

# Modelos lineales y aditivos en ecología

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# Introducción a los modelos lineales

Placeholder

Definición de modelo lineal

Correlación lineal simple

Matrices de correlación

Regresión lineal simple

Relación entre regresión y correlación

Matrices de gráficos de dispersión

Regresión lineal multiple

Variables categóricas (= *dummies*)

Test de  $t$

Test de  $t$  pareado

Análisis de la varianza

Supuestos

Colinealidad

Análisis de residuos

Transformaciones

Actividades

Ejercicios de repaso

Ejercicio 1.2

Ejercicio 1.3

Ejercicio 1.4

# Modelos lineales generalizados

Placeholder

## Datos de presencia-ausencia

GLM binomial

Diagnósticos

Bondad del ajuste

Gráfico del modelo

Interpretación de los coeficientes

Ecuación

Capacidad predictiva

## Conteos I

GLMs Poisson y quasi-Poisson

GLM Poisson

GLM quasi-Poisson

Diagnósticos

Bondad del ajuste

Ecuación

Gráfico del modelo

GLM binomial negativo

Chequear sobredispersión

Validación del modelo quasi-Poisson

Modelo binomial negativo

Validación del modelo binomial negativo

Bondad del ajuste

Ecuación

Comparaciones múltiples

Incluyendo un offset

Gráficos de los modelos

## Modelo lineal general

# Modelos no lineales

Placeholder

Regresión no paramétrica

Regresión polinómica

Funciones a trozos

Splines de regresión

Polinomios a trozos

Splines de suavizado

Modelos aditivos generalizados

GAM con otras distribuciones e interacciones

Comparación de modelos

Validación

Modelo con variables continuas (efectos principales + interacciones)

Actividades

Ejercicio 4.1

Ejercicio 4.2

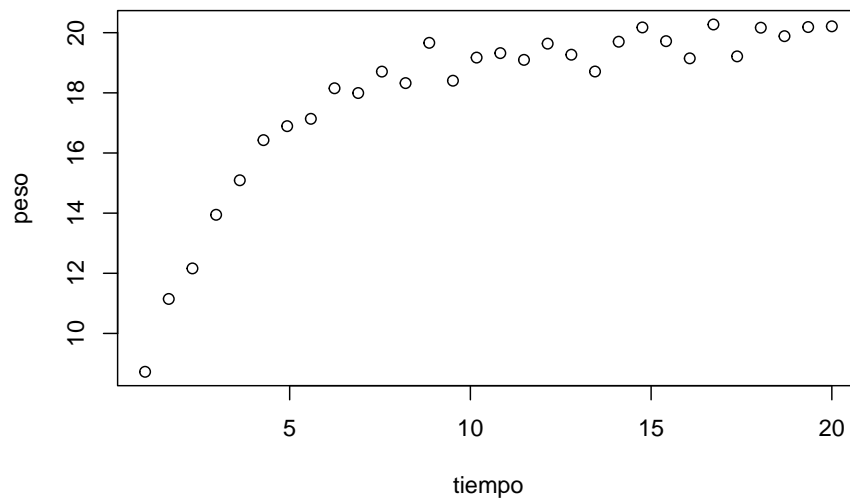
Ejercicio 4.3



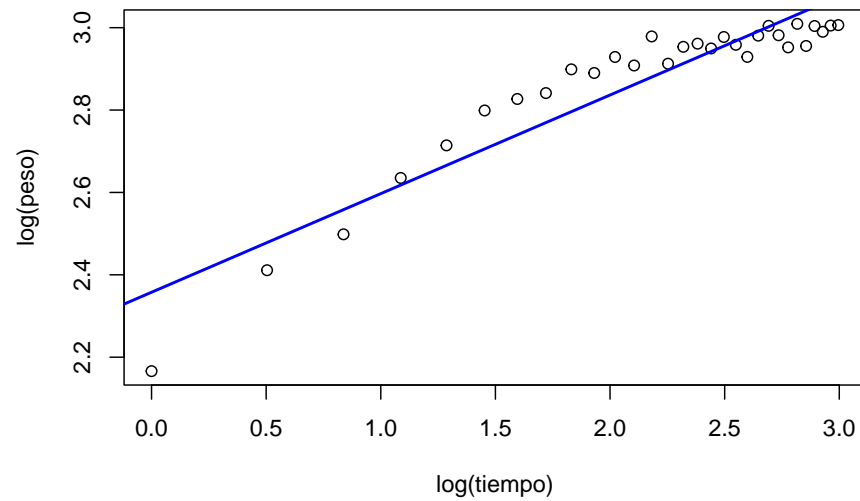
# Modelos mixtos

## Dependencia temporal

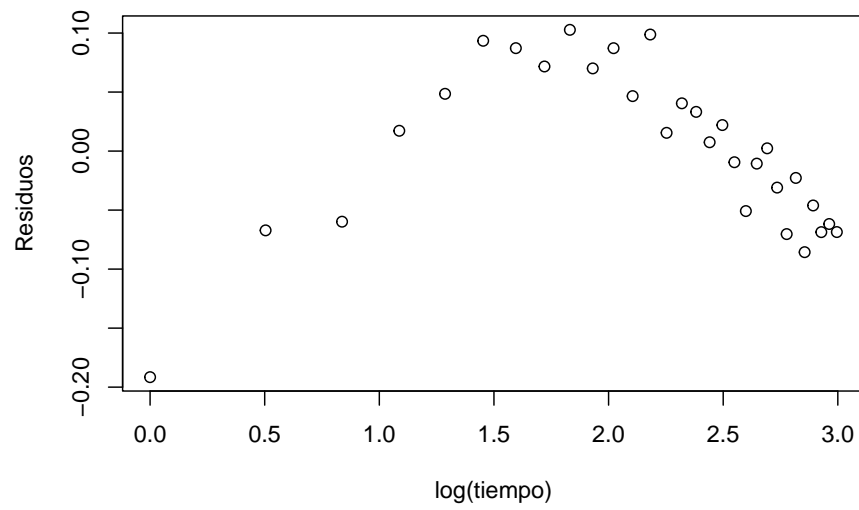
```
set.seed(101)
tiempo <- seq(1, 20, length = 30)
a <- 20
b <- 5
c <- 0.3
peso <- a - (a - b)*exp(-c*tiempo) + rnorm(n = 30, mean = 0, sd = 0.5)
plot(tiempo, peso)
```



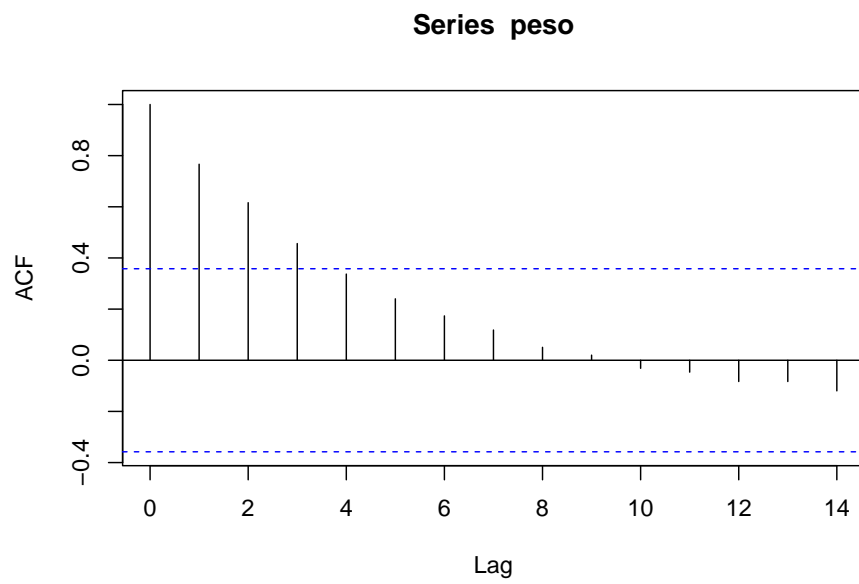
```
# Gráfico de residuos  
m.crec <- lm(log(peso) ~ log(tiempo))  
plot(log(tiempo), log(peso))  
abline(m.crec, lwd = 2, col = "blue")
```



```
plot(log(tiempo), resid(m.crec), xlab = "log(tiempo)", ylab = "Residuos")
```



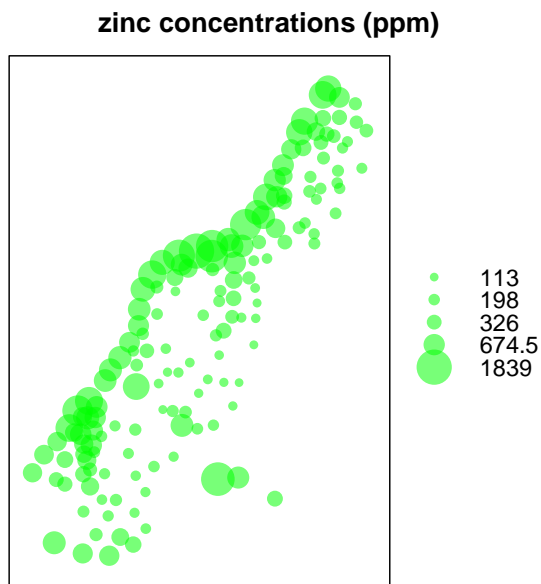
```
# Función de autocorrelación  
plot(acf(peso))
```



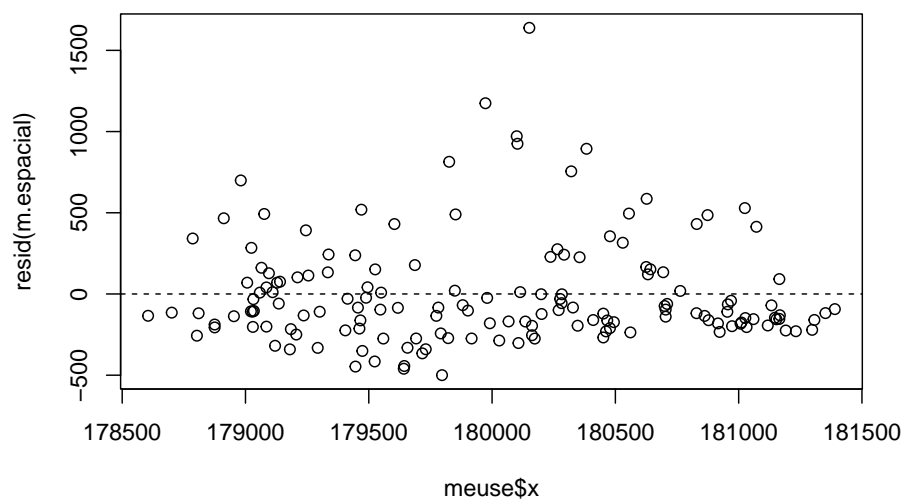
## Dependencia espacial

Ubicación (coordenadas) y concentración de metales pesados en el río Mosa (Europa).

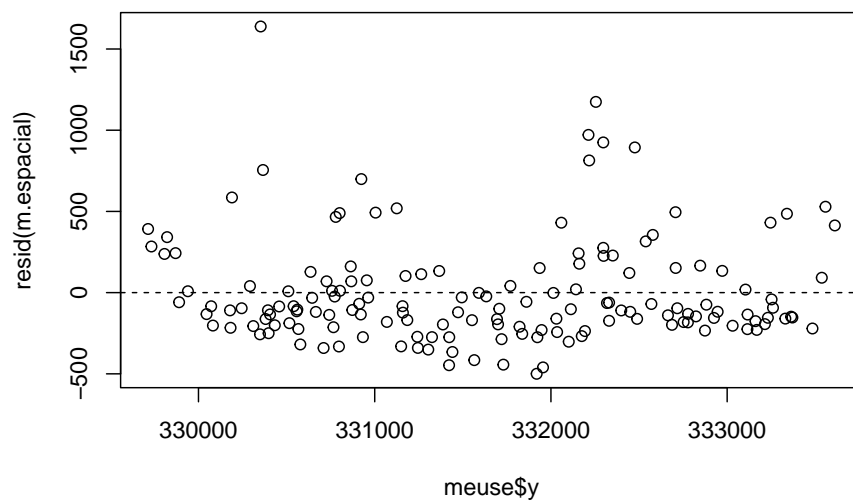
```
library(sp)
library(gstat)
library(ggplot2)
data(meuse)
coordinates(meuse) = ~x+y
bubble(meuse, "zinc", col = "#00ff0088", main = "zinc concentrations (ppm)")
```



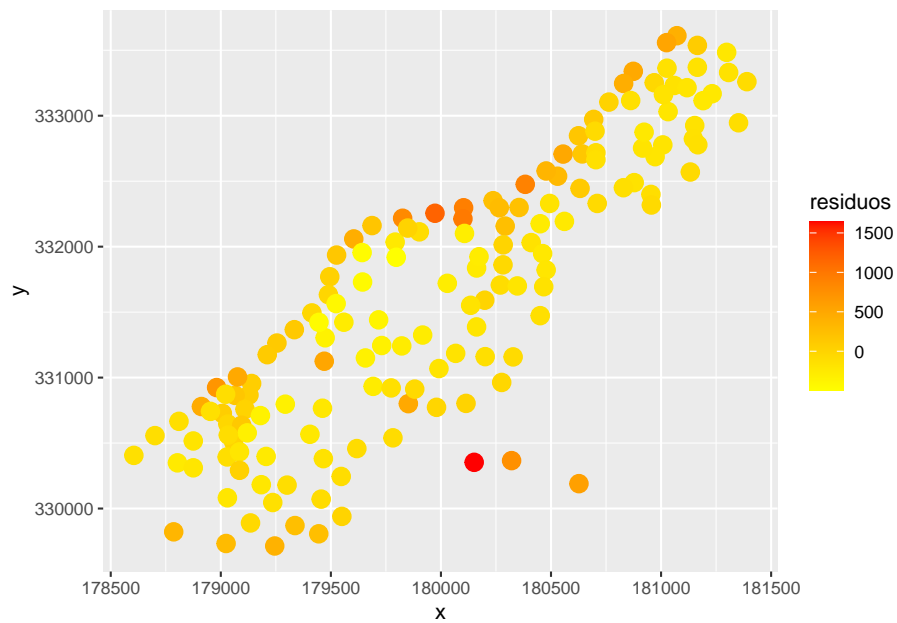
```
m.espacial <- lm(zinc ~ x + y, data = meuse)
plot(meuse$x, resid(m.espacial))
abline(a = 0, b = 0, lty = 2)
```



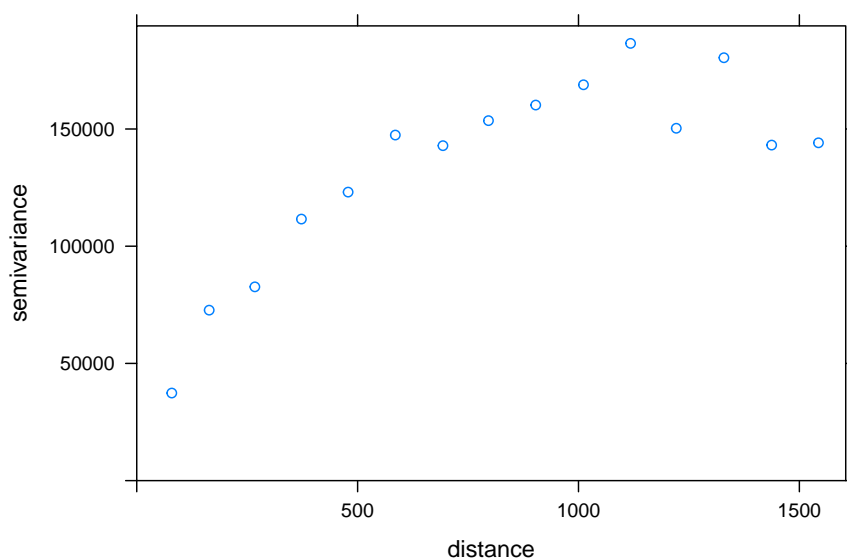
```
plot(meuse$y, resid(m.especial))  
abline(a = 0, b = 0, lty = 2)
```



```
data(meuse)
meuse$residuos <- resid(m.espacial)
ggplot(meuse, aes(x = x, y = y, col = residuos)) +
  geom_point(size = 4) +
  scale_color_gradient(low = "yellow", high = "red")
```



```
# Semivariograma
coordinates(meuse) = ~x+y
zinc.variog <- variogram(zinc ~ 1, meuse)
plot(zinc.variog)
```



