

# Gráficos

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17/09/2020

## Script para desenhar gráficos no R

Códigos de R usados no post “Qual gráfico devo fazer?”

Blog: Sobrevivendo na Ciência

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Publicado em 17 de setembro de 2020 (versão em português).

Rodado no R version 4.0.2 (2020-06-22) “Taking Off Again”

## Fonte dos dados

Neste tutorial usei como exemplo os dados de:

Gonçalves, Fernando, Ricardo S. Bovendorp, Gabrielle Beca, Carolina Bello, Raul Costa-Pereira, Renata L. Muylaert, Raissa R. Rodarte, et al. 2018. “ATLANTIC MAMMAL TRAITS: A Data Set of Morphological Traits of Mammals in the Atlantic Forest of South America.” *Ecology* 99 (2): 498–498.

## Aviso

Você pode usar este script livremente para fins não comerciais por seu próprio risco. Não assumimos nenhuma responsabilidade pelo uso deste software, não transmitimos licença ou título sob nenhuma patente, direito autoral ou mascaramento de direito de trabalho sobre o produto. Reservamo-nos o direito de fazer alterações no software sem notificação. Também não declaramos ou garantimos que esse aplicativo seja adequado para o uso especificado sem testes ou modificações adicionais. Se esse script o ajudar a produzir algum trabalho acadêmico (artigo, livro, capítulo, dissertação etc.), por favor, reconheça os autores e cite a fonte.

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## 1. Prepare o ambiente de trabalho

Defina o diretório de trabalho como sendo o mesmo onde estão este tutorial e os dados:

```
setwd(dirname(rstudioapi::getActiveDocumentContext())$path))
```

Remova todos os objetos da memória:

```
rm(list= ls())
```

## 2. Prepare os dados

Importe os dados para o R:

```
dados <- read.delim("dados.txt", sep = "\t", header = T, na = "NA")
```

Inspecione os dados para ver se estão ok:

```
head(dados)
```

```
##   ID_register ID_sp Group      order      family      genus
## 1      8970    26  Bats Chiroptera Phyllostomidae Carollia
## 2      8971    26  Bats Chiroptera Phyllostomidae Carollia
## 3      8972    26  Bats Chiroptera Phyllostomidae Carollia
## 4      8973    26  Bats Chiroptera Phyllostomidae Carollia
## 5      8974    26  Bats Chiroptera Phyllostomidae Carollia
## 6      8975    26  Bats Chiroptera Phyllostomidae Carollia
##               binomial body_mass body_length tail_length forearm  age  sex
## 1 Carollia perspicillata      15         NA         NA      40.0 adult female
## 2 Carollia perspicillata      15         NA         NA      40.0 adult female
## 3 Carollia perspicillata      17         NA         NA      41.0 adult  male
## 4 Carollia perspicillata      15         NA         NA      41.0 adult  male
## 5 Carollia perspicillata      13         NA         NA      41.0 adult female
## 6 Carollia perspicillata      18         NA         NA      41.5 adult female
## reproductive_stage status longitude latitude year collector_name
## 1                <NA>   alive -42.26196 -22.5838 1997      Marco Mello
## 2                <NA>   alive -42.26196 -22.5838 1997      Marco Mello
## 3                <NA>   alive -42.26196 -22.5838 1997      Marco Mello
## 4                <NA>   alive -42.26196 -22.5838 1997      Marco Mello
## 5                <NA>   alive -42.26196 -22.5838 1997      Marco Mello
## 6                <NA>   alive -42.26196 -22.5838 1997      Marco Mello
```

```
summary(dados)
```

```
## ID_register      ID_sp      Group      order
## Min. : 8970      Min. :26      Length:2353      Length:2353
## 1st Qu.: 9558      1st Qu.:26      Class :character  Class :character
## Median :10146      Median :26      Mode  :character  Mode  :character
## Mean :10152      Mean :26
## 3rd Qu.:10734      3rd Qu.:26
## Max. :11452      Max. :26
##
## family          genus          binomial          body_mass
## Length:2353      Length:2353      Length:2353      Min. : 6.0
## Class :character  Class :character  Class :character  1st Qu.:15.0
## Mode :character  Mode :character  Mode :character  Median :16.0
##                                     Mean :15.8
##                                     3rd Qu.:17.0
##                                     Max. :60.0
##
## body_length      tail_length      forearm      age
## Mode:logical      Mode:logical      Min. :34.07      Length:2353
## NA's:2353          NA's:2353          1st Qu.:39.08      Class :character
##                                     Median :39.90      Mode :character
##                                     Mean :39.86
##                                     3rd Qu.:40.60
##                                     Max. :45.65
##                                     NA's :339
##
## sex              reproductive_stage      status      longitude
## Length:2353      Length:2353      Length:2353      Min. : -44.86
## Class :character  Class :character  Class :character  1st Qu.: -42.26
## Mode :character  Mode :character  Mode :character  Median : -42.26
##                                     Mean : -42.31
##                                     3rd Qu.: -42.26
##                                     Max. : -42.04
##
## latitude          year      collector_name
## Min. : -23.36      Min. :1997      Length:2353
## 1st Qu.: -22.58      1st Qu.:1998      Class :character
## Median : -22.58      Median :1999      Mode :character
## Mean : -22.46      Mean :2000
## 3rd Qu.: -22.58      3rd Qu.:2000
## Max. : -19.35      Max. :2016
##
```

```
summary(dados$body_mass)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      6.0   15.0   16.0   15.8   17.0   60.0
```

Fique apenas com os dados dos morcegos abaixo de 30 g de massa corporal, como comentado no post do blog:

```
dados2 <- subset(dados, dados$body_mass < 30)
```

### 3. Histograma

Vamos começar plotando um histograma.

Primeiro, faça um resumo dos dados :

```
summary(dados2$body_mass)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      6.00  15.00   16.00   15.76   17.00   27.00
```

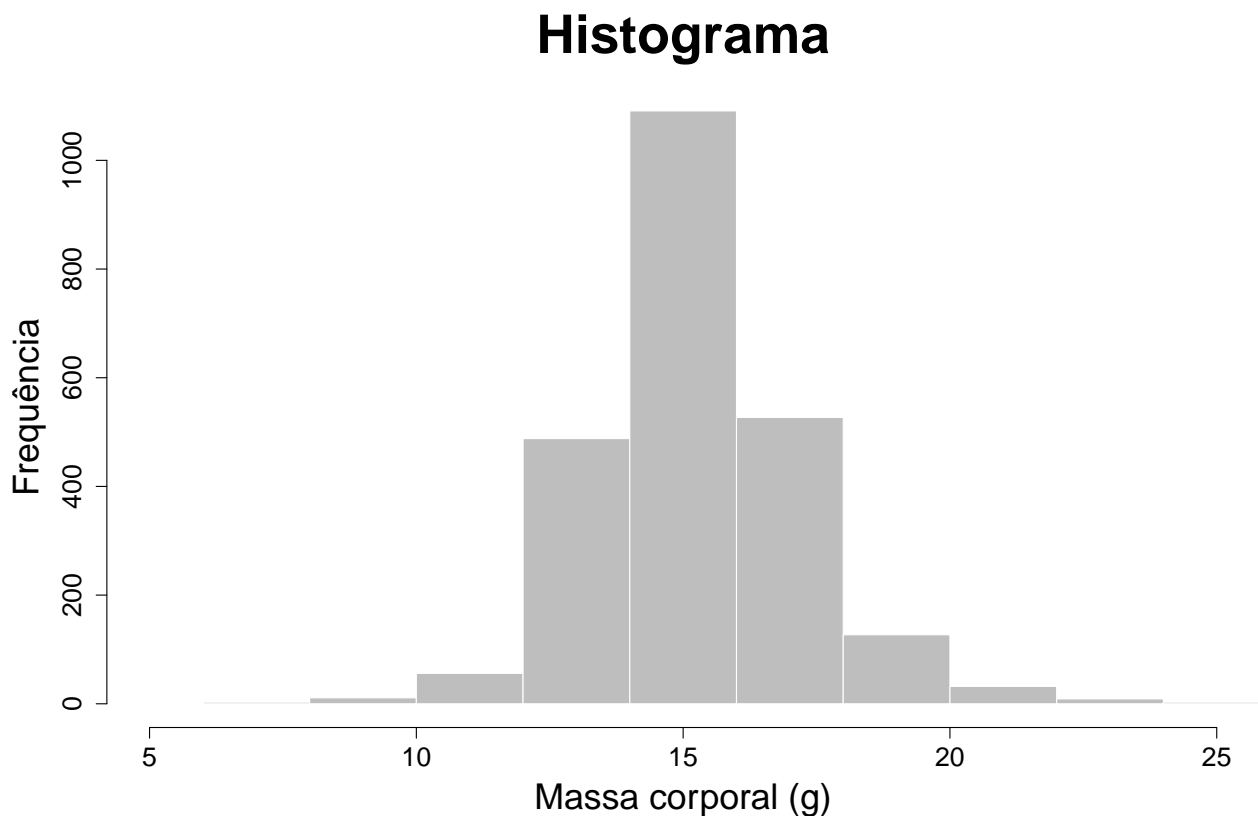
Confira o total de casos, excluindo os dados faltantes:

```
length(dados2$body_mass)-(sum(is.na(dados2$body_mass)))
```

```
## [1] 2350
```

Plote o gráfico:

```
par(mfrow=c(1,1),mar=c(5,5,5,1), bg = "white")
hist(dados2$body_mass,
     main = "Histograma",
     xlab = "Massa corporal (g)",
     ylab = "Frequência",
     col = "grey", border = "white",
     xlim=c(5,25), cex.axis = 1.5, cex.lab = 2, cex.main = 3)
```



```
par(mfrow=c(1,1))
```

## 4. Barras

Agora plote o diagrama de barras.

