

.daddy_code v2.1

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1 Allmänt

Lite allmänna funktioner som är bra att kunna.

1.1 Paket & inläsning av data

För att installera ett paket.

```
# För att installera paketet som heter palmerpenguins
install.packages("palmerpenguins")

# Stats
install.packages("MKinfer")
install.packages("lmboot")
install.packages("boot.pval")

# Matte
install.packages("pracma")
install.packages("expm")
install.packages("deSolve")

# KvantBio
install.packages("plotrix")
install.packages("scales")
```

För att använda funktioner i ett paket måste man ladda in paketet i R genom `library()`

```
# Exempel data
library(palmerpenguins)

# Stats
library(MKinfer)
library(lmboot)
library(boot.pval)

# Matte
library(pracma)
library(expm)
library(deSolve)
```

```
# KvantBio
library(plotrix)
library(scales)
```

För att läsa in data från t.ex. en .csv eller .txt fil. Öppna filen och identifiera vilka symboler som **separerar** kolumner samt används som **decimaltecken**.

```
file.choose() # Returnerar vägen till filen man väljer, hitta fönstret
↳ med alt + tab.

my_data <- read.table(
  file = file.choose(), # Välj fil interaktivt, alt. filens sökväg som
  ↳ en text string
  header = TRUE, # Om det finns namn på kolumnerna
  sep = ",", # Här används ett kommatecken för att skilja på kolumner
  dec = "." # Här används en punkt som decimaltecken
)
```

För att titta på data kan man använda

```
# View(penguins) # Öppnar som separat flik
head(penguins, # Printar de första n raderna
      n = 3)
```

```
# A tibble: 3 x 8
  species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
  <fct>   <fct>         <dbl>         <dbl>         <int>         <int>
1 Adelie Torgersen      39.1           18.7           181           3750
2 Adelie Torgersen      39.5           17.4           186           3800
3 Adelie Torgersen      40.3            18           195           3250
# i 2 more variables: sex <fct>, year <int>
```

```
tail(penguins, # Printar de sista n raderna
     n = 3)
```

```
# A tibble: 3 x 8
  species  island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
  <fct>    <fct>         <dbl>         <dbl>         <int>         <int>
1 Chinstrap Dream      49.6           18.2           193           3775
```

```

2 Chinstrap Dream          50.8          19          210          4100
3 Chinstrap Dream          50.2          18.7          198          3775
# i 2 more variables: sex <fct>, year <int>

```

För att skapa olika datastrukturer

1.2 Variabel

```

var_1 <- "Text/character string" # Någonting inuti "" är text
var_2 <- 25 # Nummer, för decimaltal 25.99
var_3 <- TRUE # Boolean, kan bara vara TRUE (T) eller FALSE (F)
var_4 <- NA # Not Available (NA), inte samma som "NA" (text string)!
var_5 <- NULL # Ingenting, tenderar att radera saker!

```

1.3 Vektor

```

vec_1 <- c() # Skapar en tom vektor
vec_1 <- c(36, 56, 48) # Skapa en vektor med tre värden
vec_1[4] <- 25 # Sätta in ett värde i index plats 4
vec_1 # Printa innehållet av variabeln (vektorn)

```

```
[1] 36 56 48 25
```

```
vec_1[2] # Printa innehållet i index 2
```

```
vec_1[c(1,3)] # Printa index 1 och 3
```

Vektorer kan innehålla namn och indexeras med namn

```

vec_2 <- c(element_1 = 99, element_2 = 100, element_3 = 101)
vec_2["element_4"] <- 102 # Sätt in ett värde med namn
vec_2

```

```

element_1 element_2 element_3 element_4
      99       100       101       102

```

```
vec_2["element_2"]
```

```
vec_2[c("element_1", "element_3")]
```

1.4 Data frame

```
df <- data.frame( # Skapa en dataframe med kolumn_namn = vektor
  vec_1, # Kolumn 1, vec_1 från tidigare
  letters = LETTERS[1:4] # Kolumn 2, lite bokstäver
)
```

df

	vec_1	letters
1	36	A
2	56	B
3	48	C
4	25	D

Man kan lägga till kolumner med \$

```
df$col_3 <- vec_2 # Kolumn 3
df
```

	vec_1	letters	col_3
1	36	A	99
2	56	B	100
3	48	C	101
4	25	D	102

Andra sätt att lägga till kolumner är med namn

```
df["col4"] <- letters[1:4]
df
```

	vec_1	letters	col_3	col4
1	36	A	99	a

2	56	B	100	b
3	48	C	101	c
4	25	D	102	d

En kolumn kan användas med \$ vilket ger en vektor (viktig distinktion vid vissa andra tillfällen).

```
df$letters # Ger en vektor, samma som med df[["letters"]]
```

Eller med indexering/namn, N.B. enkla [] ger ett subset, alltså en mindre del av samma objekt typ

```
df[3] # Ger en data frame med enbart kolumn 3
df["col4"] # Ger en data frame med kolumn "col4"
```

medan dubbla [[]] ger objektet inuti

```
df[[1]] # Ger det "mindre objektet inuti", alltså en vektor i detta fall
```

Enkla [] kan indexeras med rader och kolumner samtidigt

```
df[2] # Kolumn 2 (en data frame med en kolumn)
df[3,2] # Rad 3, kolumn 2 (en vektor av längd ett)
df[,2] # Alla rader, kolumn 2 (en vektor)
df[3, ] # Rad 3, alla kolumner (en data frame med en rad)
```

På tal om subsetting, för att ta ett subset av en data frame kan man filtrera rader baserat på ett kriterium

```
penguins_chin <- penguins[penguins$species == "Chinstrap", ]
# Utan komma läses det som att du vill filtrera kolumner! '==' är det
↪ matematiska 'lika med' (eftersom '=' är samma som '<-' )
head(penguins_chin, 3)
```

```
# A tibble: 3 x 8
  species island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
<fct>    <fct>         <dbl>         <dbl>             <int>      <int>
1 Chinstrap Dream         46.5           17.9             192       3500
2 Chinstrap Dream         50            19.5             196       3900
3 Chinstrap Dream        51.3           19.2             193       3650
# i 2 more variables: sex <fct>, year <int>
```

```
penguins_heavy <- penguins[penguins$body_mass_g > 3500, ]
head(penguins_heavy, 3)
```

```
# A tibble: 3 x 8
  species island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
  <fct>   <fct>         <dbl>         <dbl>         <int>         <int>
1 Adelie Torgersen         39.1           18.7           181           3750
2 Adelie Torgersen         39.5           17.4           186           3800
3 <NA>    <NA>              NA             NA             NA           NA
# i 2 more variables: sex <fct>, year <int>
```

Man kan även göra detta för att få en kolumn filtrerad/subset baserad på en annan kolumn.

```
penguins_chin_weight <- penguins$body_mass_g[penguins$species ==
  ↪ "Chinstrap", ]
```

Error in `penguins$body_mass_g[penguins$species == "Chinstrap",]` : incorrect number of dimensions

Det blir en error därför att nu försöker man ta både rader och kolumner (2 dimensioner) på en kolumn (kolumn/vektor har bara 1 dimension) därför att `$` ger en vektor. Om vi istället provar utan extra kommatecken för att ange rader & kolumner samtidigt fungerar det (ger en vektor). Alternativt ange kolumnen med namn istället för med `$` (ger en mindre data frame).

```
# Utan extra kommatecken
penguins_chin_weight <- penguins$body_mass_g[penguins$species ==
  ↪ "Chinstrap"]
head(penguins_chin_weight)
```

```
[1] 3500 3900 3650 3525 3725 3950
```

```
# Ange kolumnen med namn
penguins_chin_weight <- penguins[penguins$species == "Chinstrap",
  ↪ "body_mass_g"]
head(penguins_chin_weight)
```

```
# A tibble: 6 x 1
  body_mass_g
```



```

      <int>
1      3500
2      3900
3      3650
4      3525
5      3725
6      3950

```

Vi kan även bli av med NA på ett kontrollerat sätt med den här metoden. Om man vill se till att vikt och näbb längd inte har NA kan man använda funktionen `is.na()` och operatoren `!`.

```
is.na(NA) # Kolla om NA är NA
```

```
[1] TRUE
```

```
!is.na(NA) # ! neget ett TRUE/FALSE uttryck
```

```
[1] FALSE
```

```
vec_NA <- c(NA, 50)
is.na(vec_NA) # Kolla vilka element som är NA
```

```
[1] TRUE FALSE
```

```
!is.na(vec_NA)
```

```
[1] FALSE TRUE
```

```

# Alla rader där kolumnen body_mass_g inte är NA och alla kolumner
penguins_no_NA <- penguins[!is.na(penguins$body_mass_g), ]
# Alla rader där kolumnen bill_length_mm inte är NA och alla kolumner
penguins_no_NA <- penguins_no_NA[!is.na(penguins_no_NA$bill_length_mm),
↵ ]

# Tabell med antal rader & kolumner

```

```
data.frame(
  rows = c(penguins = nrow(penguins), no_NA = nrow(penguins_no_NA)),
  columns = c(penguins = ncol(penguins), no_NA = ncol(penguins_no_NA))
)
```

	rows	columns
penguins	344	8
no_NA	342	8

1.5 Matris

Vi kan skapa matriser med `rbind()` (går även att använda `cbind()` men då placeras vektorerna vertikalt från det övre vänstra hörnet, istället för horisontellt). Med `rbind()` blir matrisen som den ser ut när man skriver den.

```
rbind( # en "character matrix"
  c("a", "b"),
  c("c", "d")
)
```

	[,1]	[,2]
[1,]	"a"	"b"
[2,]	"c"	"d"

```
cbind( # skillnaden med cbind()
  c("a", "b"),
  c("c", "d")
)
```

	[,1]	[,2]
[1,]	"a"	"c"
[2,]	"b"	"d"

```
M <- rbind( # Skapar en matris radvis med namngivna rader och kolumner
  r1 = c(col1 = 0.90, col2 = 0, col3 = 0, col4 = 0, col5 = 0.45),
  r2 = c(          0,    0.45,    0,    0,    0),
  r3 = c(          0,    0.23,    0.45,    0,    0),
)
```

```

    r4 = c(          0,          0,      0.23,      0.45,          0),
    r5 = c(          0,          0,          0,      0.23,      0.20)
  )
M

```

```

      col1 col2 col3 col4 col5
r1  0.9 0.00 0.00 0.00 0.45
r2  0.0 0.45 0.00 0.00 0.00
r3  0.0 0.23 0.45 0.00 0.00
r4  0.0 0.00 0.23 0.45 0.00
r5  0.0 0.00 0.00 0.23 0.20

```

För matris matte se [Matte](#) sektionen.

Matriser kan indexeras ungefär på samma sätt som data frames.

```

M[3, 2]
M[3:5, 2:3]
M[c(3,5), c(2,3)]
M[c("r3","r5"), c("col2","col3")]

```

1.6 Lista (den riktiga listan)

I en vektor **måste** alla element vara av samma typ (numerisk/text osv.) och i en data frame **måste** alla kolumner (som är vektorer) vara lika långa.

Listor kan ha olika typer av objekt i sig och brukar användas för att bunta ihop olika objekt man vill hålla tillsammans. Till exempel är output från `t.test()` en lista.

```

my_list <- list() # En tom lista
my_list$df_1 <- df # Lägg till en data frame med $
my_list[[2]] <- var_2 # Lägg till en variabel med index, N.B. [[]]
my_list[["plats_3"]] <- vec_2 # Lägg till en vektor med namn, N.B. [[]]
my_list

```

```

$df_1
  vec_1 letters col_3 col4
1    36      A    99    a
2    56      B   100    b

```

```
3    48      C   101    c
4    25      D   102    d
```

```
[[2]]
[1] 25
```

```
$plats_3
element_1 element_2 element_3 element_4
      99      100      101      102
```

Och man få ut objekten i en lista på samma sätt.

1.7 Lite andra funktioner

Ett objekts typ heter "klass" och kan kollas med funktionen `class()`

```
class(var_1) # var_1 är text
class(var_2) # var_2 är numerisk
class(var_3) # var_3 är logical/boolean (TRUE/FALSE)
class(vec_1) # vec_1 är numerisk vektor
class(df)    # df är en data frame
class(M)     # M är en matris
class(my_list) # my_list är en lista
```

För att se till att någonting skrivs i konsolfönstret används `print()`

```
print(var_1) # Tar enbart ett objekt! Se paste()
```

```
[1] "Text/character string"
```

För att skriva ihop text m.m. används `paste()`, den tar dock enbart enskilda element (inte vektor/data frame/list

```
message <- paste(
  "Hello", "world", var_1, 55, vec_2[3], # Alla objekt man vill skriva
  ↪ ihop
  sep = " " # Separator att infoga mellan varje objekt, här ett
  ↪ mellanslag
)
print(message)
```

```
[1] "Hello world Text/character string 55 101"
```

Notera att `print()` enbart accepterar ett objekt, därav den vanliga kombinationen `print(paste(arg1, arg2))`.

```
print(paste("Nu", "klaras", "vi", "tentan!", sep = "! "))
```

```
[1] "Nu! klaras! vi! tentan!"
```

Kolla längden på saker med

```
length(vec_1) # Längden på en vektor
length(penguins) # Längden på en data frame är antalet kolumner
nrow(penguins) # För antalet rader i en data frame
ncol(penguins) # Antalet columner på en data frame
```

Få en vektor med namnen på kolumner

```
colnames(penguins)
```

```
[1] "species"          "island"            "bill_length_mm"
[4] "bill_depth_mm"    "flipper_length_mm" "body_mass_g"
[7] "sex"              "year"
```

Få alla unika element i en vektor

```
unique(penguins$species)
```

```
[1] Adelie    Gentoo    Chinstrap
Levels: Adelie Chinstrap Gentoo
```

Konvertera/tvinga (eng. `coerce`) objekt till en viss typ.

```
as.numeric() # Bra ifall en kolumn är text men ska vara siffror
as.character()
as.factor() # Kan vara viktig för ANOVA om grupperna är 1,2,3,4...
```

```
as.data.frame() # Kan tvinga en matris till data frame
as.matrix()     # Kan tvinga en data frame till matris
```

1.8 Kontrollstrukturer

Kontrollstrukturer är några speciella funktioner som möjliggör mer kontroll över vilka rader med kod som ska köras.

1.8.1 Loop

För att köra några rader kod flera gånger används loopar. Detta är exempel på for-loop.

```
vector <- c("Nu", "klarar", "vi", "tentan!")
for (variable in vector) {
  print(variable)
}
```

```
[1] "Nu"
[1] "klarar"
[1] "vi"
[1] "tentan!"
```

```
for (i in 1:4) {
  print(paste(i, ":", vector[i]))
}
```

```
[1] "1 : Nu"
[1] "2 : klarar"
[1] "3 : vi"
[1] "4 : tentan!"
```

```
n <- c()
n[1] <- 55
for (i in 1:5) {
  n[i+1] <- i
}
```

```
n
```

```
[1] 55  1  2  3  4  5
```

1.8.2 If-else

För att köra vissa rader enbart om ett visst kriterium uppfylls används if-else kombination. Resultatet av att "köra koden" i parantesen ska bli TRUE för att köra den följande koden.

```
if ("Tenta!" == "Tenta!") { # Blir TRUE
  print(TRUE)
} else {
  print(FALSE)
}
```

```
[1] TRUE
```

```
if (5^2 < 100) { # Blir TRUE
  print("Smaller")
} else {
  print("Bigger")
}
```

```
[1] "Smaller"
```

```
if (50^2 < 100) { # Blir FALSE
  print("Smaller")
} else {
  print("Bigger")
}
```

```
[1] "Bigger"
```

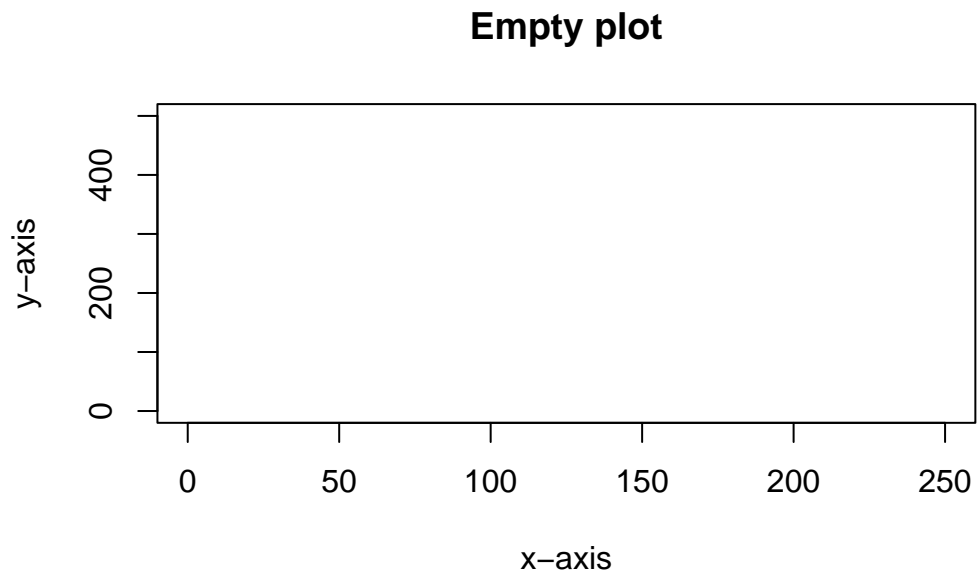
1.9 Plotting

Här följer plotfunktioner med många möjliga argument. Vissa argument visas flera gånger som alternativ.

För att kontrollera hur många plots att visa på samma gång, använd.

1.9.1 Tomt plotfönster

```
plot(  
  x = NULL,  
  y = NULL,  
  
  xlim = c(0, 250),  
  ylim = c(0, 500),  
  
  xlab = "x-axis",  
  ylab = "y-axis",  
  main = "Empty plot"  
)
```



1.9.2 Scatterplot

Om x = kontinuerlig & y = kontinuerlig ger detta ett punktdiagram eller linjediagram.

De flesta argument fungerar likadant/liknande för andra typer av plots.

```
plot(  
  # Värden för axlarna  
  x = penguins$bill_depth_mm,  
  y = penguins$body_mass_g,  
  
  # Annotering  
  xlab = "Bill depth [mm]",  
  ylab = "Body mass [g]",  
  main = "Hefty penguins!",  
  sub = "An analysis by island",  
  # ann = FALSE, # alt. ta bort alla vanliga annoteringar.  
  
  # xaxt = "n", # x-axis text = 'n' (none)  
  # yaxt = "n", # Tar bort axel markörerna  
  
  # Linjer & punkter  
  type = "p", # 'l' = line, 's' = stairs, 'p' = point,  
              # 'b' = both (line & pont), 'o' = both (overplotted),  
              # 'h' = histogram liknande, 'n' = none.  
  pch = 16, # 15 = ifylld kvadrat, 16 = ifylld prick,  
            # 17 = ifylld triangel, 18 = ifylld diamant.  
  cex = 1, # Storlek på punkt.  
  
  # lwd = 3, # Storlek på linje.  
  # lty = 1, # "blank", "solid", "dashed", "dotted",  
            # "dotdash", "longdash", "twodash".  
  
  # col = "blue", # Färg  
  col = penguins$island, # Färg baserat på faktor  
  # col = alpha("blue", 0.30) # Färg (blå) & transparens (30%)  
)  
  
# Lägg till en linje från 'a' till 'b'.  
abline(  
  # a = intercept,  
  # b = slope,
```

```

h = 4000, # y-värde för horisontella linjer
v = 14,   # x-värde för vertikala linjer
# reg = lm_objekt, # Regressionsmodell, se sektion 2.4.2.4 Predict
col = "purple"
)

# För att lägga till en legend
legend(
# x = 20, y = 6000, # x & y koordinater för legenden.

x = "topright",      # Kan ges "top", "topleft", "topright",
                     # "bottom", "bottomleft", "bottomright".
inset = 0.05,        # Avstånd till ytterkanterna som en % av plot
                     ↪ storleken.

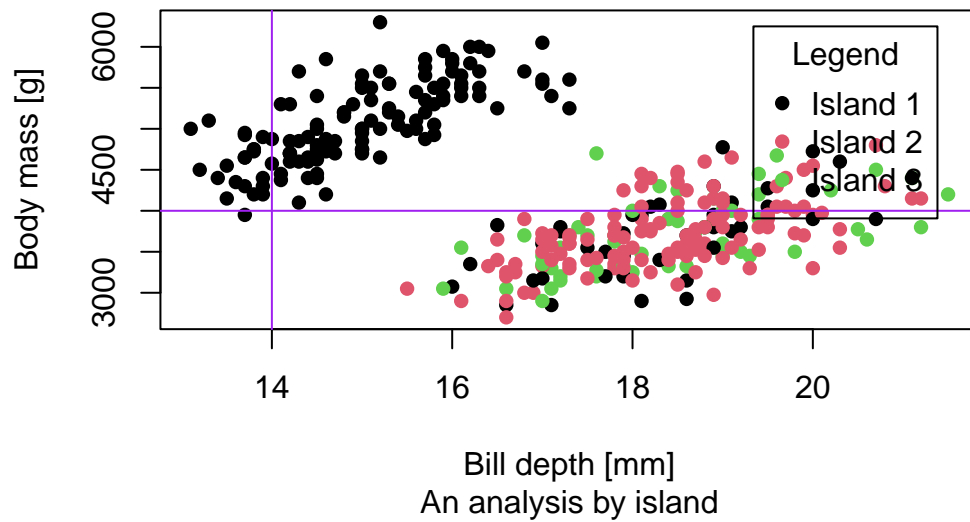
legend = c("Island 1", "Island 2", "Island 3"), # Namn i legenden.
pch = 16, # Sätt olika punkter med c(15, 16, 17). (Krävs för färger!)
col = 1:3, # Eftersom faktorn har tre grupper.
           # Kan även vara c("blue", "green", "orange").

# lty = c(1, 2, 3), # Sätt olika linje typer,
# fill = 1:3,       # Färg, men utan att ange form/linje.

title = "Legend", # Legend title
bty = "o",        # 'o' = box, 'n' = no box, eller '7', 'L', 'U', 'C'.
)

```

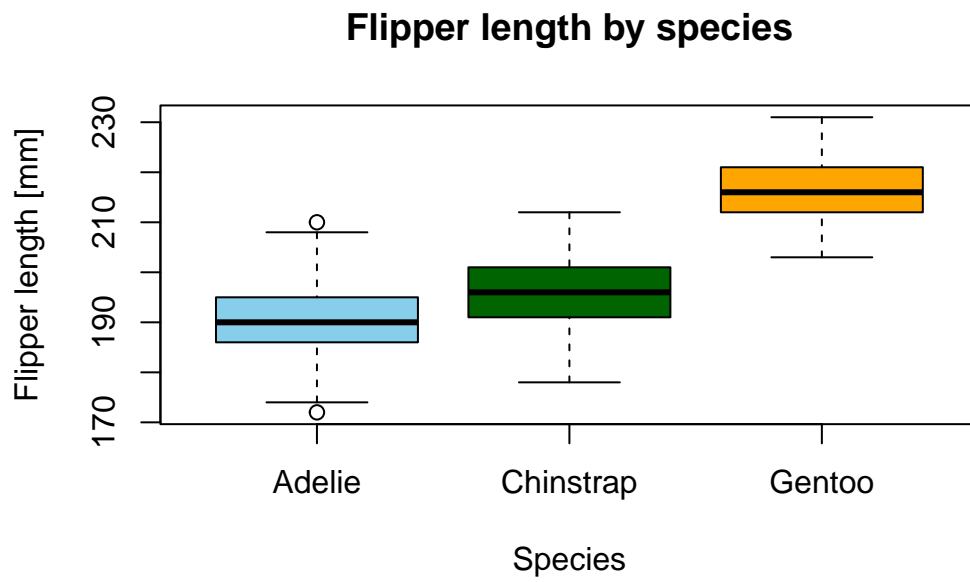
Hefty penguins!



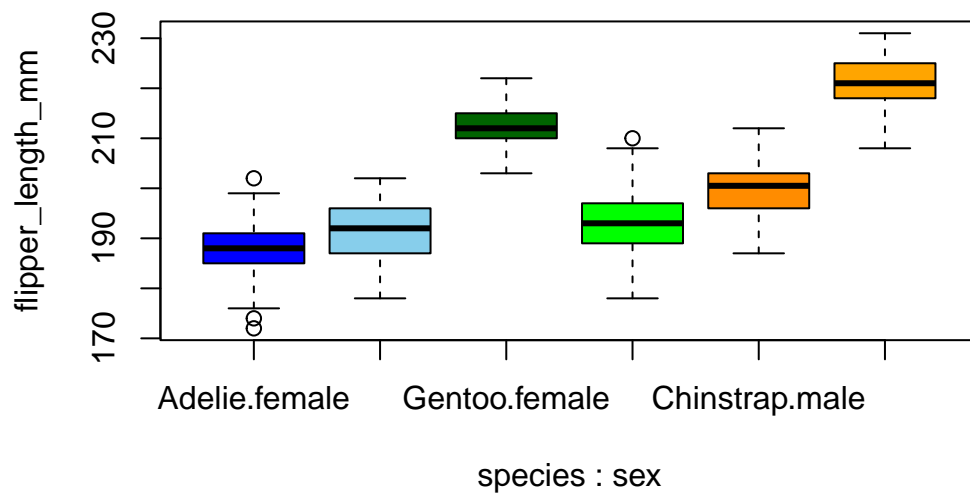
1.9.3 Boxplot

Om x = faktor & y = kontinuerlig ger detta en boxplot/låddiagram.

```
plot(  
  x = penguins$species,  
  y = penguins$flipper_length_mm,  
  
  xlab = "Species",  
  ylab = "Flipper length [mm]",  
  main = "Flipper length by species",  
  
  col = c("skyblue", "darkgreen", "orange")  
)
```



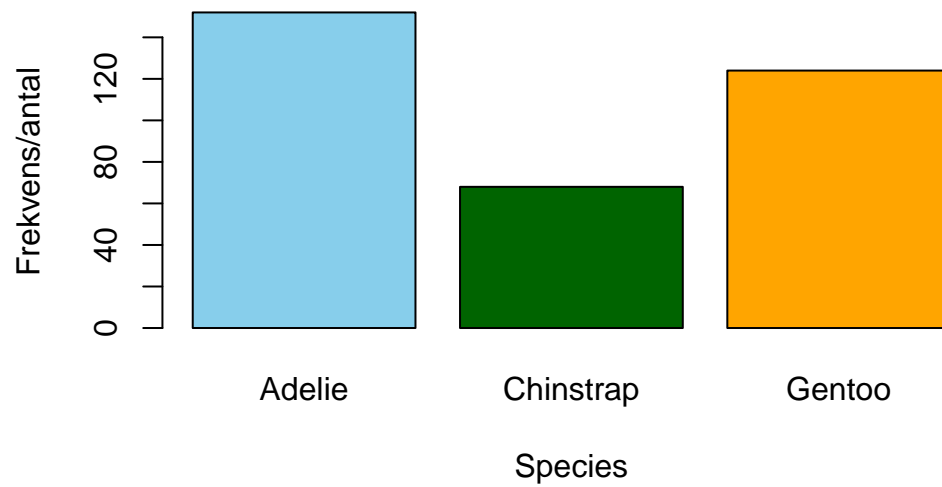
```
boxplot(  
  flipper_length_mm ~ species * sex,  
  data = penguins,  
  col = c("blue","skyblue",  
          "darkgreen","green",  
          "darkorange","orange")  
)
```



1.9.4 Barplot

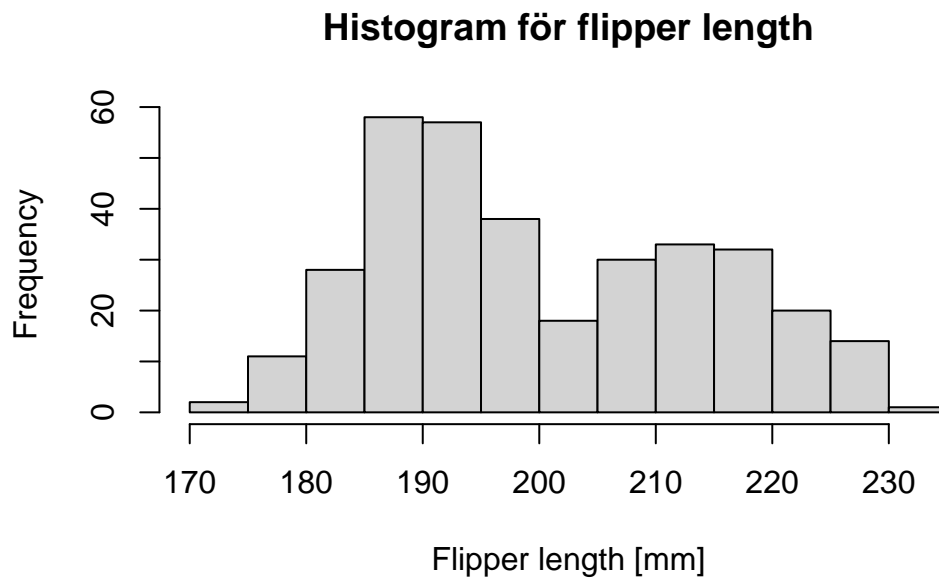
Om x = faktor & inget y ger detta en barplot/stapeldiagram.

```
plot(
  x = penguins$species,
  xlab = "Species",
  ylab = "Frekvens/antal",
  col = c("skyblue", "darkgreen", "orange")
)
```



1.9.5 Histogram

```
hist(  
  penguins$flipper_length_mm,  
  main = "Histogram för flipper length",  
  xlab = "Flipper length [mm]",  
  
  # breaks = 99,    # Hur många staplar  
  # col = "blue",   # Färg  
)
```



1.9.6 Error plot med plotCI()

Används för att illustrera medelvärdet (en punkt) \pm standardavvikelse eller standard error of the mean (SEM, se 2.1 Enkel statistik).

```
# Data för att plotta
peng_mean <- aggregate(
  flipper_length_mm ~ species,
  data = penguins,
  FUN = mean
)

peng_sd <- aggregate(
  flipper_length_mm ~ species,
  data = penguins,
  FUN = sd
)

# Plot
plotCI(
  x = c(2,3,4), # x-koordinater att placera punkter på
```

```

y = peng_mean$flipper_length_mm, # y-koordinater att placera punkter
  ↪ på

xlab = "Species",
ylab = "Flipper length [mm]",

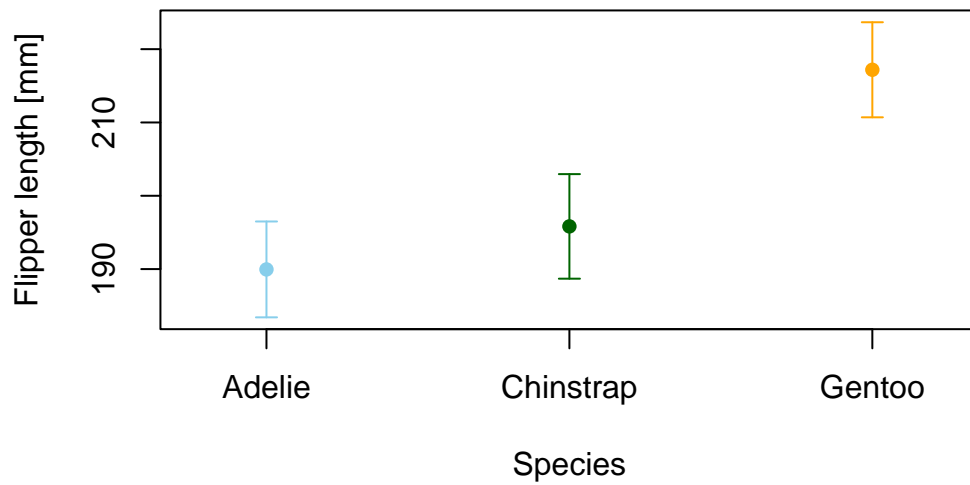
# Upper interval, alltså övre gränsen för sträcken, är lika med
# medelvärdet + standardavvikelsen
ui = peng_mean$flipper_length_mm + peng_sd$flipper_length_mm,
# Lower interval, alltså den nedre gränsen, är lika med
# medelvärdet - standardavvikelsen
li = peng_mean$flipper_length_mm - peng_sd$flipper_length_mm,

xlim = c(1.75,4.25), # För att ge lite extra plats på sidorna

xaxt = "n", # Ta bort siffrorna på x-axeln

pch = 16,
col = c("skyblue", "darkgreen", "orange")
)
axis(
  side = 1, # vilken sida/axel att lägga till (1 = botten, 2 = vänster,
  ↪ osv.)
  at = c(2,3,4), # Vid vilka x-koordinater att placera text
  labels = peng_mean$species # Lägg till arterna på x-axeln
)

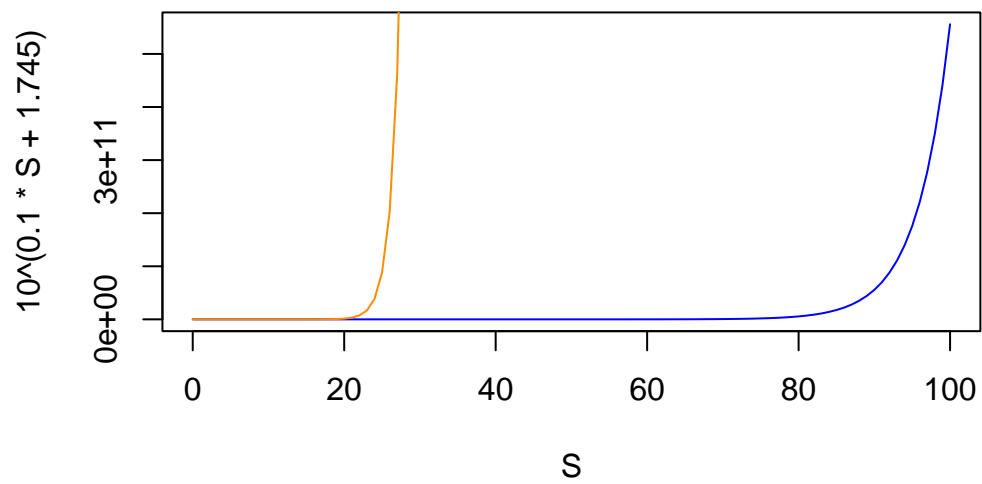
```

1.9.7 Plot av funktion

```
# Definiera en funktion som en funktion med bara ett argument.
curve_fun <- function(x) {
  10^(0.36*x+1.945)
}

curve(
  10^(0.10*S+1.745), # Matematiska funktionen att rita
  xname="S",         # Vad 'x' heter om man ger den matematiska
  ↪ funktionen direkt
  xlim=c(0,100),     # Intervallet
  col = "blue"
)
curve(
  curve_fun,          # Namn på funktionen med funktionen
  xlim = c(0,100),
  col = "darkorange",
  add = TRUE          # Lägg till linjen i existerande graf
)
```



2 Stats

2.0.1 Tolkning av p-värde

Drivna över bristningsgränsen av kursen har en student blivit galen och vandrar, med slö blick, vilset i stadsskogen. Studenten betraktar ett träd. Hur högt är trädet? Vilsen betraktar studenten ett annat träd och stapplar vidare. Vad är sannolikheten att genomsnittshöjden på de träd studenten slumpmässigt observerar skiljer sig från genomsnittshöjden på alla träd i stadsskogen? Kanske de skiljer sig från träden i fjällen?

- H_0 = Ingen skillnad mellan medelvärden
- H_1 = Skillnad mellan medelvärden

p-värdet är sannolikheten att en stackars vilsen student slumpmässigt skulle betrakta dessa träd och konstatera att deras höjd skiljer sig från resten av skogens (alltså acceptera H_1), när det i verkligheten inte finns någon skillnad mellan observerade och skogens medelvärden (alltså om H_0 är sann).

- Om p-värde $>$ alfa, alltså $p > 0.05$, säger vi att det inte finns en skillnad (acceptera H_0).
- Om p-värde $<$ alfa, alltså $p < 0.05$, säger vi att det finns en skillnad (acceptera H_1).

2.0.2 Rapportera test

Rapportera alltid testets namn, statistiken (t.ex. t-/F-värdet), frihetsgrader och p-värde, samt en mening som ger slutsatsen/tolkningen av testet. Andra relevanta saker kan också inkluderas, såsom konfidens intervall.

Exempel: Förklarande mening ([testets namn], t([frihetsgrader]) = [värdet], $p =$ [värdet]).

Det fanns en skillnad mellan Grupp 1 och den förväntade vikten ($\mu = 3000$ g) enligt internet (One sample t-test, $t(150) = 18.776$, $p < 2.2e-16$).

Tips från coachen, gör detta snyggare än jag...

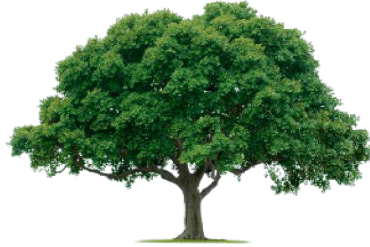
2.0.3 Formel notation

Många av funktionerna för de statistiska testen kan, eller måste, ges en formel. Formler har följande komponenter:

- *Respons*, en kontinuerlig variabel vi vill förutspå, värdet på y-axeln
- *Faktor*, en kategorisk variabel vilken delar in *Respons* i grupper (för regression är detta en kontinuerlig variabel som direkt orsakar *Respons*)

- ‘~’, skiljer *Respons* från *Faktor*, alltså ger Vänster- och Högerled (`Respons ~ Faktor`)
- ‘+’, adderar en ytterligare *Faktor* (`Respons ~ Faktor_1 + Faktor_2`)
- ‘*’, adderar en ytterligare *Faktor* **och** interaktionen (`Respons ~ Faktor_1 * Faktor_2`
)
- ‘:’, adderar enbart interaktionen (`Respons ~ Faktor_1:Faktor_2`)

Beslutsträd statistik



Blå box – gå vidare i trädet

Grön box – gå vidare till ANOVOR

Lila box – gå vidare till analys av samband

Röd box – du har nått ditt test

Svart box – testet tas inte upp på denna kurs

Figure 1: Stats flowchart 1

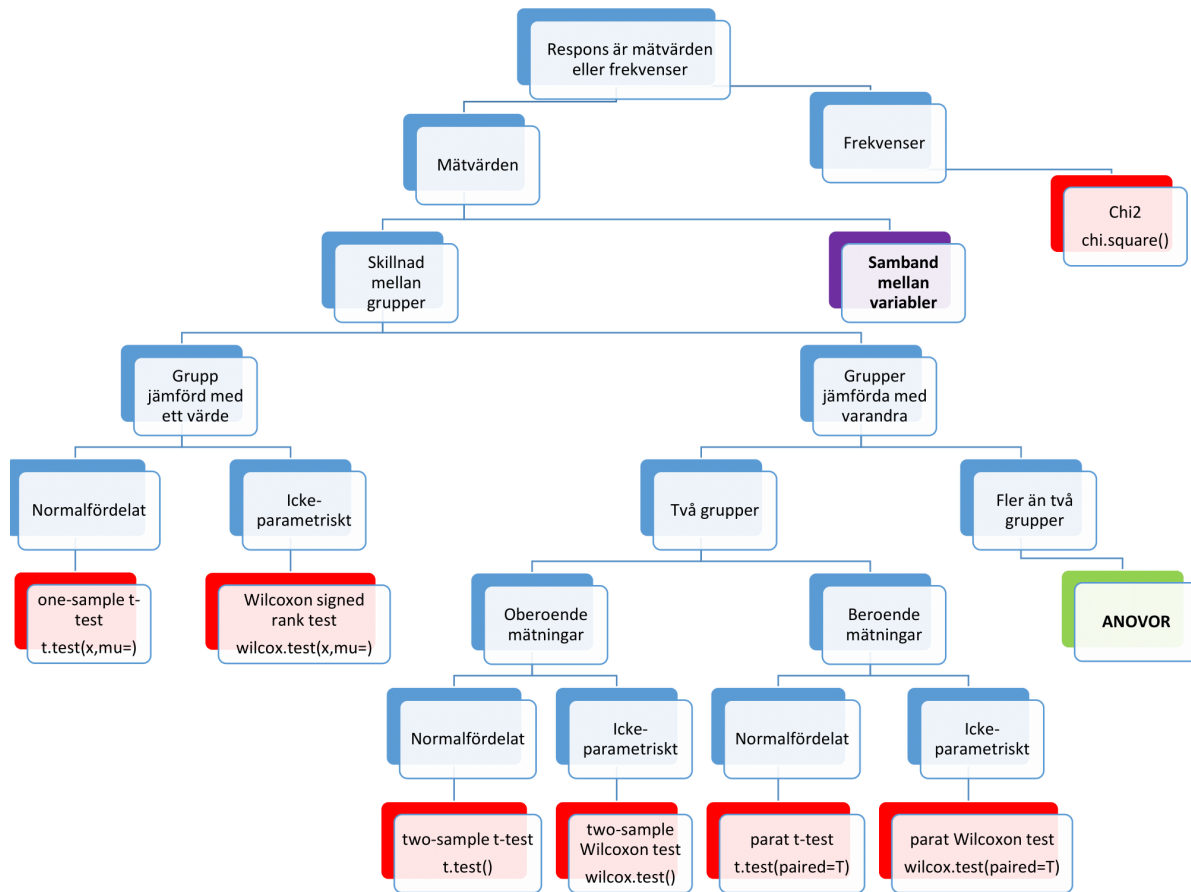


Figure 2: Stats flowchart 2

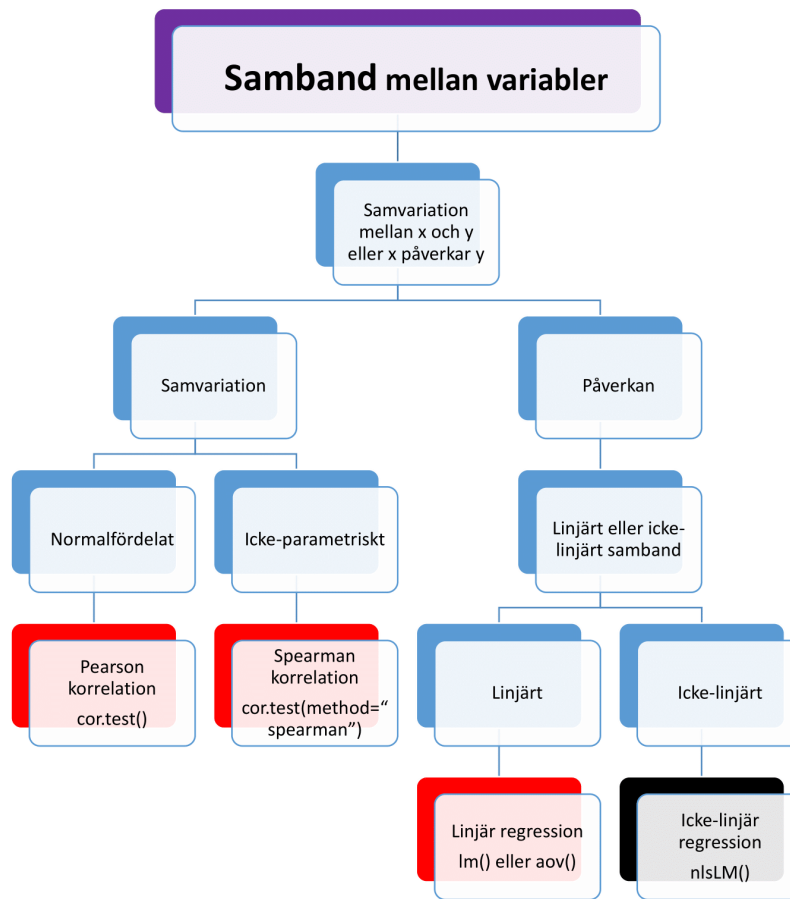


Figure 3: Stats flowchart 3

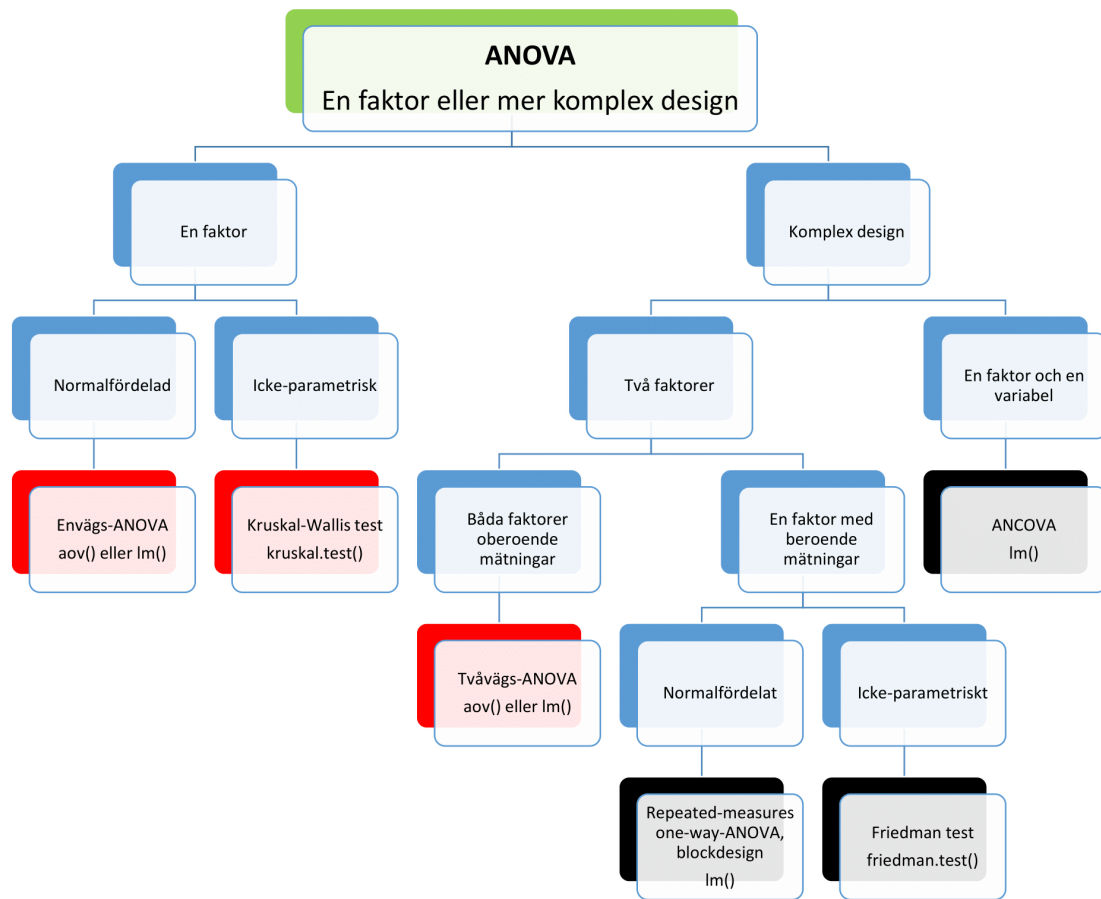


Figure 4: Stats flowchart 4

2.1 Enkel statistik

Några enkla/grundläggande statistik funktioner.

```
mean(penguins$bill_length_mm, na.rm = TRUE) # Medelvärde
```

```
[1] 43.92193
```

```
median(penguins$bill_length_mm, na.rm = TRUE) # Median
```

```
[1] 44.45
```

```
sum(penguins$bill_length_mm, na.rm = TRUE) # Summa av vektor
```

```
[1] 15021.3
```

```
sd(penguins$bill_length_mm, na.rm = TRUE) # Standardavvikelse
```

```
[1] 5.459584
```

```
# Funktioner som ger vektorer med svar. Fungerar på både matriser & data  
↪ frames!  
# N.B. stor bokstav i mitten! Finns andra funktioner med liknande namn.  
rowSums(M) # ger en (kolumn) vektor med summan för varje rad.
```

```
  r1  r2  r3  r4  r5  
1.35 0.45 0.68 0.68 0.43
```

```
colSums(M) # ger en (rad) vektor med summan för varje kolumn.
```

```
col1 col2 col3 col4 col5  
0.90 0.68 0.68 0.68 0.65
```

```
rowMeans(M) # Samma, men för medelvärde.
```

```
      r1      r2      r3      r4      r5  
0.270 0.090 0.136 0.136 0.086
```

```
colMeans(M) # Samma, men för medelvärde.
```

```
col1 col2 col3 col4 col5  
0.180 0.136 0.136 0.136 0.130
```

*# Aggregate är lite speciell. Den grupperar rader efter en faktor och
↪ applicerar en annan funktion på varje grupp.*

```
aggregate(  
  bill_length_mm ~ island,  
  data = penguins,  
  FUN = mean, # Använd 'mean' eller 'median'  
)
```

```
      island bill_length_mm  
1      Biscoe      45.25749  
2       Dream      44.16774  
3 Torgersen      38.95098
```

Standard error of the mean (SEM) finns det ingen egen funktion för, men vi kan skapa en. Formeln är $SEM = \frac{S_d}{\sqrt{n}}$, där S_d = standardavvikelse och n = antal observationer. SEM beskriver hur exakt/pålitligt medelvärdet är om det används som det sanna medelvärdet för populationen.

```
SEM <- function(x, na.rm = FALSE) {  
  # Om argumentet na.rm = TRUE, ta bort NA från x  
  if (na.rm) {  
    x <- na.omit(x)  
  }  
  
  # Beräkna SEM  
  SEM <- sd(x)/sqrt(length(x))  
  return(SEM)  
}
```

```
}

SEM(penguins$bill_length_mm, na.rm = TRUE)
```

```
[1] 0.2952205
```

2.2 Transformation

Om data inte ser nice ut, prova att transformera data (för paired/beroende transformera differensen). För denna kurs prova logaritmering.

```
log()    # Basen e
log10()  # Basen 10
```

2.3 Sannolikhet

2.3.1 Slumpade tal

Slumpa ett tal från normalfördelning. Ungefär 96 % av alla observationer i en normalfördelad population ligger inom \pm två standardavvikelser.

```
rnorm(
  n = 5,      # Antal tal
  mean = 0,   # Väntevärde för fördelningen
  sd = 1      # Standard avvikelse
)
```

```
[1] -1.1219549 -0.7548793  0.1133823  0.1916903  0.8282490
```

Slumpade tal från binomialfördelning. Ger n tal där varje tal är hur många gynnsamma utfall det blev, baserat på totalt antal försök och sannolikheten.

```
rbinom(
  n = 5,      # Antal tal
  size = 10,  # Totalt antal försök
  prob = 0.5  # Sannolikhet för gynnsamt utfall
)
```

```
[1] 6 6 4 7 7
```

Slumpade tal från en uniform fördelning (samma sannolikhet för för varje tal).

```
runif(  
  n = 5,    # Antal tal  
  min = 0,  # Nedre intervall  
  max = 10 # Övre intervall  
)
```

```
[1] 0.6287113 9.5105390 5.0900921 9.3945588 6.7392836
```

2.3.2 Binomial fördelning

Min binomiala studie:

- 20 försök
- varje försök är Ja/Nej
- 37 % sannolikhet för Ja för varje oberoende försök

För utfall med binomial fördelning används `dbinom()` för att beräkna sannolikheten för exakt x antal gynsamma utfall.

```
f5 <- dbinom(  
  x = 5, # Exakt antal 'Ja'  
  size = 20, # Totalt antal försök  
  prob = 0.37 # Sannolikheten för försöket  
)  
print(paste("Sannolikhet att exakt fem av 20 försök blir 'Ja':", f5))
```

```
[1] "Sannolikhet att exakt fem av 20 försök blir 'Ja': 0.10508981363014"
```

Dessa sannolikheter kan adderas.

```
f6 <- dbinom(  
  x = 6, # Exakt 6st Ja  
  size = 20,  
  prob = 0.37
```

```
)
print(paste("p att exakt 5-6st av 20 försök blir 'Ja':", (f5+f6)))
```

```
[1] "p att exakt 5-6st av 20 försök blir 'Ja': 0.259388349515663"
```

eller `1 - pbinom()` för att beräkna sannolikheten för alla utfall **över** det man anger.

```
f15_20 <- (1 - pbinom(
  q = 14, # utfall över det angivna
  size = 20,
  prob = 0.37
))
print(paste("p att få 15 eller fler 'Ja':",f15_20))
```

```
[1] "p att få 15 eller fler 'Ja': 0.000621595787321794"
```

Enbart `pbinom()` ger den motsatta sannolikheten (alltså 0-14 Ja) vilket är komplement till 15-20 Ja. Använd `lower.tail = FALSE` för att få 15-20 Ja istället.

```
f15_20_igen <- pbinom(
  q = 14,
  size = 20,
  prob = 0.37,
  lower.tail = FALSE # Istället för 1 - pbinom()
)
print(paste("p att få 15 eller fler 'Ja':",f15_20_igen))
```

```
[1] "p att få 15 eller fler 'Ja': 0.000621595787321803"
```

2.4 Skillnad mellan grupper

2.4.1 T-test

2.4.1.1 Krav/antaganden

- Data på intervall eller kvotskala (kontinuerlig)
- Normalfördelad (parametrisk) inom varje grupp

- Lika varians (homogen varians, ej för Welch t-test)
- Inga outliers

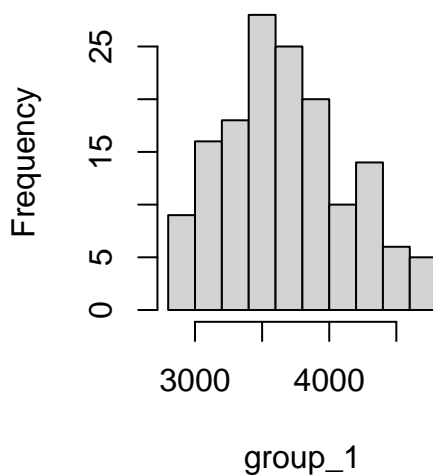
```
group_1 <- penguins$body_mass_g[penguins$species == "Adelie"]

par(mfrow = c(1,2)) # Ändrar hur många "rutor/celler" för
# plots det finns enligt rad x column. Bra vana att alltid
# ändra tillbaka till standard c(1,1) efteråt.

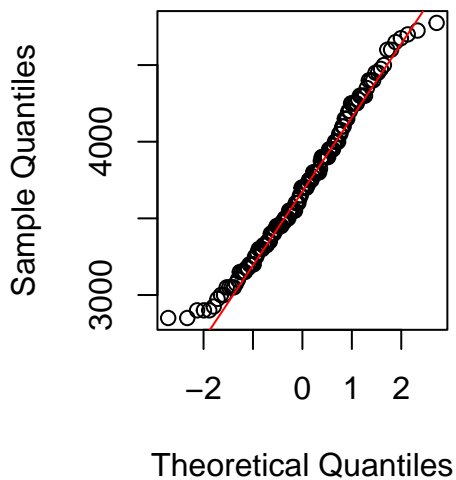
hist(group_1)

qqnorm(group_1)
qqline(group_1, col = "red")
```

Histogram of group_1



Normal Q-Q Plot



```
par(mfrow = c(1,1)) # Ändra tillbaka inställningarna.
```

2.4.1.2 Ensidigt

För att testa om en grupp med kontinuerlig data skiljer sig från ett känt eller teoretiskt väntevärde.

```

grupp_1 <- penguins$body_mass_g[penguins$species == "Adelie"]

t.test(
  x = grupp_1, # En vektor
  mu = 3000    # Väntevärdet vi hittade på internet
)

```

One Sample t-test

```

data:  grupp_1
t = 18.776, df = 150, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 3000
95 percent confidence interval:
 3626.926 3774.398
sample estimates:
mean of x
 3700.662

```

Resultat:

Det fanns en skillnad mellan Grupp 1 och den förväntade vikten enligt internet (One sample t-test, $t(150) = 18.776$, $p < 2.2e-16$).

2.4.1.3 Tvåsidigt

För att testa om det finns en skillnad mellan två grupper av kontinuerlig data.

```

grupp_1 <- penguins$body_mass_g[penguins$species == "Adelie"]
grupp_2 <- penguins$body_mass_g[penguins$species == "Gentoo"]

t.test(
  x = grupp_1, # En vektor
  y = grupp_2, # En annan vektor
)

```

Welch Two Sample t-test

```

data:  grupp_1 and grupp_2
t = -23.386, df = 249.64, p-value < 2.2e-16
alternative hypothesis: true difference in means is not equal to 0

```

```
95 percent confidence interval:
 -1491.183 -1259.525
sample estimates:
mean of x mean of y
 3700.662  5076.016
```

Alternativt sätt att skriva koden är med formel.

```
peng_groups <- penguins[ which(penguins$species == "Adelie" |
  ↪ penguins$species == "Gentoo"), ]

t.test( # Respons = mätdata & Faktor = två olika arter (alltså två
  ↪ grupper)
  body_mass_g ~ species,
  data = peng_groups
)
```

Welch Two Sample t-test

```
data: body_mass_g by species
t = -23.386, df = 249.64, p-value < 2.2e-16
alternative hypothesis: true difference in means between group Adelie and group Gentoo is not
95 percent confidence interval:
 -1491.183 -1259.525
sample estimates:
mean in group Adelie mean in group Gentoo
      3700.662           5076.016
```

Resultat:

Det fanns en skillnad mellan Grupp 1 och Grupp 2 (Welch two sample t-test, $t(249.64) = -23.386$, $p < 2.2e-16$).

2.4.1.4 Paired/beroende

First rule of Crayfish Fight Club is you do not talk about Crayfish Fight Club.

Vi studerar kräftor och vill undersöka vilken effekt storleken på klorna har på vilken kräfta som vinner strider om resurser. För att göra detta snorklar vi någonstans tropiskt och letar efter kräftor som slåss. Efter några månader "hårt arbete" har vi samlat ihop följande data. Varje rad är storleken på klorna i cm med vinnare och förlorare i respektive kolumn.


```
crayfish_fight_club <- data.frame(
  winner = c(86, 84, 75, 93, 102, 87, 88, 91, 87, 74),
  loser = c( 70, 79, 68, 85,  90, 89, 91, 82, 80, 69)
)
head(crayfish_fight_club)
```

	winner	loser
1	86	70
2	84	79
3	75	68
4	93	85
5	102	90
6	87	89

Alltså består varje rad av mätningar på två individer där grupperingen är **beroende** på vem de jämförs med, och därför gör vi ett parat t-test. (Det känns inte rimligt att jämföra vinnaren på rad tre (75 cm) med förloraren på rad fyra (85 cm) eftersom de inte stred med varandra, vilket är vad vi hade gjort om vi behandlat data som oberoende, alltså `paired = FALSE`.) Notera att för parat/beroende data måste **differensen** vara normalfördelad.

```
t.test(
  crayfish_fight_club$winner,
  crayfish_fight_club$loser,
  paired = TRUE
)
```

Paired t-test

```
data:  crayfish_fight_club$winner and crayfish_fight_club$loser
t = 3.5266, df = 9, p-value = 0.006448
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
 2.29474 10.50526
sample estimates:
mean difference
      6.4
```

Resultat:

Paired t-test, $t(9) = 3.5266$, $p = 0.006448$, Signifikant.

2.4.1.5 Wilcox-test (icke parametriskt)

För när data inte uppfyller krav för t-test eller vi vill titta på skillnader i median.

```
wilcox.test( # Motsvarar vanligt t-test för två grupper
  grupp_1,
  grupp_2
)

wilcox.test( # Med formel
  body_mass_g ~ species,
  data = peng_groups
)

wilcox.test( # Motsvarar parat t-test för beroende data
  crayfish_fight_club$winner,
  crayfish_fight_club$loser,
  paired = TRUE
)
```

```
Warning in wilcox.test.default(crayfish_fight_club$winner,
crayfish_fight_club$loser, : cannot compute exact p-value with ties
```

Wilcoxon signed rank test with continuity correction

```
data:  crayfish_fight_club$winner and crayfish_fight_club$loser
V = 52, p-value = 0.01431
alternative hypothesis: true location shift is not equal to 0
```

Resultat:

Ingen skillnad.

För denna kurs, ignorera `Warning: cannot compute exact p-value with ties`. Det betyder att det finns två av samma mätvärde vilket inte går att rangordna. (Om data är `c(25, 26, 26, 27)` är det `(1,2,3,4)` eller `(1,3,2,4)`?)

2.4.1.6 Bootstrap (icke parametriskt)

För när data inte uppfyller krav för t-test men vi behöver ett konfidensintervall. Resurskrävande, alltså om du har mycket data tar det längre tid att köra funktionen. Ekvivalent med Wilcoxon men ger konfidensintervall.

```
boot.t.test( # Med två vektorer
  grupp_1,
  grupp_2
)
```

Bootstrap Welch Two Sample t-test

```
data:  grupp_1 and grupp_2
bootstrap p-value < 2.2e-16
bootstrap difference of means (SE) = -1374.597 (58.54662)
95 percent bootstrap percentile confidence interval:
-1492.602 -1258.417
```

Results without bootstrap:

```
t = -23.386, df = 249.64, p-value < 2.2e-16
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-1491.183 -1259.525
sample estimates:
mean of x mean of y
3700.662  5076.016
```

```
boot.t.test( # Med formel
  body_mass_g ~ species,
  data = peng_groups
)
boot.t.test( # Paired/beroende data
  crayfish_fight_club$winner,
  crayfish_fight_club$loser,
  paired = TRUE
)
```

2.4.2 ANOVA

ANOVA undersöker skillnad mellan många grupper och faktorernas effekt på respons variabeln (liknande regression där kontinuerlig variabel kausalt påverkar respons).

2.4.2.1 Krav/antaganden

Anova är nästan samma som t-test,

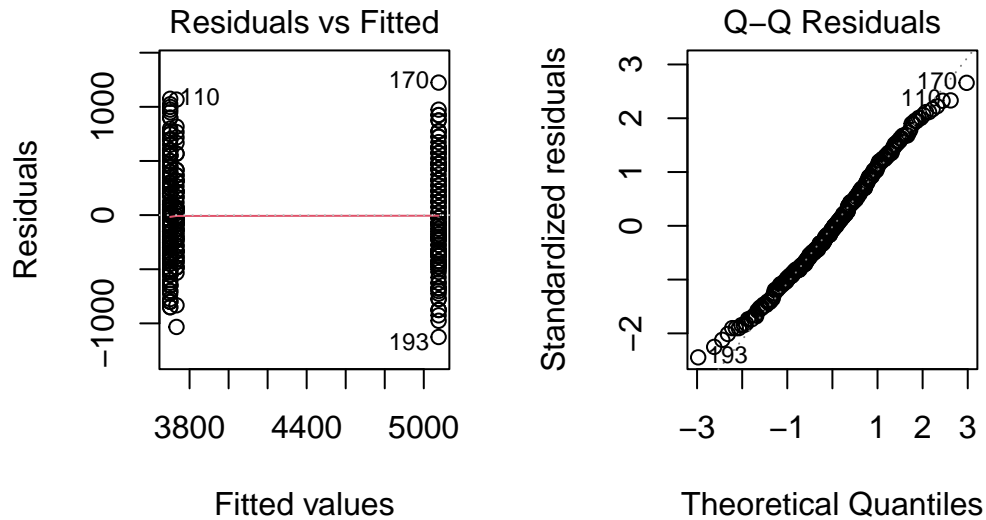
- Data på intervall eller kvotskala (kontinuerlig)
- Normalfördelad (parametrisk) inom varje grupp (**Bootstrap**)
- Lika varians (homogen varians, ej för Welch t-test)
- Inga outliers
- **Oberoende data** (vi kör inte parat/beroende i denna kurs)
- **Förutsätter lika varians mellan grupper**
- **Kan hantera fler än två grupper samt fler än en faktor**

```
# Skapa modellen, sedan diagnostik.
diagnostic_model <- aov(
  body_mass_g ~ species,
  data = penguins
)

par(mfrow = c(1,2))

plot(diagnostic_model, which = 1) # Lika varians om
# spridningen/"längden" på varje stapel med punkter är lika.

plot(diagnostic_model, which = 2) # QQ-plot för normalfördelning.
```



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

2.4.2.2 Envägs ANOVA

Envägs ANOVA innebär att vi använder en faktor (med flera grupper). Hur hittar man enkelt faktorer och grupper i ett dataset? En faktor är en kolumn med grupper. I `penguins` data frame är `penguins$species` en kolumn med grupper, alltså en faktor.

```
unique(penguins$species) # Unika element i kolumnen,
```

```
[1] Adelie    Gentoo    Chinstrap
Levels: Adelie Chinstrap Gentoo
```

```
# alltså, faktorn 'species' har grupperna 'Adelie', 'Gentoo',  
↪ 'Chinstrap'
```

ANOVA med funktionen `aov()`, `summary()` och `TukeyHSD()`.

```
anova_aov <- aov( # Skapa modell
  body_mass_g ~ species,
  data = penguins
)
summary(anova_aov) # Kolla om det fanns en skillnad mellan någon av
↳ grupperna
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
species	2	146864214	73432107	343.6	<2e-16 ***
Residuals	339	72443483	213698		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
 2 observations deleted due to missingness

```
TukeyHSD(anova_aov) # Kolla mellan vilka grupper det fanns en skillnad
```

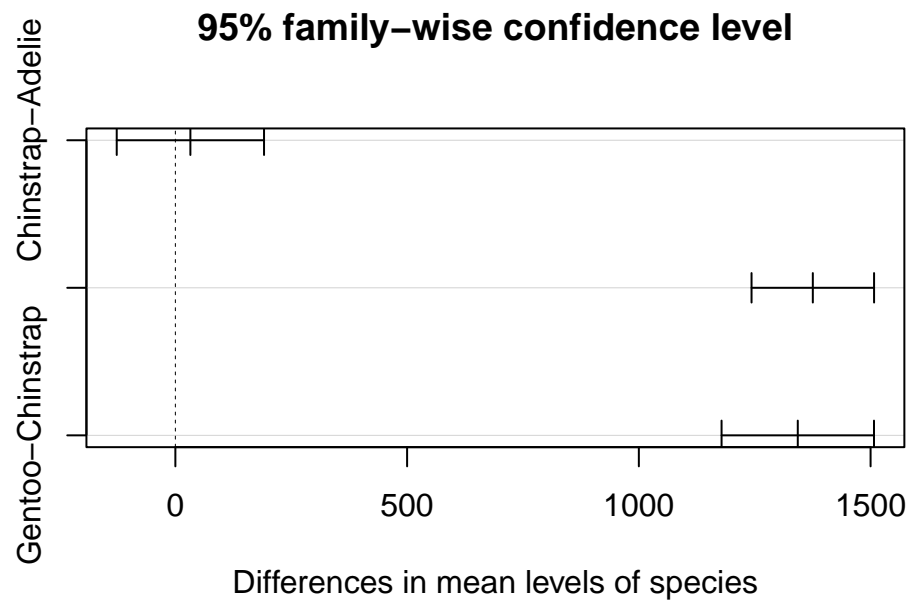
Tukey multiple comparisons of means
 95% family-wise confidence level

Fit: aov(formula = body_mass_g ~ species, data = penguins)

\$species

	diff	lwr	upr	p adj
Chinstrap-Adelie	32.42598	-126.5002	191.3522	0.8806666
Gentoo-Adelie	1375.35401	1243.1786	1507.5294	0.0000000
Gentoo-Chinstrap	1342.92802	1178.4810	1507.3750	0.0000000

```
plot(TukeyHSD(anova_aov)) # Plot
```



ANOVA med funktionen `lm()`, `anova()` och `summary()`. Detta ger problem med att göra post-hoc test (`TukeyHSD()`) för att hitta mellan vilka grupper skillnaden finns. Fördelen skulle vara att få ett intercept och möjligen bygga en matematisk modell.

```
anova_lm <- lm( # Skapa modell
  body_mass_g ~ species,
  data = penguins
)
anova(anova_lm) # Kolla om det fanns en skillnad mellan någon av
  ↳ grupperna
```

Analysis of Variance Table

Response: body_mass_g

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
species	2	146864214	73432107	343.63	< 2.2e-16 ***
Residuals	339	72443483	213698		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
summary(anova_lm) # Kolla mellan vilka grupper det fanns en skillnad
```

Call:

```
lm(formula = body_mass_g ~ species, data = penguins)
```

Residuals:

Min	1Q	Median	3Q	Max
-1126.02	-333.09	-33.09	316.91	1223.98

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3700.66	37.62	98.37	<2e-16 ***
speciesChinstrap	32.43	67.51	0.48	0.631
speciesGentoo	1375.35	56.15	24.50	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 462.3 on 339 degrees of freedom

(2 observations deleted due to missingness)

Multiple R-squared: 0.6697, Adjusted R-squared: 0.6677

F-statistic: 343.6 on 2 and 339 DF, p-value: < 2.2e-16

2.4.2.3 Tvåvägs ANOVA

Samma som envägs ANOVA men med två faktorer. Se [Formel notation](#).

```
anova2_aov <- aov( # Skapa modell
  body_mass_g ~ species * sex,
  data = penguins
)
summary(anova2_aov) # Kolla om det fanns en skillnad mellan någon av
↪ grupperna
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
species	2	145190219	72595110	758.358	< 2e-16 ***
sex	1	37090262	37090262	387.460	< 2e-16 ***
species:sex	2	1676557	838278	8.757	0.000197 ***
Residuals	327	31302628	95727		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

11 observations deleted due to missingness

```
TukeyHSD(anova2_aov) # Kolla mellan vilka grupper det fanns en skillnad
```

Tukey multiple comparisons of means
95% family-wise confidence level

```
Fit: aov(formula = body_mass_g ~ species * sex, data = penguins)
```

\$species

	diff	lwr	upr	p adj
Chinstrap-Adelie	26.92385	-80.0258	133.8735	0.8241288
Gentoo-Adelie	1386.27259	1296.3070	1476.2382	0.0000000
Gentoo-Chinstrap	1359.34874	1248.6108	1470.0866	0.0000000

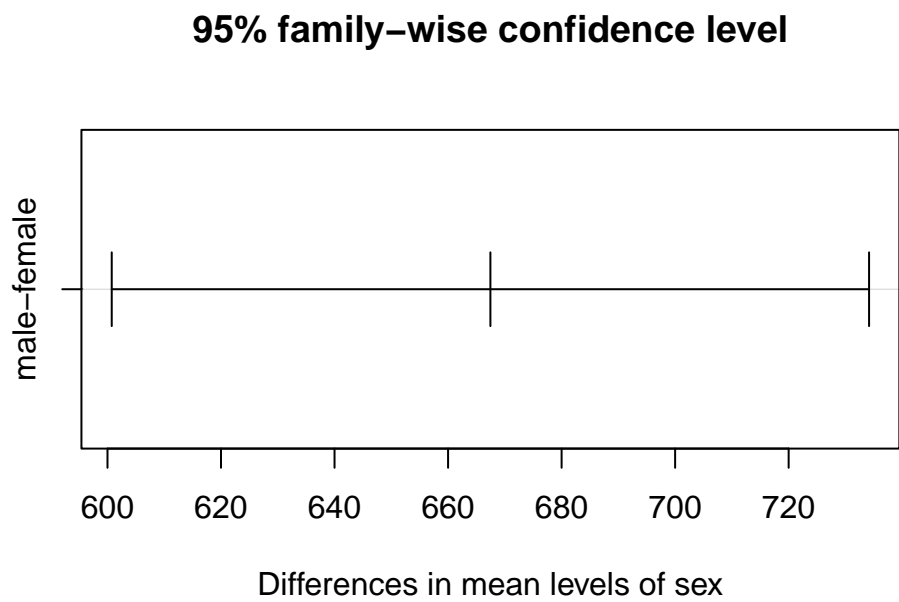
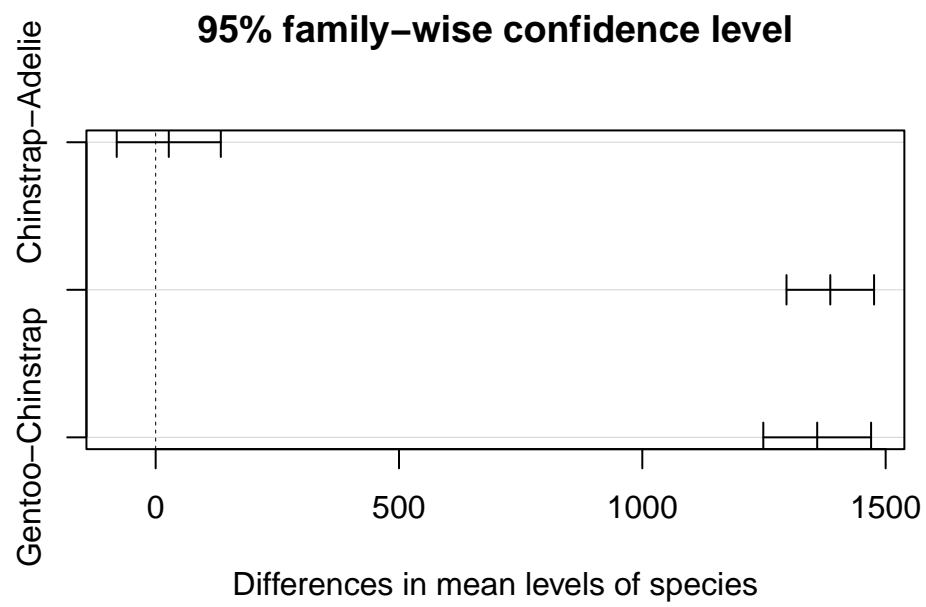
\$sex

	diff	lwr	upr	p adj
male-female	667.4577	600.7462	734.1692	0

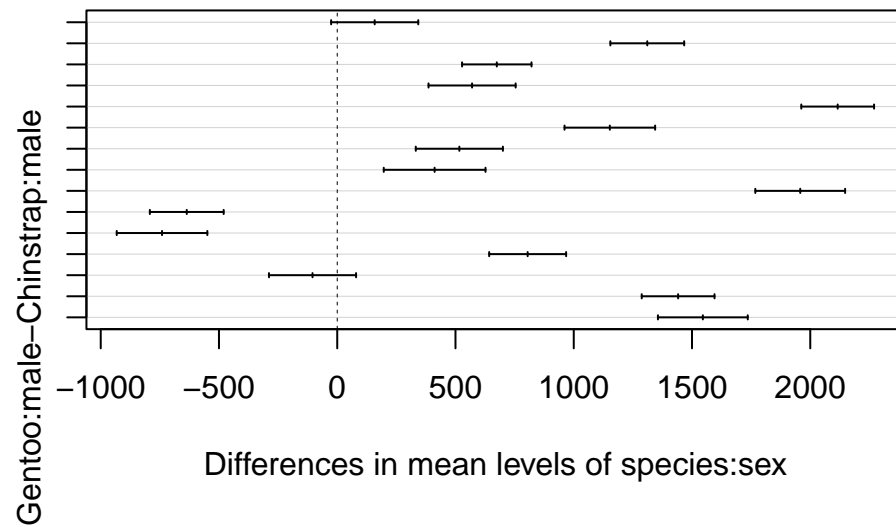
\$`species:sex`

	diff	lwr	upr	p adj
Chinstrap:female-Adelie:female	158.3703	-25.7874	342.5279	0.1376213
Gentoo:female-Adelie:female	1310.9058	1154.8934	1466.9181	0.0000000
Adelie:male-Adelie:female	674.6575	527.8486	821.4664	0.0000000
Chinstrap:male-Adelie:female	570.1350	385.9773	754.2926	0.0000000
Gentoo:male-Adelie:female	2116.0004	1962.1408	2269.8601	0.0000000
Gentoo:female-Chinstrap:female	1152.5355	960.9603	1344.1107	0.0000000
Adelie:male-Chinstrap:female	516.2873	332.1296	700.4449	0.0000000
Chinstrap:male-Chinstrap:female	411.7647	196.6479	626.8815	0.0000012
Gentoo:male-Chinstrap:female	1957.6302	1767.8040	2147.4564	0.0000000
Adelie:male-Gentoo:female	-636.2482	-792.2606	-480.2359	0.0000000
Chinstrap:male-Gentoo:female	-740.7708	-932.3460	-549.1956	0.0000000
Gentoo:male-Gentoo:female	805.0947	642.4300	967.7594	0.0000000
Chinstrap:male-Adelie:male	-104.5226	-288.6802	79.6351	0.5812048
Gentoo:male-Adelie:male	1441.3429	1287.4832	1595.2026	0.0000000
Gentoo:male-Chinstrap:male	1545.8655	1356.0392	1735.6917	0.0000000

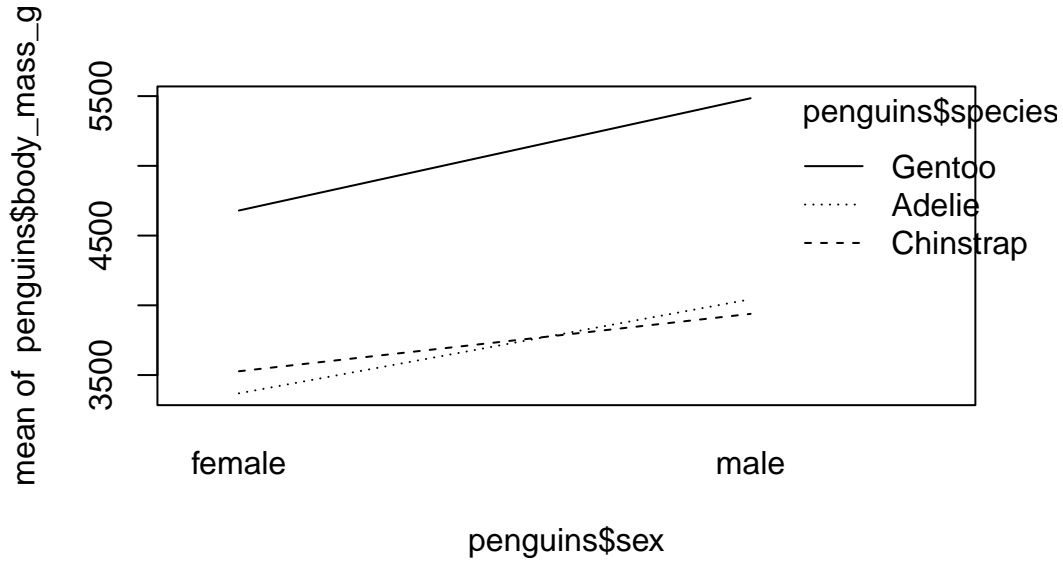
```
plot(TukeyHSD(anova2_aov)) # Plot
```



95% family-wise confidence level



```
# Interaktions plot
interaction.plot(
  x.factor = penguins$sex,          # x-axis
  trace.factor = penguins$species, # line
  response = penguins$body_mass_g, # y-axis
)
```



2.4.2.4 Kruskal-Wallis (icke parametrisk)

Icke parametrisk variant av **envägs** ANOVA

```
kruskal.test(
  body_mass_g ~ species,
  data = penguins
)
```

Kruskal-Wallis rank sum test

data: body_mass_g by species

Kruskal-Wallis chi-squared = 217.6, df = 2, p-value < 2.2e-16

Detta är utanför kursen! För att hitta mellan vilka grupper skillnaden finns (post-hoc). Kan inte hantera NA och har kraschat R...

```
pairwise.wilcox.test(
  x = penguins$body_mass_g, # Vektor med mätdata
  g = penguins$species,     #
  p.adjust.method = "holm"
```

```
)
```

Pairwise comparisons using Wilcoxon rank sum test with continuity correction

data: penguins\$body_mass_g and penguins\$species

```
      Adelie Chinstrap
Chinstrap 0.49      -
Gentoo    <2e-16 <2e-16
```

P value adjustment method: holm

2.4.2.5 Bootstrap (icke parametriskt)

Om någon av grupperna inte är normalfördelade kan man använda bootstrap. Alla grupper ska fortfarande ha samma varians.

ANOVA.boot() kan inte hantera NA, så se till att filtrera data frame.

```
# Subset to remove NA
peng_boot <- penguins[!is.na(penguins$body_mass_g), ]
peng_boot <- peng_boot[!is.na(peng_boot$species), ]
peng_boot <- peng_boot[!is.na(peng_boot$sex), ]

anova_boot <- ANOVA.boot(
  body_mass_g ~ species * sex,
  data = peng_boot,
  type = "residual" # Default,
  # type = "wild"
)
anova_boot[c("terms", "df", "p-values")]
```

```
$terms
[1] "species" "sex" "species:sex" "Residuals"
```

```
$df
[1] 2 1 2 327
```

```
$`p-values`
[1] 0 0 0
```

Detta är inte särskilt nice output format så vi undviker helst att använda `ANOVA.boot()`.

2.5 Kontinuerliga samband

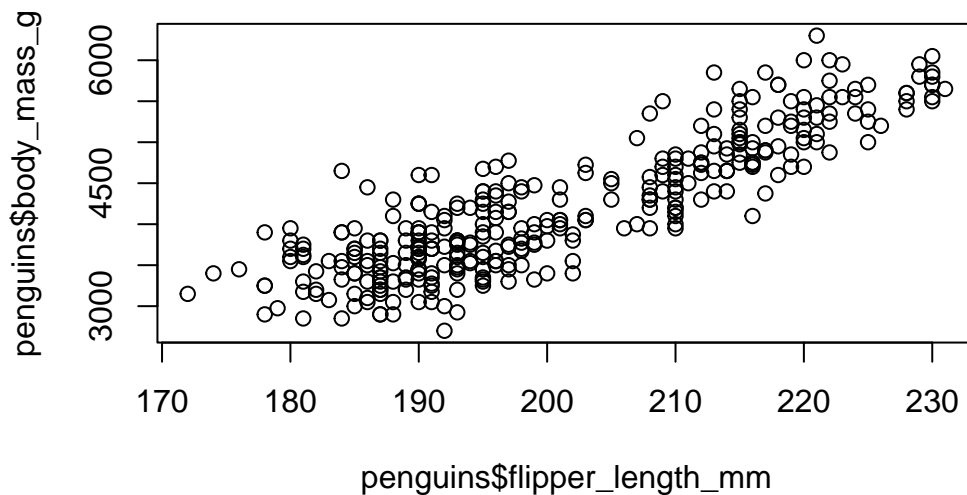
2.5.1 Samvariation/korrelation

När två kontinuerliga variabler ökar/minskar tillsammans (positiv korrelation) eller i motsatt riktning (negativ korrelation), möjligtvis till följd av en gemensam tredje (dold) variabel.

2.5.1.1 Krav/antaganden

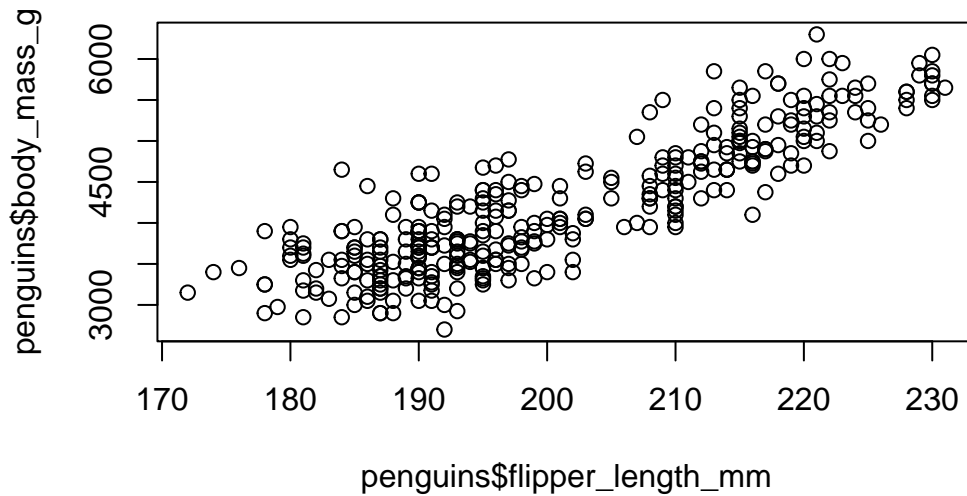
- Två kontinuerliga variabler/mätdata
- Linjärt samband (kan göras linjär genom transformation om nödvändigt)

```
plot( # Ögonmätta att sambandet inte är uppenbarligen icke-linjärt
      penguins$flipper_length_mm,
      penguins$body_mass_g
    )
```



2.5.1.2 Pearson korrelation

```
plot( # Kolla alltid data
      penguins$flipper_length_mm,
      penguins$body_mass_g
    )
```



```
cor.test(
  penguins$flipper_length_mm,
  penguins$body_mass_g
)
```

Pearson's product-moment correlation

```
data:  penguins$flipper_length_mm and penguins$body_mass_g
t = 32.722, df = 340, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.843041 0.894599
sample estimates:
cor
```

0.8712018

p-värdet tolkas som vanligt, cor är r^2 -värdet som beskriver styrka och riktning av korrelationen.

2.5.1.3 Spearman (icke parametrisk)

```
cor.test(  
  penguins$flipper_length_mm,  
  penguins$body_mass_g,  
  method = "spearman" # Specificera spearman  
)
```

Warning in cor.test.default(penguins\$flipper_length_mm, penguins\$body_mass_g, :
Cannot compute exact p-value with ties

Spearman's rank correlation rho

```
data:  penguins$flipper_length_mm and penguins$body_mass_g  
S = 1066875, p-value < 2.2e-16  
alternative hypothesis: true rho is not equal to 0  
sample estimates:  
      rho  
0.8399741
```

För denna kurs, ignorera Warning: cannot compute exact p-value with ties. Det betyder att det finns två av samma mätvärde vilket inte går att rangordna. (Om data är c(25, 26, 26, 27) är det (1,2,3,4) eller (1,3,2,4)?)

2.5.2 Regression

Regression används då en kontinuerlig variabel kausalt orsakar en annan kontinuerlig variabel.

2.5.2.1 Krav/antaganden

- Linjärt samband
- Normalfördelad (parametrisk)
- Lika varians


```

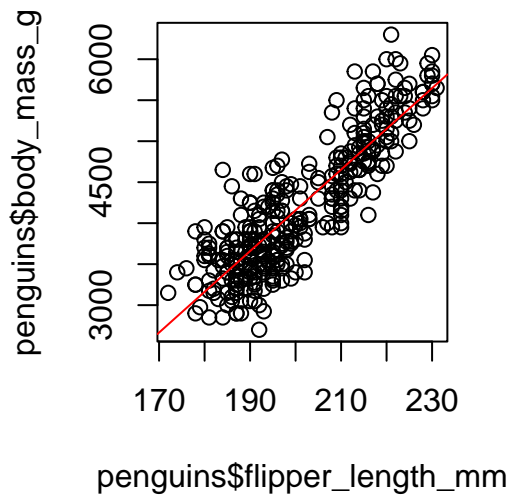
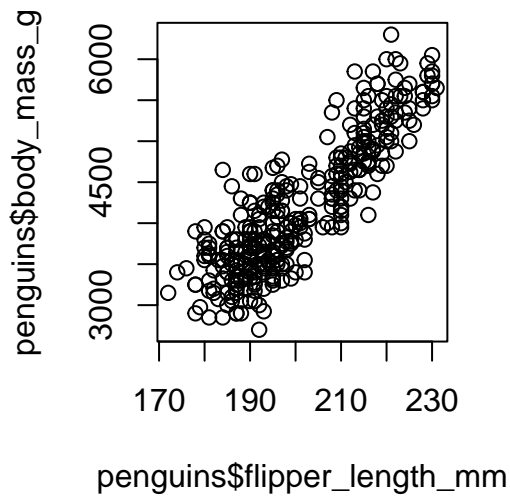
par(mfrow = c(1,2))

plot( # Ögonmätta om det finns en linjär trend.
      x = penguins$flipper_length_mm,
      y = penguins$body_mass_g
    )

# Skapa modellen, sedan diagnostik.
diagnostic_model <- aov(
  body_mass_g ~ flipper_length_mm,
  data = penguins
)

plot( # Plot med linjen från modellen som hjälp
      x = penguins$flipper_length_mm,
      y = penguins$body_mass_g
    )
abline(diagnostic_model,
       col = "red")

```



```

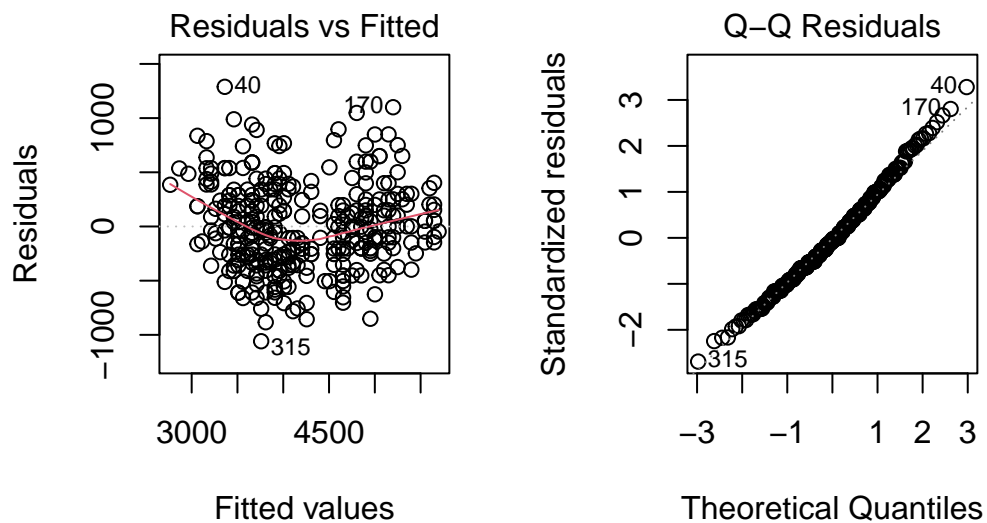
par(mfrow = c(1,1))

par(mfrow = c(1,2))

plot(diagnostic_model, which = 1) # Lika varians om
# spridningen av punkter är uniform & röda linjen är platt.

plot(diagnostic_model, which = 2) # QQ-plot för normalfördelning.

```



```

par(mfrow = c(1,1))

```

2.5.2.2 Linjär regression

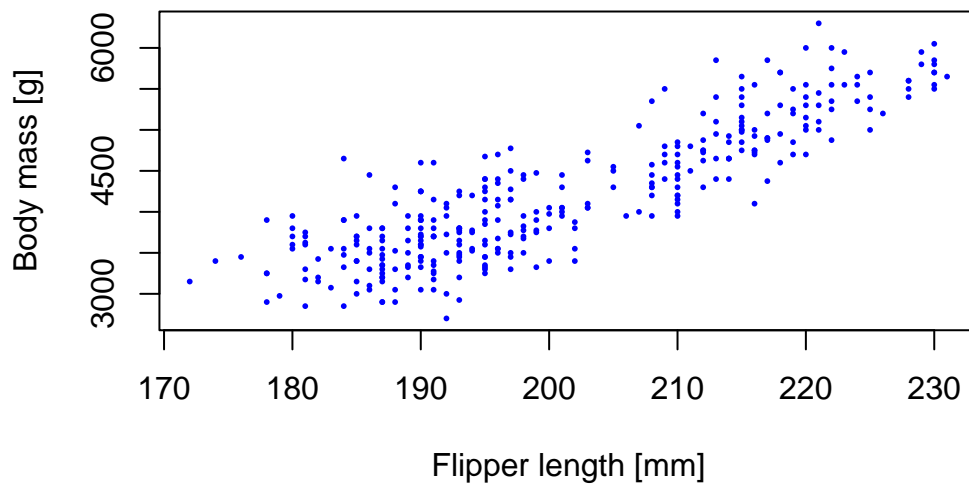
Skapas med en formel liknande för ANOVA.

Med det högst biologiska antagandet att längre fenor orsakar högre kroppsvikt (genom att pingvinerna simmar fortare och därmed kan äta mer, säger vi) enligt en linjär trend, väljer vi att göra linjär regression.

```

plot( # Scatterplot för att kolla sambandet
  penguins$flipper_length_mm,
  penguins$body_mass_g,
  pch = 16,
  cex = 0.4,
  col = "blue",
  xlab = "Flipper length [mm]",
  ylab = "Body mass [g]"
)

```



```

mass_by_flipper <- lm( # Skapa model
  body_mass_g ~ flipper_length_mm,
  data = penguins
)
summary(mass_by_flipper)

```

Call:

```
lm(formula = body_mass_g ~ flipper_length_mm, data = penguins)
```

Residuals:

Min	1Q	Median	3Q	Max
-1058.80	-259.27	-26.88	247.33	1288.69

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-5780.831	305.815	-18.90	<2e-16 ***
flipper_length_mm	49.686	1.518	32.72	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 394.3 on 340 degrees of freedom
(2 observations deleted due to missingness)

Multiple R-squared: 0.759, Adjusted R-squared: 0.7583

F-statistic: 1071 on 1 and 340 DF, p-value: < 2.2e-16

2.5.2.3 Bootstrap

Alternativt med `lm()` och sedan `boot_summary()`.

```
peng_boot <- peng_boot[!is.na(peng_boot$flipper_length_mm), ]

boot_mass_by_flipper <- lm( # Skapa model
  body_mass_g ~ flipper_length_mm,
  data = peng_boot, # Inga NA!
  method = "residual" # Default, kräver lika varians
  # och att respons & mätfel är slumpmässiga
  # (men inte x-variabeln).
  # method = "case" # Kräver lika varians och att
  # alla tre är slumpmässiga.
)
```

Warning in `lm(body_mass_g ~ flipper_length_mm, data = peng_boot, method = "residual")`: method = 'residual' is not supported. Using 'qr'

```
boot.pval::boot_summary(boot_mass_by_flipper)
```

Warning in `lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, : method = 'residual' is not supported. Using 'qr'`

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

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method = 'residual' is not supported. Using 'qr'

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method = 'residual' is not supported. Using 'qr'

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method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

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method = 'residual' is not supported. Using 'qr'

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method = 'residual' is not supported. Using 'qr'

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method = 'residual' is not supported. Using 'qr'

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method = 'residual' is not supported. Using 'qr'

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method = 'residual' is not supported. Using 'qr'

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method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
method = 'residual' is not supported. Using 'qr'

Warning in lm(formula = get(".y.boot", envir = .carEnv) ~ flipper_length_mm, :
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	Estimate	Lower.bound	Upper.bound	p.value
(Intercept)	-5872.09268	-6496.87175	-5297.84092	0.001
flipper_length_mm	50.15327	47.24389	53.23078	0.000

2.5.2.4 Predict

Om längden på fenorna orsakar kroppsmassa kan vi använda modellen för att förutse vikten på en pingvin baserat på fenornas längd.

Argumentet `newdata = data.frame()` måste innehålla samma kolumn namn som x-axeln och en vektor med de värden på x-axeln man vill förutspå y-värdet för.

```

# Data frame med nya värden att förutspå.
# Måste ha en kolumn med samma namn som x-axeln i modellen!
measured_flipper_length <- data.frame(
  flipper_length_mm = c(205, 221, 179)
)

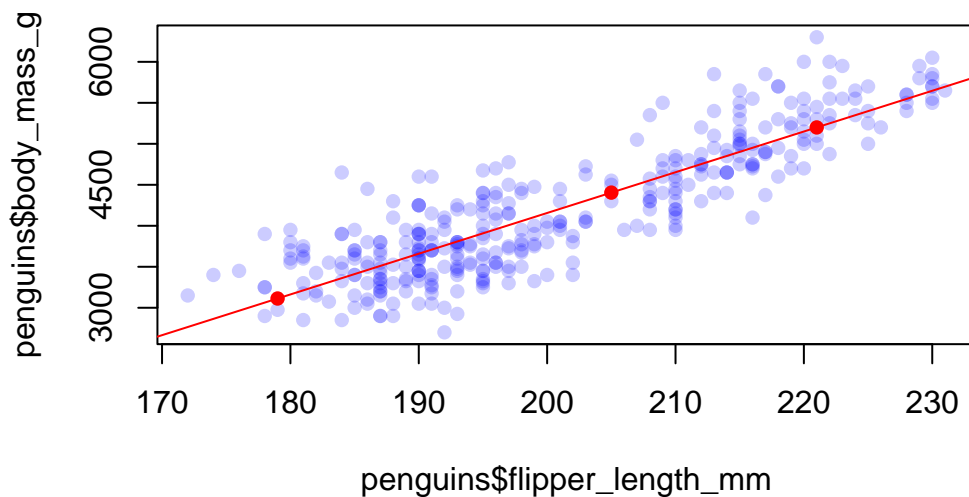
# De värden vi gissar med hjälp av modellen
estimated_weight <- predict(
  object = mass_by_flipper, # Modellen
  newdata = measured_flipper_length, # nya x-värden
  interval = "prediction" # Prediktionsintervall för en ny observation
# interval = "confidence" # Konfidensintervall för förväntade värden
)

plot(
  penguins$flipper_length_mm,
  penguins$body_mass_g,

  pch = 16,
  col = alpha("blue", 0.2)
)
points(
  x = measured_flipper_length$flipper_length_mm, # newdata
  y = estimated_weight[,1], # Gissade värden

  pch = 16,
  col = "red"
)
abline( # Lägg till linjen från modellen.
  reg = mass_by_flipper,
  col = "red",
  lwd = 1
)

```



2.6 Fördelning av frekvens data

2.6.1 Chi-square (χ^2 -test)

Det enda testet på kursen som hanterar frekvenser/räknedata. Principiellt behövs tre saker, en faktor med grupper som blir kolumner, en faktor med grupper som blir rader, individer/föremål att räkna.

Till ära av Tobbes doktorsavhandling används här data om Gemsbock och Red hartbeest och deras observerade fördelning på fyra områden.

```
bockar <- rbind(
  Gemsbock = c(FR = 5, CGA = 7, WMA = 12, NP = 67),
  Red_hartbeest = c(6, 8, 54, 13)
)
```

```
bockar
```

	FR	CGA	WMA	NP
Gemsbock	5	7	12	67
Red_hartbeest	6	8	54	13

2.6.1.1 Krav/antaganden

- Frekvens data (nominal skala)
- Väntevärdet/expected i varje cell ska vara minst 5 (Fishers exact test)

```
low_expected <- rbind(  
  c(2,3,4),  
  c(4,5,6)  
)  
low_expected_test <- chisq.test(  
  low_expected  
)
```

Warning in chisq.test(low_expected): Chi-squared approximation may be incorrect

```
low_expected_test$expected
```

```
      [,1] [,2] [,3]  
[1,] 2.25   3 3.75  
[2,] 3.75   5 6.25
```

2.6.1.2 Anpassning

Kollar om en rad data “kan anpassas” efter en fördelning, vanligen lika många i varje kategori. Så om data ser ut såhär,

```
bockar["Gemsbock", , drop = FALSE] # Det extra ', drop = FALSE' gör att  
↪ vi behåller namnet på raden (som annars försvinner mystiskt när  
↪ matrisen har bara en rad).
```

```
      FR CGA WMA NP  
Gemsbock 5   7 12 67
```

```
# Detta kan ignoreras och skulle då vara 'bockar["Gemsbock", ]'.
```

```
bockar_anpassning <- chisq.test(  
  bockar["Gemsbock", ]
```

```
)
bockar_anpassning # Visa resultatet
```

Chi-squared test for given probabilities

```
data:  bockar["Gemsbock", ]
X-squared = 115.9, df = 3, p-value < 2.2e-16
```

```
bockar_anpassning$expected # Visa väntevärden
```

```
FR    CGA    WMA    NP
22.75 22.75 22.75 22.75
```

Alternativt, anpassning mot en specifik fördelning.

```
bockar_anpassning <- chisq.test(
  bockar["Gemsbock", ],
  p = c(0.10, 0.15, 0.35, 0.40) # Totalt ska dessa bli 1
)
bockar_anpassning # Visa resultatet
```

Chi-squared test for given probabilities

```
data:  bockar["Gemsbock", ]
X-squared = 43.182, df = 3, p-value = 2.251e-09
```

```
bockar_anpassning$expected # Visa väntevärden
```

```
FR    CGA    WMA    NP
9.10 13.65 31.85 36.40
```

2.6.1.3 Oberoende

Testa slumpmässiga observationer från två olika faktorer samtidigt för att se om de kommer från samma fördelning. Innebär att alla kolumner och alla rader kan ha olika summor. Så om data ser ut såhär,

```

# Skapa ny kolumn med summan av varje rad
bockar_sums <- cbind(
  bockar,
  Row_sum = rowSums(bockar)
)
# Skapa ny rad med summan av varje kolumn
bockar_sums <- rbind(
  bockar_sums,
  Col_sum = colSums(bockar_sums)
)
bockar_sums

```

	FR	CGA	WMA	NP	Row_sum
Gemsbock	5	7	12	67	91
Red_hartbeest	6	8	54	13	81
Col_sum	11	15	66	80	172

Varken alla rader eller alla kolumner har samma summor, alltså gör vi ett oberoende test.

```

bockar_oberoende <- chisq.test(
  bockar
)
bockar_oberoende

```

Pearson's Chi-squared test

```

data:  bockar
X-squared = 62.966, df = 3, p-value = 1.365e-13

```

```

bockar_oberoende$expected

```

	FR	CGA	WMA	NP
Gemsbock	5.819767	7.936047	34.9186	42.32558
Red_hartbeest	5.180233	7.063953	31.0814	37.67442

2.6.1.4 Homogenitet

Testa slumpmässiga observationer från **en** faktor och kontrollera den andra. Innebär att **antingen** alla rader **eller** kolumner har samma summa (medan den andra varierar).

För detta behöver vi ny data. Ett stort företag vill undersöka om antalet vaccinerade anställda skiljer sig mellan avdelningarna. För att kontrollera för de olika avdelningarna slumpades 100 anställda från varje avdelning och frågade om de var vaccinerade eller inte.

```
uppsala_site <- rbind( # Data
  vaccinerad = c(RnD = 99, HR = 45, Lön = 63, IT = 76),
  ej_vaccinerade = c( 1,      55,      37,      24)
)

uppsala_site
```

	RnD	HR	Lön	IT
vaccinerad	99	45	63	76
ej_vaccinerade	1	55	37	24

Vi kan utforska företagets data lite mer genom att lägga till rad och kolumn summor.

```
# Skapa ny kolumn med summan av varje rad
uppsala_sums <- cbind(
  uppsala_site,
  Row_sum = rowSums(uppsala_site)
)
# Skapa ny rad med summan av varje kolumn
uppsala_sums <- rbind(
  uppsala_sums,
  Col_sum = colSums(uppsala_sums)
)
uppsala_sums
```

	RnD	HR	Lön	IT	Row_sum
vaccinerad	99	45	63	76	283
ej_vaccinerade	1	55	37	24	117
Col_sum	100	100	100	100	400

Detta säger oss att den faktorn är kontrollerad, alltså gör vi ett Homogenitetstest.


```
vaccin_homogen <- chisq.test(
  uppsala_site
)

vaccin_homogen
```

Pearson's Chi-squared test

```
data: uppsala_site
X-squared = 74.839, df = 3, p-value = 3.923e-16
```

```
vaccin_homogen$expected
```

	RnD	HR	Lön	IT
vaccinerad	70.75	70.75	70.75	70.75
ej_vaccinerade	29.25	29.25	29.25	29.25

2.6.2 Fisher's exact (icke parametrisk)

Ifall en eller flera celler med väntevärden/expected är < 5 kan man använda Fisher's exact test.

```
uppsala_fisher <- fisher.test(
  uppsala_site
)

uppsala_fisher # Inga expected values
```

Fisher's Exact Test for Count Data

```
data: uppsala_site
p-value < 2.2e-16
alternative hypothesis: two.sided
```

3 Matte

3.1 Matematiska beräkningar

```
1 + 1    # addition
1 - 1    # subtraktion
5 * 4    # multiplikation
6 / 2    # division
5^2      # upphöjt med

sqrt(25) # roten ur, (positiv)
exp(3)   #  $e^3$ 
log(7)   #  $\log(7)$  med basen  $e$ 
log10(7) #  $\log(7)$  med basen 10
```

Matriser

```
A <- rbind(
  c(1,2),
  c(3,4)
)
B <- rbind(
  c(5,6),
  c(7,8)
)
C <- rbind(
  c(19,22),
  c(43,50)
)
```

```
A %*% B # Matrismultiplikation
```

```
      [,1] [,2]
[1,]   19  22
[2,]   43  50
```

```
A %^% 5 # Upphöjt med, kräver att paketet 'expm' är laddat med
↪ library()
```

```

      [,1] [,2]
[1,] 1069 1558
[2,] 2337 3406

```

```

solve(A, C) # För ekvationen A %*% B = C ger solve(A,C) svaret B

```

```

      [,1] [,2]
[1,]     5     6
[2,]     7     8

```

```

solve(A)      # Med en matris antas A %*% A-invers = I alltså ges A-invers

```

```

      [,1] [,2]
[1,] -2.0  1.0
[2,]  1.5 -0.5

```

```

eigen_values_vectors <- eigen(A) # Egenvärden och egenvektorer i lista
eigen_value <- eigen_values_vectors$values[1]      # Dominant egenvärde
eigen_vector <- eigen_values_vectors$vectors[,1]  # Dess egenvektor

```

3.2 Differensekvationer

Betrakta ekv. $x_{n+2} = 4x_n$ med begynnelsevilkor $x_0 = 5$; $x_1 = 6$.

a. Hitta en explicit formel

Detta kan vi inte lösa med R.

b. Beräkna x_7

```

x <- c()
x[1] <- 5
x[2] <- 6

for (i in 1:10) {
  x[i+2] <- 0*x[i+1] + 4*x[i]
}
x[7]

```

[1] 320

Alternativt skrivsätt som ger samma sak.

```
x <- c(5,6)

for (i in 3:12) {
  x[i] <- 0*x[i-1] + 4*x[i-2]
}
x[7]
```

[1] 320

3.3 Kritiska punkter

Betrakta funktionen $f(x) = x^2 e^{1-x^2}$

- a. Visa att derivatan är $f'(x) = 2x(1 - x^2)e^{1-x^2}$

Detta kan vi inte göra (bra) i R.

- b. Bestäm kritiska punkter och avgör deras typ

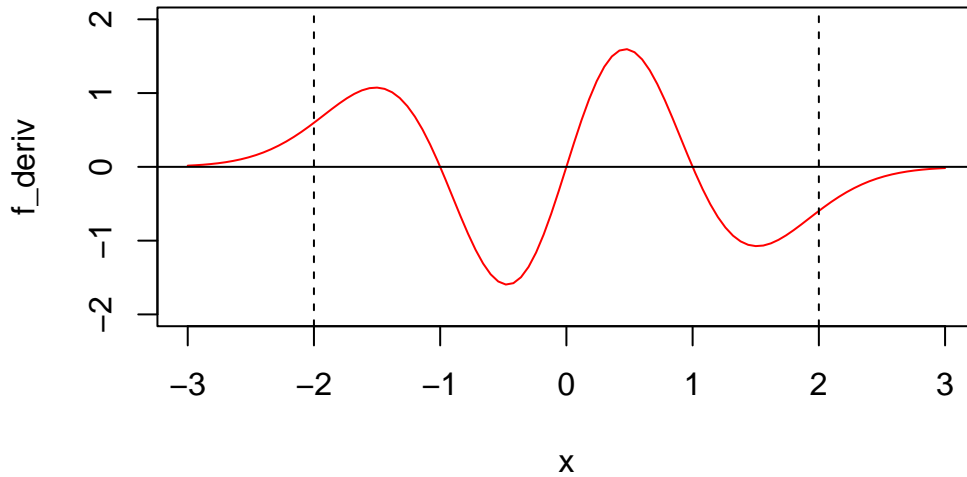
Kritiska punkter ges då $f'(x) = 0$ så vi definerar funktionerna.

```
f_av_x <- function(x) { # Funktion av funktion
  x^2*exp(1-x^2)
}
f_deriv <- function(x) { # Derivata av funktion
  fderiv(f_av_x, x)
}
```

Skapar en plot för att grafiskt hitta nollpunkterna.

```
plot( # För att grafiskt hitta intervallen för nollställen
  f_deriv,
  xlim = c(-3,3),
  ylim = c(-2,2),
  col = "red"
)
abline(h = 0) # Linje för noll
abline(v = -2, lty = 2) # Markera nedre intervall
```

```
abline(v = 2, lty = 2) # Markera övre intervall
```



Använder `uniroot()` för att hitta exakta nollställen.

```
x_1 <- uniroot(f_deriv,
               interval = c(-2, -0.5))
               )$root
x_2 <- uniroot(f_deriv,
               interval = c(-0.5, 0.5))
               )$root
x_3 <- uniroot(f_deriv,
               interval = c(0.5, 2))
               )$root

print(paste("Lösningarna är", x_1, ";", x_2, ";", x_3))
```

```
[1] "Lösningarna är -1.00001710832717 ; 0 ; 1.00001710832717"
```

Här måste man tänka till och avgöra om dessa tal egentligen ska avrundas till fina heltal eller omvandlas till bråk.

Teckentabell används för att avgöra dess typ.

- c. Funktionen största/minsta värde på intervaller $[-2,2]$
 Sätt in x-värden för punkter av intresse och jämför.
- d. Bestäm ekvationen för tangenten till $y = f(x)$ i punkten $x = 2$

```
x <- 2
slope <- f_deriv(x)
intercept <- f_av_x(x) - slope * x

print(paste("Tangentens ekv. är: f(x) =", slope, "*x +", intercept))
```

```
[1] "Tangentens ekv. är: f(x) = -0.597444820421625 *x + 1.39403791431471"
```

3.4 Matriser & diagonalisering

Betrakta matrisen $A = \begin{bmatrix} 2 & 1 \\ 1 & 2 \end{bmatrix}$

- a. Bestäm egenvärdena till A

```
A <- rbind(
  c(2,1),
  c(1,2)
)

A_eigen <- eigen(A)
A_eigen$values
```

```
[1] 3 1
```

- b. Bestäm egenvektorerna till A

```
A_eigen$vectors
```

```
      [,1]      [,2]
[1,] 0.7071068 -0.7071068
[2,] 0.7071068  0.7071068
```

- c. Diagonalisera A, d.v.s. hitta en diagonalmatris D och en inverterbar matris C, så att $A = CDC^{-1}$

```

D <- rbind(
  c(A_eigen$values[1], 0),
  c(0, A_eigen$values[2])
)
C <- rbind(
  c(A_eigen$vectors[1,1], A_eigen$vectors[1,2]),
  c(A_eigen$vectors[2,1], A_eigen$vectors[2,2])
)
C_invers <- solve(C)

C %*% D %*% C_invers # = A

```

```

      [,1] [,2]
[1,]     2     1
[2,]     1     2

```

```

C_invers %*% A %*% C # = D

```

```

      [,1] [,2]
[1,]     3     0
[2,]     0     1

```

- d. Beräkna A^8 med hjälp av svaret i c.

```

n <- 8
C %*% (D %^% n) %*% C_invers # = A %^% n

```

```

      [,1] [,2]
[1,] 3281 3280
[2,] 3280 3281

```

3.5 Diskreta dynamiska system

Betrakta det diskreta dynamiska systemet $x_{n+1} = \frac{5x_n^2}{x_n^2+6}$

- a. Bestäm systemets övergångsfunktion

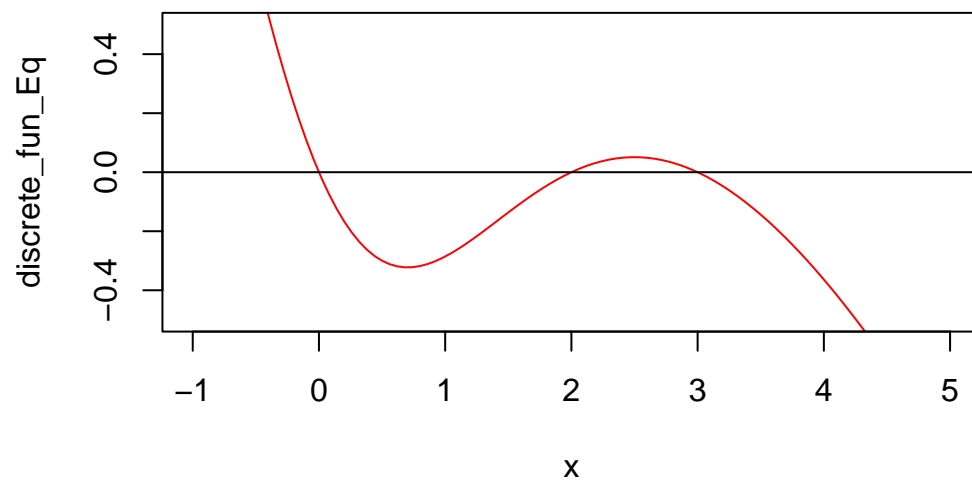
Övergångs funktion $f(x) = \frac{5x^2}{x^2+6}$

```
discrete_fun <- function(x) {
  (5*x^2)/(x^2+6)
}
```

b. Bestäm systemets tre jämviktspunkter

Lös $f(x) = x$ med `uniroot()`

```
discrete_fun_Eq <- function(x) {
  discrete_fun(x) - x
}
plot(
  discrete_fun_Eq,
  ylim = c(-0.5,0.5),
  xlim = c(-1,5),
  col = "red"
)
abline(h = 0)
```




```

x_1 <- uniroot(discrete_fun_Eq,
               interval = c(-0.5, 0.5)
               )$root
x_2 <- uniroot(discrete_fun_Eq,
               interval = c(1.5, 2.5)
               )$root
x_3 <- uniroot(discrete_fun_Eq,
               interval = c(2.5, 3.5)
               )$root

print(paste(x_1, ";", x_2, ";", x_3))

```

```
[1] "2.63729556410053e-05 ; 1.99997675765039 ; 3.00002538813349"
```

Avgör själv om dessa rötter måste avrundas eller omvandlas till bråk.

c. Avgör om de är stabila/instabila

Beroende på om derivatan är större/mindre än ett blir jämviktspunkten instabil < 1 < stabil

```

discrete_deriv <- function(x) {
  fderiv(discrete_fun, x)
}

check_stability <- function(x) {
  if (abs(x) > 1) {
    print(paste(x, "är stabil"))
  } else {
    print(paste(x, "är instabil"))
  }
}

check_stability(x_1)

```

```
[1] "2.63729556410053e-05 är instabil"
```

```
check_stability(x_2)
```

```
[1] "1.99997675765039 är stabil"
```

```
check_stability(x_3)
```

```
[1] "3.00002538813349 är stabil"
```

3.6 Differentialekvationer

```
# Funktion med ekvationssystemet att lösa
DE_fun <- function(times, # Intervall
                    y,     # Begynnelsevärden
                    parms  # Andra värden
) {
  # variabler att använda (från parms)
  alfa <- parms["alfa"]
  beta <- parms["beta"]
  delta <- parms["delta"]
  gamma <- parms["gamma"]

  # Begynnelsevärden (från y)
  B <- y["B"]
  P <- y["P"]

  # Differentialekvationen att lösa numeriskt
  # (Minst 1 ekv. men sedan är det bara att lägga till fler ekv.
  # på var sin rad. Varje ekv. måste ha ett begynnelsevärde &
  # sedan returneras i result_vec)
  dB <- alfa * B - beta * B * P
  dP <- delta * B * P - gamma * P

  # Spara & returnera resultatet (ode() är lite speciell...)
  result_vec <- c( # Först som vektor
    dB,
    dP
  )
  result_list <- list(result_vec) # Sedan som lista
  return(result_list) #Returnera
}

# Vektor med alla tidssteg (t) att sätta in
DE_time_span <- seq(
  from = 0, # Början på intervall
```

```

    to = 30, # Slut på intervall
    by = 0.1 # Steglängd
  )

  # Vektor med begynnelsevärden
  # (enklast att namnge dem och sedan indexera med namnet i fun)
  DE_init <- c(
    B = 200,
    P = 10
  )

  # Vektor med andra värden för formeln
  # (enklast att namnge dem och sedan indexera med namnet i fun)
  DE_params <- c(
    alfa = 2.5,
    beta = 0.15,
    delta = 0.02,
    gamma = 1.5
  )

  # Lösa ekvationerna numeriskt
  DE_sol <- ode(
    y = DE_init,          # Begynnelsevärden
    times = DE_time_span, # Intervall
    func = DE_fun,        # Funktionen
    parms = DE_params,    # Andra värden
    method = "rk4"        # Runge-Kutta version 4
  )

  # Konvertera till data frame för att göra den lättare att hantera
  DE_sol <- as.data.frame(DE_sol)

  # Plotta dB respektive dP mot tid
  plot( # Plot fönster & dB mot tid
    DE_sol$time,
    DE_sol$B,
    type = "l",

    col = "blue",

    xlab = "Time",

```

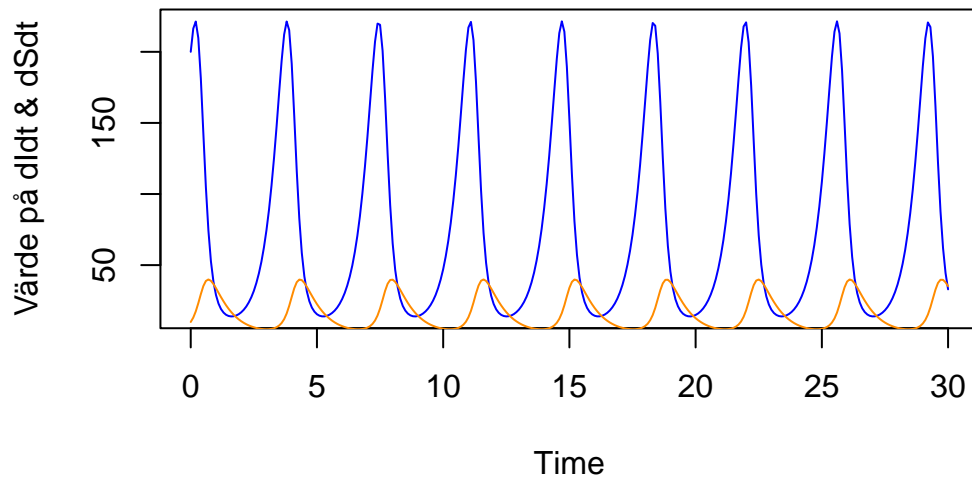
```

ylab = "Värde på dIdt & dSdt",
main = "Numerisk lösning för system av differentialekvationer"
)
lines( # Lägg till dP mot tid
  DE_sol$time,
  DE_sol$P,

  col = "darkorange"
)

```

Numerisk lösning för system av differentialekvationer



4 KvantBio

4.1 Fibonacci

```
n <- c(1,2)
for (i in 3:25) {
  n[i] <- n[i-1] + n[i-2]
}
n
```

```
[1]      1      2      3      5      8     13     21     34     55     89
[11]    144    233    377    610    987   1597   2584   4181   6765  10946
[21]  17711  28657  46368  75025 121393
```

4.2 Hantera modeller

Kunna använda modeller och lösa för saknade parametrar. Översätt de matematiska funktionerna till funktioner i R. Funktionen `uniroot()` är användbar för att hitta nollställena.

4.2.1 Allometri & energiförbrukning

$$K = P + M + E$$

Bioenergetisk modell där K = konsumtion, P = produktion/ökning i massa, M = metabolism, E = exkretion.

$$\log_{10}(O_2) = 0.36 \cdot \frac{S}{TL} + 1.945$$

Modell för citronhajars metabolism baserat på sambandet mellan simhastighet och syreförbrukning (för hajar som väger 1kg).

4.2.2 Individuell tillväxt (von Bertalanffys tillväxtekvation)

$$L(t) = L_{\infty} + (L_0 - L_{\infty}) \cdot e^{-kt}$$

Där L_{∞} är maxlängd vid oändlig tid, L_0 är längden vid $t = 0$, k är en tillväxtfaktor och t är tid/ålder.

För att hitta längden vid givet t .

```

# Parametrar
L_inf <- 85
k <- 0.00082
L_noll <- 30

# Funktion av t
growth_av_t <- function(t) {
  L_t <- L_inf + (L_noll - L_inf) * exp(-k * t)
  return(L_t)
}
growth_av_t(t = 10)

```

[1] 30.44916

För att hitta L_{∞} (eller annan okänd från funktionen) kan vi möblera om till

$$0 = L_{\infty} + (L_0 - L_{\infty}) \cdot e^{-kt} - L_t$$

och använda `uniroot()`.

```

# Parametrar
k <- 0.00082
L_noll <- 30
L_t <- 95
t <- 2000

# Funktion av L_inf
growth_av_L_inf <- function(L_inf) {
  noll_punkt <- L_inf + (L_noll - L_inf) * exp(-k * t) - L_t
  return(noll_punkt)
}

# Hitta nollpunkten med uniroot()
uniroot(
  f = growth_av_L_inf,
  interval = c(0,200)
)$root

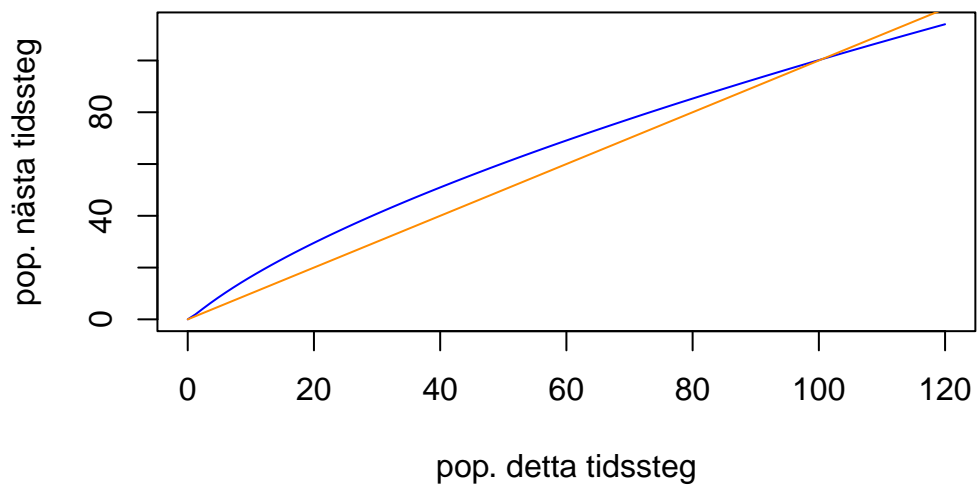
```

[1] 110.6432

4.3 Hållbart uttag

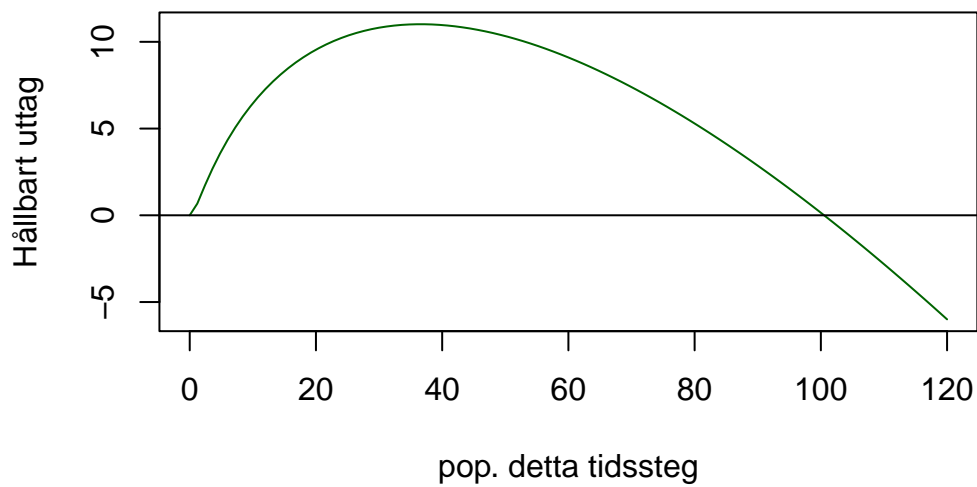
Hur tillväxer en population och vid vilken storlek kan man plocka ut så många individer som möjligt och samtidigt få en stabil population?

```
# Rekryteringsfunktion, n individer detta år ger n+x individer nästa år
recruitment <- function(n) {
  recruit <- 2.17 * sqrt(n) * log(n+1)
  return(recruit)
}
# Plot
curve(
  recruitment,
  xlim = c(0,120),
  col = "blue",
  xlab = "pop. detta tidssteg",
  ylab = "pop. nästa tidssteg"
)
curve(
  1*x,
  add = TRUE,
  col = "darkorange"
)
```



```
# Skördekurva
harvest <- function(n) {
  harvest <- recruitment(n) - n
  return(harvest)
}

# Plot
curve(
  harvest,
  xlim = c(0,120),
  xlab = "pop. detta tidssteg",
  ylab = "Hållbart uttag",
  col = "darkgreen"
)
abline(
  h = 0
)
```

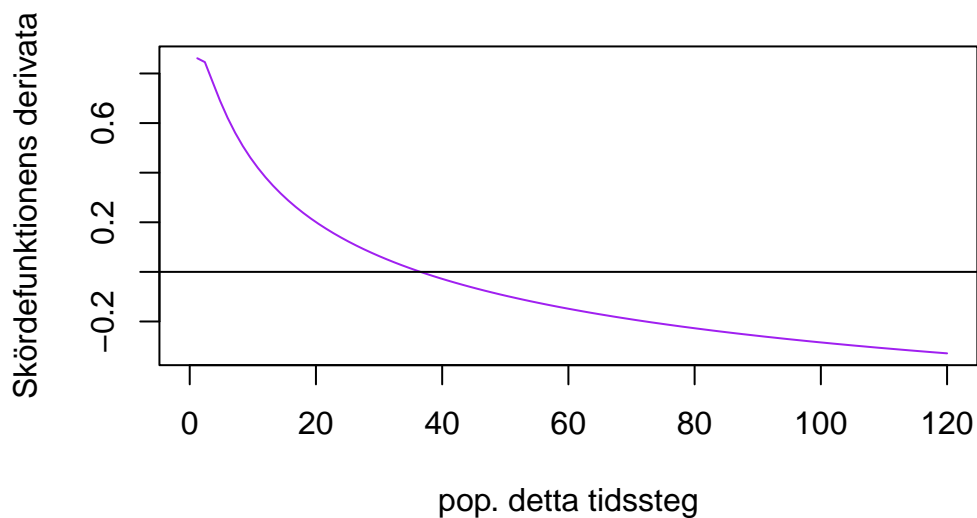
```
# Hitta x-värde för maxpunkt, alltså pop. storlek för max hållbart
↪ uttag.
```

```
# Derivata av skördefunktionen
```

```
harvest_deriv <- function(n) {
  harvest_deriv <- fderiv(harvest, n)
  return(harvest_deriv)
}
```

```
# Plot (indikerar intervallet för uniroot())
```

```
curve(
  harvest_deriv,
  xlim = c(0,120),
  xlab = "pop. detta tidssteg",
  ylab = "Skördefunktionens derivata",
  col = "purple"
)
abline(
  h = 0
)
```



```
# Hitta nollpunkt numeriskt = pop. storlek för max hållbart uttag
harvest_deriv_root <- uniroot(
  harvest_deriv,
  interval = c(20,60)
)

# Insättning av nollpunkt i skördefunktion ger max hållbart uttag
harvest(harvest_deriv_root$root)
```

```
[1] 11.0155
```

4.4 Diskret logistisk tillväxt

$$x_{n+1} = x_n + r \cdot x_n \cdot \left(1 - \frac{x_n}{k}\right)$$

Funktion för diskret logistisk tillväxt.

```
dlt <- function(n, r, k) {
  n_ny <- n + r*n*(1-n/k)
```

```

    return(n_ny)
}

```

4.4.1 Modellera en population

Definiera värden på parametrar.

```

r <- 0.36 # perkapitareproduktion (egenvärde från Leslie-matris)
k <- 600  # Bärkraft

sluttid <- 30
t <- 1:(sluttid+1)

```

En populationsutveckling med konstant r-värde.

```

n <- c(4) # Startvärde & vektor att lagra resultat i

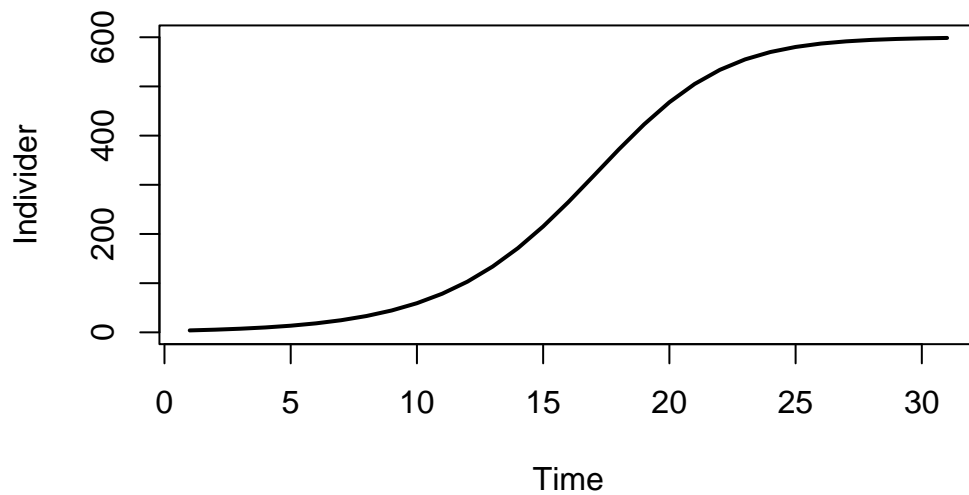
for (i in 1:sluttid) { # Loop för pop. utveckling
  n[i+1] <- dlt(n = n[i],
               r = r,
               k = k)
}

plot(
  x = t,
  y = n,
  ylim = c(0,k),

  type = "l",
  lwd = 2,

  xlab = "Time",
  ylab = "Individer"
)

```



Samma, men med varierande r-värde.

```
# r <- 0.36 # perkapitareproduktion (egenvärde från Leslie-matris)
k <- 600 # Bärkraft

sluttid <- 30
t <- 1:(sluttid+1)

n <- c(4) # Startvärde & vektor att lagra resultat i

for (i in 1:sluttid) { # Loop för pop. utveckling
  n[i+1] <- dlt(n = n[i],
               r = rnorm(n = 1,
                         mean = 0.36,
                         sd = 0.2),
               k = k)
}

plot(
  x = t,
  y = n,
```

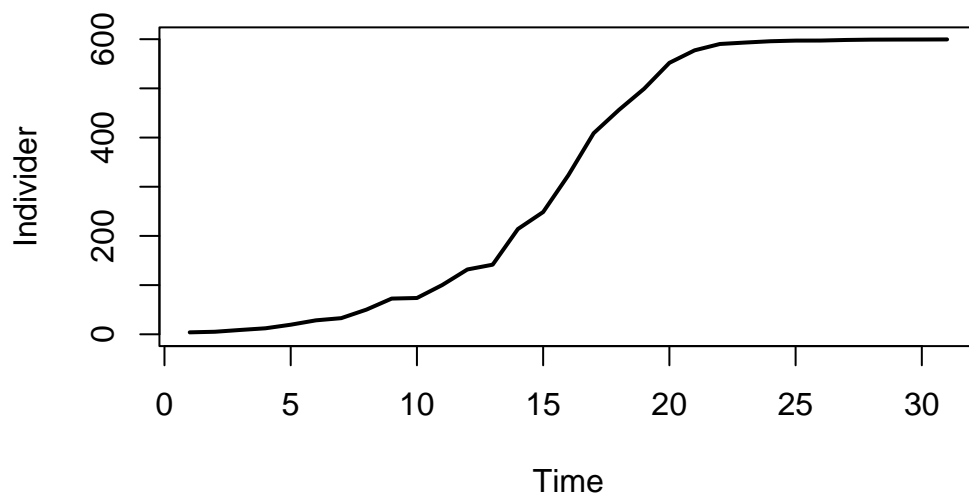
```

ylim = c(0,k),

type = "l",
lwd = 2,

xlab = "Time",
ylab = "Individer"
)

```



4.4.2 Modellera många populationer & beräkna utdöende risk

Definiera värden på parametrar.

```

# r defineras i for-loop
k <- 1000 # Bärkraft

sluttid <- 20
t <- 1:(sluttid+1)

collapse <- 10 # Färre individer = pop. dör ut

```

Skapa många linjer för hypotetiska populationers öden.

```
plot( # Skapa tom plot
      NULL,
      xlim = c(0, sluttid+1),
      ylim = c(0, 200),
      type = "l",
      xlab = "Time",
      ylab = "Individer"
)

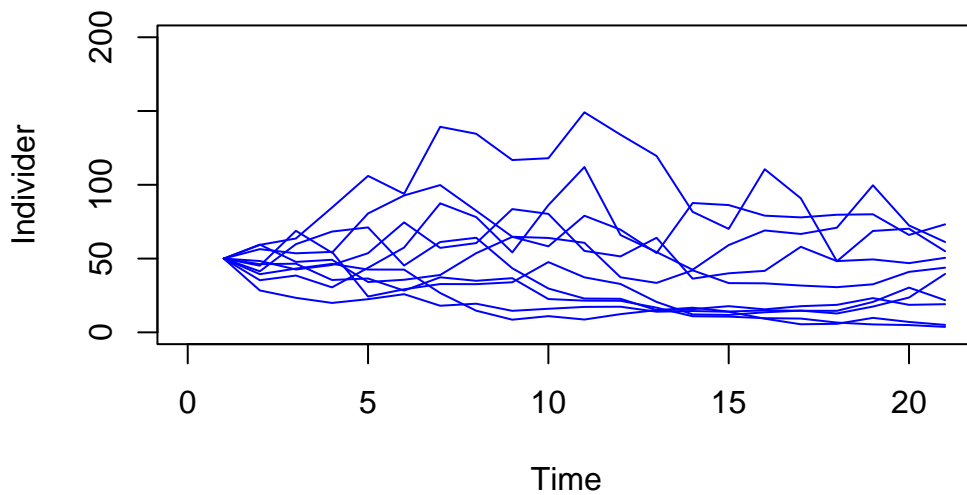
n <- c(50) # Startvärde & vektor att lagra resultat i
pop_collapse <- 0 # Räknare för hur många populationer har dött ut
attempts <- 10

for (i in 1:attempts) { # Loop för upprepade försök/linjer

  for (j in 1:sluttid) { # Loop för en linje/population
    n[j+1] <- dlt(n = n[j],
                  r = rnorm(n = 1, # slumpad reproduktion
                           mean = 0,
                           sd = 0.25),
                  k = k)
  }

  if (min(n) < collapse) { # Kolla om pop. collapsade
    pop_collapse <- pop_collapse + 1 # Addera 1 till räknare
    print(paste("Försök",i,"dog ut. