Progresión radiográfica en pacientes con Espondiloartritis Axial en tratamiento con anti-TNF

Maria Llop Vilaltella
Máster universitario en Bioinformática y bioestadística UOC-UB
Análisis de datos y técnicas de clustering

Daniel Fernandez Martinez
Marc Maceira Duch

FICHA DEL TRABAJO FINAL

Título del trabajo:	*Progresión radiográfica en pacientes con Espondiloartritis Axial en tratamiento con anti-TNF*
Nombre del autor:	*Maria Llop Vilaltella*
Nombre del consultor/a:	*Daniel Fernandez Martinez*
Nombre del PRA:	*Marc Maceira Duch*
Fecha de entrega (mm/aaaa):	05/2020
Titulación:	*Máster universitario en Bioinformática y bioestadística UOC-UB*
Área del Trabajo Final:	*Análisis de datos y técnicas de clustering*
Idioma del trabajo:	*Castellano*
Palabras clave	*Espondiloartritis axial (EspAx), anti-TNF, progresión radiográfica*

Resumen del Trabajo (máximo 250 palabras): *Con la finalidad, contexto de aplicación, metodología, resultados i conclusiones del trabajo.*

Contexto: La eficacia clínica de los anti-TNF en la espondiloartritis axial (EspAax) ha sido ampliamente demostrada en ensayos clínicos aleatorizados. Algunos estudios observacionales sugieren que el tratamiento a largo plazo con anti-TNF (más de 4 años) podrían ralentizar la progresión radiográfica en EspAax. Existen datos que sugieren que el efecto del anti-TNF en la progresión radiográfica puede estar mediado por la reducción de la actividad de la enfermedad.

Objetivo: Evaluar la relación de la actividad de la enfermedad con la progresión radiográfica en pacientes con EspAax en tratamiento con anti-TNF.

Metodología: Un total de 101 paciente de la base de datos del registro español de pacientes con Espondiloartritis en terapia biológica (REGISPONSERBIO) han sido incluidos en el análisis. Para valorar la relación de la actividad de la enfermedad (medida por ASDAS) con la progresión radiográfica se ha realizado un modelo de regresión lineal múltiple. Tomando como variable independiente de progresión radiográfica, la diferencia entre el mSASSS de seguimiento con el inicial. Los predictores del modelo se ajustan según el método AIC.

Resultados: El modelo de regresión lineal múltiple resultante es capaz de explicar el 61.8% de la variabilidad observada en la progresión radiográfica (R2: 0.6891, R2-Adjusted: 0.6182). El test F muestra que es significativo (p valor de 3.046e-10). La beta de la variable diferencia de ASDAS es de 0.893 (p= 0.011) con un IC al 95% de 0.225-1.561.

Conclusiones: Por cada punto de diferencia de ASDAS se puede esperar que la progresión radiográfica aumente un promedio de 0.89. Es decir, a menor actividad clínica medida por ASDAS menor progresión radiográfica medida por el mSASSS.

Abstract (in English, 250 words or less):

Background: Clinical efficacy of TNF inhibitors (TNFi) in axial spondyloarthritis (axSpA) has been widely probed in randomized control trials. In clinical practice, some studies suggested that long-term treatment with TNFi (more than 4 years) could slow down radiographic progression in axSpA. Furthermore, it is thought that the effect of TNFi on radiographic progression may be mediated by reducing disease activity.

Objetive: To evaluate the relationship between disease activity and radiographic progression in axSpA patients treated with TNFi

Methods: 101 patients with axSpA, from the Spanish Register of Biological Therapy in Spondyloarthritides (REGISPONSERBIO) were included in the analysis. To evaluate the relationship between disease activity (measured by ASDAS) with radiographic progression we have performed a multiple linear regression. The independent variable of radiographic progression used was the difference between the follow-up mSASSS with the initial one. The model predictors are adjusted according to the AIC method.

Results: The multiple lineal regression model can explain the 61.8% of the observed variability in radiographic progression (R2: 0.6891, R2-Adjusted: 0.6182). The F test shows that it is significant (p value of 3.046e-10). The beta of the ASDAS difference variable is 0.893 (p= 0.011) with a 95% CI of 0.225-1.561.

Conclusions: For each point of difference in ASDAS, the radiographic progression can be expected to increase by an average of 0.89. Meaning that the lower the clinical activity measured by ASDAS, the lower the radiographic progression measured by the mSASSS.

Índice

Lista de figuras

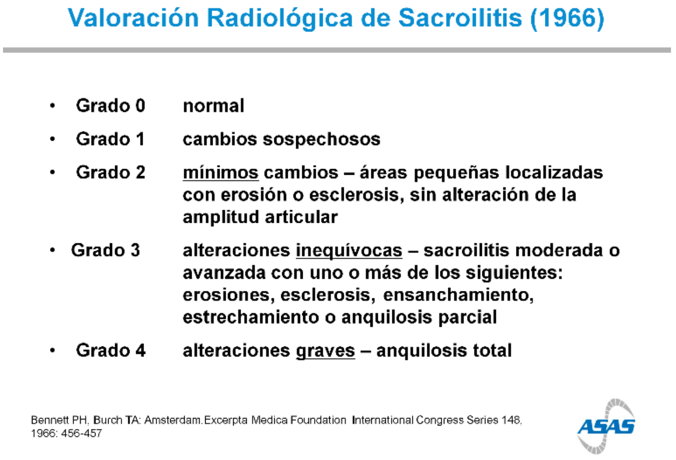
1. Introducción

1.1 Contexto y justificación del Trabajo

La Espondiloartritis axial (EspAax) es una enfermedad inflamatoria crónica con síntomas predominantemente axiales, cursa con inflamación predominantemente en las articulaciones sacroilíacas y en la columna (1). La enfermedad se asocia en un 90% de los casos con el gen HLA-B27. La prevalencia estimada entre el 0.32-1.4% (2, 3), se correlaciona con el gen HLA-B27. Los pacientes con EspAax pueden presentar otros síntomas como artritis periférica (mono o oligoartritis de los miembros inferiores), entesitis y dactilitis, así como manifestaciones extra musculoesqueléticas como la psoriasis, la uveítis y la enfermedad inflamatoria intestinal. Característicamente la enfermedad se manifiesta con dolor y rigidez, y por el desarrollo de nueva formación ósea que conlleva la anquilosis del esqueleto axial (1).

La EspAax, puede ser clasificada como EspAax-radiológica (EspAax-r) o no EspAax-no radiológica (EspAax-nr), dependiendo de la presencia o ausencia de sacroiliitis radiográfica según los criterios modificados de Nueva York, Figura 1 (4). La EspAax-nr se considera como la forma inicial o más leve de la EspAax y los pacientes no siempre desarrollan daño estructural óseo en el esqueleto axial.

Figura 1. Criterios modificados de Nueva York para la valoración de sacroiliitis radiográfica.



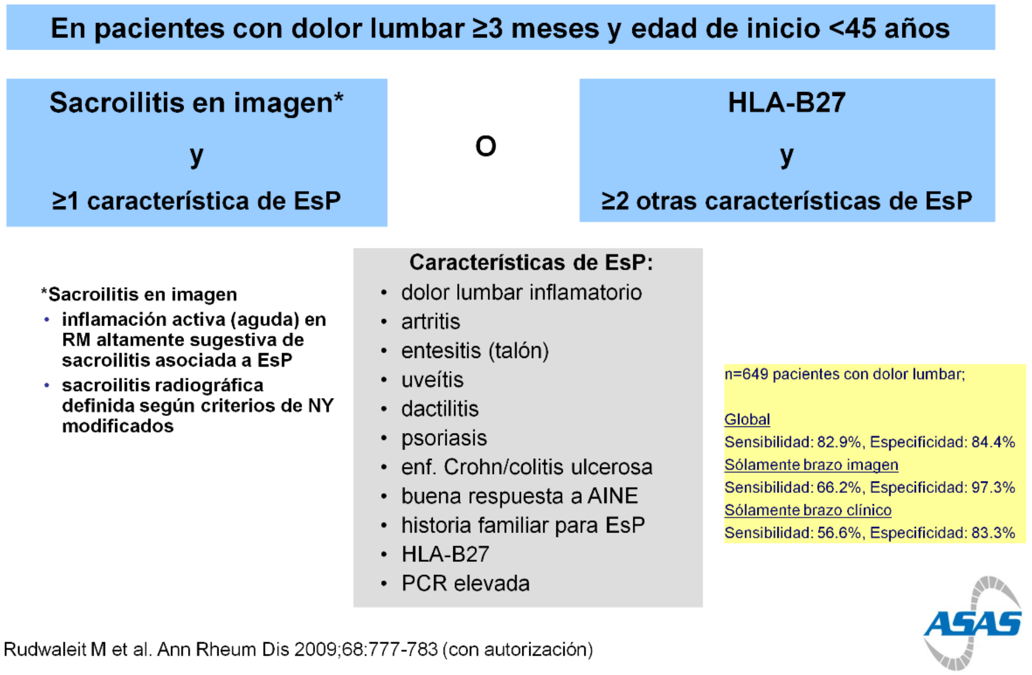
Valoración Radiológica de Sacroilitis (1966)

Grado 0	normal
Grado 1	cambios sospechosos
Grado 2	mínimos cambios – áreas pequeñas localizadas con erosión o esclerosis, sin alteración de la amplitud articular
Grado 3	alteraciones inequívocas – sacroilitis moderada o avanzada con uno o más de los siguientes: erosiones, esclerosis, ensanchamiento, estrechamiento o anquilosis parcial
Grado 4	alteraciones graves – anquilosis total

Bennett PH, Burch TA: Amsterdam.Excerpta Medica Foundation International Congress Series 148, 1966: 456-457

Los criterios de clasificación ASAS (Assesment in Spondylo Arthriits international Society) (5) se utilizan en la práctica clínica habitual como a criterios diagnósticos de EspAax (Figura 2). Su diagnóstico requiere de la presencia de dolor crónico lumbar, de más de 3 meses de duración, antes de los 45 años. También, requiere de la presencia de sacroilitis, determinada por radiografía o por resonancia magnética aparte de como mínimo una característica clínica típica de la EspAax, o bien de la presencia de HLA-B27 positivo y de dos características clínicas típicas. La sensibilidad de los criterios en los diferentes estudios difiere entre el 67 y el 87% y la especificidad entre el 62 y el 95% (6-8).

Figura 2. Criterios de clasificación ASAS para Espondiloartritis axial.



En pacientes con dolor lumbar ≥3 meses y edad de inicio <45 años

Sacroilitis en imagen*
y
≥1 característica de EsP

O

HLA-B27
y
≥2 otras características de EsP

***Sacroilitis en imagen**

- **inflamación activa (aguda) en RM altamente sugestiva de sacroilitis asociada a EsP**
- **sacroilitis radiográfica definida según criterios de NY modificados**

Características de EsP:

- dolor lumbar inflamatorio
- artritis
- entesitis (talón)
- uveítis
- dactilitis
- psoriasis
- enf. Crohn/colitis ulcerosa
- buena respuesta a AINE
- historia familiar para EsP
- HLA-B27
- PCR elevada

n=649 pacientes con dolor lumbar;

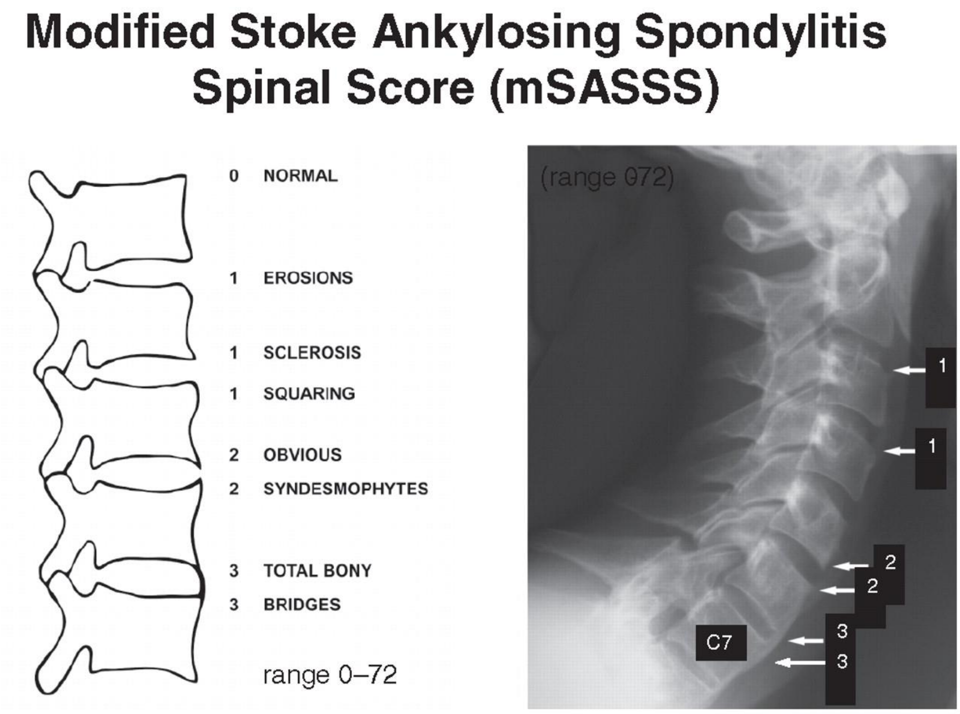
Global
Sensibilidad: 82.9%, Especificidad: 84.4%
Sólamente brazo imagen
Sensibilidad: 66.2%, Especificidad: 97.3%
Sólamente brazo clínico
Sensibilidad: 56.6%, Especificidad: 83.3%

Rudwaleit M et al. Ann Rheum Dis 2009;68:777-783 (con autorización)

Una de las mayores preocupaciones en el campo de la espondiloartritis es el desarrollo de una nueva formación ósea (sindesmofitos) en la columna vertebral debido a su contribución en la gravedad de la enfermedad. Como también es relevante en determinar si los tratamientos son eficaces para inhibir esta progresión estructural. Es por ello, que resulta de vital importancia la evaluación del daño estructural en los pacientes con EspAax. El método de imagen de elección para la evaluación de la progresión estructural son las radiografías de columna (cervical y lumbar) y el índice numérico más utilizado es el mSASSS (modified Stoke Ankylosing Spondylitis Spine

Score). El mSASSS (Figura 3) captura las esquinas vertebrales anteriores de la columna cervical y lumbar en proyección lateral, evalúa la presencia de erosiones, esclerosis, cuadratura y sindesmofitos y puentes óseos con una puntuación total de 72 (9).

Figura 3. Escala mSASSS (modified Stoke Ankylosing Spondylitis Spine Score), escala para evaluar el daño estrctural en pacientes con Espondiloartritis.



Creemers M et al. Ann Rheum Dis 2005; 64(1): 127-9

Para medir la actividad de la enfermedad, se dispone de la escala Bath Ankylosing Spondylitis Disease Activity Index (BASDAI) que fue descrito inicialmente en 1994 (10). Es un índice clínico que consiste en 6 preguntas referentes a fatiga, afectación axial, afectación articular, entesopatía y rigidez matutina (2 preguntas). Por otro lado, el Ankylosing Spondylitis Disease Activity Score (ASDAS) (11) es un índice de actividad más reciente, y es considerado actualmente como el índice de elección para medir la actividad de la enfermedad. Combina datos clínicos (cuestionarios reportados por los pacientes) y datos analíticos (la proteína C reactiva (PCR)).

Estudios previos han demostrado que la progresión estructural está asociada con la presencia de daño estructural basal (sindemosfitos), PCR elevada, fumar, diagnóstico de EspAax-radiológica y presencia de alta actividad medida por ASDAS (12). La asociación entre la presencia de daño estructural a nivel axial y la reducción de la mobilidad espinal (medida por BASMI) es bien conocida en pacientes con EspAax.

La eficacia clínica del tratamiento con inhibidores del factor de necrosis tumoral alfa (anti-TNF) en la espondiloartritis axial (EspAax) ha sido ampliamente probada en ensayos clínicos, sin embargo, su eficacia en inhibir la progresión radiográfica en este grupo de pacientes permanece incierto. En la práctica clínica habitual, algunos estudios sugieren que el tratamiento a largo plazo con anti-TNF (más de 4 años) podría ralentizar la progresión radiográfica (13). Además, se cree que el efecto del anti-TNF en la progresión radiográfica puede estar mediado por la reducción de la actividad de la enfermedad (13).

Por todo ello, resulta de vital interés conocer los factores que influyen en la progresión radiográfica en pacientes en tratamiento con anti-TNF. Y particularmente, conocer la influencia de la baja actividad en el tiempo con la progresión radiográfica en dichos pacientes. En nuestro trabajo, gracias a la cohorte longitudinal REGISPONSERBIO de pacientes con Espondiloartritis axial en tratamiento con anti-TNF, nos proponemos dar respuesta a ello.

1.2 Objetivos del Trabajo

- Evaluar la relación de la actividad de la enfermedad con la progresión radiográfica en pacientes con EspAax en tratamiento con anti-TNF.

- Evaluar el efecto de la baja actividad clínica medida por ASDAS y/o BASDAI en la progresión radiográfica en pacientes con EspAax en tratamiento con anti-TNF.

- Valorar si la baja actividad mantenida en el tiempo es más determinante que el tratamiento a largo plazo con anti-TNF en disminuir la progresión radiográfica.

1.3 Enfoque y método seguido

La evaluación de la progresión radiográfica se realizará mediante el índice numérico mSASSS. Dos lectores han evaluado las radiografías de forma independiente y con un orden cronológico conocido. Como definiciones de progresión radiográfica, disponemos:

- diferencia entre el mSASSS de seguimiento y el inical (mSASSS Progress)
- cambio en la puntuación total del mSASSS en ≥2 puntos
- desarrollo de nuevos sindesmofitos
- desarrollo de nuevos sindesmofitos o crecimiento de los sindesmofitos existentes.

Para nuestro estudio, utilizaremos la variable de progresión numérica mSASSS Progress.

Como variables de actividad se utilizarán las variables numéricas: ASDAS y BASDAI m y como escala de funcionalidad la variable numérica BASFI.

Primero se realizará un análisis descriptivo de la variable respuesta y de los factores/covariables, así como un análisis de missings y outliers. Para evaluar la relación de la actividad con la progresión radiográfica, una de las posibles estrategias a realizar es primero un análisis de regresión lineal multivariable.

1.4 Planificación del Trabajo

Para realizar el trabajo, dispongo de una base de datos clínicos obtenida en base a los datos de un registro multicéntrico español, REGISPONSERBIO, de pacientes con EspAax en tratamiento con ani-TNF, concedida por el grupo de investigación en el campo de Espondiloartritis GRESSER.

El análisis estadístico se realizará con el programo estadístico R. A continuación, expongo una planificación temporal del proyecto con el diagrama de Gantt:

Nombre	Fecha de inicio	Fecha de fin
análisis estadístico	19/10/20	14/12/20
análisis descriptivo de las variables	19/10/20	27/10/20
análisis de missings y outliers	19/10/20	27/10/20
análisis de regresión logística univariable	1/11/20	10/11/20
análisis de regresión logística multivariable	10/11/20	24/11/20
elaboración de gráficas	24/11/20	14/12/20
interpretación y redacción de resultados	14/12/20	30/12/20

Análisis de riesgo, el factor tiempo es el principal limitante para la realización del proyecto, en el primer paso de análisis descriptivo de las variables resulta crucial para entender bien las cuales son las variables respuesta y las covariables y para entender bien el modelo estadístico a realizar.

1.5 Breve sumario de productos obtenidos

Con los resultados obtenidos en base a la interpretación de los resultados de las técnicas estadísticas realizadas y con la ayuda de tablas y gráficas, esperamos poder exponer de una forma clara la relación de la actividad de la enfermedad, medida por ASDAS, con la progresión radiográfica en pacientes con EspAax en tratamiento con anti-TNF.

1.6 Breve descripción de los otros capítulos de la memoria

Este Trabajo de Final de Máster (TFM) está estructurado de la siguiente forma. El Capítulo 2 y 3, explica extensamente el material y métodos del estudio. En el Capítulo 2, se realiza una descripción de la base de datos y de las variables utilizadas para llevar a cabo el análisis, luego se realizará un análisis descriptivo de las variables incluidas. Por último, se realizará un análisis de los valores faltantes (missings). Posteriormente, en el Capítulo 3, se realiza primero un análisis de correlación de los predictores numéricos. Luego, se realizará un análisis de la variable respuesta, una validación de condiciones para la regresión lineal múltiple y luego un modelo de análisis de regresión múltiple lineal para cada variable de actividad (ASDAS y BASDAI). Por último, se realizará el ajuste de predictores del modelo de regresión lineal múltiple. En el Capítulo 4, se expondrán las conclusiones.

2. Material y métodos

2.1. Datos

Los datos con los que trabajaremos se han obtenido del registro español de pacientes con Espondiloartritis en terapia biológica (REGISPONSERBIO). Se trata de un registro observacional, longitudinal de pacientes con Espondiloartritis axial en tratamiento biológico con anti-TNF. Han participado un total de 20 centros de todo el territorio español. De los 200 pacientes incluidos en el registro, un total de 101 pacientes han sido incluidos en este estudio, en base a la disponibilidad de radiografías en el momento de inclusión del estudio y al seguimiento. La base de datos consta 66 variables, distribuidas entre variables clínicas y variables radiológicas. El registro, consta de paciente ya en tratamiento biológico previo al inicio del estudio (75%) y de pacientes que inician tratamiento biológico (25%). Al inicio del estudio, se recogieron datos demográficos, datos clínicos y radiografías. Las radiografías de seguimiento se obtuvieron en un intervalo medio de 3.45 años (±0.98 sd). La lectura radiográfica, se realizó mediante la escala mSASSS, y como progresión radiográfica se utilizaron 4 definiciones: diferencia entre el MSASSS de seguimiento con el incial, cambio en la puntuación total del mSASSS en ≥2 puntos, desarrollo de nuevos sindesmofitos y desarrollo de nuevos sindesmofitos o crecimiento de los sindesmofitos existentes. Los datos de actividad de la enfermedad (variables ASDAI, BASDAI y PCR) y de funcionalidad (variable BASFI) se han obtenido al inicio del tratamiento biológico, al inicio del estudio y luego cada 3 meses hasta un seguimiento total de 3 años.

He elegido la siguiente base de datos, porque es el único registro a nivel nacional dónde se disponen datos de actividad clínica y radiológicas de forma longitudinal con un seguimiento de 3 años. Por lo que resulta de vital interés estudiar la relación de la actividad clínica mantenida con la progresión radiográfica.

Tabla 1. Descripción de las variables al inicio del estudio, de la base de datos REGISPONSERBIO, registro español de pacientes con Espondiloartritis en terapia biológica.

Descripción de las variables	Tipo de variables	Cathegories	Median(IQR) N(%)
Edad:	Numérica		46.00 (16.00)
Sexo	Factor	Hombre	82 (81.2%)
		Mujer	19 (18.8%)
imc:	Numérica		26.02 (4.63)
imc.30: IMC > 30	Factor	No	84 (88.4%)
		Si	11 (11.6%)
tsint: Tiempo de síntomas de la enfermad al inicio del estudio	Numérica		15.00 (18.00)
hlab27:	Factor	Negativo	13 (13.1%)
		Positivo	86 (86.9%)
ea: Espondiloartritis radiográfica	Factor	Negativo	15 (14.9%)
		Positivo	86 (85.1%)
tabaco.kat: tabaco	Factor	No	70 (69.3%)
		Si	31 (30.7%)
vsg: VSG al inicio del estudio	Numérica		19.00 (29.75
basmi: BASMI al inicio del estudio	Numérica		2.87 (2.44)
uveitis: al inicio del estudio	Factor	No	79 (78.2%)
		Si	22 (21.8%)
psoriasis: PSORIASIS al inicio del estudio	Factor	No	92 (92.9%)
		Si	7 (7.1%)
enf.inf: ENF_INF al inicio del estudio	Factor	No	92 (92.9%)
		Si	7 (7.1%)
ttobio: Tipo de tto biológico al inicio del estudio	Factor	ETA	31 (30.7%)
		ADA	44 (43.6%)
		IFX	11 (10.9%)
		GOL	12 (11.9%)
		CTZ	3 (3.0%)
num.tb.prev: Número de ttos biológicos previos en el momento del inicio del estudio	Factor	No ttos previos	75 (74.3%)
		1 tto previo	20 (19.8%)
		2 ttos previos	6 (5.9%)
motivo: Motivo de cambio de tratamiento	Factor	Ineficacia	18 (72.0%)
		Efectos secundarios	7 (28.0%)
tiembio: Tiempo en tto biológico del estudio (meses)	Numérica		37.50 (70.00)
bio.inici: Tto biológico al inicio del estudio	Factor	No	25 (25.0%)
		Si	75 (75.0%)
biol.4.kat: Presencia de tto biológico durante más de 4 años al inicio del estudio	Factor	No	52 (51.5%)
		Si	49 (48.5%)

interval: Intervalo de tiempo entre RXs (entre el inicio y el seguimento)	Factor	2 años	17 (17.0%)
		3 años	38 (38.0%)
		4 años	29 (29.0%)
		5 años	15 (15.0%)
		6 años	1 (1.0%)
aine: Tto con AINEs al inicio del estudio	Factor	No	42 (42.4%)
		Si	57 (57.6%)
fame: Tto con FAME al inicio del estudio	Factor	No	81 (81.8%)
		Si	18 (18.2%)
i.basdai: BASDAI al inicio del tratamiento biológico	Numérica		5.40 (2.17)
basdai.0: BASDAI al inicio del estudio	Numérica		3.20 (3.10)
basdai.1: BASDAI a los 6 meses	Numérica		2.70 (3.00)
basdai.2: BASDAI a los 12 meses	Numérica		2.50 (2.80)
basdai.3: BASDAI a los 18 meses	Numérica		3.00 (3.60)
basdai.4: BASDAI a los 24 meses	Numérica		2.80 (3.40)
basdai.5: BASDAI a los 30 meses	Numérica		2.55 (2.92)
basdai.6: BASDAI a los 36 meses	Numérica		2.80 (3.50)
asdas.0: ASDAS al inicio del estudio	Numérica		2.06 (1.54)
asdas.1: ASDAS a los 6 meses	Numérica		1.57 (1.26)
asdas.2: ASDAS a los 12 meses	Numérica		1.83 (1.23)
asdas.3: ASDAS a los 18 meses	Numérica		1.77 (1.31)
asdas.4: ASDAS a los 24 meses	Numérica		1.67 (1.27)
asdas.5: ASDAS a los 30 meses	Numérica		1.64 (1.13)
asdas.6: ASDAS a los 36 meses	Numérica		1.68 (1.25)
pcr.0: PCR al inicio del estudio	Numérica		3.35 (8.10)
pcr.1: PCR a los 6 meses	Numérica		2.00 (3.68)
pcr.2: PCR a los 12 meses	Numérica		2.00 (4.70)
pcr.3: PCR a los 18 meses	Numérica		1.90 (4.85)
pcr.4: PCR a los 24 meses	Numérica		2.05 (4.68)
pcr.5: PCR a los 30 meses	Numérica		1.40 (5.38)
pcr.6: PCR a los 36 meses	Numérica		2.00 (5.35)
egp: Dolor global descrito por el paciente en el inicio del estudio	Numérica		3.00 (4.00)
dan: Dolor axial nocturno	Numérica		3.00 (5.00)
egm: Dolor global del paciente en la opinión del médico	Numérica		3.00 (3.50)
basfi.0: BASFI al inicio del estudio	Numérica		3.85 (4.45)
basfi.1: BASFI a los 6 meses	Numérica		2.70 (3.35)
basfi.2: BASFI a los 12 meses	Numérica		2.30 (3.70)
basfi.3: BASFI a los 18 meses	Numérica		2.80 (3.50)
basfi.4: BASFI a los 24 meses	Numérica		3.50 (3.70)
basfi.5: BASFI a los 30 meses	Numérica		3.20 (3.60)
basfi.6: BASFI a los 36 meses	Numérica		3.10 (4.00)
msasss.mean.bl: media de la puntuación Msasss al inicio	Numérica		5.00 (23.00)
msasss.mean.fl: media de la puntuación Msasss en el seguimento	Numérica		8.00 (30.00)
msasss.progress: Diferencia entre el mSASSS del inicio con el del seguimento	Numérica		0.00 (3.00)
new.syn.msasss: Nuevos sindesmofitos	Factor	No	81 (80.2%)
		Nuevos sindesmofitos	20 (19.8%)

msasss.progress.kat: Msasss increment of 2 points or more during follow-up	Factor	No	71 (70.3%)
		Incremento de dos o más puntos del mSASSS	30 (29.7%)
new.prog.syn: Nuevos o progresión de sindesmofitos existentes	Factor	No	79 (78.2%)
		Nuevos o progresión de sindesmofitos	22 (21.8%)
mind.2.synd.fl: presencia de sindesmofitos en el seguimiento	Factor	No	46 (45.5%)
		Presencia de sindesmofitos	55 (54.5%)
mind.2.synd.bl: presencia de sindesmofitos al inicio	Factor	No	50 (49.5%)
		Presencia de sindesmofitos	51 (50.5%)
pcr.iniciob: PCR al inicio del tratamiento biológico	Numérica		10.50 (22.40)
i.asdas: ASDAS al inicio del tratamient biológico	Numérica		3.40 (1.22)
hvgp: valoración global de la enfermedad al inicio	Numérica		6.00 (2.00)

2.2. Preparación de los datos para el análisis

La base de datos original consta de 66 variables, a continuación, preparamos la base datos para el análisis. Definimos como variable respuesta la variable de progresión radiográfica, numérica Msasss Progress, que se define como la diferencia de la variable del mSASSS al inicio con la de seguimiento (Msasss_BL y Msasss_FL). Eliminamos la primera variable (el número de paciente), y las variables (Msasss_BL y Msasss_FL) puesto que forman parte de la variable y (respuesta).

Además, la base de datos original consta de diferentes mediciones de las variables BASDAI, ASDAS, PCR y BASFI medidas cada 6 meses en un seguimiento total de 3 años. Para poder realizar el análisis de regresión lineal, trataremos las covariables X de las diferentes mediciones a lo largo del tiempo del mismo modo que lo hemos hecho para la variable Y, es decir, como un cálculo de diferencia entre la variable inicial con la última medición de seguimiento. Por lo tanto, en la base de datos resultante, transformamos las variables de seguimiento en una única variable. Las variables resultantes son: BASDAIDif, ASDASDif, PCRDif y BASFIDif.

2.3. Análisis descriptivo de las variables

Tras los ajustes realizados, obtenemos una base de datos con 39 variables y 101 observaciones (base_rx2). Una descripción gráfica de algunas de las variables de la base datos está representado en las Figuras 4 y 5.

Para el posterior análisis de regresión lineal, creamos también una base datos ajustada con los valores mencionados anteriormente, pero únicamente con variables numéricas (base_rx.num2). Los descriptivos de las variables se encuentran representados en la Tabla 2.

Figura 4. Boxplot y gráfico de densidad de las variables numéricas EDAD e IMC.

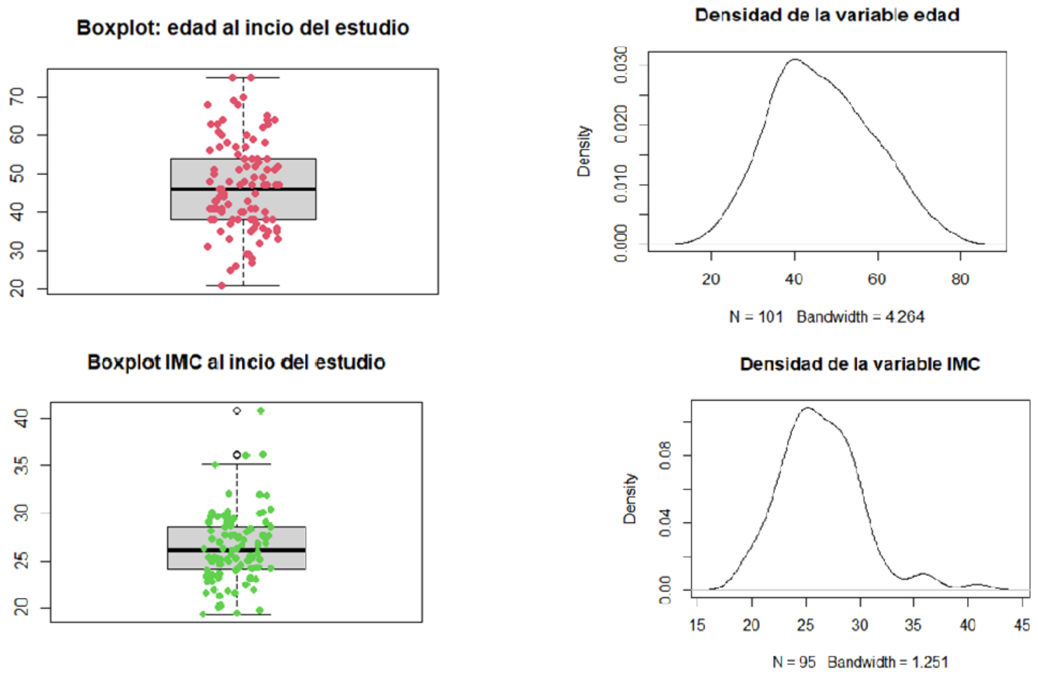


Figura 5. Histogramas de las variables tipo factor, HLA-B27, SEXO, IMC>30 y tipo de tratamiento biológico recibido.

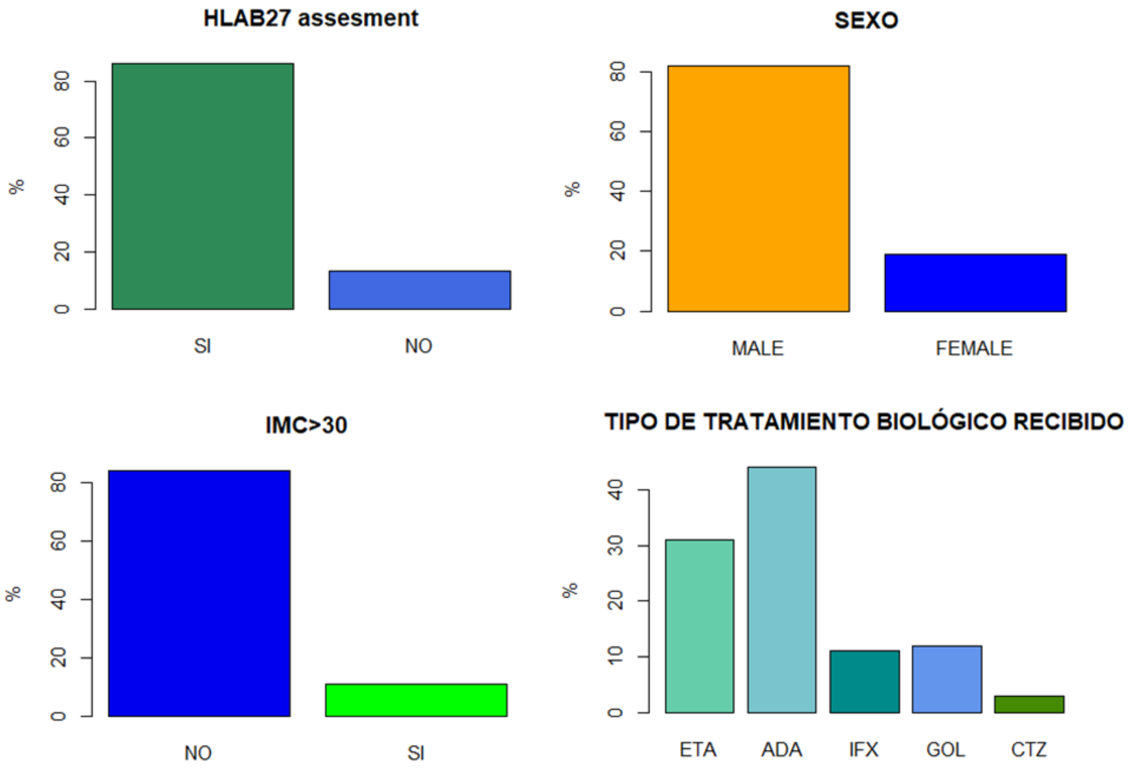


Tabla 2. Análisis descriptivo de las variables numéricas.

Variable	mean	Median	sd	min	max	var
ASDAS al inicio del tratamiento	3.4	3.5	0.8	1.5	5.3	0.7
BASDAI al inicio del tratamiento	5.3	5.4	1.8	0.7	8.8	3.3
BASMI	3.1	2.7	1.7	0.5	7.3	3
Diferencia entre ASDAS al inicio y final	-0.5	-0.3	1.2	-3.5	2	1.5
Diferencia entre el BASDAI al inicio final	-0.7	-0.1	2.1	-7	5.2	4.5
Diferencia entre el BASFI al inicio y final	-0.7	-0.2	2.6	-8.9	6.2	6.7
Diferencia entre el mSASSS al inicio y final	2	0	3.8	-2.5	21.5	14.1
Diferencia entre PCR al inicio y final	-3.6	-0.2	13.2	-88.4	28	173.5

Dolor global del paciente	4	3	2.8	0	10	7.7
Dolor global en la opinión del médico	3.4	3	2.4	0	10	5.7
Edad	46.7	46	11.9	21	75	142.2
IMC	26.4	26	3.7	19.4	40.8	13.9
Intervalo entre radiografías	3.5	3	1	2	6	1
PCR al inicio del tratamiento	18.5	11	19.2	0	98	370
Tiempo con tratamiento	45.1	42	40.1	0	132	1611.7
Tiempo síntomas	17.9	15	12.8	0	52	163.9
Valoración global del paciente al inicio del tratamiento	5.9	6	2	1	10	3.9
VSG	26.1	18	22.4	0.5	115	502.7

2.4. Análisis de missings

De la base datos ajustada hay 147 missings y en la base de datos de variables únicamente numéricas hay 128. Con el análisis de missings, vemos que los missings se concentran principalmente en 5 variables numéricas (BASMI, BASFIDif, BASDAIDif, ASDASDif, PCRDif).

Debido a que los missings se centran en las variables numéricas, sobre las variables numéricas de la base de datos original aplicamos un método de imputación de missings (Multivariate Imputation by Chained Equations). A este nuevo data.frame creado, lo unimos con las variables tipo factor, y creamos una nueva base de datos ((c_base_rx2).

3. Modelo de regresión lineal múltplie

3.1. Análisis de correlación de los predictores numéricos

Para controlar la multicolinealidad del modelo, estudiamos la correlación de los predictores numéricos. Para ellos creamos una matriz de correlaciones, las variables que están más correlacionadas (coeficiente de correlación >0.5), están representadas en la Tabla 3. Para construir el modelo de regresión, no incluiremos las variables numéricas que tienen una correlación superior a 0.7 para evitar la multicolinealidad.

Según apreciamos en la tabla, las variables EGM y EGP tienen una alta correlación 0.77. Hecho que es lógico, debido a que ambas variables expresan el grado del dolor del paciente. Por un lado, EGM, representa el grado del dolor del paciente en la opinión del médico y EGP, el grado de dolor reportado por el paciente. Por lo que, para construir el modelo, nos quedamos con la variable EGM, que en general refleja de forma más real el grado de dolor del paciente.

Otras variables que obtienen una correlación superior a 0,7, son las dos variables de actividad BASDAIDif y ASDASDif, correlación 0.728, y la variable de actividad BASDAIDif con la funcionalidad BASFIDif, correlación 0.747. Como la variable principal de interés para medir la actividad es el ASDAS, elegimos primero la variable ASDASDif para construir el modelo y la variable de funcionalidad, BASFIDif.

Tabla 3. Coeficientes de correlación superiores a 0.5 de las variables numéricas de la base de datos REGISPONSERBIO.

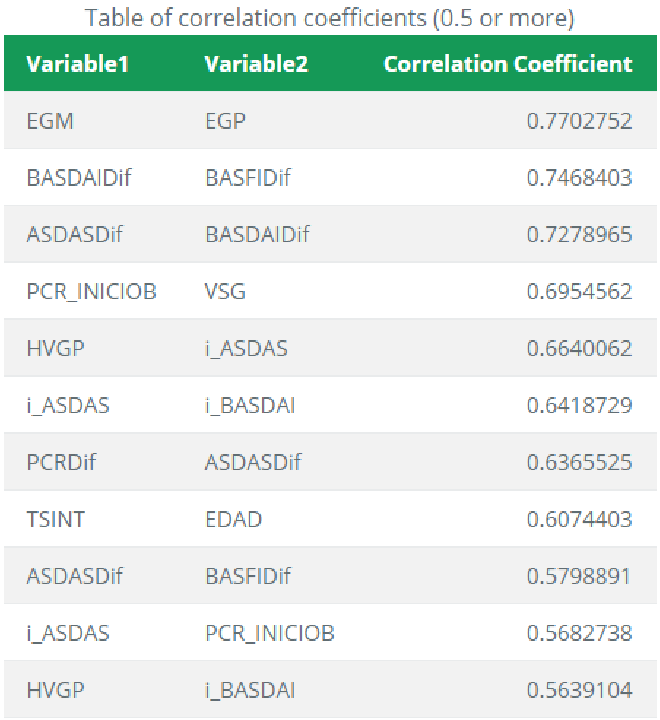
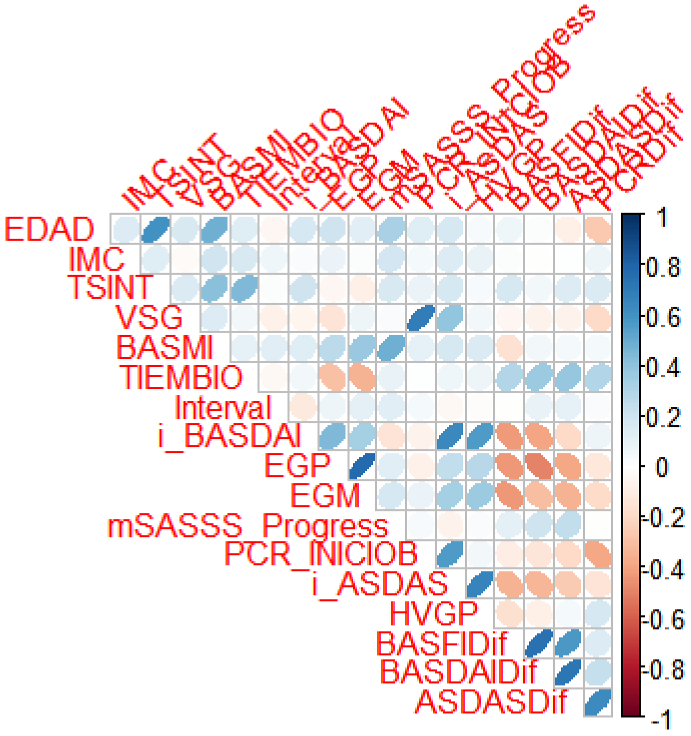


Table of correlation coefficients (0.5 or more)

Variable1	Variable2	Correlation Coefficient
EGM	EGP	0.7702752
BASDAIDif	BASFIDif	0.7468403
ASDASDif	BASDAIDif	0.7278965
PCR_INICIOB	VSG	0.6954562
HVGP	i_ASDAS	0.6640062
i_ASDAS	i_BASDAI	0.6418729
PCRDif	ASDASDif	0.6365525
TSINT	EDAD	0.6074403
ASDASDif	BASFIDif	0.5798891
i_ASDAS	PCR_INICIOB	0.5682738
HVGP	i_BASDAI	0.5639104

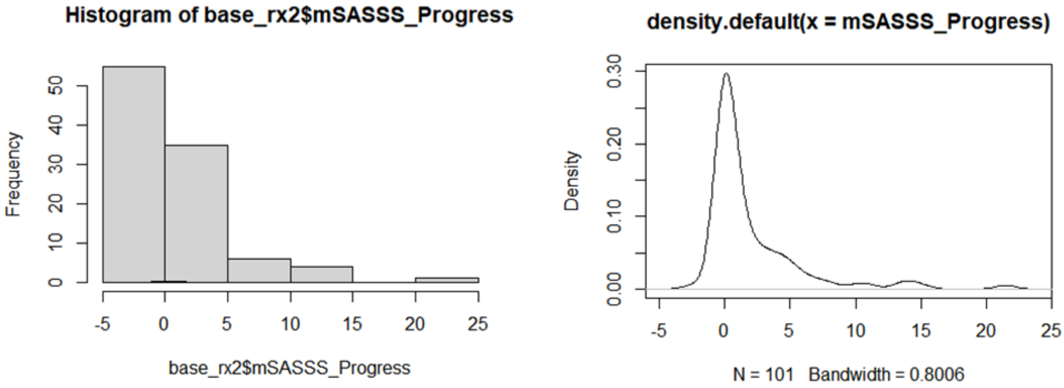
Figura 6. Correlation Plot de las variables numéricas de la base de datos REGISPONSERBIO.



3.2. Análisis de la variable respuesta

A continuación, estudiamos la variable respuesta numérica (mSASSS Progress) para ver si sigue una distribución normal. En la representación gráfica de la variable respuesta, se aprecia que la densidad es claramente asimétrica.

Figura 7. Histograma y diagrama de densidad de la variable respuesta, mSASSS Progress.

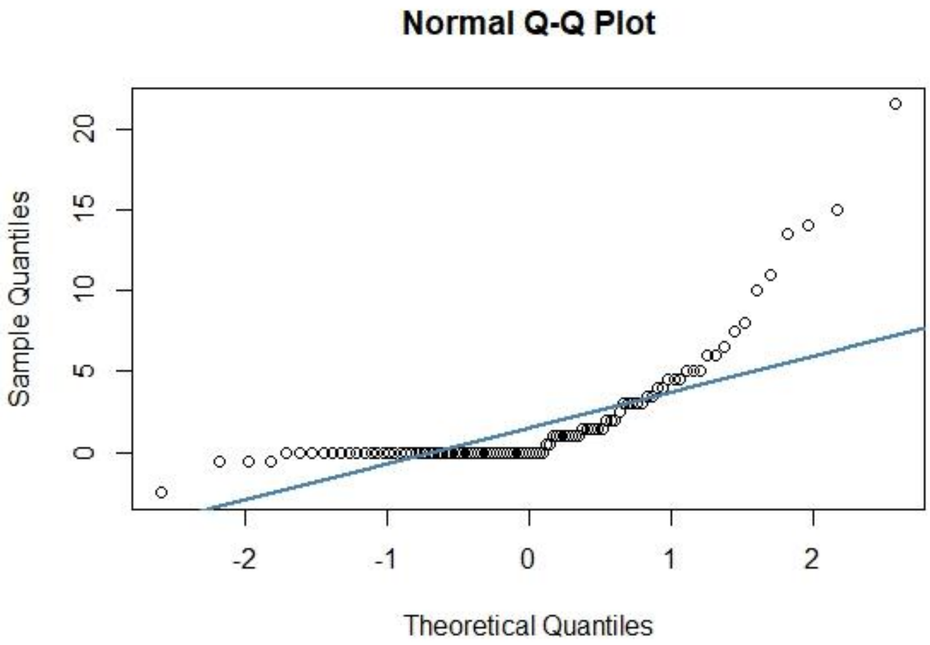


En el análisis descriptivo de la variable respuesta, la media y mediana no coincide (1.98 y 0, respectivamente), y que la kurtosis es superior a 3.

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	kurtosis	skew
-2.50	0.00	0.00	1.98	3.00	21.50	8.37	2.69

Con la gráfica qqplot, vemos que la variable respuesta no sigue una distribución normal (Figura 8). Hallazgos, que se confirman tanto en el Shapiro-Wilk's test como en el Kolmogorov-Smirnov (K-S) normality test. Pues al obtener un resultado significativo (p 2.092e-14), debemos rechazar la hipótesis nula de igualdad. Como la variable respuesta no es normal, podemos intentar una transformación para mejorar esa situación, pero antes vamos a ver si los residuos siguen la suposición de normalidad, porque si es así no es necesario transformar la variable respuesta.

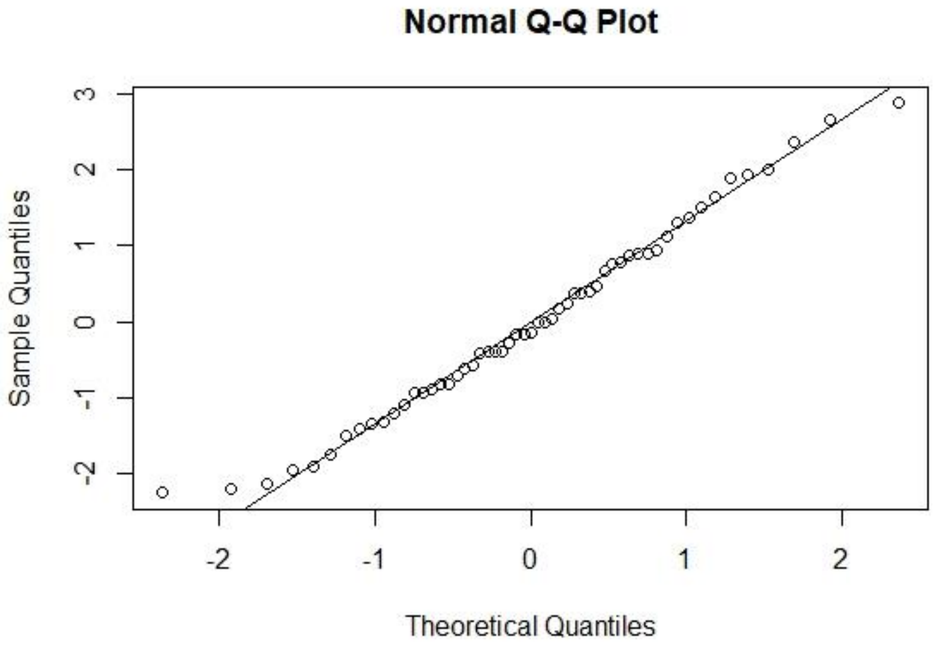
Figura 8. Q-Q Plot de la variable respuesta mSASSS Progress.



3.3. Validación de condiciones para la regresión múltiple lineal

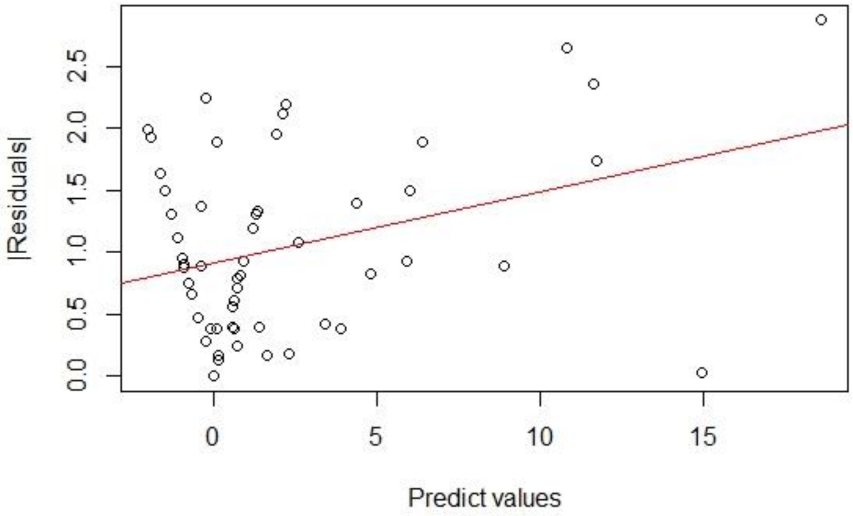
Primero realizamos un análisis de residuos para evaluar si cumplen la hipótesis de normalidad. Realizamos un gráfico Q-Q plot, donde se puede observar que los puntos se ajustan a la diagonal, lo que sugiere que los datos se ajustan a una distribución normal (Figura 9). Realizamos un test de normalidad (Shapiro-Wilks) para comprobar lo que hemos visto gráficamente y con un p-valor 0.58 permite rechazar la hipótesis nula, que nos dice que los residuos efectivamente siguen una distribución normal. Por lo tanto, al haber normalidad de los residuos, no hace falta realizar una transformación para la variable respuesta, mSASSS Progress.

Figura 9. Q-Q Plot de los residuos



Luego estudiamos la varianza de los residuos, que debe ser constante en todo el rango de observaciones. Para comprobarlo se representan los residuos gráficamente y se confirma los hallazgos con el Breusch-Pagan test. Con el test, obtenemos un resultado no significativo (p= 0.3958). Por lo que no hay evidencias de falta de homocedasticidad.

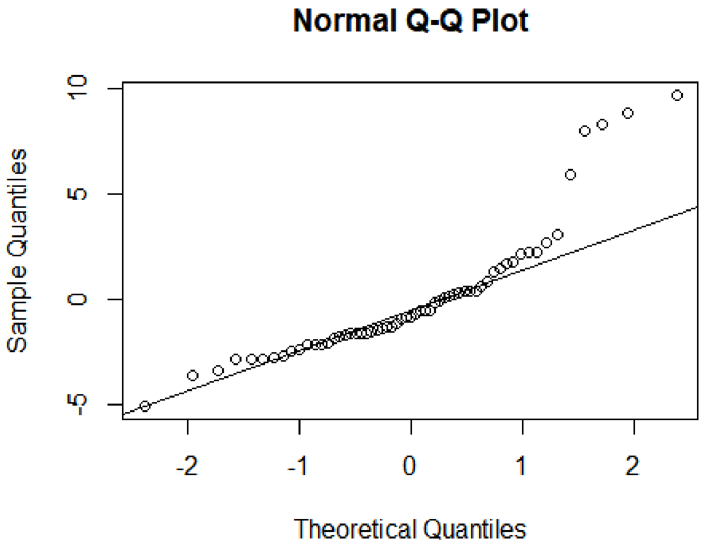
Figura 10. Representación gráfica de los residuos frente a los valores ajustados por el modelo.



Para estudiar la autocorrelación, realizamos el test D-W Statistic y al obtener también un resultado no significativo (p=0.832), no hay tampoco evidencia de autocorrelación.

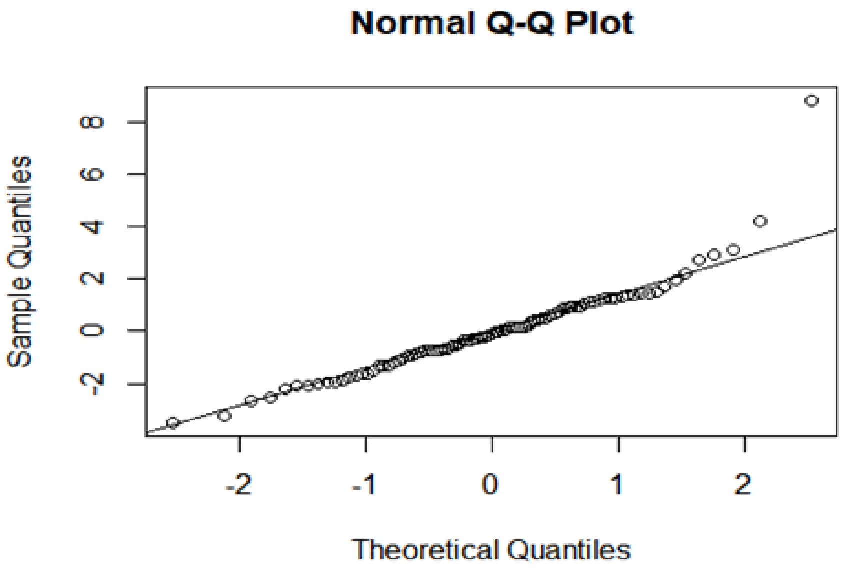
Por otro lado, cuando estudiamos las condiciones para el modelo con la base de datos únicamente numérica (base_rx.num2). En el análisis de residuos vemos que el Q-Q Plot los residuos se alejan de la normalidad, hallazgos que se confirman con el Saphiro test (p= 1.724e-06), por lo que los residuos no siguen la normalidad.

Figura 11. Q-Q Plot de los residuos de las variables numéricas.



Para la base de datos, con variables numéricas corregidas con imputación de missings (c_base_rx2). En el análisis de residuos vemos también que el Q-Q Plot los residuos se alejan de la normalidad, hallazgos que se confirman con el Saphiro test (p= 5.607e-06), por lo que los residuos no siguen la normalidad.

Figura 12. Q-Q Plot de los residuos con los missings corregidos.



3.4. Modelo de regresión múltiple lineal

Como hemos visto en el modelo, generado por la base de datos base_rx2, cumple la normalidad de los residuos, la homocedasticidad y no hay autocorrelación ni multicolinealidad. Para gestionar los missings, utilizamos la función na.action = na.omit, en el modelo resultante, 46 observaciones son eliminadas debido a los missings, quedando un total de 97 observaciones.

Con el modelo realizado, únicamente las variables EGM y la variable categórica mSASSS_Progress_Kat alcanzan la significación estadística.

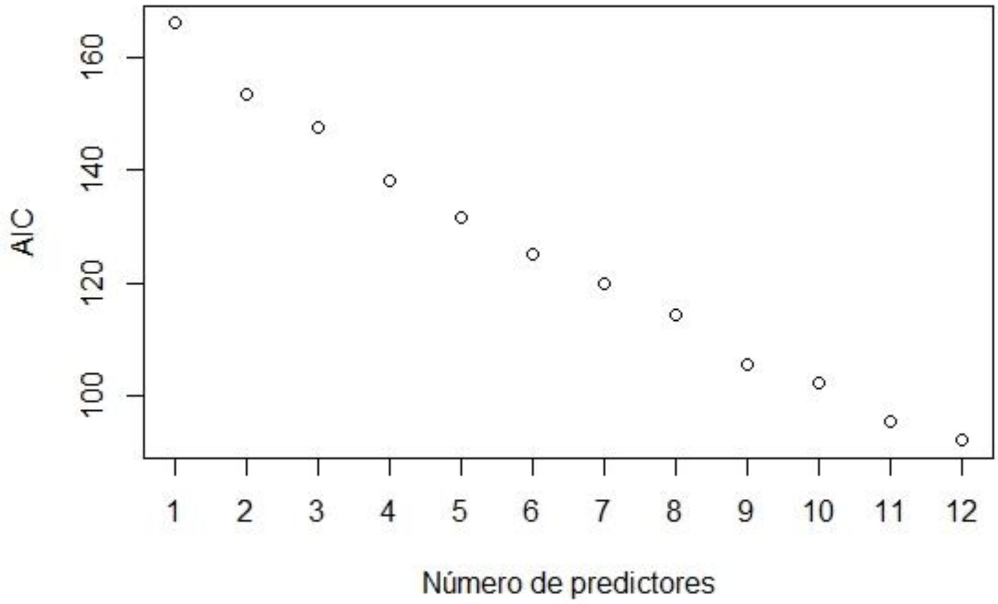
En conclusión, el modelo múltiple es capaz de explicar el 62.4% de la variabilidad observada en la progresión radiográfica (R2: 0.9197, R2-Adjusted: 0.6664). El test F muestra que es significativo (p= 0.007572). Se satisfacen todas las condiciones para este tipo de regresión múltiple.

3.5. Ajuste de predictores del modelo de regresión múltiple lineal

Por regla general, el número de observaciones debe ser como mínimo entre 10 y 20 veces el número de predictores del modelo. Como tenemos 97 observaciones, el número de predictores no debería ser mayor a 10. Por lo que debemos eliminar predictores, que no influyan en el modelo. Para ello, vamos a realizar a una regresión con variables seleccionadas por AIC.

Como apreciamos en la gráfica, el mínimo AIC se alcanza con 12 predictores, aunque con 10 también tenemos un buen resultado. Por lo que los predictores finales para el modelo son: EDAD, SEXO, HLAB27, EA, TTOBIO, EGM, New_Syn_mSASSS, mSASSS_Progress_Kat, New_Prog_Syn_Msasss y ASDASDif.

Figura 13. Selección de predictores por AIC.



Con este modelo las variables, presencia de nuevos sindesmofitos (New_Syn_mSASSS), la progresión radiográfica de > 2 puntos del mSASSS (mSASSS_Progress_Kat), y la diferencia entre el ASDAS del inicio con la variable final de seguimiento (ASDASDif), son las únicas variables significativas. La beta de la variable la progresión radiográfica de > 2 puntos del mSASSS es de 4.820 (p= 0.0003) con un IC al 95% de 2.318-7.321. Y, la beta de la variable presencia de nuevos sindesmofitos es de 5.291 (p= 0.012) con un IC al 95% de 1.278-9.304. Por último, la beta de la variable diferencia de ASDAS es de 0.893 (p= 0.011) con un IC al 95% de 0.225-1.561

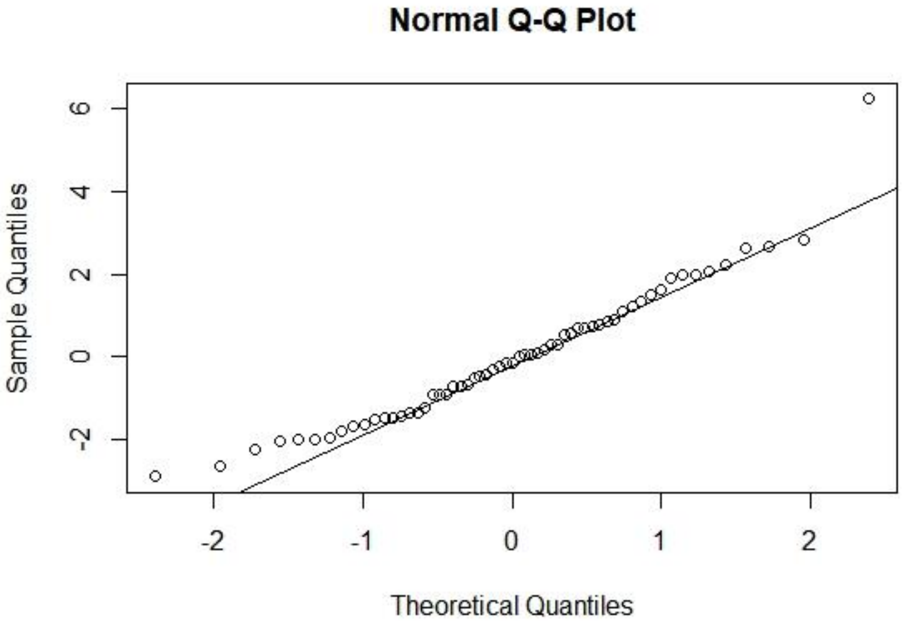
En conclusión, el modelo de regresión lineal múltiple resultante es capaz de explicar el 61.8% de la variabilidad observada en la progresión radiográfica (R2: 0.6891, R2-Adjusted: 0.6182). El test F muestra que es significativo (p valor de 3.046e-10).

3.6. Modelo de regresión lineal múltiple con variable actividad BASDAI

A continuación, repetimos el mismo proceso anterior, pero tomando la variable BASDAIDif en vez de la variable ASDASDif como variable de actividad. Como hemos visto anteriormente ambas variables son utilizadas para medir la actividad clínica de la enfermedad. Debido a que presentan una alta correlación, para evitar la multicolinealidad del modelo, realizamos un modelo de regresión lineal múltiple para cada una de estas variables.

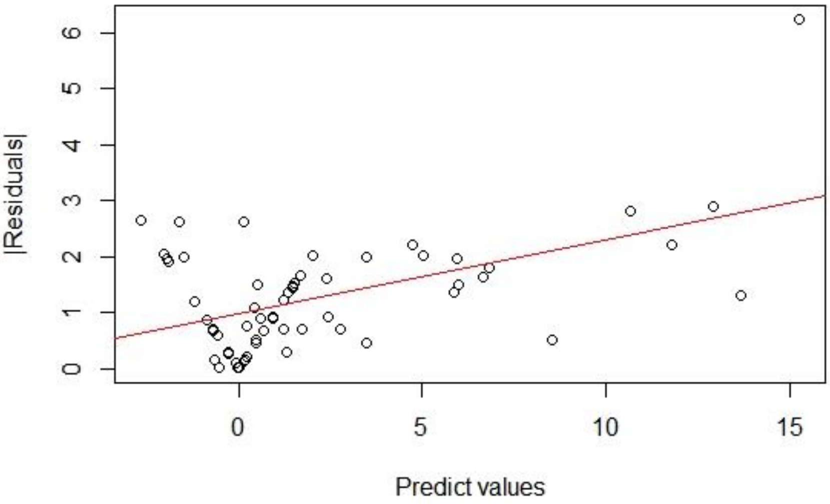
Como la variable respuesta es la misma (mSASSS_Progress) y ya hemos visto anteriormente que no sigue una distribución normal realizamos un análisis de residuos para ver si los residuos cumplen la hipótesis de normalidad. Realizamos primero un gráfico Q-Q plot, donde se puede observar que los puntos no se ajustan del todo a la diagonal, lo que sugiere que los datos no se ajustan a una distribución normal (Figura 14). Realizamos un test de normalidad (Shapiro-Wilks) para comprobar lo que hemos visto gráficamente y con un p-valor 0.0165 no se puede rechazar la hipótesis nula, que nos dice que los residuos efectivamente no siguen una distribución normal. Por lo tanto, al no haber normalidad de los residuos, se debería realizar una transformación para la variable respuesta, mSASSS Progress.

Figura 14. Q-Q plot de los residuos con la variable BASDAI de actividad.



Estudiamos también la varianza de los residuos, que debe ser constante en todo el rango de observaciones. Para comprobarlo se representan los residuos gráficamente (Figura 15) y se confirma los hallazgos con el Breusch-Pagan test. Con el test, obtenemos un resultado no significativo (p= 0.3916). Por lo que no hay evidencias de falta de homocedasticidad.

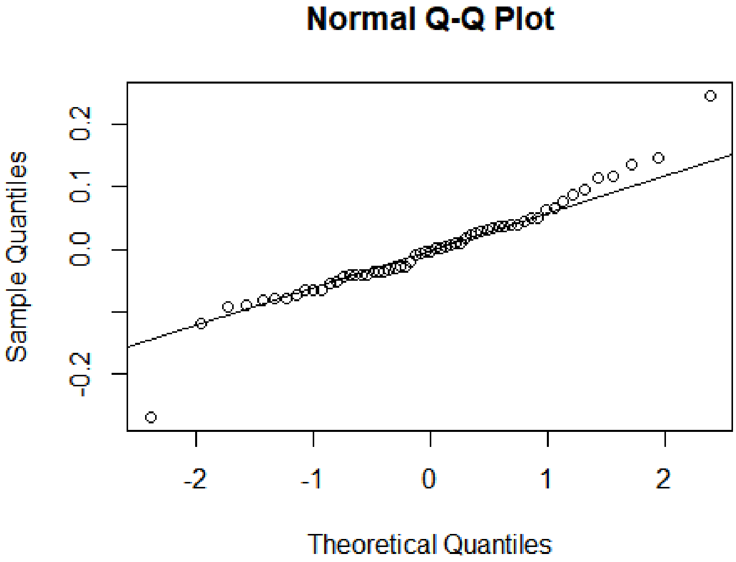
Figura 15. Representación gráfica de los residuos frente a los valores ajustados por el modelo.



Al tener valores negativos y 0 en la variable respuesta, se convierten en NaN cuando aplicamos una transformación logarítmica. Por lo tanto, debemos transformar los valores negativos y 0. Para ello, una técnica común para el manejo de valores negativos es agregar un valor constante a los datos antes de aplicar la transformación logarítmica. Como, por ejemplo: LY = log10(Y + 1 - min(Y)).

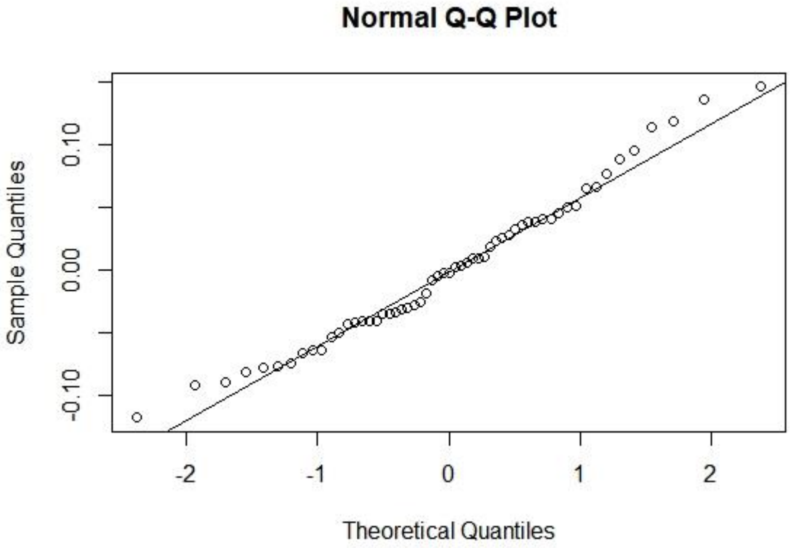
Con la variable respuesta transformada según lo indicado, realizamos ahora un análisis de residuos. Primero realizamos un gráfico Q-Q plot, por la disposición de los puntos impresiona que sigue sin satisfacerse la condición de normalidad posiblemente debido a dos datos atípicos (Figura 16). Realizamos un test de normalidad (Shapiro-Wilks) para comprobar lo que hemos visto gráficamente y con un p-valor 0.01936 no permite rechazar la hipótesis nula, lo que nos dice efectivamente que los residuos no siguen una distribución normal.

Figura 16. Q-plot de los residuos, con la variable respuesta transformada.



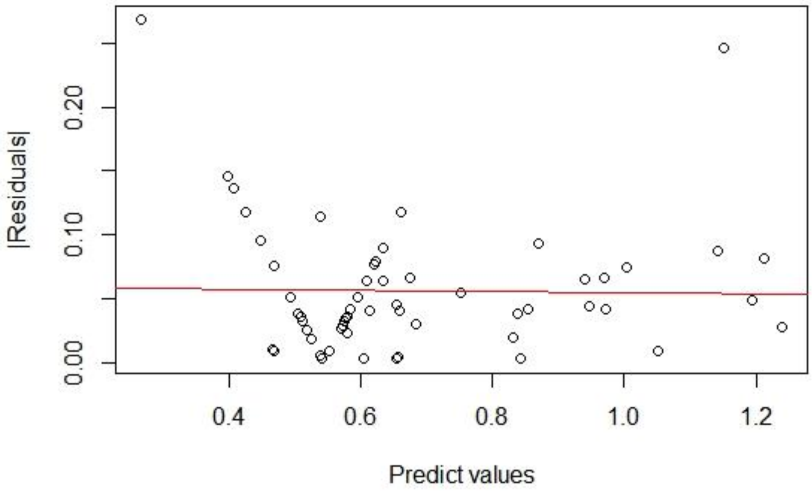
Con la función, which.max(abc1$residuals) y which.min(abc1$residuals), vemos principalmente que hay dos datos atípicos en los residuos, uno por la parte superior de la gráfica (max) y otro en la parte inferior (min), el 24 y el 41. Realizamos de nuevo el gráfico q-q plot (figura 17) y el saphiro test (p= 0.3819) sin los dos valores extremos, y se confirma que los residuos sí se distribuyen de forma normal a excepción de dos datos extremos. Es necesario estudiar en detalle la influencia de esta observación para determinar si el modelo es más preciso sin ella.

Figura 17. Q-Q plot de los residus sin los dos datos extremos.