## Introducción a los modelos mixtos

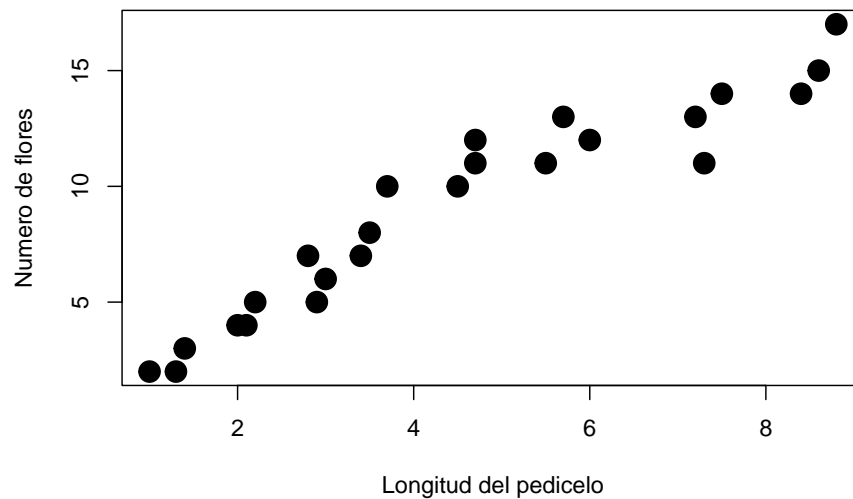
A partir de 8 plantas, se contaron el número de flores en 3 inflorescencias por planta y se midió la longitud de los pedicelos. Analizar la relación entre la longitud del pedicelo y el número de flores/inflorescencia.

```
id <- factor(sort(rep(1:8, 3)))
long.pedicelo <- c(1, 1.3, 1.4, 2, 2.2, 2.1, 2.9, 3, 2.8, 3.5, 3.4, 3.7,
                  4.5, 4.7, 4.7, 5.5, 5.7, 6, 7.2, 7.3, 7.5, 8.4, 8.8, 8.6)
nflores <- c(2, 2, 3, 4, 5, 4, 5, 6, 7, 8, 7, 10, 10, 12, 11, 11, 13, 12,
            13, 11, 14, 14, 17, 15)
plantas <- data.frame(id, long.pedicelo, nflores)
plantas
```

```
##      id long.pedicelo nflores
## 1    1           1.0        2
## 2    1           1.3        2
## 3    1           1.4        3
## 4    2           2.0        4
## 5    2           2.2        5
## 6    2           2.1        4
## 7    3           2.9        5
## 8    3           3.0        6
```

```
## 9 3 2.8 7
## 10 4 3.5 8
## 11 4 3.4 7
## 12 4 3.7 10
## 13 5 4.5 10
## 14 5 4.7 12
## 15 5 4.7 11
## 16 6 5.5 11
## 17 6 5.7 13
## 18 6 6.0 12
## 19 7 7.2 13
## 20 7 7.3 11
## 21 7 7.5 14
## 22 8 8.4 14
## 23 8 8.8 17
## 24 8 8.6 15
```

```
plot(plantas$long.pedicelo, plantas$nflores, pch = 19, cex = 2,
     xlab = "Longitud del pedicelo", ylab = "Numero de flores" )
```



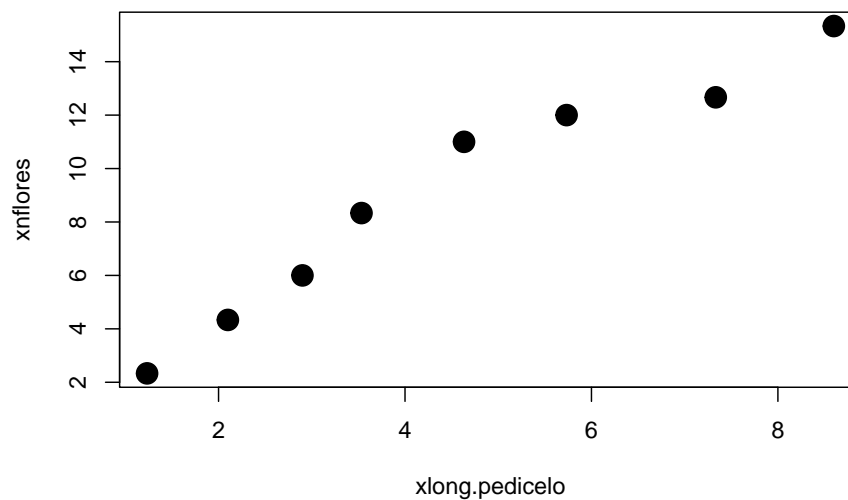
```
# Opción 1: asumimos que las observaciones son independientes
m1 <- lm(nflores ~ long.pedicelo, data = plantas)
summary(m1)
```

```
##
```



```
## Call:
## lm(formula = nflores ~ long.pedicelo, data = plantas)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.7697 -0.9116 -0.1089  0.7718  2.6725
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.2973     0.5926   2.189   0.0395 *
## long.pedicelo    1.7085     0.1159  14.739 6.99e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.368 on 22 degrees of freedom
## Multiple R-squared:  0.908, Adjusted R-squared:  0.9039
## F-statistic: 217.2 on 1 and 22 DF, p-value: 6.986e-13
```

```
# Opción 2: una media por unidad
xlong.pedicelo <- tapply(long.pedicelo, id, mean)
xnflores <- tapply(nflores, id, mean)
plot(xlong.pedicelo, xnflores, pch = 19, cex = 2)
```



```
m2 <- lm(xnflores ~ xlong.pedicelo)
summary(m2)
```

```
##
## Call:
## lm(formula = xnflores ~ xlong.pedicelo)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.1378 -0.7432 -0.4178  0.9354  1.7874
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.3328     0.8834   1.509   0.182
## xlong.pedicelo  1.7007     0.1729   9.837 6.36e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.176 on 6 degrees of freedom
## Multiple R-squared:  0.9416, Adjusted R-squared:  0.9319
## F-statistic: 96.78 on 1 and 6 DF, p-value: 6.359e-05
```

*# Opción 3: incluir el efecto de la unidad*

```
m3 <- lm(nflores ~ long.pedicelo + id, data = plantas)
summary(m3)
```

```
##
## Call:
## lm(formula = nflores ~ long.pedicelo + id, data = plantas)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5294 -0.4657 -0.1177  0.6667  1.4118
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2.745     1.832  -1.498   0.1548
## long.pedicelo    4.118     1.417   2.907   0.0108 *
## id2             -1.569     1.454  -1.079   0.2977
## id3             -3.196     2.486  -1.286   0.2181
## id4             -3.471     3.350  -1.036   0.3166
## id5             -5.333     4.879  -1.093   0.2916
## id6             -8.863     6.422  -1.380   0.1878
## id7            -14.784     8.677  -1.704   0.1090
```

```
## id8          -17.333      10.465  -1.656   0.1184
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9538 on 15 degrees of freedom
## Multiple R-squared:  0.9695, Adjusted R-squared:  0.9533
## F-statistic: 59.68 on 8 and 15 DF,  p-value: 5.532e-10
```

```
# Opción 4: modelo mixto de intercepto aleatorio
library(lme4)
```

```
## Loading required package: Matrix
```

```
library(lmerTest)
```

```
##
## Attaching package: 'lmerTest'
```

```
## The following object is masked from 'package:lme4':
```

```
##
```

```
##      lmer
```

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

```
##
```

```
##      step
```

```
m4 <- lmer(nflores ~ long.pedicelo + (1|id), data = plantas)
summary(m4)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
```

```
## lmerModLmerTest]
```

```
## Formula: nflores ~ long.pedicelo + (1 | id)
```

```
## Data: plantas
```

```
##
```

```
## REML criterion at convergence: 79.4
```

```
##
```

```
## Scaled residuals:
```

```
##      Min      1Q  Median      3Q      Max
```

```
## -1.8940 -0.4662 -0.1966  0.4627  1.6150
```

```
##
```

```
## Random effects:
```

```
## Groups   Name      Variance Std.Dev.
```

```
## id      (Intercept) 1.050    1.025
```

```
## Residual          1.015    1.007
## Number of obs: 24, groups: id, 8
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)    1.1887    0.8804 6.0833    1.35    0.225
## long.pedicelo  1.7326    0.1720 6.1198   10.07 4.91e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## long.pedicl -0.881
```

```
ranef(m4)
```

```
## $id
## (Intercept)
## 1 -0.7505424
## 2 -0.3735793
## 3 -0.1613717
## 4  0.7734991
## 5  1.3489226
## 6  0.6637327
## 7 -0.9288334
## 8 -0.5718278
##
## with conditional variances for "id"
```

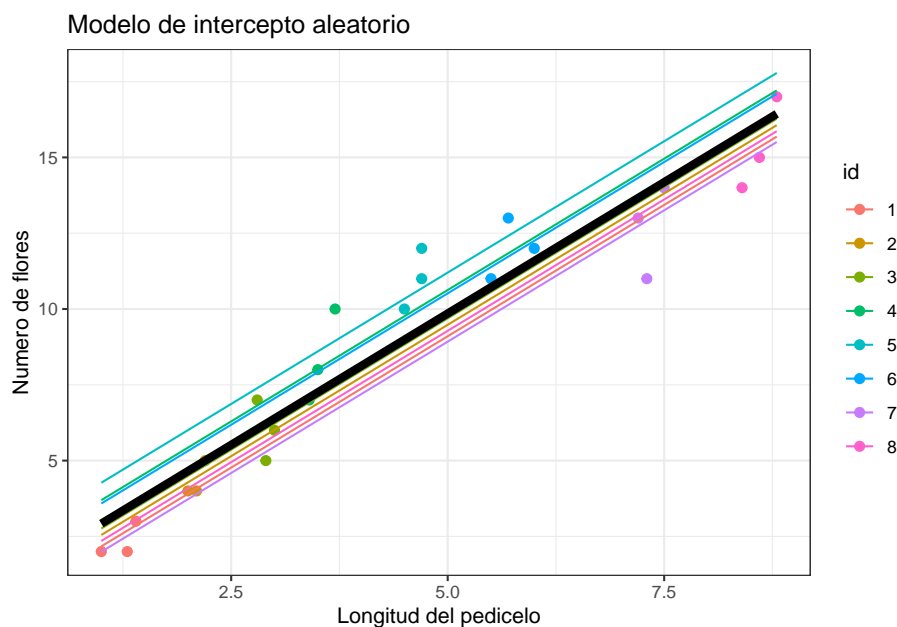
```
rand(m4) # Significancia de efectos aleatorios
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## nflores ~ long.pedicelo + (1 | id)
##      npar logLik   AIC   LRT Df Pr(>Chisq)
## <none>    4 -39.679 87.357
## (1 | id)   3 -42.174 90.349 4.9912 1    0.02548 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
long.pedicelo.new <- seq(min(plantas$long.pedicelo), max(plantas$long.pedicelo), length=100)
newdata <- expand.grid(long.pedicelo.new, plantas$id)
colnames(newdata) <- c("long.pedicelo", "id")
```

```
newdata$predy.fixed <- predict(m4, newdata = newdata, re.form = NA)
newdata$predy.rand <- predict(m4, newdata = newdata, re.form = NULL)
```

```
ggplot(data = plantas, aes(x = long.pedicelo, y = nflores, col = id)) +
  geom_point(size = 2) +
  geom_line(data = newdata, aes(x = long.pedicelo, y = predy.rand)) +
  geom_line(data = newdata, aes(x = long.pedicelo, y = predy.fixed), col = "black", size = 2) +
  xlab("Longitud del pedicelo") + ylab("Numero de flores") +
  theme_bw()
```



```
# Opción 5: modelo mixto de intercepto y pendiente aleatorios
m5 <- lmer(nflores ~ long.pedicelo + (long.pedicelo|id), data = plantas)
```

```
## boundary (singular) fit: see help('isSingular')
```

```
summary(m5)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: nflores ~ long.pedicelo + (long.pedicelo | id)
## Data: plantas
##
## REML criterion at convergence: 77.1
```

```
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.8626 -0.5465 -0.1193  0.5507  1.6903
##
## Random effects:
##   Groups    Name                Variance Std.Dev. Corr
##   id        (Intercept)         0.8215   0.9064
##           long.pedicelo         0.1895   0.4353   -1.00
## Residual                        0.9006   0.9490
## Number of obs: 24, groups: id, 8
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)   0.03828    0.66573  5.38487   0.057 0.956222
## long.pedicelo  2.08596    0.21792  4.77122   9.572 0.000271 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## long.pedicl -0.889
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
ranef(m5)
```

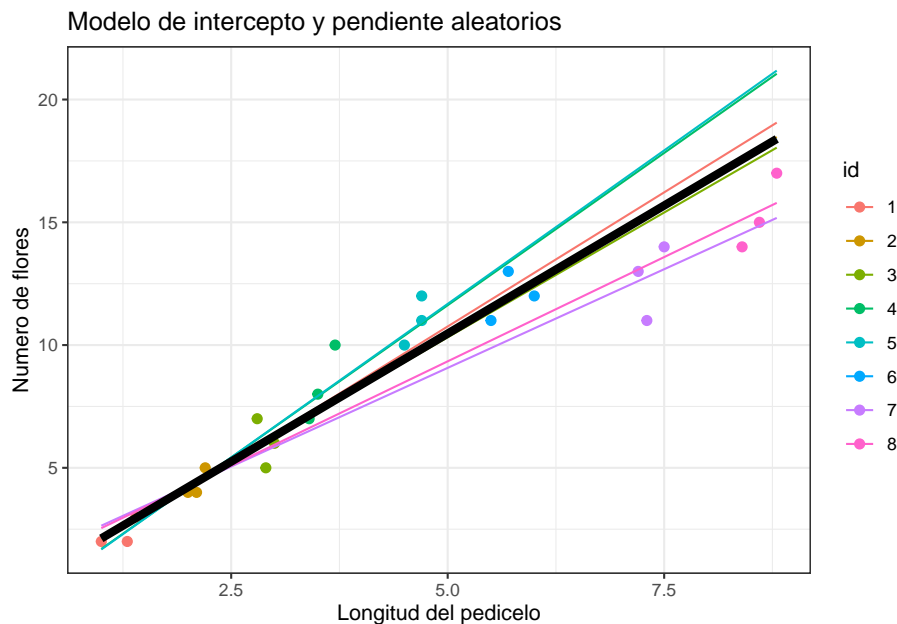
```
## $id
##   (Intercept) long.pedicelo
## 1 -0.20606623   0.098969626
## 2 -0.02342207   0.011249167
## 3  0.10951121  -0.052596116
## 4 -0.82313657   0.395336576
## 5 -0.86260770   0.414293794
## 6  0.00184916  -0.000888116
## 7  0.99686885  -0.478776830
## 8  0.80700335  -0.387588101
##
## with conditional variances for "id"
```

```
rand(m5)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
```

```
## Model:
## nflores ~ long.pedicelo + (long.pedicelo | id)
##                                     npar logLik   AIC   LRT Df Pr(>Chisq)
## <none>                             6 -38.527 89.054
## long.pedicelo in (long.pedicelo | id)  4 -39.679 87.357 2.303  2    0.3162

newdata$predy.fixed <- predict(m5, newdata = newdata, re.form = NA)
newdata$predy.rand <- predict(m5, newdata = newdata, re.form = NULL)
ggplot(data = plantas, aes(x = long.pedicelo, y = nflores, col = id)) +
  geom_point(size = 2) +
  ggtitle("Modelo de intercepto y pendiente aleatorios") +
  geom_line(data = newdata, aes(x = long.pedicelo, y = predy.rand)) +
  geom_line(data = newdata, aes(x = long.pedicelo, y = predy.fixed), col = "black", size = 2) +
  xlab("Longitud del pedicelo") + ylab("Numero de flores") +
  theme_bw()
```