Primeiro, extraia os dados de sexo:

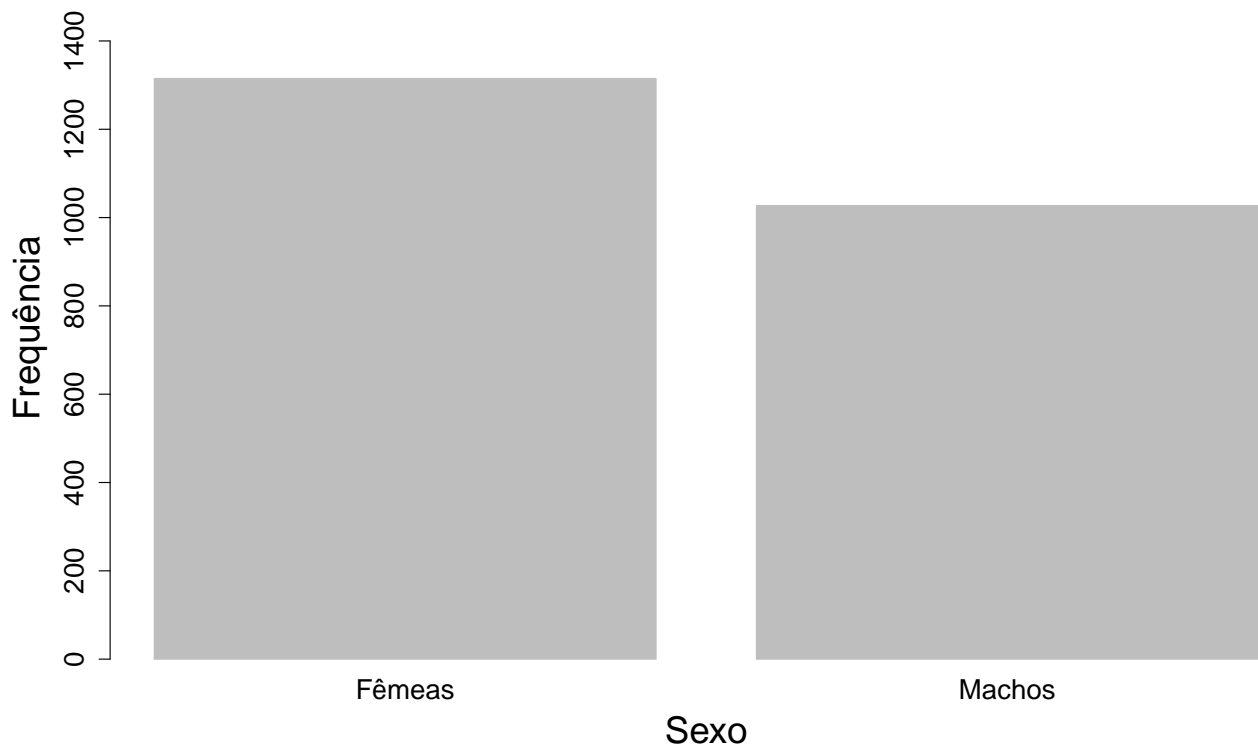
```
sexo <- table(dados2$sex)
sexo
```

```
##
## female    male
##    1315    1027
```

Plote o gráfico:

```
par(mfrow=c(1,1),mar=c(5,5,5,1), bg = "white")
barplot(sexo,
        main = "Diagrama de barras",
        xlab = "Sexo", names=c("Fêmeas","Machos"),
        ylab = "Frequência",
        col = "grey", border = "grey",
        cex = 1.5, cex.axis = 1.5, cex.lab = 2, cex.main = 3, cex.sub = 1,
        ylim=c(0,1500))
```

## Diagrama de barras



```
par(mfrow=c(1,1))
```

## 5. Barras agrupadas

Primeiro, extraia os dados de idade:

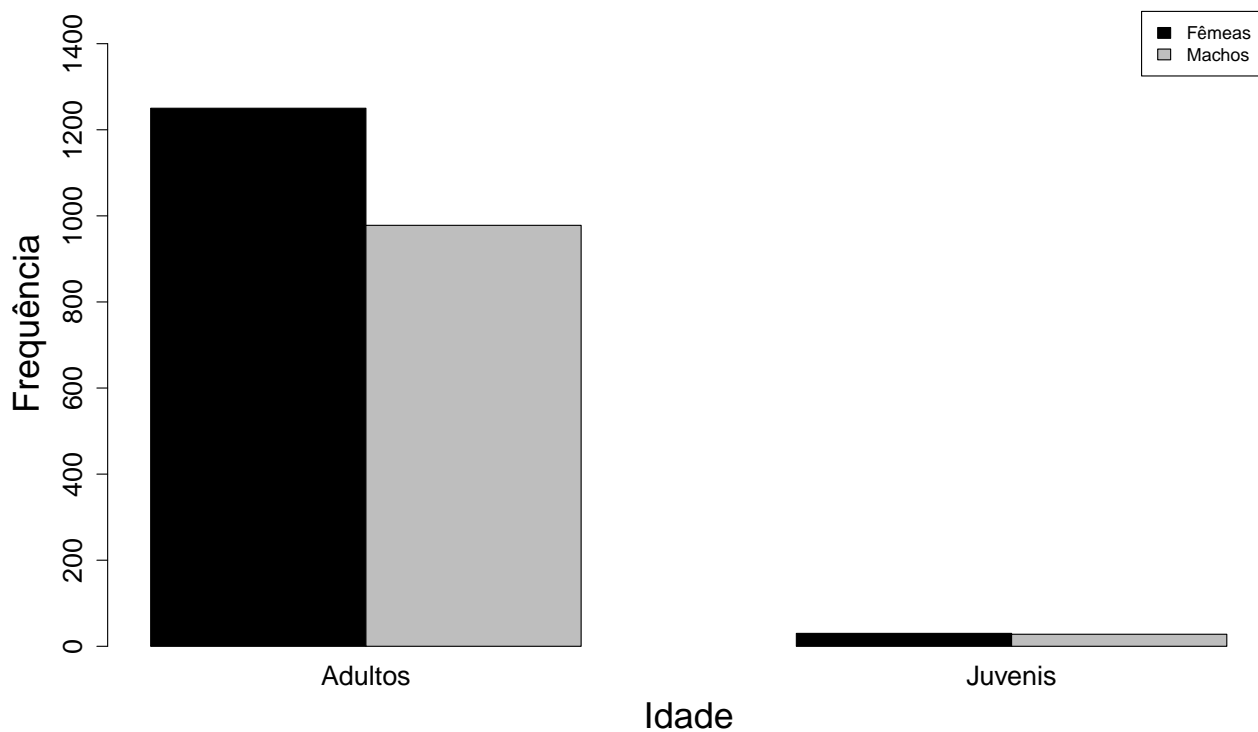
```
idade <- table(dados2$sex, dados2$age)
idade
```

```
##
##      adult juvenile
## female 1250      30
##  male   978      28
```

Plote o gráfico:

```
par(mfrow=c(1,1),mar=c(5,5,5,1), bg = "white")
barplot(idade,
        beside = T,
        main="Diagrama de barras agrupadas",
        xlab="Idade",
        ylab = "Frequência",
        col=c("black","grey"),
        names=c("Adultos","Juvenis"),
        legend = c("Fêmeas", "Machos"),
        cex = 1.5, cex.axis = 1.5, cex.lab = 2, cex.main = 3, cex.sub = 1,
        ylim=c(0,1500))
```

## Diagrama de barras agrupadas



```
par(mfrow=c(1,1))
```

## 6. Barras empilhadas

Primeiro, extraia os dados de idade:

```
idade2 <- table(dados2$sex, dados2$age)
idade2
```

```
##
##      adult juvenile
## female  1250       30
## male    978       28
```

Depois, converta os dados em porcentagens:

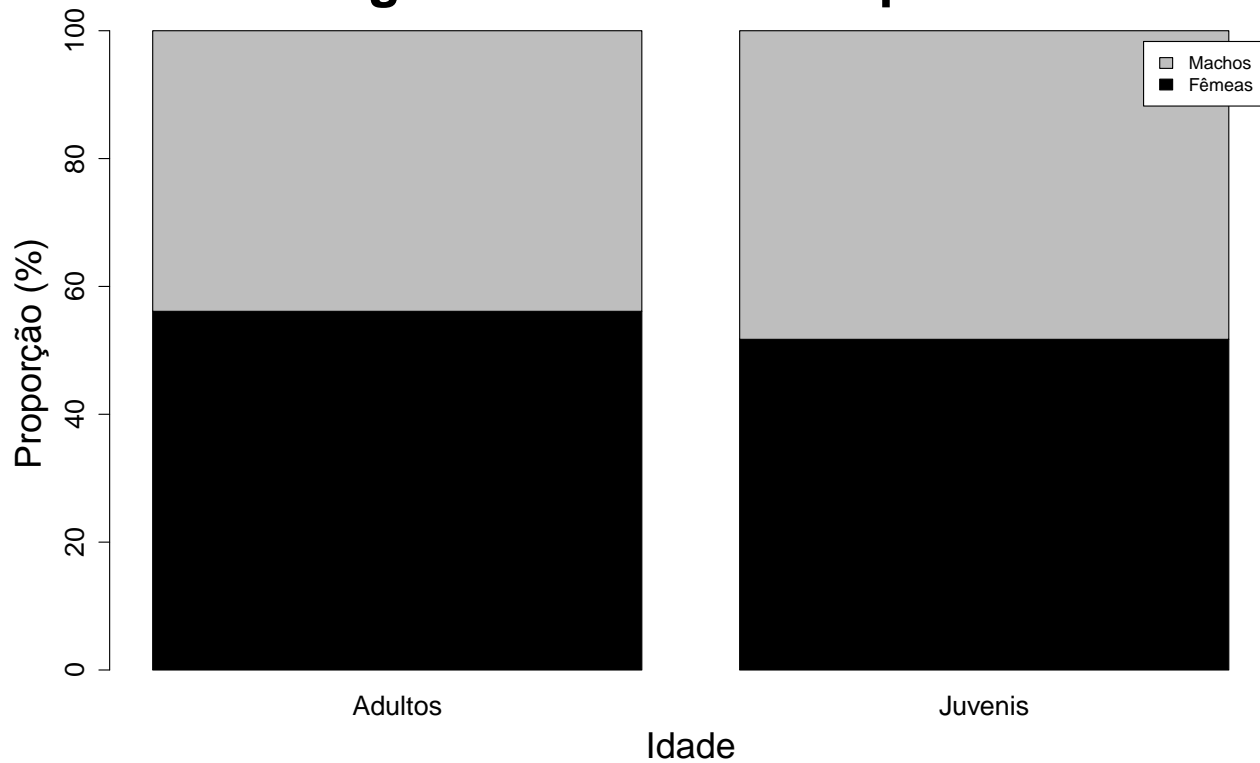
```
idade3 <- apply(idade2, 2, function(x){x*100/sum(x,na.rm=T)})
idade3
```

```
##
##      adult juvenile
## female 56.10413 51.72414
## male   43.89587 48.27586
```