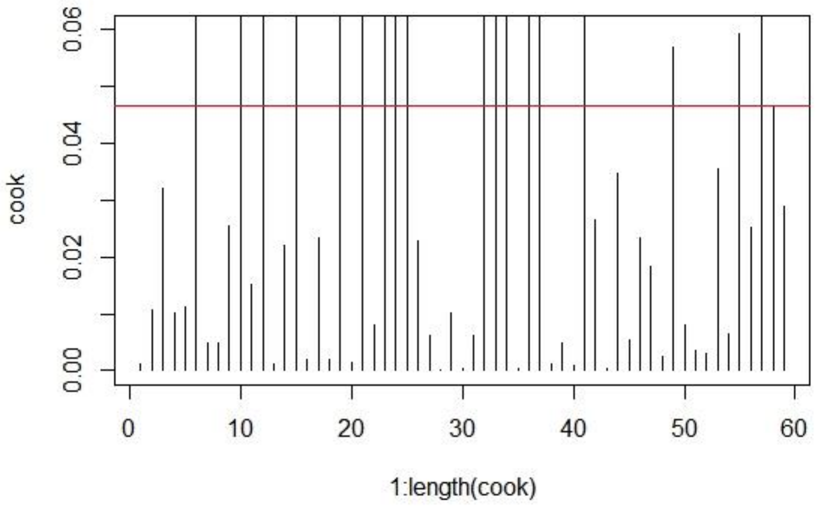
Estudiamos también la varianza de los residuos, que debe ser constante en todo el rango de observaciones. Para comprobarlo se representan los residuos gráficamente (Figura 18) y se confirma los hallazgos con el Breusch-Pagan test. Con el test, obtenemos un resultado no significativo (p= 0.2969). Por lo que no hay evidencias de falta de homocedasticidad. Ni tampoco de autocorrelación, p= 0.688, con el test D-W Statistic.

Figura 18. Representación gráfica de los residuos frente a los valores ajustados por el modelo, con la variable respuesta ajustada.



A continuación, estudiamos las observaciones influyentes. Calculamos la distancia de Cook como medida de la influencia de los puntos y la representamos contra los cuartiles de una distribución seminormal, figura 19, donde se aprecian varios valores influyentes (valores que sobrepasan al línia horitzontal).

Figura 19. Gráfico de la distancia de Cook para detectar observaciones que influyen fuertemente en los valores ajustados del modelo.



Buscamos las observaciones con un mayor residuo studentizado externamente (*jackknife residual*).

```
42       66       7        51       61       36
4.813376 4.638805 2.399791 1.816236 1.745187 1.496918
```

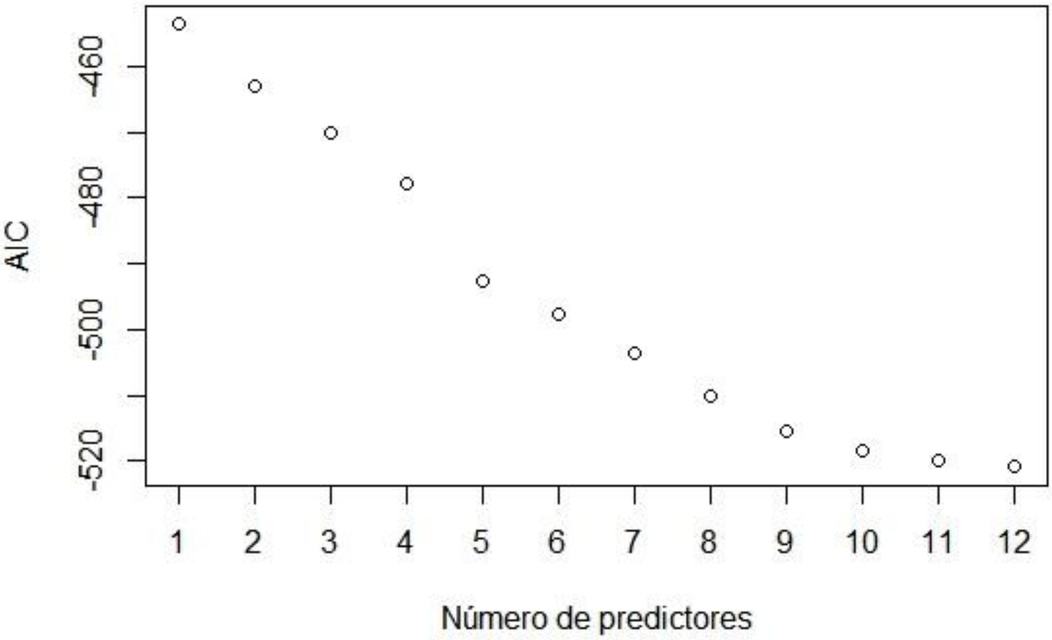
En cuanto al leverage:

```
1         15        63        57        51        14
0.9211843 0.9211843 0.9211843 0.8551536 0.8541275 0.8480441
```

En resumen, el punto 51 es un valor influyente con alto leverage y outlier. En cambio, el punto 1 es de alta influencia, tiene un alto leverage (está lejos del centro de los datos), pero no es outlier.

Por último, realizamos el modelo de regresión con variables seleccionadas por AIC. Como apreciamos en la gráfica (figura 20), el mínimo AIC se alcanza con 12 predictores, aunque con 10 también tenemos un buen resultado. Por lo que los predictores finales para el modelo son: EDAD, EA, TTOBIO, NUM_TB_PREV, MOTIVO, BIO_INICI, Mind_2_Synd_FL, mSASSS_Progress_Kat y BASDAIDif.

Figura 20. Selección de predictores por AIC.



Con este modelo las variables, EDAD, Espondilitis AnquilosantE, Tratamiento biológico con Adalimumab y certolizumab (TTBIOADA y TTOBIOCTZ), presencia de tratamiento biológico al inicio, la progresión radiográfica de > 2 puntos del mSASSS (mSASSS_Progress_Kat), y la diferencia entre el BASDAI del inicio con la variable final de seguimiento (BASDAIDif), son variables significativas. La beta de la variable diferencia de BASDAI es de 0.000122 (p= 0.011) con un IC al 95% de 0.0145-0.0414. Recordemos que la variable respuesta esta transformada, por lo que tenemos que corregir el coeficiente de la siguiente forma: (10exp(0.000122)-1)*100= 0.028. Por lo que por cada incremento en la diferencia de la progresión radiográfica, la diferencia del BASDAI aumenta en un 0.028%.

En conclusión, el modelo de regresión lineal múltiple resultante es capaz de explicar el 76.8% de la variabilidad observada en la progresión radiográfica (R2: 0.808, R2-Adjusted: 0.7679). El test F muestra que es significativo (p valor de < 2.2e-16).

4. Conclusiones

En el presente trabajo evaluamos la asociación de la actividad de la enfermedad con la progresión radiográfica en pacientes con Espondiloartritis axial tratados con anti-TNF de un registro Español (REGISPONSERBIO). Para poder evaluar dicha asociación, se ha realizado un modelo de regresión lineal múltiple, tomando como variable respuesta la progresión radiográfica. Se ha utilizado como definición de progresión radiográfica, la variable numérica, diferencia entre el mSASSS de seguimiento con el inicial. Para medir la actividad de la enfermedad, se ha utilizado el índice de elección para medir la actividad clínica de la enfermedad, el ASDAS. Disponemos de medidas de ASDAS y BASDAI (otra forma de medir la actividad de la enfermedad) al inicio del estudio y cada 6 meses hasta un seguimiento total de 3 años. Para incluir las variables de actividad en el modelo, se ha utilizado la diferencia entre el ASDAS y BASDAI del seguimiento (3er año) con la del inicio.

La duración del tratamiento biológico es un factor importante para evaluar su efecto en la progresión radiográfica en pacientes con EspAax. Según lo reportado en estudios previos, existe una asociación entre la duración del tratamiento con anti-TNF y el riesgo de progresión, sin que se observe ningún efecto del anti-TNF en un intervalo de seguimiento de 2 años. Además, se cree que el posible efecto a largo plazo del anti-TNF en la nueva formación ósea se debe a una supresión efectiva de la inflamación, ya que nuevas pruebas apoyan que los cambios inflamatorios van seguidos de la sustitución de la médula ósea subcondral por la reparación del tejido que luego estimula los osteoblastos, lo que da lugar a la nueva formación ósea.

Con los resultados obtenidos, podemos concluir que por cada punto de diferencia de ASDAS se puede esperar que la progresión radiográfica aumente un promedio de 0.89. Es decir, a menor actividad clínica medida por ASDAS menor progresión radiográfica medida por el mSASSS. Por otro lado, apreciamos sin embargo que la duración del tratamiento biológico previo (tiembio), no resulta significativa en el modelo, lo que hace suponer que es más importante el control de la enfermedad (disminución del ASDAS) que el tiempo previo en tratamiento biológico.

Con los resultados obtenidos, apreciamos también que el índice de actividad ASDAS presenta una correlación muy alta con el BASDAI (coeficiente de correlación 0.727). Cuando evaluamos el modelo, utilizando la variable BASDAI en vez del ASDAS, como variable de actividad de la enfermedad, apreciamos que hay significación estadística y por lo tanto asociación con la progresión radiográfica, pero con menor beta y por tanto menor magnitud de impacto. Lo que confirma que el ASDAS es el mejor método para medir la actividad de la enfermedad y para medir los efectos de la progresión radiográfica en pacientes tratados con anti-TNF.

En conclusión, con los resultados descritos podemos confirmar nuestra hipótesis. Los pacientes con EspAax tratados con anti-TNF que presenten un descenso de la actividad clínica, medida por ADSDAS principalmente y BASDAI, presentan una menor progresión radiográfica.

5. Glosario

EspAax: Espondiloartritis axial

EA: Espondilitis Anquilosante

ASDAS: Ankylosing Spondylitis Disease Activity Score

BASDAI: Bath Ankylosing Spondylitis Disease Activity Index

BASFI: Bath Ankylosing Spondylitis Functional Index

PCR: proteína C reactiva

VGP: valoración del dolor por el paciente

EGM: EVA (escala de dolor) Global en la opinión del Médico

EGP: EVA (escala de dolor Global en la opinión del Paciente

mSASSS: modified Stoke Ankylosing Spondylitis Spine Score

Anti-TNF: inhibidores del factor de necrosis tumoral alfa

6. Bibliografía

1. Sieper J, Poddubnyy D. Axial spondyloarthritis. Lancet. 2017;390(10089):73-84.

2. Reveille JD, Witter JP, Weisman MH. Prevalence of axial spondylarthritis in the United States: estimates from a cross-sectional survey. Arthritis Care Res (Hoboken). 2012;64(6):905-10.

3. Costantino F, Talpin A, Said-Nahal R, Goldberg M, Henny J, Chiocchia G, et al. Prevalence of spondyloarthritis in reference to HLA-B27 in the French population: results of the GAZEL cohort. Ann Rheum Dis. 2015;74(4):689-93.

4. van der Linden S, Valkenburg HA, Cats A. Evaluation of diagnostic criteria for ankylosing spondylitis. A proposal for modification of the New York criteria. Arthritis Rheum. 1984;27(4):361-8.

5. Rudwaleit M, van der Heijde D, Landewé R, Listing J, Akkoc N, Brandt J, et al. The development of Assessment of SpondyloArthritis international Society classification criteria for axial spondyloarthritis (part II): validation and final selection. Ann Rheum Dis. 2009;68(6):777-83.

6. Tomero E, Mulero J, de Miguel E, Fernández-Espartero C, Gobbo M, Descalzo MA, et al. Performance of the Assessment of Spondyloarthritis International Society criteria for the classification of spondyloarthritis in early spondyloarthritis clinics participating in the ESPERANZA programme. Rheumatology (Oxford). 2014;53(2):353-60.

7. Moltó A, Paternotte S, Comet D, Thibout E, Rudwaleit M, Claudepierre P, et al. Performances of the Assessment of SpondyloArthritis International Society axial spondyloarthritis criteria for diagnostic and classification purposes in patients visiting a rheumatologist because of chronic back pain: results from a multicenter, cross-sectional study. Arthritis Care Res (Hoboken). 2013;65(9):1472-81.

8. Song IH, Hermann K, Haibel H, Althoff CE, Althoff C, Listing J, et al. Effects of etanercept versus sulfasalazine in early axial spondyloarthritis on active inflammatory lesions as detected by whole-body MRI (ESTHER): a 48-week randomised controlled trial. Ann Rheum Dis. 2011;70(4):590-6.

9. Creemers MC, Franssen MJ, van't Hof MA, Gribnau FW, van de Putte LB, van Riel PL. Assessment of outcome in ankylosing spondylitis: an extended radiographic scoring system. Ann Rheum Dis. 2005;64(1):127-9.

10. van der Heijde D, Lie E, Kvien TK, Sieper J, Van den Bosch F, Listing J, et al. ASDAS, a highly discriminatory ASAS-endorsed disease activity score in patients with ankylosing spondylitis. Ann Rheum Dis. 2009;68(12):1811-8.

11. Sieper J, Poddubnyy D. Inflammation, new bone formation and treatment options in axial spondyloarthritis. Ann Rheum Dis. 2014;73(8):1439-41.

12. Baraliakos X, Gensler LS, D'Angelo S, Iannone F, Favalli EG, de Peyrecave N, et al. Biologic therapy and spinal radiographic progression in patients with axial spondyloarthritis: A structured literature review. Ther Adv Musculoskelet Dis. 2020;12:1759720X20906040.

13. Molnar C, Scherer A, Baraliakos X, de Hooge M, Micheroli R, Exer P, et al. TNF blockers inhibit spinal radiographic progression in ankylosing spondylitis by reducing disease activity: results from the Swiss Clinical Quality Management cohort. Ann Rheum Dis. 2018;77(1):63-9.

7. Anexos

TFM

Maria Llop

28 de octubre de 2020

Descripción de los datos

```
install.packages("readxl", repos=c("http://rstudio.org/_packages",
"http://cran.rstudio.com",dependencies=TRUE))

## Installing package into 'C:/Users/maria/OneDrive/Documentos/R/win-library/4.0'
## (as 'lib' is unspecified)

## Warning: unable to access index for repository TRUE/src/contrib:
##   scheme not supported in URL 'TRUE/src/contrib/PACKAGES'

## Warning: unable to access index for repository http://rstudio.org/_packages/bin/windows/
contrib/4.0:
##   no fue posible abrir la URL 'http://rstudio.org/_packages/bin/windows/contrib/4.0/PACKA
GES'

## Warning: unable to access index for repository TRUE/bin/windows/contrib/4.0:
##   scheme not supported in URL 'TRUE/bin/windows/contrib/4.0/PACKAGES'

## package 'readxl' successfully unpacked and MD5 sums checked

## Warning: cannot remove prior installation of package 'readxl'

## Warning in file.copy(savedcopy, lib, recursive = TRUE):
## problema al copiar C:\Users\maria\OneDrive\Documentos\R\win-
## library\4.0\00LOCK\readxl\libs\x64\readxl.dll a C:
## \Users\maria\OneDrive\Documentos\R\win-library\4.0\readxl\libs\x64\readxl.dll:
## Permission denied

## Warning: restored 'readxl'

##
## The downloaded binary packages are in
##  C:\Users\maria\AppData\Local\Temp\RtmpGGIHpg\downloaded_packages

library(readxl)

base_rx<-read_excel("C:/Users/maria/OneDrive/Documentos/TFM/variables_regisponserbio.x
lsx")

# Realizamos una descripciÃ³n de las variables, para ver como se han codificado y ver los missin
```

```
gs.
summary(base_rx)

##    NUM_PAC               EDAD            SEXO            IMC       
##  Length:101         Min.   :21.00   Min.   :1.000   Min.   :19.37  
##  Class :character   1st Qu.:38.00   1st Qu.:1.000   1st Qu.:24.05  
##  Mode  :character   Median :46.00   Median :1.000   Median :26.02  
##                     Mean   :46.68   Mean   :1.188   Mean   :26.38  
##                     3rd Qu.:54.00   3rd Qu.:1.000   3rd Qu.:28.68  
##                     Max.   :75.00   Max.   :2.000   Max.   :40.83  
##                                                     NA's   :6      
##     IMC>30           TSINT           HLAB27            EA       
##  Min.   :0.0000   Min.   : 0.00   Min.   :1.000   Min.   :1.000  
##  1st Qu.:0.0000   1st Qu.: 8.00   1st Qu.:1.000   1st Qu.:1.000  
##  Median :0.0000   Median :15.00   Median :1.000   Median :1.000  
##  Mean   :0.1158   Mean   :17.76   Mean   :1.131   Mean   :1.149  
##  3rd Qu.:0.0000   3rd Qu.:26.00   3rd Qu.:1.000   3rd Qu.:1.000  
##  Max.   :1.0000   Max.   :52.00   Max.   :2.000   Max.   :2.000  
##  NA's   :6        NA's   :4       NA's   :2                      
##    TABACO_Kat          VSG             BASMI           UVEITIS      
##  Min.   :0.0000   Min.   :  0.50   Min.   :0.5378   Min.   :0.0000  
##  1st Qu.:0.0000   1st Qu.:  9.00   1st Qu.:1.6458   1st Qu.:0.0000  
##  Median :0.0000   Median : 19.00   Median :2.8728   Median :0.0000  
##  Mean   :0.3069   Mean   : 26.65   Mean   :3.0915   Mean   :0.2178  
##  3rd Qu.:1.0000   3rd Qu.: 38.75   3rd Qu.:4.0864   3rd Qu.:0.0000  
##  Max.   :1.0000   Max.   :115.00   Max.   :7.2729   Max.   :1.0000  
##                   NA's   :3        NA's   :19                       
##    PSORIASIS          ENF_INF            TTOBIO        NUM_TB_PREV    
##  Min.   :0.00000   Min.   :0.00000   Min.   :1.000   Min.   :0.0000  
##  1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:1.000   1st Qu.:0.0000  
##  Median :0.00000   Median :0.00000   Median :2.000   Median :0.0000  
##  Mean   :0.07071   Mean   :0.07071   Mean   :2.129   Mean   :0.3168  
##  3rd Qu.:0.00000   3rd Qu.:0.00000   3rd Qu.:3.000   3rd Qu.:1.0000  
##  Max.   :1.00000   Max.   :1.00000   Max.   :5.000   Max.   :2.0000  
##  NA's   :2         NA's   :2                                          
##      MOTIVO          TIEMBIO          BIO_INICI      Biol_4_kat    
##  Min.   :0.0000   Min.   :  0.00   Min.   :0.00   Min.   :0.0000  
##  1st Qu.:0.0000   1st Qu.:  8.00   1st Qu.:0.75   1st Qu.:0.0000  
##  Median :0.0000   Median : 42.50   Median :1.00   Median :0.0000  
##  Mean   :0.3069   Mean   : 45.51   Mean   :0.75   Mean   :0.4554  
##  3rd Qu.:0.0000   3rd Qu.: 76.75   3rd Qu.:1.00   3rd Qu.:1.0000  
##  Max.   :2.0000   Max.   :132.00   Max.   :1.00   Max.   :1.0000  
##                   NA's   :1        NA's   :1                      
##     Interval         AINE             FAME           i_BASDAI    
##  Min.   :2.00   Min.   :0.0000   Min.   :0.0000   Min.   :0.700  
##  1st Qu.:3.00   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:4.225  
##  Median :3.00   Median :1.0000   Median :0.0000   Median :5.400  
##  Mean   :3.45   Mean   :0.5758   Mean   :0.1818   Mean   :5.326  
##  3rd Qu.:4.00   3rd Qu.:1.0000   3rd Qu.:0.0000   3rd Qu.:6.400  
##  Max.   :6.00   Max.   :1.0000   Max.   :1.0000   Max.   :8.800  
##  NA's   :1      NA's   :2        NA's   :2        NA's   :3      
##     BASDAI_0        BASDAI_1         BASDAI_2         BASDAI_3    
```

```
##  Min.   :0.20   Min.   :0.000   Min.   : 0.000   Min.   :0.000
##  1st Qu.:2.00   1st Qu.:1.400   1st Qu.: 1.400   1st Qu.:1.200
##  Median :3.20   Median :2.700   Median : 2.500   Median :3.000
##  Mean   :3.67   Mean   :2.902   Mean   : 3.419   Mean   :3.108
##  3rd Qu.:5.10   3rd Qu.:4.400   3rd Qu.: 4.200   3rd Qu.:4.800
##  Max.   :8.80   Max.   :8.500   Max.   :65.000   Max.   :8.000
##  NA's   :4      NA's   :4       NA's   :4        NA's   :8
##     BASDAI_4        BASDAI_5        BASDAI_6        ASDAS_0
##  Min.   :0.000   Min.   :0.000   Min.   :0.000   Min.   :0.2257
##  1st Qu.:1.200   1st Qu.:1.275   1st Qu.:1.100   1st Qu.:1.3874
##  Median :2.800   Median :2.550   Median :2.800   Median :2.0565
##  Mean   :3.075   Mean   :2.915   Mean   :2.924   Mean   :2.2160
##  3rd Qu.:4.600   3rd Qu.:4.200   3rd Qu.:4.600   3rd Qu.:2.9248
##  Max.   :8.000   Max.   :8.000   Max.   :7.300   Max.   :5.0749
##  NA's   :10      NA's   :17      NA's   :16      NA's   :5
##     ASDAS_1          ASDAS_2             ASDAS_3           ASDAS_4
##  Min.   :0.2471   Min.   :0.001737   Min.   :0.04892   Min.   :0.00058
##  1st Qu.:1.1572   1st Qu.:1.088078   1st Qu.:1.16497   1st Qu.:1.17363
##  Median :1.5738   Median :1.827288   Median :1.76656   Median :1.66660
##  Mean   :1.8249   Mean   :1.773470   Mean   :1.81523   Mean   :1.81274
##  3rd Qu.:2.4204   3rd Qu.:2.316346   3rd Qu.:2.47797   3rd Qu.:2.44173
##  Max.   :7.1255   Max.   :4.131246   Max.   :3.98374   Max.   :4.45150
##  NA's   :13       NA's   :9          NA's   :14        NA's   :22
##     ASDAS_5          ASDAS_6          PCR_0             PCR_1
##  Min.   :0.0338   Min.   :0.096   Min.   : 0.000   Min.   : 0.000
##  1st Qu.:1.0522   1st Qu.:1.143   1st Qu.: 1.000   1st Qu.: 1.000
##  Median :1.6400   Median :1.680   Median : 3.350   Median : 2.000
##  Mean   :1.7329   Mean   :1.807   Mean   : 8.181   Mean   : 4.358
##  3rd Qu.:2.1781   3rd Qu.:2.397   3rd Qu.: 9.100   3rd Qu.: 4.675
##  Max.   :4.0579   Max.   :3.988   Max.   :88.700   Max.   :61.300
##  NA's   :30       NA's   :24      NA's   :7        NA's   :3
##      PCR_2           PCR_3            PCR_4            PCR_5
##  Min.   : 0.00   Min.   : 0.000   Min.   : 0.000   Min.   : 0.000
##  1st Qu.: 0.90   1st Qu.: 0.750   1st Qu.: 0.700   1st Qu.: 0.615
##  Median : 2.00   Median : 1.900   Median : 2.050   Median : 1.400
##  Mean   : 4.36   Mean   : 4.452   Mean   : 5.368   Mean   : 4.118
##  3rd Qu.: 5.60   3rd Qu.: 5.600   3rd Qu.: 5.375   3rd Qu.: 6.000
##  Max.   :33.90   Max.   :37.000   Max.   :68.500   Max.   :65.900
##  NA's   :2       NA's   :4        NA's   :7        NA's   :10
##      PCR_6            EGP              EGM            BASFI_0
##  Min.   : 0.00   Min.   : 0.000   Min.   : 0.000   Min.   :0.000
##  1st Qu.: 0.60   1st Qu.: 2.000   1st Qu.: 1.500   1st Qu.:1.525
##  Median : 2.00   Median : 3.000   Median : 3.000   Median :3.850
##  Mean   : 4.42   Mean   : 4.031   Mean   : 3.455   Mean   :3.931
##  3rd Qu.: 5.95   3rd Qu.: 6.000   3rd Qu.: 5.000   3rd Qu.:5.975
##  Max.   :39.70   Max.   :10.000   Max.   :10.000   Max.   :9.300
##  NA's   :14      NA's   :3        NA's   :2        NA's   :3
##     BASFI_1         BASFI_2         BASFI_3         BASFI_4        BASFI_5
##  Min.   :0.000   Min.   :0.000   Min.   :0.000   Min.   :0.00   Min.   :0.000
##  1st Qu.:1.200   1st Qu.:0.550   1st Qu.:1.000   1st Qu.:1.30   1st Qu.:1.100
##  Median :2.700   Median :2.330   Median :2.800   Median :3.50   Median :3.200
##  Mean   :3.059   Mean   :2.667   Mean   :2.882   Mean   :3.34   Mean   :3.118
```

```
##  3rd Qu.:4.550   3rd Qu.:4.340   3rd Qu.:4.500   3rd Qu.:5.00   3rd Qu.:4.700  
##  Max.   :8.800   Max.   :7.890   Max.   :7.900   Max.   :8.40   Max.   :8.100  
##  NA's   :2                       NA's   :8       NA's   :12      NA's   :22     
##     BASFI_6      mSASSS_Mean_BL  mSASSS_Mean_FL  mSASSS_Progress
##  Min.   :0.000   Min.   : 0.00   Min.   : 0.00   Min.   :-2.50  
##  1st Qu.:1.100   1st Qu.: 0.00   1st Qu.: 0.00   1st Qu.: 0.00  
##  Median :3.100   Median : 5.00   Median : 8.00   Median : 0.00  
##  Mean   :3.313   Mean   :16.46   Mean   :18.44   Mean   : 1.98  
##  3rd Qu.:5.100   3rd Qu.:23.00   3rd Qu.:30.00   3rd Qu.: 3.00  
##  Max.   :8.300   Max.   :72.00   Max.   :72.00   Max.   :21.50  
##  NA's   :16                                                     
##  New_Syn_mSASSS  Prog_Syn_mSASSS  mSASSS_Progress_Kat New_Prog_Syn_Msasss
##  Min.   :0.000   Min.   :0.0000   Min.   :0.000       Min.   :0.0000     
##  1st Qu.:0.000   1st Qu.:0.0000   1st Qu.:0.000       1st Qu.:0.0000     
##  Median :0.000   Median :0.0000   Median :0.000       Median :0.0000     
##  Mean   :0.198   Mean   :0.1089   Mean   :0.297       Mean   :0.2178     
##  3rd Qu.:0.000   3rd Qu.:0.0000   3rd Qu.:1.000       3rd Qu.:0.0000     
##  Max.   :1.000   Max.   :1.0000   Max.   :1.000       Max.   :1.0000     
##                                                                          
##  Mind_2_Synd_FL   Mind_2_Synd_BL   PCR_INICIOB       i_ASDAS     
##  Min.   :0.0000   Min.   :0.000   Min.   : 0.00   Min.   :1.500  
##  1st Qu.:0.0000   1st Qu.:0.000   1st Qu.: 4.60   1st Qu.:2.700  
##  Median :1.0000   Median :1.000   Median :11.10   Median :3.500  
##  Mean   :0.5446   Mean   :0.505   Mean   :18.70   Mean   :3.402  
##  3rd Qu.:1.0000   3rd Qu.:1.000   3rd Qu.:28.05   3rd Qu.:4.000  
##  Max.   :1.0000   Max.   :1.000   Max.   :98.00   Max.   :5.300  
##                                   NA's   :2       NA's   :2      
##       HVGP       
##  Min.   : 1.000  
##  1st Qu.: 5.000  
##  Median : 6.000  
##  Mean   : 5.923  
##  3rd Qu.: 7.000  
##  Max.   :10.000  
## 
```

```r
str(base_rx)
```

```
## tibble [101 x 66] (S3: tbl_df/tbl/data.frame)
##  $ NUM_PAC           : chr [1:101] "U01001" "U01007" "U01017" "U02001" ...
##  $ EDAD              : num [1:101] 63 34 26 57 41 40 43 65 60 41 ...
##  $ SEXO              : num [1:101] 1 1 1 2 1 2 1 1 1 1 ...
##  $ IMC               : num [1:101] 26.3 26.2 24.6 28.7 21.6 ...
##  $ IMC>30            : num [1:101] 0 0 0 0 0 0 0 0 0 0 ...
##  $ TSINT             : num [1:101] 1 13 6 13 18 16 13 38 21 13 ...
##  $ HLAB27            : num [1:101] 1 1 1 1 1 2 1 1 1 1 ...
##  $ EA                : num [1:101] 1 1 1 2 1 1 2 1 1 1 ...
##  $ TABACO_Kat        : num [1:101] 0 0 0 0 1 0 1 0 1 0 ...
##  $ VSG               : num [1:101] 50 16 3 24 38 25 9 18 10 52 ...
##  $ BASMI             : num [1:101] 1.083 NA 0.979 2.947 3.265 ...
##  $ UVEITIS           : num [1:101] 0 0 0 0 1 0 0 0 0 0 ...
##  $ PSORIASIS         : num [1:101] 0 0 0 1 0 0 1 0 0 0 ...
```

```
## $ ENF_INF            : num [1:101] 0 0 0 0 0 0 0 1 0 0 ...
## $ TTOBIO             : num [1:101] 5 3 4 2 3 4 2 3 1 2 ...
## $ NUM_TB_PREV        : num [1:101] 0 0 0 1 0 0 0 0 0 0 ...
## $ MOTIVO             : num [1:101] 0 0 0 1 0 0 0 0 0 0 ...
## $ TIEMBIO            : num [1:101] 0 72 0 84 24 0 0 132 1 58 ...
## $ BIO_INICI          : num [1:101] 0 1 0 1 1 0 0 1 0 1 ...
## $ Biol_4_kat         : num [1:101] 0 1 0 1 0 0 0 1 0 1 ...
## $ Interval           : num [1:101] 4 4 3 4 4 4 4 3 3 4 ...
## $ AINE               : num [1:101] 1 1 1 1 1 1 1 1 1 1 ...
## $ FAME               : num [1:101] 1 1 0 1 0 0 1 0 0 0 ...
## $ i_BASDAI           : num [1:101] 2.2 5.9 2.2 3.8 4.5 5 8 8 7 5 ...
## $ BASDAI_0           : num [1:101] 2.2 3.9 2.2 3 2 5 8 5.5 7 3 ...
## $ BASDAI_1           : num [1:101] 2.8 2.3 1.7 5.2 1 2.5 6 6 4 3 ...
## $ BASDAI_2           : num [1:101] 1.8 3.4 1.7 3 0.5 5.5 4 65 3 1.9 ...
## $ BASDAI_3           : num [1:101] 0.6 1.8 1.7 5 1 4 5 8 1 2.4 ...
## $ BASDAI_4           : num [1:101] 1.8 1.8 1.7 6 1 5 8 5 6.1 2.8 ...
## $ BASDAI_5           : num [1:101] 1 2.7 0.8 6 1 4 8 NA 2.1 3 ...
## $ BASDAI_6           : num [1:101] 0.8 2.9 1.1 3 1 5 1 NA 2.4 3 ...
## $ ASDAS_0            : num [1:101] 3.52 3 2.05 2.45 1.18 ...
## $ ASDAS_1            : num [1:101] 1.112 1.648 1.467 2.468 0.762 ...
## $ ASDAS_2            : num [1:101] 0.44 2.68 1.865 2.367 0.492 ...
## $ ASDAS_3            : num [1:101] 0.425 1.907 0.65 2.69 2.35 ...
## $ ASDAS_4            : num [1:101] 0.795 1.426 1.534 3.209 0.79 ...
## $ ASDAS_5            : num [1:101] 0.466 2.261 1.245 2.562 1.58 ...
## $ ASDAS_6            : num [1:101] 0.402 2.851 1.055 1.903 0.957 ...
## $ PCR_0              : num [1:101] 88.7 8.8 11.3 10 2 1.6 9.2 5.4 16 2 ...
## $ PCR_1              : num [1:101] 0.3 3.1 2 3.7 1 3 2.2 4 4 2 ...
## $ PCR_2              : num [1:101] 0 9.8 5.6 5.4 0.9 2 0.4 1.3 4 2 ...
## $ PCR_3              : num [1:101] 0.5 6.1 0 4.8 37 15 0.6 3.6 1 3 ...
## $ PCR_4              : num [1:101] 0.4 2.1 2.8 5.1 1.1 4.1 0.5 20 1 2 ...
## $ PCR_5              : num [1:101] 0.2 7.5 3.22 1 7.2 6 1 NA 1 9 ...
## $ PCR_6              : num [1:101] 0.3 11 1.79 4 1.8 18 1 NA 1.5 1.9 ...
## $ EGP                : num [1:101] 3 7 1 4 2 5 9 6 10 2 ...
## $ EGM                : num [1:101] 3 7 1 4 2 5 5 3 5 1 ...
## $ BASFI_0            : num [1:101] 1.3 5.4 0.9 5.1 1.8 4.3 6 7.2 8.1 2.2 ...
## $ BASFI_1            : num [1:101] 0.8 3.5 0.6 5.9 0.8 3.4 2 7.6 4.8 1.6 ...
## $ BASFI_2            : num [1:101] 0.11 2.67 0.44 4.89 0.55 4.33 5.21 6.23 2.99 1.88 ...
## $ BASFI_3            : num [1:101] 0.1 2.7 0.4 4.9 0.5 4.3 5.1 6.3 2.9 1.8 ...
## $ BASFI_4            : num [1:101] 1.5 2.9 6 3.9 0.6 3.5 4 6.7 5.5 1.8 ...
## $ BASFI_5            : num [1:101] 4 3 0.6 5 0 4 4 NA 5.2 2.4 ...
## $ BASFI_6            : num [1:101] 0.8 5.2 1.6 3 0 4 1 NA 5 2.4 ...
## $ mSASSS_Mean_BL     : num [1:101] 2.5 2.5 0 1 34 0 0 60 4 3 ...
## $ mSASSS_Mean_FL     : num [1:101] 6 4 0 2 34 1.5 0 60 5.5 3 ...
## $ mSASSS_Progress    : num [1:101] 3.5 1.5 0 1 0 1.5 0 0 1.5 0 ...
## $ New_Syn_mSASSS     : num [1:101] 1 0 0 0 0 0 0 0 0 0 ...
## $ Prog_Syn_mSASSS    : num [1:101] 0 0 0 0 0 0 0 0 0 0 ...
## $ mSASSS_Progress_Kat: num [1:101] 1 0 0 0 0 0 0 0 0 0 ...
## $ New_Prog_Syn_Msasss: num [1:101] 1 0 0 0 0 0 0 0 0 0 ...
## $ Mind_2_Synd_FL     : num [1:101] 1 0 0 0 1 0 0 1 1 0 ...
## $ Mind_2_Synd_BL     : num [1:101] 0 0 0 0 1 0 0 1 1 0 ...
## $ PCR_INICIOB        : num [1:101] 88.7 18 11.3 26 15 16 9.2 26 16 30 ...
```

```
##  $ i_ASDAS           : num [1:101] 3.4 3.8 2.2 3.6 3 3.4 3.8 4.3 3.9 4.1 ...
##  $ HVGP              : num [1:101] 3 7 1 7 4 5 5 5 5 8 ...
```

```
# las siguientes variables no estÃ¡n bien codificadas, estÃ¡n codificadas como variables numÃ©ricas cuando en realidad son variables categÃ³ricas, corrijo el problema:
base_rx$NUM_PAC <- factor( base_rx$NUM_PAC )
base_rx$EA<- factor(base_rx$EA, labels = c("SI","NO"))
base_rx$`IMC>30`<- factor(base_rx$`IMC>30`, labels = c("NO","SI"))
base_rx$HLAB27<- factor(base_rx$HLAB27, labels = c("SI","NO"))
base_rx$SEXO<- factor(base_rx$SEXO, labels = c("MALE","FEMALE"))
base_rx$TABACO_Kat<- factor(base_rx$TABACO_Kat, labels = c("SI","NO"))
base_rx$VSG= as.numeric(base_rx$VSG)
base_rx$UVEITIS<- factor(base_rx$UVEITIS, labels = c("NO","SI"))
base_rx$PSORIASIS<- factor(base_rx$PSORIASIS, labels = c("NO","SI"))
base_rx$ENF_INF<- factor(base_rx$ENF_INF, labels = c("NO","SI"))
base_rx$TTOBIO<- factor(base_rx$TTOBIO, labels = c("ETA","ADA","IFX","GOL","CTZ"))
base_rx$NUM_TB_PREV<- factor(base_rx$NUM_TB_PREV, labels = c("treatments.0","treatments.1","treatments.2"))
base_rx$MOTIVO<- factor(base_rx$MOTIVO, labels = c("non.change","Inefficacy","Side.effects"))
base_rx$BIO_INICI<- factor(base_rx$BIO_INICI, labels = c("NO","SI"))
base_rx$Biol_4_kat<- factor(base_rx$Biol_4_kat, labels = c("NO","SI"))
base_rx$AINE<- factor(base_rx$AINE, labels = c("NO","SI"))
base_rx$FAME<- factor(base_rx$FAME, labels = c("NO","SI"))
base_rx$New_Syn_mSASSS<- factor(base_rx$New_Syn_mSASSS, labels = c("NO","SI"))
base_rx$Prog_Syn_mSASSS<- factor(base_rx$Prog_Syn_mSASSS, labels = c("NO","SI"))
base_rx$mSASSS_Progress_Kat<- factor(base_rx$mSASSS_Progress_Kat, labels = c("NO","SI"))
base_rx$New_Prog_Syn_Msasss<- factor(base_rx$New_Prog_Syn_Msasss, labels = c("NO","SI"))
base_rx$Mind_2_Synd_FL<- factor(base_rx$Mind_2_Synd_FL, labels = c("NO","SI"))
base_rx$Mind_2_Synd_BL<- factor(base_rx$Mind_2_Synd_BL, labels = c("NO","SI"))

# Ahora repetimos el proceso de descripciÃ³n de las variables:
str(base_rx)
```

```
## tibble [101 x 66] (S3: tbl_df/tbl/data.frame)
##  $ NUM_PAC           : Factor w/ 101 levels "U01001","U01007",..: 1 2 3 4 5 6 7 8 9 10 ...
##  $ EDAD              : num [1:101] 63 34 26 57 41 40 43 65 60 41 ...
##  $ SEXO              : Factor w/ 2 levels "MALE","FEMALE": 1 1 1 2 1 2 1 1 1 1 ...
##  $ IMC               : num [1:101] 26.3 26.2 24.6 28.7 21.6 ...
##  $ IMC>30            : Factor w/ 2 levels "NO","SI": 1 1 1 1 1 1 1 1 1 1 ...
##  $ TSINT             : num [1:101] 1 13 6 13 18 16 13 38 21 13 ...
##  $ HLAB27            : Factor w/ 2 levels "SI","NO": 1 1 1 1 1 2 1 1 1 1 ...
##  $ EA                : Factor w/ 2 levels "SI","NO": 1 1 1 2 1 1 2 1 1 1 ...
##  $ TABACO_Kat        : Factor w/ 2 levels "SI","NO": 1 1 1 1 2 1 2 1 2 1 ...
##  $ VSG               : num [1:101] 50 16 3 24 38 25 9 18 10 52 ...
##  $ BASMI             : num [1:101] 1.083 NA 0.979 2.947 3.265 ...
##  $ UVEITIS           : Factor w/ 2 levels "NO","SI": 1 1 1 1 2 1 1 1 1 1 ...
##  $ PSORIASIS         : Factor w/ 2 levels "NO","SI": 1 1 1 2 1 1 2 1 1 1 ...
##  $ ENF_INF           : Factor w/ 2 levels "NO","SI": 1 1 1 1 1 1 1 2 1 1 ...
##  $ TTOBIO            : Factor w/ 5 levels "ETA","ADA","IFX",..: 5 3 4 2 3 4 2 3 1 2 ...
##  $ NUM_TB_PREV       : Factor w/ 3 levels "treatments.0",..: 1 1 1 2 1 1 1 1 1 1 ...
```

```
## $ MOTIVO            : Factor w/ 3 levels "non.change","Inefficacy",..: 1 1 1 2 1 1 1 1 1 1 ...
## $ TIEMBIO           : num [1:101] 0 72 0 84 24 0 0 132 1 58 ...
## $ BIO_INICI         : Factor w/ 2 levels "NO","SI": 1 2 1 2 2 1 1 2 1 2 ...
## $ Biol_4_kat        : Factor w/ 2 levels "NO","SI": 1 2 1 2 1 1 1 2 1 2 ...
## $ Interval          : num [1:101] 4 4 3 4 4 4 4 3 3 4 ...
## $ AINE              : Factor w/ 2 levels "NO","SI": 2 2 2 2 2 2 2 2 2 2 ...
## $ FAME              : Factor w/ 2 levels "NO","SI": 2 2 1 2 1 1 2 1 1 1 ...
## $ i_BASDAI          : num [1:101] 2.2 5.9 2.2 3.8 4.5 5 8 8 7 5 ...
## $ BASDAI_0          : num [1:101] 2.2 3.9 2.2 3 2 5 8 5.5 7 3 ...
## $ BASDAI_1          : num [1:101] 2.8 2.3 1.7 5.2 1 2.5 6 6 4 3 ...
## $ BASDAI_2          : num [1:101] 1.8 3.4 1.7 3 0.5 5.5 4 65 3 1.9 ...
## $ BASDAI_3          : num [1:101] 0.6 1.8 1.7 5 1 4 5 8 1 2.4 ...
## $ BASDAI_4          : num [1:101] 1.8 1.8 1.7 6 1 5 8 5 6.1 2.8 ...
## $ BASDAI_5          : num [1:101] 1 2.7 0.8 6 1 4 8 NA 2.1 3 ...
## $ BASDAI_6          : num [1:101] 0.8 2.9 1.1 3 1 5 1 NA 2.4 3 ...
## $ ASDAS_0           : num [1:101] 3.52 3 2.05 2.45 1.18 ...
## $ ASDAS_1           : num [1:101] 1.112 1.648 1.467 2.468 0.762 ...
## $ ASDAS_2           : num [1:101] 0.44 2.68 1.865 2.367 0.492 ...
## $ ASDAS_3           : num [1:101] 0.425 1.907 0.65 2.69 2.35 ...
## $ ASDAS_4           : num [1:101] 0.795 1.426 1.534 3.209 0.79 ...
## $ ASDAS_5           : num [1:101] 0.466 2.261 1.245 2.562 1.58 ...
## $ ASDAS_6           : num [1:101] 0.402 2.851 1.055 1.903 0.957 ...
## $ PCR_0             : num [1:101] 88.7 8.8 11.3 10 2 1.6 9.2 5.4 16 2 ...
## $ PCR_1             : num [1:101] 0.3 3.1 2 3.7 1 3 2.2 4 4 2 ...
## $ PCR_2             : num [1:101] 0 9.8 5.6 5.4 0.9 2 0.4 1.3 4 2 ...
## $ PCR_3             : num [1:101] 0.5 6.1 0 4.8 37 15 0.6 3.6 1 3 ...
## $ PCR_4             : num [1:101] 0.4 2.1 2.8 5.1 1.1 4.1 0.5 20 1 2 ...
## $ PCR_5             : num [1:101] 0.2 7.5 3.22 1 7.2 6 1 NA 1 9 ...
## $ PCR_6             : num [1:101] 0.3 11 1.79 4 1.8 18 1 NA 1.5 1.9 ...
## $ EGP               : num [1:101] 3 7 1 4 2 5 9 6 10 2 ...
## $ EGM               : num [1:101] 3 7 1 4 2 5 5 3 5 1 ...
## $ BASFI_0           : num [1:101] 1.3 5.4 0.9 5.1 1.8 4.3 6 7.2 8.1 2.2 ...
## $ BASFI_1           : num [1:101] 0.8 3.5 0.6 5.9 0.8 3.4 2 7.6 4.8 1.6 ...
## $ BASFI_2           : num [1:101] 0.11 2.67 0.44 4.89 0.55 4.33 5.21 6.23 2.99 1.88 ...
## $ BASFI_3           : num [1:101] 0.1 2.7 0.4 4.9 0.5 4.3 5.1 6.3 2.9 1.8 ...
## $ BASFI_4           : num [1:101] 1.5 2.9 6 3.9 0.6 3.5 4 6.7 5.5 1.8 ...
## $ BASFI_5           : num [1:101] 4 3 0.6 5 0 4 4 NA 5.2 2.4 ...
## $ BASFI_6           : num [1:101] 0.8 5.2 1.6 3 0 4 1 NA 5 2.4 ...
## $ mSASSS_Mean_BL    : num [1:101] 2.5 2.5 0 1 34 0 0 60 4 3 ...
## $ mSASSS_Mean_FL    : num [1:101] 6 4 0 2 34 1.5 0 60 5.5 3 ...
## $ mSASSS_Progress   : num [1:101] 3.5 1.5 0 1 0 1.5 0 0 1.5 0 ...
## $ New_Syn_mSASSS    : Factor w/ 2 levels "NO","SI": 2 1 1 1 1 1 1 1 1 1 ...
## $ Prog_Syn_mSASSS   : Factor w/ 2 levels "NO","SI": 1 1 1 1 1 1 1 1 1 1 ...
## $ mSASSS_Progress_Kat: Factor w/ 2 levels "NO","SI": 2 1 1 1 1 1 1 1 1 1 ...
## $ New_Prog_Syn_Msasss: Factor w/ 2 levels "NO","SI": 2 1 1 1 1 1 1 1 1 1 ...
## $ Mind_2_Synd_FL    : Factor w/ 2 levels "NO","SI": 2 1 1 1 2 1 1 2 2 1 ...
## $ Mind_2_Synd_BL    : Factor w/ 2 levels "NO","SI": 1 1 1 1 2 1 1 2 2 1 ...
## $ PCR_INICIOB       : num [1:101] 88.7 18 11.3 26 15 16 9.2 26 16 30 ...
## $ i_ASDAS           : num [1:101] 3.4 3.8 2.2 3.6 3 3.4 3.8 4.3 3.9 4.1 ...
## $ HVGP              : num [1:101] 3 7 1 7 4 5 5 5 5 8 ...

summary(base_rx)
```

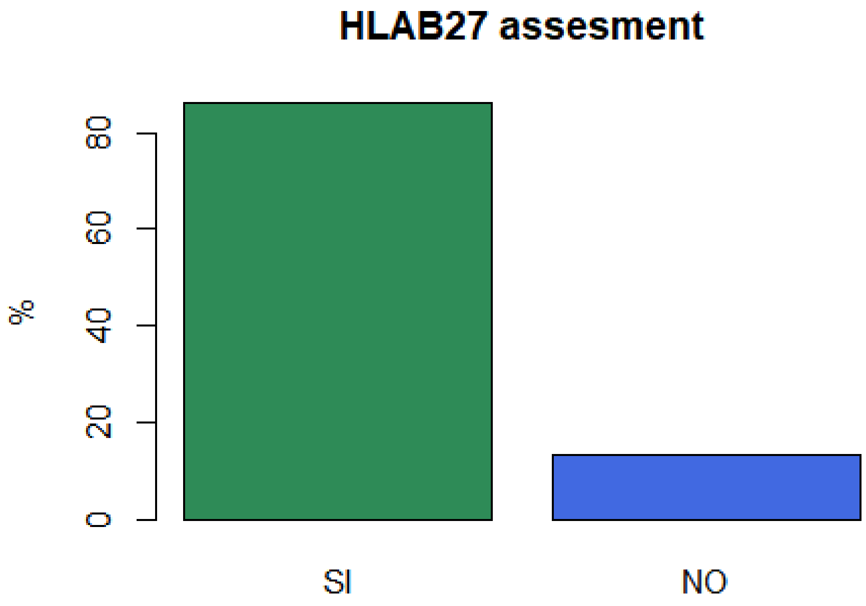
```
##    NUM_PAC       EDAD          SEXO        IMC        IMC>30
##  U01001 : 1   Min.   :21.00   MALE  :82   Min.   :19.37   NO  :84
##  U01007 : 1   1st Qu.:38.00   FEMALE:19   1st Qu.:24.05   SI  :11
##  U01017 : 1   Median :46.00               Median :26.02   NA's: 6
##  U02001 : 1   Mean   :46.68               Mean   :26.38
##  U02003 : 1   3rd Qu.:54.00               3rd Qu.:28.68
##  U02004 : 1   Max.   :75.00               Max.   :40.83
##  (Other):95                               NA's   :6
##     TSINT       HLAB27    EA     TABACO_Kat      VSG            BASMI
##  Min.   : 0.00   SI  :86   SI:86   SI:70      Min.   :  0.50   Min.   :0.5378
##  1st Qu.: 8.00   NO  :13   NO:15   NO:31      1st Qu.:  9.00   1st Qu.:1.6458
##  Median :15.00   NA's: 2                      Median : 19.00   Median :2.8728
##  Mean   :17.76                                Mean   : 26.65   Mean   :3.0915
##  3rd Qu.:26.00                                3rd Qu.: 38.75   3rd Qu.:4.0864
##  Max.   :52.00                                Max.   :115.00   Max.   :7.2729
##  NA's   :4                                    NA's   :3        NA's   :19
##  UVEITIS PSORIASIS ENF_INF   TTOBIO        NUM_TB_PREV         MOTIVO
##  NO:79   NO  :92   NO  :92   ETA:31   treatments.0:75   non.change  :77
##  SI:22   SI  : 7   SI  : 7   ADA:44   treatments.1:20   Inefficacy  :17
##          NA's: 2   NA's: 2   IFX:11   treatments.2: 6   Side.effects: 7
##                              GOL:12
##                              CTZ: 3
##
##
##     TIEMBIO       BIO_INICI Biol_4_kat    Interval      AINE      FAME
##  Min.   :  0.00   NO  :25   NO:55      Min.   :2.00   NO  :42   NO  :81
##  1st Qu.:  8.00   SI  :75   SI:46      1st Qu.:3.00   SI  :57   SI  :18
##  Median : 42.50   NA's: 1              Median :3.00   NA's: 2   NA's: 2
##  Mean   : 45.51                        Mean   :3.45
##  3rd Qu.: 76.75                        3rd Qu.:4.00
##  Max.   :132.00                        Max.   :6.00
##  NA's   :1                             NA's   :1
##     i_BASDAI       BASDAI_0       BASDAI_1       BASDAI_2
##  Min.   :0.700   Min.   :0.20   Min.   :0.000   Min.   : 0.000
##  1st Qu.:4.225   1st Qu.:2.00   1st Qu.:1.400   1st Qu.: 1.400
##  Median :5.400   Median :3.20   Median :2.700   Median : 2.500
##  Mean   :5.326   Mean   :3.67   Mean   :2.902   Mean   : 3.419
##  3rd Qu.:6.400   3rd Qu.:5.10   3rd Qu.:4.400   3rd Qu.: 4.200
##  Max.   :8.800   Max.   :8.80   Max.   :8.500   Max.   :65.000
##  NA's   :3       NA's   :4      NA's   :4       NA's   :4
##     BASDAI_3       BASDAI_4       BASDAI_5       BASDAI_6
##  Min.   :0.000   Min.   :0.000   Min.   :0.000   Min.   :0.000
##  1st Qu.:1.200   1st Qu.:1.200   1st Qu.:1.275   1st Qu.:1.100
##  Median :3.000   Median :2.800   Median :2.550   Median :2.800
##  Mean   :3.108   Mean   :3.075   Mean   :2.915   Mean   :2.924
##  3rd Qu.:4.800   3rd Qu.:4.600   3rd Qu.:4.200   3rd Qu.:4.600
##  Max.   :8.000   Max.   :8.000   Max.   :8.000   Max.   :7.300
##  NA's   :8       NA's   :10      NA's   :17      NA's   :16
##     ASDAS_0         ASDAS_1         ASDAS_2            ASDAS_3
##  Min.   :0.2257   Min.   :0.2471   Min.   :0.001737   Min.   :0.04892
##  1st Qu.:1.3874   1st Qu.:1.1572   1st Qu.:1.088078   1st Qu.:1.16497
##  Median :2.0565   Median :1.5738   Median :1.827288   Median :1.76656
```

```
##  Mean   :2.2160   Mean   :1.8249   Mean   :1.773470   Mean   :1.81523  
##  3rd Qu.:2.9248   3rd Qu.:2.4204   3rd Qu.:2.316346   3rd Qu.:2.47797  
##  Max.   :5.0749   Max.   :7.1255   Max.   :4.131246   Max.   :3.98374  
##  NA's   :5        NA's   :13       NA's   :9          NA's   :14       
##     ASDAS_4          ASDAS_5          ASDAS_6          PCR_0       
##  Min.   :0.00058   Min.   :0.0338   Min.   :0.096   Min.   : 0.000  
##  1st Qu.:1.17363   1st Qu.:1.0522   1st Qu.:1.143   1st Qu.: 1.000  
##  Median :1.66660   Median :1.6400   Median :1.680   Median : 3.350  
##  Mean   :1.81274   Mean   :1.7329   Mean   :1.807   Mean   : 8.181  
##  3rd Qu.:2.44173   3rd Qu.:2.1781   3rd Qu.:2.397   3rd Qu.: 9.100  
##  Max.   :4.45150   Max.   :4.0579   Max.   :3.988   Max.   :88.700  
##  NA's   :22        NA's   :30       NA's   :24      NA's   :7       
##      PCR_1            PCR_2           PCR_3            PCR_4       
##  Min.   : 0.000   Min.   : 0.00   Min.   : 0.000   Min.   : 0.000  
##  1st Qu.: 1.000   1st Qu.: 0.90   1st Qu.: 0.750   1st Qu.: 0.700  
##  Median : 2.000   Median : 2.00   Median : 1.900   Median : 2.050  
##  Mean   : 4.358   Mean   : 4.36   Mean   : 4.452   Mean   : 5.368  
##  3rd Qu.: 4.675   3rd Qu.: 5.60   3rd Qu.: 5.600   3rd Qu.: 5.375  
##  Max.   :61.300   Max.   :33.90   Max.   :37.000   Max.   :68.500  
##  NA's   :3        NA's   :2       NA's   :4        NA's   :7       
##      PCR_5            PCR_6            EGP              EGM        
##  Min.   : 0.000   Min.   : 0.00   Min.   : 0.000   Min.   : 0.000  
##  1st Qu.: 0.615   1st Qu.: 0.60   1st Qu.: 2.000   1st Qu.: 1.500  
##  Median : 1.400   Median : 2.00   Median : 3.000   Median : 3.000  
##  Mean   : 4.118   Mean   : 4.42   Mean   : 4.031   Mean   : 3.455  
##  3rd Qu.: 6.000   3rd Qu.: 5.95   3rd Qu.: 6.000   3rd Qu.: 5.000  
##  Max.   :65.900   Max.   :39.70   Max.   :10.000   Max.   :10.000  
##  NA's   :10       NA's   :14      NA's   :3        NA's   :2       
##     BASFI_0         BASFI_1         BASFI_2         BASFI_3         BASFI_4    
##  Min.   :0.000   Min.   :0.000   Min.   :0.000   Min.   :0.000   Min.   :0.00  
##  1st Qu.:1.525   1st Qu.:1.200   1st Qu.:0.550   1st Qu.:1.000   1st Qu.:1.30  
##  Median :3.850   Median :2.700   Median :2.330   Median :2.800   Median :3.50  
##  Mean   :3.931   Mean   :3.059   Mean   :2.667   Mean   :2.882   Mean   :3.34  
##  3rd Qu.:5.975   3rd Qu.:4.550   3rd Qu.:4.340   3rd Qu.:4.500   3rd Qu.:5.00  
##  Max.   :9.300   Max.   :8.800   Max.   :7.890   Max.   :7.900   Max.   :8.40  
##  NA's   :3       NA's   :2                        NA's   :8       NA's   :12    
##     BASFI_5         BASFI_6      mSASSS_Mean_BL  mSASSS_Mean_FL 
##  Min.   :0.000   Min.   :0.000   Min.   : 0.00   Min.   : 0.00  
##  1st Qu.:1.100   1st Qu.:1.100   1st Qu.: 0.00   1st Qu.: 0.00  
##  Median :3.200   Median :3.100   Median : 5.00   Median : 8.00  
##  Mean   :3.118   Mean   :3.313   Mean   :16.46   Mean   :18.44  
##  3rd Qu.:4.700   3rd Qu.:5.100   3rd Qu.:23.00   3rd Qu.:30.00  
##  Max.   :8.100   Max.   :8.300   Max.   :72.00   Max.   :72.00  
##  NA's   :22      NA's   :16                                      
##  mSASSS_Progress New_Syn_mSASSS Prog_Syn_mSASSS mSASSS_Progress_Kat
##  Min.   :-2.50   NO:81          NO:90           NO:71              
##  1st Qu.: 0.00   SI:20          SI:11           SI:30              
##  Median : 0.00                                                     
##  Mean   : 1.98                                                     
##  3rd Qu.: 3.00                                                     
##  Max.   :21.50                                                     
## 
```

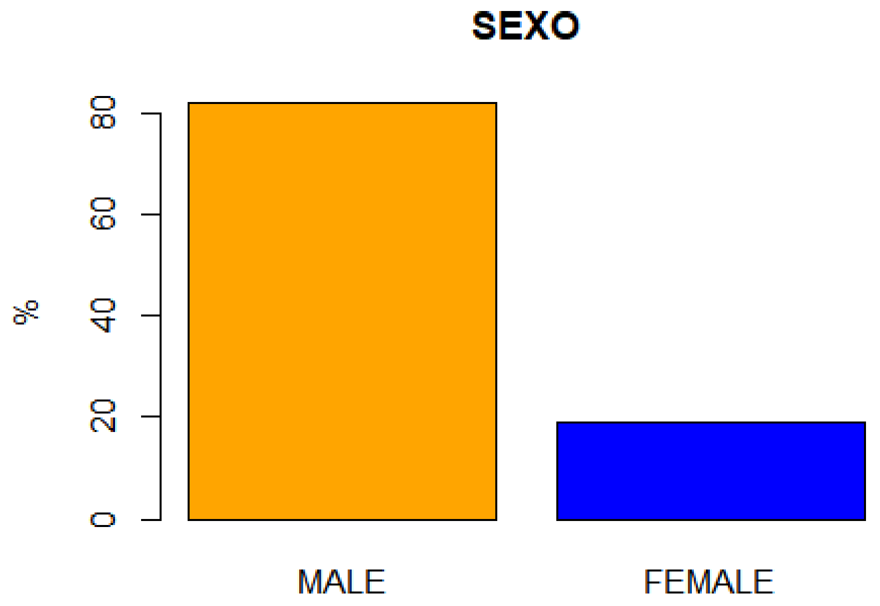
```
##  New_Prog_Syn_Msasss Mind_2_Synd_FL Mind_2_Synd_BL  PCR_INICIOB
##  NO:79               NO:46          NO:50          Min.   : 0.00
##  SI:22               SI:55          SI:51          1st Qu.: 4.60
##                                                    Median :11.10
##                                                    Mean   :18.70
##                                                    3rd Qu.:28.05
##                                                    Max.   :98.00
##                                                    NA's   :2
##     i_ASDAS          HVGP
##  Min.   :1.500   Min.   : 1.000
##  1st Qu.:2.700   1st Qu.: 5.000
##  Median :3.500   Median : 6.000
##  Mean   :3.402   Mean   : 5.923
##  3rd Qu.:4.000   3rd Qu.: 7.000
##  Max.   :5.300   Max.   :10.000
##  NA's   :2
```

AnÃ¡lisis de outliers. RepresentaciÃ³n grÃ¡fica de las variables categÃ³ricas

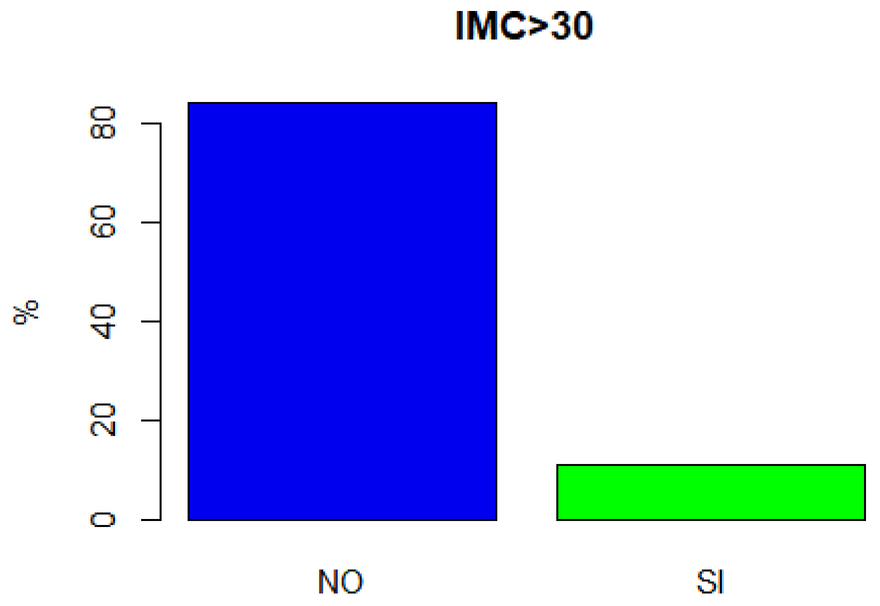
```
plot(x=base_rx$HLAB27, col=c("seagreen","royalblue"), ylab="%", main="HLAB27 assesment")
```



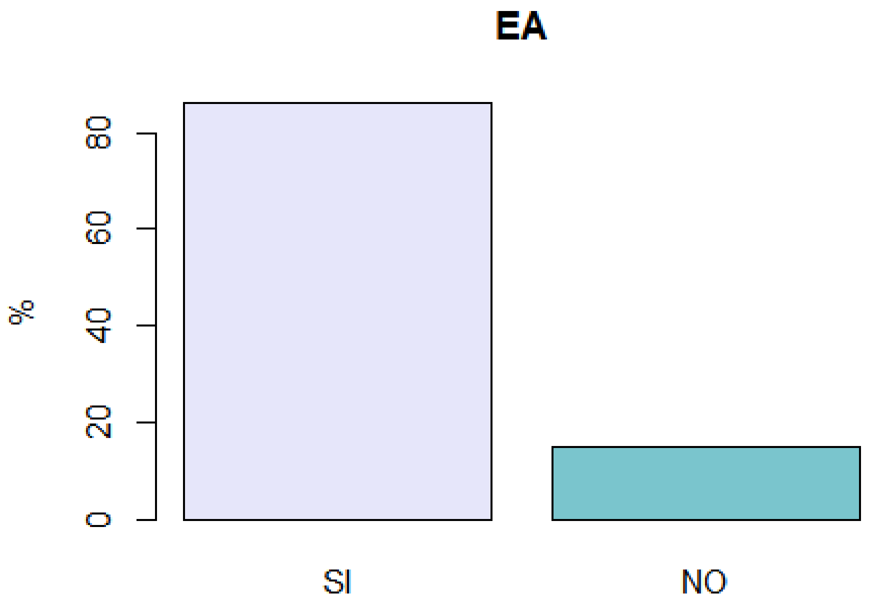
```
plot(x=base_rx$SEXO, col=c("orange","blue"), ylab="%", main="SEXO")
```



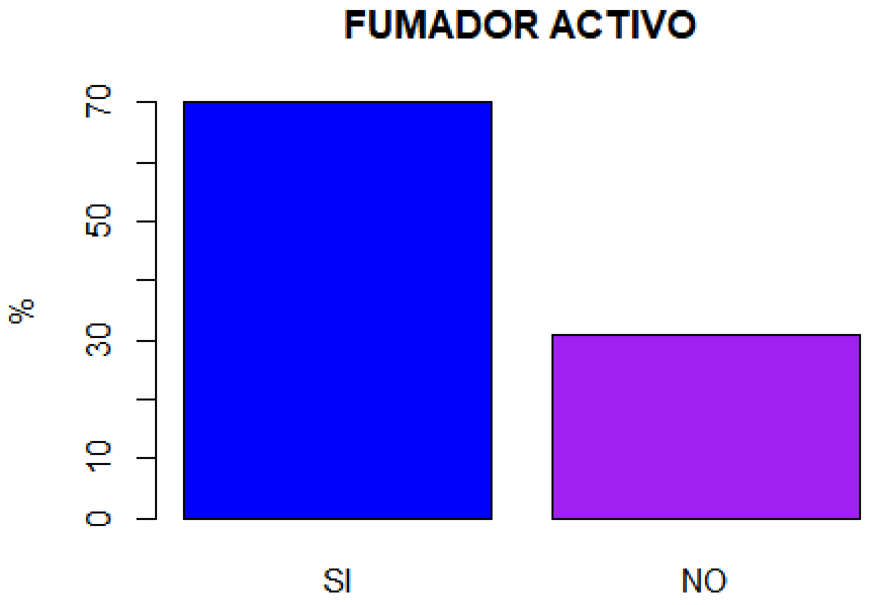
```
plot(x=base_rx$`IMC>30`, col=c("blue2","green"), ylab="%", main="IMC>30")
```



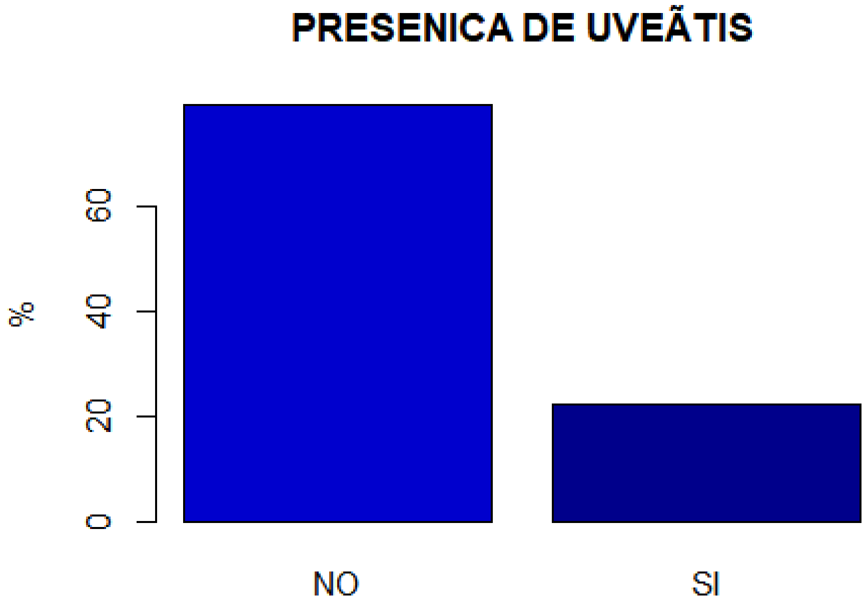
```
plot(x=base_rx$EA, col=c("lavender","cadetblue3"), ylab="%", main="EA")
```



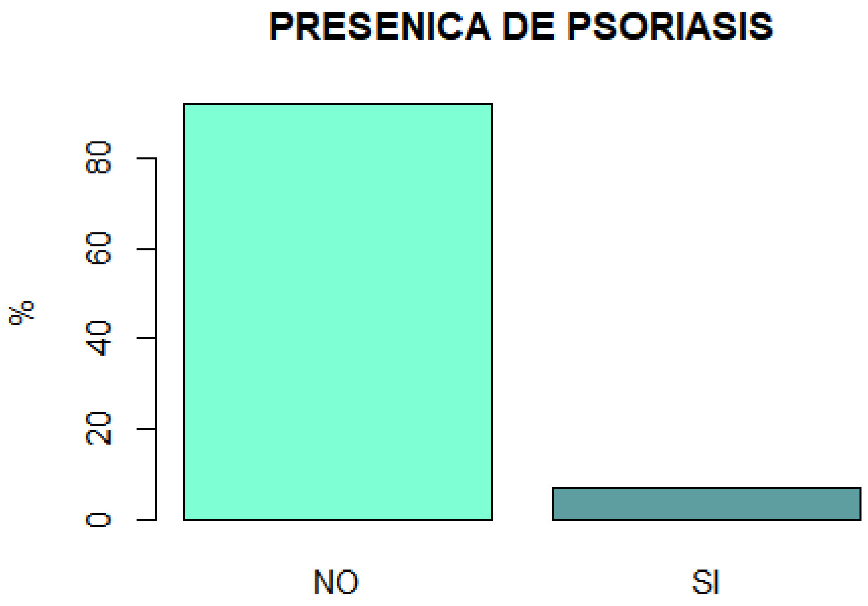
```
plot(x=base_rx$TABACO_Kat, col=c("blue","purple"), ylab="%", main="FUMADOR ACTIVO")
```



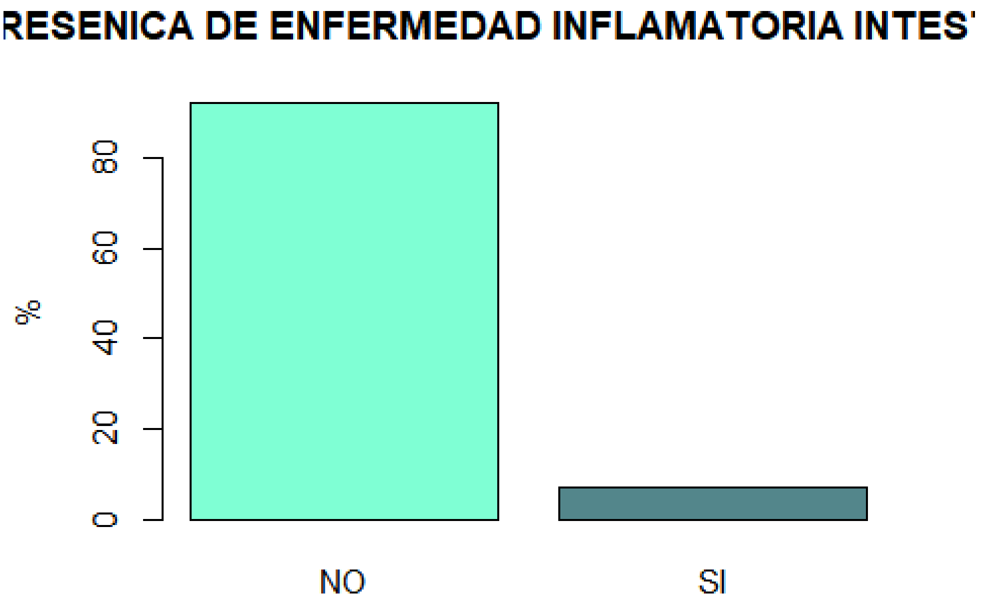
```
plot(x=base_rx$UVEITIS, col=c("blue3","blue4"), ylab="%", main="PRESENICA DE UVEÃ�TIS")
```



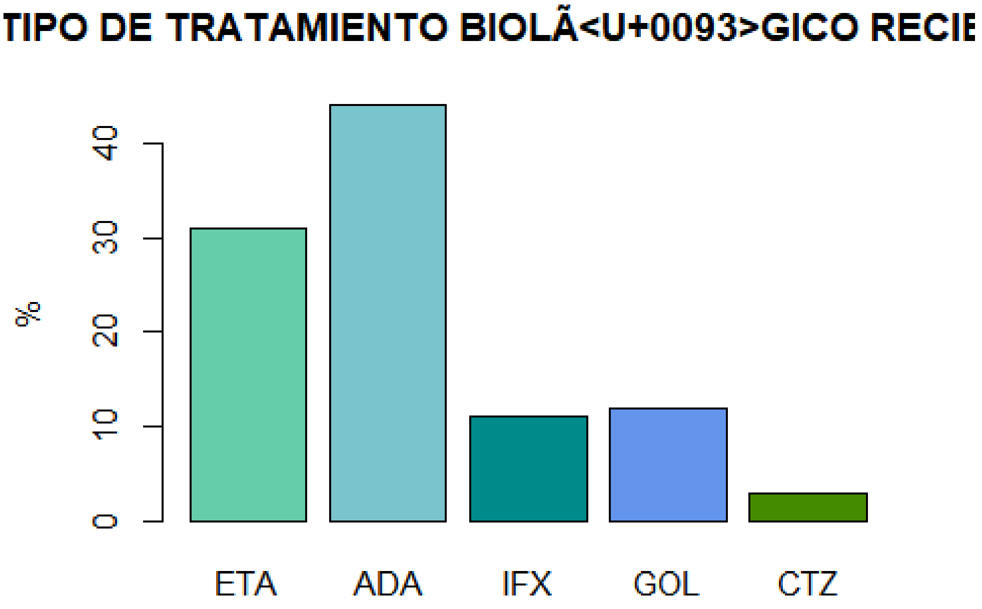
```
plot(x=base_rx$PSORIASIS, col=c("aquamarine","cadetblue"), ylab="%", main="PRESENICA DE
PSORIASIS")
```