## Un caso especial

```
library(data.table)
library(nlme)
```

```
##
```

```
## Attaching package: 'nlme'
```

```
## The following object is masked from 'package:lme4':
```

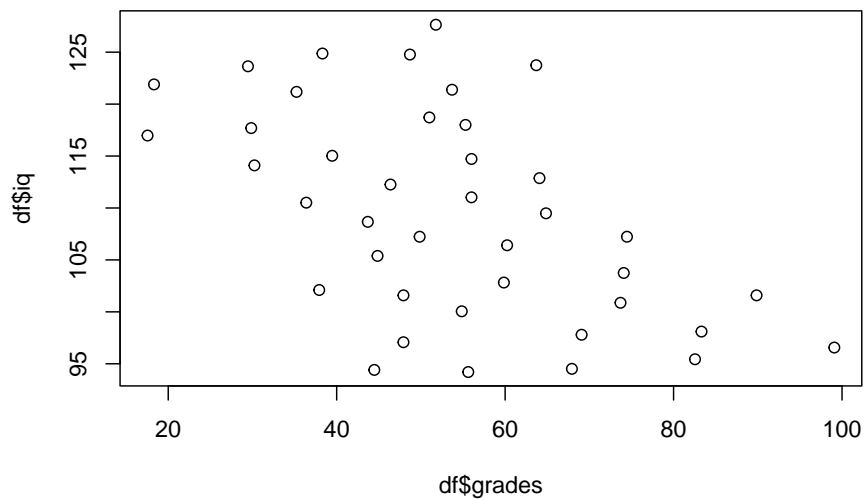
```
##
```

```
##      lmList
```

```
url <- "https://raw.githubusercontent.com/hauselin/rtutorialsite/master/data/simpsonsP
df <- fread(url)
head(df)
```

```
##      iq grades class
## 1: 94.5128 67.9295    a
## 2: 95.4359 82.5449    a
## 3: 97.7949 69.0833    a
## 4: 98.1026 83.3141    a
## 5: 96.5641 99.0833    a
## 6: 101.5897 89.8526    a
```

```
plot(df$grades, df$iq)
```

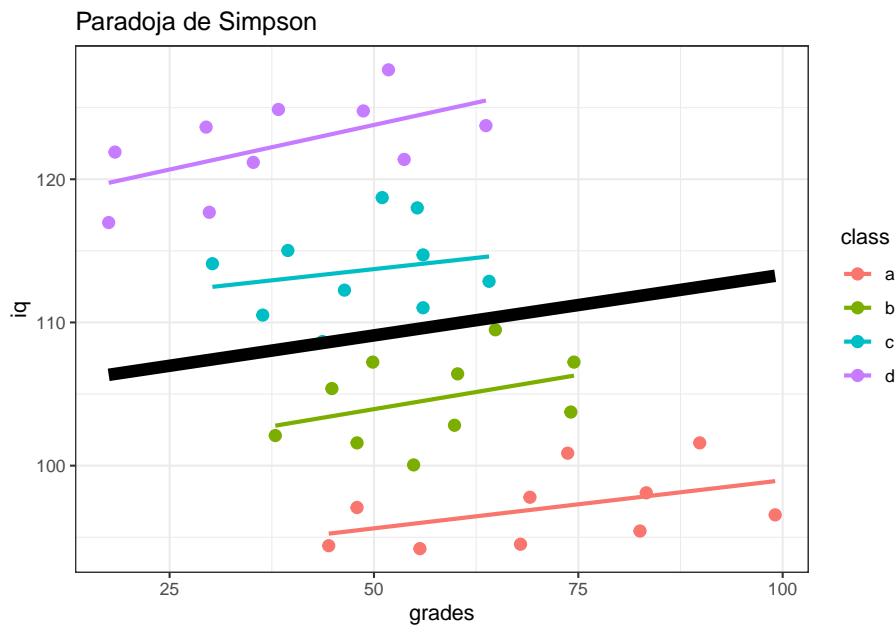


```
model.class <- lme(iq ~ grades, random = ~1|class, data = df)
predy.fixed <- predict(model.class, level = 0)
```



```
ggplot(df, aes(grades, iq, col = class)) + geom_point(size = 2.5) +
  ggtitle("Paradoja de Simpson") +
  geom_smooth(method = "lm", se = FALSE) +
  geom_line(data = data.frame(x = df$grades, y = predy.fixed), aes(x, y), col = "black", size = 3)
  theme_bw()
```

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



## Modelos lineales generalizados mixtos

Palacio et al. (2014) estudiaron la selección natural mediada por aves frugívoras sobre rasgos de los frutos de *Celtis tala* (`frutos Celtis 2013.txt`), incluyendo el diametro (`diam`), peso (`peso`), concentración de azúcares (`az`), peso de pulpa (`pulpa`), peso de semilla (`sem`) y relación peso de pulpa/peso de semilla (`pulpa.sem`). Para esto se midieron 4-10 frutos por árbol en 24 árboles y 4 parches de bosque.

### Diseño anidado

```
library(glmmTMB)
library(lme4)
library(MuMIn)
library(sjPlot)
```

```
## Registered S3 method overwritten by 'parameters':
##   method                      from
##   format.parameters_distribution datawizard
```

```
## Learn more about sjPlot with 'browseVignettes("sjPlot")'.
```

```
library(equationomatic)
celtis <- read.delim("frutos Celtis 2013.csv", sep = ";")
table(celtis$planta)
```

```
##
##   D1-145 D1-146 D1-147 D1-148 P1-10 P1-11 P1-12 P1-13 P1-2 P1-5(1)
##      26      23      19      16      29      30      30      14      27      27
## P1-5(2) P1-7   P1-8   P1-9 P2-150 P2-151 P2-152 P2-153 P2-154 P2-155
##      30      28      13      30      27      28      30      31      30      30
##   P3-1   P3-2   P3-6   P3-7
##      9      30      30      30
```

```
table(celtis$planta, celtis$parche) # Es un diseño anidado?
```

```
##
##           D1 P1 P2 P3
##   D1-145  26  0  0  0
##   D1-146  23  0  0  0
##   D1-147  19  0  0  0
##   D1-148  16  0  0  0
##   P1-10    0 29  0  0
##   P1-11    0 30  0  0
##   P1-12    0 30  0  0
##   P1-13    0 14  0  0
##   P1-2     0 27  0  0
##   P1-5(1)  0 27  0  0
##   P1-5(2)  0 30  0  0
##   P1-7     0 28  0  0
##   P1-8     0 13  0  0
##   P1-9     0 30  0  0
##   P2-150   0  0 27  0
```

```
## P2-151 0 0 28 0
## P2-152 0 0 30 0
## P2-153 0 0 31 0
## P2-154 0 0 30 0
## P2-155 0 0 30 0
## P3-1 0 0 0 9
## P3-2 0 0 0 30
## P3-6 0 0 0 30
## P3-7 0 0 0 30
```

```
lmm.m0 <- lm(sem ~ diam, data = celtis)
lmm.m1 <- glmmTMB(sem ~ diam + (1|planta), family = gaussian, data = celtis)
lmm.m2 <- glmmTMB(sem ~ diam + (1|parche/planta), family = gaussian, data = celtis)
```

```
# Comparación de modelos
AIC(lmm.m0, lmm.m1, lmm.m2)
```

```
##          df          AIC
## lmm.m0  3 -3832.245
## lmm.m1  4 -4215.268
## lmm.m2  5 -4214.188
```

```
r.squaredGLMM(lmm.m1)
```

```
## Warning: 'r.squaredGLMM' now calculates a revised statistic. See the help page.
```

```
## Warning in r.squaredGLMM.glmmTMB(lmm.m1): the effects of zero-inflation and
## dispersion model are ignored
```

```
##          R2m          R2c
## [1,] 0.3126432 0.6709598
```

```
summary(lmm.m1)
```

```
## Family: gaussian ( identity )
## Formula:          sem ~ diam + (1 | planta)
## Data: celtis
##
##          AIC          BIC    logLik deviance df.resid
## -4215.3   -4197.6    2111.6   -4223.3        612
##
## Random effects:
```

```
## Conditional model:
## Groups      Name      Variance Std.Dev.
## planta      (Intercept) 5.899e-05 0.00768
## Residual              5.417e-05 0.00736
## Number of obs: 616, groups:  planta, 24
##
## Dispersion estimate for gaussian family (sigma^2): 5.42e-05
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.0210216  0.0043376  -4.846 1.26e-06 ***
## diam         0.0080182  0.0004735  16.935 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#### # Gráfico

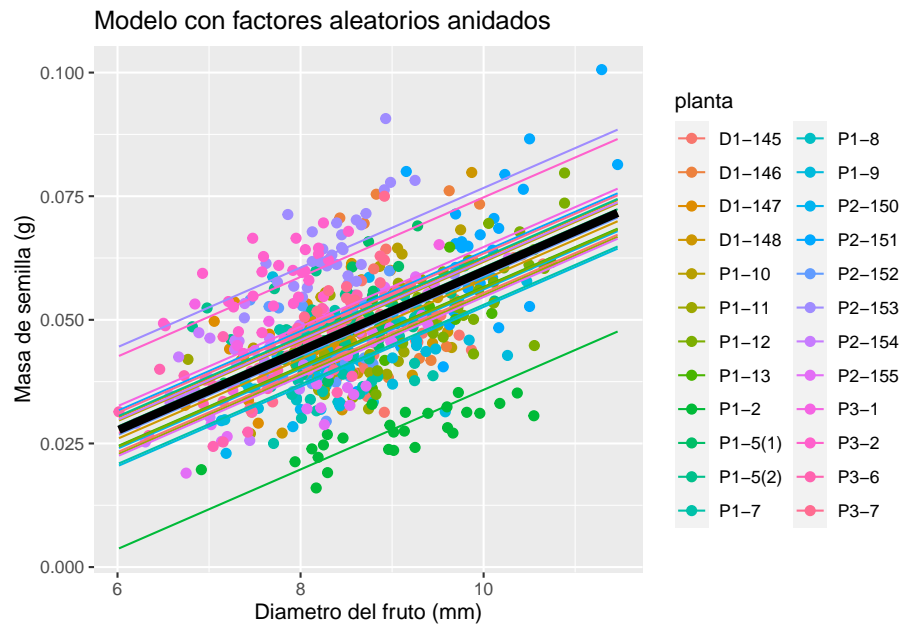
```
diam.new <- seq(min(celtis$diam, na.rm = TRUE), max(celtis$diam, na.rm = TRUE), length
newdata <- expand.grid(diam.new, celtis$planta, stringsAsFactors = TRUE)
colnames(newdata) <- c("diam", "planta")
newdata$parche <- substr(newdata$planta, 1, 2)
```

```
newdata$predy.fixed <- predict(lmm.m2, newdata = newdata, re.form = NA) # poblacional
newdata$predy.rand1 <- predict(lmm.m2, newdata = newdata, re.form = NULL) # planta
rand2 <- ranef(lmm.m2)$cond$parche
rand2.parche <- rand2[match(newdata$parche, rownames(rand2)), 1]
a <- fixef(lmm.m2)$cond[1]
b <- fixef(lmm.m2)$cond[2]
newdata$predy.rand2 <- a + b*newdata$diam + rand2.parche
```

#### # Efecto planta

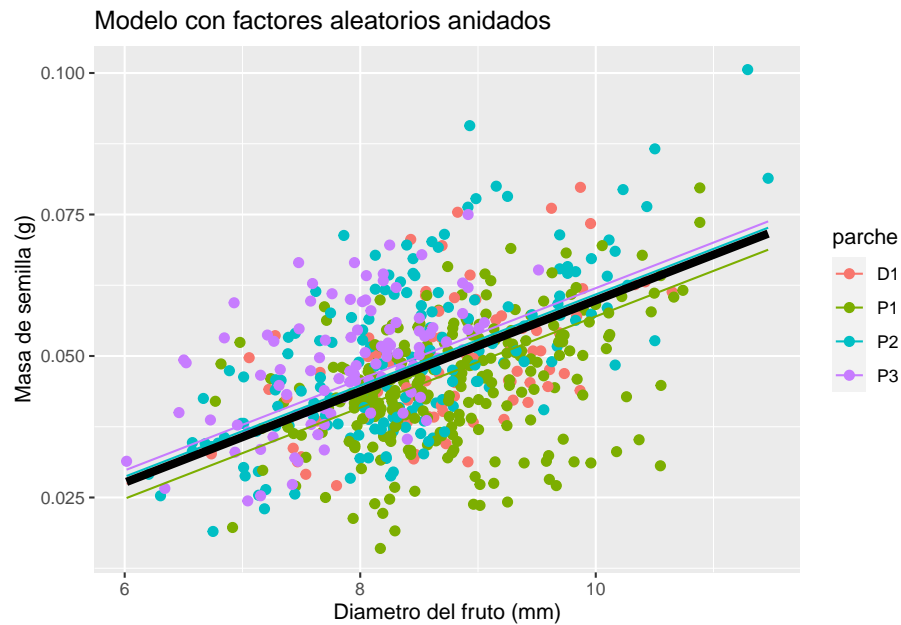
```
library(ggplot2)
ggplot(data = celtis, aes(x = diam, y = sem, col = planta)) +
  geom_point(size = 2) +
  ggtitle("Modelo con factores aleatorios anidados") +
  geom_line(data = newdata, aes(x = diam, y = predy.rand1)) +
  geom_line(data = newdata, aes(x = diam, y = predy.fixed), col = "black", size = 2) +
  xlab("Diámetro del fruto (mm)") + ylab("Masa de semilla (g)")
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```



```
# Efecto parche
ggplot(data = celtis, aes(x = diam, y = sem, col = parche)) +
  geom_point(size = 2) +
  ggtitle("Modelo con factores aleatorios anidados") +
  geom_line(data = newdata, aes(x = diam, y = predy.rand2, col = parche)) +
  geom_line(data = newdata, aes(x = diam, y = predy.fixed), col = "black", size = 2) +
  xlab("Diametro del fruto (mm)") + ylab("Masa de semilla (g)")
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```



```
# Tabla resumen
# tab_model(lmm.m2)

# Ecuaciones del modelo
lmm.m1 <- lmer(sem ~ diam + (1|planta), data = celtis)
lmm.m2 <- lmer(sem ~ diam + (1|parche/planta), data = celtis)
# extract_eq(lmm.m1)
# extract_eq(lmm.m2)
```

### Diseño cruzado

```
data(Penicillin)
str(Penicillin)

## 'data.frame': 144 obs. of 3 variables:
## $ diameter: num 27 23 26 23 23 21 27 23 26 23 ...
## $ plate : Factor w/ 24 levels "a","b","c","d",...: 1 1 1 1 1 1 2 2 2 2 ...
## $ sample : Factor w/ 6 levels "A","B","C","D",...: 1 2 3 4 5 6 1 2 3 4 ...

summary(Penicillin)

## diameter plate sample
```

```
## Min.      :18.00   a      : 6   A:24
## 1st Qu.:22.00   b      : 6   B:24
## Median :23.00   c      : 6   C:24
## Mean    :22.97   d      : 6   D:24
## 3rd Qu.:24.00   e      : 6   E:24
## Max.     :27.00   f      : 6   F:24
##                               (Other):108
```

```
table(Penicillin$plate, Penicillin$sample) # Es un diseño cruzado?
```

```
##
##      A B C D E F
## a 1 1 1 1 1 1
## b 1 1 1 1 1 1
## c 1 1 1 1 1 1
## d 1 1 1 1 1 1
## e 1 1 1 1 1 1
## f 1 1 1 1 1 1
## g 1 1 1 1 1 1
## h 1 1 1 1 1 1
## i 1 1 1 1 1 1
## j 1 1 1 1 1 1
## k 1 1 1 1 1 1
## l 1 1 1 1 1 1
## m 1 1 1 1 1 1
## n 1 1 1 1 1 1
## o 1 1 1 1 1 1
## p 1 1 1 1 1 1
## q 1 1 1 1 1 1
## r 1 1 1 1 1 1
## s 1 1 1 1 1 1
## t 1 1 1 1 1 1
## u 1 1 1 1 1 1
## v 1 1 1 1 1 1
## w 1 1 1 1 1 1
## x 1 1 1 1 1 1
```