Plote o gráfico:

```
par(mfrow=c(1,1),mar=c(5,5,5,1), bg = "white")
barplot(idade3,
        beside = F,
        main="Diagrama de barras empilhadas",
        xlab="Idade",
        ylab = "Proporção (%)",
        col=c("black","grey"),
        names=c("Adultos","Juvenis"),
        legend = c("Fêmeas", "Machos"),
        cex = 1.5, cex.axis = 1.5, cex.lab = 2, cex.main = 3, cex.sub = 1)
```

## Diagrama de barras empilhadas



```
par(mfrow=c(1,1))
```

## 7. Pizza

Use os dados de sexo que extraiu anteriormente:

```
sexo
```

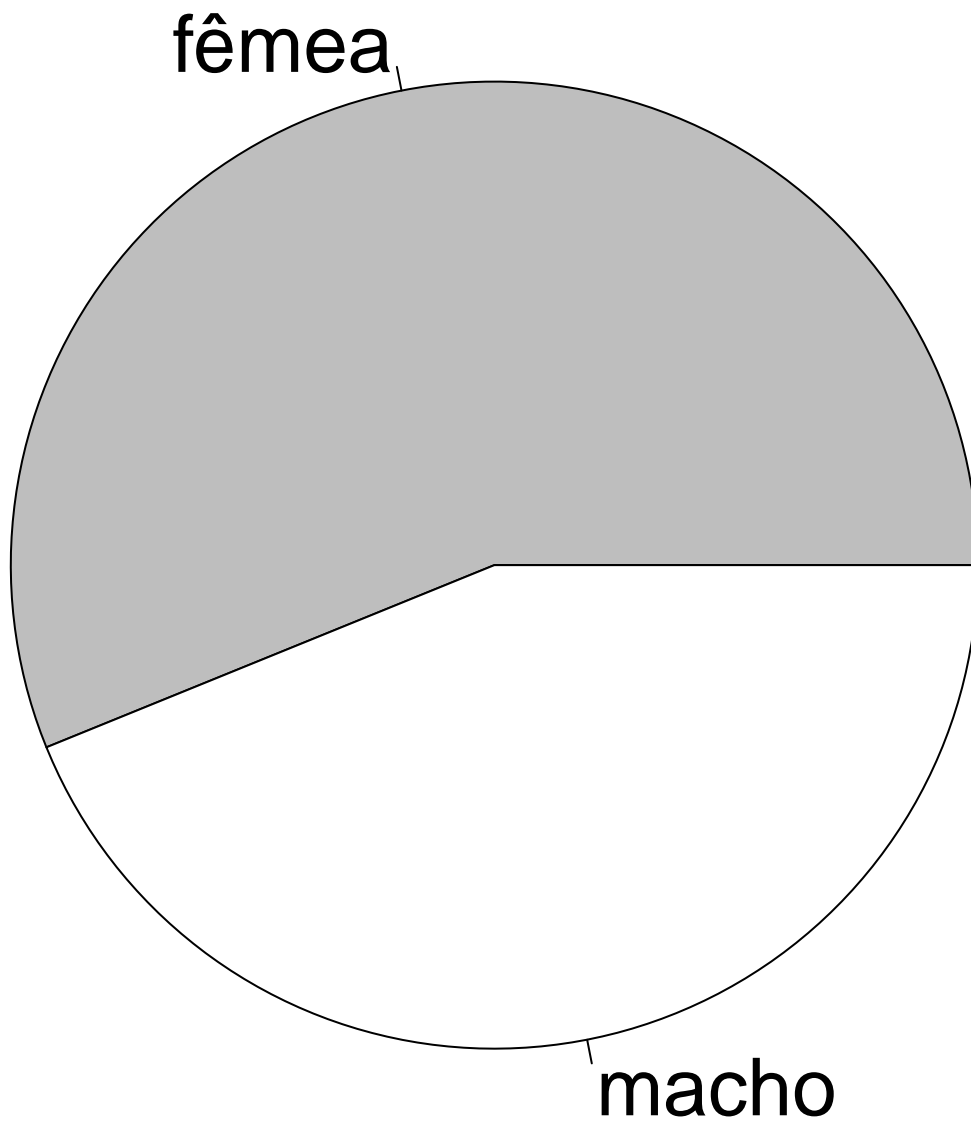
```
##  
## female    male  
##   1315    1027
```

Plote o gráfico:

```
par(mfrow=c(1,1),mar=c(1,1,5,1), bg = "white")  
pie(sexo,  
    main = "Diagrama de pizza",  
    labels = c("fêmea", "macho"),  
    col = c("grey", "white"),  
    cex = 2.5, cex.axis = 1.5, cex.lab = 2, cex.main = 3, cex.sub = 1)
```



# Diagrama de pizza



```
par(mfrow=c(1,1))
```

## 8. Caixas

Também conhecido como boxplot.

Use os dados de sexo:

```
table(dados2$sex)
```

```
##
## female   male
##    1315   1027
```

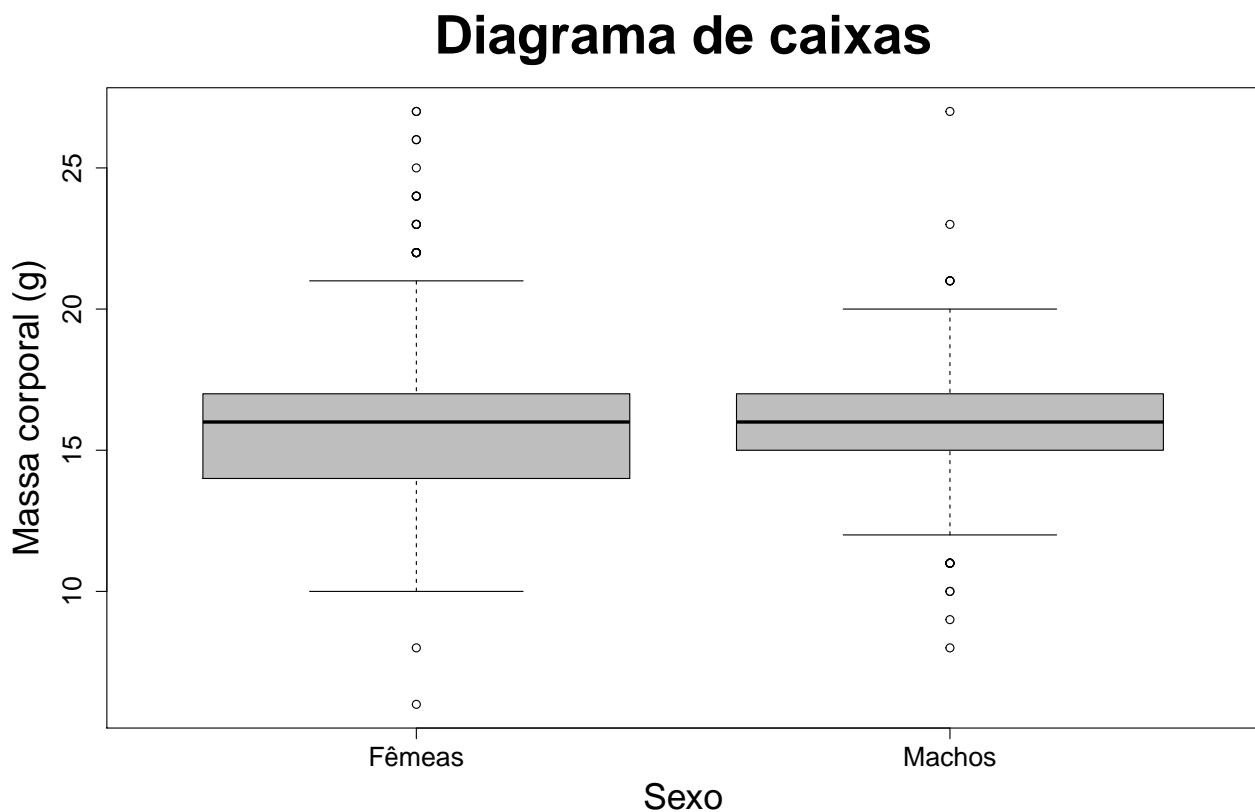
E também os dados de massa corporal:

```
summary(dados2$body_mass)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      6.00  15.00   16.00   15.76  17.00   27.00
```

Plote o gráfico:

```
par(mfrow=c(1,1),mar=c(5,5,5,1), bg = "white")
boxplot(dados2$body_mass~dados2$sex,
        main = "Diagrama de caixas",
        xlab = "Sexo", names=c("Fêmeas","Machos"),
        ylab = "Massa corporal (g)",
        col = "grey", border = "black",
        cex.axis = 1.5, cex.lab = 2, cex.main = 3)
```



```
par(mfrow=c(1,1))
```

## 9. Scatterplot

Também conhecido como diagrama de dispersão.