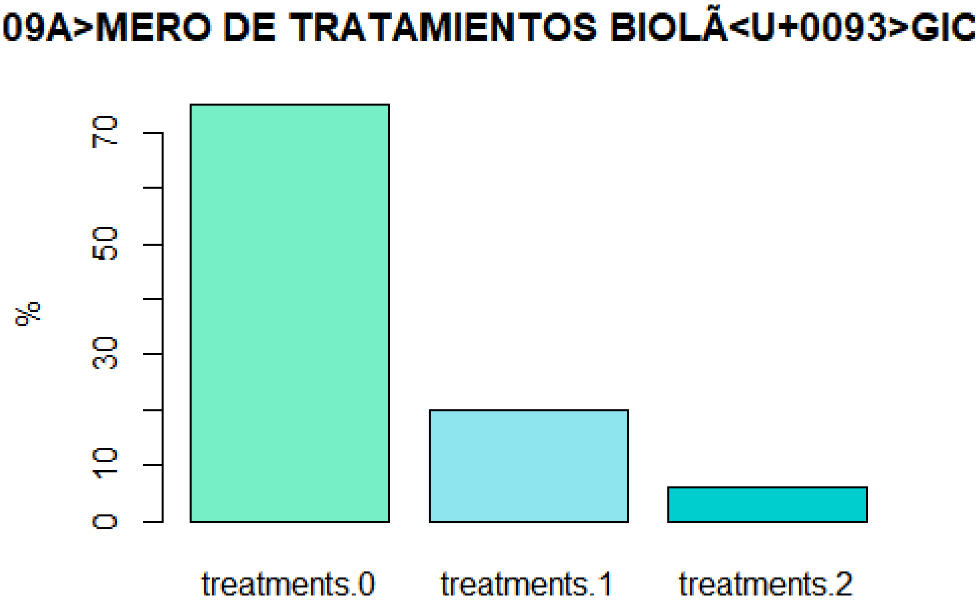
```
plot(x=base_rx$ENF_INF, col=c("aquamarine1","cadetblue4"), ylab="%", main="PRESENICA DE
ENFERMEDAD INFLAMATORIA INTESTINAL")
```



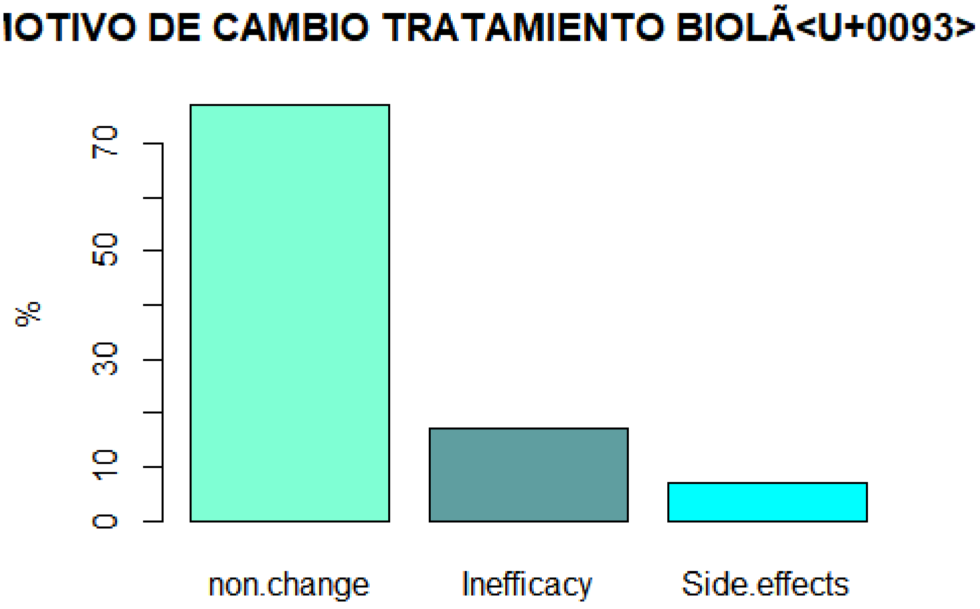
```
plot(x=base_rx$TTOBIO, col=c("aquamarine3","cadetblue3","cyan4", "cornflowerblue", "chartr
euse4"), ylab="%", main="TIPO DE TRATAMIENTO BIOLÃ“GICO RECIBIDO")
```



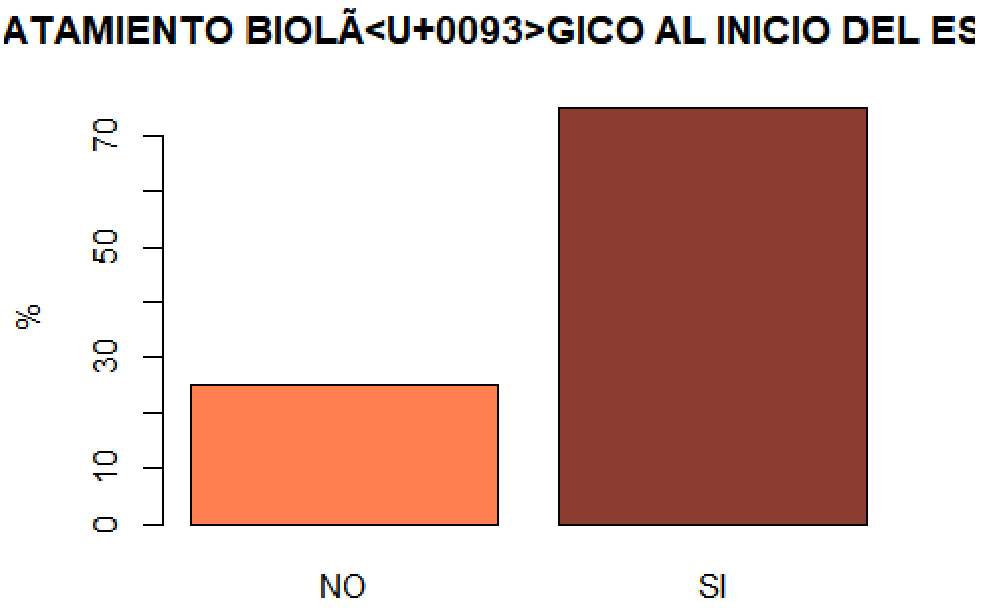
```
plot(x=base_rx$NUM_TB_PREV, col=c("aquamarine2","cadetblue2","cyan3"), ylab="%", main=
"NÃšMERO DE TRATAMIENTOS BIOLÃ“GICIS PREVIOS")
```



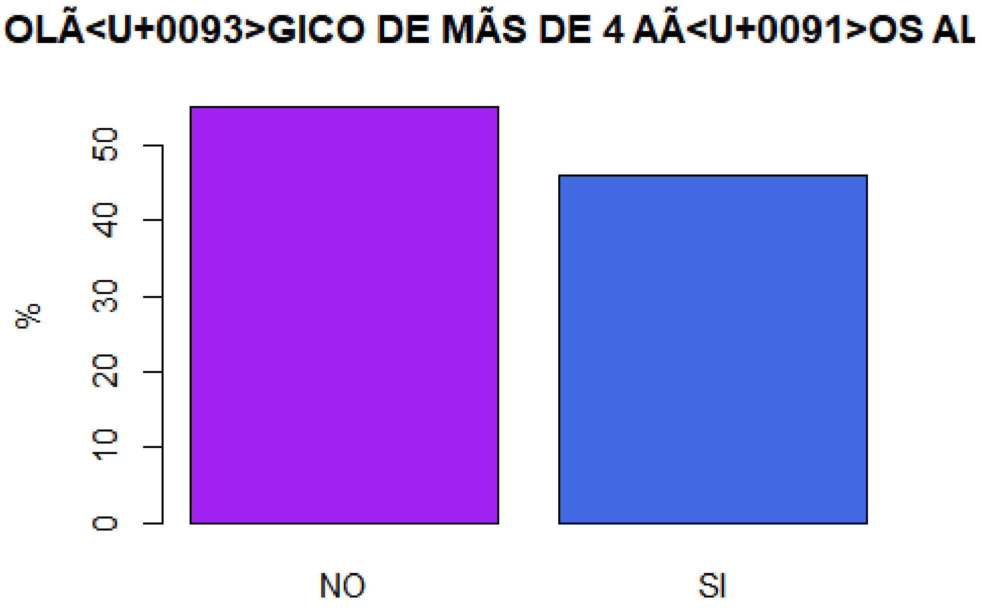
```
plot(x=base_rx$MOTIVO, col=c("aquamarine","cadetblue","cyan"), ylab="%", main="MOTIVO
DE CAMBIO TRATAMIENTO BIOLÃ“GICO")
```



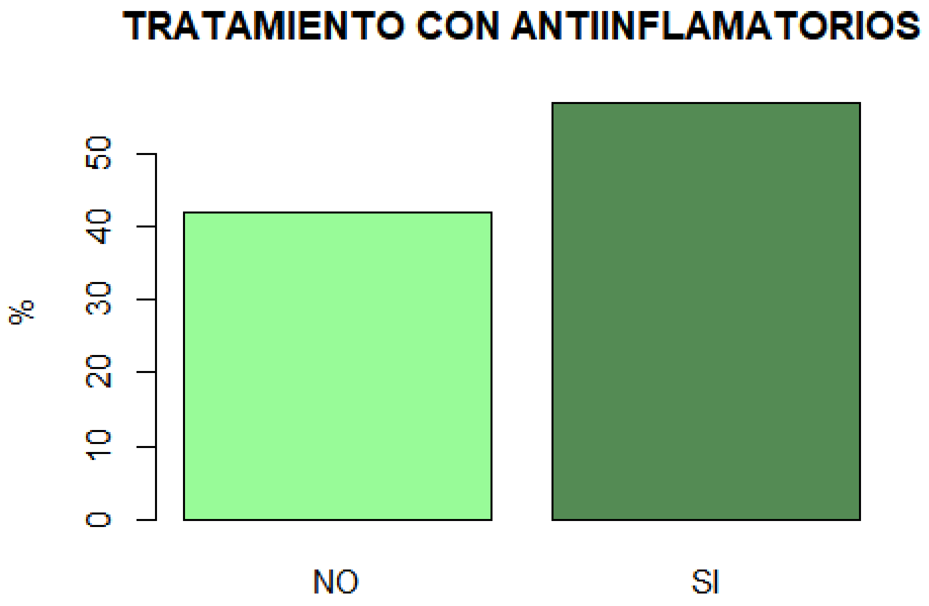
```
plot(x=base_rx$BIO_INICI, col=c("coral","coral4"), ylab="%", main="TRATAMIENTO BIOLÃ“GIC
O AL INICIO DEL ESTUDIO")
```



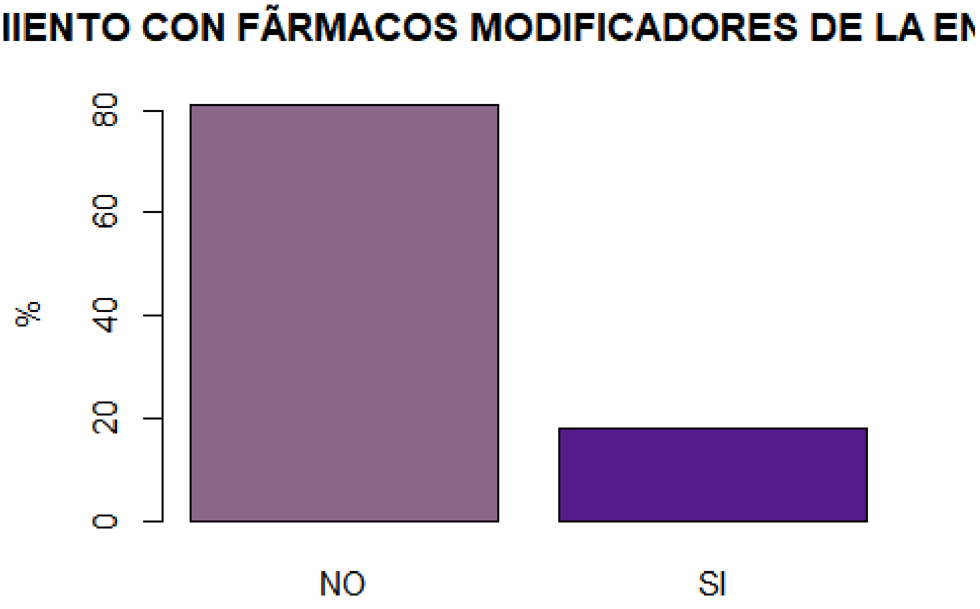
```
plot(x=base_rx$Biol_4_kat, col=c("purple","royalblue"), ylab="%", main="TRATAMIENTO BIOL
Ã“GICO DE MÃ S DE 4 AÃ‘OS AL INICIO DEL ESTUDIO")
```



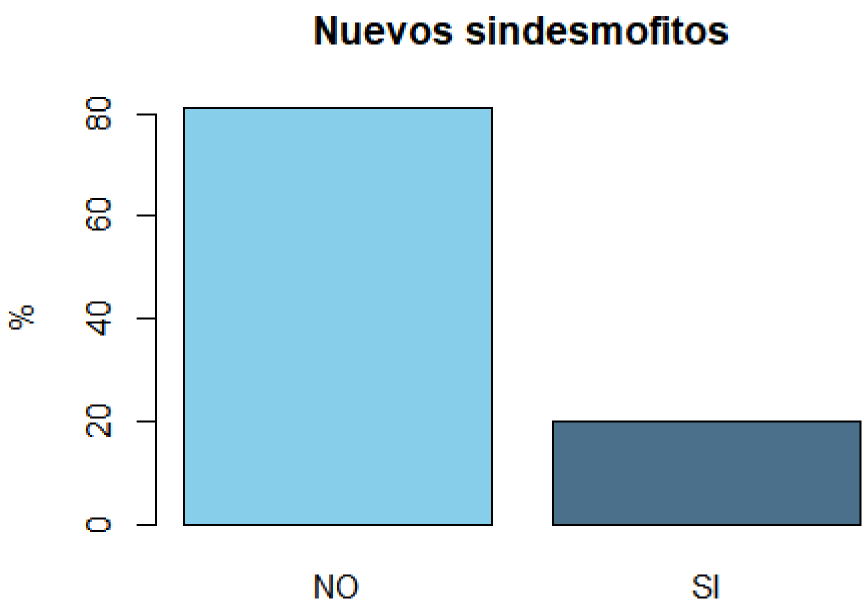
```
plot(x=base_rx$AINE, col=c("palegreen","palegreen4"), ylab="%", main="TRATAMIENTO CON
ANTIINFLAMATORIOS")
```



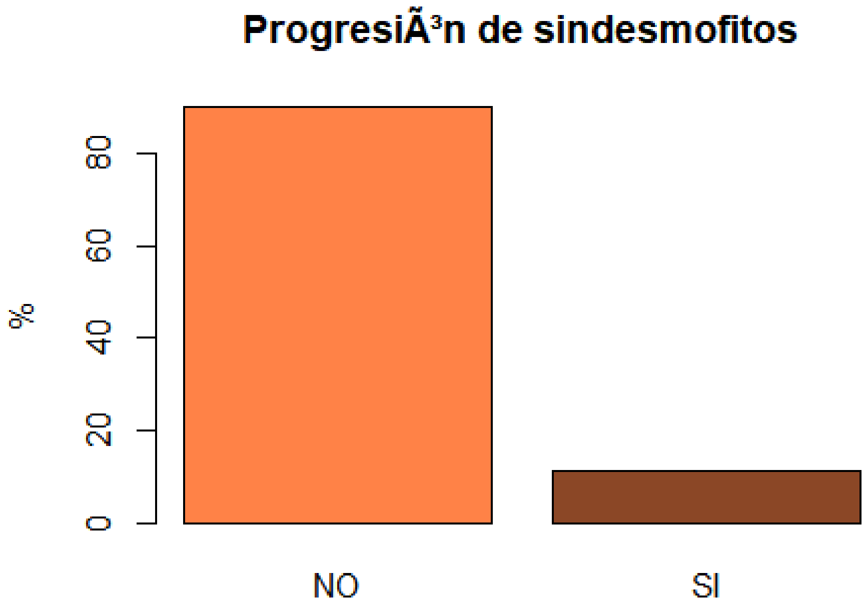
```
plot(x=base_rx$FAME, col=c("plum4","purple4"), ylab="%", main="TRATAMIENTO CON FÃ�RM
ACOS MODIFICADORES DE LA ENFERMEDAD")
```



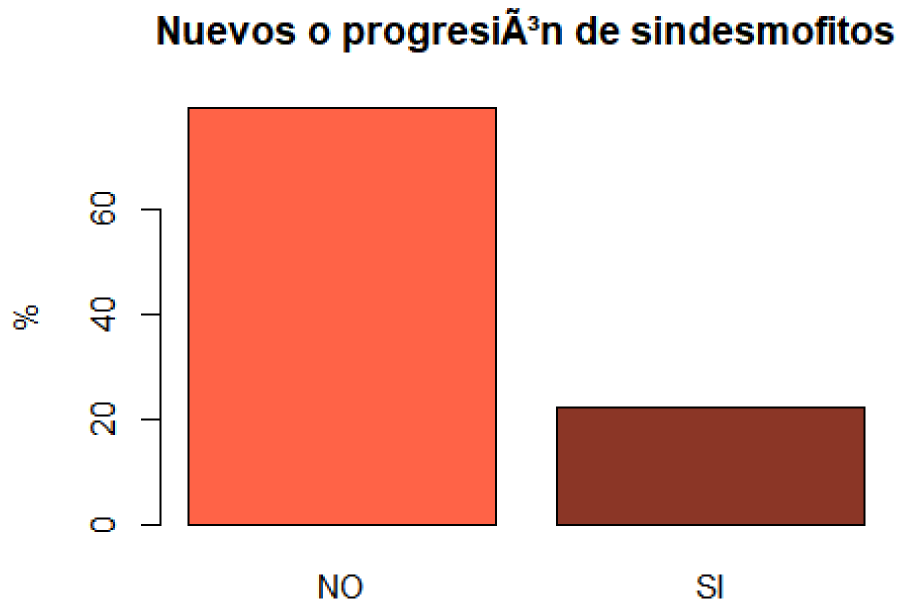
```
plot(x=base_rx$New_Syn_mSASSS, col=c("skyblue","skyblue4"), ylab="%", main="Nuevos sind
esmofitos")
```



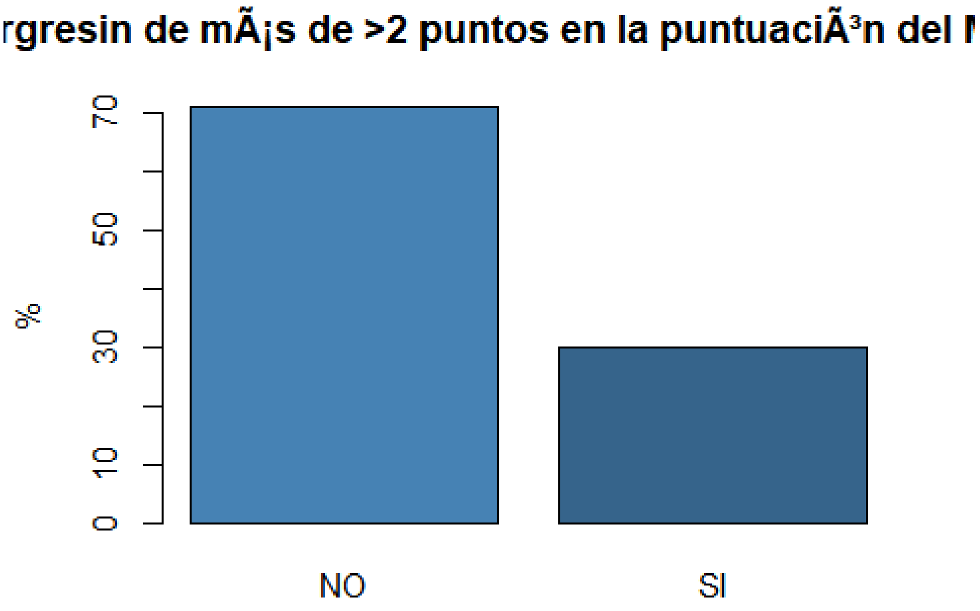
```
plot(x=base_rx$Prog_Syn_mSASSS, col=c("sienna1","sienna4"), ylab="%", main="ProgresiÃ³n d
e sindesmofitos")
```



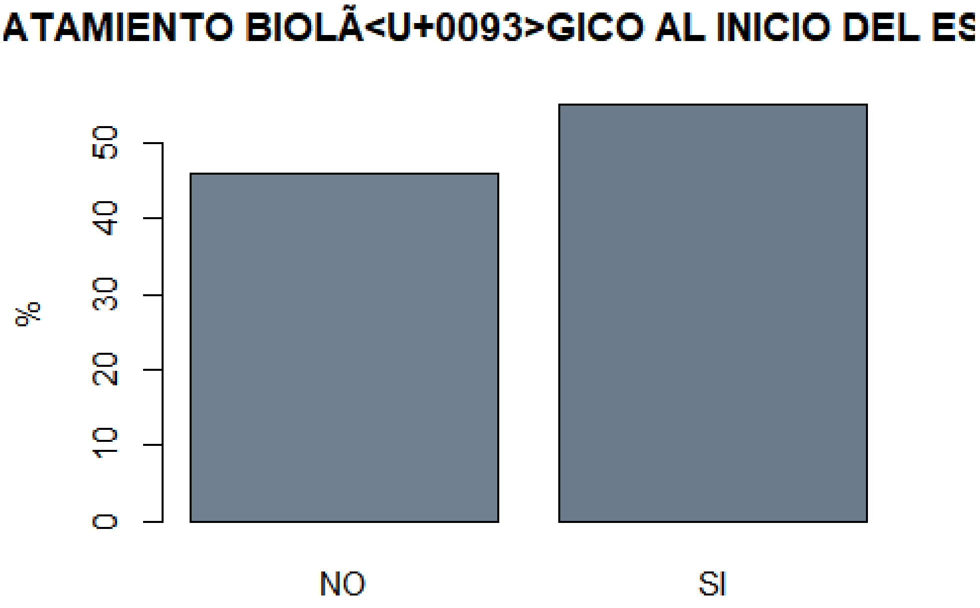
```
plot(x=base_rx$New_Prog_Syn_Msasss, col=c("tomato","tomato4"), ylab="%", main="Nuevos
o progresiÃ³n de sindesmofitos")
```



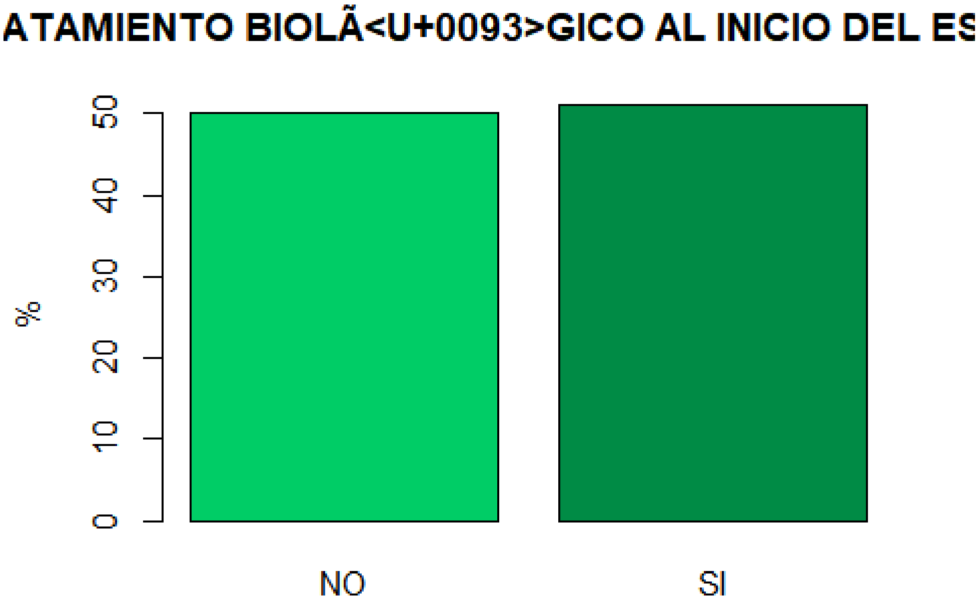
```
plot(x=base_rx$mSASSS_Progress_Kat, col=c("steelblue","steelblue4"), ylab="%", main="Porgr
esin de mÃ¡s de >2 puntos en la puntuaciÃ³n del Msasss")
```



```
plot(x=base_rx$Mind_2_Synd_FL, col=c("slategray","slategray4"), ylab="%", main="TRATAMIE
NTO BIOLÃ“GICO AL INICIO DEL ESTUDIO")
```



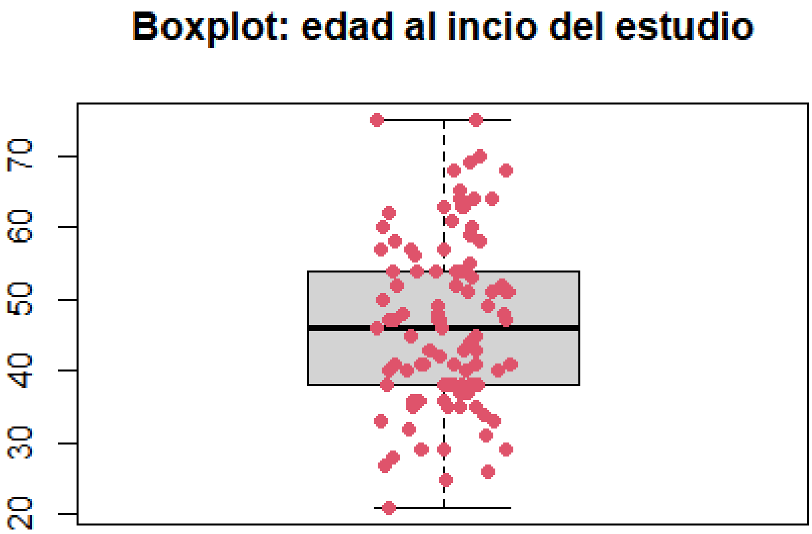
```r
plot(x=base_rx$Mind_2_Synd_BL, col=c("springgreen3","springgreen4"), ylab="%", main="TRATAMIENTO BIOLÃ“GICO AL INICIO DEL ESTUDIO")
```



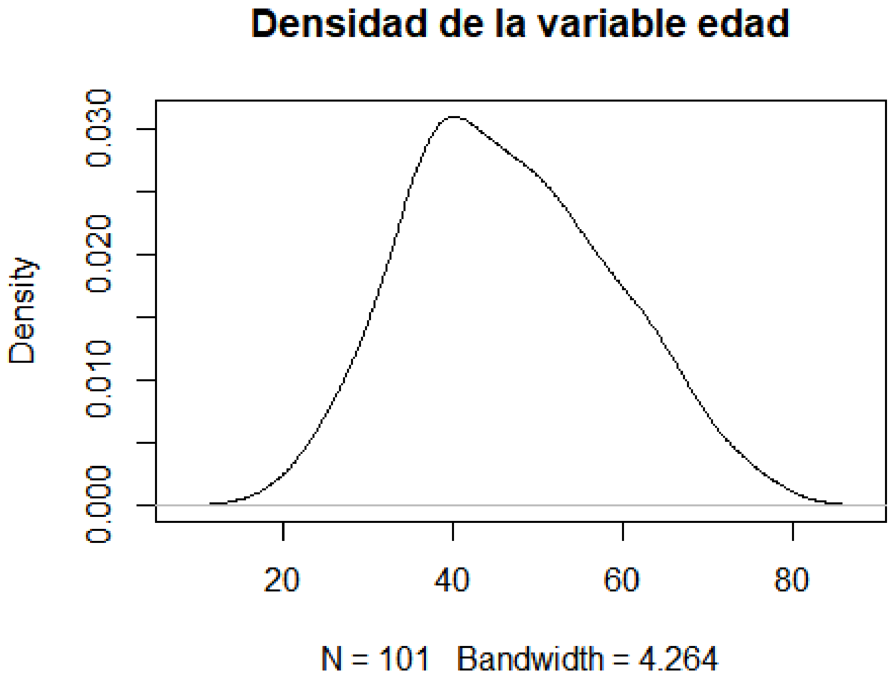
AnÃ¡lsis de outilers. Variables numÃ©ricas

Con la función stripchart observamos la dispersiÃ³n de los datos

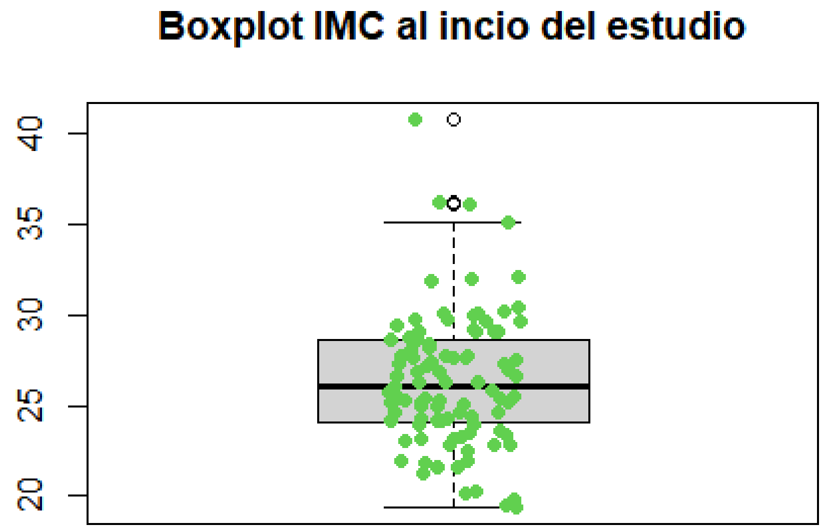
```
boxplot(x=base_rx$EDAD, main = "Boxplot: edad al incio del estudio")
stripchart(x=base_rx$EDAD, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 2)
```



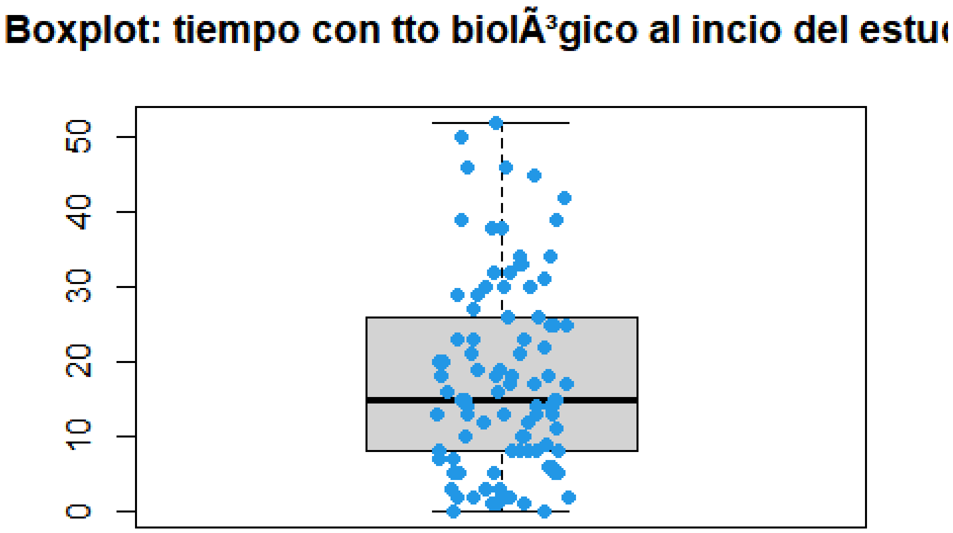
```
plot(density(base_rx$EDAD), main = "Densidad de la variable edad")
```



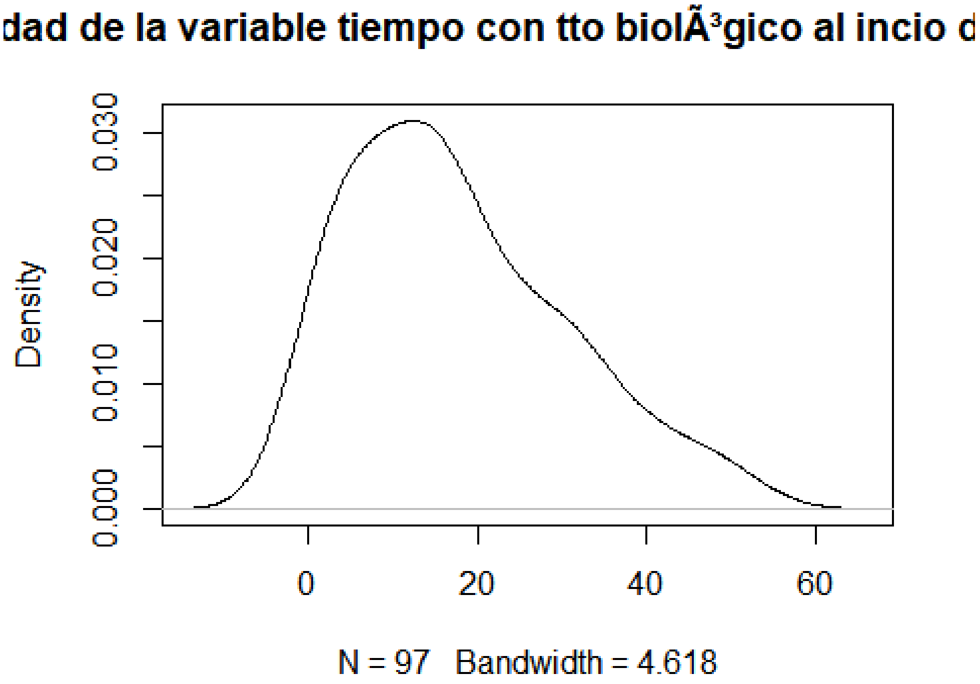
```
boxplot(x=base_rx$IMC, main = "Boxplot IMC al incio del estudio")
stripchart(x=base_rx$IMC, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 3)
```



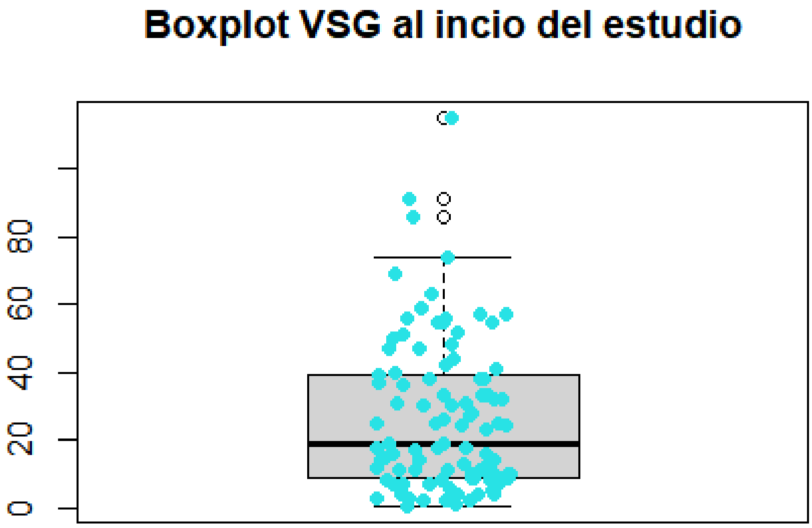
```
boxplot(x=base_rx$TSINT, main = "Boxplot: tiempo con tto biolÃ³gico al incio del estudio")
stripchart(x=base_rx$TSINT, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 4)
```



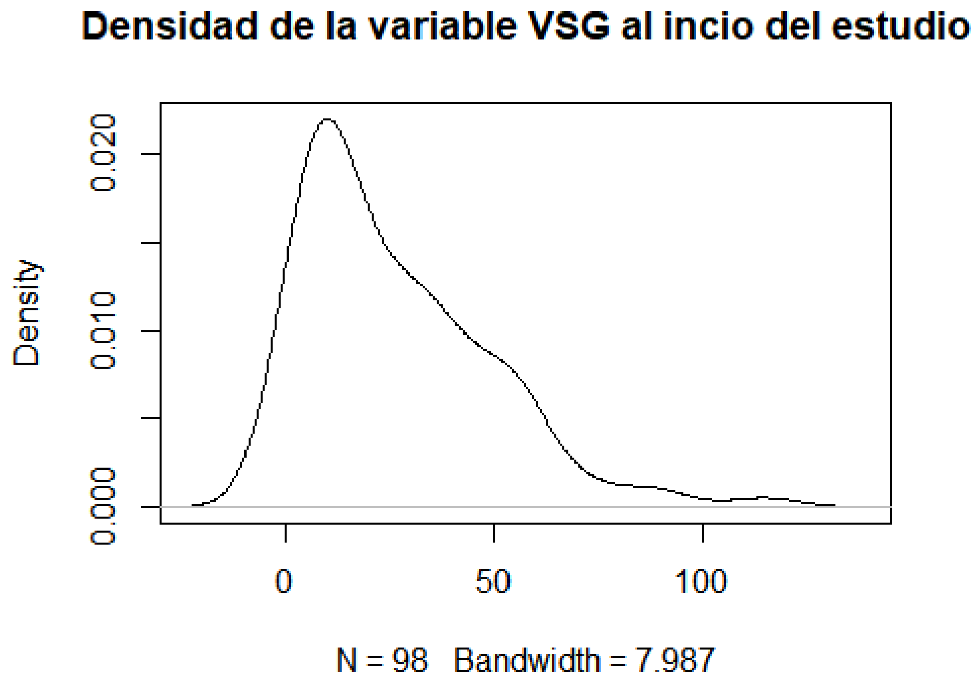
```
plot(density(base_rx$TSINT, na.rm = T), main = "Densidad de la variable tiempo con tto biolÃ³g
ico al incio del estudio")
```



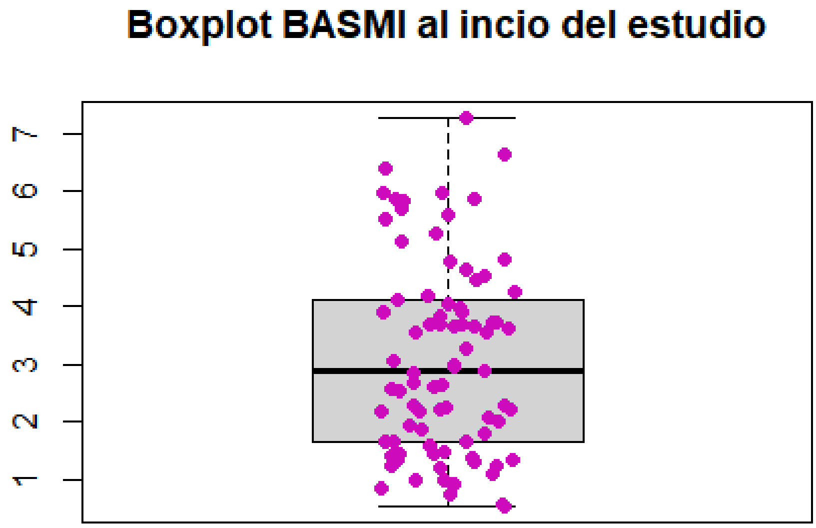
```
boxplot(x=base_rx$VSG, main = "Boxplot VSG al incio del estudio")
stripchart(x=base_rx$VSG, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 5)
```



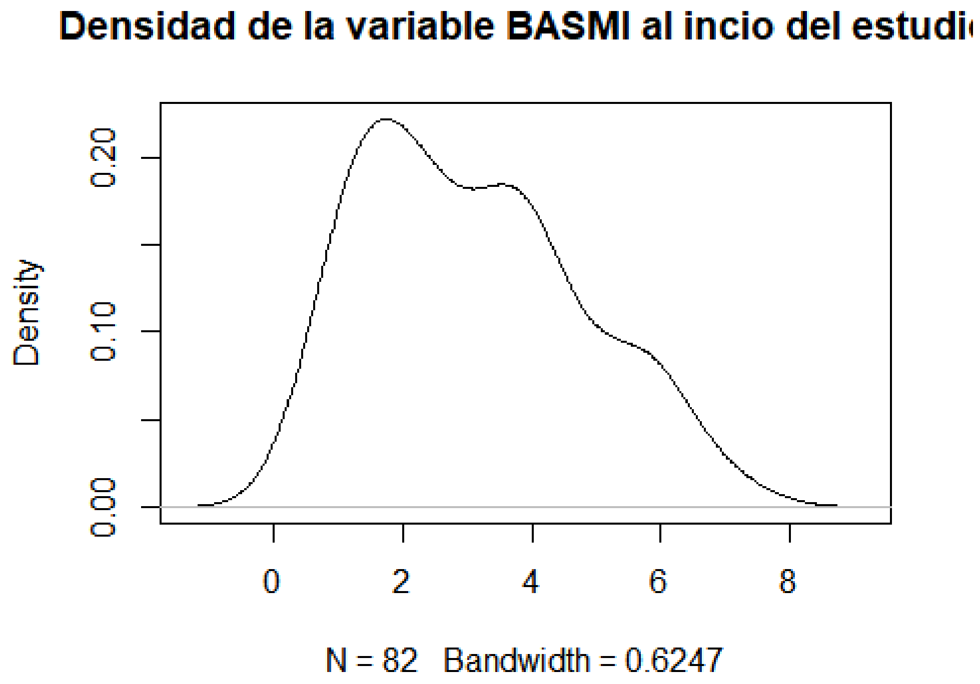
```
plot(density(base_rx$VSG, na.rm = T), main = "Densidad de la variable VSG al incio del estudio
")
```



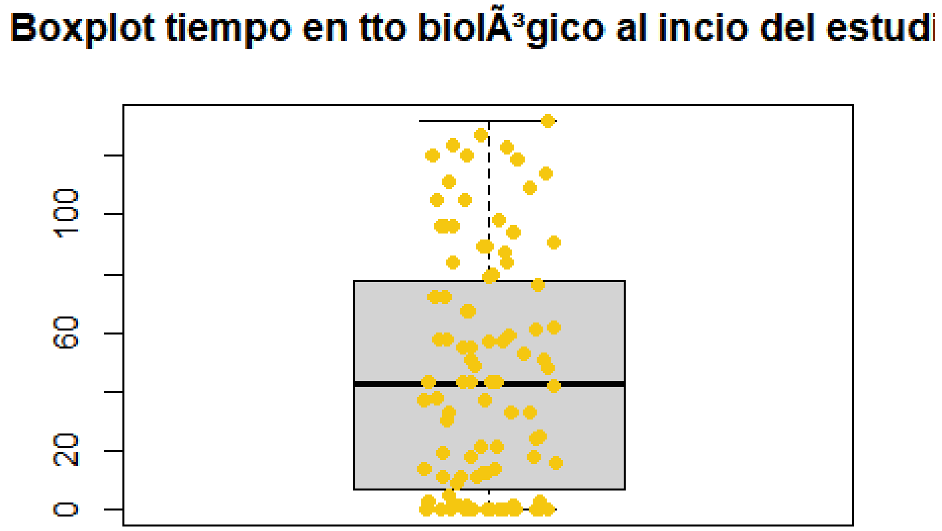
```
boxplot(x=base_rx$BASMI, main = "Boxplot BASMI al incio del estudio")
stripchart(x=base_rx$BASMI, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 6)
```



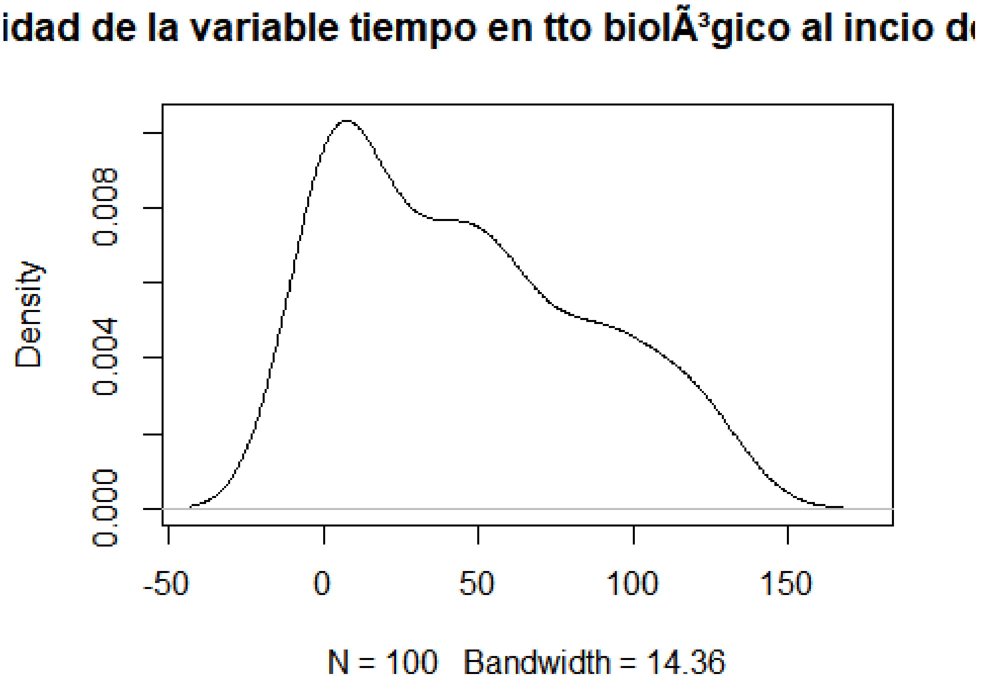
```
plot(density(base_rx$BASMI, na.rm = T), main = "Densidad de la variable BASMI al incio del est
udio")
```



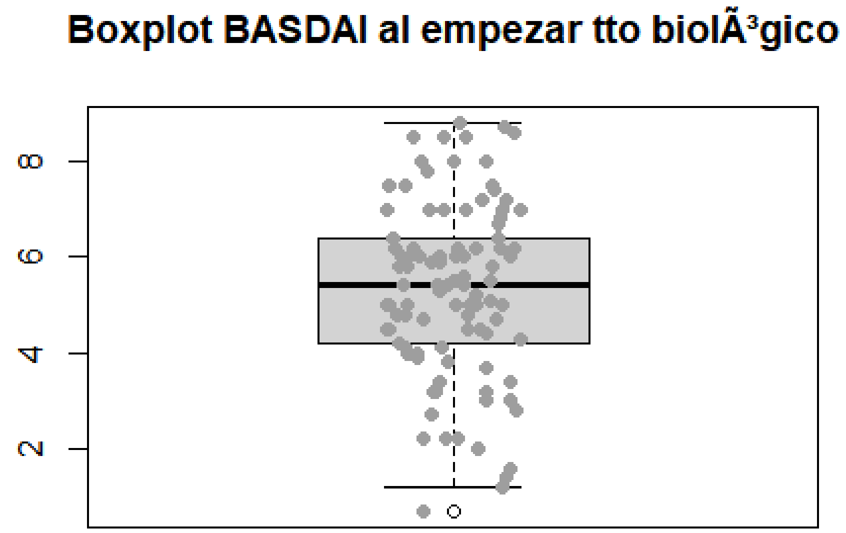
```
boxplot(x=base_rx$TIEMBIO, main = "Boxplot tiempo en tto biolÃ³gico al incio del estudio")
stripchart(x=base_rx$TIEMBIO, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 7)
```



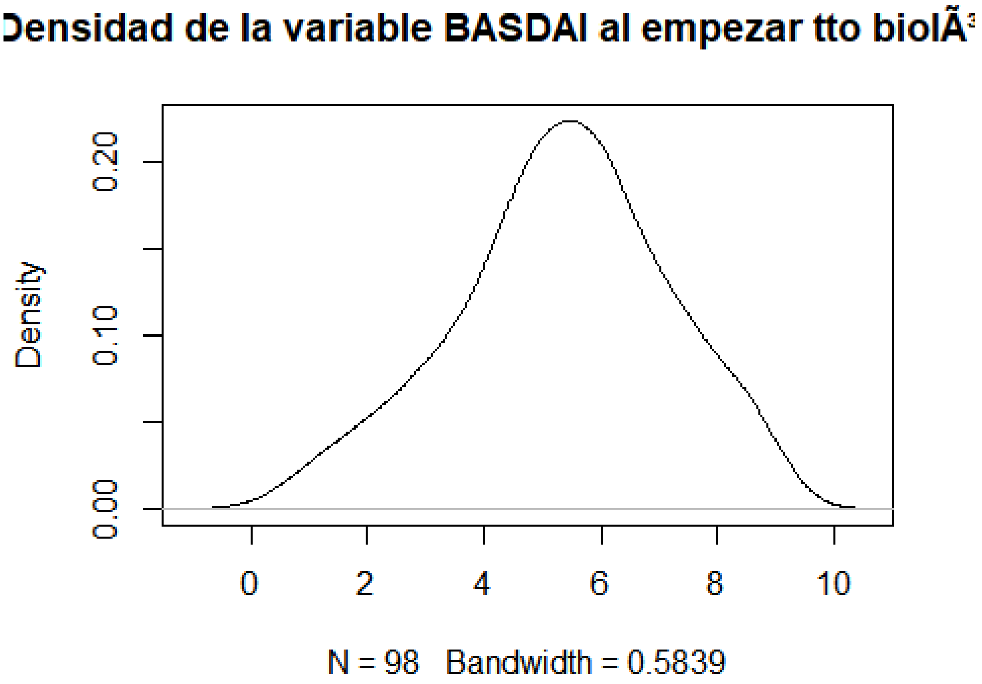
```
plot(density(base_rx$TIEMBIO, na.rm = T), main = "Densidad de la variable tiempo en tto biolÃ³gico al incio del estudio")
```



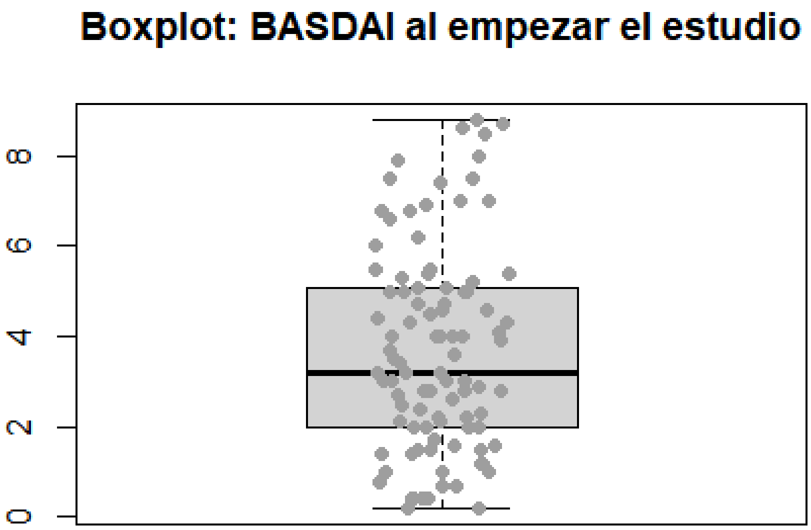
```
boxplot(x=base_rx$i_BASDAI, main = "Boxplot BASDAI al empezar tto biolÃ³gico")
stripchart(x=base_rx$i_BASDAI, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 8)
```



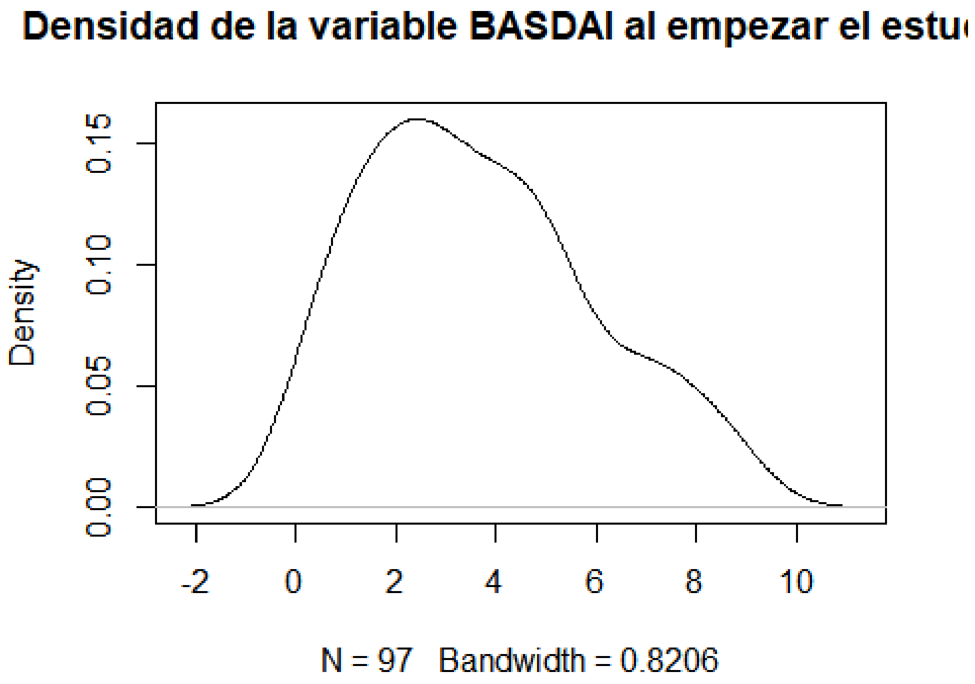
```
plot(density(base_rx$i_BASDAI, na.rm = T), main = "Densidad de la variable BASDAI al empezar
tto biolÃ³gico")
```



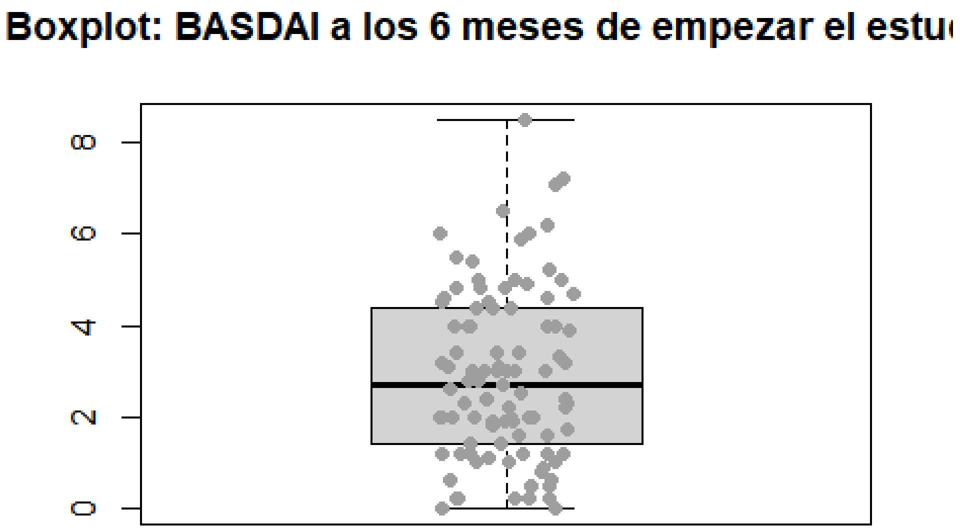
```r
boxplot(x=base_rx$BASDAI_0, main = "Boxplot: BASDAI al empezar el estudio")
stripchart(x=base_rx$BASDAI_0, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 8)
```



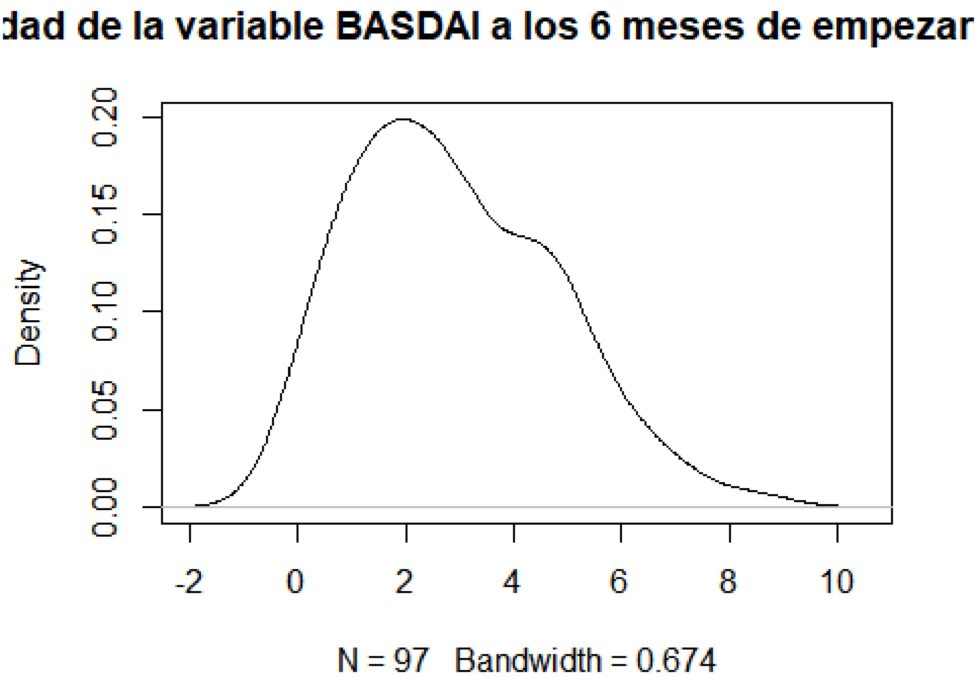
```r
plot(density(base_rx$BASDAI_0, na.rm = T), main = "Densidad de la variable BASDAI al empeza
r el estudio")
```



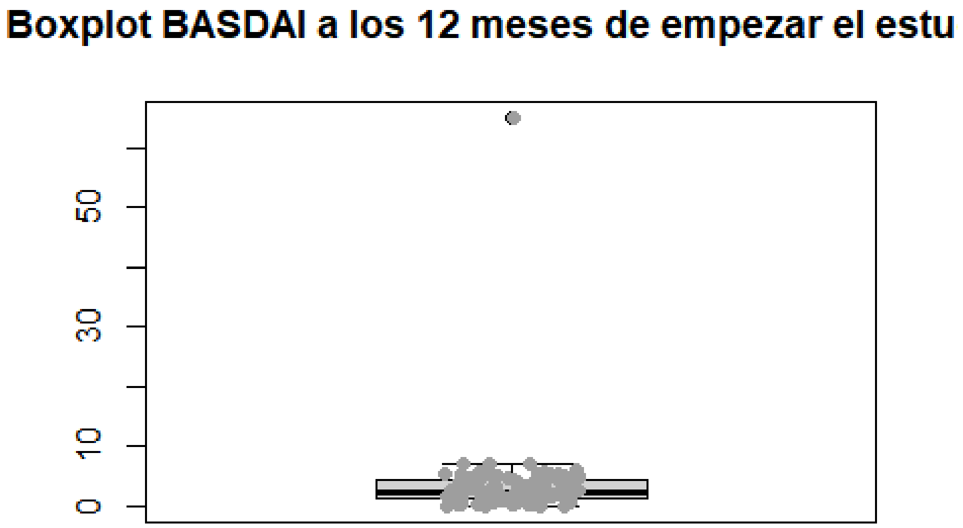
```
boxplot(x=base_rx$BASDAI_1, main = "Boxplot: BASDAI a los 6 meses de empezar el estudio")
stripchart(x=base_rx$BASDAI_1, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 8)
```



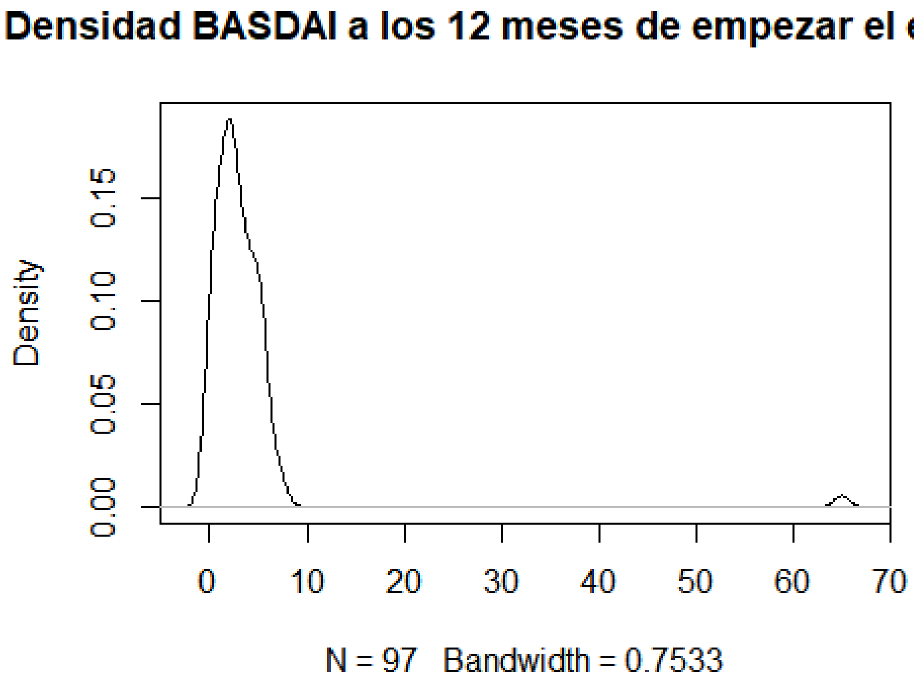
```
plot(density(base_rx$BASDAI_1, na.rm = T), main = "Densidad de la variable BASDAI a los 6 me
ses de empezar el estudio")
```



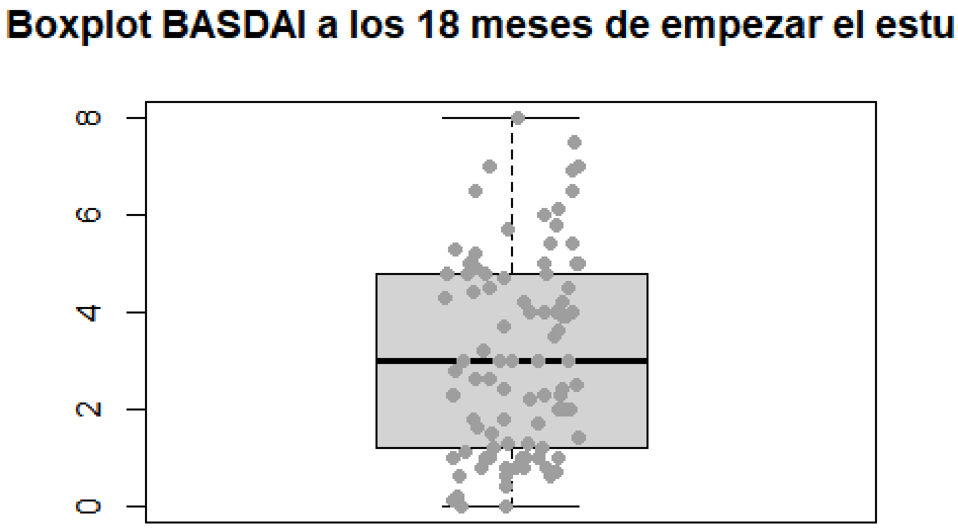
```
boxplot(x=base_rx$BASDAI_2, main = "Boxplot BASDAI a los 12 meses de empezar el estudio")
stripchart(x=base_rx$BASDAI_2, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 8)
```



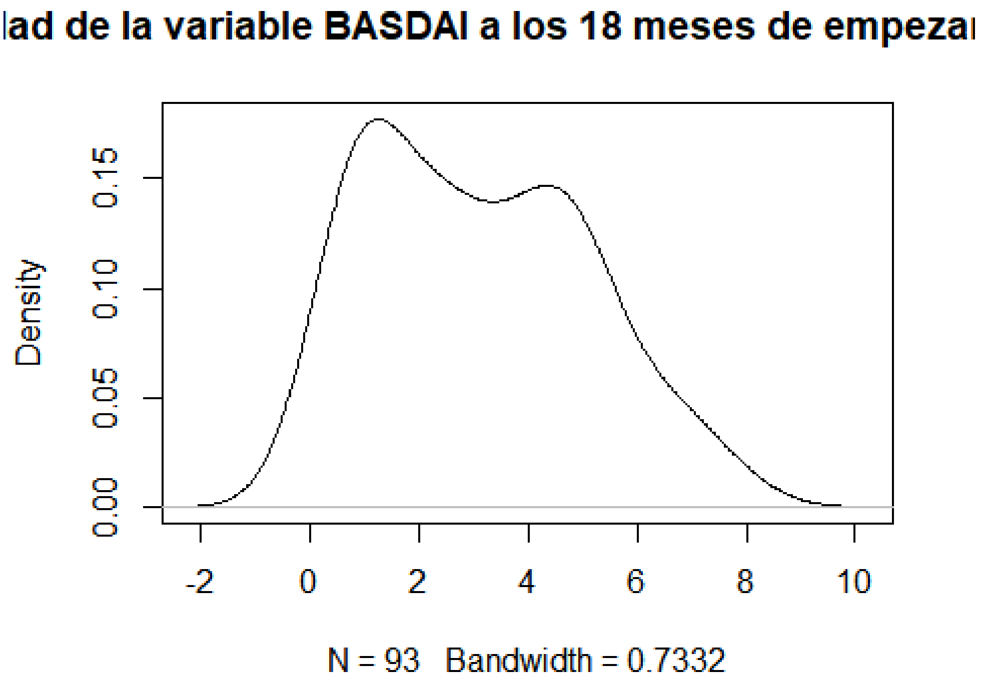
```
plot(density(base_rx$BASDAI_2, na.rm = T), main = "Densidad BASDAI a los 12 meses de empe
zar el estudio")
```



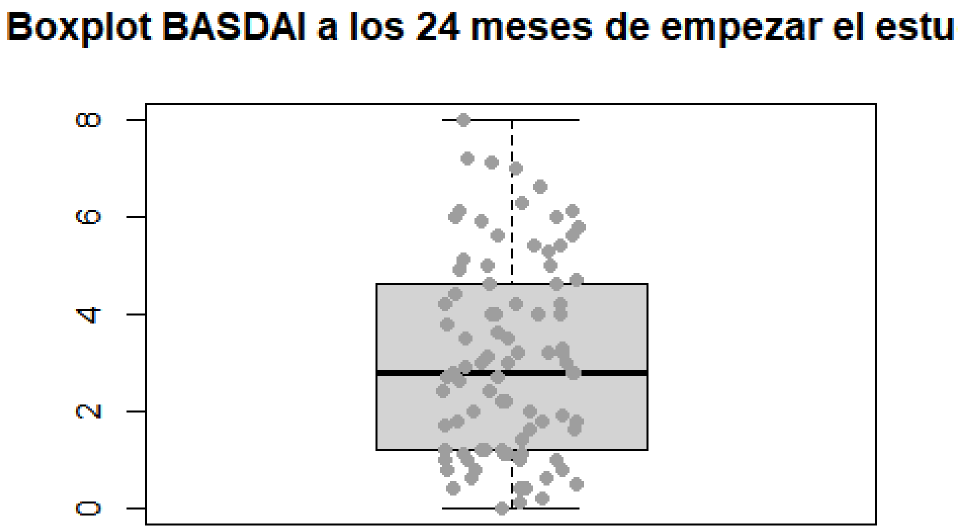
```
boxplot(x=base_rx$BASDAI_3, main = "Boxplot BASDAI a los 18 meses de empezar el estudio")
stripchart(x=base_rx$BASDAI_3, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 8)
```



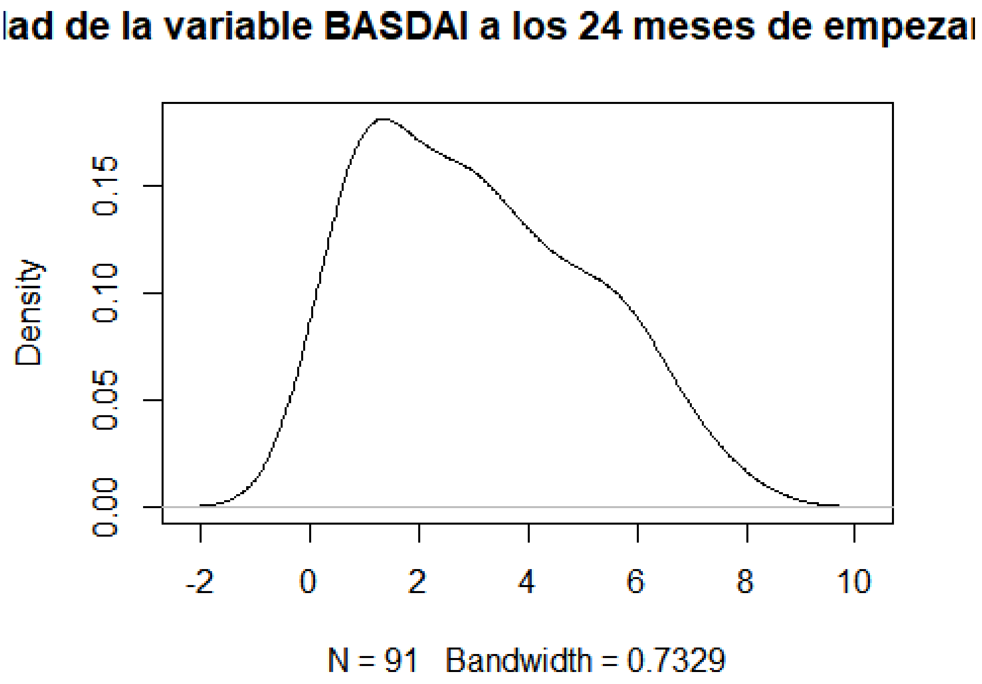
```
plot(density(base_rx$BASDAI_3, na.rm = T), main = "Densidad de la variable BASDAI a los 18 m
eses de empezar el estudio")
```



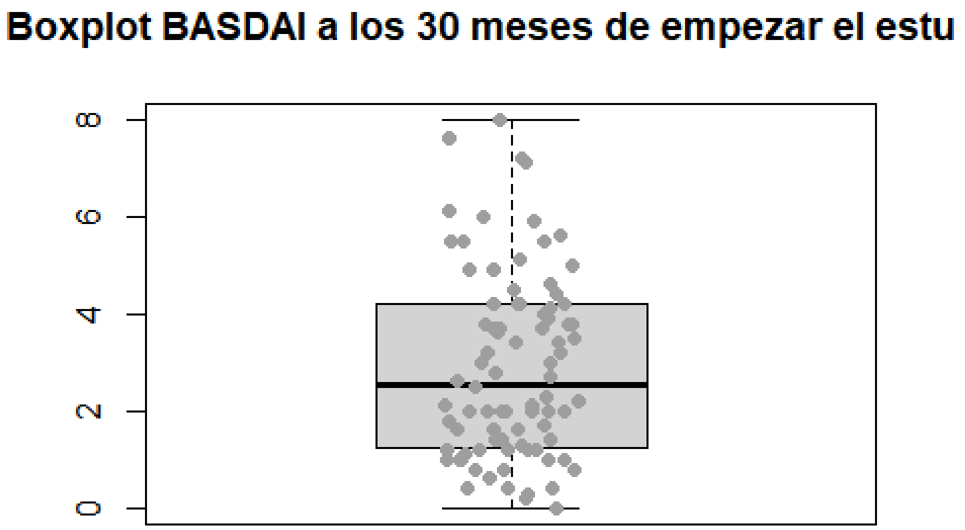
```
boxplot(x=base_rx$BASDAI_4, main = "Boxplot BASDAI a los 24 meses de empezar el estudio")
stripchart(x=base_rx$BASDAI_4, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 8)
```