```
lmm.pen <- lmer(diameter ~ 1 + (1|plate) + (1|sample), data = Penicillin)
summary(lmm.pen)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: diameter ~ 1 + (1 | plate) + (1 | sample)
##      Data: Penicillin
```

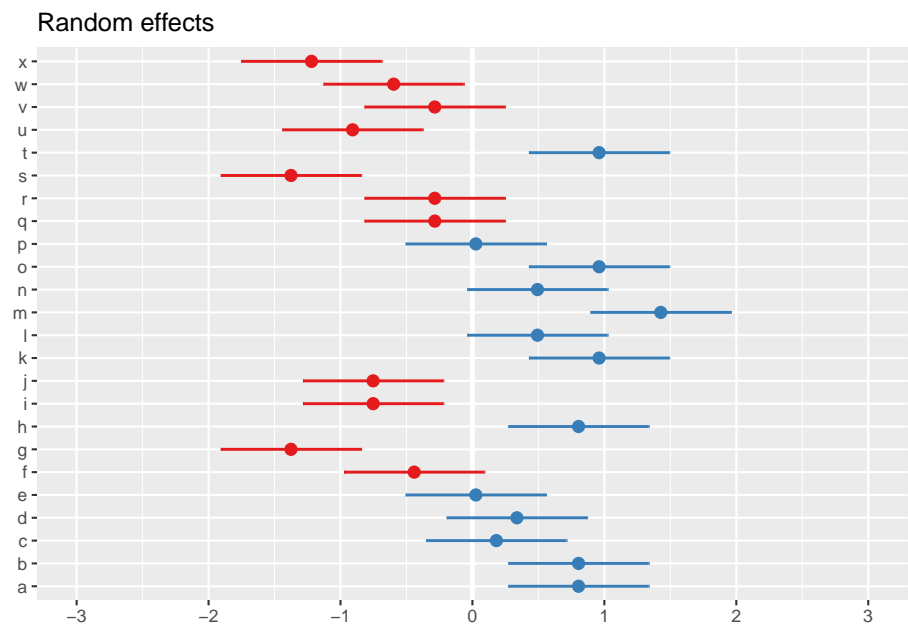
```
##
## REML criterion at convergence: 330.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.07923 -0.67140  0.06292  0.58377  2.97959
##
## Random effects:
##  Groups      Name                Variance Std.Dev.
##  plate      (Intercept)  0.7169     0.8467
##  sample      (Intercept)  3.7311     1.9316
##  Residual                    0.3024     0.5499
## Number of obs: 144, groups:  plate, 24; sample, 6
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  22.9722      0.8086   5.4866   28.41 3.62e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Tabla resumen
# tab_model(lmm.pen)

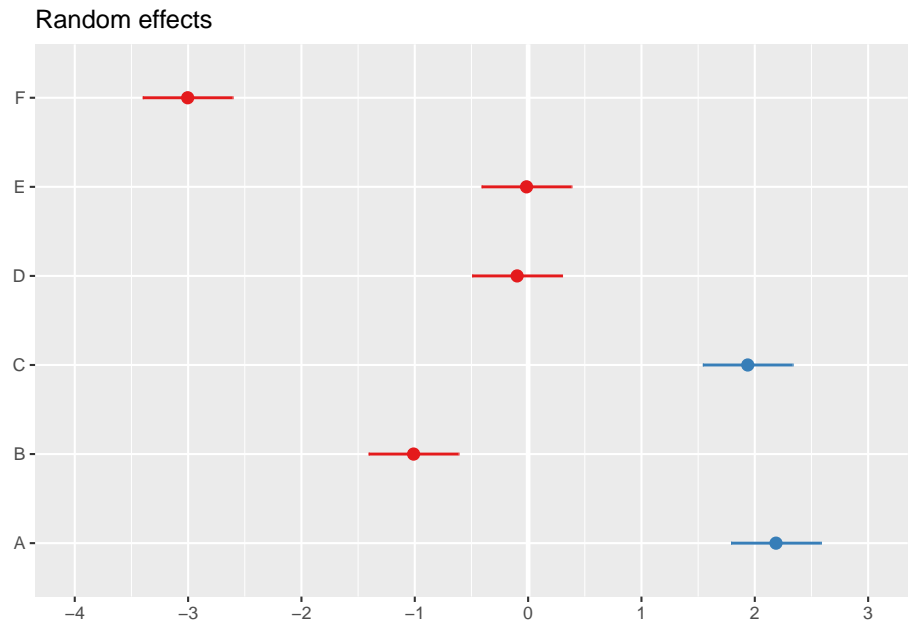
# Gráfico de efectos aleatorios
plot_model(lmm.pen, type = "re")
```

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





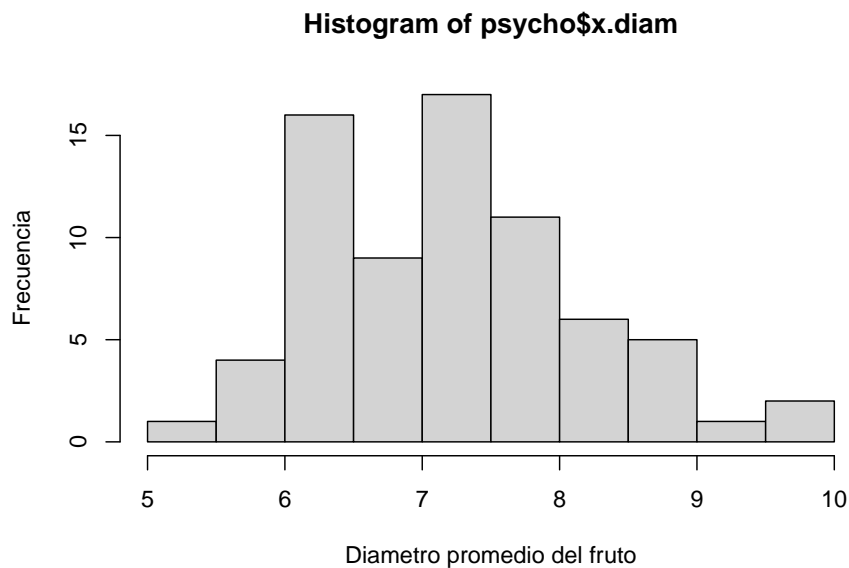
##  
## [[2]]



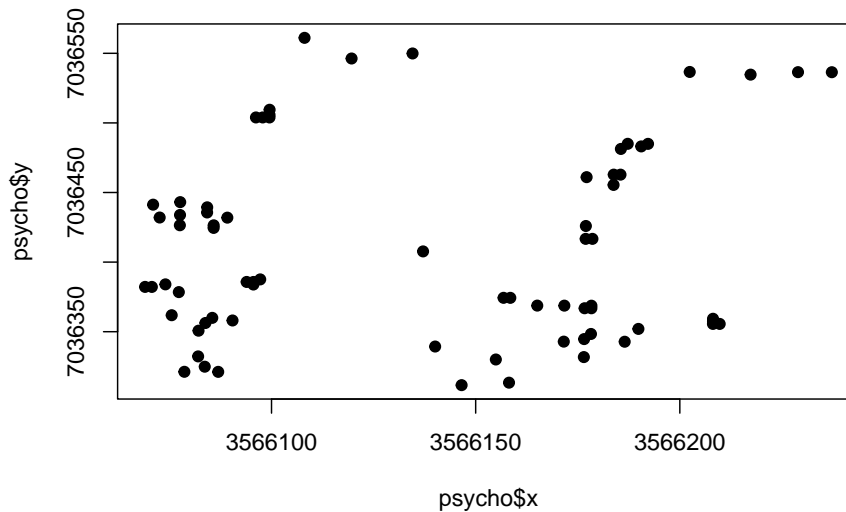
## Modelos mixtos con estructura espacial

Palacio et al. (2017) estudiaron el consumo de frutos por aves en *Psychotriacarthagenensis* en un bosque secundario pedemontano de las Yungas (Psychotria\_El\_Corte\_2012.txt). Se quiere analizar si el peso del fruto (`x.peso`) se relaciona con el número de infrutescencias (`n.infrut`).

```
library(glmTMB)
psycho <- read.table("Psychotria_El_Corte_2012.txt", header = TRUE)
hist(psycho$x.diam, xlab = "Diametro promedio del fruto", ylab = "Frecuencia")
```



```
plot(psycho$x, psycho$y, pch = 19)
```



```

psycho$pos <- numFactor(psycho$x, psycho$y)
psycho$group <- factor(rep(1, nrow(psycho)))
lm.no_espacial <- lm(x.diam ~ n.infrut, data = psycho)

glmm.espacial <- glmmTMB(x.diam ~ n.infrut + exp(pos + 0|group), family = gaussian, data = psycho)
summary(glmm.espacial)

```

```

## Family: gaussian ( identity )
## Formula:          x.diam ~ n.infrut + exp(pos + 0 | group)
## Data: psycho
##
##      AIC      BIC   logLik deviance df.resid
##    171.8    183.2   -80.9    161.8      67
##
## Random effects:
##
## Conditional model:
##   Groups   Name                                Variance Std.Dev. Corr
##   group    pos(3566146.557,7036311.599) 0.4442    0.6665
##   group    pos(3566158.168,7036313.385) 0.4442    0.6665 0.83
##   group    pos(3566086.945,7036321.145) 0.4442    0.6665 0.39 0.33
##   group    pos(3566078.659,7036321.188) 0.4442    0.6665 0.35 0.29 0.88
##   group    pos(3566083.65,7036324.855) 0.4442    0.6665 0.37 0.31 0.93 0.91
##   group    pos(3566154.94,7036330.023) 0.4442    0.6665 0.73 0.77 0.35 0.31

```

|    |                              |        |        |      |      |      |      |
|----|------------------------------|--------|--------|------|------|------|------|
| ## | pos(3566176.494,7036331.757) | 0.4442 | 0.6665 | 0.57 | 0.67 | 0.25 | 0.22 |
| ## | pos(3566082.032,7036332.251) | 0.4442 | 0.6665 | 0.35 | 0.30 | 0.83 | 0.84 |
| ## | pos(3566140.074,7036339.335) | 0.4442 | 0.6665 | 0.64 | 0.61 | 0.42 | 0.37 |
| ## | pos(3566186.495,7036342.785) | 0.4442 | 0.6665 | 0.46 | 0.53 | 0.21 | 0.18 |
| ## | pos(3566171.58,7036342.863)  | 0.4442 | 0.6665 | 0.54 | 0.61 | 0.26 | 0.23 |
| ## | pos(3566176.562,7036344.684) | 0.4442 | 0.6665 | 0.50 | 0.57 | 0.24 | 0.21 |
| ## | pos(3566178.238,7036348.369) | 0.4442 | 0.6665 | 0.47 | 0.54 | 0.23 | 0.20 |
| ## | pos(3566082.128,7036350.719) | 0.4442 | 0.6665 | 0.31 | 0.27 | 0.63 | 0.63 |
| ## | pos(3566189.858,7036352.001) | 0.4442 | 0.6665 | 0.40 | 0.46 | 0.19 | 0.17 |
| ## | pos(3566209.764,7036355.591) | 0.4442 | 0.6665 | 0.31 | 0.36 | 0.14 | 0.12 |
| ## | pos(3566208.107,7036355.599) | 0.4442 | 0.6665 | 0.31 | 0.37 | 0.14 | 0.13 |
| ## | pos(3566083.814,7036356.25)  | 0.4442 | 0.6665 | 0.31 | 0.27 | 0.58 | 0.58 |
| ## | pos(3566208.117,7036357.446) | 0.4442 | 0.6665 | 0.31 | 0.36 | 0.14 | 0.13 |
| ## | pos(3566090.453,7036358.062) | 0.4442 | 0.6665 | 0.33 | 0.29 | 0.57 | 0.55 |
| ## | pos(3566208.127,7036359.293) | 0.4442 | 0.6665 | 0.30 | 0.35 | 0.14 | 0.13 |
| ## | pos(3566085.491,7036359.935) | 0.4442 | 0.6665 | 0.30 | 0.26 | 0.55 | 0.55 |
| ## | pos(3566075.557,7036361.834) | 0.4442 | 0.6665 | 0.26 | 0.23 | 0.52 | 0.53 |
| ## | pos(3566178.335,7036366.836) | 0.4442 | 0.6665 | 0.37 | 0.41 | 0.21 | 0.18 |
| ## | pos(3566176.678,7036366.845) | 0.4442 | 0.6665 | 0.38 | 0.42 | 0.21 | 0.19 |
| ## | pos(3566178.345,7036368.683) | 0.4442 | 0.6665 | 0.37 | 0.40 | 0.20 | 0.18 |
| ## | pos(3566171.716,7036368.718) | 0.4442 | 0.6665 | 0.38 | 0.42 | 0.22 | 0.20 |
| ## | pos(3566165.087,7036368.752) | 0.4442 | 0.6665 | 0.40 | 0.42 | 0.24 | 0.22 |
| ## | pos(3566158.487,7036374.327) | 0.4442 | 0.6665 | 0.37 | 0.39 | 0.25 | 0.23 |
| ## | pos(3566156.83,7036374.336)  | 0.4442 | 0.6665 | 0.38 | 0.39 | 0.26 | 0.23 |
| ## | pos(3566077.301,7036378.446) | 0.4442 | 0.6665 | 0.23 | 0.20 | 0.41 | 0.41 |
| ## | pos(3566070.692,7036382.174) | 0.4442 | 0.6665 | 0.20 | 0.18 | 0.38 | 0.39 |
| ## | pos(3566069.035,7036382.183) | 0.4442 | 0.6665 | 0.20 | 0.18 | 0.38 | 0.39 |
| ## | pos(3566095.56,7036383.891)  | 0.4442 | 0.6665 | 0.26 | 0.23 | 0.38 | 0.37 |
| ## | pos(3566074.016,7036384.003) | 0.4442 | 0.6665 | 0.21 | 0.18 | 0.37 | 0.38 |
| ## | pos(3566095.57,7036385.737)  | 0.4442 | 0.6665 | 0.25 | 0.23 | 0.37 | 0.36 |
| ## | pos(3566093.912,7036385.746) | 0.4442 | 0.6665 | 0.25 | 0.23 | 0.37 | 0.36 |
| ## | pos(3566097.237,7036387.575) | 0.4442 | 0.6665 | 0.25 | 0.23 | 0.36 | 0.35 |
| ## | pos(3566137.117,7036407.682) | 0.4442 | 0.6665 | 0.23 | 0.23 | 0.21 | 0.20 |
| ## | pos(3566178.596,7036416.698) | 0.4442 | 0.6665 | 0.18 | 0.20 | 0.13 | 0.12 |
| ## | pos(3566176.939,7036416.707) | 0.4442 | 0.6665 | 0.19 | 0.20 | 0.13 | 0.12 |
| ## | pos(3566085.829,7036424.571) | 0.4442 | 0.6665 | 0.14 | 0.13 | 0.20 | 0.20 |
| ## | pos(3566176.987,7036425.941) | 0.4442 | 0.6665 | 0.16 | 0.17 | 0.12 | 0.11 |
| ## | pos(3566085.839,7036426.418) | 0.4442 | 0.6665 | 0.14 | 0.13 | 0.20 | 0.20 |
| ## | pos(3566077.553,7036426.461) | 0.4442 | 0.6665 | 0.13 | 0.12 | 0.20 | 0.20 |
| ## | pos(3566089.182,7036431.941) | 0.4442 | 0.6665 | 0.13 | 0.12 | 0.18 | 0.18 |
| ## | pos(3566072.61,7036432.027)  | 0.4442 | 0.6665 | 0.11 | 0.11 | 0.18 | 0.18 |
| ## | pos(3566077.591,7036433.848) | 0.4442 | 0.6665 | 0.12 | 0.11 | 0.18 | 0.18 |
| ## | pos(3566084.23,7036435.66)   | 0.4442 | 0.6665 | 0.12 | 0.11 | 0.17 | 0.17 |
| ## | pos(3566084.249,7036439.354) | 0.4442 | 0.6665 | 0.11 | 0.11 | 0.16 | 0.16 |
| ## | pos(3566071.001,7036441.27)  | 0.4442 | 0.6665 | 0.10 | 0.09 | 0.15 | 0.16 |
| ## | pos(3566077.639,7036443.082) | 0.4442 | 0.6665 | 0.10 | 0.10 | 0.15 | 0.15 |

```

##      pos(3566183.771,7036455.454) 0.4442 0.6665 0.10 0.11 0.08 0.07
##      pos(3566177.171,7036461.029) 0.4442 0.6665 0.10 0.10 0.08 0.07
##      pos(3566185.467,7036462.832) 0.4442 0.6665 0.09 0.10 0.07 0.07
##      pos(3566183.81,7036462.841) 0.4442 0.6665 0.09 0.10 0.07 0.07
##      pos(3566185.564,7036481.3) 0.4442 0.6665 0.07 0.07 0.06 0.05
##      pos(3566190.545,7036483.12) 0.4442 0.6665 0.07 0.07 0.05 0.05
##      pos(3566192.212,7036484.959) 0.4442 0.6665 0.06 0.07 0.05 0.05
##      pos(3566187.24,7036484.985) 0.4442 0.6665 0.06 0.07 0.05 0.05
##      pos(3566099.502,7036503.912) 0.4442 0.6665 0.05 0.05 0.06 0.06
##      pos(3566097.845,7036503.921) 0.4442 0.6665 0.05 0.05 0.06 0.06
##      pos(3566096.188,7036503.929) 0.4442 0.6665 0.05 0.05 0.06 0.06
##      pos(3566099.512,7036505.759) 0.4442 0.6665 0.05 0.05 0.06 0.06
##      pos(3566099.531,7036509.452) 0.4442 0.6665 0.04 0.04 0.05 0.05
##      pos(3566217.332,7036534.69) 0.4442 0.6665 0.03 0.03 0.02 0.02
##      pos(3566237.229,7036536.433) 0.4442 0.6665 0.02 0.03 0.02 0.02
##      pos(3566228.943,7036536.476) 0.4442 0.6665 0.03 0.03 0.02 0.02
##      pos(3566202.426,7036536.615) 0.4442 0.6665 0.03 0.03 0.02 0.02
##      pos(3566119.612,7036546.283) 0.4442 0.6665 0.03 0.03 0.03 0.03
##      pos(3566134.546,7036549.898) 0.4442 0.6665 0.03 0.03 0.03 0.03
##      pos(3566108.088,7036561.118) 0.4442 0.6665 0.02 0.02 0.02 0.02
## Residual 0.3628 0.6023
##
##
##
##
##
## 0.33
## 0.24 0.72
## 0.89 0.33 0.23
## 0.41 0.76 0.56 0.41
## 0.20 0.59 0.80 0.20 0.49
## 0.25 0.72 0.83 0.25 0.61 0.79
## 0.23 0.67 0.82 0.23 0.57 0.86 0.92
## 0.22 0.63 0.77 0.22 0.55 0.86 0.88 0.94
## 0.67 0.31 0.23 0.75 0.40 0.20 0.25 0.23 0.23
## 0.18 0.53 0.69 0.18 0.45 0.86 0.73 0.79 0.83 0.19
## 0.14 0.39 0.53 0.14 0.33 0.66 0.54 0.58 0.61 0.14 0.73
## 0.14 0.40 0.54 0.14 0.34 0.68 0.55 0.60 0.62 0.14 0.75 0.97
## 0.62 0.31 0.23 0.69 0.40 0.20 0.25 0.24 0.23 0.91 0.20 0.14 0.15
## 0.14 0.40 0.53 0.14 0.34 0.67 0.55 0.59 0.62 0.14 0.75 0.96 0.97 0.15
## 0.59 0.34 0.25 0.66 0.44 0.22 0.28 0.26 0.26 0.84 0.22 0.16 0.16 0.90 0.16
## 0.14 0.39 0.52 0.14 0.34 0.66 0.54 0.59 0.61 0.14 0.74 0.94 0.94 0.15 0.97
## 0.58 0.31 0.23 0.65 0.41 0.21 0.26 0.24 0.24 0.86 0.20 0.15 0.15 0.94 0.15
## 0.56 0.27 0.20 0.63 0.35 0.18 0.22 0.21 0.20 0.82 0.17 0.13 0.13 0.86 0.13
## 0.20 0.51 0.58 0.21 0.48 0.68 0.68 0.71 0.75 0.22 0.75 0.60 0.61 0.23 0.62

```

```

## 0.21 0.52 0.58 0.21 0.49 0.67 0.69 0.71 0.75 0.23 0.74 0.58 0.60 0.24 0.60
## 0.20 0.50 0.57 0.20 0.48 0.66 0.66 0.69 0.73 0.22 0.73 0.59 0.61 0.23 0.61
## 0.22 0.52 0.56 0.23 0.51 0.63 0.67 0.69 0.72 0.24 0.68 0.54 0.55 0.25 0.56
## 0.24 0.54 0.55 0.25 0.55 0.60 0.66 0.66 0.69 0.27 0.63 0.49 0.50 0.28 0.50
## 0.25 0.50 0.49 0.26 0.54 0.52 0.59 0.59 0.61 0.29 0.55 0.43 0.44 0.31 0.45
## 0.26 0.51 0.49 0.27 0.55 0.51 0.59 0.58 0.60 0.30 0.54 0.42 0.43 0.31 0.44
## 0.44 0.24 0.18 0.49 0.32 0.17 0.21 0.20 0.20 0.65 0.17 0.13 0.13 0.70 0.13
## 0.40 0.22 0.16 0.45 0.28 0.15 0.19 0.18 0.18 0.60 0.15 0.11 0.12 0.64 0.12
## 0.40 0.21 0.16 0.45 0.28 0.15 0.18 0.17 0.17 0.59 0.15 0.11 0.11 0.63 0.11
## 0.40 0.29 0.23 0.44 0.38 0.22 0.26 0.25 0.25 0.58 0.22 0.16 0.17 0.63 0.17
## 0.40 0.22 0.17 0.45 0.29 0.16 0.20 0.18 0.18 0.59 0.16 0.12 0.12 0.64 0.12
## 0.38 0.29 0.22 0.43 0.37 0.21 0.26 0.25 0.25 0.56 0.21 0.16 0.17 0.61 0.17
## 0.39 0.28 0.22 0.43 0.37 0.21 0.26 0.24 0.24 0.57 0.21 0.16 0.16 0.62 0.16
## 0.37 0.29 0.22 0.41 0.37 0.21 0.26 0.25 0.25 0.54 0.22 0.17 0.17 0.59 0.17
## 0.22 0.29 0.27 0.24 0.35 0.28 0.32 0.32 0.33 0.30 0.31 0.25 0.26 0.32 0.26
## 0.13 0.25 0.27 0.14 0.26 0.32 0.32 0.33 0.35 0.17 0.36 0.35 0.35 0.18 0.36
## 0.13 0.25 0.27 0.14 0.27 0.32 0.32 0.33 0.35 0.17 0.36 0.34 0.35 0.18 0.36
## 0.22 0.16 0.14 0.24 0.21 0.14 0.16 0.16 0.16 0.32 0.14 0.11 0.12 0.35 0.12
## 0.12 0.22 0.23 0.13 0.23 0.28 0.28 0.29 0.30 0.16 0.31 0.30 0.31 0.17 0.31
## 0.21 0.16 0.13 0.23 0.21 0.13 0.16 0.15 0.16 0.31 0.14 0.11 0.11 0.34 0.12
## 0.21 0.15 0.12 0.23 0.19 0.12 0.14 0.14 0.14 0.31 0.13 0.10 0.10 0.34 0.10
## 0.19 0.15 0.13 0.21 0.20 0.13 0.15 0.15 0.15 0.29 0.14 0.11 0.11 0.31 0.12
## 0.19 0.13 0.11 0.21 0.17 0.11 0.13 0.12 0.13 0.28 0.11 0.09 0.09 0.31 0.09
## 0.19 0.14 0.11 0.21 0.17 0.11 0.13 0.13 0.13 0.28 0.12 0.09 0.10 0.30 0.10
## 0.18 0.14 0.12 0.20 0.18 0.12 0.14 0.14 0.14 0.27 0.13 0.10 0.10 0.29 0.10
## 0.17 0.13 0.11 0.19 0.17 0.11 0.13 0.13 0.13 0.26 0.12 0.10 0.10 0.28 0.10
## 0.16 0.12 0.10 0.19 0.15 0.10 0.11 0.11 0.11 0.25 0.10 0.08 0.08 0.27 0.08
## 0.16 0.12 0.10 0.18 0.16 0.10 0.12 0.12 0.12 0.24 0.11 0.09 0.09 0.26 0.09
## 0.08 0.14 0.15 0.09 0.15 0.18 0.17 0.18 0.19 0.11 0.20 0.20 0.21 0.11 0.21
## 0.08 0.13 0.14 0.09 0.14 0.16 0.16 0.17 0.18 0.11 0.18 0.18 0.18 0.12 0.19
## 0.07 0.12 0.13 0.08 0.13 0.16 0.16 0.16 0.17 0.10 0.18 0.18 0.19 0.10 0.19
## 0.07 0.12 0.13 0.08 0.13 0.16 0.16 0.16 0.17 0.10 0.18 0.18 0.18 0.11 0.19
## 0.06 0.09 0.10 0.06 0.10 0.12 0.12 0.12 0.13 0.08 0.14 0.14 0.14 0.08 0.14
## 0.05 0.09 0.10 0.06 0.10 0.12 0.11 0.12 0.12 0.07 0.13 0.14 0.14 0.08 0.14
## 0.05 0.09 0.09 0.06 0.09 0.11 0.11 0.11 0.12 0.07 0.13 0.13 0.13 0.07 0.14
## 0.05 0.09 0.09 0.06 0.09 0.11 0.11 0.11 0.12 0.07 0.13 0.13 0.13 0.08 0.14
## 0.06 0.06 0.05 0.07 0.07 0.06 0.07 0.07 0.07 0.09 0.07 0.06 0.06 0.10 0.06
## 0.06 0.06 0.05 0.07 0.07 0.06 0.07 0.06 0.07 0.09 0.06 0.06 0.06 0.10 0.06
## 0.06 0.06 0.05 0.07 0.07 0.06 0.06 0.06 0.07 0.09 0.06 0.06 0.06 0.10 0.06
## 0.06 0.06 0.05 0.06 0.07 0.06 0.06 0.06 0.06 0.09 0.06 0.05 0.06 0.09 0.06
## 0.02 0.04 0.04 0.02 0.04 0.05 0.05 0.05 0.05 0.03 0.06 0.06 0.06 0.03 0.07
## 0.02 0.03 0.04 0.02 0.03 0.05 0.04 0.05 0.05 0.02 0.05 0.06 0.06 0.03 0.06
## 0.02 0.03 0.04 0.02 0.04 0.05 0.04 0.05 0.05 0.03 0.05 0.06 0.06 0.03 0.06
## 0.02 0.04 0.04 0.03 0.04 0.05 0.05 0.05 0.05 0.03 0.06 0.06 0.06 0.04 0.06
## 0.03 0.03 0.03 0.04 0.04 0.04 0.04 0.04 0.04 0.05 0.04 0.04 0.04 0.05 0.04

```

```
## 0.03 0.03 0.03 0.03 0.04 0.04 0.04 0.04 0.04 0.04 0.04 0.04 0.04 0.05 0.04
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##
## 0.16
## 0.92 0.15
## 0.79 0.13 0.86
## 0.26 0.62 0.24 0.21
## 0.26 0.61 0.24 0.21 0.97
## 0.26 0.62 0.24 0.20 0.97 0.96
## 0.28 0.56 0.26 0.23 0.90 0.92 0.90
## 0.31 0.51 0.29 0.25 0.81 0.83 0.82 0.90
## 0.34 0.45 0.32 0.27 0.72 0.74 0.73 0.80 0.88
## 0.35 0.44 0.33 0.28 0.70 0.72 0.71 0.78 0.86 0.97
## 0.69 0.13 0.73 0.77 0.21 0.21 0.21 0.23 0.26 0.29 0.29
## 0.62 0.12 0.66 0.72 0.19 0.19 0.19 0.21 0.23 0.26 0.26 0.89
## 0.61 0.11 0.65 0.72 0.18 0.19 0.18 0.20 0.22 0.25 0.26 0.87 0.97
## 0.67 0.17 0.67 0.63 0.27 0.28 0.27 0.30 0.33 0.38 0.38 0.75 0.68 0.66
## 0.62 0.12 0.66 0.71 0.20 0.20 0.20 0.22 0.24 0.27 0.28 0.91 0.94 0.92 0.72
## 0.65 0.17 0.65 0.62 0.27 0.28 0.27 0.30 0.33 0.37 0.38 0.74 0.68 0.66 0.97
## 0.65 0.16 0.66 0.63 0.26 0.27 0.27 0.29 0.32 0.36 0.37 0.76 0.70 0.68 0.96
## 0.63 0.17 0.63 0.60 0.28 0.28 0.28 0.31 0.34 0.38 0.39 0.71 0.66 0.64 0.94
## 0.35 0.27 0.34 0.31 0.41 0.42 0.42 0.45 0.48 0.54 0.55 0.36 0.33 0.33 0.48
## 0.20 0.37 0.19 0.17 0.46 0.46 0.48 0.47 0.46 0.49 0.48 0.19 0.17 0.17 0.25
## 0.20 0.37 0.19 0.17 0.46 0.46 0.48 0.48 0.47 0.49 0.49 0.19 0.18 0.17 0.26
## 0.36 0.12 0.37 0.38 0.19 0.19 0.19 0.21 0.22 0.26 0.26 0.49 0.50 0.50 0.53
```

|    |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
|----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| ## | 0.18 | 0.32 | 0.18 | 0.16 | 0.40 | 0.40 | 0.41 | 0.41 | 0.41 | 0.43 | 0.43 | 0.18 | 0.17 | 0.17 | 0.24 |
| ## | 0.35 | 0.12 | 0.36 | 0.37 | 0.18 | 0.19 | 0.19 | 0.20 | 0.22 | 0.25 | 0.26 | 0.47 | 0.49 | 0.48 | 0.51 |
| ## | 0.34 | 0.10 | 0.36 | 0.37 | 0.16 | 0.17 | 0.17 | 0.18 | 0.20 | 0.23 | 0.23 | 0.48 | 0.50 | 0.50 | 0.49 |
| ## | 0.32 | 0.12 | 0.33 | 0.33 | 0.18 | 0.19 | 0.19 | 0.20 | 0.22 | 0.25 | 0.25 | 0.43 | 0.44 | 0.44 | 0.47 |
| ## | 0.31 | 0.09 | 0.32 | 0.34 | 0.15 | 0.15 | 0.15 | 0.16 | 0.18 | 0.20 | 0.21 | 0.44 | 0.46 | 0.46 | 0.44 |
| ## | 0.31 | 0.10 | 0.32 | 0.33 | 0.16 | 0.16 | 0.16 | 0.17 | 0.19 | 0.21 | 0.22 | 0.43 | 0.45 | 0.45 | 0.44 |
| ## | 0.30 | 0.11 | 0.31 | 0.32 | 0.17 | 0.17 | 0.17 | 0.18 | 0.20 | 0.23 | 0.23 | 0.41 | 0.43 | 0.42 | 0.44 |
| ## | 0.29 | 0.10 | 0.29 | 0.30 | 0.16 | 0.16 | 0.16 | 0.18 | 0.19 | 0.22 | 0.22 | 0.39 | 0.40 | 0.40 | 0.42 |
| ## | 0.27 | 0.09 | 0.28 | 0.29 | 0.13 | 0.14 | 0.14 | 0.15 | 0.16 | 0.18 | 0.19 | 0.38 | 0.40 | 0.40 | 0.38 |
| ## | 0.27 | 0.09 | 0.28 | 0.29 | 0.14 | 0.15 | 0.15 | 0.16 | 0.17 | 0.20 | 0.20 | 0.37 | 0.39 | 0.39 | 0.39 |
| ## | 0.13 | 0.22 | 0.12 | 0.11 | 0.25 | 0.25 | 0.26 | 0.26 | 0.26 | 0.27 | 0.27 | 0.13 | 0.13 | 0.12 | 0.17 |
| ## | 0.13 | 0.19 | 0.12 | 0.11 | 0.23 | 0.23 | 0.24 | 0.24 | 0.24 | 0.26 | 0.25 | 0.14 | 0.13 | 0.13 | 0.18 |
| ## | 0.11 | 0.20 | 0.11 | 0.10 | 0.23 | 0.23 | 0.23 | 0.23 | 0.23 | 0.24 | 0.24 | 0.12 | 0.12 | 0.11 | 0.16 |
| ## | 0.12 | 0.19 | 0.11 | 0.10 | 0.23 | 0.23 | 0.23 | 0.23 | 0.23 | 0.24 | 0.24 | 0.12 | 0.12 | 0.12 | 0.16 |
| ## | 0.09 | 0.15 | 0.09 | 0.08 | 0.17 | 0.17 | 0.18 | 0.17 | 0.17 | 0.18 | 0.18 | 0.10 | 0.10 | 0.09 | 0.13 |
| ## | 0.08 | 0.15 | 0.08 | 0.08 | 0.17 | 0.16 | 0.17 | 0.17 | 0.16 | 0.17 | 0.17 | 0.09 | 0.09 | 0.09 | 0.12 |
| ## | 0.08 | 0.14 | 0.08 | 0.07 | 0.16 | 0.16 | 0.16 | 0.16 | 0.16 | 0.17 | 0.17 | 0.09 | 0.09 | 0.08 | 0.12 |
| ## | 0.09 | 0.14 | 0.08 | 0.08 | 0.16 | 0.16 | 0.17 | 0.16 | 0.16 | 0.17 | 0.17 | 0.09 | 0.09 | 0.09 | 0.12 |
| ## | 0.11 | 0.06 | 0.11 | 0.11 | 0.09 | 0.09 | 0.09 | 0.09 | 0.10 | 0.11 | 0.11 | 0.14 | 0.15 | 0.14 | 0.16 |
| ## | 0.11 | 0.06 | 0.11 | 0.11 | 0.09 | 0.09 | 0.09 | 0.09 | 0.10 | 0.11 | 0.11 | 0.14 | 0.15 | 0.15 | 0.16 |
| ## | 0.11 | 0.06 | 0.11 | 0.11 | 0.09 | 0.09 | 0.09 | 0.09 | 0.10 | 0.11 | 0.11 | 0.14 | 0.15 | 0.15 | 0.16 |
| ## | 0.10 | 0.06 | 0.10 | 0.11 | 0.09 | 0.09 | 0.09 | 0.09 | 0.10 | 0.11 | 0.11 | 0.14 | 0.14 | 0.14 | 0.15 |
| ## | 0.10 | 0.06 | 0.10 | 0.10 | 0.08 | 0.08 | 0.08 | 0.09 | 0.09 | 0.10 | 0.10 | 0.13 | 0.13 | 0.13 | 0.14 |
| ## | 0.04 | 0.07 | 0.03 | 0.03 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.04 | 0.04 | 0.04 | 0.05 |
| ## | 0.03 | 0.06 | 0.03 | 0.03 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.03 | 0.03 | 0.03 | 0.04 |
| ## | 0.03 | 0.06 | 0.03 | 0.03 | 0.07 | 0.07 | 0.07 | 0.07 | 0.06 | 0.07 | 0.07 | 0.03 | 0.03 | 0.03 | 0.04 |
| ## | 0.04 | 0.07 | 0.04 | 0.04 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.08 | 0.07 | 0.04 | 0.04 | 0.04 | 0.06 |
| ## | 0.05 | 0.04 | 0.05 | 0.05 | 0.05 | 0.06 | 0.06 | 0.06 | 0.06 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 | 0.08 |
| ## | 0.05 | 0.04 | 0.05 |      |      |      |      |      |      |      |      |      |      |      |      |



[illegible]

[illegible]

[illegible]



```
##
##
##
##
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##
##
##
##
##
##
##
##
## 0.16
## 0.12 0.74
## 0.13 0.83 0.88
## 0.19 0.79 0.59 0.66
## 0.52 0.22 0.16 0.18 0.28
## 0.44 0.27 0.20 0.23 0.34 0.79
## 0.45 0.18 0.13 0.15 0.22 0.75 0.64
##
## Number of obs: 72, groups: group, 1
##
## Dispersion estimate for gaussian family (sigma^2): 0.363
##
## Conditional model:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept) 7.085923   0.344658  20.559   <2e-16 ***
## n.infrut    0.005973   0.005773   1.035    0.301
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

AIC(lm.no_espacial, glmm.espacial)

##           df      AIC
## lm.no_espacial  3 204.1418
## glmm.espacial   5 171.8000
```

## Modelos mixtos con filogenia

Lislevand & Thomas (2006) estudiaron la evolución del tamaño del huevo en aves playeras (`data(shorebirds)`). En particular, nos interesa analizar la relación

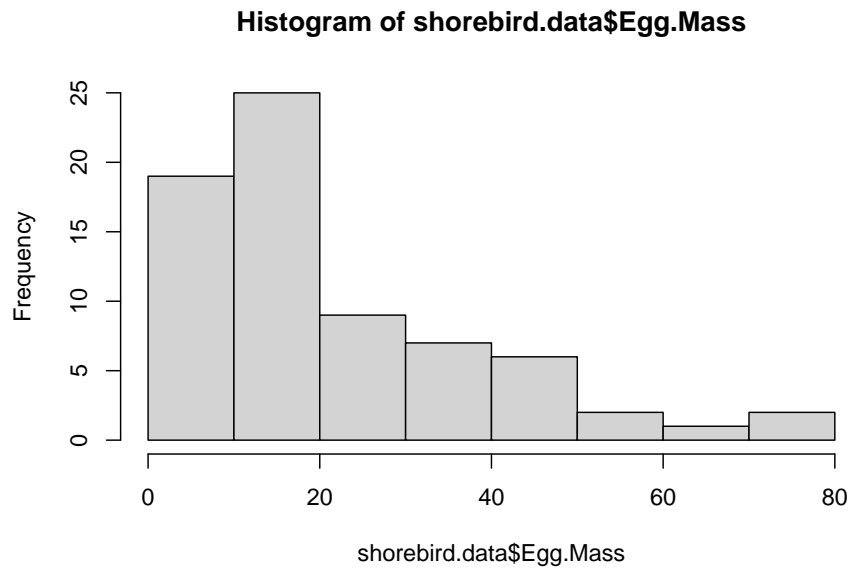
```
library(caper)
```

```
## Loading required package: MASS
```

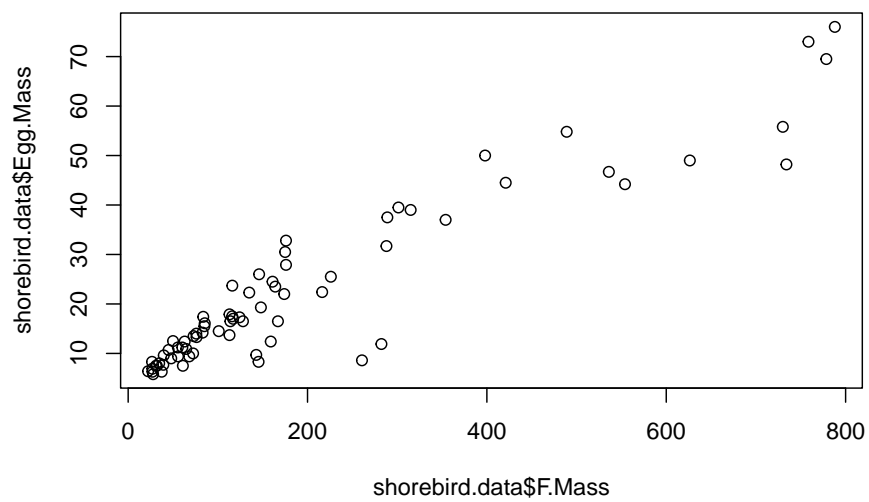
```
## Registered S3 method overwritten by 'caper':
##   method      from
##   nobs.pglis MuMIn
```

[illegible]

```
shorebird <- comparative.data(phy = shorebird.tree, data = shorebird.data, names.col =
hist(shorebird.data$Egg.Mass)
```



```
plot(shorebird.data$F.Mass, shorebird.data$Egg.Mass)
```



```
normal.phyloglmm <- pgls(log(Egg.Mass) ~ F.Mass, data = shorebird)
summary(normal.phyloglmm)
```

```
##
## Call:
## pgls(formula = log(Egg.Mass) ~ F.Mass, data = shorebird)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.194516 -0.046257 -0.005145  0.027299  0.166274
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [Fix] : 1.000
## delta [Fix] : 1.000
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.40680667  0.28666687   8.3958 3.775e-12 ***
## F.Mass        0.00229913  0.00029862   7.6991 7.095e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06234 on 69 degrees of freedom
## Multiple R-squared: 0.4621, Adjusted R-squared: 0.4543
## F-statistic: 59.28 on 1 and 69 DF, p-value: 7.095e-11
```

```
normal.glm <- glm(log(Egg.Mass) ~ F.Mass, data = shorebird.data)
summary(normal.glm)
```

```
##
## Call:
## glm(formula = log(Egg.Mass) ~ F.Mass, data = shorebird.data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.89508  -0.25844   0.03603   0.29072   0.68572
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.3015653  0.0604762  38.06  <2e-16 ***
## F.Mass        0.0028587  0.0002132  13.41  <2e-16 ***
## ---
```



```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.1339951)
##
##      Null deviance: 33.3279  on 70  degrees of freedom
## Residual deviance:  9.2457  on 69  degrees of freedom
## AIC: 62.754
##
## Number of Fisher Scoring iterations: 2

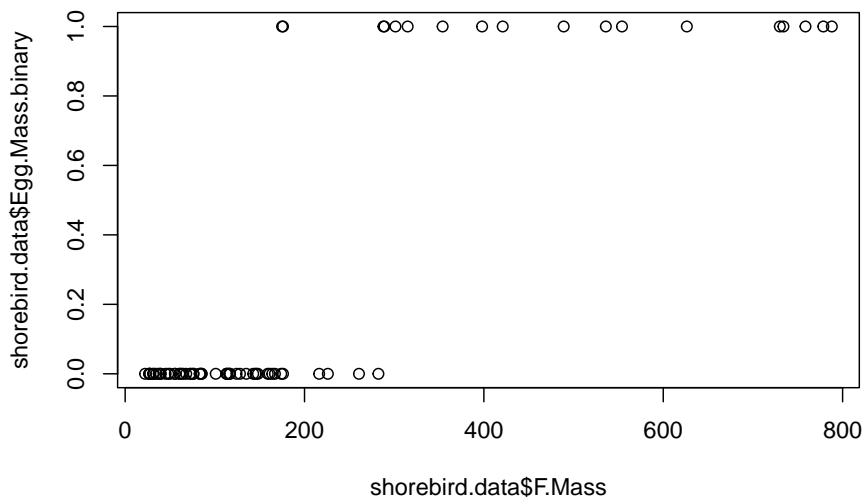
AIC(normal.phyloglmm, normal.glm)

##              df      AIC
## normal.phyloglmm  2 20.61397
## normal.glm        3 62.75396

library(phylolm)

## Registered S3 methods overwritten by 'phylolm':
##   method      from
##   logLik.phylolm MuMIn
##   nobs.phylolm   MuMIn

shorebird.data$Egg.Mass.binary <- ifelse(shorebird.data$Egg.Mass > 30, 1, 0)
plot(shorebird.data$F.Mass, shorebird.data$Egg.Mass.binary)
```



```

binomial.glm <- phyloglm(Egg.Mass.binary ~ F.Mass, phy = shorebird.tree, data = shorebird.data)

## Warning in phyloglm(Egg.Mass.binary ~ F.Mass, phy = shorebird.tree, data = shorebird.data):
## You can increase this bound by increasing 'btol'.

summary(binomial.glm)

##
## Call:
## phyloglm(formula = Egg.Mass.binary ~ F.Mass, data = shorebird.data,
##          phy = shorebird.tree, method = "logistic_MPLE", btol = 30,
##          boot = 100)
##          AIC          logLik Pen.logLik
##      27.484      -10.742       -5.899
##
## Method: logistic_MPLE
## Mean tip height: 81.872
## Parameter estimate(s):
## alpha: 0.01221473
##          bootstrap mean: 0.01221439 (on log scale, then back transformed)
##          so possible downward bias.
##          bootstrap 95% CI: (0.012214,0.01221667)
##
## Coefficients:
##              Estimate      StdErr    z.value lowerbootCI upperbootCI  p.value
## (Intercept) -7.3788576  2.4647338 -2.9937747  -7.3788804    -7.3788  0.002755
## F.Mass       0.0284749  0.0089727  3.1735091   0.0249895     0.0373  0.001506
##
## (Intercept) **
## F.Mass      **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Note: Wald-type p-values for coefficients, conditional on alpha=0.01221473
##          Parametric bootstrap results based on 100 fitted replicates

```

## Modelos aditivos generalizados mixtos

Gillibrand et al. (2007) analizaron la bioluminiscencia pelágica (Sources) a lo largo de un gradiente de profundidad (SampleDepth) en el NE del Océano Atlántico (ISIT.txt).

```
library(ggplot2)
library(mgcv)

## This is mgcv 1.8-40. For overview type 'help("mgcv-package")'.

library(itsadug)

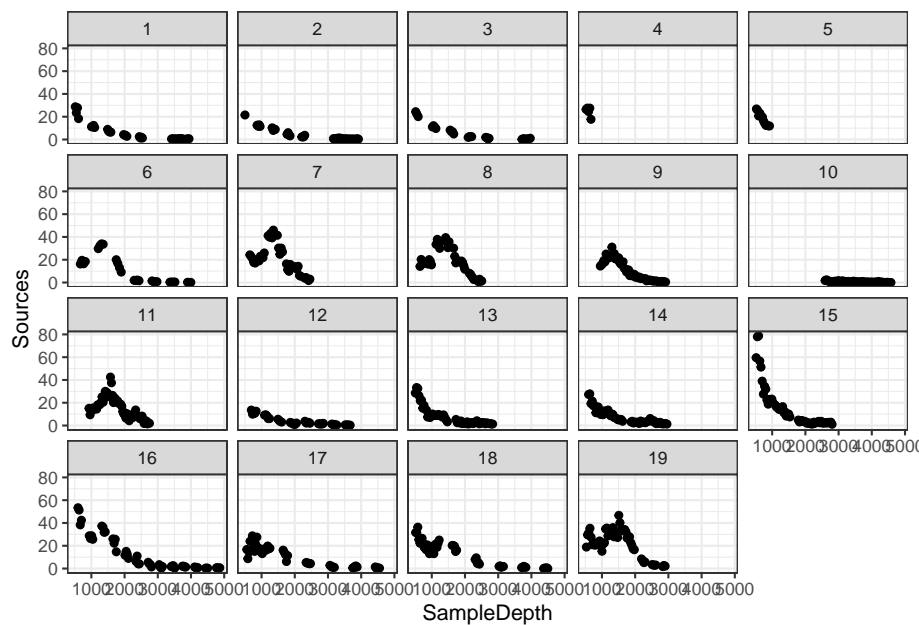
## Loading required package: plotfunctions

##
## Attaching package: 'plotfunctions'

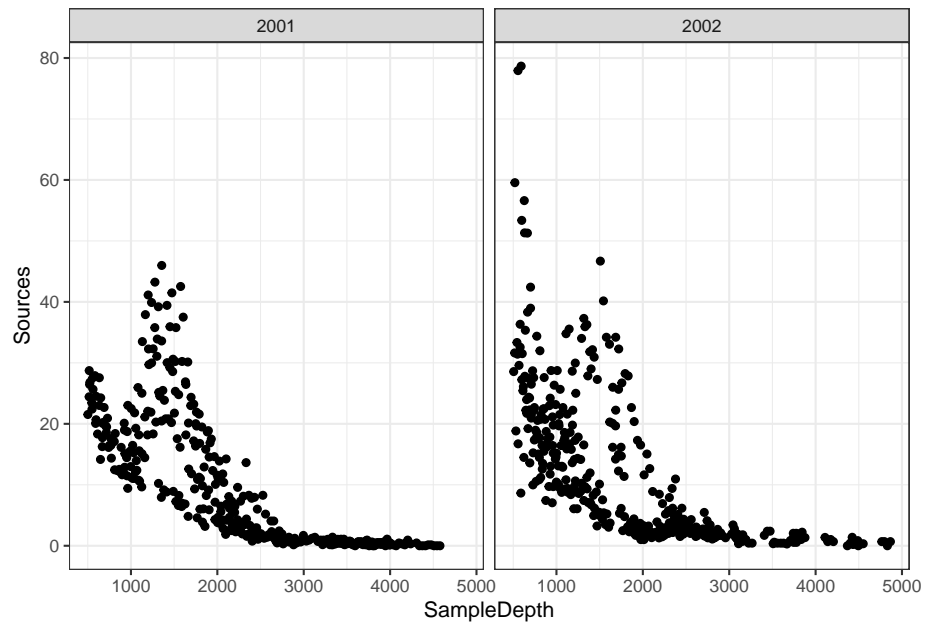
## The following object is masked from 'package:ggplot2':
##
##     alpha

## Loaded package itsadug 2.4 (see 'help("itsadug")' ).

biolum <- read.table("ISIT.txt", header = TRUE)
biolum$Station <- as.factor(biolum$Station)
biolum$Year <- as.factor(biolum$Year)
ggplot(data = biolum, aes(x = SampleDepth, y = Sources)) +
  geom_point() + facet_wrap(~Station) +
  theme_bw()
```

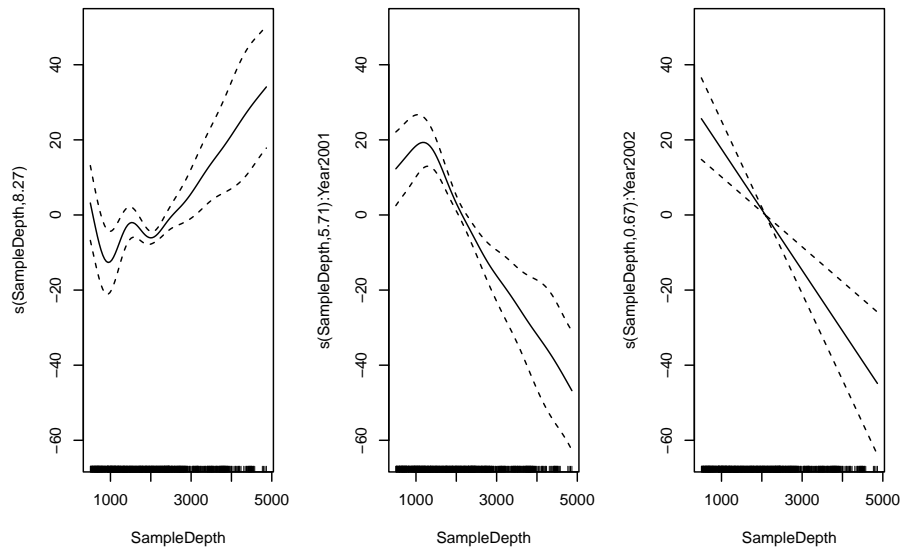


```
ggplot(data = biolum, aes(x = SampleDepth, y = Sources)) +
  geom_point() + facet_wrap(~Year) +
  theme_bw()
```



## Ajuste de modelos

```
# Sin efectos aleatorios
gam0 <- gam(Sources ~ Year + s(SampleDepth) + s(SampleDepth, by = Year), family = gaussian)
layout(matrix(1:3, 1, 3))
plot(gam0)
```



```
layout(1)
```

```
# Intercepto aleatorio
```

```
gamm1 <- gam(Sources ~ Year + s(SampleDepth) + s(Station, bs = "re"), family = gaussian, data = biolum)
```

```
# Intercepto + pendiente aleatorios
```

```
gamm2 <- gam(Sources ~ Year + s(SampleDepth) +  
             s(Station, bs = "re") + # Intercepto aleatorio  
             s(SampleDepth, Station, bs = "re"), # Pendiente aleatoria  
             family = gaussian, data = biolum)
```

```
# Intercepto + "smooth" aleatorios
```

```
gamm3 <- gam(Sources ~ Year + s(SampleDepth, Station, bs = "fs", m = 1, k = 5), # Smooth aleatorios  
             family = gaussian, data = biolum)
```

```
# Comparación de estructuras de efectos aleatorios
```

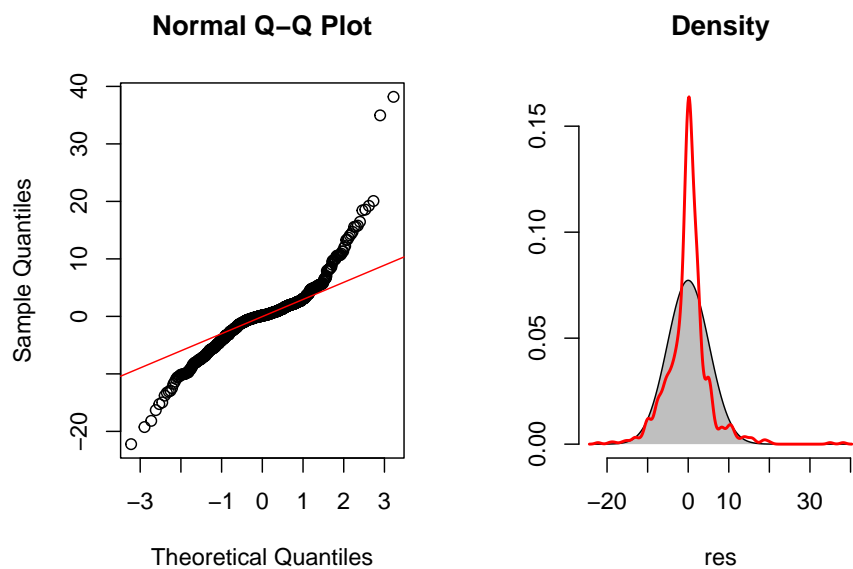
```
AIC(gam0, gamm1, gamm2, gamm3)
```

```
##           df      AIC  
## gam0  17.64724 5289.443  
## gamm1 27.86427 5084.019  
## gamm2 42.97891 4914.160  
## gamm3 85.56720 4452.836
```

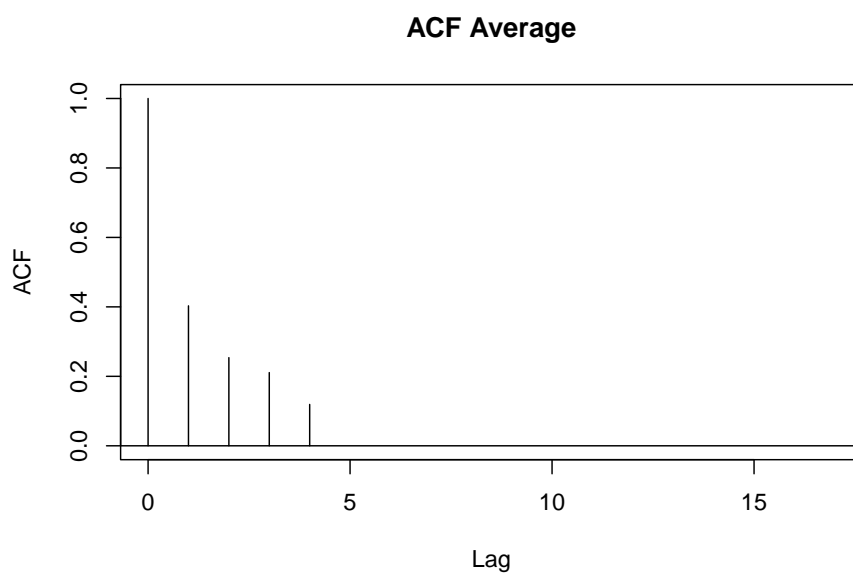
```
summary(gamm2)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## Sources ~ Year + s(SampleDepth) + s(Station, bs = "re") + s(SampleDepth,
##   Station, bs = "re")
##
## Parametric coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)   8.7423     1.4018   6.236 7.49e-10 ***
## Year2002      2.3588     0.8287   2.846 0.00454 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##               edf Ref.df      F p-value
## s(SampleDepth)   8.857  8.992 5.304e+01 <2e-16 ***
## s(Station)       17.250 17.000 3.501e+03 <2e-16 ***
## s(SampleDepth,Station) 14.122 18.000 5.927e+10 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Rank: 47/49
## R-sq.(adj) =  0.796   Deviance explained = 80.6%
## GCV = 29.692   Scale est. = 28.112     n = 789
```

```
layout(matrix(1:2, 1, 2))
check_resid(gamm2, split_pred = "Station", select = 1:2, ask = F)
```



```
layout(1)
acf_resid(gamm2, split_pred = "Station")
```



```
gamtabs(gamm2, type = "HTML")
```

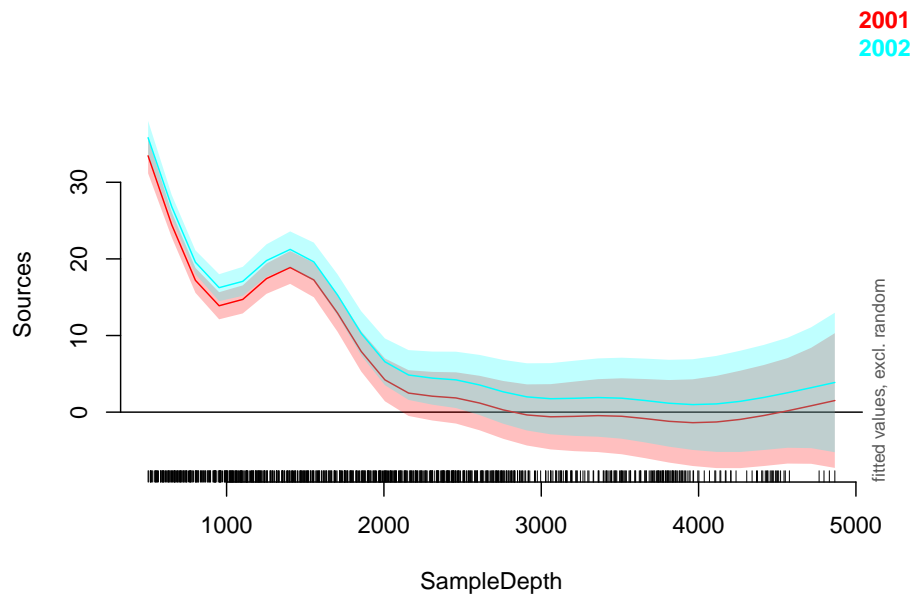
```
## <!-- html table generated in R 4.2.0 by xtable 1.8-4 package -->
## <!-- Thu Apr 28 13:22:27 2022 -->
## <table border=1>
## <caption align="bottom"> </caption>
## <tr> <td> A. parametric coefficients </td> <td align="right"> Estimate </td> <td align="right"> 1.423 </td> <td align="right"> 0.828 </td> </tr>
## <tr> <td> (Intercept) </td> <td align="right"> 8.7423 </td> <td align="right"> 1.423 </td> <td align="right"> 0.828 </td> </tr>
## <tr> <td> Year2002 </td> <td align="right"> 2.3588 </td> <td align="right"> 0.828 </td> <td align="right"> 0.828 </td> </tr>
## <tr> <td> B. smooth terms </td> <td align="right"> edf </td> <td align="right"> 17.2500 </td> <td align="right"> 14.1217 </td> </tr>
## <tr> <td> s(SampleDepth) </td> <td align="right"> 8.8572 </td> <td align="right"> 17.2500 </td> <td align="right"> 14.1217 </td> </tr>
## <tr> <td> s(Station) </td> <td align="right"> 17.2500 </td> <td align="right"> 17.2500 </td> <td align="right"> 14.1217 </td> </tr>
## <tr> <td> s(SampleDepth,Station) </td> <td align="right"> 14.1217 </td> <td align="right"> 14.1217 </td> <td align="right"> 14.1217 </td> </tr>
## <a name=tab.gam></a>
## </table>
```

## Gráficos

```
# Efectos fijos
plot_smooth(gamm2, view = "SampleDepth", plot_all = "Year", rm.ranef = TRUE)
```

```
## Summary:
## * Year : factor; set to the value(s): 2001, 2002.
## * SampleDepth : numeric predictor; with 30 values ranging from 501.000000 to 4866.000000.
## * Station : factor; set to the value(s): 14. (Might be canceled as random effect, c
## * NOTE : The following random effects columns are canceled: s(Station),s(SampleDepth)
##
```





```
plot_parametric(gamm2, pred = list(Year = c("2001", "2002")), rm.ranef = TRUE)
```

```
## Summary:
```

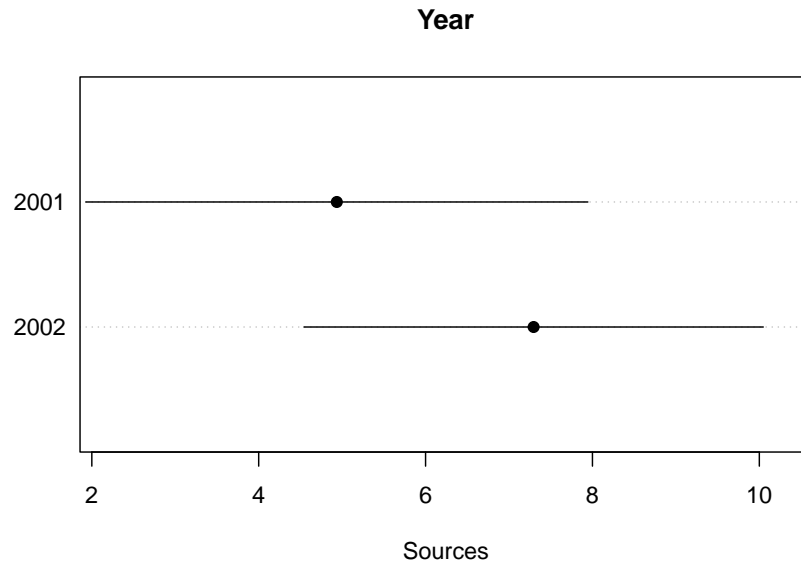
```
## * Year : factor; set to the value(s): 2001, 2002.
```

```
## * SampleDepth : numeric predictor; set to the value(s): 1969.5.
```

```
## * Station : factor; set to the value(s): 14. (Might be canceled as random effect, check below)
```

```
## * NOTE : The following random effects columns are canceled: s(Station),s(SampleDepth,Station)
```

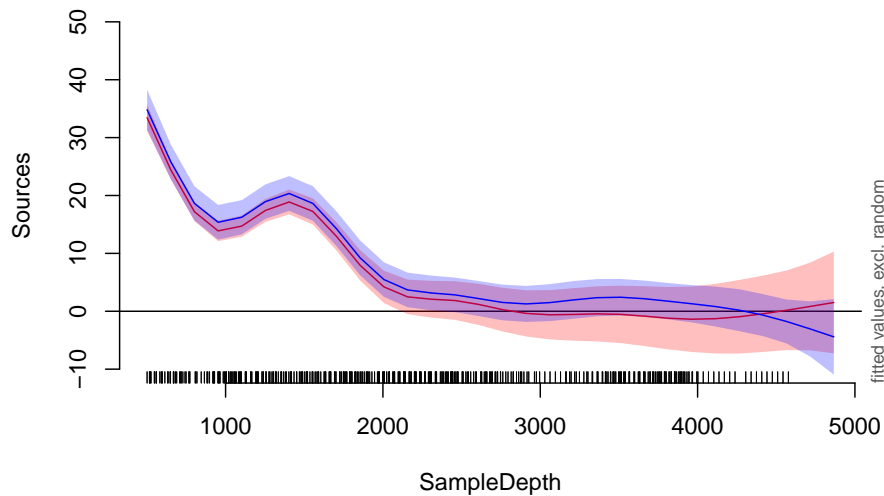
```
##
```



```
# Efectos aleatorios
plot_smooth(gamm2, view = "SampleDepth", cond = list(Year = "2001", Station = "3"), col = "red")
```

```
## Summary:
## * Year : factor; set to the value(s): 2001.
## * SampleDepth : numeric predictor; with 30 values ranging from 501.000000 to 4866.000000.
## * Station : factor; set to the value(s): 3. (Might be canceled as random effect, check model)
## * NOTE : The following random effects columns are canceled: s(Station),s(SampleDepth)
##
```

```
plot_smooth(gamm1, view = "SampleDepth", cond = list(Year = "2001", Station = "16"), col = "red")
```



```
## Summary:
## * Year : factor; set to the value(s): 2001.
## * SampleDepth : numeric predictor; with 30 values ranging from 501.000000 to 4866.000000.
## * Station : factor; set to the value(s): 16. (Might be canceled as random effect, check below)
## * NOTE : The following random effects columns are canceled: s(Station)
##
```

## Autocorrelación temporal

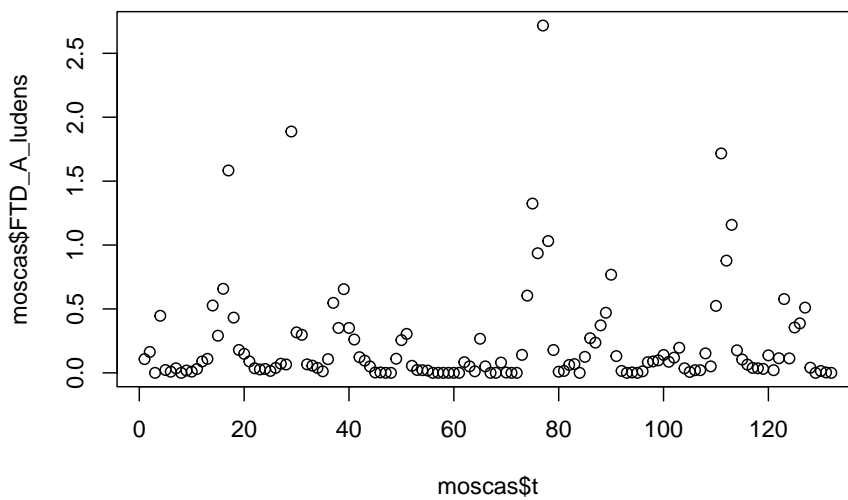
Aluja et al. (2012) estudiaron los factores que determinan la dinámica poblacional de especies de moscas de la fruta (Tephritidae) durante 11 años en Veracruz, México (Aluja\_et\_al\_Tephritidae.txt). Las variables utilizadas son el (log) número de capturas diarias (FTD) y el sesgo sexual de captura (SBC) de distintas especies del género *Anastrepha* y los índices de oscilación del Atlántico Norte (NAOI) y Sur (SOI).

```
library(visreg)
moscas <- read.table("Aluja_et_al_Tephritidae.txt", header = TRUE)
str(moscas)
```

```
## 'data.frame':   132 obs. of  13 variables:
## $ Date          : chr  "January_1994" "February_1994" "March_1994" "April_1994" ...
## $ FTD_A_ludens   : num  0.1075 0.1637 0 0.4464 0.0222 ...
```

```
## $ SBC_A_ludens      : num  0.554 0.377 NA 0.563 0.225 0.25 0.448 NA 0.25 0.333 ...
## $ FTD_A_obliqua    : num  0.067 0.0692 0.1304 0.1406 1.0201 ...
## $ SBC_A_obliqua    : num  0.688 0.639 0.417 0.328 0.273 0.358 0.334 0.556 1 NA ...
## $ FTD_A_serpentina: num  0.0022 0.0201 0.25 0.9643 2.971 ...
## $ SBC_A_serpentina: num  1 0.048 0.269 0.267 0.285 0.333 0.503 0.45 NA NA ...
## $ AP.MZ            : num  69 125.4 21.2 73.5 70.8 ...
## $ MAT.MZ           : num  15.3 17.4 18.4 22 24.7 ...
## $ AP.JC            : num  173.3 4.2 8.6 43 112.5 ...
## $ MAT.JC           : num  15.1 17.1 17.6 20.8 22.8 ...
## $ SOI              : num  -0.5 -0.1 -2.2 -2.9 -1.7 -1.5 -2.9 -3 -3 -2.6 ...
## $ NAOI             : num  1 0.5 1.3 1.1 -0.6 1.5 1.3 0.4 -1.3 -1 ...
```

```
moscas$t <- 1:nrow(moscas)
plot(moscas$t, moscas$FTD_A_ludens)
```

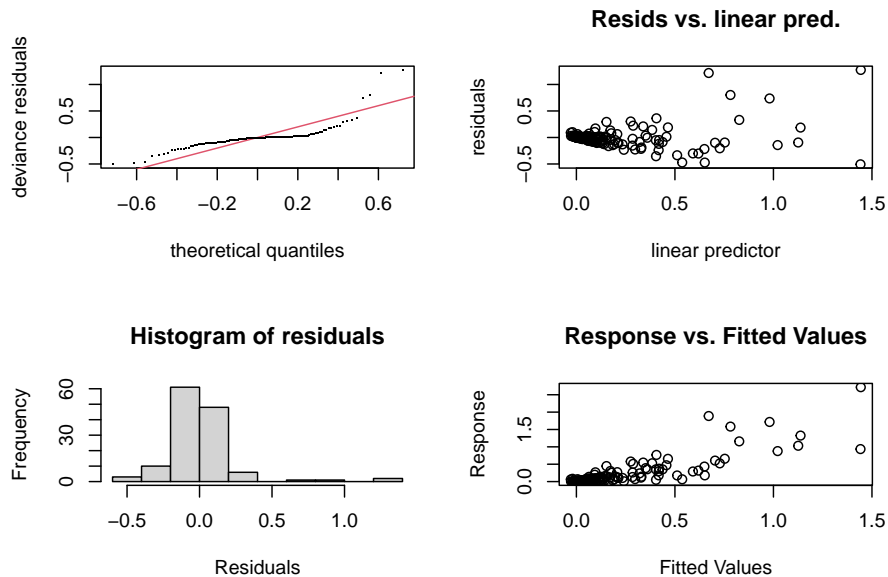


```
gam1 <- gam(FTD_A_ludens ~ s(t, k = 60), family = gaussian, data = moscas)
summary(gam1)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## FTD_A_ludens ~ s(t, k = 60)
```

```
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.22251    0.02345   9.488 2.41e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##             edf Ref.df    F p-value
## s(t) 37.69  45.25 3.938 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.556   Deviance explained = 68.4%
## GCV = 0.1027   Scale est. = 0.072604   n = 132
```

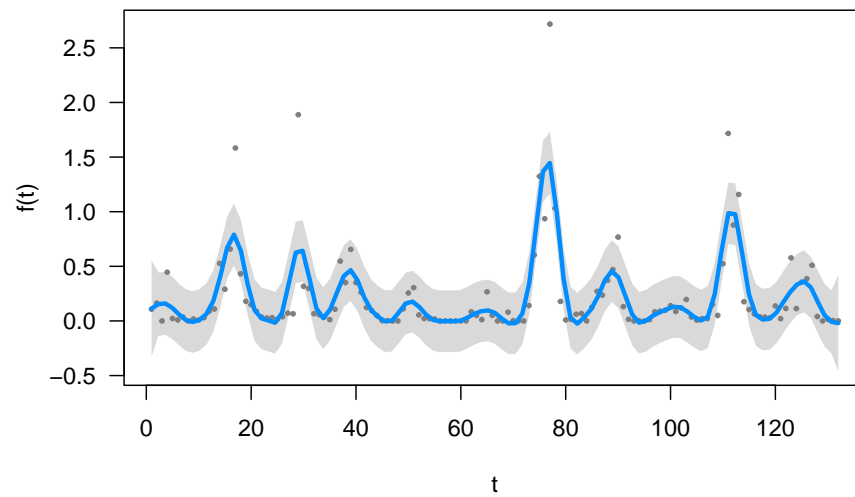
```
gam.check(gam1)
```



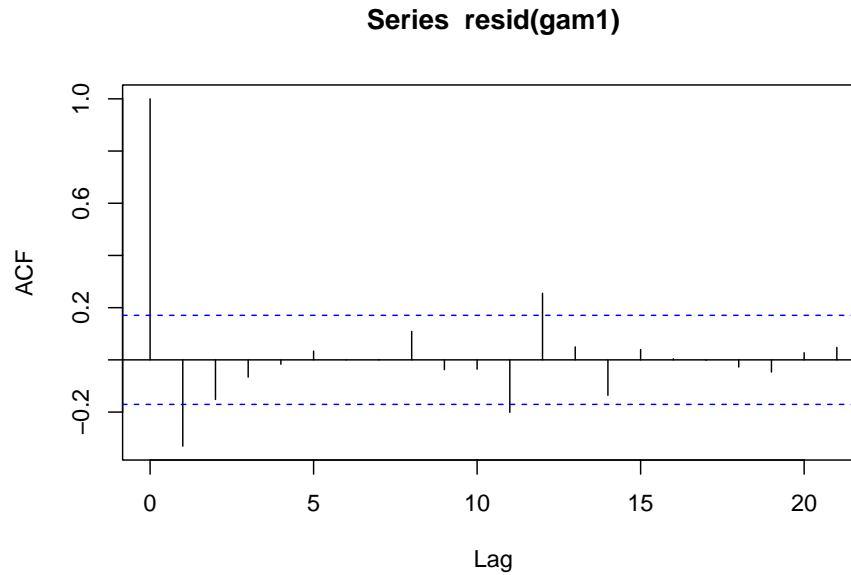
```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 5 iterations.
## The RMS GCV score gradient at convergence was 4.207139e-08 .
## The Hessian was positive definite.
## Model rank = 60 / 60
```

```
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##          k'  edf k-index p-value
## s(t) 59.0 37.7   1.34     1
```

```
visreg(fit = gam1, xvar = "t")
```



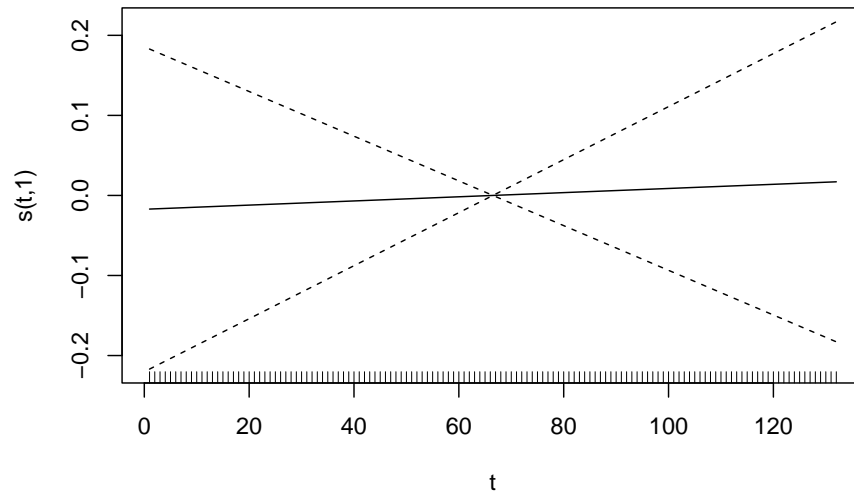
```
acf(resid(gam1))
```



```
gamm.ar1 <- gamm(FTD_A_ludens ~ s(t, k = 60), family = gaussian, correlation = corAR1(form = ~ t))
summary(gamm.ar1$gam)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## FTD_A_ludens ~ s(t, k = 60)
##
## Parametric coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.22017    0.05896   3.734 0.000281 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##      edf Ref.df      F p-value
## s(t)   1      1 0.029  0.865
##
## R-sq.(adj) = -0.00687
##  Scale est. = 0.16172  n = 132
```

```
plot(gamm.ar1$gam)
```



```
AIC(gam1, gamm.ar1$lme)
```

```
##              df      AIC
## gam1         39.68512  61.98908
## gamm.ar1$lme  5.00000 109.58570
```

## Actividades

### Ejercicio 5.1

Las siguientes variables corresponden a de datos de actividad fotosintética bajo dos concentraciones de nutrientes aplicados a las mismas 10 plantas (la planta 1 se encuentra primera en ambos vectores, la planta 2 se encuentra segunda y así sucesivamente):

```
fotosint_N1 <- c(1.42, 1.4, 1.44, 1.44, 1.42, 1.46, 1.49, 1.5, 1.42, 1.48) foto-
sint_N2 <- c(1.38, 1.36, 1.47, 1.39, 1.43, 1.41, 1.43, 1.45, 1.36, 1.46)
```

- En base al diseño experimental, identifique posibles efectos fijos y aleatorios. Justifique.



- Considere un modelo adecuado para relacionar el efecto de los tratamientos sobre la actividad fotosintética.
- Realice un gráfico que muestre los efectos aleatorios, e interprete la varianza del efecto aleatorio y la residual.
- Utilice un test de  $t$  pareado para analizar este conjunto de datos. Compare los parámetros de los efectos fijos estimados de ambos análisis ¿Qué puede concluir?
- Grafique los individuos vs la tasa fotosintética y distinga cada tratamiento con un color diferente. Conceptualmente y teniendo en cuenta este gráfico, así como el de efectos aleatorios ¿Qué piensa que pasaría si ajustara un modelo mixto de intercepto y pendiente aleatorios a este conjunto de datos? Compruebelo.

### Ejercicio 5.2

Palacio et al. (2014) realizaron conteos de 44 especies de aves a lo largo de un año en 10 puntos de muestreos (`id`) localizados en un bosque de ligustro y arbustales circundantes (`habitat.type`). El set de datos corresponde a `abundancia_aves.txt`.

- Analice los factores que se relacionan con la abundancia total de individuos y con las siguientes dos especies: Tordo músico (`agebad`) y Benteveo (`pitsul`).
- Identifique los efectos fijos y aleatorios incluidos en cada modelo.
- Según el problema de estudio y el modelo especificado ¿A qué tipo de diseño corresponde?
- En base a los resultados obtenidos ¿Tiene sentido incluir efectos aleatorios? Justifique.
- ¿Puede hipotetizar algo sobre la distribuciones de probabilidad utilizada para cada especie y para la abundancia total?

### Ejercicio 5.3

La base de datos `ChickWeight` (paquete `datasets`) contiene información sobre el peso (`weight`) de un grupo de pollos (`Chick`) versus el tiempo (`Time`) bajo diferentes dietas (`Diet`).

- Grafique la relación peso vs tiempo para cada individuo y dieta.

- Considere un modelo adecuado en base a la exploración de datos realizada para relacionar el crecimiento bajo distintas dietas.
- Muestre uno o más gráficos que represente el modelo ajustado.

### Ejercicio 5.4

Johnson & Manoukis (2021) analizaron la relación entre el número de capturas de la Broca del Café (*Hypothenemus hampei*, Curculionidae) y distintas variables climáticas en cafetales de Hawai (<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0257861>). El archivo corresponde a `Weather_CBB_flight.xls`. Los metadatos están en el archivo `README_JohnsonManoukisPLOSONE2021.xls`.

- Ajuste un modelo que relacione el número de capturas con variables climáticas. Para esto, construya un modelo saturado y compare primero diferentes estructuras de efectos aleatorios. Luego, realice una selección de modelos considerando diferentes efectos fijos.

### Ejercicio 5.5

Price et al. (2015) realizaron conteos de salamandras (`count`) en cursos de agua en 23 sitios (`site`) muestreados 4 veces cada uno (`sample`). En cada curso tomaron las siguientes variables (estandarizadas): minería (`mined`), cobertura (`cover`), días desde la última precipitación (`DOP`), temperatura del agua (`Wtemp`) y día del año (`DOY`).

La base de datos está disponible en el objeto `Salamander` del paquete `glmmTMB`.

- En base a hipótesis biológicas, construya un modelo que explique la abundancia de salamandras en sitios minados y no minados.