Use os dados de comprimento do antebraço:

```
summary(dados2$forearm)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.     NA's  
##    34.07  39.08   39.90   39.86  40.60   45.65     339
```

Confira o total de casos, excluindo os dados faltantes:

```
length(dados2$forearm)-(sum(is.na(dados2$forearm)))
```

```
## [1] 2011
```

E também os dados de massa corporal:

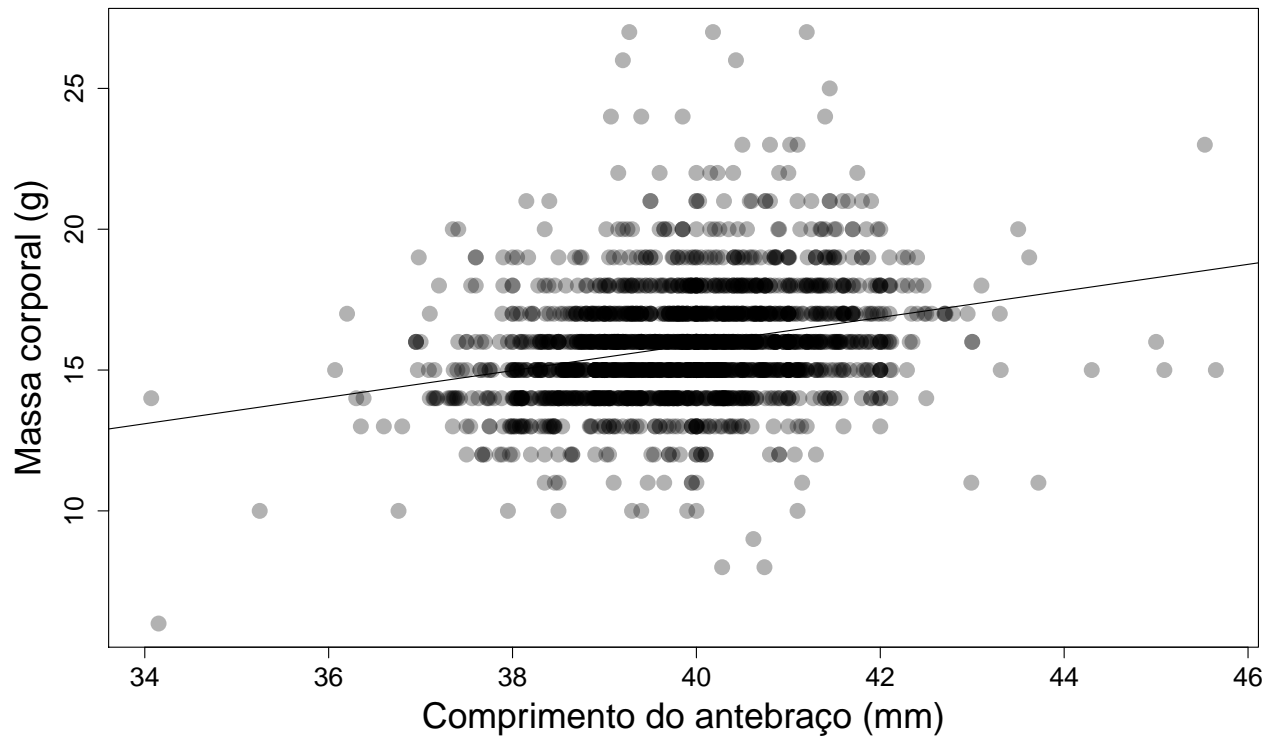
```
summary(dados2$body_mass)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.  
##     6.00  15.00   16.00   15.76  17.00   27.00
```

Plote o gráfico:

```
par(mfrow=c(1,1),mar=c(5,5,5,1), bg = "white")  
plot(dados2$body_mass~dados2$forearm,  
     main = "Diagrama de dispersão",  
     xlab = "Comprimento do antebraço (mm)",  
     ylab = "Massa corporal (g)",  
     pch = 16, col = adjustcolor("black", alpha.f = 0.3),  
     cex.axis = 1.5, cex.lab = 2, cex.main = 3, cex = 2)  
abline(lm(dados2$body_mass~dados2$forearm))
```

## Diagrama de dispersão



```
par(mfrow=c(1,1))
```

### 10. Linha

Primeiro, extraia e inspecione os dados dos anos:

```
anos <- tapply(dados2$body_mass, dados2$year, mean)
anos
```

```
##      1997      1998      1999      2000      2001      2013      2014      2015
## 16.17834 15.95773 15.54389 15.95540 15.52312 13.71429 15.35484 14.57143
##      2016
## 15.47368
```

```
class(anos)
```

```
## [1] "array"
```

Converta o formato dos dados:

```
anos2 <- as.data.frame(anos)
anos2
```

```
##      anos
## 1997 16.17834
```

```
## 1998 15.95773
## 1999 15.54389
## 2000 15.95540
## 2001 15.52312
## 2013 13.71429
## 2014 15.35484
## 2015 14.57143
## 2016 15.47368
```

Renomeie as linhas:

```
anos2$year <- row.names(anos2)
anos2$year
```

```
## [1] "1997" "1998" "1999" "2000" "2001" "2013" "2014" "2015" "2016"
```

Selecione apenas os anos anteriores a 2013:

```
anos3 <- subset(anos2, anos2$year < 2013)
anos3
```

```
##      anos year
## 1997 16.17834 1997
## 1998 15.95773 1998
## 1999 15.54389 1999
## 2000 15.95540 2000
## 2001 15.52312 2001
```

Confira o total de casos, excluindo os dados faltantes:

```
anosN <- subset(dados2, dados2$year < 2013)
head(anosN)
```

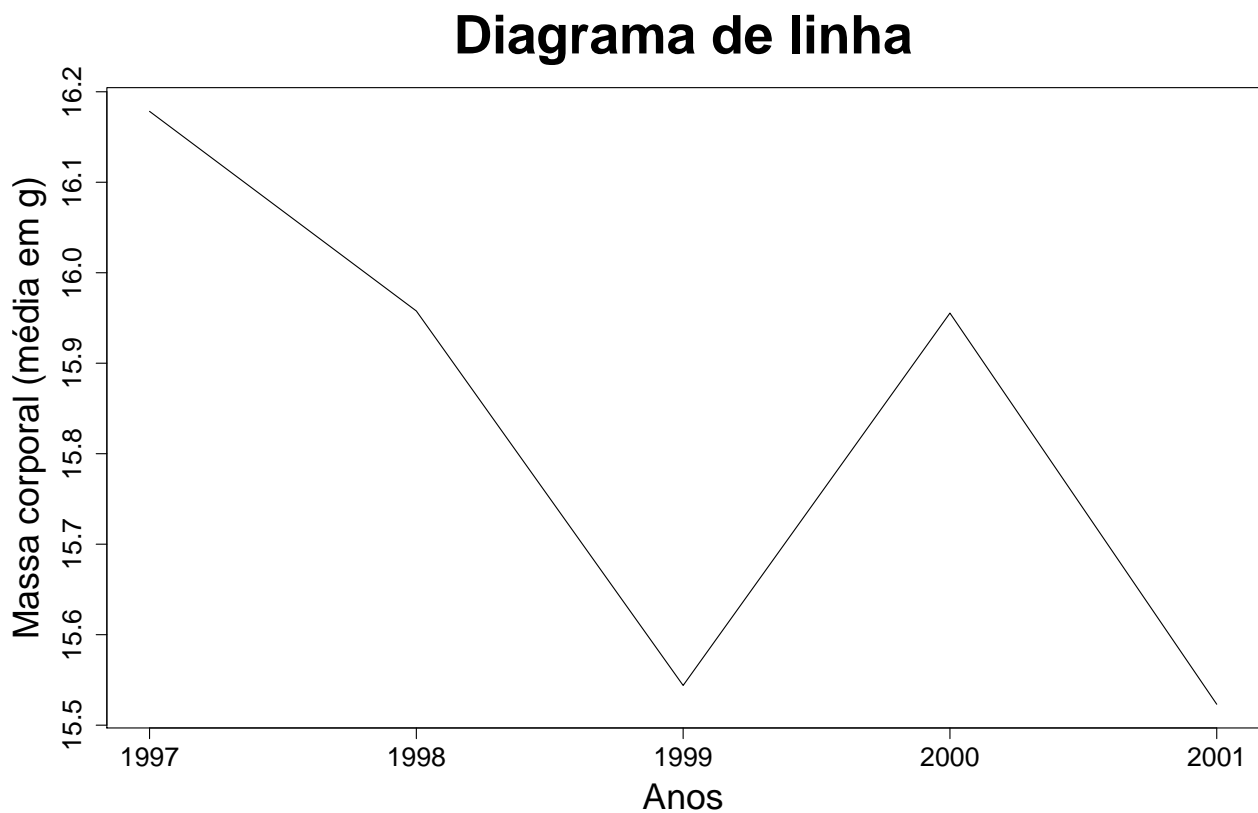
```
##   ID_register ID_sp Group      order      family      genus
## 1      8970    26   Bats Chiroptera Phyllostomidae Carollia
## 2      8971    26   Bats Chiroptera Phyllostomidae Carollia
## 3      8972    26   Bats Chiroptera Phyllostomidae Carollia
## 4      8973    26   Bats Chiroptera Phyllostomidae Carollia
## 5      8974    26   Bats Chiroptera Phyllostomidae Carollia
## 6      8975    26   Bats Chiroptera Phyllostomidae Carollia
##               binomial body_mass body_length tail_length forearm  age  sex
## 1 Carollia perspicillata      15      NA      NA      NA 40.0 adult female
## 2 Carollia perspicillata      15      NA      NA      NA 40.0 adult female
## 3 Carollia perspicillata      17      NA      NA      NA 41.0 adult  male
## 4 Carollia perspicillata      15      NA      NA      NA 41.0 adult  male
## 5 Carollia perspicillata      13      NA      NA      NA 41.0 adult female
## 6 Carollia perspicillata      18      NA      NA      NA 41.5 adult female
## reproductive_stage status longitude latitude year collector_name
## 1      <NA>   alive -42.26196 -22.5838 1997      Marco Mello
## 2      <NA>   alive -42.26196 -22.5838 1997      Marco Mello
## 3      <NA>   alive -42.26196 -22.5838 1997      Marco Mello
## 4      <NA>   alive -42.26196 -22.5838 1997      Marco Mello
## 5      <NA>   alive -42.26196 -22.5838 1997      Marco Mello
## 6      <NA>   alive -42.26196 -22.5838 1997      Marco Mello
```

```
nrow(anosN)
```

```
## [1] 2253
```

Plote o gráfico:

```
par(mfrow=c(1,1),mar=c(5,5,5,1), bg = "white")
plot(anos3$anos ~ anos3$year, type = "l",
     main = "Diagrama de linha",
     xlab = "Anos",
     ylab = "Massa corporal (média em g)",
     cex.axis = 1.5, cex.lab = 2, cex.main = 3, cex = 2)
```



```
par(mfrow=c(1,1))
```