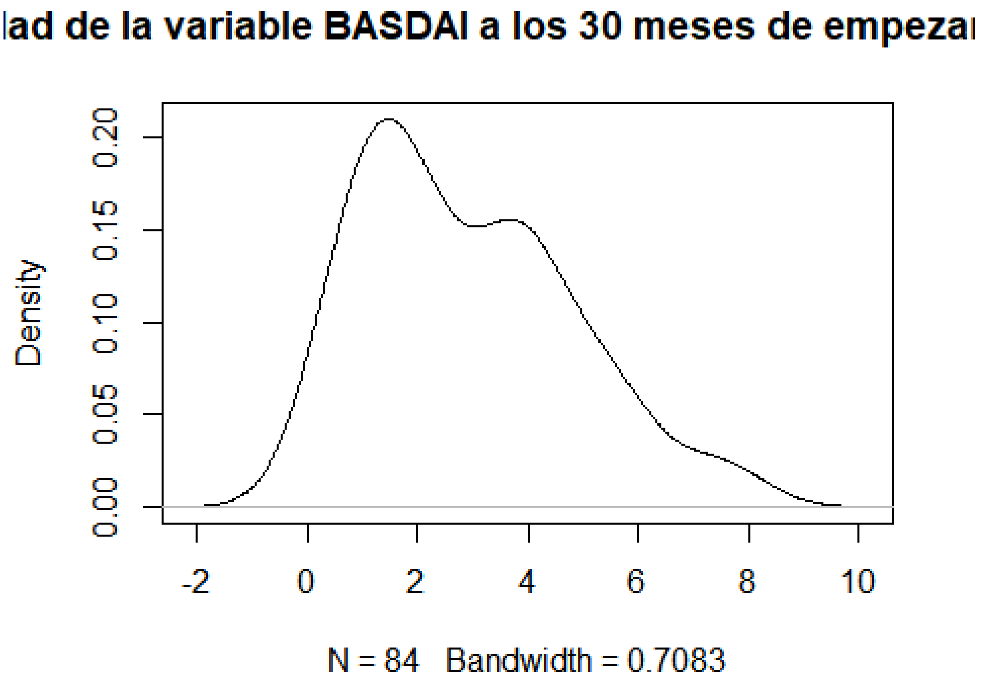
```
plot(density(base_rx$BASDAI_4, na.rm = T), main = "Densidad de la variable BASDAI a los 24 m
eses de empezar el estudio")
```



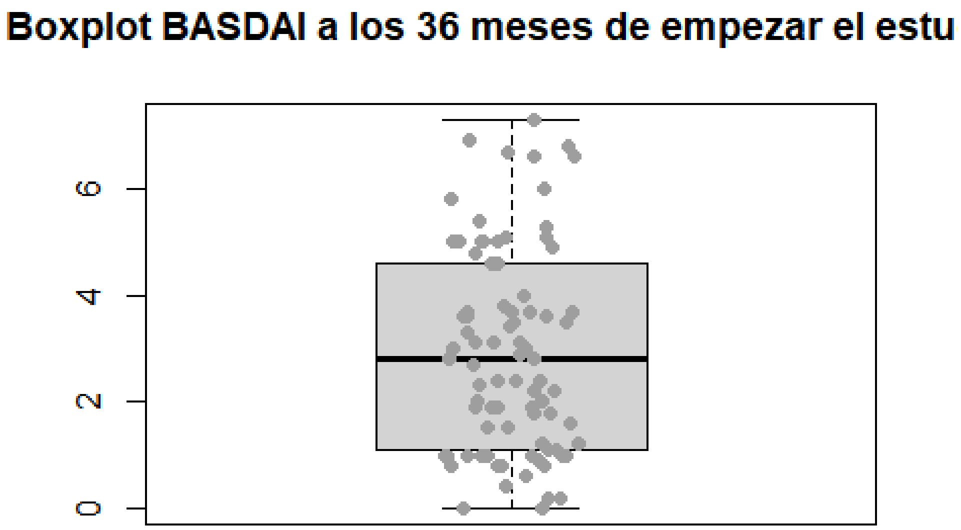
```
boxplot(x=base_rx$BASDAI_5, main = "Boxplot BASDAI a los 30 meses de empezar el estudio")
stripchart(x=base_rx$BASDAI_5, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 8)
```



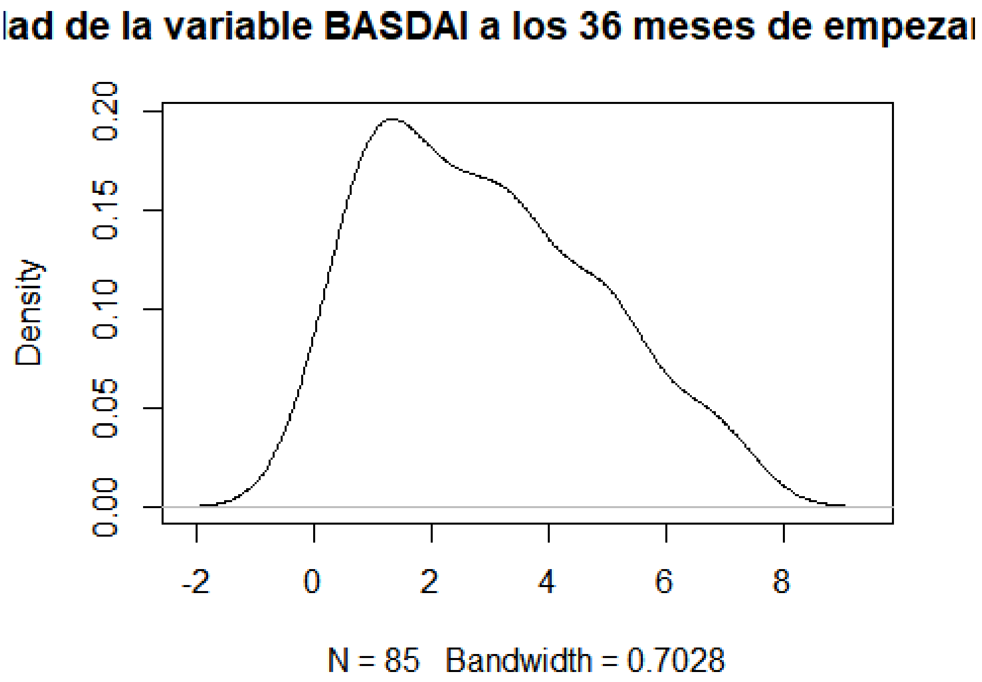
```
plot(density(base_rx$BASDAI_5, na.rm = T), main = "Densidad de la variable BASDAI a los 30 meses de empezar el estudio")
```



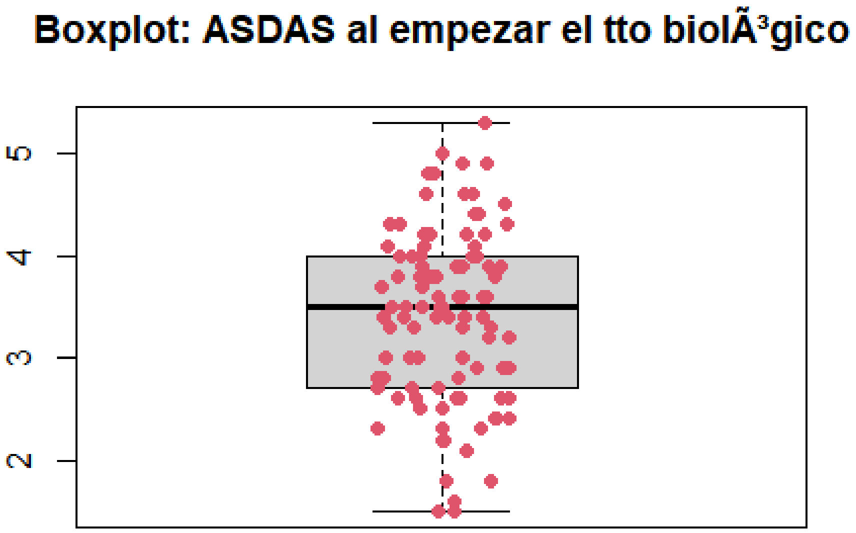
```
boxplot(x=base_rx$BASDAI_6, main = "Boxplot BASDAI a los 36 meses de empezar el estudio")
stripchart(x=base_rx$BASDAI_6, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 8)
```



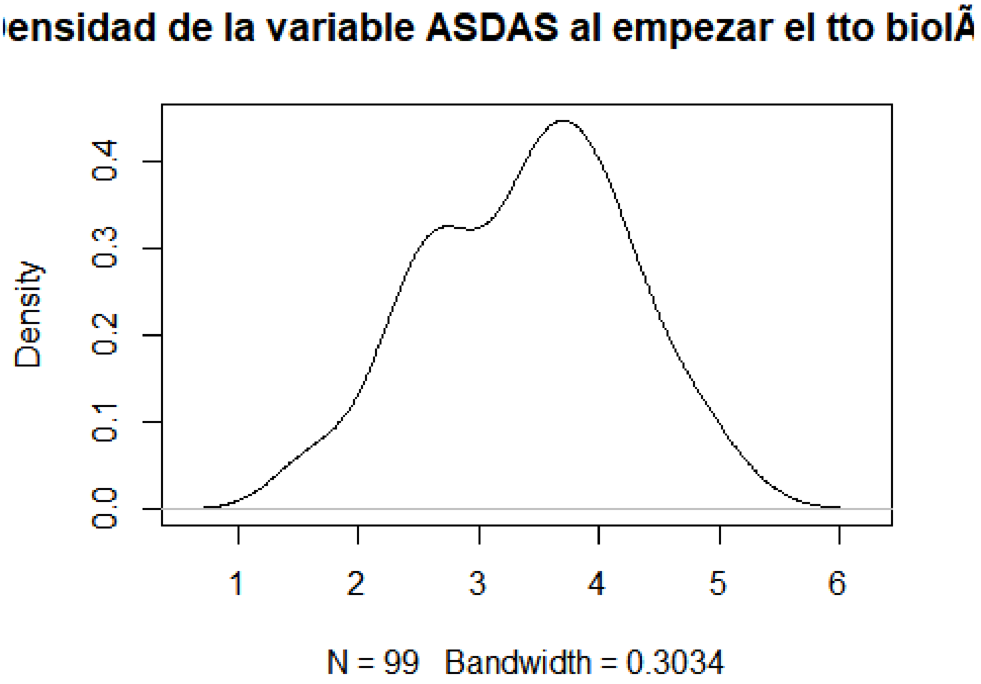
```
plot(density(base_rx$BASDAI_6, na.rm = T), main = "Densidad de la variable BASDAI a los 36 m
eses de empezar el estudio")
```



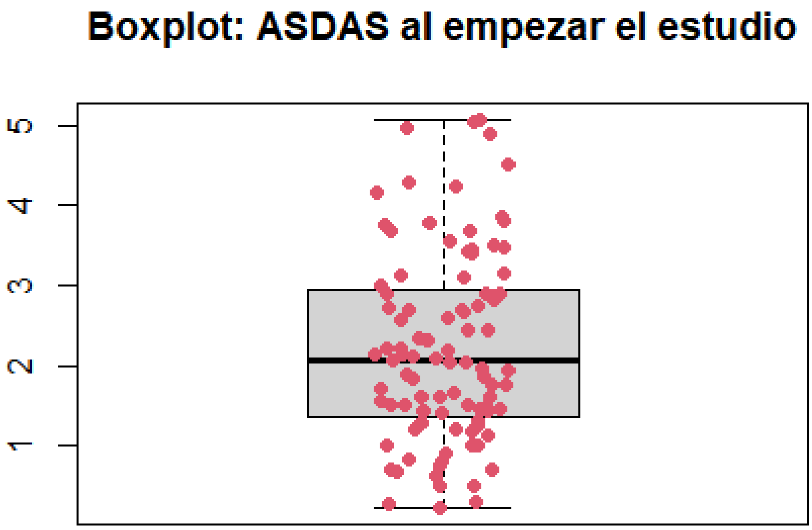
```
boxplot(x=base_rx$i_ASDAS, main = "Boxplot: ASDAS al empezar el tto biolÃ³gico")
stripchart(x=base_rx$i_ASDAS, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 10)
```



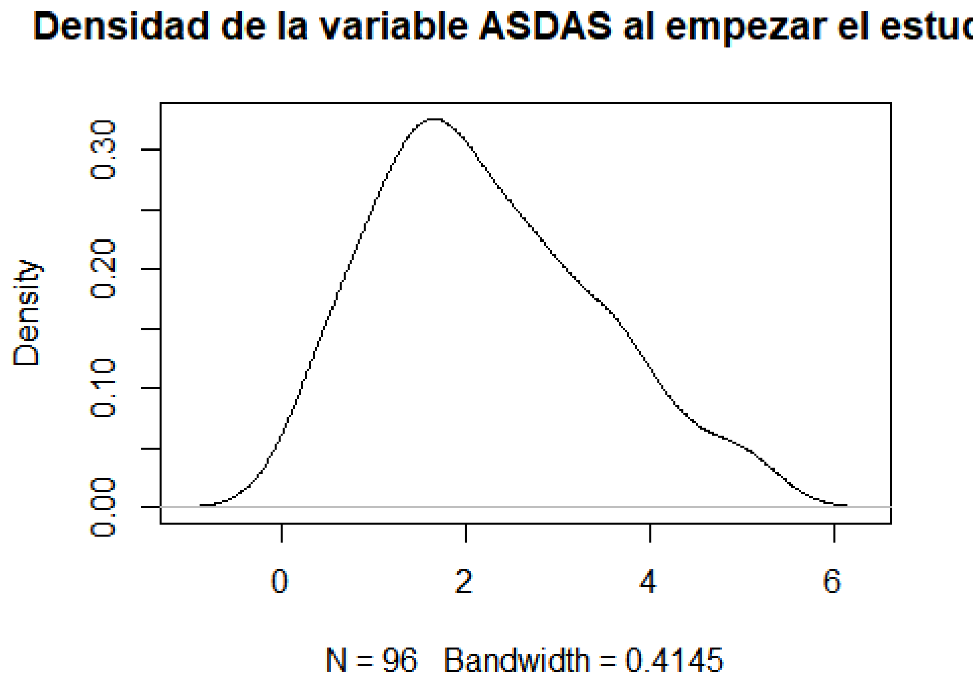
```
plot(density(base_rx$i_ASDAS, na.rm = T), main = "Densidad de la variable ASDAS al empezar
el tto biolÃ³gico")
```



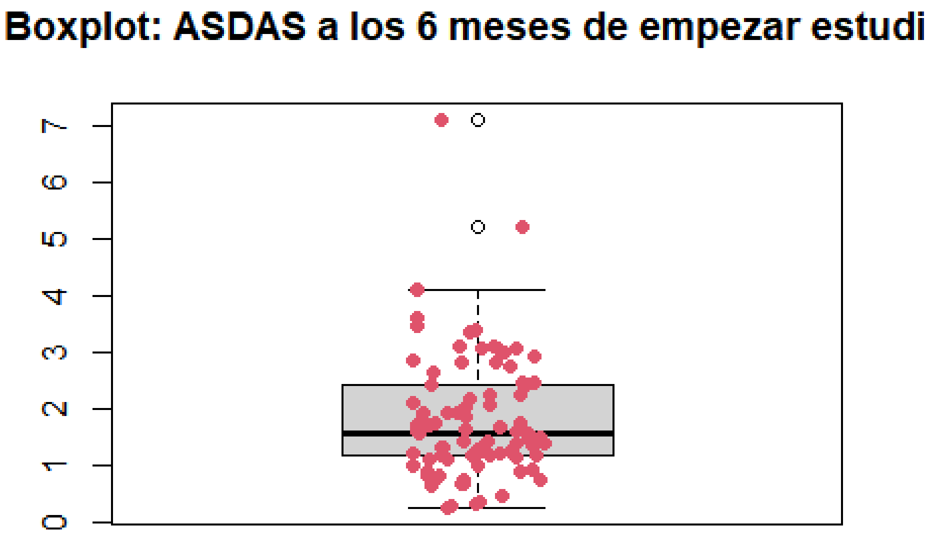
```
boxplot(x=base_rx$ASDAS_0, main = "Boxplot: ASDAS al empezar el estudio")
stripchart(x=base_rx$ASDAS_0, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 10
)
```



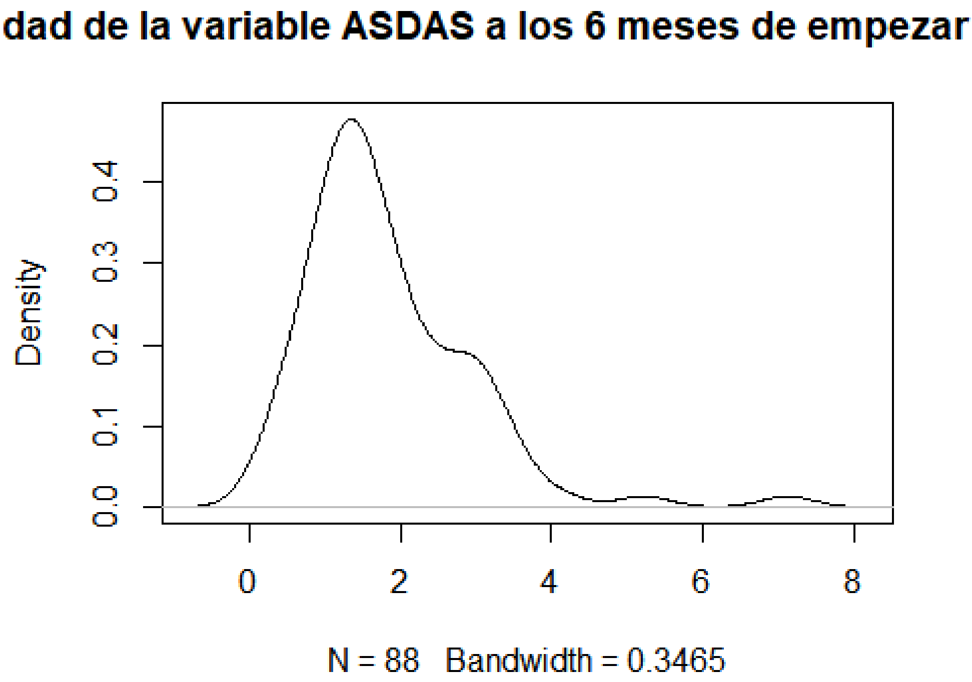
```
plot(density(base_rx$ASDAS_0, na.rm = T), main = "Densidad de la variable ASDAS al empezar
el estudio")
```



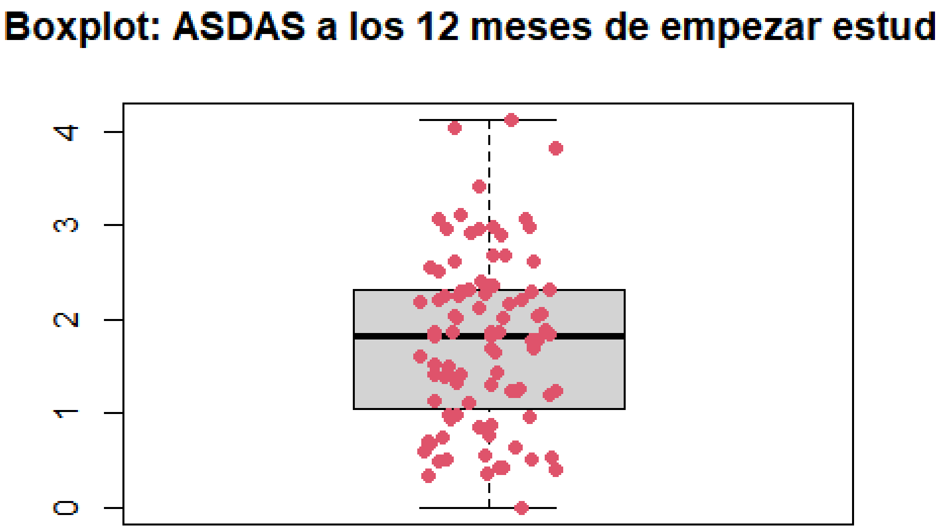
```
boxplot(x=base_rx$ASDAS_1, main = "Boxplot: ASDAS a los 6 meses de empezar estudio")
stripchart(x=base_rx$ASDAS_1, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 10
)
```



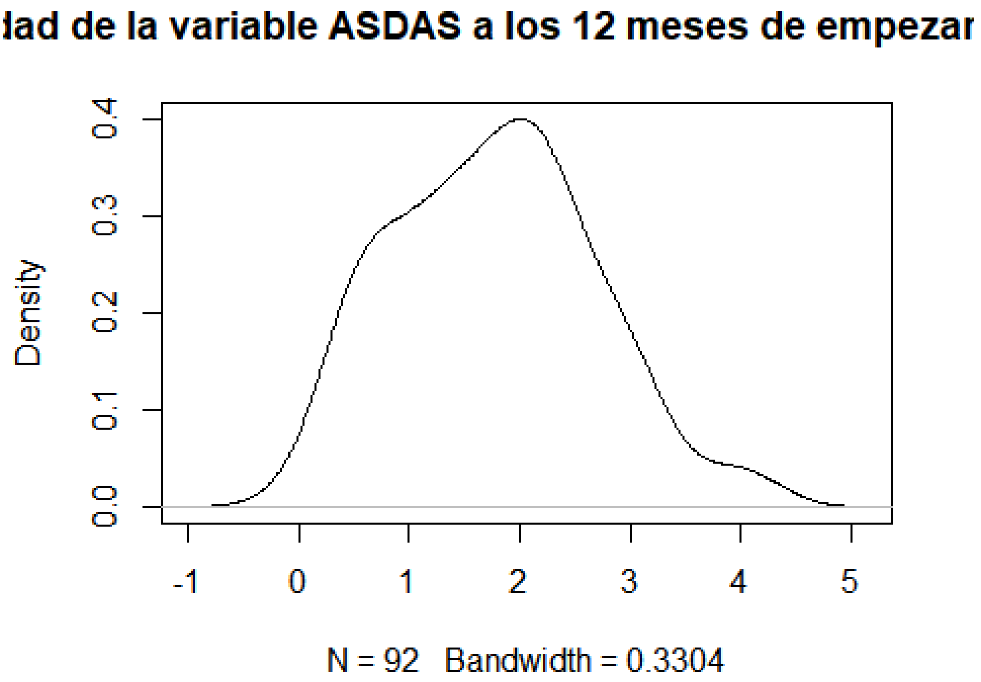
```
plot(density(base_rx$ASDAS_1, na.rm = T), main = "Densidad de la variable ASDAS a los 6 mes
es de empezar el estudio")
```



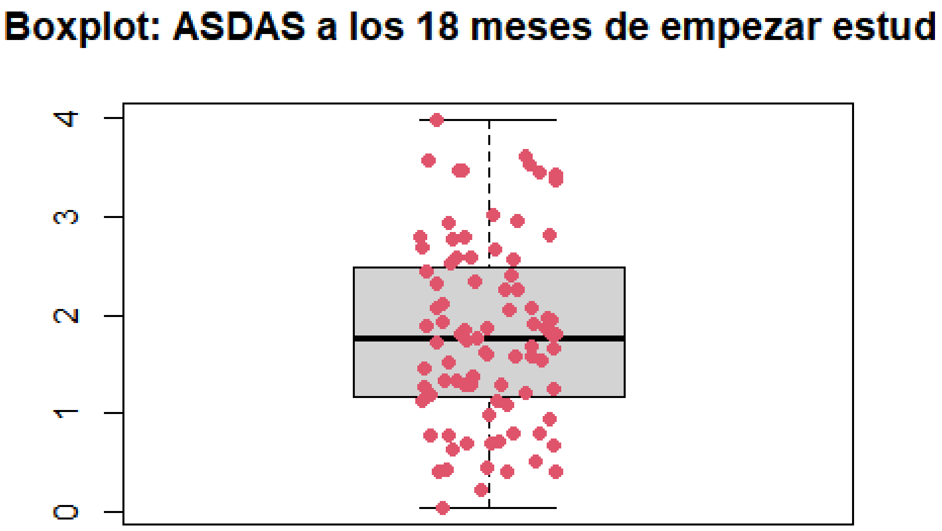
```
boxplot(x=base_rx$ASDAS_2, main = "Boxplot: ASDAS a los 12 meses de empezar estudio")
stripchart(x=base_rx$ASDAS_2, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 10
)
```



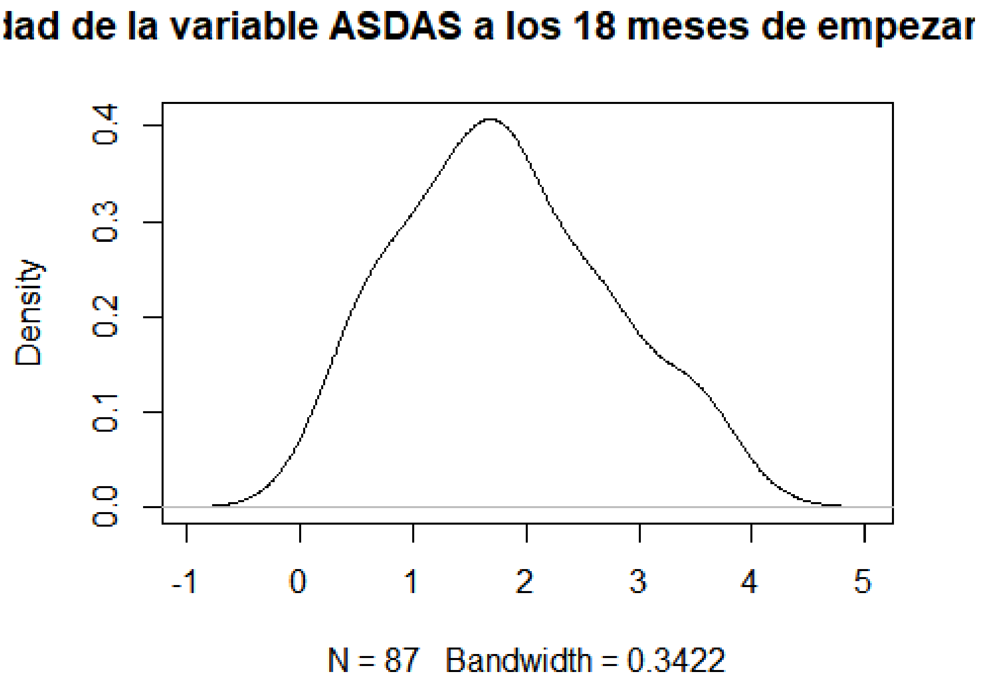
```
plot(density(base_rx$ASDAS_2, na.rm = T), main = "Densidad de la variable ASDAS a los 12 me
ses de empezar el estudio")
```



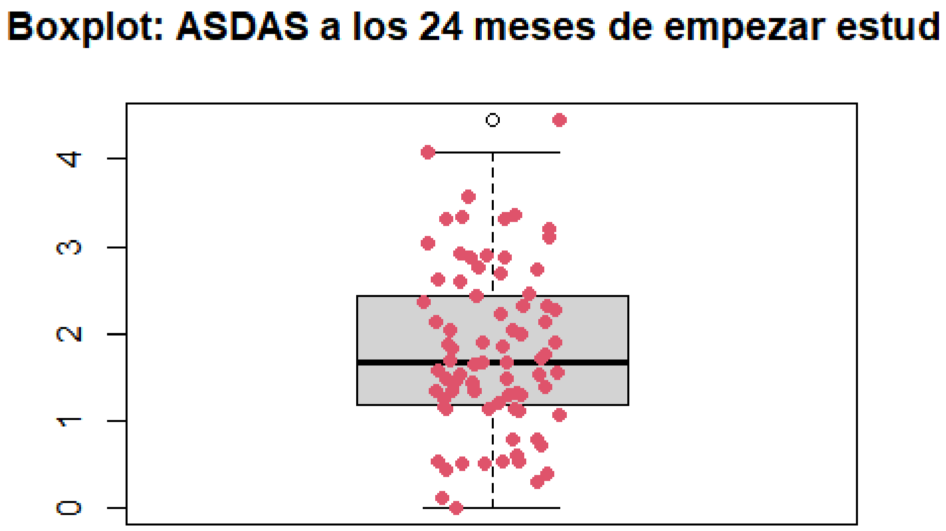
```
boxplot(x=base_rx$ASDAS_3, main = "Boxplot: ASDAS a los 18 meses de empezar estudio")
stripchart(x=base_rx$ASDAS_3, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 10
)
```



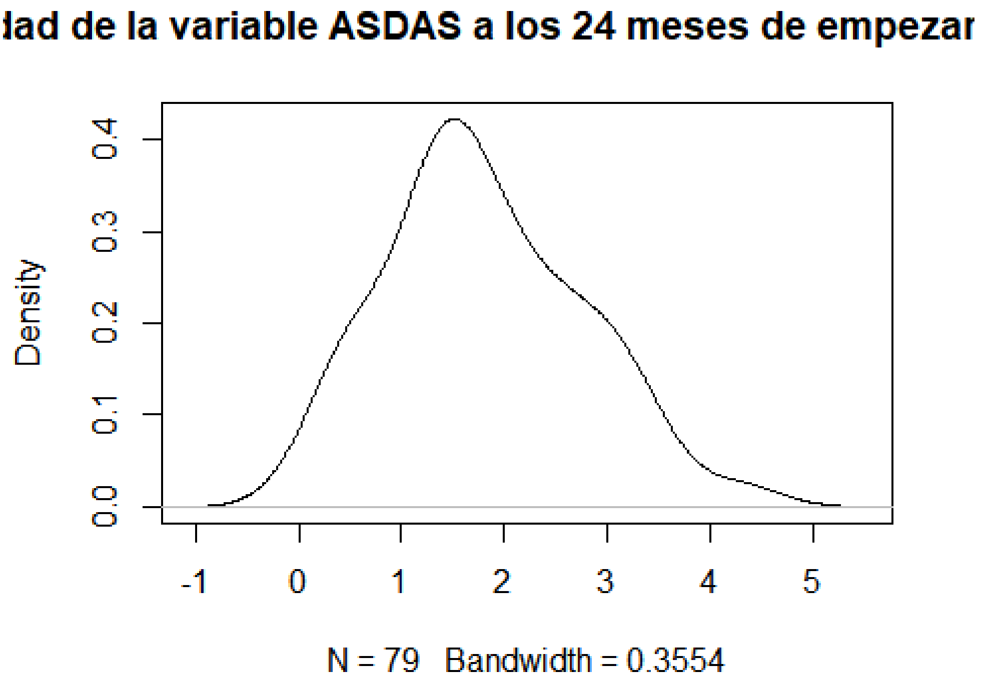
```
plot(density(base_rx$ASDAS_3, na.rm = T), main = "Densidad de la variable ASDAS a los 18 me
ses de empezar el estudio")
```



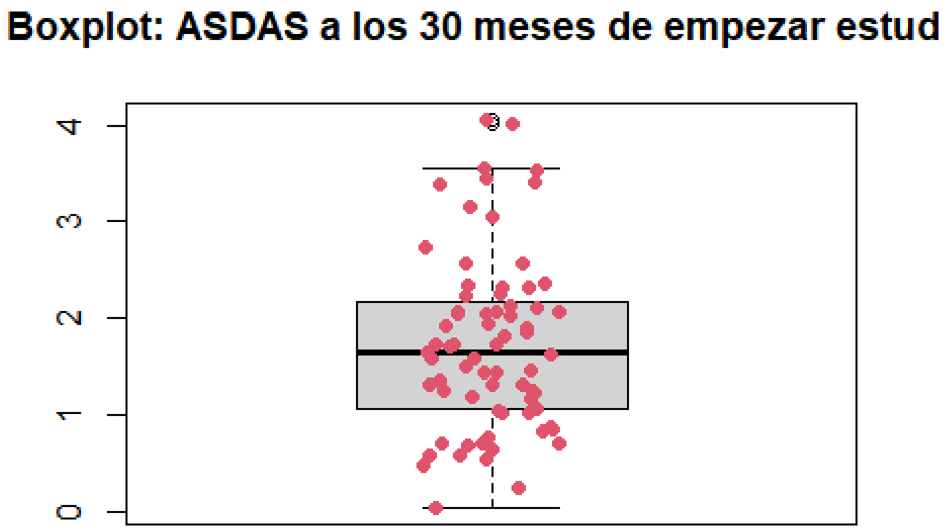
```
boxplot(x=base_rx$ASDAS_4, main = "Boxplot: ASDAS a los 24 meses de empezar estudio")
stripchart(x=base_rx$ASDAS_4, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 10
)
```



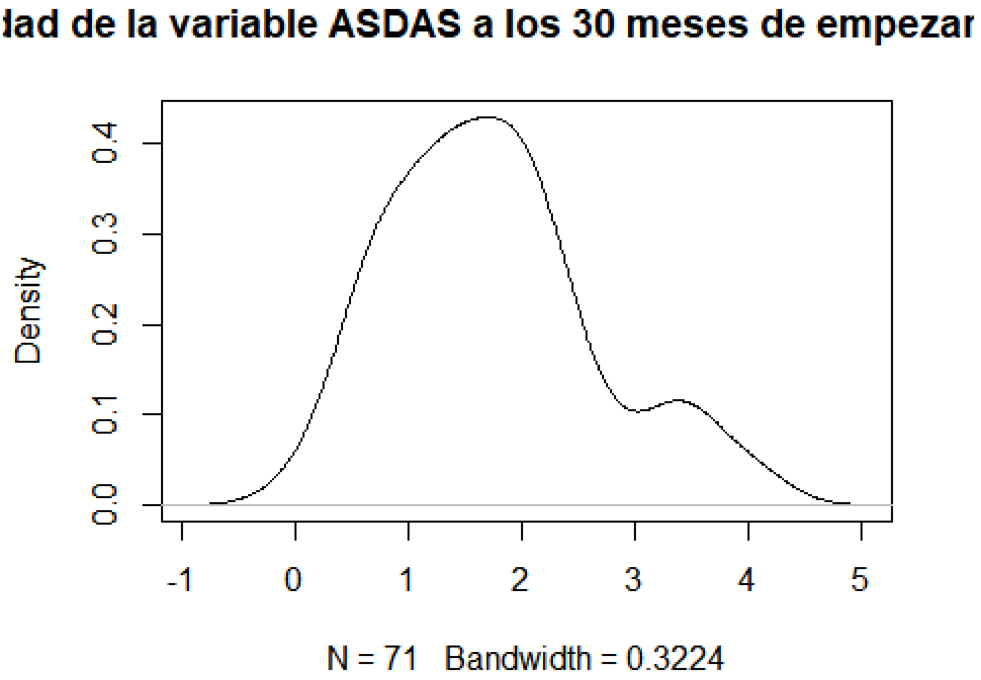
```
plot(density(base_rx$ASDAS_4, na.rm = T), main = "Densidad de la variable ASDAS a los 24 me
ses de empezar el estudio")
```



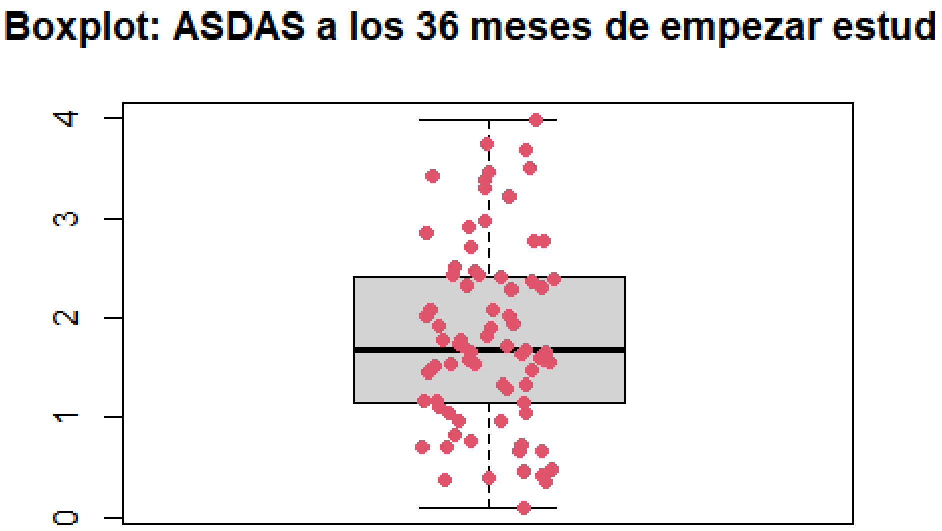
```
boxplot(x=base_rx$ASDAS_5, main = "Boxplot: ASDAS a los 30 meses de empezar estudio")
stripchart(x=base_rx$ASDAS_5, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 10
)
```



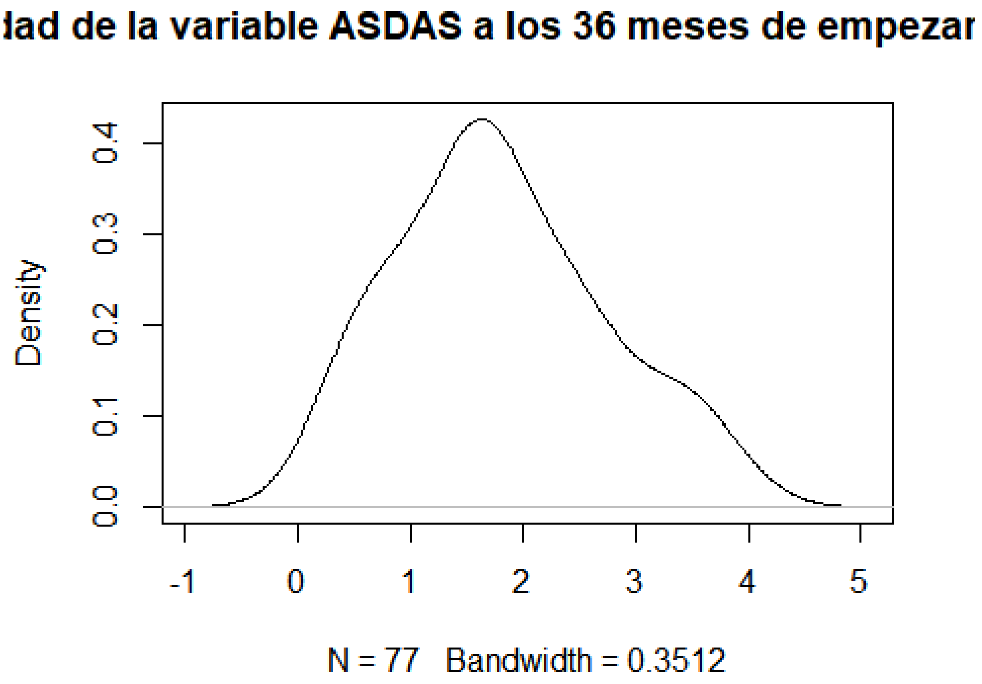
```
plot(density(base_rx$ASDAS_5, na.rm = T), main = "Densidad de la variable ASDAS a los 30 me
ses de empezar el estudio")
```



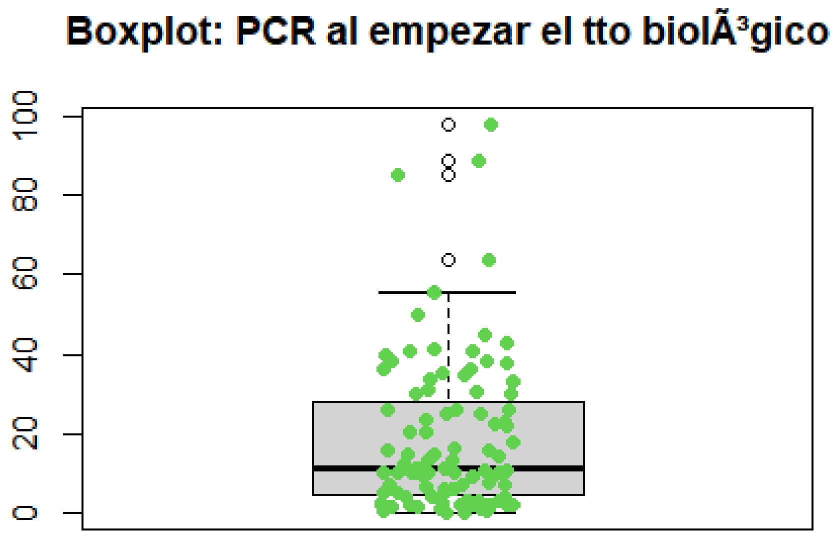
```
boxplot(x=base_rx$ASDAS_6, main = "Boxplot: ASDAS a los 36 meses de empezar estudio")
stripchart(x=base_rx$ASDAS_6, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 10
)
```



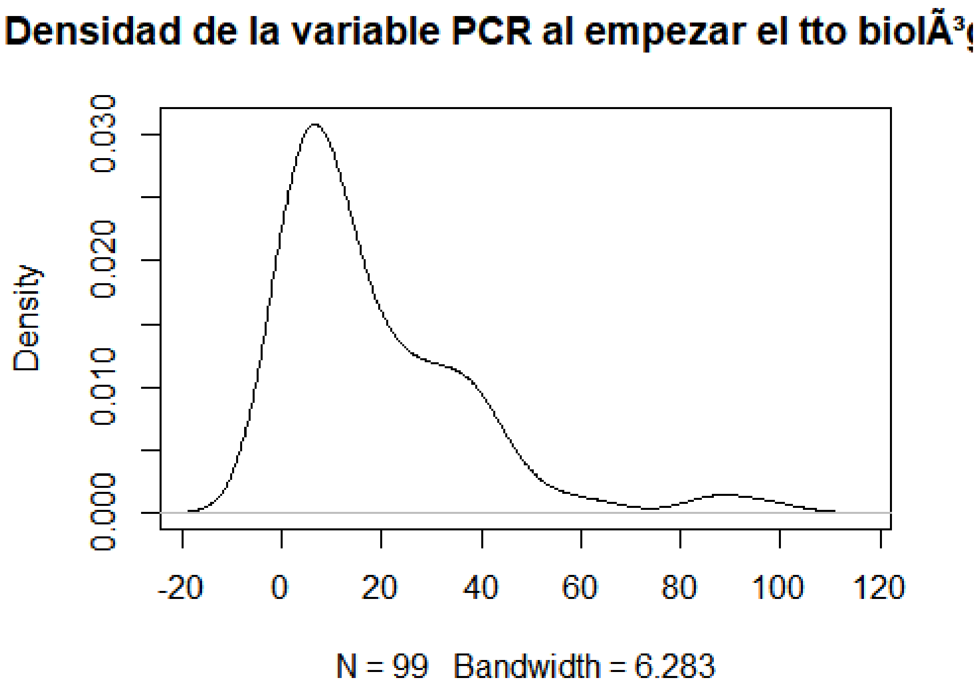
```
plot(density(base_rx$ASDAS_6, na.rm = T), main = "Densidad de la variable ASDAS a los 36 me
ses de empezar el estudio")
```



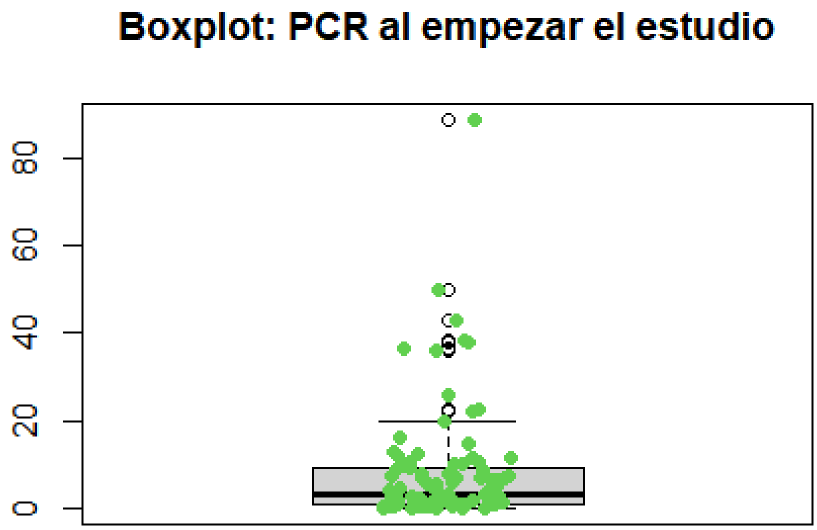
```
boxplot(x=base_rx$PCR_INICIOB, main = "Boxplot: PCR al empezar el tto biolÃ³gico")
stripchart(x=base_rx$PCR_INICIOB, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col
= 11)
```



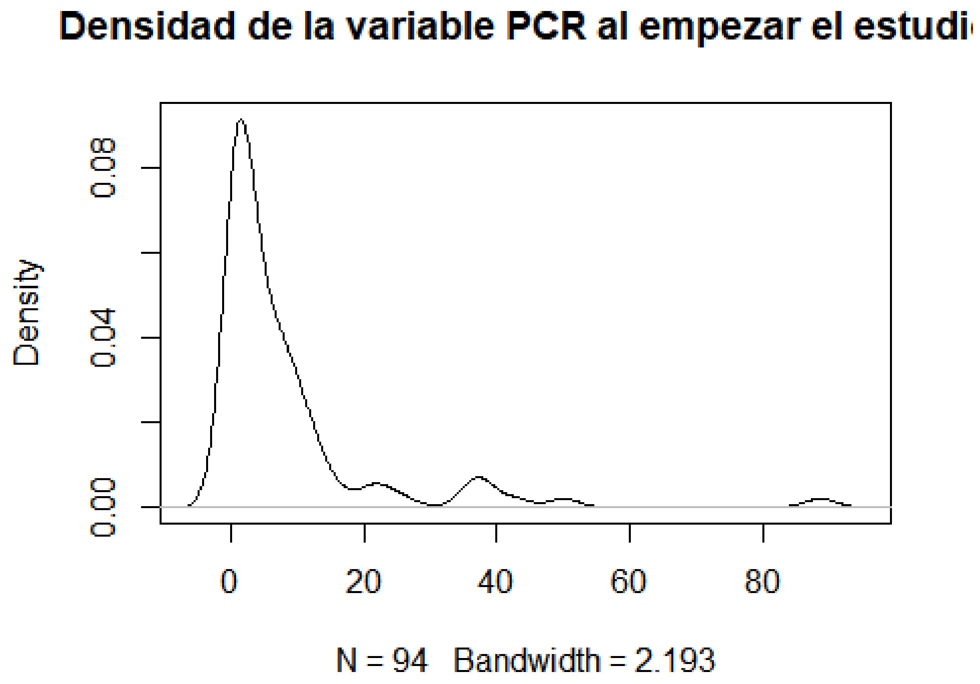
```
plot(density(base_rx$PCR_INICIOB, na.rm = T), main = "Densidad de la variable PCR al empeza
r el tto biolÃ³gico")
```



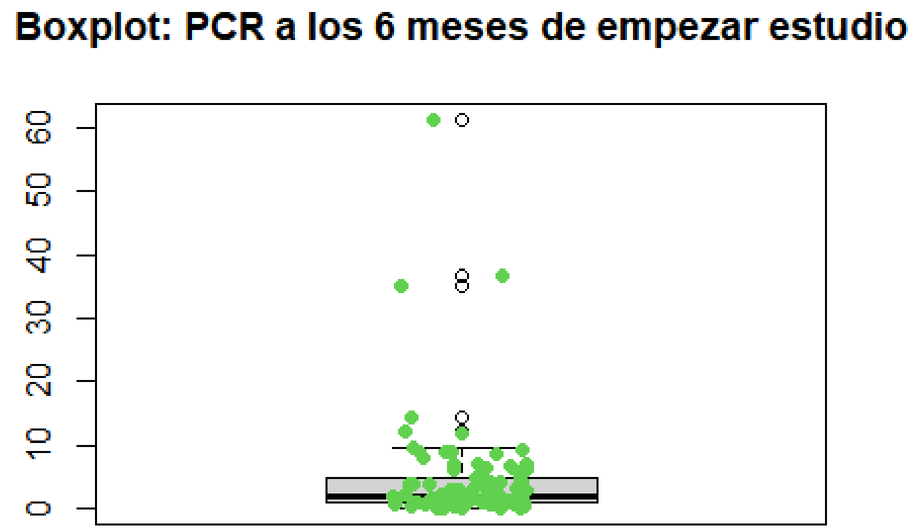
```
boxplot(x=base_rx$PCR_0, main = "Boxplot: PCR al empezar el estudio")
stripchart(x=base_rx$PCR_0, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 11)
```



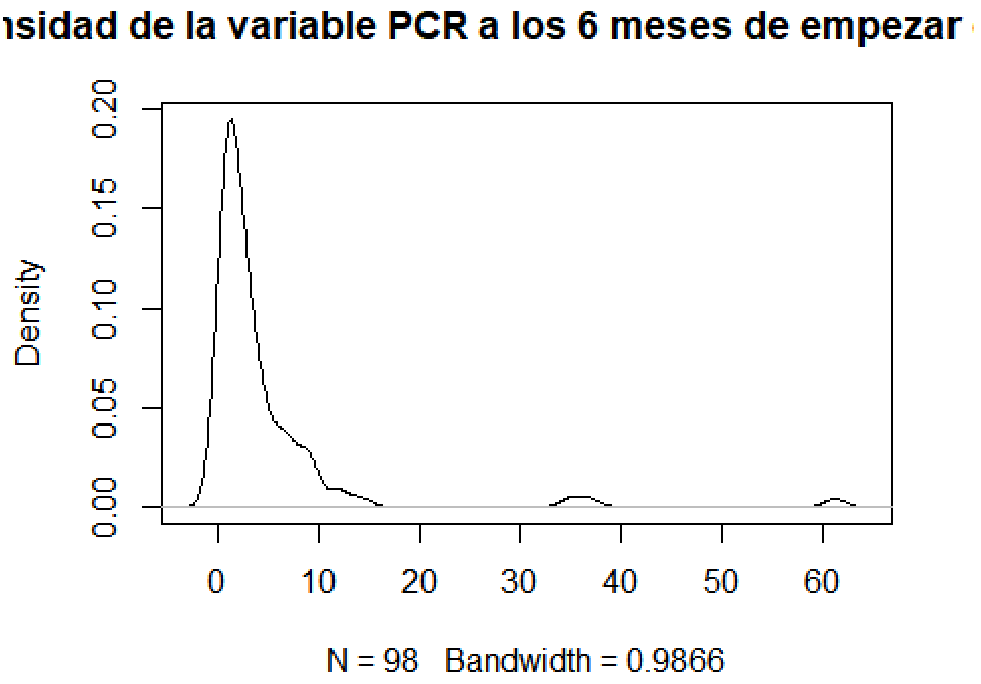
```
plot(density(base_rx$PCR_0, na.rm = T), main = "Densidad de la variable PCR al empezar el est
udio")
```



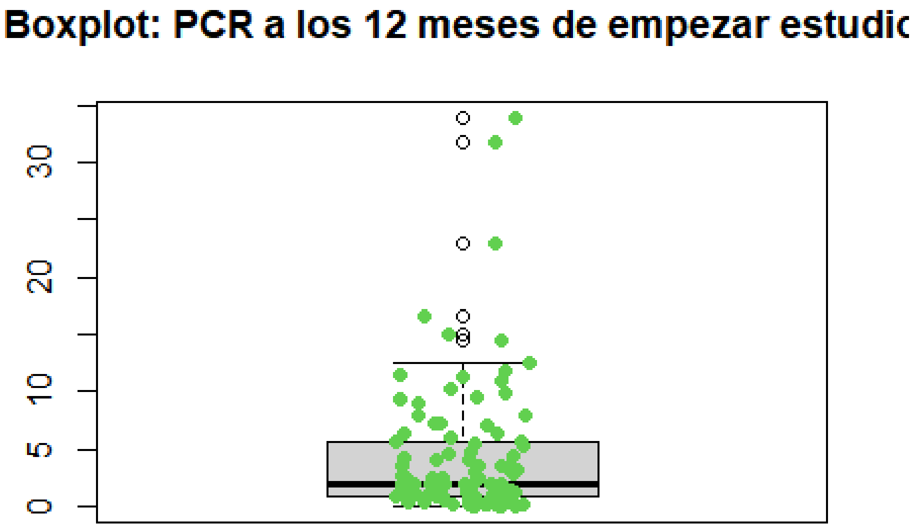
```
boxplot(x=base_rx$PCR_1, main = "Boxplot: PCR a los 6 meses de empezar estudio")
stripchart(x=base_rx$PCR_1, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 11)
```



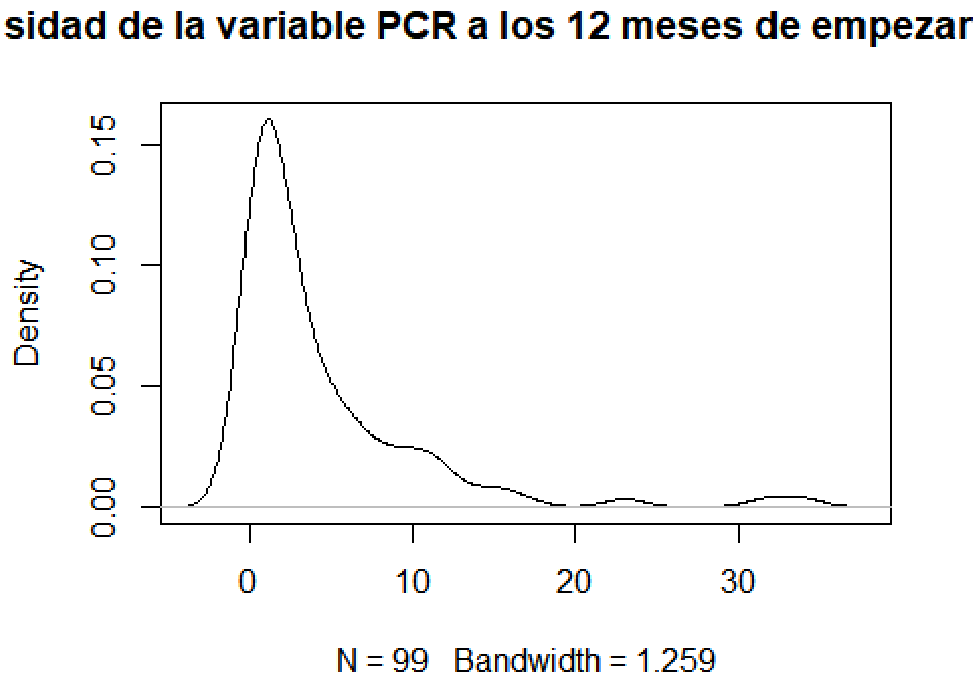
```
plot(density(base_rx$PCR_1, na.rm = T), main = "Densidad de la variable PCR a los 6 meses de
empezar estudio")
```



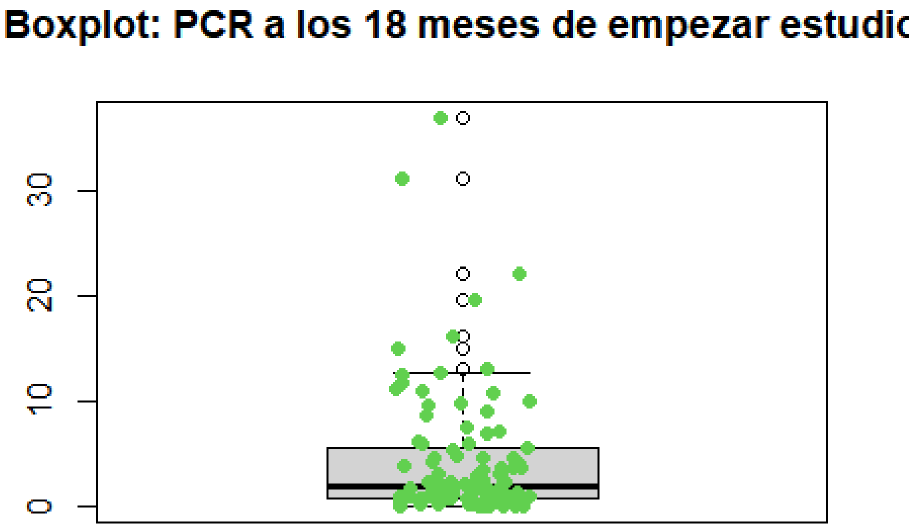
```
boxplot(x=base_rx$PCR_2, main = "Boxplot: PCR a los 12 meses de empezar estudio")
stripchart(x=base_rx$PCR_2, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 11)
```



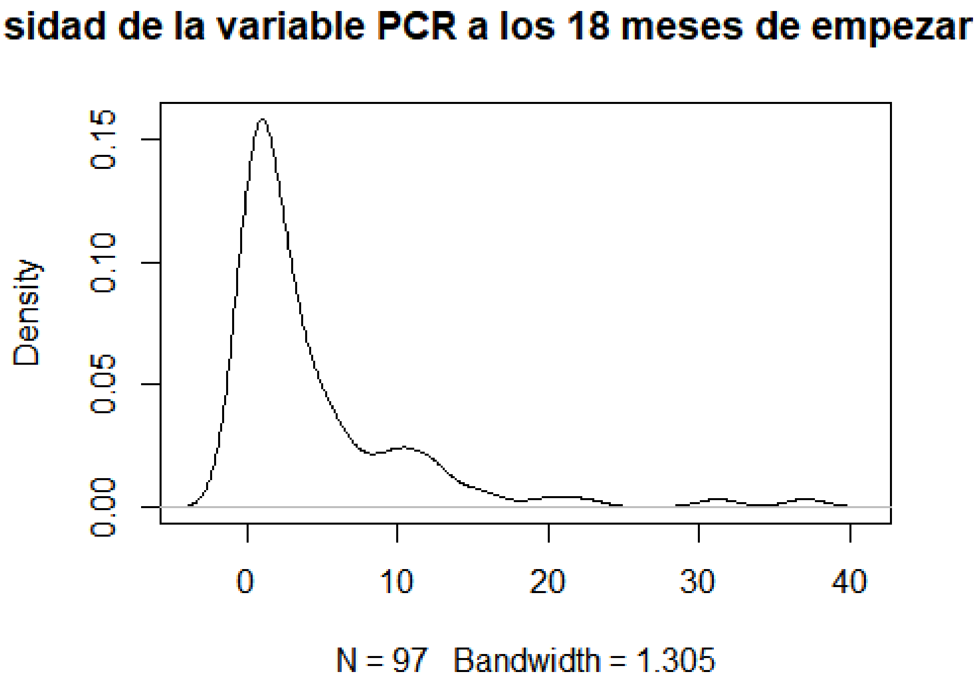
```
plot(density(base_rx$PCR_2, na.rm = T), main = "Densidad de la variable PCR a los 12 meses d
e empezar estudio")
```



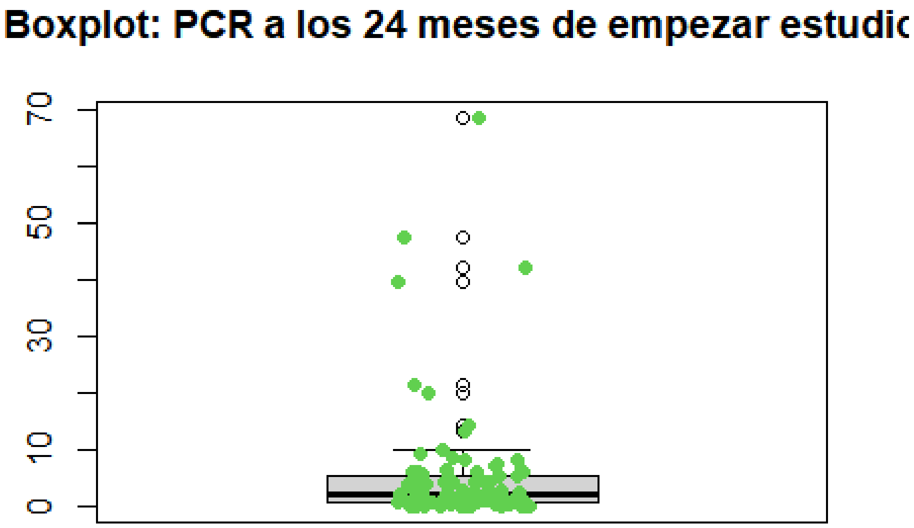
```
boxplot(x=base_rx$PCR_3, main = "Boxplot: PCR a los 18 meses de empezar estudio")
stripchart(x=base_rx$PCR_3, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 11)
```



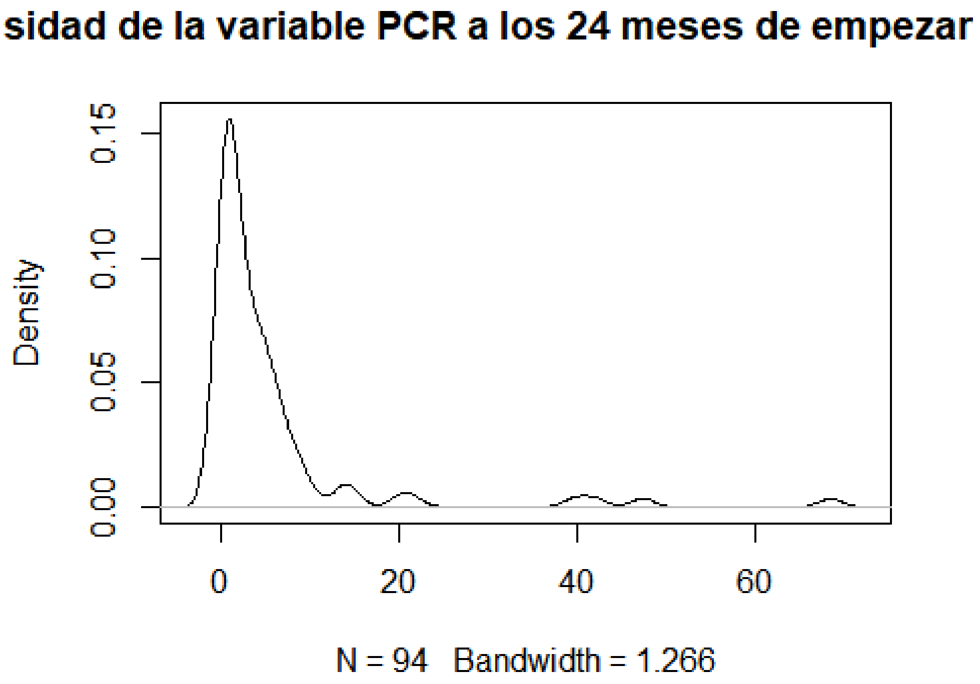
```
plot(density(base_rx$PCR_3, na.rm = T), main = "Densidad de la variable PCR a los 18 meses d
e empezar estudio")
```



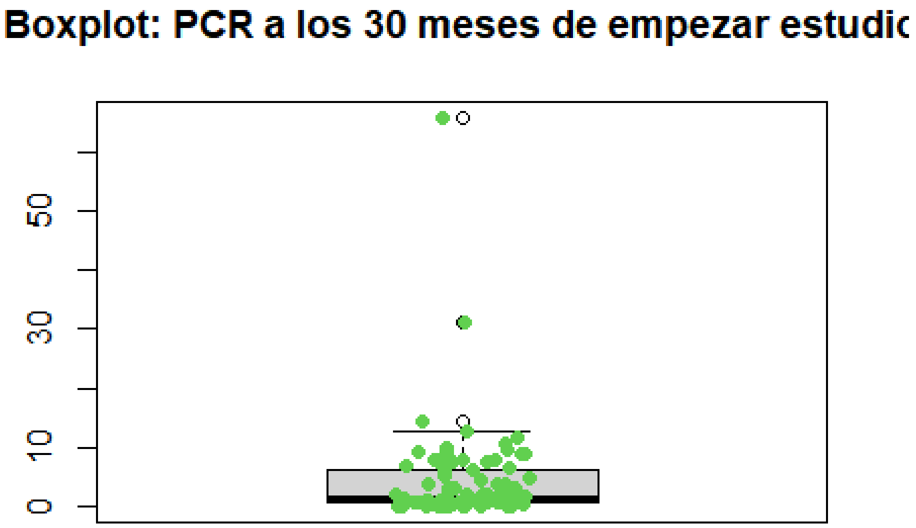
```r
boxplot(x=base_rx$PCR_4, main = "Boxplot: PCR a los 24 meses de empezar estudio")
stripchart(x=base_rx$PCR_4, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 11)
```



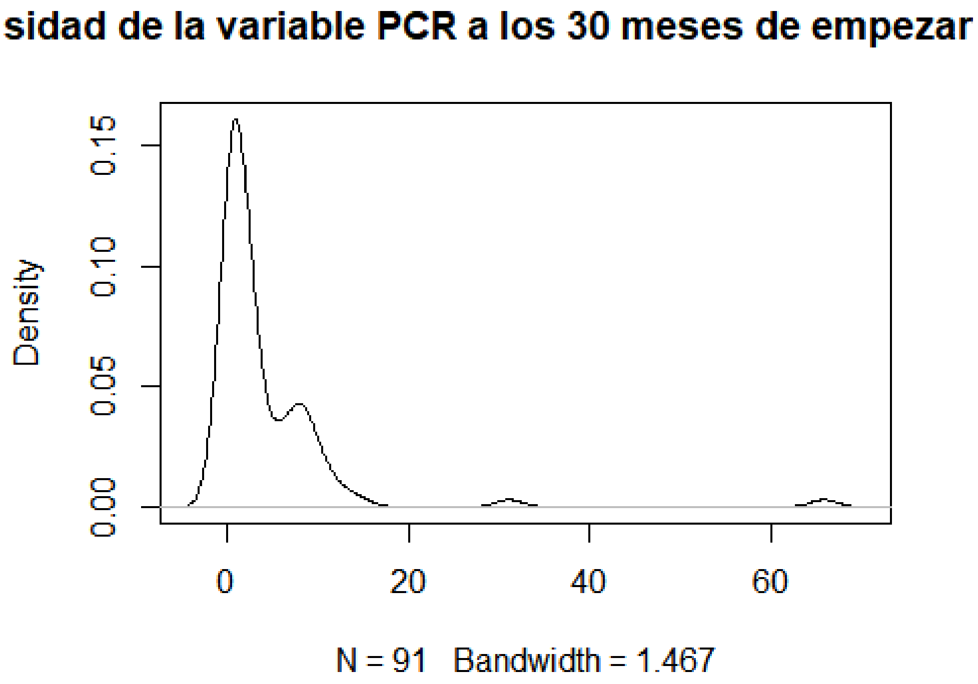
```r
plot(density(base_rx$PCR_4, na.rm = T), main = "Densidad de la variable PCR a los 24 meses d
e empezar estudio")
```



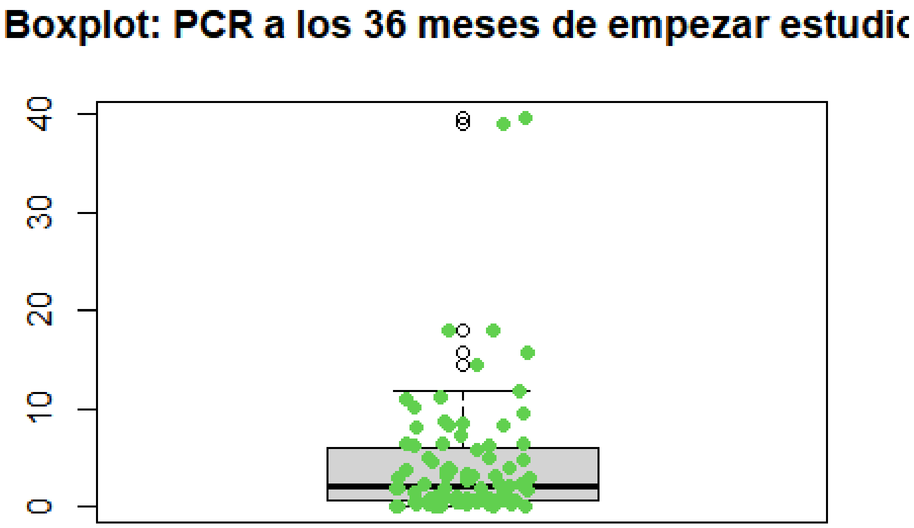
```
boxplot(x=base_rx$PCR_5, main = "Boxplot: PCR a los 30 meses de empezar estudio")
stripchart(x=base_rx$PCR_5, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 11)
```



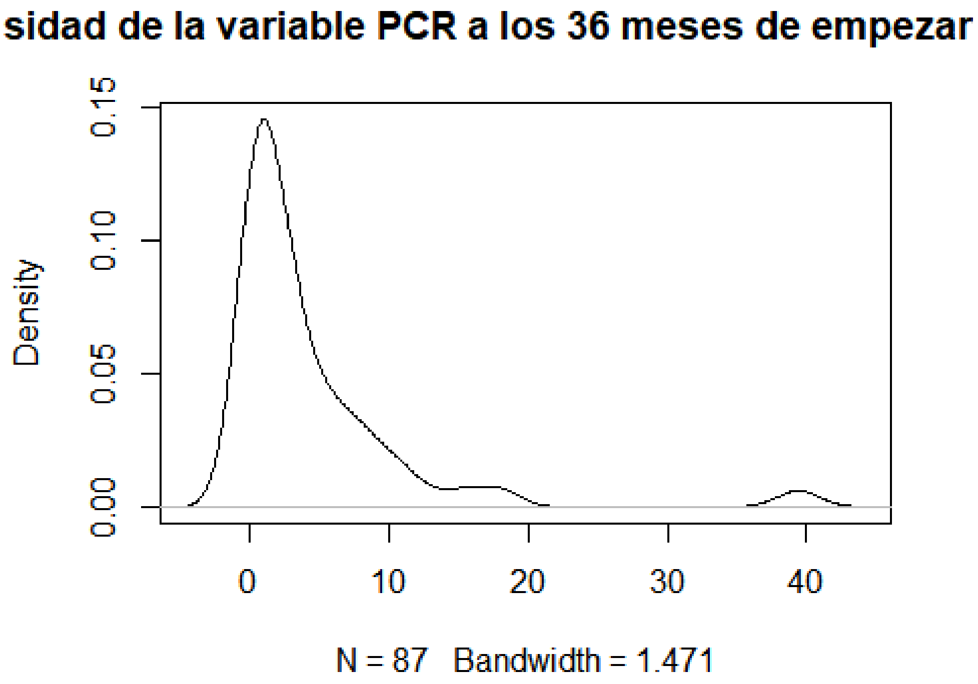
```
plot(density(base_rx$PCR_5, na.rm = T), main = "Densidad de la variable PCR a los 30 meses d
e empezar estudio")
```



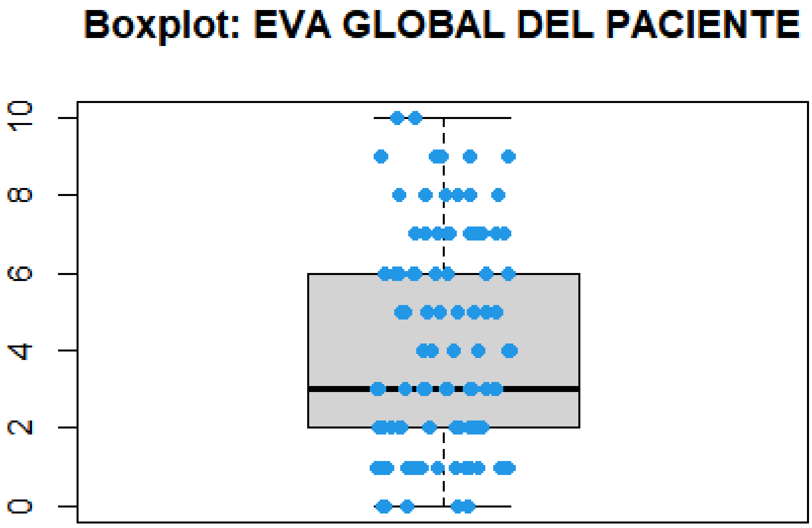
```
boxplot(x=base_rx$PCR_6, main = "Boxplot: PCR a los 36 meses de empezar estudio")
stripchart(x=base_rx$PCR_6, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 11)
```