## 11. Pareado

Para fazer este gráfico você precisará do pacote ggplot2:

```
library(ggplot2)
```

Resuma os dados de massa corporal por ano:

```

massa <- tapply(dados2$body_mass, dados2$year, mean)
massa

```

```

##      1997      1998      1999      2000      2001      2013      2014      2015
## 16.17834 15.95773 15.54389 15.95540 15.52312 13.71429 15.35484 14.57143
##      2016
## 15.47368

```

Resuma os dados por sexo e ano:

```

massa2 <- aggregate(x=dados2$body_mass,
                     by=list(dados2$year,dados2$sex),
                     FUN=mean)
colnames(massa2) <- c("ano", "sexo", "massa")
head(massa2)

```

```

##   ano  sexo  massa
## 1 1997 female 16.54839
## 2 1998 female 16.05755
## 3 1999 female 15.53776
## 4 2000 female 16.04115
## 5 2001 female 15.48387
## 6 2013 female 13.33333

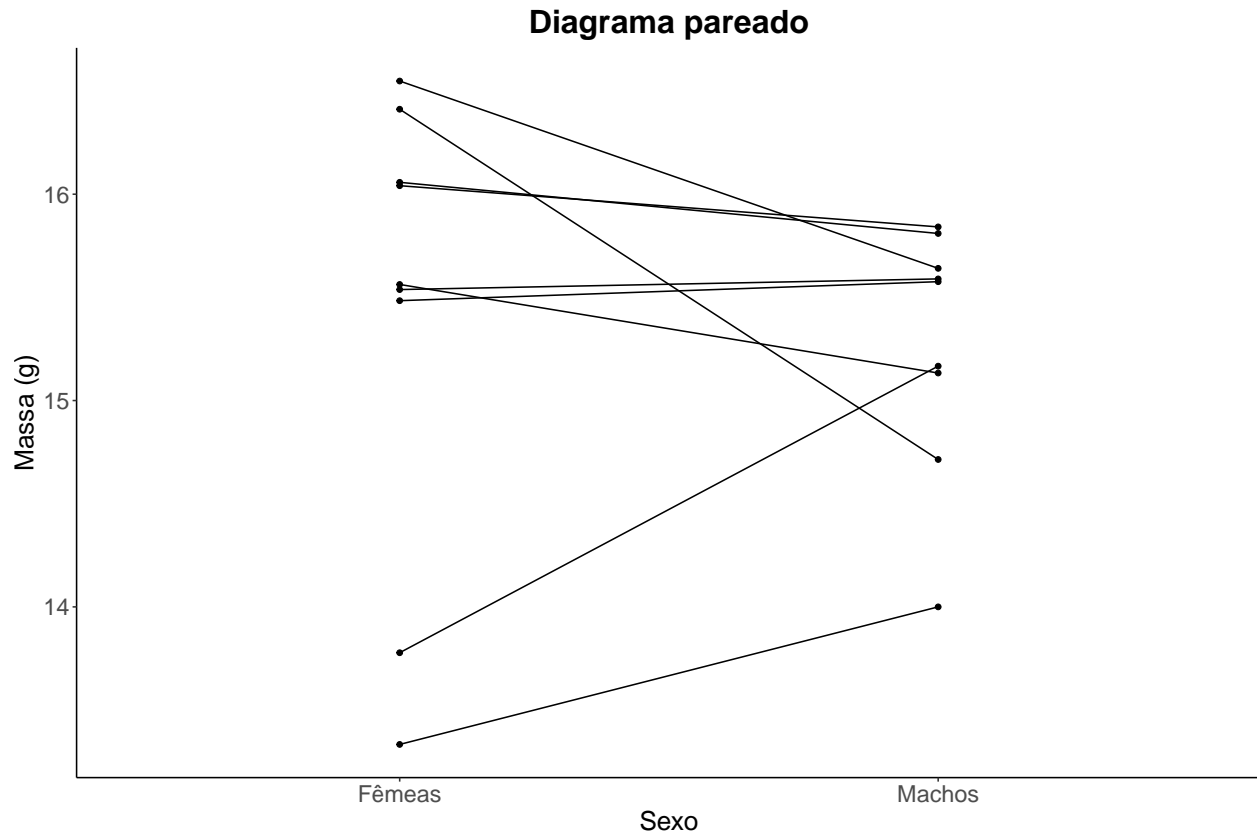
```

Plote o gráfico:

```

p1 <- ggplot(massa2, aes(x = sexo, y = massa)) +
  geom_line(aes(group = ano)) +
  geom_point() +
  ggtitle("Diagrama pareado") +
  xlab("Sexo") + ylab("Massa (g)") +
  theme(panel.background = element_rect(fill = NA),
        axis.line = element_line(size = 0.5, colour = "black"),
        plot.title = element_text(color="black", size=22, face="bold", hjust = 0.5),
        axis.title.x = element_text(color="black", size=18, face="plain"),
        axis.title.y = element_text(color="black", size=18, face="plain"),
        axis.text = element_text(size = 16)) +
  scale_x_discrete(labels = c('Fêmeas', 'Machos'))
p1

```



## 12. Logístico

Para fazer este gráfico você precisará de mais 2 pacotes:

```
library(lme4)
```

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

```
library(reshape2)
```

Separe os dados das fêmeas e inspecione-os:

```
femeas<- read.delim("femeas.txt", header=T)
head(femeas)
```

```
##   ID_register ID_sp Group      order      family      genus
## 1      8970    26   Bats Chiroptera Phyllostomidae Carollia
## 2      8971    26   Bats Chiroptera Phyllostomidae Carollia
## 3      8974    26   Bats Chiroptera Phyllostomidae Carollia
## 4      8975    26   Bats Chiroptera Phyllostomidae Carollia
## 5      8979    26   Bats Chiroptera Phyllostomidae Carollia
## 6      8981    26   Bats Chiroptera Phyllostomidae Carollia
##                                binomial body_mass body_length tail_length forearm  age  sex
## 1 Carollia perspicillata          15          NA          NA         40.0 adult female
```



```
## 2 Carollia perspicillata      15      NA      NA      40.0 adult female
## 3 Carollia perspicillata      13      NA      NA      41.0 adult female
## 4 Carollia perspicillata      18      NA      NA      41.5 adult female
## 5 Carollia perspicillata      14      NA      NA      38.5 adult female
## 6 Carollia perspicillata      15      NA      NA      40.0 adult female
##   reproductive_stage status longitude latitude year collector_name
## 1                <NA>   alive  -42.26196 -22.5838 1997   Marco Mello
## 2                <NA>   alive  -42.26196 -22.5838 1997   Marco Mello
## 3                <NA>   alive  -42.26196 -22.5838 1997   Marco Mello
## 4                <NA>   alive  -42.26196 -22.5838 1997   Marco Mello
## 5                <NA>   alive  -42.26196 -22.5838 1997   Marco Mello
## 6                <NA>   alive  -42.26196 -22.5838 1997   Marco Mello
```

Veja as dimensões dos dados:

```
nrow(femeas)
```

```
## [1] 1318
```

```
ncol(femeas)
```

```
## [1] 19
```

Confira o padrão geral dos dados:

```
summary(femeas$body_mass)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      6.00  14.00   16.00   15.92  17.00   60.00
```

Separe apenas os casos em que as fêmeas tenham massa corporal menor do que 30 g:

```
femeas2 <- subset(femeas, femeas$body_mass < 30)
head(femeas2)
```

```
##   ID_register ID_sp Group      order      family      genus
## 1      8970    26  Bats Chiroptera Phyllostomidae Carollia
## 2      8971    26  Bats Chiroptera Phyllostomidae Carollia
## 3      8974    26  Bats Chiroptera Phyllostomidae Carollia
## 4      8975    26  Bats Chiroptera Phyllostomidae Carollia
## 5      8979    26  Bats Chiroptera Phyllostomidae Carollia
## 6      8981    26  Bats Chiroptera Phyllostomidae Carollia
##               binomial body_mass body_length tail_length forearm  age  sex
## 1 Carollia perspicillata      15      NA      NA      40.0 adult female
## 2 Carollia perspicillata      15      NA      NA      40.0 adult female
## 3 Carollia perspicillata      13      NA      NA      41.0 adult female
## 4 Carollia perspicillata      18      NA      NA      41.5 adult female
## 5 Carollia perspicillata      14      NA      NA      38.5 adult female
## 6 Carollia perspicillata      15      NA      NA      40.0 adult female
##   reproductive_stage status longitude latitude year collector_name
## 1                <NA>   alive  -42.26196 -22.5838 1997   Marco Mello
```

```
## 2          <NA>  alive -42.26196 -22.5838 1997    Marco Mello
## 3          <NA>  alive -42.26196 -22.5838 1997    Marco Mello
## 4          <NA>  alive -42.26196 -22.5838 1997    Marco Mello
## 5          <NA>  alive -42.26196 -22.5838 1997    Marco Mello
## 6          <NA>  alive -42.26196 -22.5838 1997    Marco Mello
```

Presuma que as fêmeas com dados faltantes estavam inativas:

```
femeas2$reproductive_stage[is.na(femeas2$reproductive_stage)] <- "inactive"
```

Transforme os dados reprodutivos em binários:

```
femeas2$reproductive_stage2 <- ifelse(femeas2$reproductive_stage == "pregnant", 1, 0)
```

Calcule um modelo logístico para a relação entre estado reprodutivo e massa corporal:

```
fit1 = glm(femeas2$reproductive_stage2~femeas2$body_mass, family=binomial)
summary(fit1)
```

```
##
## Call:
## glm(formula = femeas2$reproductive_stage2 ~ femeas2$body_mass,
##      family = binomial)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.9843  -0.3209  -0.1772  -0.1202   3.8132
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -15.85761     1.14639  -13.83  <2e-16 ***
## femeas2$body_mass  0.78072     0.06324   12.35  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 732.19  on 1314  degrees of freedom
## Residual deviance: 479.21  on 1313  degrees of freedom
## AIC: 483.21
##
## Number of Fisher Scoring iterations: 6
```

```
res1 = anova(fit1, test="Chisq")
res1
```

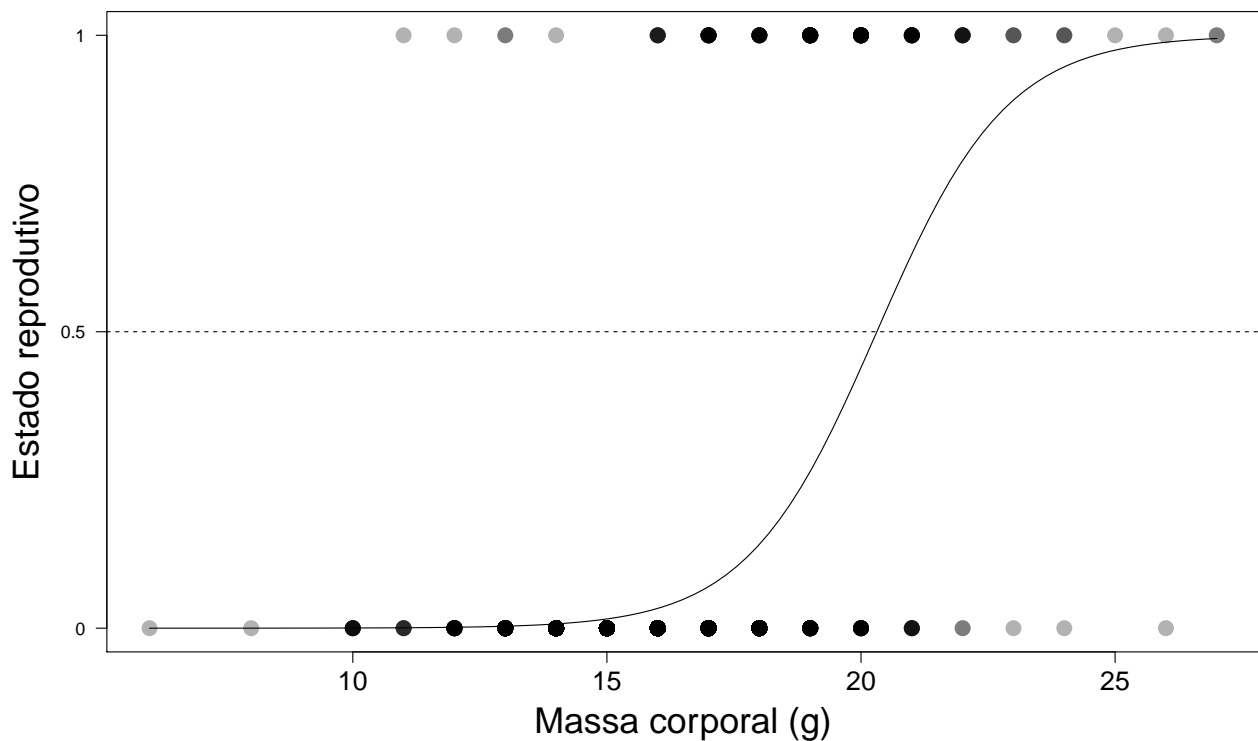
```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: femeas2$reproductive_stage2
```

```
##
## Terms added sequentially (first to last)
##
##
##              Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                                1314      732.19
## femeas2$body_mass  1    252.97      1313      479.21 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Plote o gráfico:

```
par(mfrow=c(1,1),mar=c(5,5,5,1), bg = "white")
plot(femeas2$reproductive_stage2~femeas2$body_mass,
     main = "Diagrama logístico",
     xlab = "Massa corporal (g)",
     ylab = "Estado reprodutivo",
     cex.axis = 1.5, cex.lab = 2, cex.main = 3, cex = 2,
     pch = 16, col = adjustcolor("black", alpha.f = 0.3),
     yaxt="n")
axis(2, at=c(0,0.5,1.0),labels=c(0, 0.5, 1.0), col.axis="black", las=2)
abline(h=0.5, col="black", lty=2)
curve (exp(fit1$coefficients[[1]]+fit1$coefficients[[2]]*x)/(1+exp(fit1$coefficients[[1]]+fit1$coefficients[[2]]*x)), col="black", lty=1, lwd=2)
```

## Diagrama logístico



```
par(mfrow=c(1,1))
```

## 13. Mapa

Para fazer este gráfico você precisará de mais alguns pacotes:

```
library(ggplot2)
library(ggmap)
```

```
## Google's Terms of Service: https://cloud.google.com/maps-platform/terms/.
```

```
## Please cite ggmap if you use it! See citation("ggmap") for details.
```

```
library(ggsn)
```

```
## Loading required package: grid
```

```
library(maps)
library(mapdata)
library(ggrepel)
```

Importe os dados com as coordenadas geográficas dos locais de estudo:

```
pontos = read.delim("pontos.txt", na.strings = "NA")
head(pontos)
```

```
##   longitude  latitude year
## 1 -44.86393 -23.35661 1999
## 2 -44.86393 -23.35661 1999
## 3 -44.86393 -23.35661 1999
## 4 -44.86393 -23.35661 1999
## 5 -44.86393 -23.35661 1999
## 6 -44.86393 -23.35661 1999
```

Melhore os nomes das colunas:

```
colnames(pontos) = c("long", "lat", "year")
head(pontos)
```

```
##           long          lat year
## 1 -44.86393 -23.35661 1999
## 2 -44.86393 -23.35661 1999
## 3 -44.86393 -23.35661 1999
## 4 -44.86393 -23.35661 1999
## 5 -44.86393 -23.35661 1999
## 6 -44.86393 -23.35661 1999
```

Transforme os anos em categorias:

```
pontos$year = as.factor(pontos$year)
class(pontos$year)
```

```
## [1] "factor"
```

```
write.csv(pontos, "pontos.csv", row.names=F)
```

Importe o mapa do Brasil e defina os limites a serem usados:

```
area <-map_data("world", region="Brazil", zoom=1)
head(area)
```

```
##           long      lat group order region      subregion
## 1 -48.48589 -27.76699     1     1 Brazil Ilha de Santa Catarina
## 2 -48.55459 -27.81221     1     2 Brazil Ilha de Santa Catarina
## 3 -48.54219 -27.57480     1     3 Brazil Ilha de Santa Catarina
## 4 -48.50518 -27.49551     1     4 Brazil Ilha de Santa Catarina
## 5 -48.46474 -27.43633     1     5 Brazil Ilha de Santa Catarina
## 6 -48.41489 -27.39961     1     6 Brazil Ilha de Santa Catarina
```

```
min(pontos$long)
```

```
## [1] -44.86393
```

```
max(pontos$long)
```

```
## [1] -42.03627
```

```
min(pontos$lat)
```

```
## [1] -23.35661
```

```
max(pontos$lat)
```

```
## [1] -19.35353
```

```
longs<-c(min(pontos$long)-0.01, max(pontos$long)+0.01)
lats<-c(min(pontos$lat)-0.01, max(pontos$lat)+0.01)
```

Plote o gráfico:

```
g1 <- ggplot() + geom_polygon(data = area,
                             aes(x=long, y = lat, group = group),
                             fill = "lightgrey", color = "lightgrey") +
  #xlim(longs) +
  #ylim(lats) +
  coord_fixed(1.1) +
  geom_polygon(data = area,
              aes(x = long, y = lat, group = group),
              color = "white", fill = NA, size = 0.04) +
  geom_point(data = pontos, aes(x = long, y = lat),
            color = "red",
            size = 2,
```

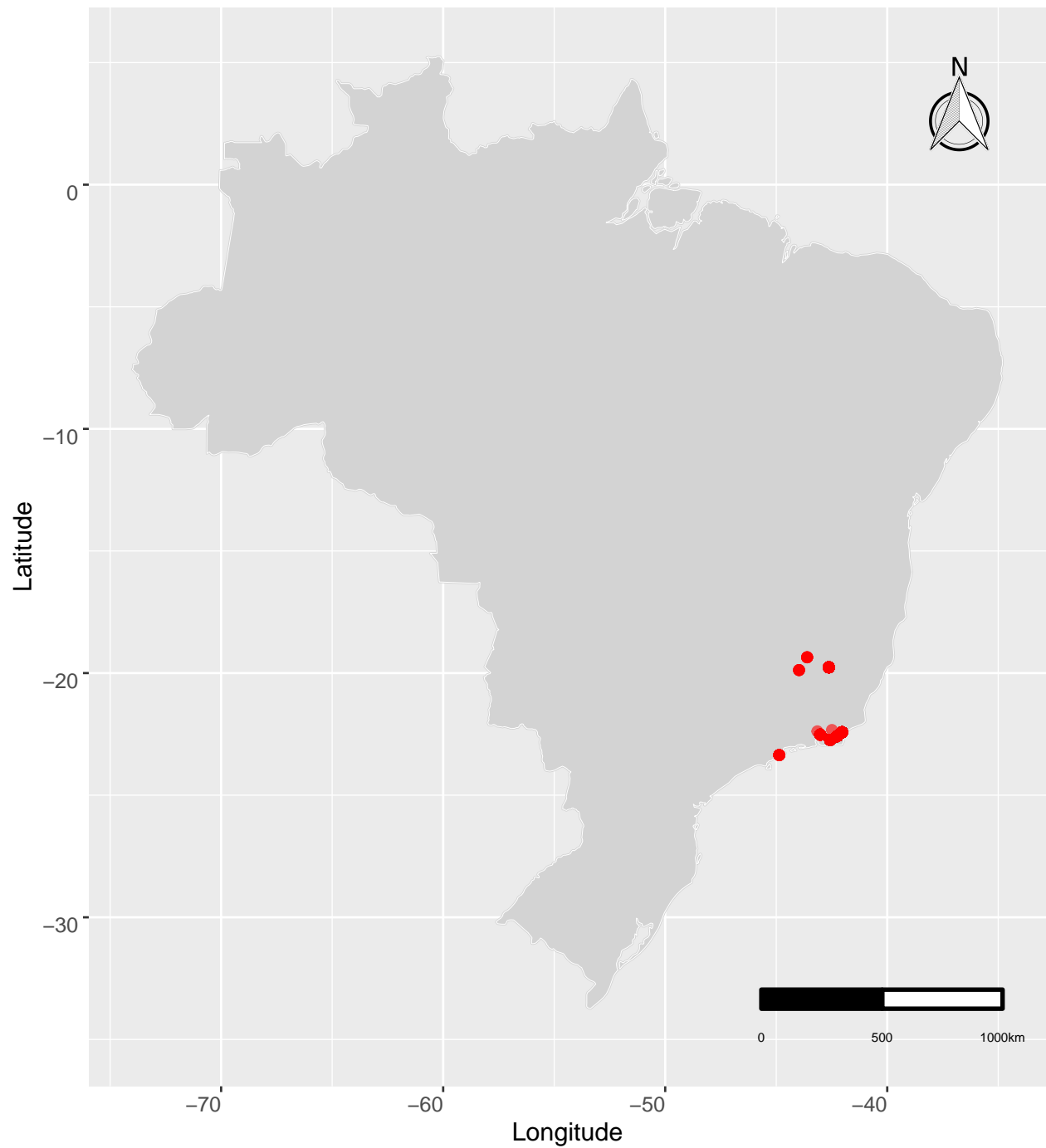
```

        alpha = 0.6) +
ggtitle("Mapa") +
labs(x="Longitude", y = "Latitude") +
theme(text = element_text(size=14),
      plot.title = element_text(size=20, hjust=0.5),
      axis.text.x = element_text(size = 10, angle=0, hjust=1),
      axis.text.y = element_text(size = 10, angle=0, vjust=1),
      axis.title.x = element_text(size = 12, angle=0),
      axis.title.y = element_text(size = 12, angle=90))

g1 +
  ggsm::scalebar(area, dist = 500,
    location = "bottomright",
    transform = TRUE,
    dist_unit = "km",
    st.dist = 0.03,
    st.size = 2,
    model = 'WGS84') +
  ggsm::north(area, scale = .1)

```

## Mapa



### 14. Grafo

Para desenhar este gráfico você precisará de mais um pacote:

```
library(bipartite)
```

```
## Loading required package: vegan
```

```

## Loading required package: permute

## Loading required package: lattice

## This is vegan 2.5-6

## Loading required package: sna

## Loading required package: statnet.common

##
## Attaching package: 'statnet.common'

## The following object is masked from 'package:base':
##
##     order

## Loading required package: network

## network: Classes for Relational Data
## Version 1.16.0 created on 2019-11-30.
## copyright (c) 2005, Carter T. Butts, University of California-Irvine
##             Mark S. Handcock, University of California -- Los Angeles
##             David R. Hunter, Penn State University
##             Martina Morris, University of Washington
##             Skye Bender-deMoll, University of Washington
## For citation information, type citation("network").
## Type help("network-package") to get started.

## sna: Tools for Social Network Analysis
## Version 2.5 created on 2019-12-09.
## copyright (c) 2005, Carter T. Butts, University of California-Irvine
## For citation information, type citation("sna").
## Type help(package="sna") to get started.

## This is bipartite 2.15.
## For latest changes see versionlog in ?"bipartite-package". For citation see: citation("bipartite").
## Have a nice time plotting and analysing two-mode networks.

##
## Attaching package: 'bipartite'

## The following object is masked from 'package:vegan':
##
##     nullmodel

```

Importe os dados como um objeto usável pelo pacote bipartite:



```

grafo <- read.delim("grafo.txt",
                    row.names=1,
                    header=TRUE)

head(grafo)

```

```

##      a1940 a1941 a1961 a1963 a1970 a1971 a1973 a1974 a1975 a1977 a1978 a1983
## Anocau    0     0     0     0     0     0     0     0     0     0     0     0
## Anogeo    0     0     0     0     0     0     0     0     0     0     0     0
## Artcin    0     0     0     0     0     0     0     0     0     0     0     0
## Artfim    0     0     0     0     0     0     0     0     0     0     0     0
## Artgno    0     0     0     0     0     0     0     0     0     0     0     0
## Artlit    0     0     0     0     0     0     0     0     0     0     0     0
##      a1984 a1989 a1991 a1992 a1993 a1995 a1997 a1998 a1999 a2000 a2001 a2002
## Anocau    0     0     0     0     0     0     1     0     6    29     9     1
## Anogeo    0     0     0     0     0     0     3     2     4     9     1     2
## Artcin    0     0     0     0     0     0    15    37    28    11     0     0
## Artfim    0     0     0     0     0     0     1    57    46    84    87    62
## Artgno    0     0     0     0     0     0     0     3     4     0     0     0
## Artlit    0     0     0     0     0     0    23    81   109   101    67    30
##      a2003 a2004 a2005 a2006 a2007 a2008 a2009 a2010 a2011 a2012 a2013 a2014
## Anocau     1    11     2    13    30     3     1     2    17    28    47    19
## Anogeo     0     0     0    10    29     1     2     2    16     4    10    18
## Artcin     0     2     2     3    43     2     0     0    47    43    16   110
## Artfim     0     4    19    42    43    23    11    21    16    30    25   105
## Artgno     0     0     0     0     0     0     0     0     0     0     0     0
## Artlit     0    20    36   189   360    42    22   131   139   227   306   350
##      a2015 a2016 a2017
## Anocau    16    26     5
## Anogeo     2     0     1
## Artcin    67    61     0
## Artfim     5   103     3
## Artgno     0     0     0
## Artlit    101   177    65

```

Plote o gráfico usando o pacote bipartite:

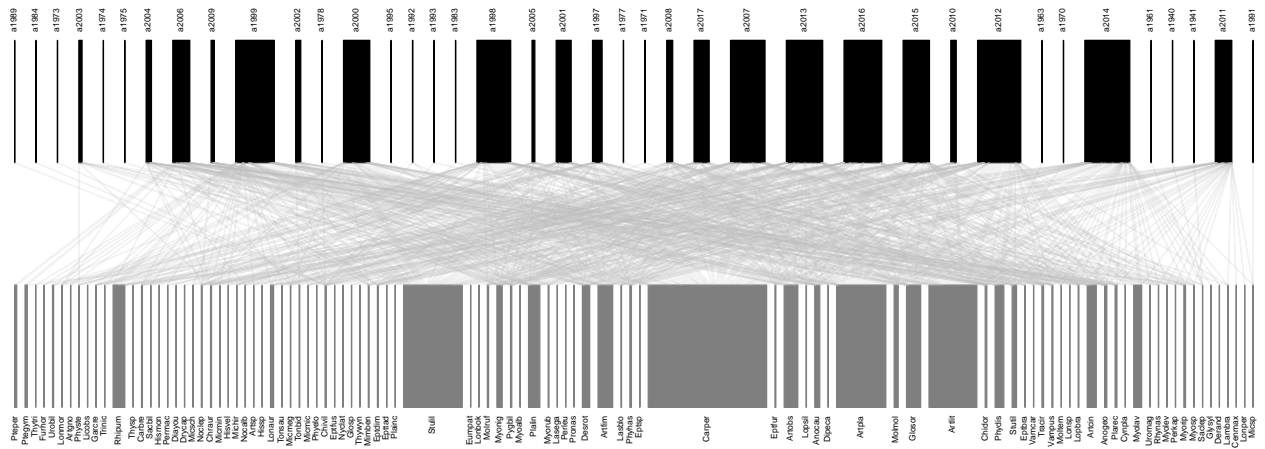
```

par(mfrow=c(1,1),mar=c(1,1,5,1), bg = "white")
plotweb(grafo,method = "cca",
        text.rot = 90, empty = TRUE, labsize = .70, ybig = 0.9, arrow = "no",
        col.interaction = adjustcolor("grey", alpha.f = 0.2),
        bor.col.interaction = adjustcolor("grey", alpha.f = 0.2),
        col.high = "black",
        bor.col.high="black",
        col.low="grey50",
        bor.col.low="grey50",
        high.lablength = NULL, low.lablength = NULL,
        sequence=NULL, low.abun = NULL, high.abun = NULL,
        low.abun.col = NULL, bor.low.abun.col = NULL,
        high.abun.col = NULL, bor.high.abun.col= NULL,
        text.high.col = "black",text.low.col = "black",
        adj.high=NULL, adj.low=NULL, plot.axes = FALSE,
        low.y=0.6, high.y=1.0, add=FALSE,

```

```
y.lim=NULL, x.lim=NULL, low.plot=TRUE)
title("Grafo", cex.main=3, col.main="black")
```

# Grafo



```
par(mfrow=c(1,1))
```

Agora você precisará de mais um pacote para desenhar o gráfico de outra maneira:

```
library(igraph)
```

```
##
## Attaching package: 'igraph'

## The following object is masked from 'package:bipartite':
##
## strength

## The following objects are masked from 'package:sna':
##
## betweenness, bonpow, closeness, components, degree, dyad.census,
## evcent, hierarchy, is.connected, neighborhood, triad.census

## The following objects are masked from 'package:network':
##
## %c%, %s%, add.edges, add.vertices, delete.edges, delete.vertices,
## get.edge.attribute, get.edges, get.vertex.attribute, is.bipartite,
## is.directed, list.edge.attributes, list.vertex.attributes,
## set.edge.attribute, set.vertex.attribute
```

```
## The following object is masked from 'package:vegan':
##
##     diversity

## The following object is masked from 'package:permute':
##
##     permute

## The following objects are masked from 'package:stats':
##
##     decompose, spectrum

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

Transforme os dados para o formato de um objeto do pacote igraph:

```
grafo2 <- graph_from_incidence_matrix(grafo,
                                     directed = FALSE,
                                     weighted = T,
                                     add.names = NULL)
```

Inspecione o objeto:

```
grafo2
```

```
## IGRAPH 6cf65d0 UNWB 137 707 --
## + attr: type (v/l), name (v/c), weight (e/n)
## + edges from 6cf65d0 (vertex names):
## [1] Anocau--a1997 Anocau--a1999 Anocau--a2000 Anocau--a2001 Anocau--a2002
## [6] Anocau--a2003 Anocau--a2004 Anocau--a2005 Anocau--a2006 Anocau--a2007
## [11] Anocau--a2008 Anocau--a2009 Anocau--a2010 Anocau--a2011 Anocau--a2012
## [16] Anocau--a2013 Anocau--a2014 Anocau--a2015 Anocau--a2016 Anocau--a2017
## [21] Anogeo--a1997 Anogeo--a1998 Anogeo--a1999 Anogeo--a2000 Anogeo--a2001
## [26] Anogeo--a2002 Anogeo--a2006 Anogeo--a2007 Anogeo--a2008 Anogeo--a2009
## [31] Anogeo--a2010 Anogeo--a2011 Anogeo--a2012 Anogeo--a2013 Anogeo--a2014
## [36] Anogeo--a2015 Anogeo--a2017 Artcin--a1997 Artcin--a1998 Artcin--a1999
## + ... omitted several edges
```

```
E(grafo2)
```

```
## + 707/707 edges from 6cf65d0 (vertex names):
## [1] Anocau--a1997 Anocau--a1999 Anocau--a2000 Anocau--a2001 Anocau--a2002
## [6] Anocau--a2003 Anocau--a2004 Anocau--a2005 Anocau--a2006 Anocau--a2007
## [11] Anocau--a2008 Anocau--a2009 Anocau--a2010 Anocau--a2011 Anocau--a2012
## [16] Anocau--a2013 Anocau--a2014 Anocau--a2015 Anocau--a2016 Anocau--a2017
## [21] Anogeo--a1997 Anogeo--a1998 Anogeo--a1999 Anogeo--a2000 Anogeo--a2001
## [26] Anogeo--a2002 Anogeo--a2006 Anogeo--a2007 Anogeo--a2008 Anogeo--a2009
## [31] Anogeo--a2010 Anogeo--a2011 Anogeo--a2012 Anogeo--a2013 Anogeo--a2014
## [36] Anogeo--a2015 Anogeo--a2017 Artcin--a1997 Artcin--a1998 Artcin--a1999
## [41] Artcin--a2000 Artcin--a2004 Artcin--a2005 Artcin--a2006 Artcin--a2007
## [46] Artcin--a2008 Artcin--a2011 Artcin--a2012 Artcin--a2013 Artcin--a2014
## + ... omitted several edges
```

```
V(grafo2)
```

```
## + 137/137 vertices, named, from 6cf65d0:
##   [1] Anocau Anogeo Artcin Artfim Artgno Artlit Artobs Artpla Artsp  Carbre
##  [11] Carper Cenmax Chidor Chivil Chraur Cynpla Derand Desrot Diayou Dipec
##  [21] Drycap Eptbra Eptdim Eptfur Eptfus Eptsp  Epttad Eumpat Furhor Garcr
##  [31] Glosor Glosp  Glysyl Hismon Hissp  Hisvel Lambra Lasblo Lasega Licob
##  [41] Lonbok Lonmor Lonper Lonsp  Lonaur Lopbra Lopsil Michir Micmeg Micmic
##  [51] Micmin Micsch Micsp  Mimbem Moltem Molmol Molruf Myoalb Myolav Myolev
##  [61] Myonig Myorip Myorub Myosp  Nocalb Noclep Nyclat Perkap Perleu Permac
##  [71] Physte Phydis Phyelo Phyhas Plainc Plalin Plarec Pronas Ptegy
##  [81] Pygbil Rhipum Rhynas Sacbil Saclep Stulil Stutil Thysp  Thytri Thywyn
##  [91] Tonbid Tonsau Tracir Trinic Urobil Uromag Vampus Vamcar a1940 a1941
## + ... omitted several vertices
```

Confira a estrutura bipartida do grafo, com 2 classes de nós:

```
bipartite_mapping(grafo2)
```

```
## $res
## [1] TRUE
##
## $type
##   [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##  [13] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##  [25] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##  [37] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##  [49] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##  [61] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##  [73] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##  [85] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##  [97] FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
## [109]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
## [121]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
## [133]  TRUE  TRUE  TRUE  TRUE  TRUE
```

Converta as classes de nós em binárias:

```
ifelse(V(grafo2)$type == FALSE, 0, 1)
```

```
##   [1] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##  [38] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##  [75] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1
## [112] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
```

```
V(grafo2)$type
```

```
##   [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##  [13] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##  [25] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

```
## [37] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [49] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [61] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [73] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [85] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [97] FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [109] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [121] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [133] TRUE TRUE TRUE TRUE TRUE
```

Defina as cores das classes de nós:

```
colors <- ifelse(V(grafo2)$type == 0, "black", "grey50")
colors
```

```
## [1] "black" "black" "black" "black" "black" "black" "black" "black"
## [9] "black" "black" "black" "black" "black" "black" "black" "black"
## [17] "black" "black" "black" "black" "black" "black" "black" "black"
## [25] "black" "black" "black" "black" "black" "black" "black" "black"
## [33] "black" "black" "black" "black" "black" "black" "black" "black"
## [41] "black" "black" "black" "black" "black" "black" "black" "black"
## [49] "black" "black" "black" "black" "black" "black" "black" "black"
## [57] "black" "black" "black" "black" "black" "black" "black" "black"
## [65] "black" "black" "black" "black" "black" "black" "black" "black"
## [73] "black" "black" "black" "black" "black" "black" "black" "black"
## [81] "black" "black" "black" "black" "black" "black" "black" "black"
## [89] "black" "black" "black" "black" "black" "black" "black" "black"
## [97] "black" "black" "grey50" "grey50" "grey50" "grey50" "grey50" "grey50"
## [105] "grey50" "grey50" "grey50" "grey50" "grey50" "grey50" "grey50" "grey50"
## [113] "grey50" "grey50" "grey50" "grey50" "grey50" "grey50" "grey50" "grey50"
## [121] "grey50" "grey50" "grey50" "grey50" "grey50" "grey50" "grey50" "grey50"
## [129] "grey50" "grey50" "grey50" "grey50" "grey50" "grey50" "grey50" "grey50"
## [137] "grey50"
```

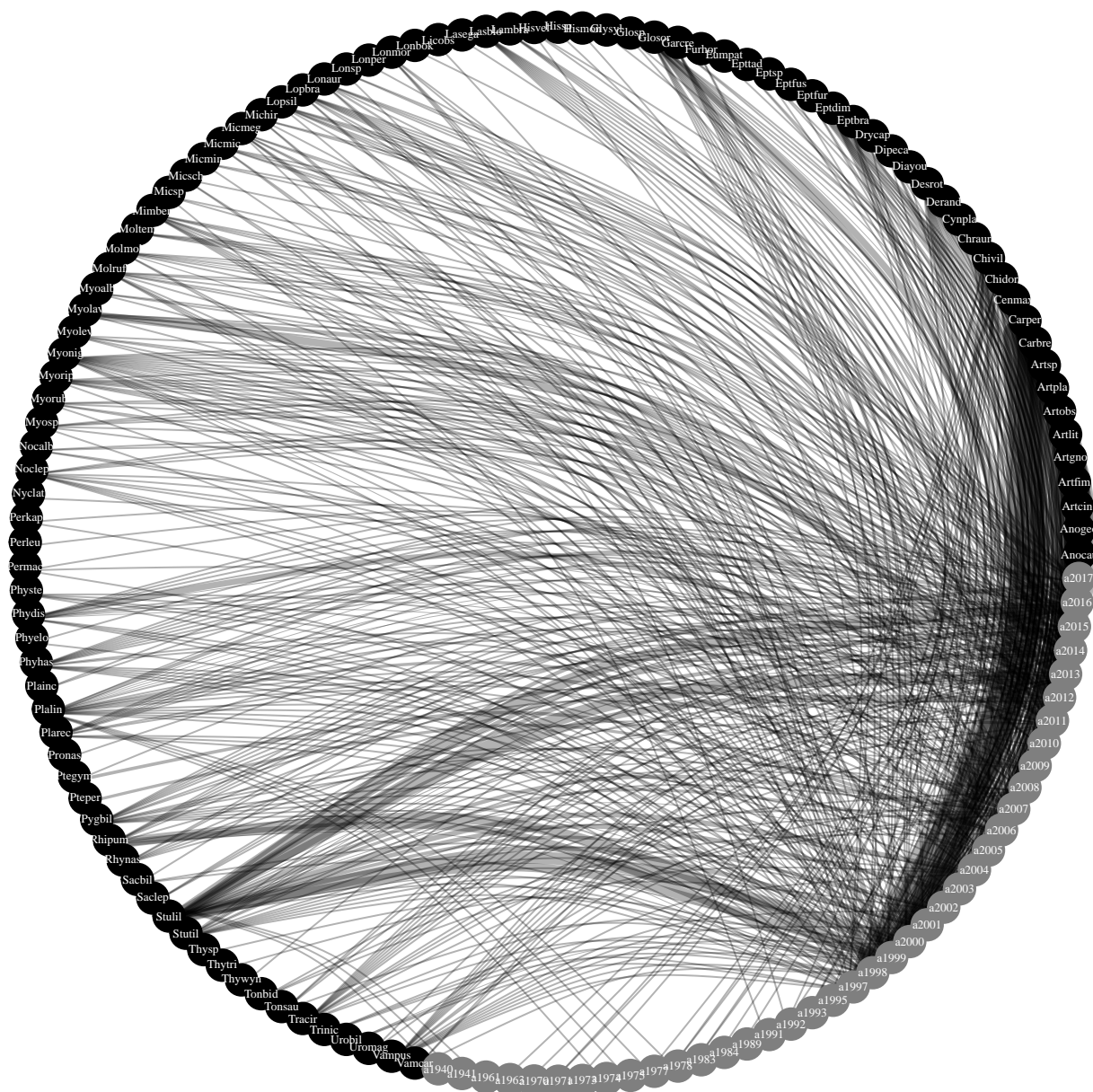
Defina a espessura das conexões:

```
E(grafo2)$width = scale(E(grafo2)$weight)
```

Plote o gráfico:

```
par(mfrow=c(1,1),mar=c(1,1,5,1), bg = "white")
plot(grafo2,
     vertex.color = colors,
     vertex.frame.color= colors,
     vertex.size=6,
     vertex.label.cex=.4,
     vertex.label = V(grafo2)$names,
     vertex.label.color = "white",
     edge.color = adjustcolor("black", alpha.f = .3),
     edge.width = E(grafo2)$width*2,
     edge.curved = 0.3,
     layout=layout_in_circle)
title("Grafo",cex.main=3,col.main="black")
```

# Grafo



```
par(mfrow=c(1,1))
```