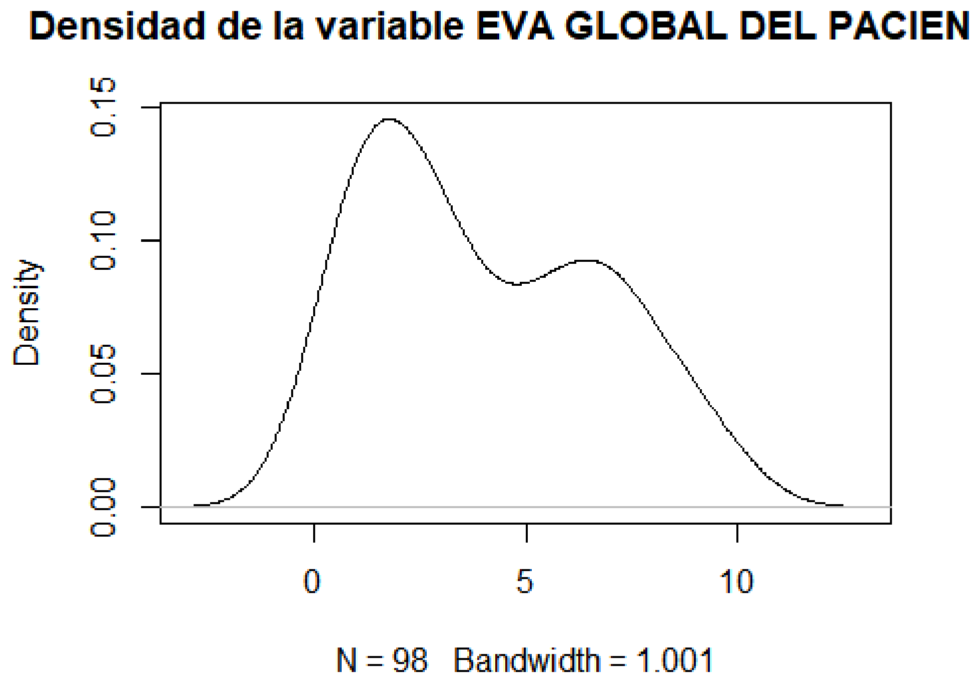
```
plot(density(base_rx$PCR_6, na.rm = T), main = "Densidad de la variable PCR a los 36 meses d
e empezar estudio")
```



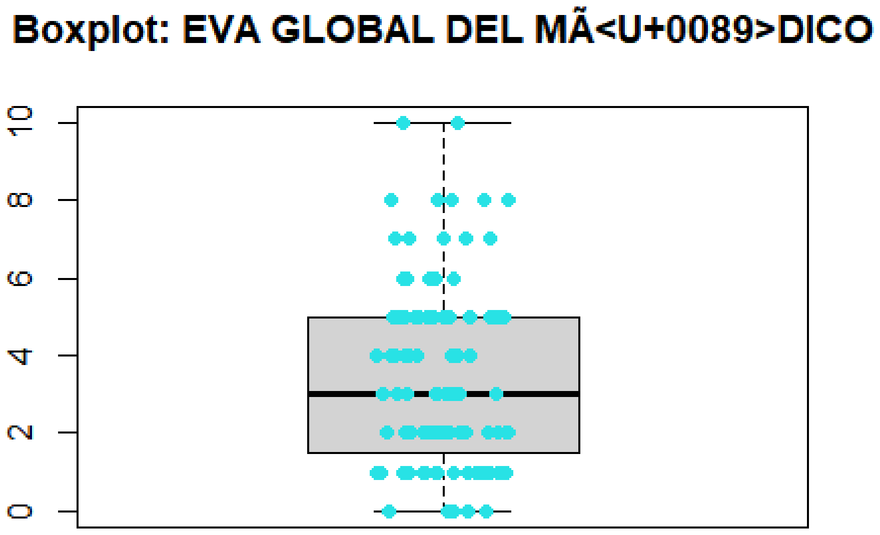
```
boxplot(x=base_rx$EGP, main = "Boxplot: EVA GLOBAL DEL PACIENTE")
stripchart(x=base_rx$EGP, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 12)
```



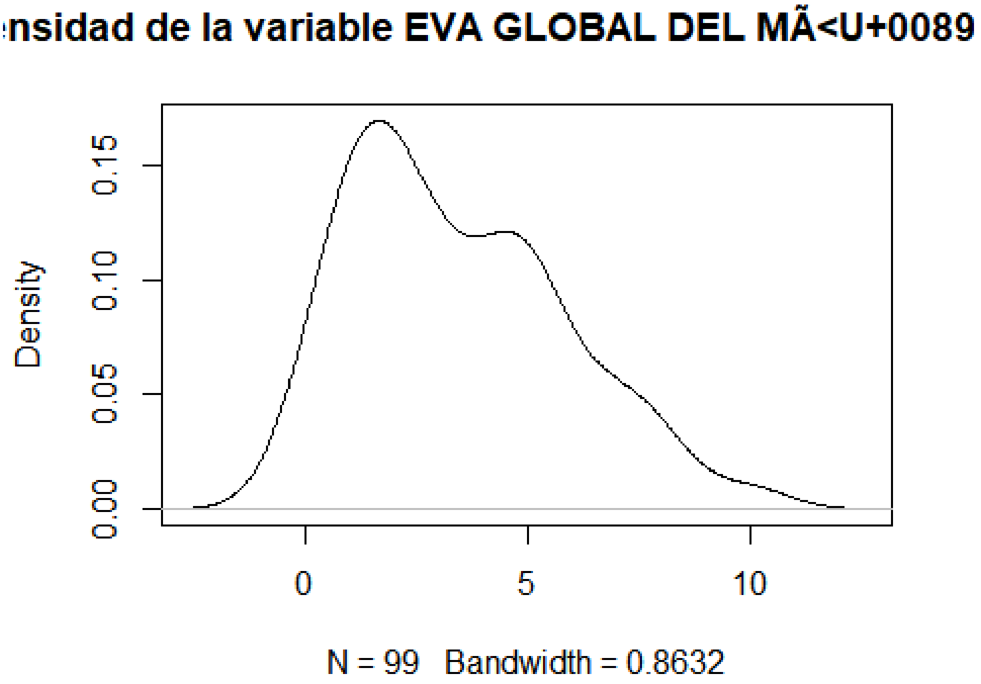
```
plot(density(base_rx$EGP, na.rm = T), main = "Densidad de la variable EVA GLOBAL DEL PACIE
NTE")
```



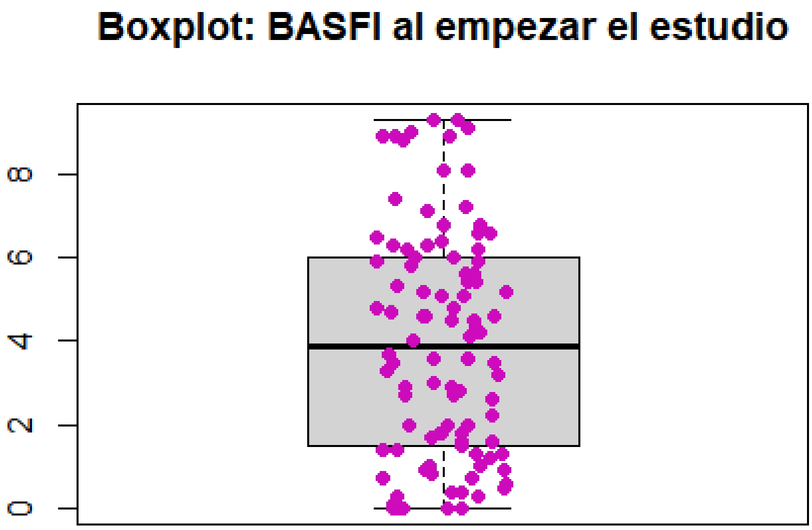
```
boxplot(x=base_rx$EGM, main = "Boxplot: EVA GLOBAL DEL MÃ‰DICO")
stripchart(x=base_rx$EGM, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 13)
```



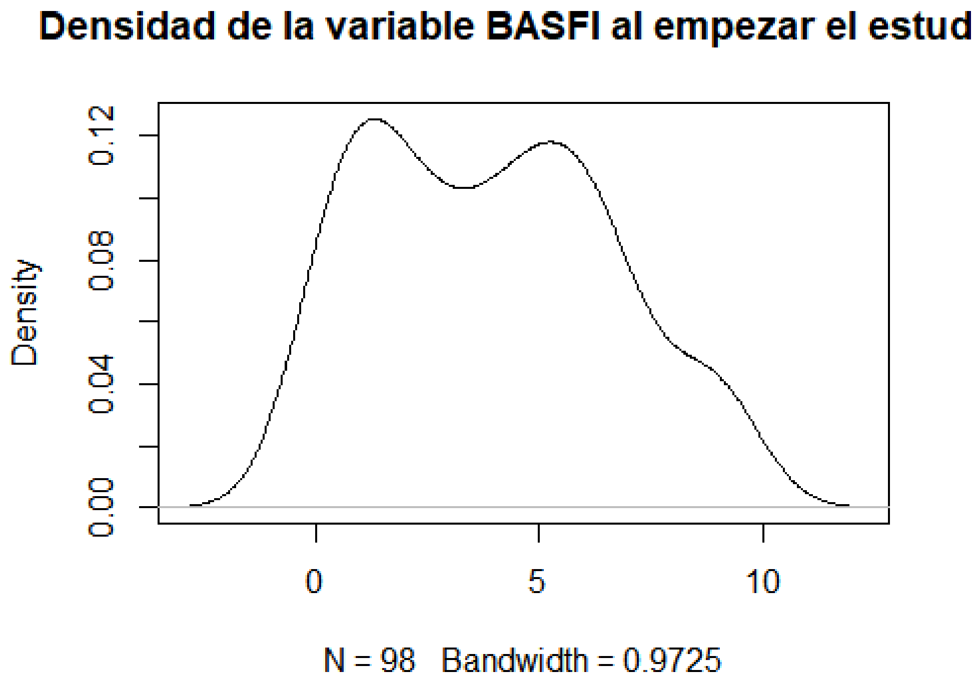
```
plot(density(base_rx$EGM, na.rm = T), main = "Densidad de la variable EVA GLOBAL DEL MÃ
‰DICO")
```



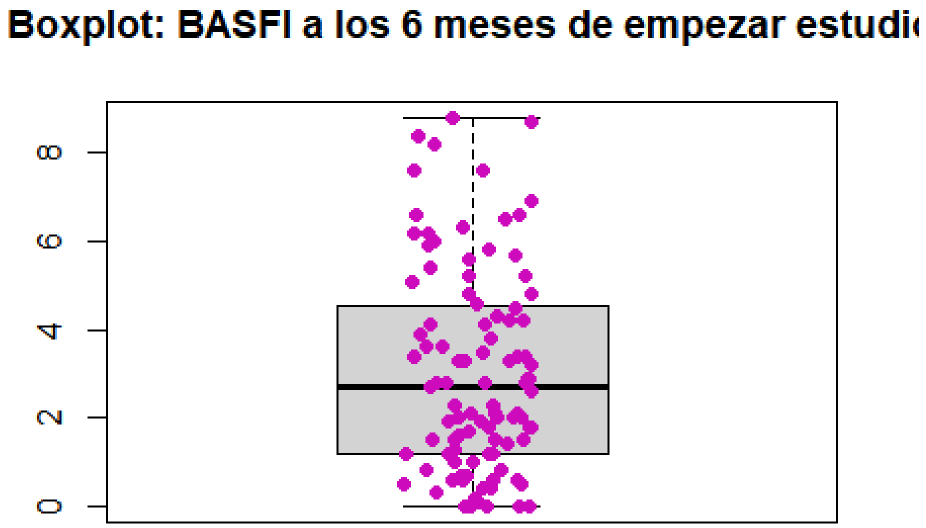
```
boxplot(x=base_rx$BASFI_0, main = "Boxplot: BASFI al empezar el estudio")
stripchart(x=base_rx$BASFI_0, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 14)
```



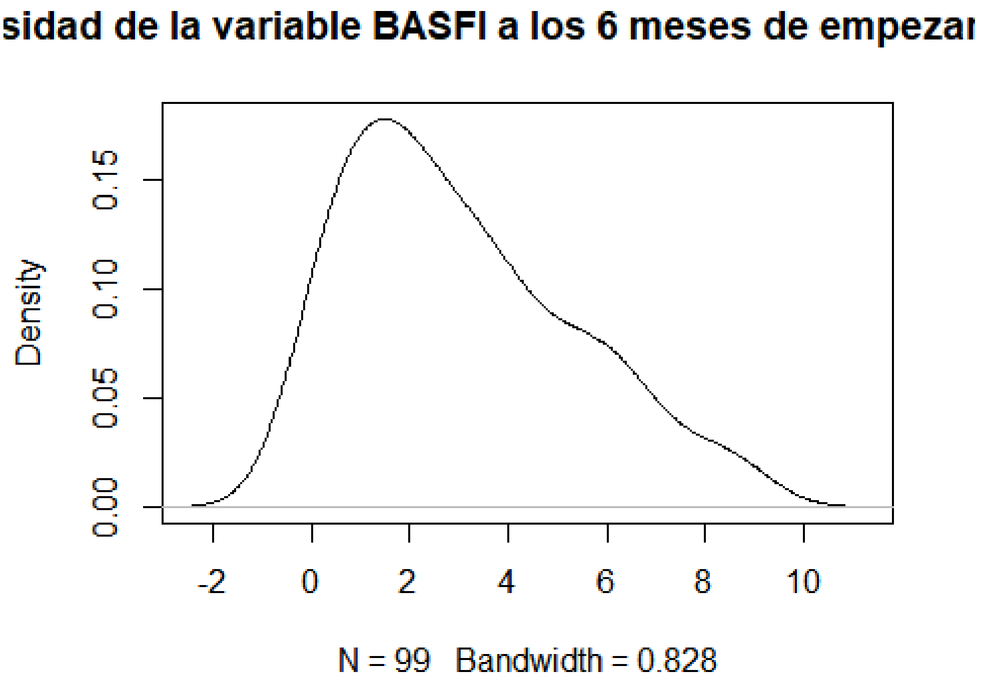
```
plot(density(base_rx$BASFI_0, na.rm = T), main = "Densidad de la variable BASFI al empezar el
estudio")
```



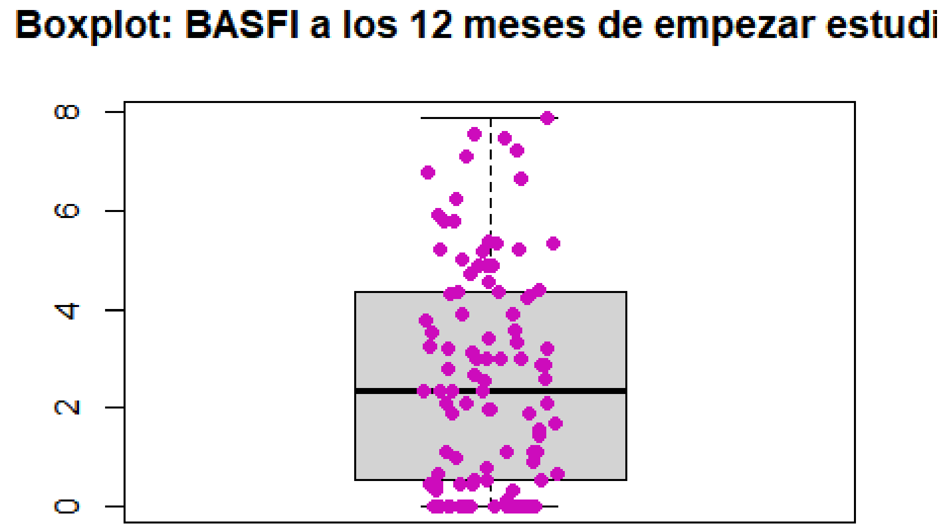
```
boxplot(x=base_rx$BASFI_1, main = "Boxplot: BASFI a los 6 meses de empezar estudio")
stripchart(x=base_rx$BASFI_1, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 14)
```



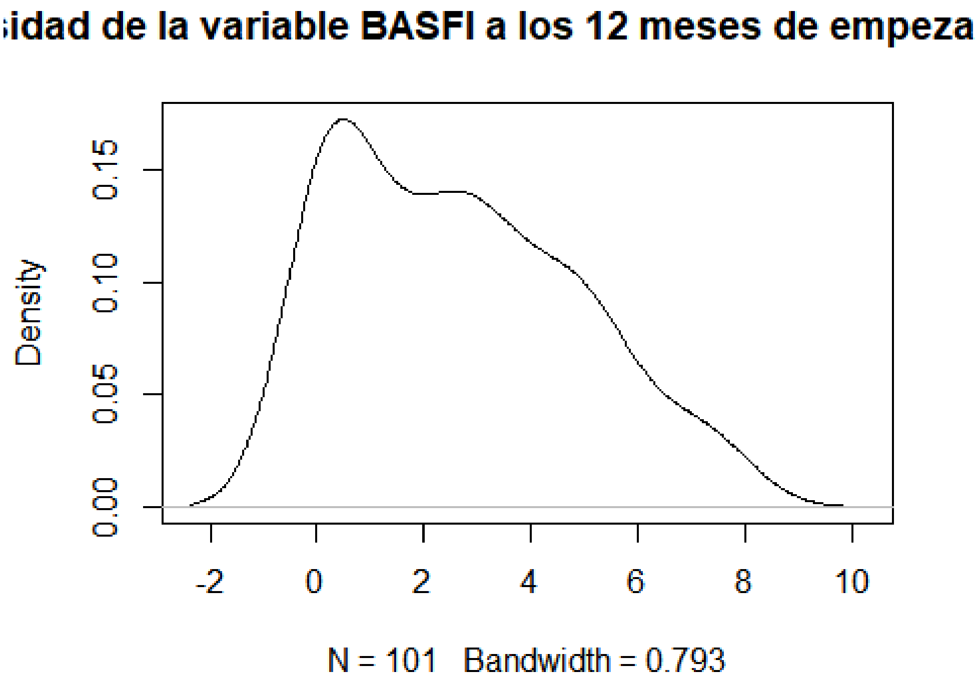
```
plot(density(base_rx$BASFI_1, na.rm = T), main = "Densidad de la variable BASFI a los 6 meses
de empezar estudio")
```



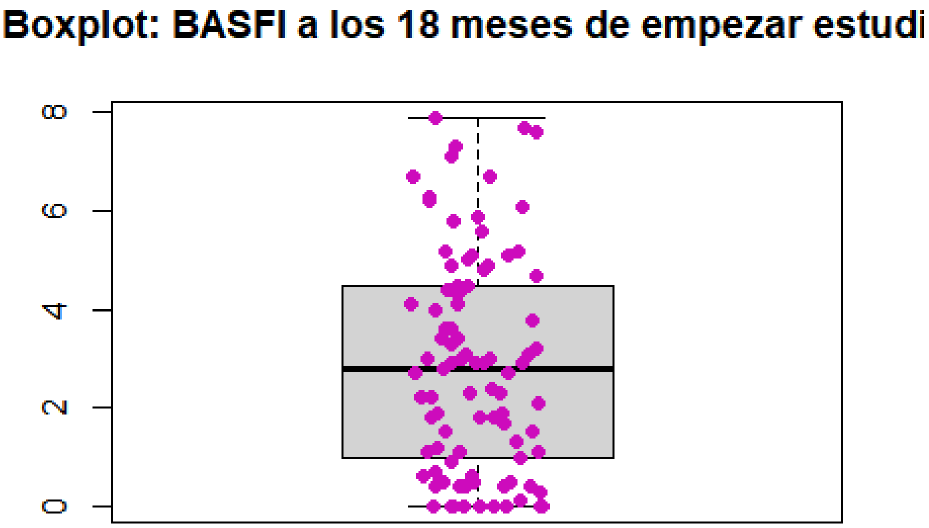
```
boxplot(x=base_rx$BASFI_2, main = "Boxplot: BASFI a los 12 meses de empezar estudio")
stripchart(x=base_rx$BASFI_2, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 14)
```



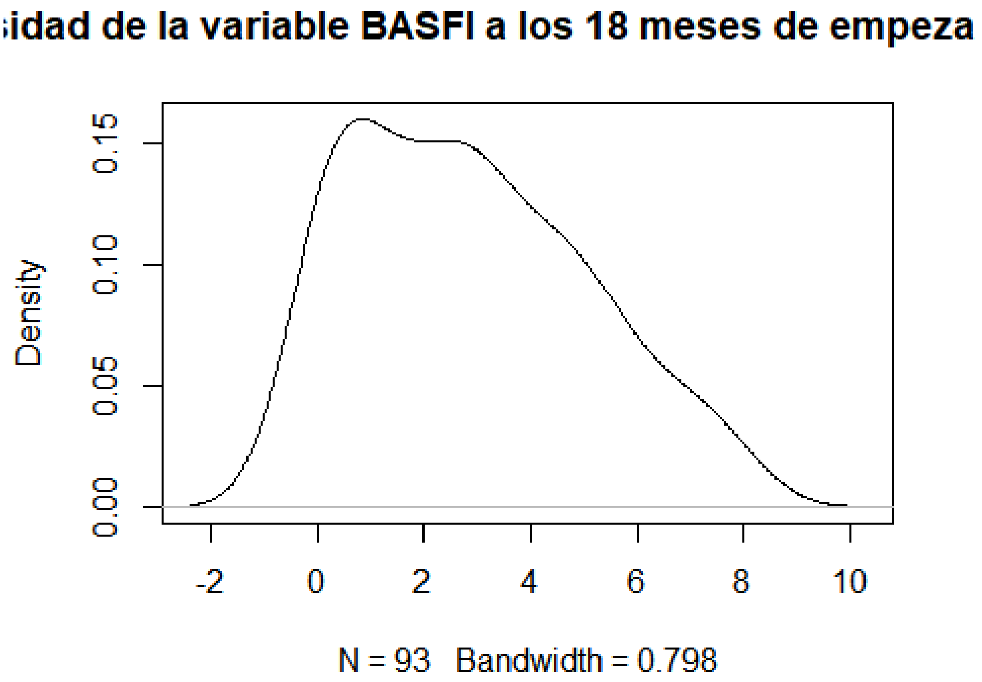
```
plot(density(base_rx$BASFI_2, na.rm = T), main = "Densidad de la variable BASFI a los 12 mese
s de empezar estudio")
```



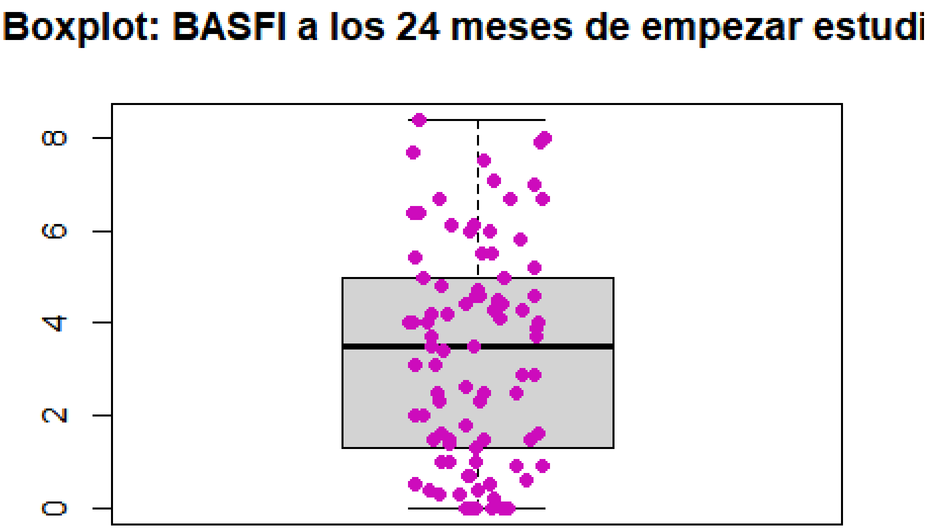
```r
boxplot(x=base_rx$BASFI_3, main = "Boxplot: BASFI a los 18 meses de empezar estudio")
stripchart(x=base_rx$BASFI_3, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 14)
```



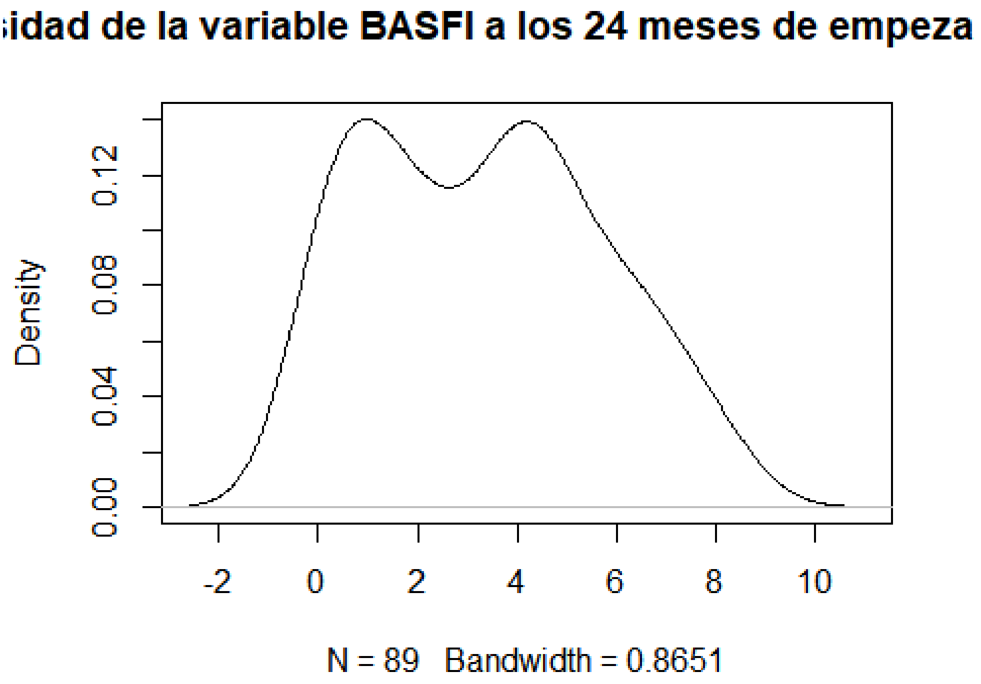
```r
plot(density(base_rx$BASFI_3, na.rm = T), main = "Densidad de la variable BASFI a los 18 mese
s de empezar estudio")
```



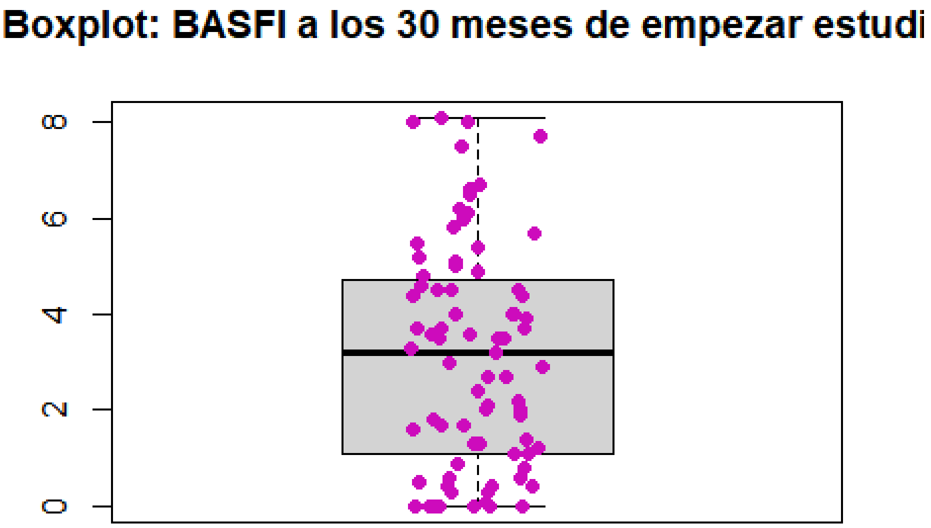
```
boxplot(x=base_rx$BASFI_4, main = "Boxplot: BASFI a los 24 meses de empezar estudio")
stripchart(x=base_rx$BASFI_4, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 14)
```



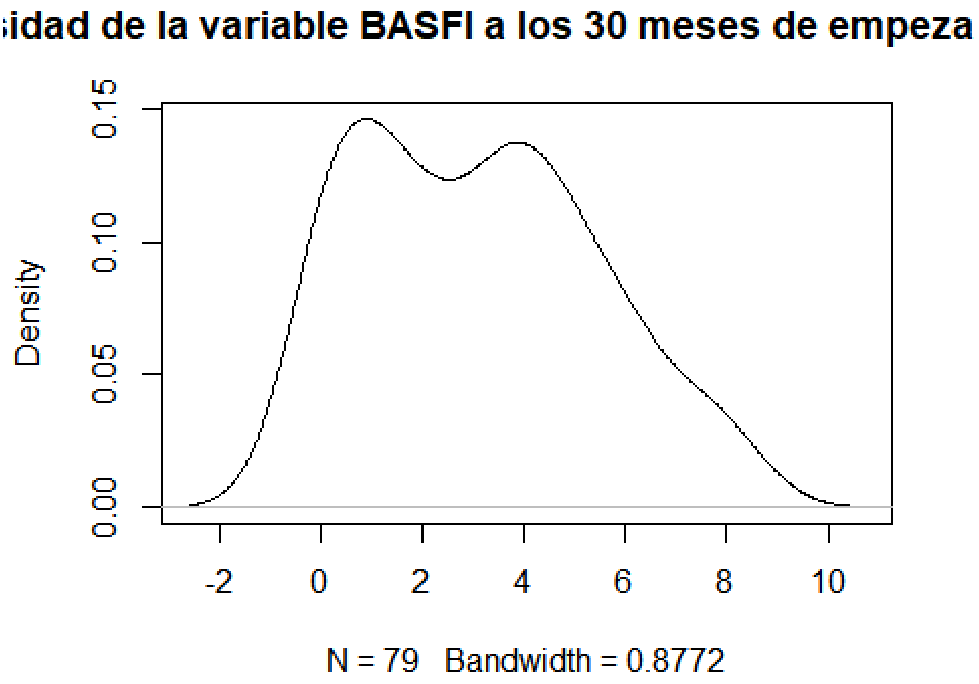
```
plot(density(base_rx$BASFI_4, na.rm = T), main = "Densidad de la variable BASFI a los 24 mese
s de empezar estudio")
```



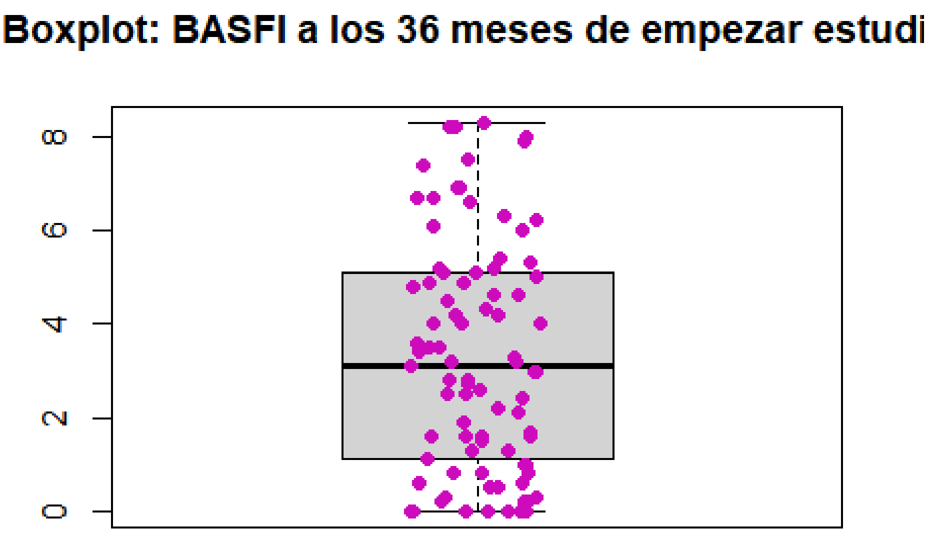
```r
boxplot(x=base_rx$BASFI_5, main = "Boxplot: BASFI a los 30 meses de empezar estudio")
stripchart(x=base_rx$BASFI_5, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 14)
```



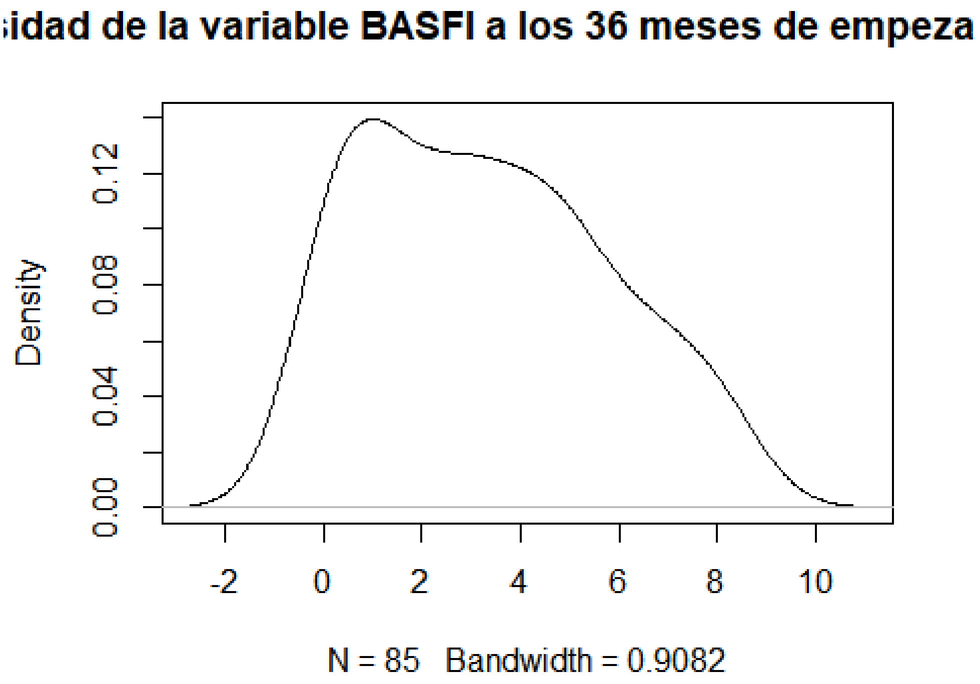
```r
plot(density(base_rx$BASFI_5, na.rm = T), main = "Densidad de la variable BASFI a los 30 mese
s de empezar estudio")
```



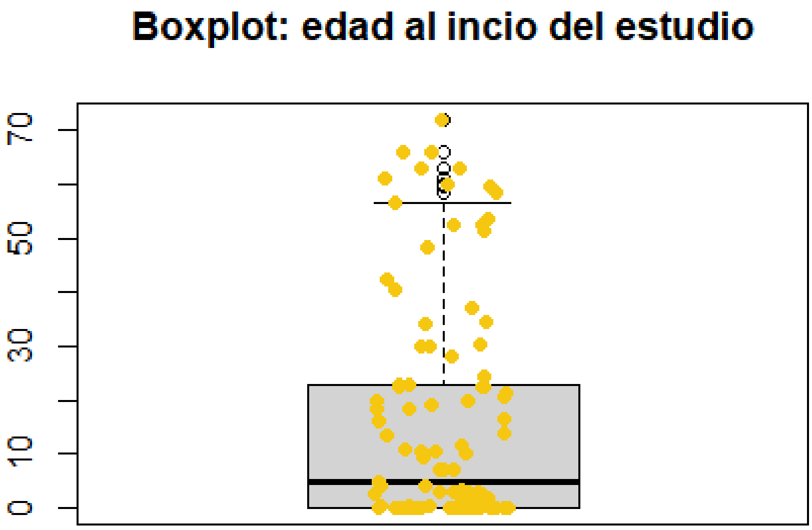
```
boxplot(x=base_rx$BASFI_6, main = "Boxplot: BASFI a los 36 meses de empezar estudio")
stripchart(x=base_rx$BASFI_6, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 14)
```



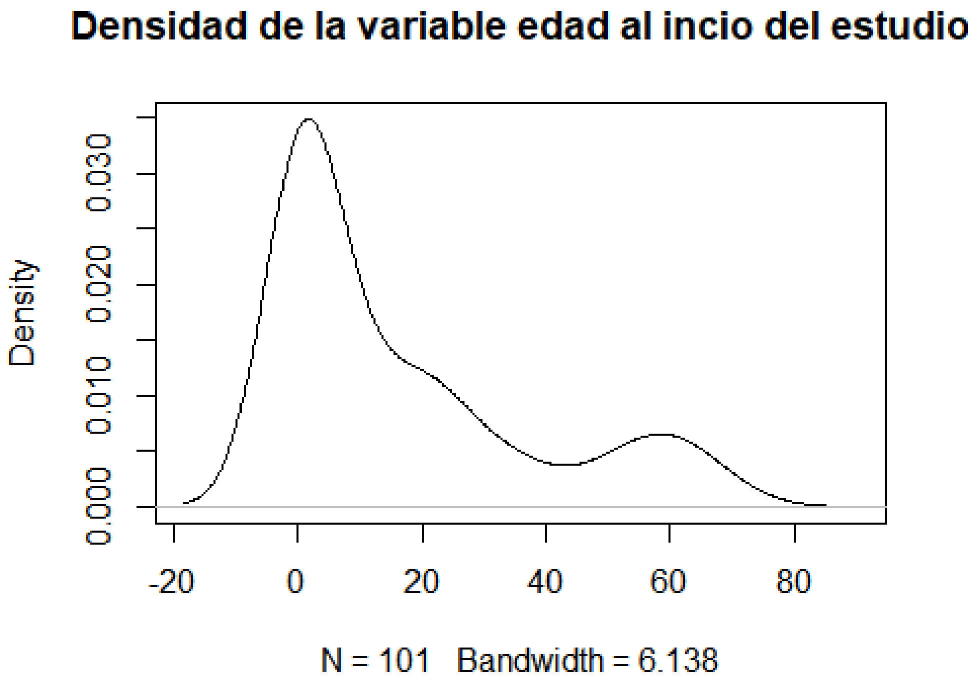
```
plot(density(base_rx$BASFI_6, na.rm = T), main = "Densidad de la variable BASFI a los 36 mese
s de empezar estudio")
```



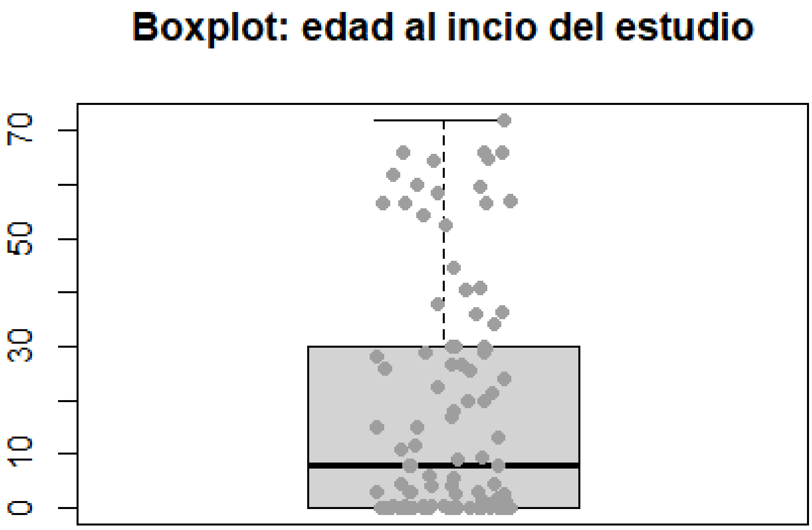
```
boxplot(x=base_rx$mSASSS_Mean_BL, main = "Boxplot: edad al incio del estudio")
stripchart(x=base_rx$mSASSS_Mean_BL, method = "jitter", pch=16, add= TRUE, vertical= TRUE
, col = 15)
```



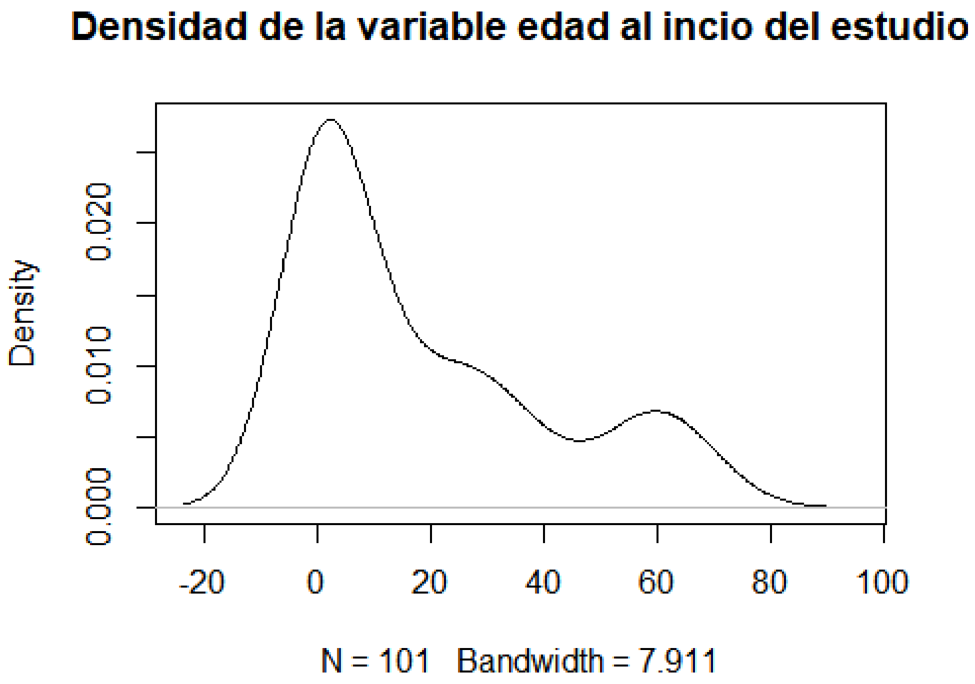
```
plot(density(base_rx$mSASSS_Mean_BL, na.rm = T), main = "Densidad de la variable edad al in
cio del estudio")
```


Densidad de la variable edad al incio del estudio

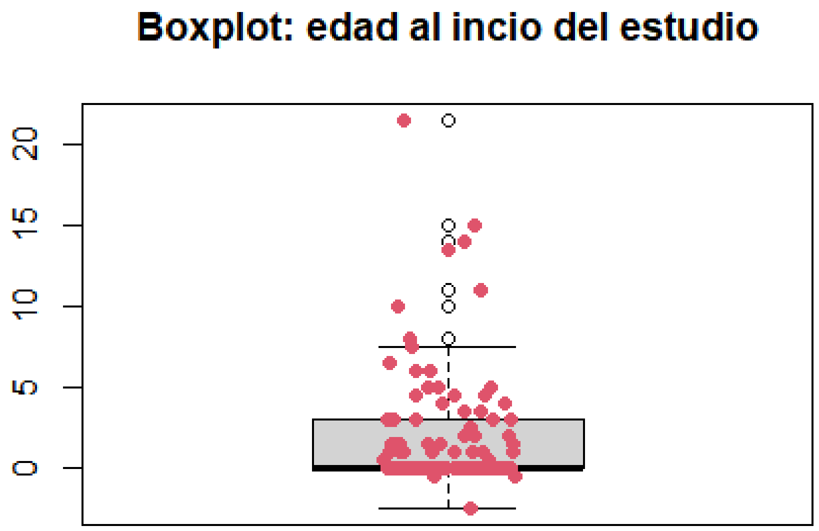
```
boxplot(x=base_rx$mSASSS_Mean_FL, main = "Boxplot: edad al incio del estudio")
stripchart(x=base_rx$mSASSS_Mean_FL, na.rm = T, method = "jitter", pch=16, add= TRUE, vertical= TRUE, col = 16)

## Warning in plot.xy(xy.coords(x, y), type = type, ...): "na.rm" is not a
## graphical parameter
```


Boxplot: edad al incio del estudio

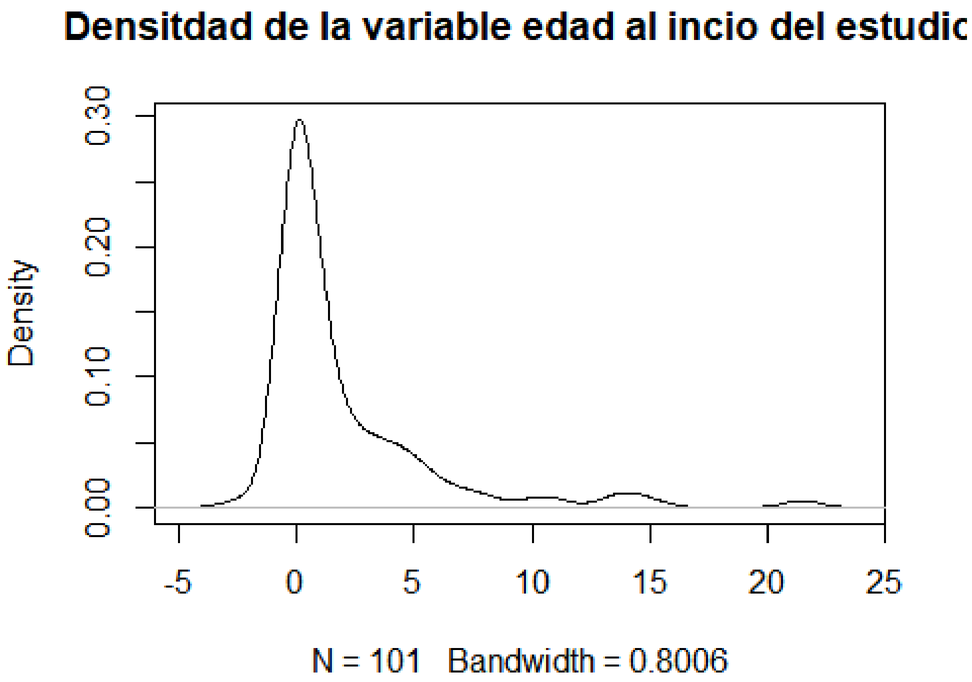
```
plot(density(base_rx$mSASSS_Mean_FL, na.rm = T), main = "Densidad de la variable edad al in
cio del estudio")
```



```
boxplot(x=base_rx$mSASSS_Progress, main = "Boxplot: edad al incio del estudio")
stripchart(x=base_rx$mSASSS_Progress, method = "jitter", pch=16, add= TRUE, vertical= TRUE,
col = 18)
```



```
plot(density(base_rx$mSASSS_Progress, na.rm = T), main = "Densitdad de la variable edad al in
cio del estudio")
```



Ajustamos las covariables, de medidas repetidos en el tiempo, de la misma forma que ajustamos la variable respuesta. Del mismo modo elimino las variables mSASSS_Mean_BL y mSASSS_Mean_FL porque la diferencia de ellas, es la variable respuesta, la variable y (mSASSS_Progress)

```
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union

base_rx1 <-
  base_rx %>%
  mutate( BASFIDif = (BASFI_6-BASFI_0), BASDAIDif = (BASDAI_6-BASDAI_0
), ASDASDif = (ASDAS_6-ASDAS_0), PCRDif = (PCR_6-PCR_0))
summary(base_rx1)

##      NUM_PAC         EDAD            SEXO          IMC            IMC>30
##  U01001 : 1   Min.   :21.00   MALE  :82   Min.   :19.37   NO  :84
##  U01007 : 1   1st Qu.:38.00   FEMALE:19   1st Qu.:24.05   SI  :11
##  U01017 : 1   Median :46.00               Median :26.02   NA's: 6
##  U02001 : 1   Mean   :46.68               Mean   :26.38
```

```
##  U02003 : 1   3rd Qu.:54.00               3rd Qu.:28.68
##  U02004 : 1   Max.   :75.00               Max.   :40.83
##  (Other):95                               NA's   :6
##      TSINT        HLAB27    EA     TABACO_Kat      VSG
BASMI
##  Min.   : 0.00   SI  :86   SI:86   SI:70      Min.   :  0.50   Min.
:0.5378
##  1st Qu.: 8.00   NO  :13   NO:15   NO:31      1st Qu.:  9.00   1st
Qu.:1.6458
##  Median :15.00   NA's: 2                      Median : 19.00   Medi
an :2.8728
##  Mean   :17.76                                Mean   : 26.65   Mean
:3.0915
##  3rd Qu.:26.00                                3rd Qu.: 38.75   3rd
Qu.:4.0864
##  Max.   :52.00                                Max.   :115.00   Max.
:7.2729
##  NA's   :4                                    NA's   :3        NA's
:19
##  UVEITIS PSORIASIS ENF_INF   TTOBIO         NUM_TB_PREV          MO
TIVO
##  NO:79   NO  :92   NO  :92   ETA:31   treatments.0:75   non.change
:77
##  SI:22   SI  : 7   SI  : 7   ADA:44   treatments.1:20   Inefficacy
:17
##          NA's: 2   NA's: 2   IFX:11   treatments.2: 6   Side.effect
s: 7
##                              GOL:12
##                              CTZ: 3
##
##
##     TIEMBIO       BIO_INICI Biol_4_kat    Interval      AINE      F
AME
##  Min.   :  0.00   NO  :25   NO:55      Min.   :2.00   NO  :42   NO
:81
##  1st Qu.:  8.00   SI  :75   SI:46      1st Qu.:3.00   SI  :57   SI
:18
##  Median : 42.50   NA's: 1              Median :3.00   NA's: 2   NA'
s: 2
##  Mean   : 45.51                        Mean   :3.45
##  3rd Qu.: 76.75                        3rd Qu.:4.00
##  Max.   :132.00                        Max.   :6.00
##  NA's   :1                             NA's   :1
##     i_BASDAI        BASDAI_0       BASDAI_1        BASDAI_2
##  Min.   :0.700   Min.   :0.20   Min.   :0.000   Min.   : 0.000
##  1st Qu.:4.225   1st Qu.:2.00   1st Qu.:1.400   1st Qu.: 1.400
##  Median :5.400   Median :3.20   Median :2.700   Median : 2.500
##  Mean   :5.326   Mean   :3.67   Mean   :2.902   Mean   : 3.419
##  3rd Qu.:6.400   3rd Qu.:5.10   3rd Qu.:4.400   3rd Qu.: 4.200
##  Max.   :8.800   Max.   :8.80   Max.   :8.500   Max.   :65.000
##  NA's   :3       NA's   :4      NA's   :4       NA's   :4
##     BASDAI_3        BASDAI_4        BASDAI_5        BASDAI_6
##  Min.   :0.000   Min.   :0.000   Min.   :0.000   Min.   :0.000
##  1st Qu.:1.200   1st Qu.:1.200   1st Qu.:1.275   1st Qu.:1.100
```

```
##  Median :3.000   Median :2.800   Median :2.550   Median :2.800  
##  Mean   :3.108   Mean   :3.075   Mean   :2.915   Mean   :2.924  
##  3rd Qu.:4.800   3rd Qu.:4.600   3rd Qu.:4.200   3rd Qu.:4.600  
##  Max.   :8.000   Max.   :8.000   Max.   :8.000   Max.   :7.300  
##  NA's   :8       NA's   :10      NA's   :17      NA's   :16     
##     ASDAS_0          ASDAS_1          ASDAS_2            ASDAS_3 
##  Min.   :0.2257   Min.   :0.2471   Min.   :0.001737   Min.   :0.048
92  
##  1st Qu.:1.3874   1st Qu.:1.1572   1st Qu.:1.088078   1st Qu.:1.164
97  
##  Median :2.0565   Median :1.5738   Median :1.827288   Median :1.766
56  
##  Mean   :2.2160   Mean   :1.8249   Mean   :1.773470   Mean   :1.815
23  
##  3rd Qu.:2.9248   3rd Qu.:2.4204   3rd Qu.:2.316346   3rd Qu.:2.477
97  
##  Max.   :5.0749   Max.   :7.1255   Max.   :4.131246   Max.   :3.983
74  
##  NA's   :5        NA's   :13       NA's   :9          NA's   :14   
##     ASDAS_4           ASDAS_5           ASDAS_6           PCR_0       
##  Min.   :0.00058   Min.   :0.0338   Min.   :0.096   Min.   : 0.000  
##  1st Qu.:1.17363   1st Qu.:1.0522   1st Qu.:1.143   1st Qu.: 1.000  
##  Median :1.66660   Median :1.6400   Median :1.680   Median : 3.350  
##  Mean   :1.81274   Mean   :1.7329   Mean   :1.807   Mean   : 8.181  
##  3rd Qu.:2.44173   3rd Qu.:2.1781   3rd Qu.:2.397   3rd Qu.: 9.100  
##  Max.   :4.45150   Max.   :4.0579   Max.   :3.988   Max.   :88.700  
##  NA's   :22        NA's   :30       NA's   :24      NA's   :7       
##      PCR_1            PCR_2           PCR_3            PCR_4       
##  Min.   : 0.000   Min.   : 0.00   Min.   : 0.000   Min.   : 0.000  
##  1st Qu.: 1.000   1st Qu.: 0.90   1st Qu.: 0.750   1st Qu.: 0.700  
##  Median : 2.000   Median : 2.00   Median : 1.900   Median : 2.050  
##  Mean   : 4.358   Mean   : 4.36   Mean   : 4.452   Mean   : 5.368  
##  3rd Qu.: 4.675   3rd Qu.: 5.60   3rd Qu.: 5.600   3rd Qu.: 5.375  
##  Max.   :61.300   Max.   :33.90   Max.   :37.000   Max.   :68.500  
##  NA's   :3        NA's   :2       NA's   :4        NA's   :7       
##      PCR_5            PCR_6            EGP              EGM        
##  Min.   : 0.000   Min.   : 0.00   Min.   : 0.000   Min.   : 0.000  
##  1st Qu.: 0.615   1st Qu.: 0.60   1st Qu.: 2.000   1st Qu.: 1.500  
##  Median : 1.400   Median : 2.00   Median : 3.000   Median : 3.000  
##  Mean   : 4.118   Mean   : 4.42   Mean   : 4.031   Mean   : 3.455  
##  3rd Qu.: 6.000   3rd Qu.: 5.95   3rd Qu.: 6.000   3rd Qu.: 5.000  
##  Max.   :65.900   Max.   :39.70   Max.   :10.000   Max.   :10.000  
##  NA's   :10       NA's   :14      NA's   :3        NA's   :2       
##     BASFI_0         BASFI_1         BASFI_2         BASFI_3     
BASFI_4   
##  Min.   :0.000   Min.   :0.000   Min.   :0.000   Min.   :0.000   Mi
n.   :0.00  
##  1st Qu.:1.525   1st Qu.:1.200   1st Qu.:0.550   1st Qu.:1.000   1s
t Qu.:1.30  
##  Median :3.850   Median :2.700   Median :2.330   Median :2.800   Me
dian :3.50  
##  Mean   :3.931   Mean   :3.059   Mean   :2.667   Mean   :2.882   Me
an   :3.34  
##  3rd Qu.:5.975   3rd Qu.:4.550   3rd Qu.:4.340   3rd Qu.:4.500   3r
```

```
d Qu.:5.00
##  Max.   :9.300   Max.   :8.800   Max.   :7.890   Max.   :7.900   Ma
x.   :8.40
##  NA's   :3       NA's   :2                         NA's   :8       NA
's   :12
##     BASFI_5          BASFI_6      mSASSS_Mean_BL  mSASSS_Mean_FL
##  Min.   :0.000   Min.   :0.000   Min.   : 0.00   Min.   : 0.00
##  1st Qu.:1.100   1st Qu.:1.100   1st Qu.: 0.00   1st Qu.: 0.00
##  Median :3.200   Median :3.100   Median : 5.00   Median : 8.00
##  Mean   :3.118   Mean   :3.313   Mean   :16.46   Mean   :18.44
##  3rd Qu.:4.700   3rd Qu.:5.100   3rd Qu.:23.00   3rd Qu.:30.00
##  Max.   :8.100   Max.   :8.300   Max.   :72.00   Max.   :72.00
##  NA's   :22      NA's   :16
##  mSASSS_Progress New_Syn_mSASSS Prog_Syn_mSASSS mSASSS_Progress_Kat
##  Min.   :-2.50   NO:81          NO:90           NO:71
##  1st Qu.: 0.00   SI:20          SI:11           SI:30
##  Median : 0.00
##  Mean   : 1.98
##  3rd Qu.: 3.00
##  Max.   :21.50
##
##  New_Prog_Syn_Msasss Mind_2_Synd_FL Mind_2_Synd_BL  PCR_INICIOB
##  NO:79               NO:46          NO:50          Min.   : 0.00
##  SI:22               SI:55          SI:51          1st Qu.: 4.60
##                                                    Median :11.10
##                                                    Mean   :18.70
##                                                    3rd Qu.:28.05
##                                                    Max.   :98.00
##                                                    NA's   :2
##     i_ASDAS            HVGP           BASFIDif          BASDAIDif
##  Min.   :1.500   Min.   : 1.000   Min.   :-8.9000   Min.   :-7.0000
##  1st Qu.:2.700   1st Qu.: 5.000   1st Qu.:-1.8000   1st Qu.:-1.1000
##  Median :3.500   Median : 6.000   Median :-0.2000   Median :-0.1000
##  Mean   :3.402   Mean   : 5.923   Mean   :-0.5667   Mean   :-0.5354
##  3rd Qu.:4.000   3rd Qu.: 7.000   3rd Qu.: 0.6250   3rd Qu.: 0.4750
##  Max.   :5.300   Max.   :10.000   Max.   : 6.2000   Max.   : 5.2000
##  NA's   :2                        NA's   :17        NA's   :19
##     ASDASDif           PCRDif
##  Min.   :-3.4650   Min.   :-88.40
##  1st Qu.:-1.0300   1st Qu.: -5.40
##  Median :-0.2247   Median : -0.20
##  Mean   :-0.3908   Mean   : -4.14
##  3rd Qu.: 0.2567   3rd Qu.:  1.00
##  Max.   : 1.9947   Max.   : 28.00
##  NA's   :28        NA's   :20
```

```
base_rx2 <- base_rx1[,c(-1,-25:-45,-48:-56)]
summary(base_rx2)
```

```
##       EDAD          SEXO          IMC          IMC>30        TSINT
##  Min.   :21.00   MALE  :82   Min.   :19.37   NO  :84   Min.   : 0.0
0
##  1st Qu.:38.00   FEMALE:19   1st Qu.:24.05   SI  :11   1st Qu.: 8.0
0
```

```
##  Median :46.00               Median :26.02   NA's: 6   Median :15.0
0
##  Mean   :46.68               Mean   :26.38             Mean   :17.7
6
##  3rd Qu.:54.00               3rd Qu.:28.68             3rd Qu.:26.0
0
##  Max.   :75.00               Max.   :40.83             Max.   :52.0
0
##                              NA's   :6                 NA's   :4
##   HLAB27    EA     TABACO_Kat      VSG             BASMI        UVE
ITIS
##  SI  :86   SI:86   SI:70      Min.   :  0.50   Min.   :0.5378   NO:
79
##  NO  :13   NO:15   NO:31      1st Qu.:  9.00   1st Qu.:1.6458   SI:
22
##  NA's: 2                      Median : 19.00   Median :2.8728
##                               Mean   : 26.65   Mean   :3.0915
##                               3rd Qu.: 38.75   3rd Qu.:4.0864
##                               Max.   :115.00   Max.   :7.2729
##                               NA's   :3        NA's   :19
##  PSORIASIS ENF_INF   TTOBIO         NUM_TB_PREV          MOTIVO
##  NO  :92   NO  :92   ETA:31   treatments.0:75   non.change  :77
##  SI  : 7   SI  : 7   ADA:44   treatments.1:20   Inefficacy  :17
##  NA's: 2   NA's: 2   IFX:11   treatments.2: 6   Side.effects: 7
##                      GOL:12
##                      CTZ: 3
##
##
##     TIEMBIO       BIO_INICI Biol_4_kat    Interval      AINE      F
AME
##  Min.   :  0.00   NO  :25   NO:55      Min.   :2.00   NO  :42   NO
:81
##  1st Qu.:  8.00   SI  :75   SI:46      1st Qu.:3.00   SI  :57   SI
:18
##  Median : 42.50   NA's: 1              Median :3.00   NA's: 2   NA'
s: 2
##  Mean   : 45.51                        Mean   :3.45
##  3rd Qu.: 76.75                        3rd Qu.:4.00
##  Max.   :132.00                        Max.   :6.00
##  NA's   :1                             NA's   :1
##     i_BASDAI          EGP              EGM         mSASSS_Progress
##  Min.   :0.700   Min.   : 0.000   Min.   : 0.000   Min.   :-2.50
##  1st Qu.:4.225   1st Qu.: 2.000   1st Qu.: 1.500   1st Qu.: 0.00
##  Median :5.400   Median : 3.000   Median : 3.000   Median : 0.00
##  Mean   :5.326   Mean   : 4.031   Mean   : 3.455   Mean   : 1.98
##  3rd Qu.:6.400   3rd Qu.: 6.000   3rd Qu.: 5.000   3rd Qu.: 3.00
##  Max.   :8.800   Max.   :10.000   Max.   :10.000   Max.   :21.50
##  NA's   :3       NA's   :3        NA's   :2
##  New_Syn_mSASSS Prog_Syn_mSASSS mSASSS_Progress_Kat New_Prog_Syn_Ms
asss
##  NO:81          NO:90           NO:71               NO:79
##  SI:20          SI:11           SI:30               SI:22
##
##
```

```
##
##
##
##  Mind_2_Synd_FL Mind_2_Synd_BL  PCR_INICIOB       i_ASDAS
HVGP
##  NO:46          NO:50          Min.   : 0.00   Min.   :1.500   Min.
: 1.000
##  SI:55          SI:51          1st Qu.: 4.60   1st Qu.:2.700   1st
Qu.: 5.000
##                                Median :11.10   Median :3.500   Medi
an : 6.000
##                                Mean   :18.70   Mean   :3.402   Mean
: 5.923
##                                3rd Qu.:28.05   3rd Qu.:4.000   3rd
Qu.: 7.000
##                                Max.   :98.00   Max.   :5.300   Max.
:10.000
##                                NA's   :2       NA's   :2
##     BASFIDif         BASDAIDif          ASDASDif           PCRDif
##  Min.   :-8.9000   Min.   :-7.0000   Min.   :-3.4650   Min.   :-88.
40
##  1st Qu.:-1.8000   1st Qu.:-1.1000   1st Qu.:-1.0300   1st Qu.: -5.
40
##  Median :-0.2000   Median :-0.1000   Median :-0.2247   Median : -0.
20
##  Mean   :-0.5667   Mean   :-0.5354   Mean   :-0.3908   Mean   : -4.
14
##  3rd Qu.: 0.6250   3rd Qu.: 0.4750   3rd Qu.: 0.2567   3rd Qu.:  1.
00
##  Max.   : 6.2000   Max.   : 5.2000   Max.   : 1.9947   Max.   : 28.
00
##  NA's   :17        NA's   :19        NA's   :28        NA's   :20
```

```
base_rx21 <- base_rx1[,c(-1,-25:-46,-48:-56,-68)]
summary(base_rx21)
```

```
##       EDAD           SEXO         IMC          IMC>30       TSINT
##  Min.   :21.00   MALE  :82   Min.   :19.37   NO  :84   Min.   : 0.0
0
##  1st Qu.:38.00   FEMALE:19   1st Qu.:24.05   SI  :11   1st Qu.: 8.0
0
##  Median :46.00               Median :26.02   NA's: 6   Median :15.0
0
##  Mean   :46.68               Mean   :26.38             Mean   :17.7
6
##  3rd Qu.:54.00               3rd Qu.:28.68             3rd Qu.:26.0
0
##  Max.   :75.00               Max.   :40.83             Max.   :52.0
0
##                              NA's   :6                 NA's   :4
##   HLAB27     EA      TABACO_Kat      VSG             BASMI         UVE
ITIS
##  SI  :86   SI:86   SI:70      Min.   :  0.50   Min.   :0.5378   NO:
79
```

```
##  NO  :13   NO:15   NO:31      1st Qu.:  9.00   1st Qu.:1.6458   SI:
22
##  NA's: 2                      Median : 19.00   Median :2.8728
##                               Mean   : 26.65   Mean   :3.0915
##                               3rd Qu.: 38.75   3rd Qu.:4.0864
##                               Max.   :115.00   Max.   :7.2729
##                               NA's   :3        NA's   :19
##  PSORIASIS ENF_INF   TTOBIO         NUM_TB_PREV          MOTIVO
##  NO  :92   NO  :92   ETA:31   treatments.0:75   non.change  :77
##  SI  : 7   SI  : 7   ADA:44   treatments.1:20   Inefficacy  :17
##  NA's: 2   NA's: 2   IFX:11   treatments.2: 6   Side.effects: 7
##                      GOL:12
##                      CTZ: 3
##
##
##     TIEMBIO       BIO_INICI Biol_4_kat    Interval      AINE       F
AME
##  Min.   :  0.00   NO  :25   NO:55      Min.   :2.00   NO  :42   NO
:81
##  1st Qu.:  8.00   SI  :75   SI:46      1st Qu.:3.00   SI  :57   SI
:18
##  Median : 42.50   NA's: 1              Median :3.00   NA's: 2   NA'
s: 2
##  Mean   : 45.51                        Mean   :3.45
##  3rd Qu.: 76.75                        3rd Qu.:4.00
##  Max.   :132.00                        Max.   :6.00
##  NA's   :1                             NA's   :1
##     i_BASDAI          EGM         mSASSS_Progress New_Syn_mSASSS
##  Min.   :0.700   Min.   : 0.000   Min.   :-2.50   NO:81
##  1st Qu.:4.225   1st Qu.: 1.500   1st Qu.: 0.00   SI:20
##  Median :5.400   Median : 3.000   Median : 0.00
##  Mean   :5.326   Mean   : 3.455   Mean   : 1.98
##  3rd Qu.:6.400   3rd Qu.: 5.000   3rd Qu.: 3.00
##  Max.   :8.800   Max.   :10.000   Max.   :21.50
##  NA's   :3       NA's   :2
##  Prog_Syn_mSASSS mSASSS_Progress_Kat New_Prog_Syn_Msasss Mind_2_Syn
d_FL
##  NO:90           NO:71               NO:79               NO:46
##  SI:11           SI:30               SI:22               SI:55
##
##
##
##
##
##  Mind_2_Synd_BL  PCR_INICIOB       i_ASDAS          HVGP
##  NO:50          Min.   : 0.00   Min.   :1.500   Min.   : 1.000
##  SI:51          1st Qu.: 4.60   1st Qu.:2.700   1st Qu.: 5.000
##                 Median :11.10   Median :3.500   Median : 6.000
##                 Mean   :18.70   Mean   :3.402   Mean   : 5.923
##                 3rd Qu.:28.05   3rd Qu.:4.000   3rd Qu.: 7.000
##                 Max.   :98.00   Max.   :5.300   Max.   :10.000
##                 NA's   :2       NA's   :2
##     BASFIDif          ASDASDif          PCRDif
##  Min.   :-8.9000   Min.   :-3.4650   Min.   :-88.40
```

```
##  1st Qu.:-1.8000   1st Qu.:-1.0300   1st Qu.: -5.40
##  Median :-0.2000   Median :-0.2247   Median : -0.20
##  Mean   :-0.5667   Mean   :-0.3908   Mean   : -4.14
##  3rd Qu.: 0.6250   3rd Qu.: 0.2567   3rd Qu.:  1.00
##  Max.   : 6.2000   Max.   : 1.9947   Max.   : 28.00
##  NA's   :17        NA's   :28        NA's   :20

base_rx22 <- base_rx1[,c(-1,-25:-46,-48:-56,-67,-69)]
summary(base_rx22)

##       EDAD           SEXO         IMC         IMC>30       TSINT
##  Min.   :21.00   MALE  :82   Min.   :19.37   NO  :84   Min.   : 0.0
0
##  1st Qu.:38.00   FEMALE:19   1st Qu.:24.05   SI  :11   1st Qu.: 8.0
0
##  Median :46.00               Median :26.02   NA's: 6   Median :15.0
0
##  Mean   :46.68               Mean   :26.38             Mean   :17.7
6
##  3rd Qu.:54.00               3rd Qu.:28.68             3rd Qu.:26.0
0
##  Max.   :75.00               Max.   :40.83             Max.   :52.0
0
##                              NA's   :6                 NA's   :4
##   HLAB27    EA     TABACO_Kat      VSG             BASMI        UVE
ITIS
##  SI  :86   SI:86   SI:70      Min.   :  0.50   Min.   :0.5378   NO:
79
##  NO  :13   NO:15   NO:31      1st Qu.:  9.00   1st Qu.:1.6458   SI:
22
##  NA's: 2                      Median : 19.00   Median :2.8728
##                               Mean   : 26.65   Mean   :3.0915
##                               3rd Qu.: 38.75   3rd Qu.:4.0864
##                               Max.   :115.00   Max.   :7.2729
##                               NA's   :3        NA's   :19
##  PSORIASIS ENF_INF   TTOBIO         NUM_TB_PREV          MOTIVO
##  NO  :92   NO  :92   ETA:31   treatments.0:75   non.change  :77
##  SI  : 7   SI  : 7   ADA:44   treatments.1:20   Inefficacy  :17
##  NA's: 2   NA's: 2   IFX:11   treatments.2: 6   Side.effects: 7
##                      GOL:12
##                      CTZ: 3
##
##
##     TIEMBIO       BIO_INICI Biol_4_kat    Interval       AINE       F
AME
##  Min.   :  0.00   NO  :25   NO:55      Min.   :2.00   NO  :42   NO
:81
##  1st Qu.:  8.00   SI  :75   SI:46      1st Qu.:3.00   SI  :57   SI
:18
##  Median : 42.50   NA's: 1              Median :3.00   NA's: 2   NA'
s: 2
##  Mean   : 45.51                        Mean   :3.45
##  3rd Qu.: 76.75                        3rd Qu.:4.00
##  Max.   :132.00                        Max.   :6.00
```

```
##  NA's   :1                            NA's   :1
##     i_BASDAI          EGM         mSASSS_Progress New_Syn_mSASSS
##  Min.   :0.700   Min.   : 0.000   Min.   :-2.50   NO:81
##  1st Qu.:4.225   1st Qu.: 1.500   1st Qu.: 0.00   SI:20
##  Median :5.400   Median : 3.000   Median : 0.00
##  Mean   :5.326   Mean   : 3.455   Mean   : 1.98
##  3rd Qu.:6.400   3rd Qu.: 5.000   3rd Qu.: 3.00
##  Max.   :8.800   Max.   :10.000   Max.   :21.50
##  NA's   :3       NA's   :2
##  Prog_Syn_mSASSS mSASSS_Progress_Kat New_Prog_Syn_Msasss Mind_2_Syn
d_FL
##  NO:90           NO:71               NO:79               NO:46
##  SI:11           SI:30               SI:22               SI:55
##
##
##
##
##
##  Mind_2_Synd_BL  PCR_INICIOB       i_ASDAS           HVGP
##  NO:50          Min.   : 0.00   Min.   :1.500   Min.   : 1.000
##  SI:51          1st Qu.: 4.60   1st Qu.:2.700   1st Qu.: 5.000
##                 Median :11.10   Median :3.500   Median : 6.000
##                 Mean   :18.70   Mean   :3.402   Mean   : 5.923
##                 3rd Qu.:28.05   3rd Qu.:4.000   3rd Qu.: 7.000
##                 Max.   :98.00   Max.   :5.300   Max.   :10.000
##                 NA's   :2       NA's   :2
##    BASDAIDif           PCRDif
##  Min.   :-7.0000   Min.   :-88.40
##  1st Qu.:-1.1000   1st Qu.: -5.40
##  Median :-0.1000   Median : -0.20
##  Mean   :-0.5354   Mean   : -4.14
##  3rd Qu.: 0.4750   3rd Qu.:  1.00
##  Max.   : 5.2000   Max.   : 28.00
##  NA's   :19        NA's   :20
```

```
base_rx3 <- base_rx1[,c(-1,-25:-45,-48:-56,-58:-61)]
summary(base_rx3)
```

```
##       EDAD            SEXO          IMC           IMC>30        TSINT
##  Min.   :21.00   MALE  :82   Min.   :19.37   NO  :84   Min.   : 0.0
0
##  1st Qu.:38.00   FEMALE:19   1st Qu.:24.05   SI  :11   1st Qu.: 8.0
0
##  Median :46.00               Median :26.02   NA's: 6   Median :15.0
0
##  Mean   :46.68               Mean   :26.38             Mean   :17.7
6
##  3rd Qu.:54.00               3rd Qu.:28.68             3rd Qu.:26.0
0
##  Max.   :75.00               Max.   :40.83             Max.   :52.0
0
##                              NA's   :6                 NA's   :4
##   HLAB27     EA      TABACO_Kat       VSG             BASMI          UVE
ITIS
```

```
##  SI  :86   SI:86   SI:70      Min.   :  0.50   Min.   :0.5378   NO:
79
##  NO  :13   NO:15   NO:31      1st Qu.:  9.00   1st Qu.:1.6458   SI:
22
##  NA's: 2                      Median : 19.00   Median :2.8728
##                               Mean   : 26.65   Mean   :3.0915
##                               3rd Qu.: 38.75   3rd Qu.:4.0864
##                               Max.   :115.00   Max.   :7.2729
##                               NA's   :3        NA's   :19
##  PSORIASIS ENF_INF   TTOBIO         NUM_TB_PREV          MOTIVO
##  NO  :92   NO  :92   ETA:31   treatments.0:75   non.change  :77
##  SI  : 7   SI  : 7   ADA:44   treatments.1:20   Inefficacy  :17
##  NA's: 2   NA's: 2   IFX:11   treatments.2: 6   Side.effects: 7
##                      GOL:12
##                      CTZ: 3
##
##
##     TIEMBIO       BIO_INICI Biol_4_kat    Interval      AINE       F
AME
##  Min.   :  0.00   NO  :25   NO:55      Min.   :2.00   NO  :42   NO
:81
##  1st Qu.:  8.00   SI  :75   SI:46      1st Qu.:3.00   SI  :57   SI
:18
##  Median : 42.50   NA's: 1              Median :3.00   NA's: 2   NA'
s: 2
##  Mean   : 45.51                        Mean   :3.45
##  3rd Qu.: 76.75                        3rd Qu.:4.00
##  Max.   :132.00                        Max.   :6.00
##  NA's   :1                             NA's   :1
##     i_BASDAI          EGP              EGM         mSASSS_Progress
##  Min.   :0.700   Min.   : 0.000   Min.   : 0.000   Min.   :-2.50
##  1st Qu.:4.225   1st Qu.: 2.000   1st Qu.: 1.500   1st Qu.: 0.00
##  Median :5.400   Median : 3.000   Median : 3.000   Median : 0.00
##  Mean   :5.326   Mean   : 4.031   Mean   : 3.455   Mean   : 1.98
##  3rd Qu.:6.400   3rd Qu.: 6.000   3rd Qu.: 5.000   3rd Qu.: 3.00
##  Max.   :8.800   Max.   :10.000   Max.   :10.000   Max.   :21.50
##  NA's   :3       NA's   :3        NA's   :2
##  Mind_2_Synd_FL Mind_2_Synd_BL  PCR_INICIOB       i_ASDAS
HVGP
##  NO:46          NO:50           Min.   : 0.00   Min.   :1.500   Min.
: 1.000
##  SI:55          SI:51           1st Qu.: 4.60   1st Qu.:2.700   1st
Qu.: 5.000
##                                 Median :11.10   Median :3.500   Medi
an : 6.000
##                                 Mean   :18.70   Mean   :3.402   Mean
: 5.923
##                                 3rd Qu.:28.05   3rd Qu.:4.000   3rd
Qu.: 7.000
##                                 Max.   :98.00   Max.   :5.300   Max.
:10.000
##                                 NA's   :2       NA's   :2
##     BASFIDif         BASDAIDif          ASDASDif           PCRDif
##  Min.   :-8.9000   Min.   :-7.0000   Min.   :-3.4650   Min.   :-88.
```

```
40
##  1st Qu.:-1.8000   1st Qu.:-1.1000   1st Qu.:-1.0300   1st Qu.: -5.
40
##  Median :-0.2000   Median :-0.1000   Median :-0.2247   Median : -0.
20
##  Mean   :-0.5667   Mean   :-0.5354   Mean   :-0.3908   Mean   : -4.
14
##  3rd Qu.: 0.6250   3rd Qu.: 0.4750   3rd Qu.: 0.2567   3rd Qu.:  1.
00
##  Max.   : 6.2000   Max.   : 5.2000   Max.   : 1.9947   Max.   : 28.
00
##  NA's   :17        NA's   :19        NA's   :28        NA's   :20
```

```
library(psych)
describe(base_rx2)
```

```
##                       vars   n  mean    sd median trimmed   mad    m
in    max
## EDAD                     1 101 46.68 11.92  46.00   46.37 11.86  21.
00  75.00
## SEXO*                    2 101  1.19  0.39   1.00    1.11  0.00   1.
00   2.00
## IMC                      3  95 26.38  3.74  26.02   26.18  3.49  19.
37  40.83
## IMC>30*                  4  95  1.12  0.32   1.00    1.03  0.00   1.
00   2.00
## TSINT                    5  97 17.76 12.81  15.00   16.65 13.34   0.
00  52.00
## HLAB27*                  6  99  1.13  0.34   1.00    1.05  0.00   1.
00   2.00
## EA*                      7 101  1.15  0.36   1.00    1.06  0.00   1.
00   2.00
## TABACO_Kat*              8 101  1.31  0.46   1.00    1.26  0.00   1.
00   2.00
## VSG                      9  98 26.65 22.53  19.00   24.02 19.27   0.
50 115.00
## BASMI                   10  82  3.09  1.68   2.87    2.98  1.82   0.
54   7.27
## UVEITIS*                11 101  1.22  0.41   1.00    1.15  0.00   1.
00   2.00
## PSORIASIS*              12  99  1.07  0.26   1.00    1.00  0.00   1.
00   2.00
## ENF_INF*                13  99  1.07  0.26   1.00    1.00  0.00   1.
00   2.00
## TTOBIO*                 14 101  2.13  1.07   2.00    2.00  1.48   1.
00   5.00
## NUM_TB_PREV*            15 101  1.32  0.58   1.00    1.20  0.00   1.
00   3.00
## MOTIVO*                 16 101  1.31  0.60   1.00    1.17  0.00   1.
00   3.00
## TIEMBIO                 17 100 45.51 40.09  42.50   41.90 51.89   0.
00 132.00
## BIO_INICI*              18 100  1.75  0.44   2.00    1.81  0.00   1.
00   2.00
```

```
## Biol_4_kat*            19 101  1.46  0.50   1.00    1.44  0.00   1.
00   2.00
## Interval               20 100  3.45  0.98   3.00    3.42  1.48   2.
00   6.00
## AINE*                  21  99  1.58  0.50   2.00    1.59  0.00   1.
00   2.00
## FAME*                  22  99  1.18  0.39   1.00    1.11  0.00   1.
00   2.00
## i_BASDAI               23  98  5.33  1.83   5.40    5.38  1.70   0.
70   8.80
## EGP                    24  98  4.03  2.78   3.00    3.88  2.97   0.
00  10.00
## EGM                    25  99  3.45  2.40   3.00    3.27  2.97   0.
00  10.00
## mSASSS_Progress        26 101  1.98  3.75   0.00    1.12  0.00  -2.
50  21.50
## New_Syn_mSASSS*        27 101  1.20  0.40   1.00    1.12  0.00   1.
00   2.00
## Prog_Syn_mSASSS*       28 101  1.11  0.31   1.00    1.01  0.00   1.
00   2.00
## mSASSS_Progress_Kat*   29 101  1.30  0.46   1.00    1.25  0.00   1.
00   2.00
## New_Prog_Syn_Msasss*   30 101  1.22  0.41   1.00    1.15  0.00   1.
00   2.00
## Mind_2_Synd_FL*        31 101  1.54  0.50   2.00    1.56  0.00   1.
00   2.00
## Mind_2_Synd_BL*        32 101  1.50  0.50   2.00    1.51  0.00   1.
00   2.00
## PCR_INICIOB            33  99 18.70 19.39  11.10   15.72 13.49   0.
00  98.00
## i_ASDAS                34  99  3.40  0.85   3.50    3.41  0.89   1.
50   5.30
## HVGP                   35 101  5.92  1.99   6.00    6.02  1.48   1.
00  10.00
## BASFIDif               36  84 -0.57  2.42  -0.20   -0.47  1.63  -8.
90   6.20
## BASDAIDif              37  82 -0.54  1.99  -0.10   -0.37  1.33  -7.
00   5.20
## ASDASDif               38  73 -0.39  1.15  -0.22   -0.32  0.77  -3.
46   1.99
## PCRDif                 39  81 -4.14 13.70  -0.20   -1.86  3.41 -88.
40  28.00
##                       range  skew kurtosis   se
## EDAD                 54.00  0.27    -0.59 1.19
## SEXO*                 1.00  1.57     0.48 0.04
## IMC                  21.46  0.84     1.71 0.38
## IMC>30*               1.00  2.36     3.63 0.03
## TSINT                52.00  0.69    -0.29 1.30
## HLAB27*               1.00  2.15     2.65 0.03
## EA*                   1.00  1.95     1.81 0.04
## TABACO_Kat*           1.00  0.82    -1.33 0.05
## VSG                 114.50  1.22     1.58 2.28
## BASMI                 6.74  0.47    -0.76 0.19
## UVEITIS*              1.00  1.35    -0.19 0.04
```

```
## PSORIASIS*            1.00  3.30    8.97 0.03
## ENF_INF*              1.00  3.30    8.97 0.03
## TTOBIO*               4.00  0.90    0.04 0.11
## NUM_TB_PREV*          2.00  1.64    1.60 0.06
## MOTIVO*               2.00  1.75    1.88 0.06
## TIEMBIO             132.00  0.50   -0.99 4.01
## BIO_INICI*            1.00 -1.14   -0.71 0.04
## Biol_4_kat*           1.00  0.18   -1.99 0.05
## Interval              4.00  0.23   -0.73 0.10
## AINE*                 1.00 -0.30   -1.93 0.05
## FAME*                 1.00  1.62    0.65 0.04
## i_BASDAI              8.10 -0.26   -0.35 0.18
## EGP                  10.00  0.38   -1.10 0.28
## EGM                  10.00  0.62   -0.37 0.24
## mSASSS_Progress      24.00  2.69    8.37 0.37
## New_Syn_mSASSS*       1.00  1.49    0.23 0.04
## Prog_Syn_mSASSS*      1.00  2.47    4.16 0.03
## mSASSS_Progress_Kat*  1.00  0.88   -1.25 0.05
## New_Prog_Syn_Msasss*  1.00  1.35   -0.19 0.04
## Mind_2_Synd_FL*       1.00 -0.18   -1.99 0.05
## Mind_2_Synd_BL*       1.00 -0.02   -2.02 0.05
## PCR_INICIOB          98.00  1.79    3.82 1.95
## i_ASDAS               3.80 -0.15   -0.58 0.08
## HVGP                  9.00 -0.41   -0.29 0.20
## BASFIDif             15.10 -0.45    1.67 0.26
## BASDAIDif            12.20 -0.73    1.71 0.22
## ASDASDif              5.46 -0.58    0.28 0.13
## PCRDif              116.40 -3.28   16.60 1.52
```

```
describe(base_rx3)
```

```
##                    vars   n  mean    sd median trimmed   mad   min
max  range
## EDAD                  1 101 46.68 11.92  46.00   46.37 11.86 21.00  7
5.00  54.00
## SEXO*                 2 101  1.19  0.39   1.00    1.11  0.00  1.00
2.00   1.00
## IMC                   3  95 26.38  3.74  26.02   26.18  3.49 19.37  4
0.83  21.46
## IMC>30*               4  95  1.12  0.32   1.00    1.03  0.00  1.00
2.00   1.00
## TSINT                 5  97 17.76 12.81  15.00   16.65 13.34  0.00  5
2.00  52.00
## HLAB27*               6  99  1.13  0.34   1.00    1.05  0.00  1.00
2.00   1.00
## EA*                   7 101  1.15  0.36   1.00    1.06  0.00  1.00
2.00   1.00
## TABACO_Kat*           8 101  1.31  0.46   1.00    1.26  0.00  1.00
2.00   1.00
## VSG                   9  98 26.65 22.53  19.00   24.02 19.27  0.50 11
5.00 114.50
## BASMI                10  82  3.09  1.68   2.87    2.98  1.82  0.54
7.27   6.74
## UVEITIS*             11 101  1.22  0.41   1.00    1.15  0.00  1.00
```

```
2.00   1.00
## PSORIASIS*         12  99  1.07  0.26   1.00    1.00  0.00   1.00
2.00   1.00
## ENF_INF*           13  99  1.07  0.26   1.00    1.00  0.00   1.00
2.00   1.00
## TTOBIO*            14 101  2.13  1.07   2.00    2.00  1.48   1.00
5.00   4.00
## NUM_TB_PREV*       15 101  1.32  0.58   1.00    1.20  0.00   1.00
3.00   2.00
## MOTIVO*            16 101  1.31  0.60   1.00    1.17  0.00   1.00
3.00   2.00
## TIEMBIO            17 100 45.51 40.09  42.50   41.90 51.89   0.00 13
2.00 132.00
## BIO_INICI*         18 100  1.75  0.44   2.00    1.81  0.00   1.00
2.00   1.00
## Biol_4_kat*        19 101  1.46  0.50   1.00    1.44  0.00   1.00
2.00   1.00
## Interval           20 100  3.45  0.98   3.00    3.42  1.48   2.00
6.00   4.00
## AINE*              21  99  1.58  0.50   2.00    1.59  0.00   1.00
2.00   1.00
## FAME*              22  99  1.18  0.39   1.00    1.11  0.00   1.00
2.00   1.00
## i_BASDAI           23  98  5.33  1.83   5.40    5.38  1.70   0.70
8.80   8.10
## EGP                24  98  4.03  2.78   3.00    3.88  2.97   0.00  1
0.00  10.00
## EGM                25  99  3.45  2.40   3.00    3.27  2.97   0.00  1
0.00  10.00
## mSASSS_Progress    26 101  1.98  3.75   0.00    1.12  0.00  -2.50  2
1.50  24.00
## Mind_2_Synd_FL*    27 101  1.54  0.50   2.00    1.56  0.00   1.00
2.00   1.00
## Mind_2_Synd_BL*    28 101  1.50  0.50   2.00    1.51  0.00   1.00
2.00   1.00
## PCR_INICIOB        29  99 18.70 19.39  11.10   15.72 13.49   0.00  9
8.00  98.00
## i_ASDAS            30  99  3.40  0.85   3.50    3.41  0.89   1.50
5.30   3.80
## HVGP               31 101  5.92  1.99   6.00    6.02  1.48   1.00  1
0.00   9.00
## BASFIDif           32  84 -0.57  2.42  -0.20   -0.47  1.63  -8.90
6.20  15.10
## BASDAIDif          33  82 -0.54  1.99  -0.10   -0.37  1.33  -7.00
5.20  12.20
## ASDASDif           34  73 -0.39  1.15  -0.22   -0.32  0.77  -3.46
1.99   5.46
## PCRDif             35  81 -4.14 13.70  -0.20   -1.86  3.41 -88.40  2
8.00 116.40
##                   skew kurtosis   se
## EDAD              0.27    -0.59 1.19
## SEXO*             1.57     0.48 0.04
## IMC               0.84     1.71 0.38
## IMC>30*           2.36     3.63 0.03
```

```
## TSINT            0.69    -0.29 1.30
## HLAB27*          2.15     2.65 0.03
## EA*              1.95     1.81 0.04
## TABACO_Kat*      0.82    -1.33 0.05
## VSG              1.22     1.58 2.28
## BASMI            0.47    -0.76 0.19
## UVEITIS*         1.35    -0.19 0.04
## PSORIASIS*       3.30     8.97 0.03
## ENF_INF*         3.30     8.97 0.03
## TTOBIO*          0.90     0.04 0.11
## NUM_TB_PREV*     1.64     1.60 0.06
## MOTIVO*          1.75     1.88 0.06
## TIEMBIO          0.50    -0.99 4.01
## BIO_INICI*      -1.14    -0.71 0.04
## Biol_4_kat*      0.18    -1.99 0.05
## Interval         0.23    -0.73 0.10
## AINE*           -0.30    -1.93 0.05
## FAME*            1.62     0.65 0.04
## i_BASDAI        -0.26    -0.35 0.18
## EGP              0.38    -1.10 0.28
## EGM              0.62    -0.37 0.24
## mSASSS_Progress  2.69     8.37 0.37
## Mind_2_Synd_FL* -0.18    -1.99 0.05
## Mind_2_Synd_BL* -0.02    -2.02 0.05
## PCR_INICIOB      1.79     3.82 1.95
## i_ASDAS         -0.15    -0.58 0.08
## HVGP            -0.41    -0.29 0.20
## BASFIDif        -0.45     1.67 0.26
## BASDAIDif       -0.73     1.71 0.22
## ASDASDif        -0.58     0.28 0.13
## PCRDif          -3.28    16.60 1.52
```

```
base_rx.num<-base_rx[,c(-1,-3,-5,-7,-8,-9,-12,-13,-14,-15,-16,-17,-19,
-20,-22,-23,-58,-59,-60,-61,-62,-63)] # data frame con únicamente vari
ables numéricas

library(psych)
describe(base_rx.num)
```

```
##                 vars   n  mean    sd median trimmed   mad   min
max  range
## EDAD               1 101 46.68 11.92  46.00   46.37 11.86 21.00   75
.00  54.00
## IMC                2  95 26.38  3.74  26.02   26.18  3.49 19.37   40
.83  21.46
## TSINT              3  97 17.76 12.81  15.00   16.65 13.34  0.00   52
.00  52.00
## VSG                4  98 26.65 22.53  19.00   24.02 19.27  0.50  115
.00 114.50
## BASMI              5  82  3.09  1.68   2.87    2.98  1.82  0.54    7
.27   6.74
## TIEMBIO            6 100 45.51 40.09  42.50   41.90 51.89  0.00  132
.00 132.00
## Interval           7 100  3.45  0.98   3.00    3.42  1.48  2.00    6
```

```
.00   4.00
## i_BASDAI            8  98  5.33  1.83   5.40    5.38  1.70  0.70   8
.80   8.10
## BASDAI_0            9  97  3.67  2.28   3.20    3.54  2.52  0.20   8
.80   8.60
## BASDAI_1           10  97  2.90  1.87   2.70    2.79  2.22  0.00   8
.50   8.50
## BASDAI_2           11  97  3.42  6.59   2.50    2.73  2.22  0.00  65
.00  65.00
## BASDAI_3           12  93  3.11  2.02   3.00    2.99  2.67  0.00   8
.00   8.00
## BASDAI_4           13  91  3.07  2.01   2.80    2.96  2.37  0.00   8
.00   8.00
## BASDAI_5           14  84  2.92  1.91   2.55    2.77  2.00  0.00   8
.00   8.00
## BASDAI_6           15  85  2.92  1.90   2.80    2.79  2.52  0.00   7
.30   7.30
## ASDAS_0            16  96  2.22  1.20   2.06    2.15  1.23  0.23   5
.07   4.85
## ASDAS_1            17  88  1.82  1.10   1.57    1.72  0.80  0.25   7
.13   6.88
## ASDAS_2            18  92  1.77  0.91   1.83    1.74  0.87  0.00   4
.13   4.13
## ASDAS_3            19  87  1.82  0.93   1.77    1.78  0.95  0.05   3
.98   3.93
## ASDAS_4            20  79  1.81  0.96   1.67    1.78  0.88  0.00   4
.45   4.45
## ASDAS_5            21  71  1.73  0.92   1.64    1.66  0.88  0.03   4
.06   4.02
## ASDAS_6            22  77  1.81  0.93   1.68    1.77  0.97  0.10   3
.99   3.89
## PCR_0              23  94  8.18 13.25   3.35    5.12  4.23  0.00  88
.70  88.70
## PCR_1              24  98  4.36  8.03   2.00    2.83  1.93  0.00  61
.30  61.30
## PCR_2              25  99  4.36  5.95   2.00    3.22  2.37  0.00  33
.90  33.90
## PCR_3              26  97  4.45  6.33   1.90    3.19  2.52  0.00  37
.00  37.00
## PCR_4              27  94  5.37 10.46   2.05    2.94  2.89  0.00  68
.50  68.50
## PCR_5              28  91  4.12  8.00   1.40    2.73  1.82  0.00  65
.90  65.90
## PCR_6              29  87  4.42  6.81   2.00    3.05  2.52  0.00  39
.70  39.70
## EGP                30  98  4.03  2.78   3.00    3.88  2.97  0.00  10
.00  10.00
## EGM                31  99  3.45  2.40   3.00    3.27  2.97  0.00  10
.00  10.00
## BASFI_0            32  98  3.93  2.70   3.85    3.80  3.34  0.00   9
.30   9.30
## BASFI_1            33  99  3.06  2.31   2.70    2.87  2.22  0.00   8
.80   8.80
## BASFI_2            34 101  2.67  2.22   2.33    2.48  2.80  0.00   7
```

```
.89   7.89
## BASFI_3           35  93  2.88  2.20   2.80    2.73  2.52  0.00   7
.90   7.90
## BASFI_4           36  89  3.34  2.36   3.50    3.24  2.97  0.00   8
.40   8.40
## BASFI_5           37  79  3.12  2.34   3.20    2.98  2.82  0.00   8
.10   8.10
## BASFI_6           38  85  3.31  2.45   3.10    3.17  2.97  0.00   8
.30   8.30
## mSASSS_Mean_BL    39 101 16.46 20.92   5.00   12.80  7.41  0.00  72
.00  72.00
## mSASSS_Mean_FL    40 101 18.44 22.12   8.00   15.10 11.86  0.00  72
.00  72.00
## mSASSS_Progress   41 101  1.98  3.75   0.00    1.12  0.00 -2.50  21
.50  24.00
## PCR_INICIOB       42  99 18.70 19.39  11.10   15.72 13.49  0.00  98
.00  98.00
## i_ASDAS           43  99  3.40  0.85   3.50    3.41  0.89  1.50   5
.30   3.80
## HVGP              44 101  5.92  1.99   6.00    6.02  1.48  1.00  10
.00   9.00
##                  skew kurtosis   se
## EDAD              0.27    -0.59 1.19
## IMC               0.84     1.71 0.38
## TSINT             0.69    -0.29 1.30
## VSG               1.22     1.58 2.28
## BASMI             0.47    -0.76 0.19
## TIEMBIO           0.50    -0.99 4.01
## Interval          0.23    -0.73 0.10
## i_BASDAI         -0.26    -0.35 0.18
## BASDAI_0          0.47    -0.66 0.23
## BASDAI_1          0.53    -0.32 0.19
## BASDAI_2          8.41    75.78 0.67
## BASDAI_3          0.36    -0.88 0.21
## BASDAI_4          0.42    -0.87 0.21
## BASDAI_5          0.62    -0.39 0.21
## BASDAI_6          0.46    -0.79 0.21
## ASDAS_0           0.48    -0.49 0.12
## ASDAS_1           1.71     5.06 0.12
## ASDAS_2           0.28    -0.44 0.09
## ASDAS_3           0.28    -0.70 0.10
## ASDAS_4           0.38    -0.35 0.11
## ASDAS_5           0.61    -0.13 0.11
## ASDAS_6           0.36    -0.60 0.11
## PCR_0             3.34    14.15 1.37
## PCR_1             4.88    27.71 0.81
## PCR_2             2.75     9.26 0.60
## PCR_3             2.70     8.90 0.64
## PCR_4             3.90    16.88 1.08
## PCR_5             5.52    37.64 0.84
## PCR_6             3.35    13.58 0.73
## EGP               0.38    -1.10 0.28
## EGM               0.62    -0.37 0.24
## BASFI_0           0.27    -1.02 0.27
```

```
## BASFI_1          0.67    -0.47 0.23
## BASFI_2          0.49    -0.81 0.22
## BASFI_3          0.46    -0.79 0.23
## BASFI_4          0.24    -1.05 0.25
## BASFI_5          0.35    -0.92 0.26
## BASFI_6          0.35    -0.99 0.27
## mSASSS_Mean_BL   1.18     0.09 2.08
## mSASSS_Mean_FL   0.98    -0.42 2.20
## mSASSS_Progress  2.69     8.37 0.37
## PCR_INICIOB      1.79     3.82 1.95
## i_ASDAS         -0.15    -0.58 0.08
## HVGP            -0.41    -0.29 0.20
```

```
base_rx.num1 <-
  base_rx.num %>%
  mutate( BASFIDif = (BASFI_6-BASFI_0), BASDAIDif = (BASDAI_6-BASDAI_0
), ASDASDif = (ASDAS_6-ASDAS_0), PCRDif = (PCR_6-PCR_0))
summary(base_rx.num1)
```

```
##       EDAD            IMC            TSINT            VSG
##  Min.   :21.00   Min.   :19.37   Min.   : 0.00   Min.   :  0.50
##  1st Qu.:38.00   1st Qu.:24.05   1st Qu.: 8.00   1st Qu.:  9.00
##  Median :46.00   Median :26.02   Median :15.00   Median : 19.00
##  Mean   :46.68   Mean   :26.38   Mean   :17.76   Mean   : 26.65
##  3rd Qu.:54.00   3rd Qu.:28.68   3rd Qu.:26.00   3rd Qu.: 38.75
##  Max.   :75.00   Max.   :40.83   Max.   :52.00   Max.   :115.00
##                  NA's   :6       NA's   :4       NA's   :3
##      BASMI           TIEMBIO          Interval       i_BASDAI
##  Min.   :0.5378   Min.   :  0.00   Min.   :2.00   Min.   :0.700
##  1st Qu.:1.6458   1st Qu.:  8.00   1st Qu.:3.00   1st Qu.:4.225
##  Median :2.8728   Median : 42.50   Median :3.00   Median :5.400
##  Mean   :3.0915   Mean   : 45.51   Mean   :3.45   Mean   :5.326
##  3rd Qu.:4.0864   3rd Qu.: 76.75   3rd Qu.:4.00   3rd Qu.:6.400
##  Max.   :7.2729   Max.   :132.00   Max.   :6.00   Max.   :8.800
##  NA's   :19       NA's   :1        NA's   :1      NA's   :3
##     BASDAI_0       BASDAI_1        BASDAI_2         BASDAI_3
##  Min.   :0.20   Min.   :0.000   Min.   : 0.000   Min.   :0.000
##  1st Qu.:2.00   1st Qu.:1.400   1st Qu.: 1.400   1st Qu.:1.200
##  Median :3.20   Median :2.700   Median : 2.500   Median :3.000
##  Mean   :3.67   Mean   :2.902   Mean   : 3.419   Mean   :3.108
##  3rd Qu.:5.10   3rd Qu.:4.400   3rd Qu.: 4.200   3rd Qu.:4.800
##  Max.   :8.80   Max.   :8.500   Max.   :65.000   Max.   :8.000
##  NA's   :4      NA's   :4       NA's   :4        NA's   :8
##     BASDAI_4        BASDAI_5        BASDAI_6        ASDAS_0
##  Min.   :0.000   Min.   :0.000   Min.   :0.000   Min.   :0.2257
##  1st Qu.:1.200   1st Qu.:1.275   1st Qu.:1.100   1st Qu.:1.3874
##  Median :2.800   Median :2.550   Median :2.800   Median :2.0565
##  Mean   :3.075   Mean   :2.915   Mean   :2.924   Mean   :2.2160
##  3rd Qu.:4.600   3rd Qu.:4.200   3rd Qu.:4.600   3rd Qu.:2.9248
##  Max.   :8.000   Max.   :8.000   Max.   :7.300   Max.   :5.0749
##  NA's   :10      NA's   :17      NA's   :16      NA's   :5
##     ASDAS_1          ASDAS_2            ASDAS_3           ASDAS_4
##  Min.   :0.2471   Min.   :0.001737   Min.   :0.04892   Min.   :0.00
058
```

```
##  1st Qu.:1.1572   1st Qu.:1.088078   1st Qu.:1.16497   1st Qu.:1.17
363
##  Median :1.5738   Median :1.827288   Median :1.76656   Median :1.66
660
##  Mean   :1.8249   Mean   :1.773470   Mean   :1.81523   Mean   :1.81
274
##  3rd Qu.:2.4204   3rd Qu.:2.316346   3rd Qu.:2.47797   3rd Qu.:2.44
173
##  Max.   :7.1255   Max.   :4.131246   Max.   :3.98374   Max.   :4.45
150
##  NA's   :13       NA's   :9          NA's   :14        NA's   :22
##     ASDAS_5          ASDAS_6          PCR_0            PCR_1
##  Min.   :0.0338   Min.   :0.096   Min.   : 0.000   Min.   : 0.000
##  1st Qu.:1.0522   1st Qu.:1.143   1st Qu.: 1.000   1st Qu.: 1.000
##  Median :1.6400   Median :1.680   Median : 3.350   Median : 2.000
##  Mean   :1.7329   Mean   :1.807   Mean   : 8.181   Mean   : 4.358
##  3rd Qu.:2.1781   3rd Qu.:2.397   3rd Qu.: 9.100   3rd Qu.: 4.675
##  Max.   :4.0579   Max.   :3.988   Max.   :88.700   Max.   :61.300
##  NA's   :30       NA's   :24      NA's   :7        NA's   :3
##      PCR_2           PCR_3            PCR_4            PCR_5
##  Min.   : 0.00   Min.   : 0.000   Min.   : 0.000   Min.   : 0.000
##  1st Qu.: 0.90   1st Qu.: 0.750   1st Qu.: 0.700   1st Qu.: 0.615
##  Median : 2.00   Median : 1.900   Median : 2.050   Median : 1.400
##  Mean   : 4.36   Mean   : 4.452   Mean   : 5.368   Mean   : 4.118
##  3rd Qu.: 5.60   3rd Qu.: 5.600   3rd Qu.: 5.375   3rd Qu.: 6.000
##  Max.   :33.90   Max.   :37.000   Max.   :68.500   Max.   :65.900
##  NA's   :2       NA's   :4        NA's   :7        NA's   :10
##      PCR_6            EGP              EGM             BASFI_0
##  Min.   : 0.00   Min.   : 0.000   Min.   : 0.000   Min.   :0.000
##  1st Qu.: 0.60   1st Qu.: 2.000   1st Qu.: 1.500   1st Qu.:1.525
##  Median : 2.00   Median : 3.000   Median : 3.000   Median :3.850
##  Mean   : 4.42   Mean   : 4.031   Mean   : 3.455   Mean   :3.931
##  3rd Qu.: 5.95   3rd Qu.: 6.000   3rd Qu.: 5.000   3rd Qu.:5.975
##  Max.   :39.70   Max.   :10.000   Max.   :10.000   Max.   :9.300
##  NA's   :14      NA's   :3        NA's   :2        NA's   :3
##     BASFI_1         BASFI_2         BASFI_3         BASFI_4
BASFI_5
##  Min.   :0.000   Min.   :0.000   Min.   :0.000   Min.   :0.00   Min
.   :0.000
##  1st Qu.:1.200   1st Qu.:0.550   1st Qu.:1.000   1st Qu.:1.30   1st
Qu.:1.100
##  Median :2.700   Median :2.330   Median :2.800   Median :3.50   Med
ian :3.200
##  Mean   :3.059   Mean   :2.667   Mean   :2.882   Mean   :3.34   Mea
n   :3.118
##  3rd Qu.:4.550   3rd Qu.:4.340   3rd Qu.:4.500   3rd Qu.:5.00   3rd
Qu.:4.700
##  Max.   :8.800   Max.   :7.890   Max.   :7.900   Max.   :8.40   Max
.   :8.100
##  NA's   :2                       NA's   :8       NA's   :12     NA'
s   :22
##     BASFI_6      mSASSS_Mean_BL  mSASSS_Mean_FL  mSASSS_Progress
##  Min.   :0.000   Min.   : 0.00   Min.   : 0.00   Min.   :-2.50
##  1st Qu.:1.100   1st Qu.: 0.00   1st Qu.: 0.00   1st Qu.: 0.00
```

```
##  Median :3.100   Median : 5.00   Median : 8.00   Median : 0.00
##  Mean   :3.313   Mean   :16.46   Mean   :18.44   Mean   : 1.98
##  3rd Qu.:5.100   3rd Qu.:23.00   3rd Qu.:30.00   3rd Qu.: 3.00
##  Max.   :8.300   Max.   :72.00   Max.   :72.00   Max.   :21.50
##  NA's   :16
##   PCR_INICIOB       i_ASDAS           HVGP           BASFIDif
##  Min.   : 0.00   Min.   :1.500   Min.   : 1.000   Min.   :-8.9000
##  1st Qu.: 4.60   1st Qu.:2.700   1st Qu.: 5.000   1st Qu.:-1.8000
##  Median :11.10   Median :3.500   Median : 6.000   Median :-0.2000
##  Mean   :18.70   Mean   :3.402   Mean   : 5.923   Mean   :-0.5667
##  3rd Qu.:28.05   3rd Qu.:4.000   3rd Qu.: 7.000   3rd Qu.: 0.6250
##  Max.   :98.00   Max.   :5.300   Max.   :10.000   Max.   : 6.2000
##  NA's   :2       NA's   :2                        NA's   :17
##    BASDAIDif          ASDASDif           PCRDif
##  Min.   :-7.0000   Min.   :-3.4650   Min.   :-88.40
##  1st Qu.:-1.1000   1st Qu.:-1.0300   1st Qu.: -5.40
##  Median :-0.1000   Median :-0.2247   Median : -0.20
##  Mean   :-0.5354   Mean   :-0.3908   Mean   : -4.14
##  3rd Qu.: 0.4750   3rd Qu.: 0.2567   3rd Qu.:  1.00
##  Max.   : 5.2000   Max.   : 1.9947   Max.   : 28.00
##  NA's   :19        NA's   :28        NA's   :20
```

```
base_rx.num2<-base_rx.num1[,c(-9:-29,-32:-40)]
summary(base_rx.num2)
```

```
##       EDAD            IMC            TSINT            VSG
##  Min.   :21.00   Min.   :19.37   Min.   : 0.00   Min.   :  0.50
##  1st Qu.:38.00   1st Qu.:24.05   1st Qu.: 8.00   1st Qu.:  9.00
##  Median :46.00   Median :26.02   Median :15.00   Median : 19.00
##  Mean   :46.68   Mean   :26.38   Mean   :17.76   Mean   : 26.65
##  3rd Qu.:54.00   3rd Qu.:28.68   3rd Qu.:26.00   3rd Qu.: 38.75
##  Max.   :75.00   Max.   :40.83   Max.   :52.00   Max.   :115.00
##                  NA's   :6       NA's   :4       NA's   :3
##      BASMI          TIEMBIO          Interval        i_BASDAI
##  Min.   :0.5378   Min.   :  0.00   Min.   :2.00   Min.   :0.700
##  1st Qu.:1.6458   1st Qu.:  8.00   1st Qu.:3.00   1st Qu.:4.225
##  Median :2.8728   Median : 42.50   Median :3.00   Median :5.400
##  Mean   :3.0915   Mean   : 45.51   Mean   :3.45   Mean   :5.326
##  3rd Qu.:4.0864   3rd Qu.: 76.75   3rd Qu.:4.00   3rd Qu.:6.400
##  Max.   :7.2729   Max.   :132.00   Max.   :6.00   Max.   :8.800
##  NA's   :19       NA's   :1        NA's   :1      NA's   :3
##       EGP              EGM          mSASSS_Progress  PCR_INICIOB
##  Min.   : 0.000   Min.   : 0.000   Min.   :-2.50   Min.   : 0.00
##  1st Qu.: 2.000   1st Qu.: 1.500   1st Qu.: 0.00   1st Qu.: 4.60
##  Median : 3.000   Median : 3.000   Median : 0.00   Median :11.10
##  Mean   : 4.031   Mean   : 3.455   Mean   : 1.98   Mean   :18.70
##  3rd Qu.: 6.000   3rd Qu.: 5.000   3rd Qu.: 3.00   3rd Qu.:28.05
##  Max.   :10.000   Max.   :10.000   Max.   :21.50   Max.   :98.00
##  NA's   :3        NA's   :2                        NA's   :2
##     i_ASDAS          HVGP           BASFIDif          BASDAIDif
##  Min.   :1.500   Min.   : 1.000   Min.   :-8.9000   Min.   :-7.0000
##  1st Qu.:2.700   1st Qu.: 5.000   1st Qu.:-1.8000   1st Qu.:-1.1000
##  Median :3.500   Median : 6.000   Median :-0.2000   Median :-0.1000
##  Mean   :3.402   Mean   : 5.923   Mean   :-0.5667   Mean   :-0.5354
```

```
##  3rd Qu.:4.000   3rd Qu.: 7.000   3rd Qu.: 0.6250   3rd Qu.: 0.4750
##  Max.   :5.300   Max.   :10.000   Max.   : 6.2000   Max.   : 5.2000
##  NA's   :2                        NA's   :17        NA's   :19
##     ASDASDif           PCRDif
##  Min.   :-3.4650   Min.   :-88.40
##  1st Qu.:-1.0300   1st Qu.: -5.40
##  Median :-0.2247   Median : -0.20
##  Mean   :-0.3908   Mean   : -4.14
##  3rd Qu.: 0.2567   3rd Qu.:  1.00
##  Max.   : 1.9947   Max.   : 28.00
##  NA's   :28        NA's   :20
```

```
library(dplyr)
library(tidyr)
library(broom)

base_rx.num2 <-base_rx.num2[complete.cases(base_rx.num2), ]
sumstat <- base_rx.num2 %>%
   # Select and rename five variables
    select(
        `Edad` = EDAD,
        `IMC` = IMC,
        `Tiempo sintomas` = TSINT,
        `VSG` = VSG,
        `BASMI` = BASMI,
        `Tiempo con tratamiento` = TIEMBIO,
        `Intervalo entre radiografías` = Interval,
        `BASDAI al inicio del tratamiento` = i_BASDAI,
        `Dolor global del paciente` = EGP,
        `Dolor global en la opinión del médico` = EGM,
        `Diferencia entre el mSASSS al inicio y final` = mSASSS_Progre
ss,
        `PCR al inicio del tratamiento` = PCR_INICIOB,
        `ASDAS al inicio del tratamiento` = i_ASDAS,
        `Valoración global del paciente al inicio del tratamiento` = H
VGP,
        `Diferencia entre el BASFI al inicio y final` = BASFIDif,
        `Diferencia entre el BASDAI al inicio final` = BASDAIDif,
        `Diferencia entre ASDAS al inicio y final` = ASDASDif,
        `Diferencia entre PCR al inicio y final` = PCRDif
        ) %>%
    # Find the mean, st. dev., min, and max for each variable
    summarise_each(funs(mean, median, sd, min, max, var)) %>%

   # Move summary stats to columns
    gather(key, value, everything()) %>%
    separate(key, into = c("variable", "stat"), sep = "_") %>%
    spread(stat, value) %>%

    # Set order of summary statistics
    select(variable, mean, median, sd, min, max, var) %>%

    # Round all numeric variables to one decimal point
    mutate_each(funs(round(., 1)), -variable)
```

```
## Warning: `summarise_each_()` is deprecated as of dplyr 0.7.0.
## Please use `across()` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_warnings()` to see where this warning was gen
erated.
```

```
## Warning: `funs()` is deprecated as of dplyr 0.8.0.
## Please use a list of either functions or lambdas:
##
##   # Simple named list:
##   list(mean = mean, median = median)
##
##   # Auto named with `tibble::lst()`:
##   tibble::lst(mean, median)
##
##   # Using lambdas
##   list(~ mean(., trim = .2), ~ median(., na.rm = TRUE))
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_warnings()` to see where this warning was gen
erated.
```

```
## Warning: `mutate_each_()` is deprecated as of dplyr 0.7.0.
## Please use `across()` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_warnings()` to see where this warning was gen
erated.
```

```
sumstat
```

```
## # A tibble: 18 x 7
##    variable                                 mean median    sd   min
max    var
##    <chr>                                   <dbl>  <dbl> <dbl> <dbl>
<dbl>  <dbl>
##  1 ASDAS al inicio del tratamiento           3.4    3.4   0.7   2.1
5.3    0.5
##  2 BASDAI al inicio del tratamiento          5      5     1.9   0.7
8.5    3.4
##  3 BASMI                                     3.2    2.9   1.7   0.5
6.6    2.7
##  4 Diferencia entre ASDAS al inicio y fin~  -0.4   -0.3   1.1  -3.5
1.8    1.3
##  5 Diferencia entre el BASDAI al inicio f~  -0.4    0     2    -7
5.2    4
##  6 Diferencia entre el BASFI al inicio y ~  -0.3   -0.1   2.1  -5.5
6.2    4.2
##  7 Diferencia entre el mSASSS al inicio y~   2.2    0     4.4  -2.5
21.5   19.4
##  8 Diferencia entre PCR al inicio y final   -4.5   -0.4  15   -88.4
28    224.
##  9 Dolor global del paciente                 3.7    3     2.6   0
10      6.7
## 10 Dolor global en la opinión del médico     3.3    3     2.3   0
8      5.1
## 11 Edad                                     48.2   47    11.5  25
```

```
75    133.
## 12 IMC                                      26.9   26.7   4    19.8
40.8   16.1
## 13 Intervalo entre radiografías              3.5    3     0.9   2
5      0.8
## 14 PCR al inicio del tratamiento            18.4   11.3  17.8   0.5
88.7  318.
## 15 Tiempo con tratamiento                   47.5   48    37.7   0
124   1425.
## 16 Tiempo sintomas                          18.7   16    12.4   0
52    154.
## 17 Valoración global del paciente al inic~   5.8    6     2     1
10       3.8
## 18 VSG                                      28.5   24.8  24.2   0.5
115    588.
```

```
write.table(sumstat, file = "sumstats.txt", sep = ",", quote = FALSE,
row.names = F)
```

```
library(dlookr)
```

```
## Loading required package: mice
```

```
##
## Attaching package: 'mice'
```

```
## The following object is masked from 'package:stats':
##
##     filter
```

```
## The following objects are masked from 'package:base':
##
##     cbind, rbind
```

```
## Registered S3 method overwritten by 'quantmod':
##   method            from
##   as.zoo.data.frame zoo
```

```
##
## Attaching package: 'dlookr'
```

```
## The following object is masked from 'package:psych':
##
##     describe
```

```
## The following object is masked from 'package:base':
##
##     transform
```

```
library(ISLR)
library(SmartEDA)
```

```
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2
```

```r
library(dplyr)
eda_report(base_rx.num2, mSASSS_Progress, output_format = "html")
```

```
## Warning: Unquoting language objects with `!!!` is deprecated as of
rlang 0.4.0.
## Please use `!!` instead.
##
##   # Bad:
##   dplyr::select(data, !!!enquo(x))
##
##   # Good:
##   dplyr::select(data, !!enquo(x))    # Unquote single quosure
##   dplyr::select(data, !!!enquos(x))  # Splice list of quosures
##
## This warning is displayed once per session.
```

```
##
##
## processing file: EDA_Report.Rmd
```

```
##
  |
  |
|   0%
  |
  |...
|   4%
##    inline R code fragments
##
##
  |
  |.....
|   7%
## label: setup (with options)
## List of 1
##  $ include: logi FALSE
##
##
  |
  |........
|  11%
##   ordinary text without R code
##
##
  |
  |..........
|  15%
## label: enrironment (with options)
## List of 3
##  $ echo   : logi FALSE
##  $ warning: logi FALSE
##  $ message: logi FALSE
```

```
##
## Attaching package: 'magrittr'
```

```
## The following object is masked from 'package:tidyr':
##
##     extract

##
## Attaching package: 'ggplot2'

## The following objects are masked from 'package:psych':
##
##     %+%, alpha

##
## Attaching package: 'gridExtra'

## The following object is masked from 'package:dplyr':
##
##     combine

##
## Attaching package: 'moments'

## The following objects are masked from 'package:dlookr':
##
##     kurtosis, skewness

##
## Attaching package: 'kableExtra'

## The following object is masked from 'package:dplyr':
##
##     group_rows

##
  |
  |.............
|  19%
##   ordinary text without R code
##
##
  |
  |................
|  22%
## label: udf (with options)
## List of 3
##  $ echo   : logi FALSE
##  $ warning: logi FALSE
##  $ message: logi FALSE
##
##
  |
  |..................
|  26%
##   ordinary text without R code
##
##
  |
```

```
  |.....................
|  30%
## label: check_variables (with options)
## List of 4
##  $ echo   : logi FALSE
##  $ warning: logi FALSE
##  $ message: logi FALSE
##  $ comment: chr ""
##
##
  |
  |.......................
|  33%
##    inline R code fragments
##
##
  |
  |..........................
|  37%
## label: info_variables (with options)
## List of 5
##  $ echo   : logi FALSE
##  $ warning: logi FALSE
##  $ message: logi FALSE
##  $ comment: chr ""
##  $ results: chr "asis"
##
##
  |
  |.............................
|  41%
##    inline R code fragments
##
##
  |
  |...............................
|  44%
## label: describe_univariate (with options)
## List of 4
##  $ echo   : logi FALSE
##  $ warning: logi FALSE
##  $ message: logi FALSE
##  $ comment: chr ""

## Warning in png(file, width = 1 + k * w, height = h): 'width=13, hei
ght=13' are
## unlikely values in pixels

##
  |
  |..................................
|  48%
##   ordinary text without R code
##
```

```
##
  |
  |....................................
|  52%
## label: normality (with options)
## List of 7
##  $ echo      : logi FALSE
##  $ warning   : logi FALSE
##  $ message   : logi FALSE
##  $ comment   : chr ""
##  $ fig.height: num 4
##  $ fig.width : num 6
##  $ results   : chr "asis"

## Warning in log(x): Se han producido NaNs

## Warning in sqrt(x): Se han producido NaNs

## Warning in log(x): Se han producido NaNs

## Warning in sqrt(x): Se han producido NaNs

## Warning in log(x): Se han producido NaNs

## Warning in sqrt(x): Se han producido NaNs

## Warning in log(x): Se han producido NaNs

## Warning in sqrt(x): Se han producido NaNs

## Warning in log(x): Se han producido NaNs

## Warning in sqrt(x): Se han producido NaNs

## Warning in log(x): Se han producido NaNs

## Warning in sqrt(x): Se han producido NaNs

## Warning in log(x): Se han producido NaNs

## Warning in sqrt(x): Se han producido NaNs

## Warning in log(x): Se han producido NaNs

## Warning in sqrt(x): Se han producido NaNs

## Warning in log(x): Se han producido NaNs

## Warning in sqrt(x): Se han producido NaNs

## Warning in log(x): Se han producido NaNs

## Warning in sqrt(x): Se han producido NaNs

## Warning in log(x): Se han producido NaNs

## Warning in sqrt(x): Se han producido NaNs

## Warning in log(x): Se han producido NaNs
```

```
## Warning in sqrt(x): Se han producido NaNs

##
  |
  |.......................................
|  56%
##   ordinary text without R code
##
##
  |
  |.........................................
|  59%
## label: correlations (with options)
## List of 4
##  $ echo   : logi FALSE
##  $ warning: logi FALSE
##  $ message: logi FALSE
##  $ comment: chr ""
##
##
  |
  |............................................
|  63%
##   ordinary text without R code
##
##
  |
  |...............................................
|  67%
## label: plot_correlations (with options)
## List of 6
##  $ echo      : logi FALSE
##  $ warning   : logi FALSE
##  $ message   : logi FALSE
##  $ comment   : chr ""
##  $ fig.height: num 4
##  $ fig.width : num 6

##
  |
  |.................................................
|  70%
##   ordinary text without R code
##
##
  |
  |....................................................
|  74%
## label: numeric_variables (with options)
## List of 7
##  $ echo      : logi FALSE
##  $ warning   : logi FALSE
##  $ message   : logi FALSE
##  $ comment   : chr ""
```

```
##  $ fig.height: num 4
##  $ fig.width : num 8
##  $ results   : chr "asis"

## `geom_smooth()` using formula 'y ~ x'

## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'

##
  |
  |......................................................
|  78%
##   ordinary text without R code
##
##
  |
  |.........................................................
|  81%
## label: category_variables (with options)
## List of 7
##  $ echo      : logi FALSE
##  $ warning   : logi FALSE
##  $ message   : logi FALSE
##  $ comment   : chr ""
##  $ fig.height: num 4
##  $ fig.width : num 7
##  $ results   : chr "asis"
##
##
  |
  |............................................................
|  85%
##   ordinary text without R code
##
##
  |
  |..............................................................
|  89%
## label: group_correlations (with options)
## List of 4
```

```
##  $ echo   : logi FALSE
##  $ warning: logi FALSE
##  $ message: logi FALSE
##  $ comment: chr ""
##
##
  |
  |.................................................................
|  93%
##   ordinary text without R code
##
##
  |
  |...................................................................
|  96%
## label: plot_group_correlations (with options)
## List of 6
##  $ echo      : logi FALSE
##  $ warning   : logi FALSE
##  $ message   : logi FALSE
##  $ comment   : chr ""
##  $ fig.height: num 4
##  $ fig.width : num 6
##
##
  |
  |...................................................................
...| 100%
##   ordinary text without R code
```

```
## output file: EDA_Report.knit.md
```

```
## "C:/Program Files/RStudio/bin/pandoc/pandoc" +RTS -K512m -RTS EDA_R
eport.utf8.md --to html4 --from markdown+autolink_bare_uris+tex_math_s
ingle_backslash --output pandoc3c586e5316fc.html --email-obfuscation n
one --self-contained --standalone --section-divs --table-of-contents -
-toc-depth 3 --template "C:/Users/maria/OneDrive/Documentos/R/win-libr
ary/4.0/prettydoc/resources/templates/cayman.html" --highlight-style p
ygments --number-sections --include-in-header "C:\Users\maria\AppData\
Local\Temp\Rtmp4GADut\rmarkdown-str3c585d172210.html" --mathjax --vari
able "mathjax-url:https://mathjax.rstudio.com/latest/MathJax.js?config
=TeX-AMS-MML_HTMLorMML" --css "C:\Users\maria\AppData\Local\Temp\Rtmp4
GADut\EDA_Report_files/style.css"
```

```
##
## Output created: C:\Users\maria\AppData\Local\Temp\Rtmp4GADut/EDA_Re
port.html
```

```
str(base_rx.num2)
```

```
## tibble [59 x 18] (S3: tbl_df/tbl/data.frame)
##  $ EDAD           : num [1:59] 63 26 57 41 40 43 60 41 51 38 ...
##  $ IMC            : num [1:59] 26.3 24.6 28.7 21.6 27.7 ...
##  $ TSINT          : num [1:59] 1 6 13 18 16 13 21 13 33 2 ...
##  $ VSG            : num [1:59] 50 3 24 38 25 9 10 52 48 33 ...
```

```
##  $ BASMI          : num [1:59] 1.083 0.979 2.947 3.265 2.202 ...
##  $ TIEMBIO        : num [1:59] 0 0 84 24 0 0 1 58 59 14 ...
##  $ Interval       : num [1:59] 4 3 4 4 4 4 3 4 3 4 ...
##  $ i_BASDAI       : num [1:59] 2.2 2.2 3.8 4.5 5 8 7 5 7 6 ...
##  $ EGP            : num [1:59] 3 1 4 2 5 9 10 2 1 6 ...
##  $ EGM            : num [1:59] 3 1 4 2 5 5 5 1 1 4 ...
##  $ mSASSS_Progress: num [1:59] 3.5 0 1 0 1.5 0 1.5 0 0 0 ...
##  $ PCR_INICIOB    : num [1:59] 88.7 11.3 26 15 16 9.2 16 30 31 5 ..
.
##  $ i_ASDAS        : num [1:59] 3.4 2.2 3.6 3 3.4 3.8 3.9 4.1 4.5 3.
3 ...
##  $ HVGP           : num [1:59] 3 1 7 4 5 5 5 8 7 7 ...
##  $ BASFIDif       : num [1:59] -0.5 0.7 -2.1 -1.8 -0.3 ...
##  $ BASDAIDif      : num [1:59] -1.4 -1.1 0 -1 0 -7 -4.6 0 1.8 -2.5
...
##  $ ASDASDif       : num [1:59] -3.116 -0.99 -0.547 -0.22 1.794 ...
##  $ PCRDif         : num [1:59] -88.4 -9.51 -6 -0.2 16.4 -8.2 -14.5
-0.1 -0.2 1 ...
```

Análisis de missings

```
#De la base de datos original:
sum(is.na(base_rx))
```

```
## [1] 353
```

```
sum(is.na(base_rx.num))
```

```
## [1] 336
```

```
# Hay 353 valores missing, y en la base de datos de variabes únicament
e numéricas hay 336.

#De la base de datos ajustada:
sum(is.na(base_rx2))
```

```
## [1] 147
```

```
sum(is.na(base_rx.num2))
```

```
## [1] 0
```

```
# Hay 147 valores missing, y en la base de datos de variabes únicament
e numéricas hay 128.
colSums(is.na(base_rx))
```

```
##             NUM_PAC                EDAD                SEXO
IMC
##                   0                   0                   0
6
##              IMC>30               TSINT              HLAB27
EA
##                   6                   4                   2
0
##          TABACO_Kat                 VSG               BASMI
UVEITIS
```

```
##                    0                   3                  19                   
0
##            PSORIASIS             ENF_INF              TTOBIO 
NUM_TB_PREV
##                    2                   2                   0 
0
##               MOTIVO             TIEMBIO           BIO_INICI 
Biol_4_kat
##                    0                   1                   1 
0
##             Interval                AINE                FAME 
i_BASDAI
##                    1                   2                   2 
3
##             BASDAI_0            BASDAI_1            BASDAI_2 
BASDAI_3
##                    4                   4                   4 
8
##             BASDAI_4            BASDAI_5            BASDAI_6 
ASDAS_0
##                   10                  17                  16 
5
##              ASDAS_1             ASDAS_2             ASDAS_3 
ASDAS_4
##                   13                   9                  14 
22
##              ASDAS_5             ASDAS_6               PCR_0 
PCR_1
##                   30                  24                   7 
3
##                PCR_2               PCR_3               PCR_4 
PCR_5
##                    2                   4                   7 
10
##                PCR_6                 EGP                 EGM 
BASFI_0
##                   14                   3                   2 
3
##              BASFI_1             BASFI_2             BASFI_3 
BASFI_4
##                    2                   0                   8 
12
##              BASFI_5             BASFI_6      mSASSS_Mean_BL        mS
ASSS_Mean_FL
##                   22                  16                   0 
0
##      mSASSS_Progress      New_Syn_mSASSS     Prog_Syn_mSASSS mSASSS_
Progress_Kat
##                    0                   0                   0 
0
## New_Prog_Syn_Msasss      Mind_2_Synd_FL      Mind_2_Synd_BL 
PCR_INICIOB
##                    0                   0                   0 
2
```

```
##             i_ASDAS                HVGP
##                   2                   0

#vemos que los missings se concentran principalmente en 5 variables nu
méricas (BASMI, BASFIDif, BASDAIDif,ASDASDif,PCRDif)

# Multivariate Imputation by Chained Equations de las variables numéri
cas
library(mice)
miceMod <- mice(base_rx.num[, !names(base_rx.num) %in% "medv"], method
="rf")

## 
##  iter imp variable
##   1   1  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
```

```
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   1   2  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
```

```
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   1   3  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
```

```
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   1   4  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval
```

```
## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?
```

```
## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   1   5  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?
```

```
## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   2   1  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
```

```
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   2   2  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
```

```
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   2   3  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
```

```
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
```

```
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   2   4  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
```

```
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   2   5  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?
```

```
## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   3   1  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?
```

```
## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   3   2  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
```

```
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
```

```
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   3   3  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
```

```
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   3   4  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
```

```
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   3   5  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?
```

```
## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   4   1  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?
```

```
## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?
```

```
##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   4   2  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?
```

```
## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   4   3  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
```

```
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   4   4  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
```

```
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   4   5  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
```

```
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
```

```
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   5   1  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
```

```
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   5   2  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?
```

```
## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   5   3  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?
```

```
## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S
##   5   4  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
```

```
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
```

```
S
##   5   5  IMC  TSINT  VSG  BASMI  TIEMBIO  Interval

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
```

```
do
## regression?

## Warning in randomForest.default(x = xobs, y = yobs, ntree = 1, ...)
: The
## response has five or fewer unique values. Are you sure you want to
do
## regression?

##   i_BASDAI  BASDAI_0  BASDAI_1  BASDAI_2  BASDAI_3  BASDAI_4  BASDA
I_5  BASDAI_6  ASDAS_0  ASDAS_1  ASDAS_2  ASDAS_3  ASDAS_4  ASDAS_5  A
SDAS_6  PCR_0  PCR_1  PCR_2  PCR_3  PCR_4  PCR_5  PCR_6  EGP  EGM  BAS
FI_0  BASFI_1  BASFI_3  BASFI_4  BASFI_5  BASFI_6  PCR_INICIOB  i_ASDA
S

## Warning: Number of logged events: 950
```

```r
c_base_rx.num<- complete(miceMod)
anyNA(c_base_rx.num)
```

```
## [1] FALSE
```

```r
summary(c_base_rx.num)
```

```
##       EDAD             IMC             TSINT             VSG       
##  Min.   :21.00   Min.   :19.37   Min.   : 0.00   Min.   :  0.5  
##  1st Qu.:38.00   1st Qu.:23.94   1st Qu.: 8.00   1st Qu.:  9.0  
##  Median :46.00   Median :26.02   Median :15.00   Median : 19.0  
##  Mean   :46.68   Mean   :26.38   Mean   :17.84   Mean   : 26.3  
##  3rd Qu.:54.00   3rd Qu.:28.69   3rd Qu.:26.00   3rd Qu.: 38.0  
##  Max.   :75.00   Max.   :40.83   Max.   :52.00   Max.   :115.0  
##      BASMI            TIEMBIO          Interval        i_BASDAI    
##  Min.   :0.5378   Min.   :  0.0   Min.   :2.000   Min.   :0.700  
##  1st Qu.:1.5881   1st Qu.:  9.0   1st Qu.:3.000   1st Qu.:4.200  
##  Median :2.8480   Median : 42.0   Median :3.000   Median :5.400  
##  Mean   :3.1584   Mean   : 45.2   Mean   :3.446   Mean   :5.315  
##  3rd Qu.:4.1775   3rd Qu.: 76.0   3rd Qu.:4.000   3rd Qu.:6.400  
##  Max.   :7.2729   Max.   :132.0   Max.   :6.000   Max.   :8.800  
##     BASDAI_0        BASDAI_1       BASDAI_2        BASDAI_3    
BASDAI_4   
##  Min.   :0.200   Min.   :0.00   Min.   : 0.00   Min.   :0.000   Min
.   :0.000  
##  1st Qu.:2.000   1st Qu.:1.40   1st Qu.: 1.40   1st Qu.:1.000   1st 
Qu.:1.200  
##  Median :3.200   Median :2.80   Median : 2.50   Median :2.800   Med
ian :2.800  
##  Mean   :3.611   Mean   :2.94   Mean   : 3.36   Mean   :3.011   Mea
n   :3.015  
##  3rd Qu.:5.000   3rd Qu.:4.40   3rd Qu.: 4.10   3rd Qu.:4.700   3rd 
Qu.:4.400  
##  Max.   :8.800   Max.   :8.50   Max.   :65.00   Max.   :8.000   Max
.   :8.000  
##     BASDAI_5       BASDAI_6         ASDAS_0          ASDAS_1      
##  Min.   :0.00   Min.   :0.000   Min.   :0.2257   Min.   :0.2471  
##  1st Qu.:1.40   1st Qu.:1.000   1st Qu.:1.4166   1st Qu.:1.1572  
```

```
##  Median :2.70   Median :2.400   Median :2.0966   Median :1.5609  
##  Mean   :2.96   Mean   :2.832   Mean   :2.2336   Mean   :1.7996  
##  3rd Qu.:4.20   3rd Qu.:4.000   3rd Qu.:3.0000   3rd Qu.:2.4395  
##  Max.   :8.00   Max.   :7.300   Max.   :5.0749   Max.   :7.1255  
##     ASDAS_2           ASDAS_3           ASDAS_4           ASDAS_5      
##  Min.   :0.001737   Min.   :0.04892   Min.   :0.00058   Min.   :0.0
338  
##  1st Qu.:1.118372   1st Qu.:1.13776   1st Qu.:1.29202   1st Qu.:1.1
620  
##  Median :1.837270   Median :1.76656   Median :1.68322   Median :1.6
142  
##  Mean   :1.769730   Mean   :1.81207   Mean   :1.85161   Mean   :1.7
300  
##  3rd Qu.:2.307195   3rd Qu.:2.43783   3rd Qu.:2.45260   3rd Qu.:2.1
218  
##  Max.   :4.131246   Max.   :3.98374   Max.   :4.45150   Max.   :4.0
579  
##     ASDAS_6          PCR_0            PCR_1            PCR_2       
##  Min.   :0.096   Min.   : 0.000   Min.   : 0.000   Min.   : 0.000  
##  1st Qu.:1.108   1st Qu.: 1.000   1st Qu.: 1.000   1st Qu.: 0.900  
##  Median :1.641   Median : 3.600   Median : 2.000   Median : 2.000  
##  Mean   :1.753   Mean   : 8.228   Mean   : 4.324   Mean   : 4.377  
##  3rd Qu.:2.359   3rd Qu.: 9.200   3rd Qu.: 4.700   3rd Qu.: 5.600  
##  Max.   :3.988   Max.   :88.700   Max.   :61.300   Max.   :33.900  
##      PCR_3           PCR_4            PCR_5           PCR_6       
##  Min.   : 0.00   Min.   : 0.000   Min.   : 0.00   Min.   : 0.000  
##  1st Qu.: 0.75   1st Qu.: 0.700   1st Qu.: 0.60   1st Qu.: 0.600  
##  Median : 2.00   Median : 2.000   Median : 1.30   Median : 1.800  
##  Mean   : 4.52   Mean   : 5.149   Mean   : 3.95   Mean   : 4.291  
##  3rd Qu.: 5.90   3rd Qu.: 5.300   3rd Qu.: 6.00   3rd Qu.: 5.800  
##  Max.   :37.00   Max.   :68.500   Max.   :65.90   Max.   :39.700  
##       EGP             EGM            BASFI_0         BASFI_1     
##  Min.   : 0.00   Min.   : 0.000   Min.   :0.000   Min.   :0.000  
##  1st Qu.: 2.00   1st Qu.: 1.000   1st Qu.:1.600   1st Qu.:1.200  
##  Median : 3.00   Median : 3.000   Median :3.700   Median :2.800  
##  Mean   : 4.02   Mean   : 3.416   Mean   :3.912   Mean   :3.086  
##  3rd Qu.: 6.00   3rd Qu.: 5.000   3rd Qu.:5.900   3rd Qu.:4.600  
##  Max.   :10.00   Max.   :10.000   Max.   :9.300   Max.   :8.800  
##     BASFI_2         BASFI_3         BASFI_4         BASFI_5        
BASFI_6    
##  Min.   :0.000   Min.   :0.000   Min.   :0.000   Min.   :0.000   Mi
n.   :0.00  
##  1st Qu.:0.550   1st Qu.:1.100   1st Qu.:1.400   1st Qu.:0.900   1s
t Qu.:1.00  
##  Median :2.330   Median :2.700   Median :3.500   Median :3.000   Me
dian :2.80  
##  Mean   :2.667   Mean   :2.847   Mean   :3.364   Mean   :3.062   Me
an   :3.24  
##  3rd Qu.:4.340   3rd Qu.:4.400   3rd Qu.:5.000   3rd Qu.:4.800   3r
d Qu.:5.00  
##  Max.   :7.890   Max.   :7.900   Max.   :8.400   Max.   :8.100   Ma
x.   :8.30  
##  mSASSS_Mean_BL  mSASSS_Mean_FL  mSASSS_Progress  PCR_INICIOB    
##  Min.   : 0.00   Min.   : 0.00   Min.   :-2.50   Min.   : 0.00  
```

```
##  1st Qu.: 0.00   1st Qu.: 0.00   1st Qu.: 0.00   1st Qu.: 4.20  
##  Median : 5.00   Median : 8.00   Median : 0.00   Median :11.10  
##  Mean   :16.46   Mean   :18.44   Mean   : 1.98   Mean   :18.64  
##  3rd Qu.:23.00   3rd Qu.:30.00   3rd Qu.: 3.00   3rd Qu.:30.00  
##  Max.   :72.00   Max.   :72.00   Max.   :21.50   Max.   :98.00  
##     i_ASDAS           HVGP       
##  Min.   :1.500   Min.   : 1.000  
##  1st Qu.:2.700   1st Qu.: 5.000  
##  Median :3.500   Median : 6.000  
##  Mean   :3.416   Mean   : 5.923  
##  3rd Qu.:4.000   3rd Qu.: 7.000  
##  Max.   :5.300   Max.   :10.000  
```

Ajustamos el data frame con los missings corregidos

```
c_base_rx.num1 <-
  c_base_rx.num %>%
  mutate( BASFIDif = (BASFI_6-BASFI_0), BASDAIDif = (BASDAI_6-BASDAI_0
), ASDASDif = (ASDAS_6-ASDAS_0), PCRDif = (PCR_6-PCR_0))
summary(base_rx.num1)
```

```
##       EDAD             IMC            TSINT             VSG         
##  Min.   :21.00   Min.   :19.37   Min.   : 0.00   Min.   :  0.50  
##  1st Qu.:38.00   1st Qu.:24.05   1st Qu.: 8.00   1st Qu.:  9.00  
##  Median :46.00   Median :26.02   Median :15.00   Median : 19.00  
##  Mean   :46.68   Mean   :26.38   Mean   :17.76   Mean   : 26.65  
##  3rd Qu.:54.00   3rd Qu.:28.68   3rd Qu.:26.00   3rd Qu.: 38.75  
##  Max.   :75.00   Max.   :40.83   Max.   :52.00   Max.   :115.00  
##                  NA's   :6       NA's   :4       NA's   :3       
##      BASMI           TIEMBIO           Interval        i_BASDAI    
##  Min.   :0.5378   Min.   :  0.00   Min.   :2.00   Min.   :0.700  
##  1st Qu.:1.6458   1st Qu.:  8.00   1st Qu.:3.00   1st Qu.:4.225  
##  Median :2.8728   Median : 42.50   Median :3.00   Median :5.400  
##  Mean   :3.0915   Mean   : 45.51   Mean   :3.45   Mean   :5.326  
##  3rd Qu.:4.0864   3rd Qu.: 76.75   3rd Qu.:4.00   3rd Qu.:6.400  
##  Max.   :7.2729   Max.   :132.00   Max.   :6.00   Max.   :8.800  
##  NA's   :19       NA's   :1        NA's   :1      NA's   :3      
##     BASDAI_0        BASDAI_1        BASDAI_2         BASDAI_3    
##  Min.   :0.20   Min.   :0.000   Min.   : 0.000   Min.   :0.000  
##  1st Qu.:2.00   1st Qu.:1.400   1st Qu.: 1.400   1st Qu.:1.200  
##  Median :3.20   Median :2.700   Median : 2.500   Median :3.000  
##  Mean   :3.67   Mean   :2.902   Mean   : 3.419   Mean   :3.108  
##  3rd Qu.:5.10   3rd Qu.:4.400   3rd Qu.: 4.200   3rd Qu.:4.800  
##  Max.   :8.80   Max.   :8.500   Max.   :65.000   Max.   :8.000  
##  NA's   :4      NA's   :4       NA's   :4        NA's   :8      
##     BASDAI_4        BASDAI_5        BASDAI_6         ASDAS_0      
##  Min.   :0.000   Min.   :0.000   Min.   :0.000   Min.   :0.2257  
##  1st Qu.:1.200   1st Qu.:1.275   1st Qu.:1.100   1st Qu.:1.3874  
##  Median :2.800   Median :2.550   Median :2.800   Median :2.0565  
##  Mean   :3.075   Mean   :2.915   Mean   :2.924   Mean   :2.2160  
##  3rd Qu.:4.600   3rd Qu.:4.200   3rd Qu.:4.600   3rd Qu.:2.9248  
##  Max.   :8.000   Max.   :8.000   Max.   :7.300   Max.   :5.0749  
##  NA's   :10      NA's   :17      NA's   :16      NA's   :5       
##     ASDAS_1          ASDAS_2            ASDAS_3             ASDAS_4     
```

```
##  Min.   :0.2471   Min.   :0.001737   Min.   :0.04892   Min.   :0.00
058
##  1st Qu.:1.1572   1st Qu.:1.088078   1st Qu.:1.16497   1st Qu.:1.17
363
##  Median :1.5738   Median :1.827288   Median :1.76656   Median :1.66
660
##  Mean   :1.8249   Mean   :1.773470   Mean   :1.81523   Mean   :1.81
274
##  3rd Qu.:2.4204   3rd Qu.:2.316346   3rd Qu.:2.47797   3rd Qu.:2.44
173
##  Max.   :7.1255   Max.   :4.131246   Max.   :3.98374   Max.   :4.45
150
##  NA's   :13       NA's   :9          NA's   :14        NA's   :22
##     ASDAS_5          ASDAS_6          PCR_0            PCR_1
##  Min.   :0.0338   Min.   :0.096   Min.   : 0.000   Min.   : 0.000
##  1st Qu.:1.0522   1st Qu.:1.143   1st Qu.: 1.000   1st Qu.: 1.000
##  Median :1.6400   Median :1.680   Median : 3.350   Median : 2.000
##  Mean   :1.7329   Mean   :1.807   Mean   : 8.181   Mean   : 4.358
##  3rd Qu.:2.1781   3rd Qu.:2.397   3rd Qu.: 9.100   3rd Qu.: 4.675
##  Max.   :4.0579   Max.   :3.988   Max.   :88.700   Max.   :61.300
##  NA's   :30       NA's   :24      NA's   :7        NA's   :3
##      PCR_2           PCR_3            PCR_4            PCR_5
##  Min.   : 0.00   Min.   : 0.000   Min.   : 0.000   Min.   : 0.000
##  1st Qu.: 0.90   1st Qu.: 0.750   1st Qu.: 0.700   1st Qu.: 0.615
##  Median : 2.00   Median : 1.900   Median : 2.050   Median : 1.400
##  Mean   : 4.36   Mean   : 4.452   Mean   : 5.368   Mean   : 4.118
##  3rd Qu.: 5.60   3rd Qu.: 5.600   3rd Qu.: 5.375   3rd Qu.: 6.000
##  Max.   :33.90   Max.   :37.000   Max.   :68.500   Max.   :65.900
##  NA's   :2       NA's   :4        NA's   :7        NA's   :10
##      PCR_6            EGP              EGM            BASFI_0
##  Min.   : 0.00   Min.   : 0.000   Min.   : 0.000   Min.   :0.000
##  1st Qu.: 0.60   1st Qu.: 2.000   1st Qu.: 1.500   1st Qu.:1.525
##  Median : 2.00   Median : 3.000   Median : 3.000   Median :3.850
##  Mean   : 4.42   Mean   : 4.031   Mean   : 3.455   Mean   :3.931
##  3rd Qu.: 5.95   3rd Qu.: 6.000   3rd Qu.: 5.000   3rd Qu.:5.975
##  Max.   :39.70   Max.   :10.000   Max.   :10.000   Max.   :9.300
##  NA's   :14      NA's   :3        NA's   :2        NA's   :3
##     BASFI_1         BASFI_2         BASFI_3         BASFI_4
BASFI_5
##  Min.   :0.000   Min.   :0.000   Min.   :0.000   Min.   :0.00   Min
.   :0.000
##  1st Qu.:1.200   1st Qu.:0.550   1st Qu.:1.000   1st Qu.:1.30   1st
Qu.:1.100
##  Median :2.700   Median :2.330   Median :2.800   Median :3.50   Med
ian :3.200
##  Mean   :3.059   Mean   :2.667   Mean   :2.882   Mean   :3.34   Mea
n   :3.118
##  3rd Qu.:4.550   3rd Qu.:4.340   3rd Qu.:4.500   3rd Qu.:5.00   3rd
Qu.:4.700
##  Max.   :8.800   Max.   :7.890   Max.   :7.900   Max.   :8.40   Max
.   :8.100
##  NA's   :2                       NA's   :8       NA's   :12     NA'
s   :22
##     BASFI_6      mSASSS_Mean_BL  mSASSS_Mean_FL  mSASSS_Progress
```

```
##  Min.   :0.000   Min.   : 0.00   Min.   : 0.00   Min.   :-2.50
##  1st Qu.:1.100   1st Qu.: 0.00   1st Qu.: 0.00   1st Qu.: 0.00
##  Median :3.100   Median : 5.00   Median : 8.00   Median : 0.00
##  Mean   :3.313   Mean   :16.46   Mean   :18.44   Mean   : 1.98
##  3rd Qu.:5.100   3rd Qu.:23.00   3rd Qu.:30.00   3rd Qu.: 3.00
##  Max.   :8.300   Max.   :72.00   Max.   :72.00   Max.   :21.50
##  NA's   :16
##   PCR_INICIOB       i_ASDAS           HVGP           BASFIDif
##  Min.   : 0.00   Min.   :1.500   Min.   : 1.000   Min.   :-8.9000
##  1st Qu.: 4.60   1st Qu.:2.700   1st Qu.: 5.000   1st Qu.:-1.8000
##  Median :11.10   Median :3.500   Median : 6.000   Median :-0.2000
##  Mean   :18.70   Mean   :3.402   Mean   : 5.923   Mean   :-0.5667
##  3rd Qu.:28.05   3rd Qu.:4.000   3rd Qu.: 7.000   3rd Qu.: 0.6250
##  Max.   :98.00   Max.   :5.300   Max.   :10.000   Max.   : 6.2000
##  NA's   :2       NA's   :2                        NA's   :17
##    BASDAIDif          ASDASDif           PCRDif
##  Min.   :-7.0000   Min.   :-3.4650   Min.   :-88.40
##  1st Qu.:-1.1000   1st Qu.:-1.0300   1st Qu.: -5.40
##  Median :-0.1000   Median :-0.2247   Median : -0.20
##  Mean   :-0.5354   Mean   :-0.3908   Mean   : -4.14
##  3rd Qu.: 0.4750   3rd Qu.: 0.2567   3rd Qu.:  1.00
##  Max.   : 5.2000   Max.   : 1.9947   Max.   : 28.00
##  NA's   :19        NA's   :28        NA's   :20
```

```
c_base_rx.num2<-c_base_rx.num1[,c(-9:-29,-32:-40)]

c_base_rx2= cbind(c_base_rx.num2,base_rx [,c(3,5,7,8,9,12,13,14,15,16,
17,19,20,22,23,58,59,60,61,62,63)])
summary(c_base_rx2)
```

```
##       EDAD            IMC            TSINT            VSG
##  Min.   :21.00   Min.   :19.37   Min.   : 0.00   Min.   :  0.5
##  1st Qu.:38.00   1st Qu.:23.94   1st Qu.: 8.00   1st Qu.:  9.0
##  Median :46.00   Median :26.02   Median :15.00   Median : 19.0
##  Mean   :46.68   Mean   :26.38   Mean   :17.84   Mean   : 26.3
##  3rd Qu.:54.00   3rd Qu.:28.69   3rd Qu.:26.00   3rd Qu.: 38.0
##  Max.   :75.00   Max.   :40.83   Max.   :52.00   Max.   :115.0
##      BASMI           TIEMBIO         Interval        i_BASDAI
##  Min.   :0.5378   Min.   :  0.0   Min.   :2.000   Min.   :0.700
##  1st Qu.:1.5881   1st Qu.:  9.0   1st Qu.:3.000   1st Qu.:4.200
##  Median :2.8480   Median : 42.0   Median :3.000   Median :5.400
##  Mean   :3.1584   Mean   : 45.2   Mean   :3.446   Mean   :5.315
##  3rd Qu.:4.1775   3rd Qu.: 76.0   3rd Qu.:4.000   3rd Qu.:6.400
##  Max.   :7.2729   Max.   :132.0   Max.   :6.000   Max.   :8.800
##       EGP             EGM         mSASSS_Progress  PCR_INICIOB
##  Min.   : 0.00   Min.   : 0.000   Min.   :-2.50   Min.   : 0.00
##  1st Qu.: 2.00   1st Qu.: 1.000   1st Qu.: 0.00   1st Qu.: 4.20
##  Median : 3.00   Median : 3.000   Median : 0.00   Median :11.10
##  Mean   : 4.02   Mean   : 3.416   Mean   : 1.98   Mean   :18.64
##  3rd Qu.: 6.00   3rd Qu.: 5.000   3rd Qu.: 3.00   3rd Qu.:30.00
##  Max.   :10.00   Max.   :10.000   Max.   :21.50   Max.   :98.00
##     i_ASDAS           HVGP           BASFIDif         BASDAIDif
##  Min.   :1.500   Min.   : 1.000   Min.   :-8.9000   Min.   :-7.8000
##  1st Qu.:2.700   1st Qu.: 5.000   1st Qu.:-1.8000   1st Qu.:-1.7000
```

```
##  Median :3.500   Median : 6.000   Median :-0.2000   Median :-0.1000
##  Mean   :3.416   Mean   : 5.923   Mean   :-0.6723   Mean   :-0.7792
##  3rd Qu.:4.000   3rd Qu.: 7.000   3rd Qu.: 0.7000   3rd Qu.: 0.5000
##  Max.   :5.300   Max.   :10.000   Max.   : 6.2000   Max.   : 5.2000
##     ASDASDif           PCRDif            SEXO     IMC>30    HLAB27
EA
##  Min.   :-3.5373   Min.   :-88.400   MALE  :82   NO  :84   SI  :86
SI:86
##  1st Qu.:-1.0443   1st Qu.: -5.400   FEMALE:19   SI  :11   NO  :13
NO:15
##  Median :-0.2886   Median : -0.200               NA's: 6   NA's: 2
##  Mean   :-0.4804   Mean   : -3.937
##  3rd Qu.: 0.2043   3rd Qu.:  1.000
##  Max.   : 1.9947   Max.   : 28.000
##  TABACO_Kat UVEITIS PSORIASIS ENF_INF   TTOBIO         NUM_TB_PREV
##  SI:70      NO:79   NO  :92   NO  :92   ETA:31   treatments.0:75
##  NO:31      SI:22   SI  : 7   SI  : 7   ADA:44   treatments.1:20
##                     NA's: 2   NA's: 2   IFX:11   treatments.2: 6
##                                         GOL:12
##                                         CTZ: 3
##
##           MOTIVO   BIO_INICI Biol_4_kat   AINE      FAME     New_Syn
_mSASSS
##  non.change  :77   NO  :25   NO:55      NO  :42   NO  :81   NO:81
##  Inefficacy  :17   SI  :75   SI:46      SI  :57   SI  :18   SI:20
##  Side.effects: 7   NA's: 1              NA's: 2   NA's: 2
##
##
##
##  Prog_Syn_mSASSS mSASSS_Progress_Kat New_Prog_Syn_Msasss Mind_2_Syn
d_FL
##  NO:90           NO:71               NO:79               NO:46
##  SI:11           SI:30               SI:22               SI:55
##
##
##
##
##  Mind_2_Synd_BL
##  NO:50
##  SI:51
##
##
##
##
```

Analizamos la relación entre variables numéricas

```
round(cor(x = c_base_rx.num2, method = "pearson"), 3)
```

```
##                    EDAD   IMC TSINT   VSG  BASMI TIEMBIO Interval
i_BASDAI
## EDAD               1.000 0.129 0.602 0.159 0.479   0.118   -0.056
0.164
## IMC                0.129 1.000 0.142 0.032 0.175   0.153    0.061
```

```
0.018
## TSINT            0.602 0.142  1.000  0.133  0.416   0.408    0.058
0.193
## VSG              0.159 0.032  0.133  1.000  0.079   0.072   -0.066
-0.045
## BASMI            0.479 0.175  0.416  0.079  1.000   0.195    0.124
0.132
## TIEMBIO          0.118 0.153  0.408  0.072  0.195   1.000   -0.033
0.051
## Interval        -0.056 0.061  0.058 -0.066  0.124  -0.033    1.000
-0.140
## i_BASDAI         0.164 0.018  0.193 -0.045  0.132   0.051   -0.140
1.000
## EGP              0.199 0.054  0.002 -0.137  0.169  -0.297    0.071
0.434
## EGM              0.122 0.013 -0.068  0.084  0.289  -0.347    0.108
0.330
## mSASSS_Progress  0.327 0.181  0.163  0.033  0.432   0.091    0.124
-0.140
## PCR_INICIOB      0.150 0.058  0.064  0.689  0.052   0.010    0.038
-0.054
## i_ASDAS          0.172 0.140  0.142  0.379  0.097   0.047   -0.072
0.622
## HVGP             0.033 0.061 -0.006  0.069  0.103   0.060   -0.022
0.553
## BASFIDif         0.163 0.076  0.155 -0.006 -0.063   0.297    0.114
-0.372
## BASDAIDif       -0.015 0.030  0.088 -0.029  0.069   0.344    0.174
-0.432
## ASDASDif        -0.018 0.027  0.164 -0.051  0.012   0.380    0.102
-0.240
## PCRDif          -0.169 0.030  0.151 -0.179 -0.012   0.283   -0.043
0.048
##                    EGP    EGM mSASSS_Progress PCR_INICIOB i_ASDAS
HVGP
## EDAD             0.199  0.122           0.327       0.150   0.172
0.033
## IMC              0.054  0.013           0.181       0.058   0.140
0.061
## TSINT            0.002 -0.068           0.163       0.064   0.142 -
0.006
## VSG             -0.137  0.084           0.033       0.689   0.379
0.069
## BASMI            0.169  0.289           0.432       0.052   0.097
0.103
## TIEMBIO         -0.297 -0.347           0.091       0.010   0.047
0.060
## Interval         0.071  0.108           0.124       0.038  -0.072 -
0.022
## i_BASDAI         0.434  0.330          -0.140      -0.054   0.622
0.553
## EGP              1.000  0.749           0.123      -0.085   0.200
0.276
## EGM              0.749  1.000           0.180       0.062   0.290
```

```
0.372
## mSASSS_Progress  0.123  0.180           1.000       0.041   -0.075
0.023
## PCR_INICIOB     -0.085  0.062           0.041       1.000    0.569
0.038
## i_ASDAS          0.200  0.290          -0.075       0.569    1.000
0.634
## HVGP             0.276  0.372           0.023       0.038    0.634
1.000
## BASFIDif        -0.478 -0.456           0.099      -0.037   -0.198 -
0.179
## BASDAIDif       -0.541 -0.386           0.209      -0.052   -0.237 -
0.099
## ASDASDif        -0.465 -0.396           0.217      -0.108   -0.162
0.046
## PCRDif          -0.114 -0.187           0.026      -0.361   -0.198
0.079
##                 BASFIDif BASDAIDif ASDASDif PCRDif
## EDAD               0.163    -0.015   -0.018 -0.169
## IMC                0.076     0.030    0.027  0.030
## TSINT              0.155     0.088    0.164  0.151
## VSG               -0.006    -0.029   -0.051 -0.179
## BASMI             -0.063     0.069    0.012 -0.012
## TIEMBIO            0.297     0.344    0.380  0.283
## Interval           0.114     0.174    0.102 -0.043
## i_BASDAI          -0.372    -0.432   -0.240  0.048
## EGP               -0.478    -0.541   -0.465 -0.114
## EGM               -0.456    -0.386   -0.396 -0.187
## mSASSS_Progress    0.099     0.209    0.217  0.026
## PCR_INICIOB       -0.037    -0.052   -0.108 -0.361
## i_ASDAS           -0.198    -0.237   -0.162 -0.198
## HVGP              -0.179    -0.099    0.046  0.079
## BASFIDif           1.000     0.747    0.590  0.164
## BASDAIDif          0.747     1.000    0.697  0.165
## ASDASDif           0.590     0.697    1.000  0.556
## PCRDif             0.164     0.165    0.556  1.000
```

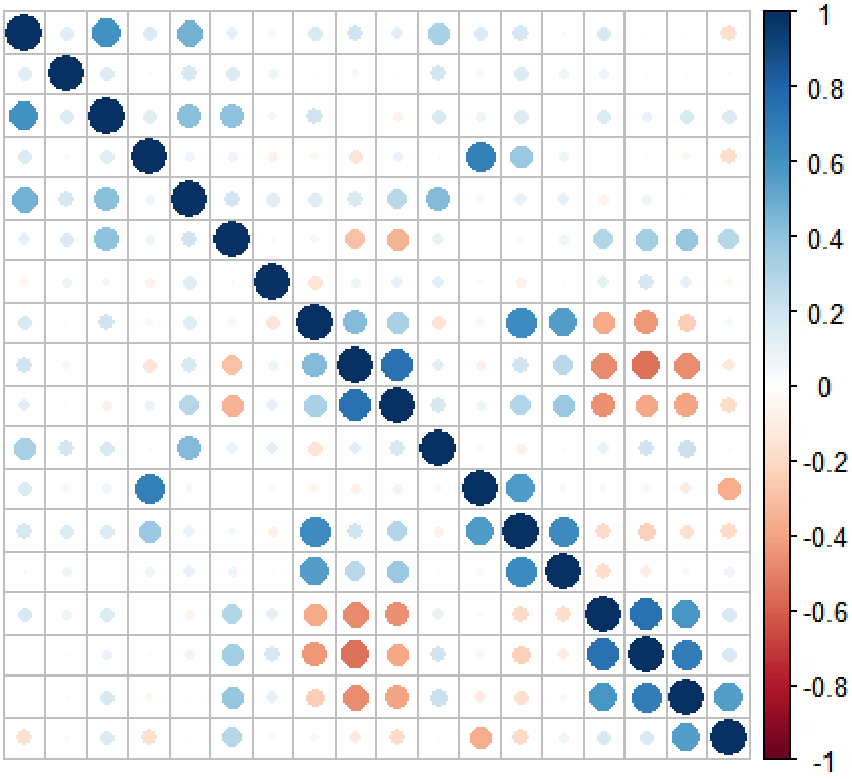
```
library(corrplot)
```

```
## corrplot 0.84 loaded
```

```
m<-cor(c_base_rx.num2)
head(round(m,2))
```

```
##           EDAD  IMC TSINT  VSG BASMI TIEMBIO Interval i_BASDAI   EGP
EGM
## EDAD     1.00 0.13  0.60 0.16  0.48    0.12    -0.06     0.16  0.20
0.12
## IMC      0.13 1.00  0.14 0.03  0.17    0.15     0.06     0.02  0.05
0.01
## TSINT    0.60 0.14  1.00 0.13  0.42    0.41     0.06     0.19  0.00
-0.07
## VSG      0.16 0.03  0.13 1.00  0.08    0.07    -0.07    -0.04 -0.14
0.08
## BASMI    0.48 0.17  0.42 0.08  1.00    0.20     0.12     0.13  0.17
```

```
0.29
## TIEMBIO 0.12 0.15  0.41 0.07  0.20    1.00    -0.03     0.05 -0.30
-0.35
##          mSASSS_Progress PCR_INICIOB i_ASDAS  HVGP BASFIDif BASDAIDi
f ASDASDif
## EDAD               0.33        0.15    0.17  0.03     0.16     -0.0
2    -0.02
## IMC                0.18        0.06    0.14  0.06     0.08      0.0
3     0.03
## TSINT              0.16        0.06    0.14 -0.01     0.15      0.0
9     0.16
## VSG                0.03        0.69    0.38  0.07    -0.01     -0.0
3    -0.05
## BASMI              0.43        0.05    0.10  0.10    -0.06      0.0
7     0.01
## TIEMBIO            0.09        0.01    0.05  0.06     0.30      0.3
4     0.38
##          PCRDif
## EDAD      -0.17
## IMC        0.03
## TSINT      0.15
## VSG       -0.18
## BASMI     -0.01
## TIEMBIO    0.28

corrplot(m, method = "circle", tl.pos="n")
```



```
# La correlación positiva está representada en azul, y la correlación
negativa en rojo. La intensidad del del color y el tamaño del círculo
son proporcionales al coeficiente de correlación.
```

Análisis de regresión lineal univariable y análisis de correlación de las variables

```
attach(c_base_rx.num)
b<-lm(mSASSS_Progress~EDAD,data=c_base_rx.num)
summary(b)
```

```
##
## Call:
## lm(formula = mSASSS_Progress ~ EDAD, data = c_base_rx.num)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.2771 -2.0128 -0.9391  0.2077 17.3258
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -2.82464    1.44047  -1.961 0.052698 .
## EDAD         0.10292    0.02991   3.442 0.000848 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.566 on 99 degrees of freedom
## Multiple R-squared:  0.1069, Adjusted R-squared:  0.09784
## F-statistic: 11.85 on 1 and 99 DF,  p-value: 0.0008483
```

```
cor.test(mSASSS_Progress,EDAD, method = "spearman")
```

```
## Warning in cor.test.default(mSASSS_Progress, EDAD, method = "spearm
an"): Cannot
## compute exact p-value with ties
```

```
##
##  Spearman's rank correlation rho
##
## data:  mSASSS_Progress and EDAD
## S = 122594, p-value = 0.00374
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.285997
```

```
c<-lm(mSASSS_Progress~IMC,data=c_base_rx.num)
summary(c)
```

```
##
## Call:
## lm(formula = mSASSS_Progress ~ IMC, data = c_base_rx.num)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.6821 -1.8668 -1.2592  0.6264 17.7018
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -2.8955     2.6867  -1.078   0.2838
```

```
## IMC           0.1848     0.1009   1.832   0.0699 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.711 on 99 degrees of freedom
## Multiple R-squared:  0.03279,    Adjusted R-squared:  0.02302
## F-statistic: 3.357 on 1 and 99 DF,  p-value: 0.06994
```

```
cor.test(mSASSS_Progress,IMC, method = "spearman")
```

```
## Warning in cor.test.default(mSASSS_Progress, IMC, method = "spearma
n"): Cannot
## compute exact p-value with ties

##
##  Spearman's rank correlation rho
##
## data:  mSASSS_Progress and IMC
## S = 136602, p-value = 0.04032
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.204416
```

```
d<-lm(mSASSS_Progress~TSINT,data=c_base_rx.num)
summary(d)
```

```
##
## Call:
## lm(formula = mSASSS_Progress ~ TSINT, data = c_base_rx.num)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.5824 -1.8456 -1.2771  0.4649 18.2332
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.13498    0.63490   1.788   0.0769 .
## TSINT        0.04737    0.02890   1.639   0.1043
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.723 on 99 degrees of freedom
## Multiple R-squared:  0.02642,    Adjusted R-squared:  0.01659
## F-statistic: 2.687 on 1 and 99 DF,  p-value: 0.1043
```

```
cor.test(mSASSS_Progress,TSINT, method = "spearman")
```

```
## Warning in cor.test.default(mSASSS_Progress, TSINT, method = "spear
man"): Cannot
## compute exact p-value with ties

##
##  Spearman's rank correlation rho
##
## data:  mSASSS_Progress and TSINT
```

```
## S = 146835, p-value = 0.1485
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.1448178
```

```
e<-lm(mSASSS_Progress~VSG,data=c_base_rx.num)
summary(e)
```

```
##
## Call:
## lm(formula = mSASSS_Progress ~ VSG, data = c_base_rx.num)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.3474 -1.9840 -1.8583  0.8192 19.5378
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.836482   0.580375   3.164  0.00207 **
## VSG         0.005465   0.016836   0.325  0.74617
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.771 on 99 degrees of freedom
## Multiple R-squared:  0.001063,   Adjusted R-squared:  -0.009027
## F-statistic: 0.1054 on 1 and 99 DF,  p-value: 0.7462
```

```
cor.test(mSASSS_Progress,VSG, method = "spearman")
```

```
## Warning in cor.test.default(mSASSS_Progress, VSG, method = "spearma
n"): Cannot
## compute exact p-value with ties
```

```
##
##  Spearman's rank correlation rho
##
## data:  mSASSS_Progress and VSG
## S = 169531, p-value = 0.9002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##        rho
## 0.01263013
```

```
f<-lm(mSASSS_Progress~BASMI,data=c_base_rx.num)
summary(f)
```

```
##
## Call:
## lm(formula = mSASSS_Progress ~ BASMI, data = c_base_rx.num)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.4813 -1.5879 -0.5962  0.4510 16.2866
##
```

```
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept)  -0.9500     0.7013  -1.355    0.179    
## BASMI         0.9277     0.1945   4.771 6.34e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 3.402 on 99 degrees of freedom
## Multiple R-squared:  0.1869, Adjusted R-squared:  0.1787 
## F-statistic: 22.76 on 1 and 99 DF,  p-value: 6.335e-06
```

```
cor.test(mSASSS_Progress,BASMI, method = "spearman")
```

```
## Warning in cor.test.default(mSASSS_Progress, BASMI, method = "spear
man"): Cannot
## compute exact p-value with ties
```

```
## 
##  Spearman's rank correlation rho
## 
## data:  mSASSS_Progress and BASMI
## S = 95796, p-value = 3.688e-06
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho 
## 0.4420714
```

```
g<-lm(mSASSS_Progress~TIEMBIO,data=c_base_rx.num)
summary(g)
```

```
## 
## Call:
## lm(formula = mSASSS_Progress ~ TIEMBIO, data = c_base_rx.num)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -4.0954 -2.0296 -1.5954  0.7513 18.9596 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 1.595437   0.565656   2.821  0.00579 **
## TIEMBIO     0.008513   0.009391   0.906  0.36689   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 3.758 on 99 degrees of freedom
## Multiple R-squared:  0.008232,  Adjusted R-squared:  -0.001786 
## F-statistic: 0.8217 on 1 and 99 DF,  p-value: 0.3669
```

```
cor.test(mSASSS_Progress,TIEMBIO, method = "spearman")
```

```
## Warning in cor.test.default(mSASSS_Progress, TIEMBIO, method = "spe
arman"):
## Cannot compute exact p-value with ties
```

```
##
##  Spearman's rank correlation rho
##
## data:  mSASSS_Progress and TIEMBIO
## S = 164738, p-value = 0.6873
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##        rho
## 0.04054722
```

```
h<-lm(mSASSS_Progress~Interval,data=c_base_rx.num)
summary(h)
```

```
##
## Call:
## lm(formula = mSASSS_Progress ~ Interval, data = c_base_rx.num)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.7453 -1.7672 -1.2892  0.7547 19.2547
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.3331     1.3753   0.242    0.809
## Interval      0.4781     0.3842   1.244    0.216
##
## Residual standard error: 3.744 on 99 degrees of freedom
## Multiple R-squared:  0.0154, Adjusted R-squared:  0.00545
## F-statistic: 1.548 on 1 and 99 DF,  p-value: 0.2164
```

```
cor.test(mSASSS_Progress,Interval, method = "spearman")
```

```
## Warning in cor.test.default(mSASSS_Progress, Interval, method = "sp
earman"):
## Cannot compute exact p-value with ties
```

```
##
##  Spearman's rank correlation rho
##
## data:  mSASSS_Progress and Interval
## S = 153995, p-value = 0.3048
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.1031182
```

```
i<-lm(mSASSS_Progress~i_BASDAI,data=c_base_rx.num)
summary(i)
```

```
##
## Call:
## lm(formula = mSASSS_Progress ~ i_BASDAI, data = c_base_rx.num)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
```

```
## -3.8754 -1.9845 -1.4914  0.6163 18.4423
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.5218     1.1539   3.052  0.00292 **
## i_BASDAI     -0.2901     0.2055  -1.411  0.16132
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.736 on 99 degrees of freedom
## Multiple R-squared:  0.01972,    Adjusted R-squared:  0.009817
## F-statistic: 1.991 on 1 and 99 DF,  p-value: 0.1613
```

```
cor.test(mSASSS_Progress,i_BASDAI, method = "spearman")
```

```
## Warning in cor.test.default(mSASSS_Progress, i_BASDAI, method = "sp
earman"):
## Cannot compute exact p-value with ties
```

```
##
##  Spearman's rank correlation rho
##
## data:  mSASSS_Progress and i_BASDAI
## S = 183897, p-value = 0.4802
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##         rho
## -0.07103595
```

```
j<-lm(mSASSS_Progress~EGP,data=c_base_rx.num)
summary(j)
```

```
##
## Call:
## lm(formula = mSASSS_Progress ~ EGP, data = c_base_rx.num)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.1482 -1.8090 -1.4734  0.5196 19.3553
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.3055     0.6628   1.970   0.0517 .
## EGP           0.1678     0.1364   1.231   0.2214
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.745 on 99 degrees of freedom
## Multiple R-squared:  0.01507,    Adjusted R-squared:  0.005119
## F-statistic: 1.515 on 1 and 99 DF,  p-value: 0.2214
```

```
cor.test(mSASSS_Progress,EGP, method = "spearman")
```

```
## Warning in cor.test.default(mSASSS_Progress, EGP, method = "spearma
n"): Cannot
## compute exact p-value with ties
```

```
##
##  Spearman's rank correlation rho
##
## data:  mSASSS_Progress and EGP
## S = 141747, p-value = 0.08102
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.1744509
```

```r
l<-lm(mSASSS_Progress~EGM,data=c_base_rx.num)
summary(l)
```

```
##
## Call:
## lm(formula = mSASSS_Progress ~ EGM, data = c_base_rx.num)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.4898 -1.8631 -1.2997  0.2286 19.0736
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.0180     0.6451   1.578   0.1177
## EGM           0.2817     0.1549   1.819   0.0719 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.712 on 99 degrees of freedom
## Multiple R-squared:  0.03234,    Adjusted R-squared:  0.02257
## F-statistic: 3.309 on 1 and 99 DF,  p-value: 0.07193
```

```r
cor.test(mSASSS_Progress,EGM, method = "spearman")
```

```
## Warning in cor.test.default(mSASSS_Progress, EGM, method = "spearma
n"): Cannot
## compute exact p-value with ties
```

```
##
##  Spearman's rank correlation rho
##
## data:  mSASSS_Progress and EGM
## S = 140236, p-value = 0.06661
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.1832498
```

```r
r<-lm(mSASSS_Progress~PCR_INICIOB,data=c_base_rx.num)
summary(r)
```

```
##
## Call:
## lm(formula = mSASSS_Progress ~ PCR_INICIOB, data = c_base_rx.num)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.3659 -1.9451 -1.8422  0.7716 19.4299
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.832707   0.522521   3.507 0.000682 ***
## PCR_INICIOB 0.007914   0.019516   0.405 0.685990
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.77 on 99 degrees of freedom
## Multiple R-squared:  0.001658,   Adjusted R-squared:  -0.008426
## F-statistic: 0.1644 on 1 and 99 DF,  p-value: 0.686
```

```
cor.test(mSASSS_Progress,PCR_INICIOB, method = "spearman")
```

```
## Warning in cor.test.default(mSASSS_Progress, PCR_INICIOB, method =
"spearman"):
## Cannot compute exact p-value with ties
```

```
##
##  Spearman's rank correlation rho
##
## data:  mSASSS_Progress and PCR_INICIOB
## S = 167716, p-value = 0.8178
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##        rho
## 0.02320423
```

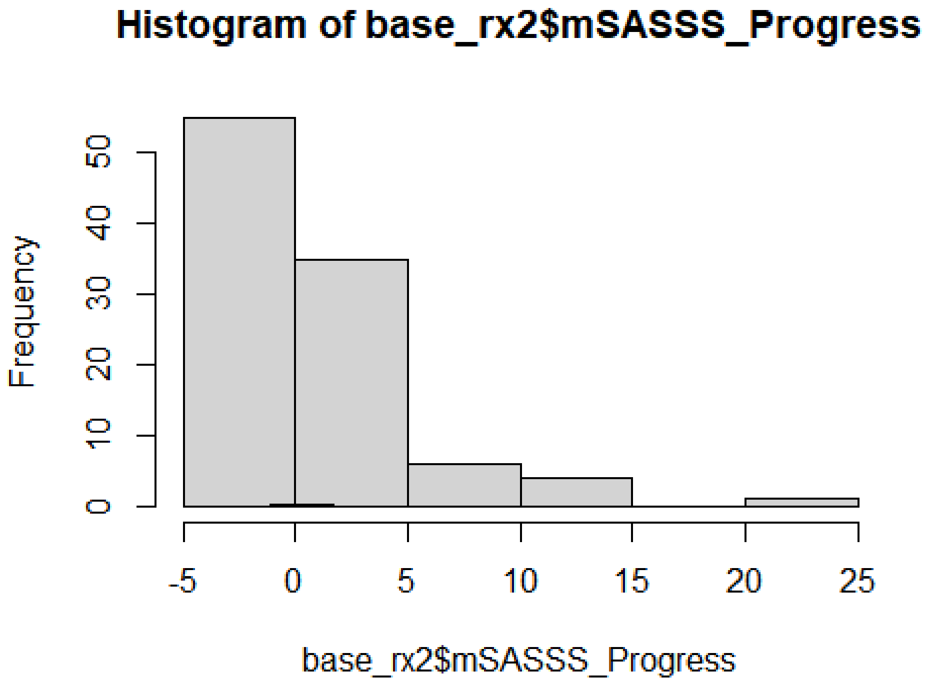
```
s<-lm(mSASSS_Progress~i_ASDAS,data=c_base_rx.num)
summary(s)
```

```
##
## Call:
## lm(formula = mSASSS_Progress ~ i_ASDAS, data = c_base_rx.num)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.4198 -2.0182 -1.6246  0.4898 19.2850
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.1006     1.5419   2.011    0.047 *
## i_ASDAS      -0.3280     0.4379  -0.749    0.456
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.763 on 99 degrees of freedom
```

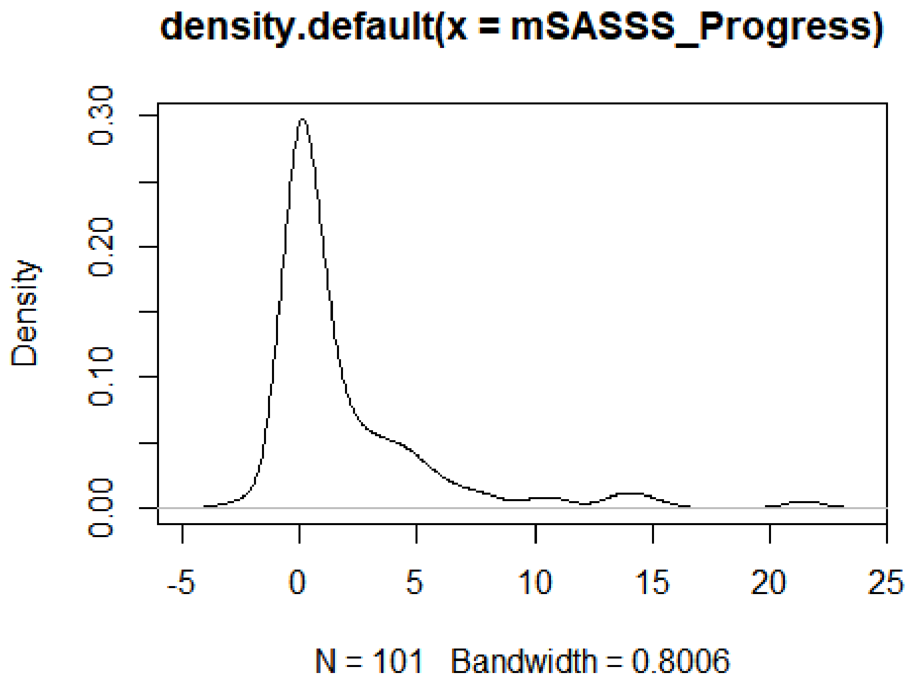
```
## Multiple R-squared:  0.005636,   Adjusted R-squared:  -0.004408
## F-statistic: 0.5611 on 1 and 99 DF,  p-value: 0.4556

cor.test(mSASSS_Progress,i_ASDAS, method = "spearman")

## Warning in cor.test.default(mSASSS_Progress, i_ASDAS, method = "spe
arman"):
## Cannot compute exact p-value with ties

##
##  Spearman's rank correlation rho
##
## data:  mSASSS_Progress and i_ASDAS
## S = 183572, p-value = 0.492
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##         rho
## -0.06914314
```

Análisis de la variable respuesta (mSASSS_Progress), numérica

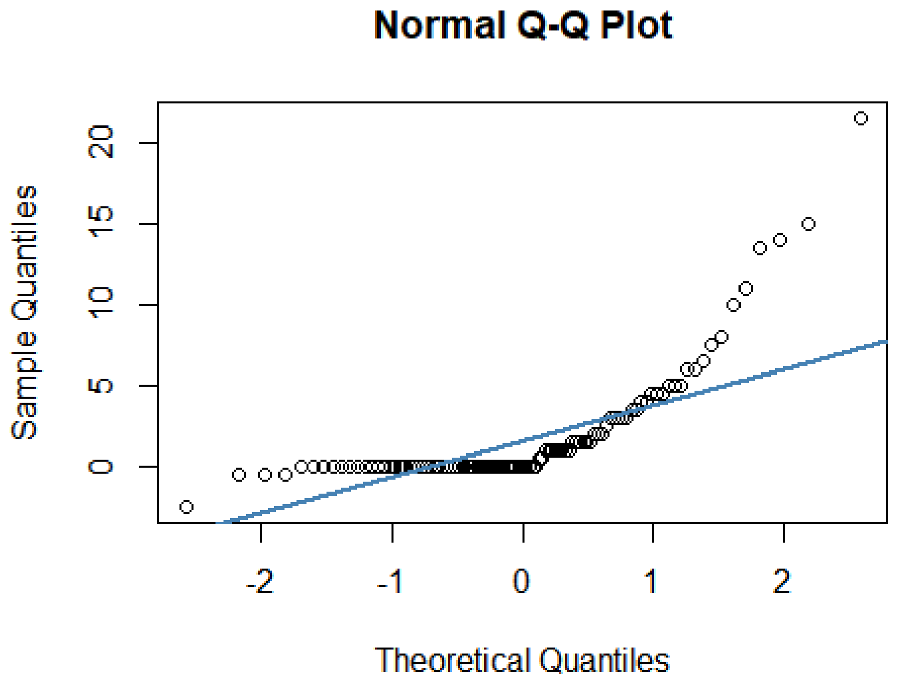
```
attach(base_rx2)

## The following objects are masked from c_base_rx.num:
##
##     BASMI, EDAD, EGM, EGP, HVGP, i_ASDAS, i_BASDAI, IMC, Interval,
##     mSASSS_Progress, PCR_INICIOB, TIEMBIO, TSINT, VSG

hist(base_rx2$mSASSS_Progress)
lines(density(mSASSS_Progress))
```



```
plot(density(mSASSS_Progress))
```



```
# Parece que la densidad es claramente asimétrica.

qqnorm(base_rx2$mSASSS_Progress)
qqline(base_rx2$mSASSS_Progress, col = "steelblue", lwd = 2)
```



```
summary(base_rx2$mSASSS_Progress)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   -2.50    0.00    0.00    1.98    3.00   21.50
```

```
shapiro.test(base_rx2$mSASSS_Progress)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  base_rx2$mSASSS_Progress
## W = 0.63869, p-value = 2.092e-14
```

En el análisis descrptivos de la variable respuesta, vemos que la media y mediana no coincide, y que la kurtosis es superior a 3. Tanto en el Shapiro-Wilk's test como en el Kolmogorov-Smirnov (K-S) normality test vemos que la variable respuesta, no sigue una distribución normal. Pues al obtener un resultado significativo (p < a 0,05), debemos rechazar la hipótesis nula de igualdad. Como la variable respuesta no es normal, podemos intentar una transformación para mejorar esa situación, pero antes vamos a ver si los residuos siguen la suposición de normalidad y homocedasticidad.

```
attach(base_rx2)
```

```
## The following objects are masked from base_rx2 (pos = 3):
##
##     AINE, ASDASDif, BASDAIDif, BASFIDif, BASMI, BIO_INICI, Biol_4_k
at,
##     EA, EDAD, EGM, EGP, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BAS
DAI,
##     IMC, IMC>30, Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO,
##     mSASSS_Progress, mSASSS_Progress_Kat, New_Prog_Syn_Msasss,
##     New_Syn_mSASSS, NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSAS
SS,
##     PSORIASIS, SEXO, TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, V
SG
```

```
## The following objects are masked from c_base_rx.num:
##
##     BASMI, EDAD, EGM, EGP, HVGP, i_ASDAS, i_BASDAI, IMC, Interval,
##     mSASSS_Progress, PCR_INICIOB, TIEMBIO, TSINT, VSG
```

```
a<-lm(mSASSS_Progress~ ., data=base_rx2, na.action = na.omit)
summary(a)
```

```
##
## Call:
## lm(formula = mSASSS_Progress ~ ., data = base_rx2, na.action = na.o
mit)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.0835 -0.8788 -0.1220  0.8867  2.7176
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)               6.030490  13.395121   0.450  0.66131
## EDAD                      0.076896   0.095442   0.806  0.43749
```

```
## SEXOFEMALE                -1.681685   2.615599  -0.643  0.53343
## IMC                       -0.033612   0.253970  -0.132  0.89710
## `IMC>30`SI                -0.037253   3.009490  -0.012  0.99035
## TSINT                      0.081354   0.100625   0.808  0.43595
## HLAB27NO                  -5.040693   2.797895  -1.802  0.09905 .
## EANO                      -0.063666   5.218556  -0.012  0.99048
## TABACO_KatNO               0.725666   2.349126   0.309  0.76316
## VSG                        0.065548   0.060919   1.076  0.30497
## BASMI                     -0.845203   0.716373  -1.180  0.26295
## UVEITISSI                 -0.026928   1.973453  -0.014  0.98936
## PSORIASISSI                3.106432   3.351841   0.927  0.37393
## ENF_INFSI                  4.710392   4.354606   1.082  0.30253
## TTOBIOADA                 -3.037611   2.053408  -1.479  0.16712
## TTOBIOIFX                  0.410255   2.700656   0.152  0.88201
## TTOBIOGOL                 -3.172484   4.399943  -0.721  0.48593
## TTOBIOCTZ                 -5.425373   4.128656  -1.314  0.21556
## NUM_TB_PREVtreatments.1 -4.314352   6.012165  -0.718  0.48796
## NUM_TB_PREVtreatments.2 -3.024290   7.419758  -0.408  0.69139
## MOTIVOInefficacy           5.409123   5.805011   0.932  0.37144
## MOTIVOSide.effects         1.273170   5.501541   0.231  0.82124
## TIEMBIO                   -0.014120   0.044600  -0.317  0.75747
## BIO_INICISI               -2.875136   2.600103  -1.106  0.29242
## Biol_4_katSI               1.508230   2.541654   0.593  0.56491
## Interval                   0.012851   0.994240   0.013  0.98992
## AINESI                     0.330936   1.847061   0.179  0.86106
## FAMESI                    -1.886349   2.837520  -0.665  0.51988
## i_BASDAI                  -0.339930   0.839083  -0.405  0.69316
## EGP                        0.374793   0.690786   0.543  0.59825
## EGM                        0.641881   0.622347   1.031  0.32450
## New_Syn_mSASSSSI           7.897362   4.922208   1.604  0.13692
## Prog_Syn_mSASSSSI          0.804746   3.195528   0.252  0.80581
## mSASSS_Progress_KatSI      7.508523   2.288661   3.281  0.00732 **
## New_Prog_Syn_MsasssSI     -6.756748   5.282319  -1.279  0.22718
## Mind_2_Synd_FLSI          -3.497963   3.594456  -0.973  0.35139
## Mind_2_Synd_BLSI           2.459721   3.650972   0.674  0.51440
## PCR_INICIOB                0.007389   0.134302   0.055  0.95711
## i_ASDAS                   -1.629755   3.200426  -0.509  0.62065
## HVGP                      -0.050671   0.757349  -0.067  0.94786
## BASFIDif                   0.072305   0.810919   0.089  0.93055
## BASDAIDif                 -0.120637   0.674872  -0.179  0.86138
## ASDASDif                   1.934157   1.712446   1.129  0.28273
## PCRDif                    -0.022665   0.134179  -0.169  0.86893
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.772 on 11 degrees of freedom
##   (46 observations deleted due to missingness)
## Multiple R-squared:  0.9235, Adjusted R-squared:  0.6244
## F-statistic: 3.087 on 43 and 11 DF,  p-value: 0.02385
```

```
modelo<-update(a, .~. -BASDAIDif -EGP)
summary(modelo)
```

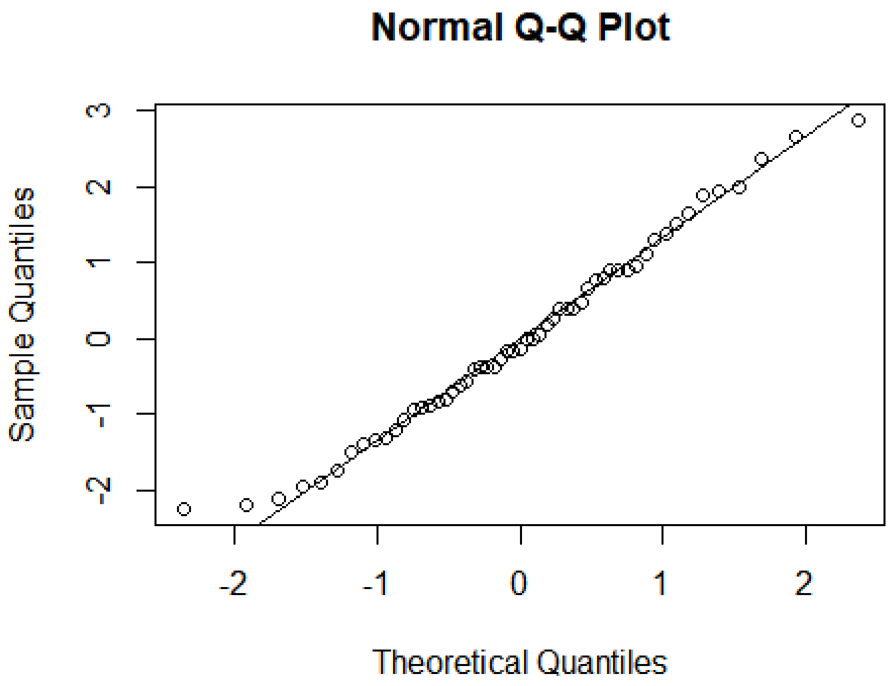
```
##
## Call:
## lm(formula = mSASSS_Progress ~ EDAD + SEXO + IMC + `IMC>30` +
##     TSINT + HLAB27 + EA + TABACO_Kat + VSG + BASMI + UVEITIS +
##     PSORIASIS + ENF_INF + TTOBIO + NUM_TB_PREV + MOTIVO + TIEMBIO +
##     BIO_INICI + Biol_4_kat + Interval + AINE + FAME + i_BASDAI +
##     EGM + New_Syn_mSASSS + Prog_Syn_mSASSS + mSASSS_Progress_Kat +
##     New_Prog_Syn_Msasss + Mind_2_Synd_FL + Mind_2_Synd_BL + PCR_INI
CIOB +
##     i_ASDAS + HVGP + BASFIDif + ASDASDif + PCRDif, data = base_rx2,
##     na.action = na.omit)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.2495 -0.9135 -0.1335  0.8903  2.8754
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              3.279166  11.544312   0.284  0.78085
## EDAD                     0.105811   0.080815   1.309  0.21310
## SEXOFEMALE              -1.366577   2.418556  -0.565  0.58167
## IMC                     -0.030907   0.236522  -0.131  0.89803
## `IMC>30`SI               0.159458   2.652687   0.060  0.95298
## TSINT                    0.086091   0.094628   0.910  0.37949
## HLAB27NO                -4.835809   2.439601  -1.982  0.06900 .
## EANO                     0.898020   4.438945   0.202  0.84281
## TABACO_KatNO             1.242937   2.061128   0.603  0.55686
## VSG                      0.049249   0.047083   1.046  0.31462
## BASMI                   -0.978005   0.652077  -1.500  0.15755
## UVEITISSI                0.234858   1.760230   0.133  0.89590
## PSORIASISSI              2.652616   3.103625   0.855  0.40820
## ENF_INFSI                4.797201   4.092863   1.172  0.26219
## TTOBIOADA               -3.291948   1.720120  -1.914  0.07792 .
## TTOBIOIFX                0.519086   2.529191   0.205  0.84057
## TTOBIOGOL               -2.952448   4.111204  -0.718  0.48537
## TTOBIOCTZ               -5.536354   3.859320  -1.435  0.17503
## NUM_TB_PREVtreatments.1 -4.310685   5.525908  -0.780  0.44931
## NUM_TB_PREVtreatments.2 -3.793466   6.723062  -0.564  0.58219
## MOTIVOInefficacy         5.415986   5.425952   0.998  0.33642
## MOTIVOSide.effects       1.497152   5.029598   0.298  0.77066
## TIEMBIO                 -0.022553   0.040463  -0.557  0.58675
## BIO_INICISI             -2.984814   2.384523  -1.252  0.23272
## Biol_4_katSI             2.139469   2.161978   0.990  0.34044
## Interval                 0.221040   0.851297   0.260  0.79920
## AINESI                   0.849680   1.548010   0.549  0.59239
## FAMESI                  -2.517002   2.358806  -1.067  0.30536
## i_BASDAI                -0.084631   0.700072  -0.121  0.90563
## EGM                      0.891908   0.398355   2.239  0.04328 *
## New_Syn_mSASSSSI         7.005377   4.388975   1.596  0.13447
## Prog_Syn_mSASSSSI        0.708655   2.765453   0.256  0.80177
## mSASSS_Progress_KatSI    7.709396   2.140348   3.602  0.00322 **
## New_Prog_Syn_MsasssSI   -5.686655   4.730863  -1.202  0.25079
## Mind_2_Synd_FLSI        -2.835653   3.276390  -0.865  0.40246
## Mind_2_Synd_BLSI         1.767413   3.320724   0.532  0.60354
```

```
## PCR_INICIOB              0.023364   0.122191   0.191  0.85131
## i_ASDAS                 -1.838684   2.949624  -0.623  0.54383
## HVGP                     0.066306   0.613889   0.108  0.91564
## BASFIDif                 0.221046   0.483612   0.457  0.65516
## ASDASDif                 1.371442   1.444511   0.949  0.35973
## PCRDif                   0.008344   0.119027   0.070  0.94518
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.612 on 13 degrees of freedom
##   (46 observations deleted due to missingness)
## Multiple R-squared:  0.9197, Adjusted R-squared:  0.6664
## F-statistic: 3.631 on 41 and 13 DF,  p-value: 0.007572
```

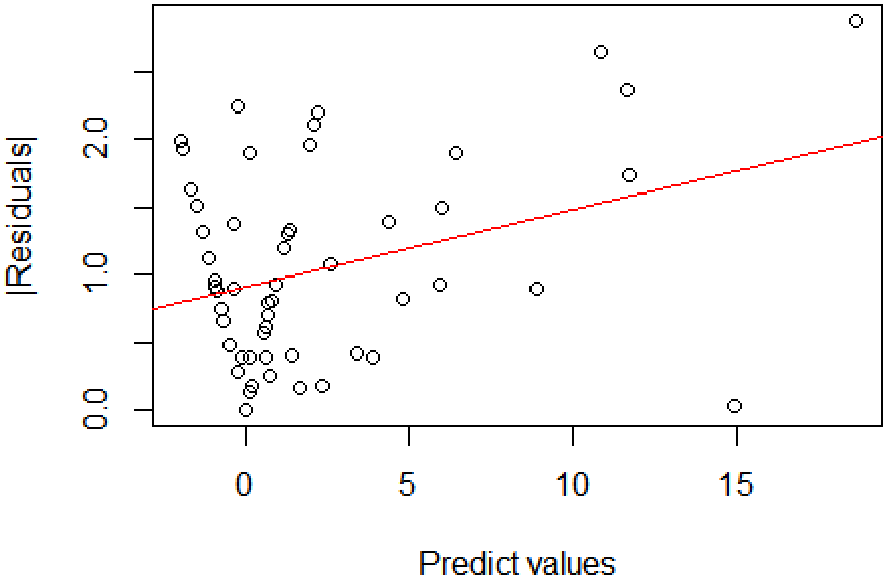
```r
fitted(modelo)
```

```
##             1             3             4             5
6
##  3.883109e+00 -7.540416e-01  7.511298e-01  2.116825e+00  7.109927e-
01
##             7             9            10            11
12
## -1.505862e+00  1.664959e+00 -1.310363e+00  5.649057e-01 -1.996754e+
00
##            13            14            15            16
17
## -1.638241e+00  6.398036e+00  6.168910e-01  1.334632e-01  2.582696e+
00
##            19            20            21            34
35
## -3.959460e-01  9.341081e-01 -2.172219e-01 -1.068590e-15  6.121443e-
01
##            36            42            44            45
46
## -3.704619e-01 -2.504826e-01  4.398667e+00  7.091628e-01 -1.929421e+
00
##            47            49            50            51
56
##  6.061890e-01 -8.847289e-01 -2.353672e-03  1.306331e+00  5.930905e+
00
##            57            59            61            62
63
## -6.646363e-01  1.396165e+00 -1.119954e+00  1.019641e-01  1.168910e-
01
##            64            65            66            67
68
##  1.496427e+01 -9.531105e-01  1.862463e+01  4.826957e+00 -1.115725e-
01
##            69            70            71            72
73
##  1.174049e+01  1.953745e+00  1.711572e-01  2.198770e+00  8.896140e+
00
##            75            76            85            86
87
```

```
##   2.320867e+00  1.163738e+01 -4.786596e-01 -9.051875e-01  6.002216e+
00
##            88            89            94            96            
97
##   3.421602e+00  8.114250e-01  1.197917e+00  1.085277e+01  1.333130e+
00

#  46 observaciones elimianadas debido a los missingn, quedando un tot
al de 97 observaciones.

qqnorm(modelo$residuals)
qqline(modelo$residuals)
```



```
shapiro.test(modelo$residuals)

## 
##  Shapiro-Wilk normality test
## 
## data:  modelo$residuals
## W = 0.98209, p-value = 0.5818

# Se rechaza la hipótesis nula, por lo que hay normalidad de los resid
uos

plot(fitted(modelo),abs(residuals(modelo)),xlab="Predict values", ylab
="|Residuals|")
abline(lm(abs(residuals(modelo)) ~ fitted(modelo)), col="red", lwd=1.5
)
```



```
library(lmtest)

## Loading required package: zoo

##
## Attaching package: 'zoo'

## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric

bptest(modelo)

##
##  studentized Breusch-Pagan test
##
## data:  modelo
## BP = 42.753, df = 41, p-value = 0.3958

# No hay evidencias de falta de homocedasticidad.
```

Validación de condiciones para la regresión múltiple lineal, como ya hemos analizado los residuos y la homocedasticidad. Valoramos ahora la correlación.

```
library(car)

## Loading required package: carData

##
## Attaching package: 'car'
```

```
## The following object is masked from 'package:psych':
##
##     logit

## The following object is masked from 'package:dplyr':
##
##     recode

dwt(modelo, alternative = "two.sided")

##  lag Autocorrelation D-W Statistic p-value
##    1     0.005012348      1.968281   0.824
##  Alternative hypothesis: rho != 0

# No hay evidencia de autocorrelación
```

Identificación de posibles valores atípicos o influyentes

```
library(car)
outlierTest(modelo)

## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##    rstudent unadjusted p-value Bonferroni p
## 66  3.51269          0.0042807      0.23116

# No hay datos atípicos
```

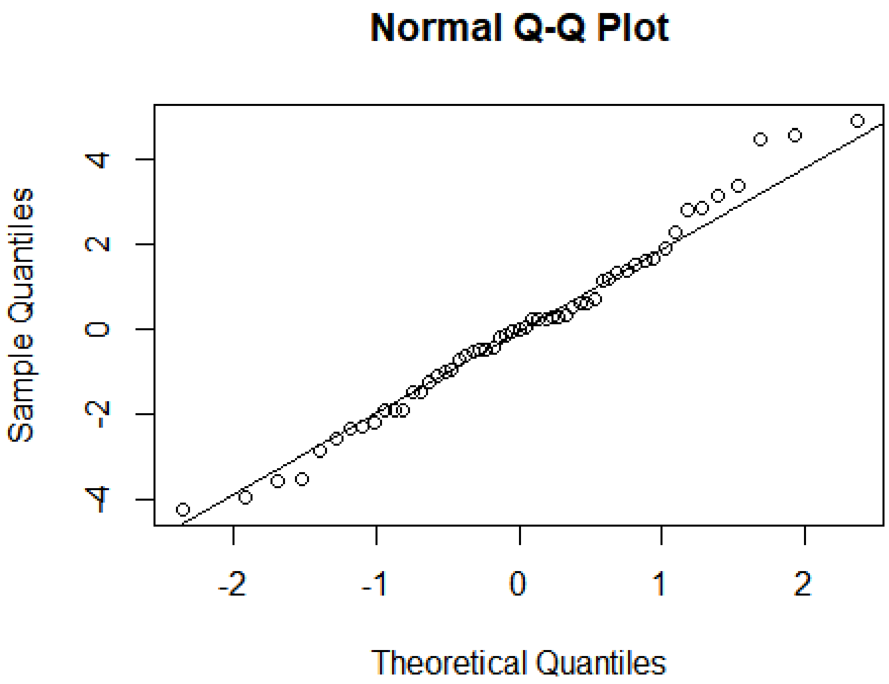
Conclusión

El modelo múltiple es capaz de explicar el 62.4% de la variabilidad observada en la progresión radiográfica (R2: 0.9235, R2-Adjusted: 0.6244).El test F muestra que es significativo (0.02385). Se satisfacen todas las condiciones para este tipo de regresión múltiple.

```
attach(base_rx3)

## The following objects are masked from base_rx2 (pos = 7):
##
##     AINE, ASDASDif, BASDAIDif, BASFIDif, BASMI, BIO_INICI, Biol_4_k
at,
##     EA, EDAD, EGM, EGP, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BAS
DAI,
##     IMC, IMC>30, Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO,
##     mSASSS_Progress, NUM_TB_PREV, PCR_INICIOB, PCRDif, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx2 (pos = 8):
##
##     AINE, ASDASDif, BASDAIDif, BASFIDif, BASMI, BIO_INICI, Biol_4_k
at,
##     EA, EDAD, EGM, EGP, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BAS
DAI,
##     IMC, IMC>30, Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO,
##     mSASSS_Progress, NUM_TB_PREV, PCR_INICIOB, PCRDif, PSORIASIS, S
```

```
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from c_base_rx.num:
##
##     BASMI, EDAD, EGM, EGP, HVGP, i_ASDAS, i_BASDAI, IMC, Interval,
##     mSASSS_Progress, PCR_INICIOB, TIEMBIO, TSINT, VSG

a3<-lm(mSASSS_Progress~ ., na.action= na.omit, data=base_rx3)
summary(a3)

##
## Call:
## lm(formula = mSASSS_Progress ~ ., data = base_rx3, na.action = na.o
mit)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -4.236 -1.350  0.000  1.249  4.897
##
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  8.103692  16.992383   0.477    0.640
## EDAD                        -0.003886   0.125016  -0.031    0.976
## SEXOFEMALE                  -2.243199   3.656405  -0.613    0.549
## IMC                         -0.108577   0.358271  -0.303    0.766
## `IMC>30`SI                  -1.097715   4.171210  -0.263    0.796
## TSINT                        0.045964   0.142208   0.323    0.751
## HLAB27NO                    -1.896123   3.860162  -0.491    0.630
## EANO                        -2.841619   7.070704  -0.402    0.693
## TABACO_KatNO                -0.216501   2.868730  -0.075    0.941
## VSG                         -0.019563   0.065021  -0.301    0.768
## BASMI                        0.416655   0.851084   0.490    0.632
## UVEITISSI                   -1.159512   2.654264  -0.437    0.668
## PSORIASISSI                  3.137099   4.752488   0.660    0.519
## ENF_INFSI                    3.609225   6.030499   0.598    0.558
## TTOBIOADA                   -4.247040   2.686738  -1.581    0.135
## TTOBIOIFX                   -0.546824   3.833681  -0.143    0.888
## TTOBIOGOL                   -1.636413   5.776941  -0.283    0.781
## TTOBIOCTZ                   -6.491962   5.877194  -1.105    0.287
## NUM_TB_PREVtreatments.1     -8.992542   8.412075  -1.069    0.302
## NUM_TB_PREVtreatments.2    -11.086607   9.511212  -1.166    0.262
## MOTIVOInefficacy             9.432894   8.162722   1.156    0.266
## MOTIVOSide.effects           5.104385   7.522292   0.679    0.508
## TIEMBIO                      0.044958   0.050599   0.889    0.388
## BIO_INICISI                 -2.551808   3.305274  -0.772    0.452
## Biol_4_katSI                -1.221309   3.298691  -0.370    0.716
## Interval                     0.401322   1.348680   0.298    0.770
## AINESI                      -2.294849   2.447854  -0.937    0.363
## FAMESI                       2.819417   3.758669   0.750    0.465
## i_BASDAI                    -1.057945   1.173140  -0.902    0.381
## EGP                          0.719047   0.834054   0.862    0.402
## EGM                          0.135346   0.806780   0.168    0.869
## Mind_2_Synd_FLSI            -1.583067   5.027610  -0.315    0.757
## Mind_2_Synd_BLSI             3.469850   5.045243   0.688    0.502
```

```
## PCR_INICIOB              0.137779   0.174083   0.791    0.441
## i_ASDAS                 -0.997510   4.468997  -0.223    0.826
## HVGP                     0.334195   1.033858   0.323    0.751
## BASFIDif                 0.109019   0.940209   0.116    0.909
## BASDAIDif               -0.110290   0.857289  -0.129    0.899
## ASDASDif                 0.977816   2.290934   0.427    0.676
## PCRDif                   0.022501   0.171042   0.132    0.897
##
## Residual standard error: 3.984 on 15 degrees of freedom
##   (46 observations deleted due to missingness)
## Multiple R-squared:  0.7844, Adjusted R-squared:  0.2239
## F-statistic:   1.4 on 39 and 15 DF,  p-value: 0.245

#Análisis de residuos
qqnorm(a3$residuals)
qqline(a3$residuals)
```



```
shapiro.test(a3$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  a3$residuals
## W = 0.98334, p-value = 0.6412

# Los residuos siguen la normalidad

library(lmtest)
bptest(a3)

##
##  studentized Breusch-Pagan test
```

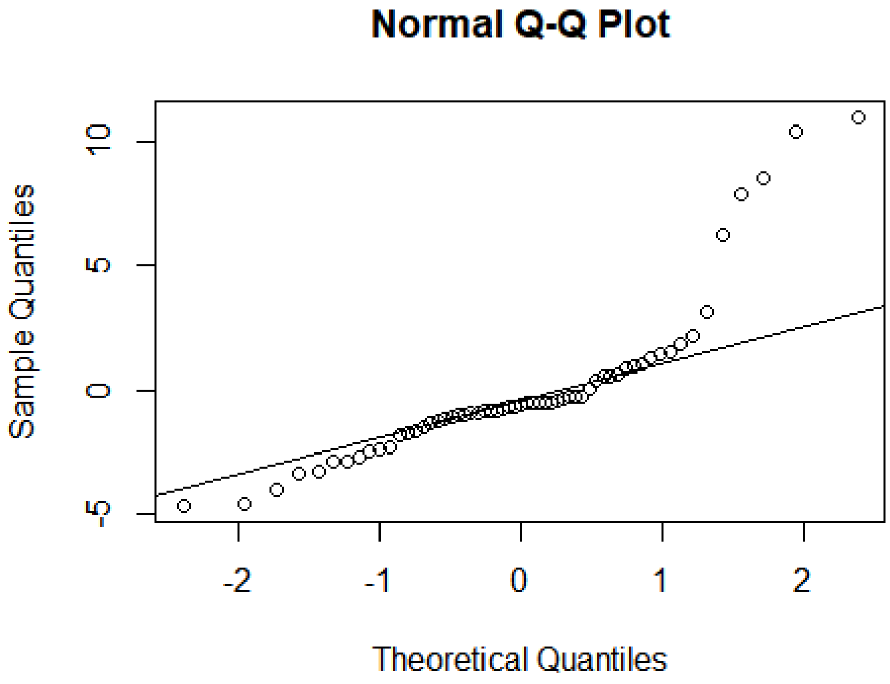
```
##
## data:  a3
## BP = 45.736, df = 39, p-value = 0.2126

# No hay evidencias de falta de homocedasticidad.

library(car)
dwt(a3,alternative = "two.sided")

##  lag Autocorrelation D-W Statistic p-value
##    1      -0.1210956      2.221821   0.636
##  Alternative hypothesis: rho != 0

# No hay evidencia de autocorrelación
```

Conclusión

El modelo múltiple es capaz de explicar el 22.4% de la variabilidad observada en la progresión radiográfica (R2: 0.7844, R2-Adjusted: 0.2239).El test F muestra que NO es significativo (0.245).

```
attach(base_rx.num2)

## The following objects are masked from base_rx3:
##
##     ASDASDif, BASDAIDif, BASFIDif, BASMI, EDAD, EGM, EGP, HVGP,
##     i_ASDAS, i_BASDAI, IMC, Interval, mSASSS_Progress, PCR_INICIOB,
##     PCRDif, TIEMBIO, TSINT, VSG

## The following objects are masked from base_rx2 (pos = 8):
##
##     ASDASDif, BASDAIDif, BASFIDif, BASMI, EDAD, EGM, EGP, HVGP,
##     i_ASDAS, i_BASDAI, IMC, Interval, mSASSS_Progress, PCR_INICIOB,
##     PCRDif, TIEMBIO, TSINT, VSG

## The following objects are masked from base_rx2 (pos = 9):
##
##     ASDASDif, BASDAIDif, BASFIDif, BASMI, EDAD, EGM, EGP, HVGP,
##     i_ASDAS, i_BASDAI, IMC, Interval, mSASSS_Progress, PCR_INICIOB,
##     PCRDif, TIEMBIO, TSINT, VSG

## The following objects are masked from c_base_rx.num:
##
##     BASMI, EDAD, EGM, EGP, HVGP, i_ASDAS, i_BASDAI, IMC, Interval,
##     mSASSS_Progress, PCR_INICIOB, TIEMBIO, TSINT, VSG

a2<-lm(mSASSS_Progress~ ., data=base_rx.num2)
summary(a2)

##
## Call:
## lm(formula = mSASSS_Progress ~ ., data = base_rx.num2)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.6650 -1.4206 -0.5989  0.5910 10.9876
##
```

```
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -6.30755    6.27543  -1.005    0.321
## EDAD         0.07762    0.08274   0.938    0.354
## IMC          0.02270    0.14503   0.157    0.876
## TSINT       -0.05750    0.06973  -0.825    0.414
## VSG         -0.03316    0.03730  -0.889    0.379
## BASMI        0.80028    0.54226   1.476    0.148
## TIEMBIO      0.01685    0.01915   0.880    0.384
## Interval     0.50775    0.66034   0.769    0.446
## i_BASDAI    -0.87809    0.58810  -1.493    0.143
## EGP          0.45201    0.39417   1.147    0.258
## EGM          0.26407    0.52132   0.507    0.615
## PCR_INICIOB  0.03217    0.08768   0.367    0.716
## i_ASDAS      0.76942    2.24528   0.343    0.734
## HVGP         0.02271    0.51083   0.044    0.965
## BASFIDif    -0.03336    0.43809  -0.076    0.940
## BASDAIDif   -0.19473    0.52683  -0.370    0.714
## ASDASDif     1.66904    1.07943   1.546    0.130
## PCRDif      -0.03104    0.06995  -0.444    0.660
##
## Residual standard error: 3.763 on 41 degrees of freedom
## Multiple R-squared:  0.4834, Adjusted R-squared:  0.2692
## F-statistic: 2.257 on 17 and 41 DF,  p-value: 0.01685

#Análisis de residuOs
qqnorm(a2$residuals)
qqline(a2$residuals)
```



```
shapiro.test(a2$residuals)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  a2$residuals
## W = 0.7963, p-value = 1.311e-07
```

```r
# Los residuos no siguen la normalidad

library(lmtest)
bptest(a2)
```

```
##
##  studentized Breusch-Pagan test
##
## data:  a2
## BP = 8.9985, df = 17, p-value = 0.9403
```

```r
# No hay evidencias de falta de homocedasticidad.

library(car)
dwt(a2,alternative = "two.sided")
```

```
##  lag Autocorrelation D-W Statistic p-value
##    1      -0.2147223      2.416146   0.114
##  Alternative hypothesis: rho != 0
```

```r
# No hay evidencia de autocorrelación
```

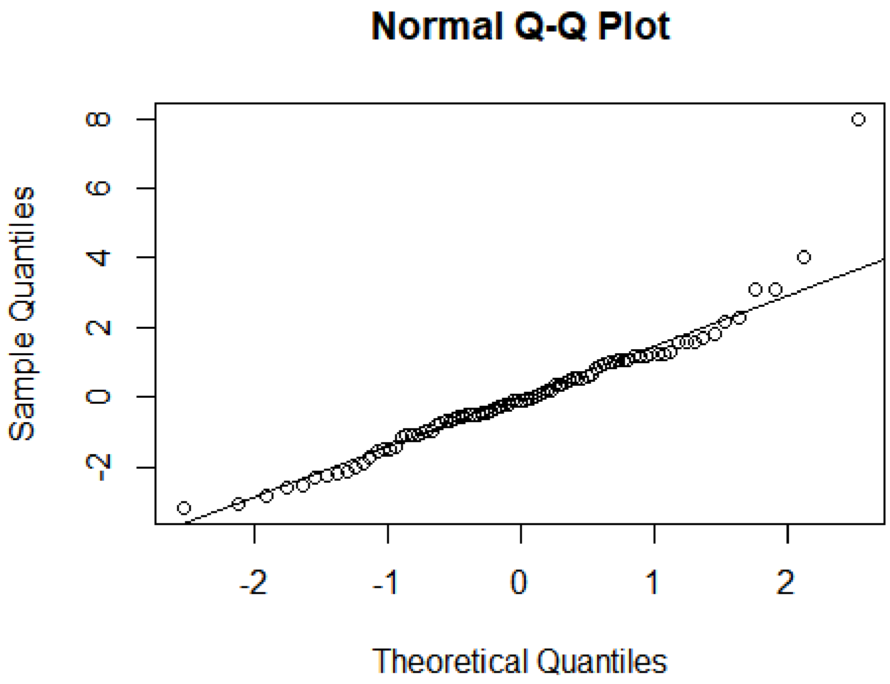
Conclusión, este modelo múltiple es capaz de explicar el 32.6% de la variabilidad observada en la progresión radiográfica (R2: 0.5235, R2-Adjusted: 0.326).El test F muestra que es significativo (0.005458). Sin embargo, el análisis de los residuos muestra que no siguen la normalidad.

```r
attach(c_base_rx2)
```

```
## The following objects are masked from base_rx.num2:
##
##     ASDASDif, BASDAIDif, BASFIDif, BASMI, EDAD, EGM, EGP, HVGP,
##     i_ASDAS, i_BASDAI, IMC, Interval, mSASSS_Progress, PCR_INICIOB,
##     PCRDif, TIEMBIO, TSINT, VSG

## The following objects are masked from base_rx3:
##
##     AINE, ASDASDif, BASDAIDif, BASFIDif, BASMI, BIO_INICI, Biol_4_k
at,
##     EA, EDAD, EGM, EGP, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BAS
DAI,
##     IMC, IMC>30, Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO,
##     mSASSS_Progress, NUM_TB_PREV, PCR_INICIOB, PCRDif, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx2 (pos = 9):
##
##     AINE, ASDASDif, BASDAIDif, BASFIDif, BASMI, BIO_INICI, Biol_4_k
at,
```

```
##     EA, EDAD, EGM, EGP, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BAS
DAI,
##     IMC, IMC>30, Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO,
##     mSASSS_Progress, mSASSS_Progress_Kat, New_Prog_Syn_Msasss,
##     New_Syn_mSASSS, NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSAS
SS,
##     PSORIASIS, SEXO, TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, V
SG

## The following objects are masked from base_rx2 (pos = 10):
##
##     AINE, ASDASDif, BASDAIDif, BASFIDif, BASMI, BIO_INICI, Biol_4_k
at,
##     EA, EDAD, EGM, EGP, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BAS
DAI,
##     IMC, IMC>30, Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO,
##     mSASSS_Progress, mSASSS_Progress_Kat, New_Prog_Syn_Msasss,
##     New_Syn_mSASSS, NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSAS
SS,
##     PSORIASIS, SEXO, TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, V
SG

## The following objects are masked from c_base_rx.num:
##
##     BASMI, EDAD, EGM, EGP, HVGP, i_ASDAS, i_BASDAI, IMC, Interval,
##     mSASSS_Progress, PCR_INICIOB, TIEMBIO, TSINT, VSG

a4<-lm(mSASSS_Progress~ ., data=c_base_rx2)
summary(a4)

##
## Call:
## lm(formula = mSASSS_Progress ~ ., data = c_base_rx2)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.1847 -0.9599 -0.1242  0.9775  7.9780
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)             -0.432440   3.693996  -0.117   0.9073
## EDAD                     0.081921   0.042793   1.914   0.0619 .
## IMC                     -0.003432   0.132654  -0.026   0.9795
## TSINT                   -0.003237   0.041008  -0.079   0.9374
## VSG                      0.029065   0.020344   1.429   0.1600
## BASMI                   -0.116478   0.249814  -0.466   0.6433
## TIEMBIO                  0.016939   0.019102   0.887   0.3799
## Interval                 0.043426   0.375553   0.116   0.9085
## i_BASDAI                -0.408141   0.367417  -1.111   0.2725
## EGP                      0.298590   0.249372   1.197   0.2374
## EGM                      0.085729   0.236838   0.362   0.7191
## PCR_INICIOB             -0.044345   0.033021  -1.343   0.1860
## i_ASDAS                  0.691693   1.015520   0.681   0.4993
## HVGP                    -0.053475   0.285021  -0.188   0.8520
## BASFIDif                -0.234562   0.201987  -1.161   0.2517
```

```
## BASDAIDif                 0.138215   0.285341   0.484   0.6305
## ASDASDif                  0.965751   0.503800   1.917   0.0616 .
## PCRDif                   -0.006256   0.037187  -0.168   0.8672
## SEXOFEMALE               -1.672282   0.983481  -1.700   0.0960 .
## `IMC>30`SI                1.205225   1.497020   0.805   0.4250
## HLAB27NO                 -1.697130   1.013916  -1.674   0.1011
## EANO                      1.203685   1.339031   0.899   0.3735
## TABACO_KatNO             -0.110267   0.726659  -0.152   0.8801
## UVEITISSI                 0.214601   0.819317   0.262   0.7946
## PSORIASISSI              -1.262357   1.393738  -0.906   0.3699
## ENF_INFSI                -0.091538   1.583879  -0.058   0.9542
## TTOBIOADA                -1.863147   0.801557  -2.324   0.0247 *
## TTOBIOIFX                 0.054218   1.235601   0.044   0.9652
## TTOBIOGOL                -0.526924   1.619044  -0.325   0.7463
## TTOBIOCTZ                -2.201403   2.048448  -1.075   0.2883
## NUM_TB_PREVtreatments.1   1.808198   2.026637   0.892   0.3770
## NUM_TB_PREVtreatments.2  -0.634034   2.708435  -0.234   0.8160
## MOTIVOIneffícacy         -0.880702   2.236344  -0.394   0.6956
## MOTIVOSide.effects       -2.001092   2.290223  -0.874   0.3869
## BIO_INICISI              -1.925112   1.174174  -1.640   0.1081
## Biol_4_katSI             -1.121438   1.266724  -0.885   0.3807
## AINESI                   -1.442735   0.735905  -1.960   0.0561 .
## FAMESI                    1.283016   0.981828   1.307   0.1979
## New_Syn_mSASSSSI          6.049405   2.353675   2.570   0.0135 *
## Prog_Syn_mSASSSSI         0.902780   1.478001   0.611   0.5444
## mSASSS_Progress_KatSI     5.487751   1.221006   4.494 4.85e-05 ***
## New_Prog_Syn_MsasssSI    -5.513072   2.802110  -1.967   0.0553 .
## Mind_2_Synd_FLSI         -2.652211   2.074171  -1.279   0.2076
## Mind_2_Synd_BLSI          2.064728   2.088418   0.989   0.3281
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.293 on 45 degrees of freedom
##   (12 observations deleted due to missingness)
## Multiple R-squared:  0.8261, Adjusted R-squared:   0.66
## F-statistic: 4.972 on 43 and 45 DF,  p-value: 1.989e-07

#Análisis de residuis
qqnorm(a4$residuals)
qqline(a4$residuals)
```



```
shapiro.test(a4$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  a4$residuals
## W = 0.92064, p-value = 4.247e-05

# pero los residuos no siguen la normalidad

library(lmtest)
bptest(a4)

##
##  studentized Breusch-Pagan test
##
## data:  a4
## BP = 55.722, df = 43, p-value = 0.09237

# No hay evidencias de falta de homocedasticidad.

library(car)
dwt(a4,alternative = "two.sided")

##  lag Autocorrelation D-W Statistic p-value
##    1     -0.06955701      2.137721   0.672
##  Alternative hypothesis: rho != 0

# No hay evidencia de autocorrelación
```

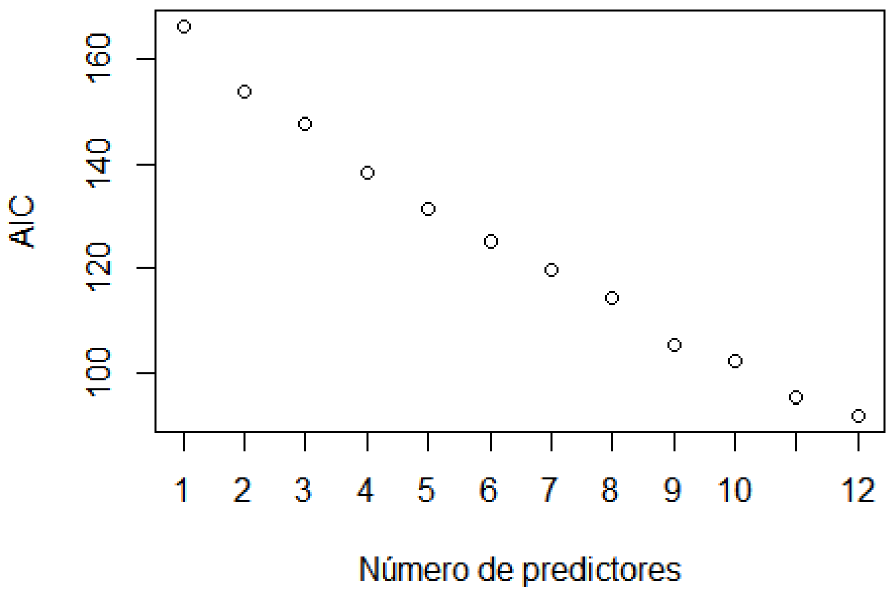
Conclusión, este modelo múltiple es capaz de explicar el 66.6% de la variabilidad observada en la progresión radiográfica (R2: 0.8296, R2-Adjusted: 0.6668).El test F muestra que es significativo (1.365e-07). Sin embargo, el análisis de los residuos muestra que no siguen la normalidad.

Por lo que elejimos el primer modelo.

Por regla general, el número de observaciones debe ser como mínimo entre 10 y 20 veces el número de predictores del modelo. Como tenemos 97 observaciones, el número de predictores no debería ser mayor a 10. Por lo que debemos elemimnar predictores, que no influyan en el modelo. Para ello, vamos a realizar a una regresión con variables seleccionadas por AIC

```
library(leaps)
attach(base_rx21)

## The following objects are masked from c_base_rx2:
##
##     AINE, ASDASDif, BASFIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDA
D,
##     EGM, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>3
0,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx.num2:
##
##     ASDASDif, BASFIDif, BASMI, EDAD, EGM, HVGP, i_ASDAS, i_BASDAI,
IMC,
##     Interval, mSASSS_Progress, PCR_INICIOB, PCRDif, TIEMBIO, TSINT,
VSG

## The following objects are masked from base_rx3:
##
##     AINE, ASDASDif, BASFIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDA
D,
##     EGM, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>3
0,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, PSORIASIS, SEXO, TABACO_Kat,
##     TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx2 (pos = 11):
##
##     AINE, ASDASDif, BASFIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDA
D,
##     EGM, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>3
0,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
```

```
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx2 (pos = 12):
##
##     AINE, ASDASDif, BASFIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDA
D,
##     EGM, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>3
0,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from c_base_rx.num:
##
##     BASMI, EDAD, EGM, HVGP, i_ASDAS, i_BASDAI, IMC, Interval,
##     mSASSS_Progress, PCR_INICIOB, TIEMBIO, TSINT, VSG

b <- regsubsets( mSASSS_Progress~ ., data=base_rx21, na.action = na.om
it, nvmax=12)
rs <- summary(b)
n <- nrow(base_rx21)
k <- length(rs$rss) # Número de variables predictoras
p <- k + 1 # Número de parámetros (incluye la intercepción)
(AIC <- n*log(rs$rss/n) + (2:p)*2)

##  [1] 166.12733 153.54661 147.48753 138.12852 131.52924 125.24759 11
9.94576
##  [8] 114.31560 105.63619 102.32931  95.34395  92.00777

plot(1:k, AIC, ylab="AIC", xlab="Número de predictores", axes=F)
box(); axis(1,at=1:k); axis(2)
```



El mínimo AIC se alcanza con 12 predictores, aunque con 10 también tenemos un buen resultado.

```
rs$outmat[10,]
```

```
##                     EDAD              SEXOFEMALE
IMC
##                      "*"                     " "
" "
##               `IMC>30`SI                   TSINT                HLAB
27NO
##                      " "                     " "
" "
##                     EANO            TABACO_KatNO
VSG
##                      "*"                     " "
" "
##                    BASMI               UVEITISSI             PSORIAS
ISSI
##                      " "                     " "
" "
##                ENF_INFSI               TTOBIOADA               TTOBI
OIFX
##                      " "                     "*"
" "
##                TTOBIOGOL               TTOBIOCTZ NUM_TB_PREVtreatmen
ts.1
##                      "*"                     "*"
" "
## NUM_TB_PREVtreatments.2        MOTIVOInefficacy      MOTIVOSide.eff
ects
##                      "*"                     " "
```

```
" "
##                 TIEMBIO             BIO_INICISI            Biol_4_k
atSI
##                     " "                     "*"
" "
##                Interval                  AINESI                  FA
MESI
##                     " "                     " "
" "
##                i_BASDAI                     EGM        New_Syn_mSAS
SSSI
##                     " "                     " "
"*"
##       Prog_Syn_mSASSSSI   mSASSS_Progress_KatSI   New_Prog_Syn_Msas
ssSI
##                     " "                     "*"
" "
##        Mind_2_Synd_FLSI        Mind_2_Synd_BLSI             PCR_INI
CIOB
##                     " "                     " "
" "
##                 i_ASDAS                    HVGP                BASF
IDif
##                     " "                     " "
" "
##                ASDASDif                  PCRDif
##                     "*"                     " "
```

```
attach(base_rx21)
```

```
## The following objects are masked from base_rx21 (pos = 3):
## 
##     AINE, ASDASDif, BASFIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDA
D,
##     EGM, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>3
0,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG
```

```
## The following objects are masked from c_base_rx2:
## 
##     AINE, ASDASDif, BASFIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDA
D,
##     EGM, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>3
0,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG
```

```
## The following objects are masked from base_rx.num2:
##
##     ASDASDif, BASFIDif, BASMI, EDAD, EGM, HVGP, i_ASDAS, i_BASDAI,
IMC,
##     Interval, mSASSS_Progress, PCR_INICIOB, PCRDif, TIEMBIO, TSINT,
VSG

## The following objects are masked from base_rx3:
##
##     AINE, ASDASDif, BASFIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDA
D,
##     EGM, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>3
0,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, PSORIASIS, SEXO, TABACO_Kat,
##     TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx2 (pos = 12):
##
##     AINE, ASDASDif, BASFIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDA
D,
##     EGM, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>3
0,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx2 (pos = 13):
##
##     AINE, ASDASDif, BASFIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDA
D,
##     EGM, ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>3
0,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from c_base_rx.num:
##
##     BASMI, EDAD, EGM, HVGP, i_ASDAS, i_BASDAI, IMC, Interval,
##     mSASSS_Progress, PCR_INICIOB, TIEMBIO, TSINT, VSG

s.aic<-lm(mSASSS_Progress ~ EDAD + SEXO  + HLAB27 + EA + TTOBIO + EGM
+ New_Syn_mSASSS +
    mSASSS_Progress_Kat + New_Prog_Syn_Msasss + ASDASDif, na.action =
na.omit)
summary(s.aic)
```

```
##
## Call:
## lm(formula = mSASSS_Progress ~ EDAD + SEXO + HLAB27 + EA + TTOBIO +
##     EGM + New_Syn_mSASSS + mSASSS_Progress_Kat + New_Prog_Syn_Msass
s +
##     ASDASDif, na.action = na.omit)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -7.5558 -1.0077 -0.3158  0.6955  9.8685
##
## Coefficients:
##                        Estimate Std. Error t value Pr(>|t|)
## (Intercept)            -1.43128    1.51491  -0.945 0.348751
## EDAD                    0.04491    0.03157   1.423 0.160307
## SEXOFEMALE             -0.19701    0.90764  -0.217 0.828939
## HLAB27NO               -0.60798    1.01252  -0.600 0.550577
## EANO                    1.19672    1.03091   1.161 0.250547
## TTOBIOADA              -1.17795    0.77237  -1.525 0.132761
## TTOBIOIFX               0.15510    1.07691   0.144 0.885989
## TTOBIOGOL              -1.57378    1.38653  -1.135 0.261105
## TTOBIOCTZ              -1.89162    2.04345  -0.926 0.358505
## EGM                     0.24254    0.16317   1.486 0.142691
## New_Syn_mSASSSSI        5.29174    2.04740   2.585 0.012334 *
## mSASSS_Progress_KatSI   4.82019    1.27623   3.777 0.000381 ***
## New_Prog_Syn_MsasssSI  -3.05319    2.29198  -1.332 0.188123
## ASDASDif                0.89338    0.34092   2.621 0.011234 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.626 on 57 degrees of freedom
##   (30 observations deleted due to missingness)
## Multiple R-squared:  0.6891, Adjusted R-squared:  0.6182
## F-statistic:  9.72 on 13 and 57 DF,  p-value: 3.046e-10
```

```
coef(s.aic)
```

```
##           (Intercept)                  EDAD            SEXOFEMALE
##           -1.43127676            0.04491406           -0.19701044
##              HLAB27NO                  EANO             TTOBIOADA
##           -0.60798117            1.19671506           -1.17794570
##             TTOBIOIFX             TTOBIOGOL             TTOBIOCTZ
##            0.15510074           -1.57377609           -1.89161660
##                   EGM      New_Syn_mSASSSSI mSASSS_Progress_KatSI
##            0.24253902            5.29173534            4.82019415
## New_Prog_Syn_MsasssSI              ASDASDif
##           -3.05319384            0.89338432
```

Este valor indica que por cada difrencia entres el ASDAS inicial con el final, la odds estimada de progressión se multiplica por ese número. El intervalo de confianza es

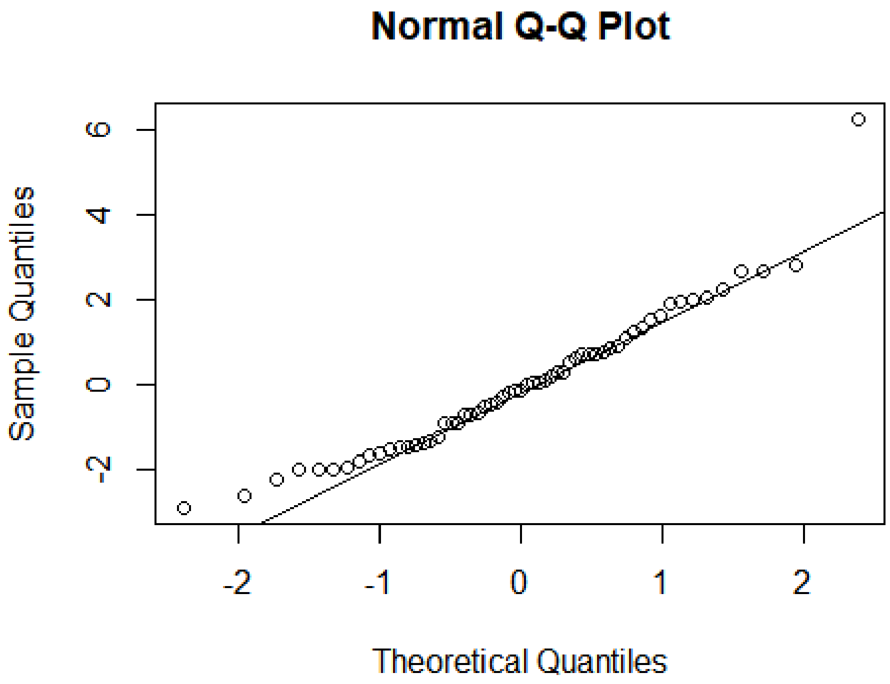
```
(summary(s.aic)$coefficients["New_Syn_mSASSSSI",1] +
qnorm(c(0.025,0.975)) * summary(s.aic)$coefficients["New_Syn_mSASSSSI"
,2])
```

```
## [1] 1.278914 9.304557

(summary(s.aic)$coefficients["mSASSS_Progress_KatSI",1] +
qnorm(c(0.025,0.975)) * summary(s.aic)$coefficients["mSASSS_Progress_K
atSI",2])

## [1] 2.318822 7.321566

(summary(s.aic)$coefficients["ASDASDif",1] +
qnorm(c(0.025,0.975)) * summary(s.aic)$coefficients["ASDASDif",2])

## [1] 0.2251996 1.5615691

attach(base_rx22)

## The following objects are masked from base_rx21 (pos = 3):
##
##     AINE, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM, ENF_INF, FAM
E,
##     HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30, Interval,
##     Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progress,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx21 (pos = 4):
##
##     AINE, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM, ENF_INF, FAM
E,
##     HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30, Interval,
##     Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progress,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from c_base_rx2:
##
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx.num2:
##
##     BASDAIDif, BASMI, EDAD, EGM, HVGP, i_ASDAS, i_BASDAI, IMC,
##     Interval, mSASSS_Progress, PCR_INICIOB, PCRDif, TIEMBIO, TSINT,
VSG

## The following objects are masked from base_rx3:
##
```

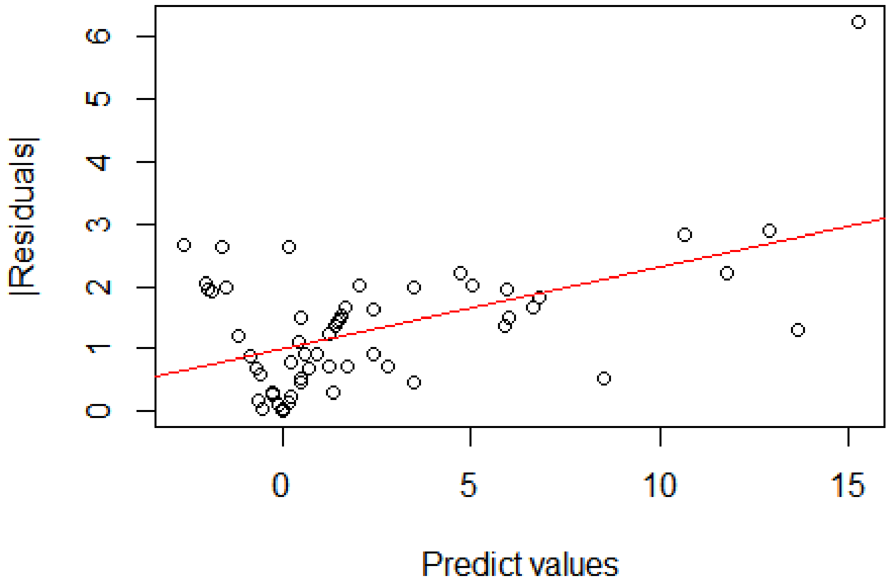
```
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, PSORIASIS, SEXO, TABACO_Kat,
##     TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx2 (pos = 13):
##
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx2 (pos = 14):
##
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from c_base_rx.num:
##
##     BASMI, EDAD, EGM, HVGP, i_ASDAS, i_BASDAI, IMC, Interval,
##     mSASSS_Progress, PCR_INICIOB, TIEMBIO, TSINT, VSG

abc<-lm(mSASSS_Progress~ ., data=base_rx22, na.action = na.omit)
summary(abc)

##
## Call:
## lm(formula = mSASSS_Progress ~ ., data = base_rx22, na.action = na.
omit)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.9083 -1.3655 -0.1359  0.8913  6.2356
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)             -5.378305   9.852182  -0.546  0.59184
## EDAD                     0.157102   0.083216   1.888  0.07527 .
## SEXOFEMALE              -1.000685   2.306875  -0.434  0.66960
## IMC                      0.089652   0.224743   0.399  0.69465
## `IMC>30`SI               0.542955   2.667651   0.204  0.84100
## TSINT                    0.001852   0.091952   0.020  0.98415
## HLAB27NO                -4.500475   2.458216  -1.831  0.08374 .
```

```
## EANO                     1.760100   3.519349   0.500  0.62305
## TABACO_KatNO             1.215674   1.951695   0.623  0.54117
## VSG                      0.068615   0.039662   1.730  0.10074
## BASMI                   -0.771863   0.561888  -1.374  0.18640
## UVEITISSI                0.719321   1.616122   0.445  0.66156
## PSORIASISSI             -1.742260   2.573706  -0.677  0.50705
## ENF_INFSI                2.161013   4.266984   0.506  0.61869
## TTOBIOADA               -2.491257   1.437645  -1.733  0.10022
## TTOBIOIFX                0.262128   2.283534   0.115  0.90988
## TTOBIOGOL               -0.673301   4.048884  -0.166  0.86978
## TTOBIOCTZ               -3.458348   4.090163  -0.846  0.40892
## NUM_TB_PREVtreatments.1  3.014191   3.692527   0.816  0.42500
## NUM_TB_PREVtreatments.2  3.854029   5.161996   0.747  0.46494
## MOTIVOInefficacy        -1.589475   3.762311  -0.422  0.67768
## MOTIVOSide.effects      -4.524821   4.255796  -1.063  0.30174
## TIEMBIO                  0.009117   0.039738   0.229  0.82113
## BIO_INICISI             -3.761606   2.478690  -1.518  0.14649
## Biol_4_katSI            -0.028936   2.101266  -0.014  0.98916
## Interval                 0.408044   0.752932   0.542  0.59451
## AINESI                   0.402600   1.563484   0.258  0.79971
## FAMESI                  -1.297081   2.480959  -0.523  0.60748
## i_BASDAI                -0.239530   0.737635  -0.325  0.74913
## EGM                      0.452444   0.341935   1.323  0.20234
## New_Syn_mSASSSSI         7.996090   4.394555   1.820  0.08550 .
## Prog_Syn_mSASSSSI       -1.202146   2.894825  -0.415  0.68285
## mSASSS_Progress_KatSI    7.911277   2.231201   3.546  0.00231 **
## New_Prog_Syn_MsasssSI   -6.335959   4.855007  -1.305  0.20832
## Mind_2_Synd_FLSI        -2.170821   3.431615  -0.633  0.53495
## Mind_2_Synd_BLSI         0.904186   3.500986   0.258  0.79913
## PCR_INICIOB             -0.071352   0.065928  -1.082  0.29342
## i_ASDAS                 -0.016251   2.571380  -0.006  0.99503
## HVGP                     0.055180   0.592719   0.093  0.92686
## BASDAIDif                0.537715   0.462403   1.163  0.26007
## PCRDif                   0.059146   0.070315   0.841  0.41129
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.975 on 18 degrees of freedom
##   (42 observations deleted due to missingness)
## Multiple R-squared:  0.8578, Adjusted R-squared:  0.5418
## F-statistic: 2.715 on 40 and 18 DF,  p-value: 0.0127
```

```
qqnorm(abc$residuals)
qqline(abc$residuals)
```



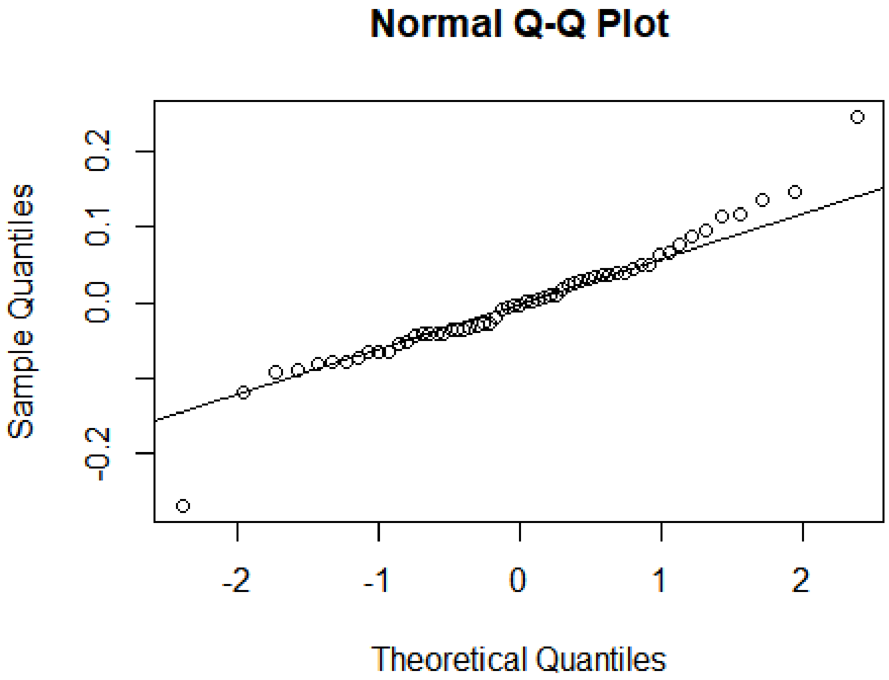
```
shapiro.test(abc$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  abc$residuals
## W = 0.94982, p-value = 0.01651

# No se rechaza la hipótesis nula, por lo que no hay normalidad de los residuos
plot(fitted(abc),abs(residuals(abc)),xlab="Predict values", ylab="|Residuals|")
abline(lm(abs(residuals(abc)) ~ fitted(abc)), col="red", lwd=1.5)
```



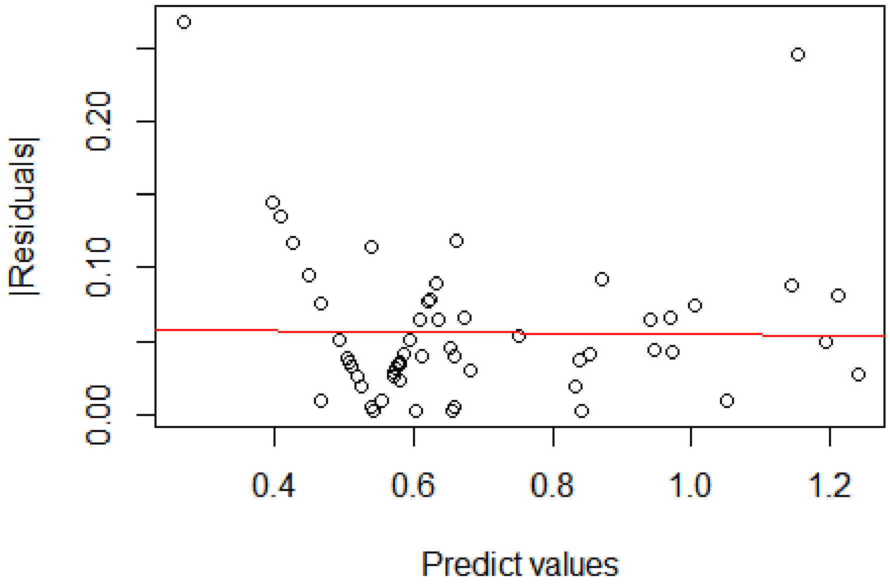
```
library(lmtest)
bptest(abc)

##
##  studentized Breusch-Pagan test
##
## data:  abc
## BP = 41.823, df = 40, p-value = 0.3916

library(car)
dwt(abc,alternative = "two.sided")

##  lag Autocorrelation D-W Statistic p-value
##    1     -0.04275237      2.056578    0.97
##  Alternative hypothesis: rho != 0

Y = c (3.5,1.5,0,1,0,1.5,0,0.,1.5,0,0,0,0,4.5,1,0,1.5,0,0.5,0,-0.5,0,0
,0,0,0,0,3,0,6,0,0,3,0,0,1.0,0.0,4.0,0.0,1.5,0.0,-2.5,5.0,3.0,0.0,0.0,
1.0,5.0,0.0,0.0,0.0,4.5,0.0,0.0,6.5,5.0,0.0,3.0,1.0,0.0,0.0,2.0,0.5,15
.0,0.0,21.5,4.0,-0.5,10.0,0.0,0.0,0.0,8.0,2.0,2.5,14.0,3.5,1.0,0.0,0.0
,0.0,0.0,-0.5,1.5,0.0,0.0,4.5,3.0,0.0,1.0,0.0,11.0,7.5,0.0,0,13.5,0.0,
1.0,0.0,6.0,2.0)
LY = log10(Y + 1 - min(Y))
abc1<-lm(LY~ .-mSASSS_Progress, data=base_rx22, na.action = na.omit)
summary(abc1)

##
## Call:
## lm(formula = LY ~ . - mSASSS_Progress, data = base_rx22, na.action
= na.omit)
##
## Residuals:
```

```
##       Min        1Q    Median        3Q       Max 
## -0.268261 -0.041747 -0.002465  0.039164  0.246168 
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)   
## (Intercept)              2.313e-01  4.533e-01   0.510  0.61612   
## EDAD                     8.508e-03  3.829e-03   2.222  0.03936 * 
## SEXOFEMALE              -1.145e-02  1.061e-01  -0.108  0.91526   
## IMC                      9.242e-05  1.034e-02   0.009  0.99297   
## `IMC>30`SI               2.183e-02  1.228e-01   0.178  0.86083   
## TSINT                   -3.076e-03  4.231e-03  -0.727  0.47663   
## HLAB27NO                -6.550e-02  1.131e-01  -0.579  0.56973   
## EANO                     1.070e-01  1.619e-01   0.661  0.51699   
## TABACO_KatNO            -1.558e-02  8.981e-02  -0.174  0.86417   
## VSG                      1.979e-03  1.825e-03   1.085  0.29244   
## BASMI                   -1.222e-02  2.585e-02  -0.473  0.64207   
## UVEITISSI               -2.197e-02  7.436e-02  -0.295  0.77102   
## PSORIASISSI             -3.071e-02  1.184e-01  -0.259  0.79834   
## ENF_INFSI                5.423e-03  1.963e-01   0.028  0.97827   
## TTOBIOADA               -1.309e-01  6.615e-02  -1.979  0.06332 . 
## TTOBIOIFX                2.622e-02  1.051e-01   0.250  0.80578   
## TTOBIOGOL                3.872e-02  1.863e-01   0.208  0.83771   
## TTOBIOCTZ               -1.417e-01  1.882e-01  -0.753  0.46123   
## NUM_TB_PREVtreatments.1 -2.300e-02  1.699e-01  -0.135  0.89382   
## NUM_TB_PREVtreatments.2 -1.280e-01  2.375e-01  -0.539  0.59647   
## MOTIVOInefficacy         9.166e-02  1.731e-01   0.529  0.60296   
## MOTIVOSide.effects      -5.195e-02  1.958e-01  -0.265  0.79382   
## TIEMBIO                  1.142e-03  1.829e-03   0.625  0.54009   
## BIO_INICISI             -1.296e-01  1.141e-01  -1.137  0.27064   
## Biol_4_katSI            -2.922e-02  9.669e-02  -0.302  0.76598   
## Interval                 1.659e-02  3.465e-02   0.479  0.63780   
## AINESI                  -1.846e-02  7.194e-02  -0.257  0.80038   
## FAMESI                  -9.641e-03  1.142e-01  -0.084  0.93363   
## i_BASDAI                 1.658e-03  3.394e-02   0.049  0.96159   
## EGM                      1.295e-03  1.573e-02   0.082  0.93531   
## New_Syn_mSASSSSI         2.344e-01  2.022e-01   1.159  0.26152   
## Prog_Syn_mSASSSSI        1.257e-03  1.332e-01   0.009  0.99258   
## mSASSS_Progress_KatSI    3.524e-01  1.027e-01   3.433  0.00297 **
## New_Prog_Syn_MsasssSI   -2.139e-01  2.234e-01  -0.957  0.35110   
## Mind_2_Synd_FLSI         3.428e-02  1.579e-01   0.217  0.83060   
## Mind_2_Synd_BLSI         2.868e-02  1.611e-01   0.178  0.86067   
## PCR_INICIOB             -2.462e-03  3.034e-03  -0.812  0.42759   
## i_ASDAS                  4.040e-02  1.183e-01   0.341  0.73674   
## HVGP                    -9.490e-03  2.727e-02  -0.348  0.73190   
## BASDAIDif                2.968e-02  2.128e-02   1.395  0.18000   
## PCRDif                   1.923e-03  3.235e-03   0.594  0.55972   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.1369 on 18 degrees of freedom
##   (42 observations deleted due to missingness)
## Multiple R-squared:  0.8972, Adjusted R-squared:  0.6688 
## F-statistic: 3.929 on 40 and 18 DF,  p-value: 0.001425
```

```
qqnorm(abc1$residuals)
qqline(abc1$residuals)
```



```
shapiro.test(abc1$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  abc1$residuals
## W = 0.9513, p-value = 0.01936

which.max(abc1$residuals)

## 66
## 41

which.min(abc1$residuals)

## 42
## 24

shapiro.test(abc1$residuals[c(-24,-41)])

##
##  Shapiro-Wilk normality test
##
## data:  abc1$residuals[c(-24, -41)]
## W = 0.97796, p-value = 0.3819

plot(fitted(abc1),abs(residuals(abc1)),xlab="Predict values", ylab="|R
esiduals|")
abline(lm(abs(residuals(abc1)) ~ fitted(abc1)), col="red", lwd=1.5)
```



```
library(lmtest)
bptest(abc1)

##
##  studentized Breusch-Pagan test
##
## data:  abc1
## BP = 44.25, df = 40, p-value = 0.2969

library(car)
dwt(abc1,alternative = "two.sided")

##  lag Autocorrelation D-W Statistic p-value
##    1      0.01571134      1.963515    0.62
##  Alternative hypothesis: rho != 0

library(car)
outlierTest(abc1)

##     rstudent unadjusted p-value Bonferroni p
## 42 -4.813376         0.00016221    0.0095705
## 66  4.638805         0.00023484    0.0138550

summary(influence.measures(abc1))

## Potentially influential observations of
##   lm(formula = LY ~ . - mSASSS_Progress, data = base_rx22, na.actio
n = na.omit) :
##
##    dfb.1_ dfb.EDAD dfb.SEXO dfb.IMC  dfb.`IMC dfb.TSIN dfb.HLAB dfb
.EANO
## 1    0.00   0.00     0.02     0.00     0.01    -0.01     0.01    -0
```

```
.01
## 3    0.29  -0.21    -0.06    -0.06    -0.07     0.08    -0.06    -0
.06
## 4    0.26  -0.23    -0.22    -0.10     0.34     0.13    -0.02    -0
.02
## 5    0.11  -0.13     0.05     0.21    -0.16     0.13     0.06    -0
.13
## 6    0.02  -0.02     0.23     0.10    -0.05    -0.15     0.26    -0
.12
## 7   -0.33  -0.10    -1.04_*  -0.06     0.62     0.55     0.23     0
.77
## 9   -0.07   0.10     0.12     0.07    -0.05    -0.04    -0.05    -0
.08
## 11  -0.04  -0.01     0.16     0.08     0.03    -0.24    -0.16     0
.00
## 13  -0.17  -0.05     0.12     0.23     0.04    -0.10     0.06     0
.06
## 14  -0.20   0.45     0.01    -0.19     0.01    -0.40    -0.06    -0
.04
## 15   0.00   0.00     0.02     0.00     0.01    -0.01     0.01    -0
.01
## 19   0.01  -0.08     0.01     0.02    -0.07     0.05     0.00    -0
.02
## 21   0.00   0.00    -0.02     0.01    -0.02    -0.06    -0.05    -0
.09
## 35   0.08  -0.10     0.07     0.03    -0.05    -0.02     0.07    -0
.06
## 36   0.94  -0.16    -0.49    -1.19_*   0.66     0.16     0.65     0
.29
## 38   0.01  -0.06     0.21     0.10    -0.04    -0.16     0.00    -0
.12
## 40  -0.48   0.02    -0.05    -0.11     0.32    -0.09    -0.14     0
.54
## 42  -0.67   1.34_*  -0.50    -0.13    -0.14    -1.01_*   1.23_*   0
.62
## 43  -0.38   0.27    -0.08     0.26    -0.02    -0.15    -0.17     0
.15
## 44   0.13  -0.01     0.26    -0.10     0.17    -0.16     0.04    -0
.10
## 45  -0.05   0.03    -0.03     0.02    -0.02    -0.10    -0.08    -0
.04
## 46   0.00   0.00     0.00     0.00     0.00     0.01     0.00     0
.00
## 47  -0.10  -0.02     0.01     0.08    -0.02    -0.02    -0.16    -0
.01
## 49   0.03  -0.03    -0.01     0.00    -0.02     0.01     0.01     0
.01
## 50  -0.04  -0.03    -0.01     0.01    -0.02    -0.01    -0.05     0
.05
## 51  -0.39  -0.93     0.30     1.02_*  -1.07_*  -0.15    -0.07    -2
.70_*
## 57   0.03  -0.22    -0.30     0.41    -0.19     0.30    -0.13     0
.18
## 59  -0.01   0.00     0.00     0.01     0.00     0.00    -0.02    -0
```

```
.01
## 63   0.00   0.00     0.02     0.00     0.01    -0.01     0.01    -0
.01
## 64  -0.02   0.04    -0.04     0.04    -0.06     0.00    -0.12     0
.06
## 65  -0.02   0.00    -0.05     0.00     0.00     0.02    -0.04     0
.04
## 66  -0.43   0.72    -0.20     0.84     0.19     0.48    -0.96    -0
.24
## 68  -0.03   0.01    -0.03     0.00     0.02     0.00     0.00     0
.01
## 70  -0.04  -0.01    -0.13    -0.12     0.08    -0.07     0.14     0
.03
## 71   0.05  -0.16    -0.21     0.28    -0.32     0.12     0.01     0
.11
## 73   0.00  -0.02    -0.04    -0.02     0.07     0.07     0.07     0
.06
## 76  -0.08   0.18    -0.01     0.07    -0.01    -0.15    -0.08    -0
.06
## 85   0.00  -0.01     0.03     0.04    -0.09     0.00    -0.05    -0
.08
## 86   0.06  -0.03     0.07     0.00    -0.03    -0.07     0.04    -0
.02
## 87   0.08   0.13    -0.24    -0.07     0.10     0.14    -0.05     0
.15
## 88  -0.04   0.01     0.07     0.14    -0.14    -0.02    -0.01    -0
.01
## 94  -0.02   0.04     0.11    -0.25     0.30    -0.01    -0.30    -0
.05
## 97  -0.04   0.22    -0.20    -0.19    -0.04     0.13     0.19    -0
.02
## 99  -0.04   0.09    -0.12     0.11    -0.13     0.07     0.01     0
.12
##    dfb.TABA dfb.VSG  dfb.BASM dfb.UVEI dfb.PSOR dfb.ENF_ dfb.TTOBIO
A
## 1    0.00    -0.02    -0.01    -0.01    -0.01     0.00     0.01
## 3   -0.10     0.03    -0.03    -0.05     0.02     0.02    -0.01
## 4   -0.13     0.24    -0.09    -0.10    -0.37     0.08     0.13
## 5   -0.20    -0.12    -0.14    -0.18    -0.08     0.06     0.03
## 6   -0.20     0.01     0.10    -0.15    -0.08    -0.07     0.19
## 7   -0.02    -0.15    -0.06    -0.79     0.20    -0.60     0.90
## 9    0.09    -0.08     0.03    -0.08    -0.02     0.01    -0.04
## 11   0.06    -0.10     0.18     0.13     0.08     0.07     0.04
## 13  -0.06     0.10     0.11     0.12    -0.06    -0.10    -0.04
## 14   0.24    -0.54     0.22     0.34     0.12     0.00     0.28
## 15   0.00    -0.02    -0.01    -0.01    -0.01     0.00     0.01
## 19  -0.03    -0.04    -0.07    -0.01     0.04     0.00    -0.07
## 21  -0.01     0.07     0.05    -0.04     0.01     0.04     0.02
## 35  -0.05     0.04     0.04    -0.01     0.02     0.00     0.03
## 36  -0.45    -0.55     0.69     0.26     0.39    -0.48    -0.38
## 38  -0.01    -0.06     0.19    -0.12    -0.07     0.01     0.16
## 40   0.21    -0.09     0.18     0.31    -0.95    -0.25    -0.12
## 42  -1.49_*   0.35     0.65    -1.63_*   0.86    -0.81    -1.18_*
## 43   0.15     0.32    -0.41     0.00    -0.24    -0.19     0.36
```

```
## 44  -0.10     0.19     0.11    -0.06     0.01    -0.05     0.24
## 45   0.18    -0.03     0.00    -0.05     0.03     0.07     0.01
## 46   0.00     0.01     0.00    -0.01     0.00     0.00     0.01
## 47   0.02    -0.07     0.01    -0.01    -0.02     0.22     0.05
## 49   0.00    -0.04     0.01     0.01    -0.02    -0.01    -0.02
## 50   0.10    -0.04     0.04     0.00    -0.05    -0.20     0.01
## 51   0.41    -1.77_*   0.99    -0.12     1.09_*   2.48_*  -0.49
## 57   0.05     0.19    -0.64     0.22    -0.06    -0.31     0.24
## 59  -0.02     0.00    -0.01     0.00     0.01    -0.01     0.01
## 63   0.00    -0.02    -0.01    -0.01    -0.01     0.00     0.01
## 64  -0.01     0.14    -0.15     0.12     0.07     0.01    -0.11
## 65   0.07    -0.03     0.01     0.01     0.00     0.00     0.00
## 66   0.80     0.41    -0.71    -0.17    -0.86     0.46    -0.04
## 68  -0.01     0.01     0.03     0.04     0.02     0.00    -0.02
## 70  -0.19     0.05     0.14     0.05     0.04    -0.07     0.07
## 71   0.03     0.01    -0.30     0.13    -0.07    -0.16    -0.10
## 73   0.03    -0.11     0.01     0.00    -0.03    -0.06     0.03
## 76  -0.03     0.08     0.05     0.02     0.02     0.10    -0.11
## 85   0.05    -0.05    -0.09     0.09     0.01     0.06    -0.02
## 86  -0.04     0.05     0.03    -0.01    -0.01    -0.03     0.01
## 87  -0.06    -0.15     0.06     0.32     0.28     0.08    -0.61
## 88   0.00    -0.06     0.05    -0.11    -0.25    -0.02     0.04
## 94   0.29    -0.04    -0.21     0.37     0.06     0.31    -0.19
## 97   0.04    -0.12    -0.14    -0.01    -0.05    -0.10     0.07
## 99   0.02     0.11     0.09     0.20     0.06    -0.05    -0.19
##    dfb.TTOBIOI dfb.TTOBIOG dfb.TTOBIOC dfb.NUM_TB_PREV.1 dfb.NUM_TB
_PREV.2
## 1    0.01        0.00        0.04        0.01              0.01
## 3   -0.01        0.12       -0.19       -0.02              0.05
## 4    0.19        0.03       -0.03        0.26              0.26
## 5   -0.26       -0.22       -0.06        0.06             -0.07
## 6    0.14        0.02        0.04       -0.08             -0.08
## 7    0.63        0.32        0.30        0.09             -0.70
## 9   -0.04       -0.14       -0.04       -0.07             -0.04
## 11   0.01        0.11        0.09        0.10             -0.14
## 13   0.02        0.05       -0.01        0.04              0.05
## 14   0.18        0.25        0.10        0.13              0.57
## 15   0.01        0.00        0.04        0.01              0.01
## 19  -0.12       -0.04       -0.05       -0.07             -0.05
## 21  -0.03        0.00        0.01        0.00              0.04
## 35   0.00       -0.13       -0.06       -0.02             -0.02
## 36   0.17        0.03       -0.33       -0.35             -0.57
## 38   0.07       -0.14        0.05       -0.01             -0.02
## 40  -0.39        0.40        0.11        1.31_*            1.04_*
## 42   0.97        1.02_*     -0.02       -1.69_*           -1.85_*
## 43   0.27        0.21        0.14        0.45              0.34
## 44   0.10       -0.15       -0.08        0.01             -0.01
## 45  -0.12        0.05        0.12        0.08              0.09
## 46   0.00        0.00        0.00        0.00              0.01
## 47  -0.02        0.04        0.09        0.00              0.00
## 49   0.00       -0.02       -0.01        0.00             -0.02
## 50   0.05        0.10       -0.03        0.00              0.02
## 51  -0.28       -0.23        0.28       -0.62             -0.87
## 57  -0.01       -0.11       -0.34        0.18             -0.09
```

```
## 59  -0.01       -0.01        0.02        0.00              0.00
## 63   0.01        0.00       -0.13        0.01              0.01
## 64  -0.10        0.04       -0.09        0.03              0.09
## 65   0.01        0.05        0.00        0.02             -0.01
## 66   0.94       -0.56        0.33        0.43              0.92
## 68   0.00        0.03       -0.01       -0.01             -0.02
## 70   0.08        0.16        0.03       -0.18             -0.08
## 71  -0.07        0.05       -0.07        0.04              0.04
## 73   0.01        0.00       -0.01        0.04             -0.02
## 76   0.07        0.01        0.01        0.00             -0.04
## 85  -0.16       -0.07       -0.04       -0.01              0.00
## 86   0.01       -0.02        0.00       -0.01              0.03
## 87  -0.27       -0.01       -0.36       -0.09             -0.16
## 88   0.04       -0.05        0.06        0.11              0.07
## 94  -0.23       -0.14        0.01        0.22              0.14
## 97   0.07       -0.03       -0.07       -0.07             -0.42
## 99  -0.19        0.02       -0.10        0.01             -0.03
##    dfb.MOTIVOI dfb.MOTIVOS dfb.TIEM dfb.BIO_ dfb.B_4_ dfb.Intr dfb.
AINE
## 1   -0.02       -0.01        0.00     0.00     0.00     0.00     0.
00
## 3    0.04       -0.05        0.10    -0.21     0.00    -0.06    -0.
03
## 4   -0.36       -0.16       -0.22    -0.01     0.14    -0.14    -0.
24
## 5   -0.12       -0.07        0.14    -0.12    -0.07    -0.24    -0.
08
## 6    0.06        0.03        0.18    -0.20    -0.07     0.00     0.
02
## 7   -0.12        0.86       -0.61    -0.04    -0.20     0.48    -0.
94
## 9    0.05        0.04        0.00    -0.10    -0.02    -0.06     0.
14
## 11  -0.19       -0.13       -0.10     0.23     0.06    -0.02    -0.
07
## 13   0.00       -0.04       -0.08     0.14     0.12     0.05     0.
04
## 14  -0.16        0.00       -0.40     0.49     0.37    -0.19     0.
00
## 15  -0.02       -0.01        0.00     0.00     0.00     0.00     0.
00
## 19   0.04        0.05        0.04     0.04    -0.06     0.07     0.
03
## 21  -0.03       -0.02        0.05     0.06    -0.04    -0.01    -0.
02
## 35   0.00       -0.03        0.03    -0.09     0.02    -0.05     0.
02
## 36   0.82        0.29        0.04    -0.18    -0.19    -0.37    -0.
21
## 38  -0.05       -0.07        0.00    -0.01    -0.07    -0.20     0.
10
## 40  -1.28_*     -0.97        0.30     0.04    -0.40     0.69    -0.
18
## 42   1.40_*      1.47_*      0.48     1.39_*  -0.36    -0.07    -2.
```

```
02_*
## 43  -0.31        -0.14        -0.17    0.10     -0.19     0.17     -0.
33
## 44   0.01        -0.25         0.13   -0.17     -0.21    -0.09     -0.
11
## 45  -0.07        -0.09        -0.12    0.10      0.13     0.05      0.
04
## 46   0.00         0.00         0.00    0.00     -0.01     0.00      0.
01
## 47   0.02         0.05        -0.03    0.13     -0.03    -0.01      0.
06
## 49  -0.01        -0.01        -0.01    0.01      0.01    -0.03     -0.
01
## 50   0.06         0.02        -0.04    0.00      0.01     0.05     -0.
07
## 51   0.29         0.72         0.17    0.46     -0.67     0.19     -0.
63
## 57   0.03         0.41         0.03   -0.22     -0.71    -0.20     -0.
24
## 59  -0.01         0.01         0.00    0.02     -0.01    -0.01      0.
02
## 63  -0.02        -0.01         0.00    0.00      0.00     0.00      0.
00
## 64  -0.06        -0.05        -0.01    0.01      0.04     0.10      0.
05
## 65  -0.02         0.00        -0.04    0.01      0.01     0.02     -0.
03
## 66  -0.21        -0.39         0.99   -0.68     -0.69     0.01      0.
56
## 68   0.01         0.01        -0.03    0.02      0.02     0.03     -0.
04
## 70   0.18         0.21         0.14   -0.02      0.04     0.12     -0.
04
## 71  -0.02        -0.21         0.17   -0.01     -0.16    -0.19      0.
02
## 73  -0.02         0.02        -0.05    0.00     -0.03    -0.02     -0.
04
## 76  -0.05        -0.02        -0.08    0.00      0.04    -0.08     -0.
10
## 85  -0.01        -0.02         0.17   -0.07     -0.14     0.03      0.
02
## 86  -0.01         0.05         0.11   -0.04     -0.03    -0.08      0.
00
## 87  -0.07         0.01        -0.25   -0.04      0.20    -0.09      0.
03
## 88  -0.10        -0.08        -0.01    0.02     -0.04     0.00      0.
00
## 94  -0.12        -0.16        -0.15   -0.09     -0.09     0.11      0.
27
## 97   0.17         0.16        -0.05   -0.07      0.08    -0.06      0.
08
## 99  -0.01         0.04         0.07   -0.15     -0.09    -0.17      0.
10
##    dfb.FAME dfb.i_BA dfb.EGM  dfb.N_S_ dfb.P_S_ dfb.mSAS dfb.N_P_ d
```

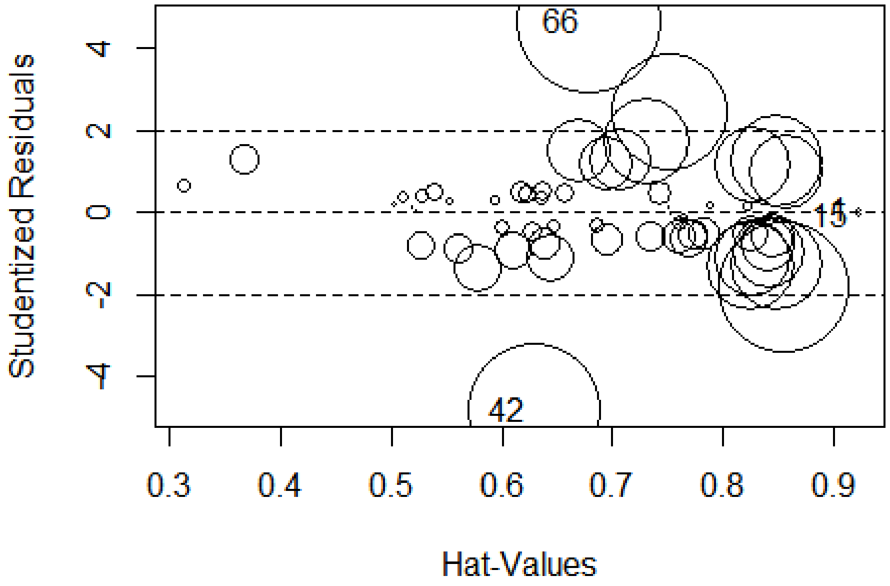
```
fb.M_2_S_F
## 1    0.01      0.02     -0.02     -0.01     -0.01      0.01      0.02
0.03
## 3    0.01      0.00      0.01     -0.01     -0.11      0.00      0.01
-0.05
## 4    0.05      0.43     -0.02      0.05     -0.03      0.28     -0.03
0.17
## 5    0.22     -0.04      0.19     -0.08     -0.12      0.03      0.13
0.01
## 6    0.05      0.11     -0.08     -0.04     -0.06     -0.07      0.03
0.07
## 7    1.08_*    0.97     -0.45     -0.65      0.28     -0.30      0.77
0.49
## 9    0.00     -0.10     -0.02     -0.06     -0.02     -0.06      0.04
-0.05
## 11  -0.02      0.03      0.01     -0.15      0.15     -0.02      0.10
0.09
## 13  -0.20      0.19     -0.05      0.23      0.06     -0.01     -0.18
-0.17
## 14  -0.33      0.07      0.05      1.29_*   0.43      0.06     -1.30_*
0.04
## 15   0.01      0.02     -0.02     -0.01     -0.01      0.01      0.02
-0.16
## 19   0.03     -0.01      0.05     -0.01     -0.03     -0.12      0.06
0.04
## 21   0.08     -0.06      0.10      0.03      0.03     -0.01     -0.05
-0.04
## 35   0.03      0.05     -0.01     -0.01     -0.09     -0.02      0.04
0.01
## 36  -0.41      0.41     -0.45     -0.17     -0.29     -0.01      0.02
-0.10
## 38   0.08      0.03     -0.08     -0.07     -0.04      0.18     -0.04
0.05
## 40   0.14     -0.11     -0.27      0.16      0.10     -0.18     -0.21
0.05
## 42   0.51      0.74     -1.41_*  -0.41      0.63     -1.37_*    0.20
0.91
## 43  -0.08     -0.10      0.15     -0.08     -0.26      0.08      0.14
0.14
## 44   0.00      0.22     -0.16     -0.02     -0.13     -0.25      0.16
0.05
## 45  -0.03     -0.14      0.05     -0.07     -0.03      0.03      0.06
-0.05
## 46   0.00     -0.01      0.00      0.00      0.00      0.00      0.00
0.00
## 47   0.02      0.03      0.12      0.09      0.04     -0.06     -0.05
0.02
## 49   0.04     -0.03      0.00     -0.03      0.01      0.00      0.02
0.01
## 50  -0.02     -0.05     -0.02     -0.01      0.00     -0.06     -0.02
-0.03
## 51   2.53_*  -1.59_*  -0.56     -0.97      0.70     -1.54_*    0.87
0.54
## 57   0.06      0.28      0.17     -0.23     -0.44     -0.19      0.37
```

```
0.15
## 59   0.01     0.02     0.02     0.02     0.01     0.00     0.00
0.01
## 63   0.01     0.02    -0.02    -0.01    -0.01     0.01     0.02
0.03
## 64  -0.10     0.08     0.13     0.17     0.10     0.02    -0.12
0.00
## 65   0.01     0.02    -0.03    -0.04     0.00    -0.03     0.03
0.02
## 66  -0.54    -1.35_*   1.40_*   0.75    -1.90_*   0.91     0.10
-1.01_*
## 68   0.00     0.01    -0.02     0.00     0.02    -0.01    -0.02
0.02
## 70   0.01     0.08     0.04     0.16     0.02    -0.08    -0.15
0.05
## 71  -0.03     0.00     0.31     0.07    -0.12     0.10    -0.07
-0.09
## 73   0.00    -0.05     0.02    -0.01     0.08    -0.01    -0.02
0.07
## 76   0.07    -0.01    -0.16     0.03     0.22     0.07    -0.08
0.00
## 85   0.04    -0.10     0.06     0.00    -0.04    -0.06     0.04
-0.03
## 86  -0.02     0.04     0.03     0.06    -0.02    -0.03    -0.03
-0.05
## 87  -0.05     0.07     0.04    -0.42    -0.25     0.07     0.21
0.19
## 88   0.13    -0.06     0.01    -0.05     0.03    -0.15     0.08
0.01
## 94  -0.09    -0.29    -0.10    -0.08    -0.05     0.34     0.10
-0.12
## 97  -0.12    -0.01     0.01    -0.22     0.00     0.05     0.17
-0.10
## 99   0.01    -0.08    -0.39     0.09     0.05    -0.04    -0.05
0.01
##    dfb.M_2_S_B dfb.PCR_ dfb.i_AS dfb.HVGP dfb.BASD dfb.PCRD dffit
cov.r
## 1   -0.03        0.04    -0.02     0.01    -0.01    -0.03     0.21
130.94_*
## 3    0.08        0.15    -0.20     0.09    -0.09    -0.07     0.65
18.07_*
## 4   -0.22        0.06    -0.20    -0.13    -0.10     0.12    -1.12
31.72_*
## 5   -0.06        0.11    -0.06    -0.05    -0.06     0.18    -0.63
15.88_*
## 6   -0.02        0.05    -0.06    -0.12    -0.12     0.15     0.66
14.24_*
## 7   -0.62       -0.16     0.28    -0.49    -0.38     0.50     4.18
0.00
## 9    0.07       -0.08     0.16    -0.15     0.05     0.02     0.44
14.55_*
## 11  -0.10        0.10    -0.07     0.03    -0.09     0.05    -1.00
24.58_*
## 13   0.16       -0.08    -0.05    -0.08    -0.03    -0.34     0.77
```

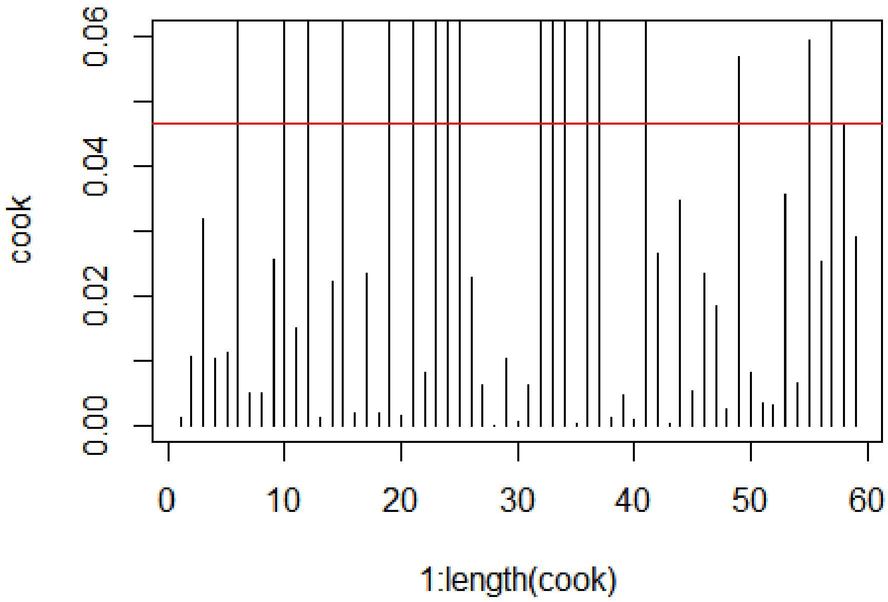
```
24.83_*
## 14  -0.10        0.08     0.23    -0.22     0.11    -0.21    -2.98
1.75
## 15   0.16        0.04    -0.02     0.01    -0.01    -0.03    -0.21
130.94_*
## 19   0.03        0.00     0.00    -0.02     0.03    -0.01     0.27
20.23_*
## 21   0.03       -0.07     0.04    -0.04    -0.04    -0.02     0.28
47.04_*
## 35   0.02        0.04    -0.07    -0.04     0.00     0.01    -0.24
42.59_*
## 36  -0.01        0.90    -0.44     0.45    -0.14    -0.22     2.13
0.20
## 38  -0.06        0.02     0.08    -0.18     0.07     0.14     0.56
17.51_*
## 40   0.00       -0.28     0.37     0.20     0.03    -0.29     2.48
2.98
## 42   0.03       -0.28     0.36    -0.78     0.71    -0.60    -6.28_
*   0.00
## 43  -0.19       -0.76     0.35    -0.18     0.27    -0.09    -1.74
16.74_*
## 44  -0.06        0.00     0.03    -0.32     0.08     0.06    -0.95
17.89_*
## 45   0.04        0.00     0.08    -0.04     0.02     0.12    -0.49
25.42_*
## 46   0.00        0.00     0.00     0.00     0.00     0.00     0.03
21.87_*
## 47   0.00       -0.05     0.07    -0.09     0.07     0.02     0.63
16.69_*
## 49  -0.01        0.01     0.01    -0.01     0.00     0.01     0.14
41.46_*
## 50   0.09        0.04     0.02     0.07     0.00    -0.11    -0.49
17.77_*
## 51  -0.39        0.17     0.79     0.28    -0.65     0.90    -4.39
0.05
## 57  -0.06        0.58    -0.26     0.16     0.47     0.31     2.36
7.87_*
## 59  -0.02       -0.02     0.01    -0.03     0.01     0.03    -0.12
41.73_*
## 63  -0.03        0.04    -0.02     0.01    -0.01    -0.03    -0.21
130.94_*
## 64   0.02       -0.08    -0.10     0.04     0.11    -0.09     0.43
22.05_*
## 65  -0.03        0.03    -0.01     0.06     0.09    -0.02     0.18
19.27_*
## 66   0.38       -0.47     0.18    -0.16    -0.36     1.07_*   6.74_
*   0.00
## 68  -0.03        0.00     0.01     0.01     0.00    -0.02     0.10
21.21_*
## 70   0.03       -0.08     0.02    -0.03    -0.12    -0.11    -0.46
22.30_*
## 71   0.14        0.24    -0.33     0.42    -0.03    -0.04    -0.96
23.79_*
## 73  -0.08        0.03     0.04     0.04     0.08    -0.01     0.31
```

```
55.61_*
## 76  -0.06       -0.07     0.08    -0.02    -0.05     0.10     0.56
11.87_*
## 85   0.01       -0.05     0.06    -0.05     0.05     0.03     0.37
15.63_*
## 86   0.05        0.00    -0.08     0.01    -0.06    -0.05     0.34
21.10_*
## 87  -0.24        0.34    -0.19     0.34     0.28    -0.03    -1.19
16.28_*
## 88  -0.01        0.05    -0.02     0.01    -0.07     0.13    -0.50
35.90_*
## 94  -0.08       -0.17     0.42    -0.12     0.24     0.14    -1.00
12.05_*
## 97   0.08       -0.09     0.19    -0.14     0.16    -0.16    -1.36
30.19_*
## 99  -0.01       -0.22     0.02     0.15     0.04    -0.15    -1.07
18.16_*
##    cook.d hat  
## 1    0.00   0.92
## 3    0.01   0.66
## 4    0.03   0.83
## 5    0.01   0.63
## 6    0.01   0.62
## 7    0.34   0.75
## 9    0.00   0.53
## 11   0.03   0.78
## 13   0.02   0.74
## 14   0.21   0.85
## 15   0.00   0.92
## 19   0.00   0.55
## 21   0.00   0.79
## 35   0.00   0.77
## 36   0.10   0.67
## 38   0.01   0.62
## 40   0.15   0.83
## 42   0.43   0.63
## 43   0.08   0.84
## 44   0.02   0.73
## 45   0.01   0.69
## 46   0.00   0.52
## 47   0.01   0.64
## 49   0.00   0.75
## 50   0.01   0.60
## 51   0.42   0.85
## 57   0.14   0.86
## 59   0.00   0.75
## 63   0.00   0.92
## 64   0.00   0.64
## 65   0.00   0.50
## 66   0.52   0.68
## 68   0.00   0.52
## 70   0.01   0.65
## 71   0.02   0.77
## 73   0.00   0.82
```

```
## 76   0.01   0.54
## 85   0.00   0.51
## 86   0.00   0.59
## 87   0.04   0.77
## 88   0.01   0.76
## 94   0.03   0.70
## 97   0.05   0.85
## 99   0.03   0.76

influencePlot(abc1)
```



```
##        StudRes       Hat        CookD
## 1    0.0623331 0.9211843 0.001172496
## 15  -0.0623331 0.9211843 0.001172496
## 42  -4.8133759 0.6302185 0.431566423
## 66   4.6388049 0.6785118 0.517635056

cook <- cooks.distance(abc1)
plot(1:length(cook), cook, ylim=c(0,0.06), type = "h")
abline(h=4/((n-p-2)), col="red")
```



```
stud <- rstudent(abc1)
head(sort(abs(stud),decreasing=TRUE))
```

```
##       42       66        7       51       61       36
## 4.813376 4.638805 2.399791 1.816236 1.745187 1.496918
```

```
hatv <- hatvalues(abc1)
head(sort(hatv,decreasing=T))
```

```
##         1        15        63        57        51        14
## 0.9211843 0.9211843 0.9211843 0.8551536 0.8541275 0.8480441
```

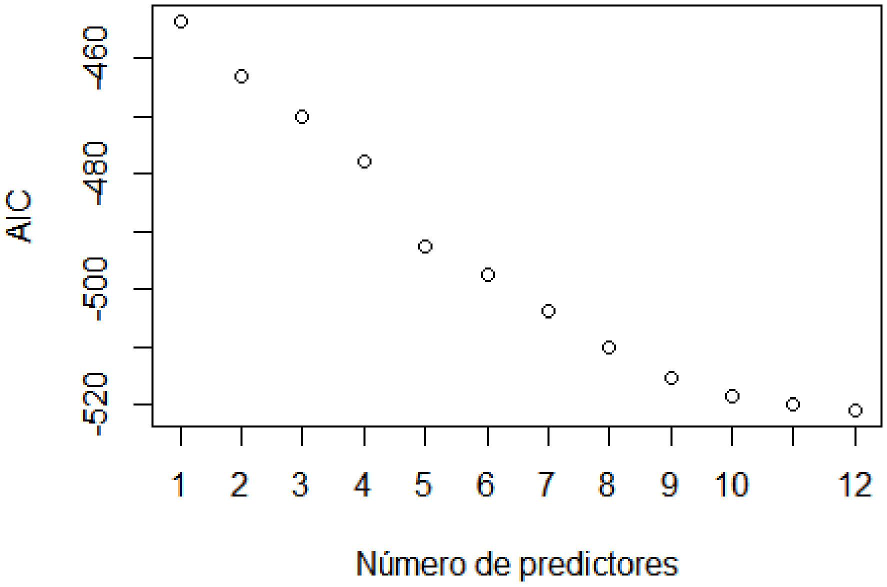
```
library(leaps)
attach(base_rx22)
```

```
## The following objects are masked from base_rx22 (pos = 3):
##
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG
```

```
## The following objects are masked from base_rx21 (pos = 4):
##
##     AINE, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM, ENF_INF, FAM
E,
##     HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30, Interval,
##     Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progress,
```

```
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx21 (pos = 5):
##
##     AINE, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM, ENF_INF, FAM
E,
##     HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30, Interval,
##     Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progress,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from c_base_rx2:
##
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx.num2:
##
##     BASDAIDif, BASMI, EDAD, EGM, HVGP, i_ASDAS, i_BASDAI, IMC,
##     Interval, mSASSS_Progress, PCR_INICIOB, PCRDif, TIEMBIO, TSINT,
VSG

## The following objects are masked from base_rx3:
##
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, PSORIASIS, SEXO, TABACO_Kat,
##     TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx2 (pos = 14):
##
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx2 (pos = 15):
##
```

```
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from c_base_rx.num:
##
##     BASMI, EDAD, EGM, HVGP, i_ASDAS, i_BASDAI, IMC, Interval,
##     mSASSS_Progress, PCR_INICIOB, TIEMBIO, TSINT, VSG

b1 <- regsubsets(LY~ .-mSASSS_Progress, data=base_rx22, na.action = na
.omit, nvmax=12)
rs1 <- summary(b1)
n1 <- nrow(base_rx22)
k1 <- length(rs1$rss) # Número de variables predictoras
p1 <- k1 + 1 # Número de parámetros (incluye la intercepción)
(AIC <- n*log(rs1$rss/n1) + (2:p1)*2)

##  [1] -453.6466 -463.1659 -470.0006 -477.9064 -492.6002 -497.5672 -5
03.6312
##  [8] -510.2430 -515.3117 -518.4770 -519.9174 -520.9258

plot(1:k1, AIC, ylab="AIC", xlab="Número de predictores", axes=F)
box(); axis(1,at=1:k1); axis(2)
```



```
rs1$outmat[10,]
```

```
##                         EDAD                   SEXOFEMALE                    
IMC
##                          "*"                          " "                    
" "
##                   `IMC>30`SI                        TSINT                 HLAB
27NO
##                          " "                          " "                    
" "
##                         EANO                 TABACO_KatNO                    
VSG
##                          "*"                          " "                    
" "
##                        BASMI                    UVEITISSI             PSORIAS
ISSI
##                          " "                          " "                    
" "
##                     ENF_INFSI                    TTOBIOADA                TTOBI
OIFX
##                          " "                          "*"                    
" "
##                     TTOBIOGOL                   TTOBIOCTZ NUM_TB_PREVtreatmen
ts.1
##                          " "                          "*"                    
" "
## NUM_TB_PREVtreatments.2         MOTIVOInefficacy       MOTIVOSide.eff
ects
##                          "*"                          "*"                    
" "
##                      TIEMBIO                   BIO_INICISI             Biol_4_k
atSI
##                          " "                          "*"                    
" "
##                     Interval                       AINESI                   FA
MESI
##                          " "                          " "                    
" "
##                      i_BASDAI                          EGM         New_Syn_mSAS
SSSI
##                          " "                          " "                    
" "
##          Prog_Syn_mSASSSSI   mSASSS_Progress_KatSI   New_Prog_Syn_Msas
ssSI
##                          " "                          "*"                    
" "
##            Mind_2_Synd_FLSI          Mind_2_Synd_BLSI              PCR_INI
CIOB
##                          "*"                          " "                    
" "
##                       i_ASDAS                         HVGP                BASDA
IDif
##                          " "                          " "                    
"*"
##                        PCRDif
##                          " "
```

```
attach(base_rx22)

## The following objects are masked from base_rx22 (pos = 3):
##
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx22 (pos = 4):
##
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx21 (pos = 5):
##
##     AINE, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM, ENF_INF, FAM
E,
##     HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30, Interval,
##     Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progress,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx21 (pos = 6):
##
##     AINE, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM, ENF_INF, FAM
E,
##     HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30, Interval,
##     Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progress,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from c_base_rx2:
##
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
```

```
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx.num2:
##
##     BASDAIDif, BASMI, EDAD, EGM, HVGP, i_ASDAS, i_BASDAI, IMC,
##     Interval, mSASSS_Progress, PCR_INICIOB, PCRDif, TIEMBIO, TSINT,
VSG

## The following objects are masked from base_rx3:
##
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, PSORIASIS, SEXO, TABACO_Kat,
##     TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx2 (pos = 15):
##
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from base_rx2 (pos = 16):
##
##     AINE, BASDAIDif, BASMI, BIO_INICI, Biol_4_kat, EA, EDAD, EGM,
##     ENF_INF, FAME, HLAB27, HVGP, i_ASDAS, i_BASDAI, IMC, IMC>30,
##     Interval, Mind_2_Synd_BL, Mind_2_Synd_FL, MOTIVO, mSASSS_Progre
ss,
##     mSASSS_Progress_Kat, New_Prog_Syn_Msasss, New_Syn_mSASSS,
##     NUM_TB_PREV, PCR_INICIOB, PCRDif, Prog_Syn_mSASSS, PSORIASIS, S
EXO,
##     TABACO_Kat, TIEMBIO, TSINT, TTOBIO, UVEITIS, VSG

## The following objects are masked from c_base_rx.num:
##
##     BASMI, EDAD, EGM, HVGP, i_ASDAS, i_BASDAI, IMC, Interval,
##     mSASSS_Progress, PCR_INICIOB, TIEMBIO, TSINT, VSG

s.aic1<-lm(LY ~ EDAD + EA + TTOBIO + NUM_TB_PREV + MOTIVO + BIO_INICI
+ Mind_2_Synd_FL+ mSASSS_Progress_Kat + BASDAIDif, na.action = na.omit
)
summary(s.aic1)

##
## Call:
## lm(formula = LY ~ EDAD + EA + TTOBIO + NUM_TB_PREV + MOTIVO +
##     BIO_INICI + Mind_2_Synd_FL + mSASSS_Progress_Kat + BASDAIDif,
##     na.action = na.omit)
```

```
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.44770 -0.05367 -0.01084  0.05426  0.32929
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              0.552830   0.059747   9.253 1.35e-13 ***
## EDAD                     0.003388   0.001228   2.758 0.007484 **
## EANO                     0.083079   0.038317   2.168 0.033699 *
## TTOBIOADA               -0.086619   0.029872  -2.900 0.005046 **
## TTOBIOIFX                0.038237   0.044039   0.868 0.388352
## TTOBIOGOL               -0.081640   0.048821  -1.672 0.099142 .
## TTOBIOCTZ               -0.209352   0.074456  -2.812 0.006457 **
## NUM_TB_PREVtreatments.1  0.024798   0.083548   0.297 0.767530
## NUM_TB_PREVtreatments.2 -0.181983   0.104824  -1.736 0.087146 .
## MOTIVOInefficacy         0.053790   0.088756   0.606 0.546532
## MOTIVOSide.effects      -0.087947   0.092211  -0.954 0.343636
## BIO_INICISI             -0.130944   0.037371  -3.504 0.000822 ***
## Mind_2_Synd_FLSI         0.030141   0.033644   0.896 0.373520
## mSASSS_Progress_KatSI    0.342374   0.034759   9.850 1.18e-14 ***
## BASDAIDif                0.028008   0.006865   4.080 0.000122 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1073 on 67 degrees of freedom
##   (19 observations deleted due to missingness)
## Multiple R-squared:  0.808,  Adjusted R-squared:  0.7679
## F-statistic: 20.14 on 14 and 67 DF,  p-value: < 2.2e-16
```

```
coef(s.aic1)
```

```
##             (Intercept)                    EDAD
EANO
##              0.55282970              0.00338837              0.0830
7935
##               TTOBIOADA               TTOBIOIFX               TTOBI
OGOL
##             -0.08661902              0.03823681             -0.0816
3998
##               TTOBIOCTZ NUM_TB_PREVtreatments.1 NUM_TB_PREVtreatmen
ts.2
##             -0.20935230              0.02479779             -0.1819
8295
##          MOTIVOInefficacy      MOTIVOSide.effects             BIO_INI
CISI
##              0.05379000             -0.08794693             -0.1309
4378
##          Mind_2_Synd_FLSI   mSASSS_Progress_KatSI               BASDA
IDif
##              0.03014132              0.34237371              0.0280
0761
```

```
(summary(s.aic1)$coefficients["BASDAIDif",1] +
qnorm(c(0.025,0.975)) * summary(s.aic1)$coefficients["BASDAIDif",2])
```

```
## [1] 0.01455265 0.04146257
```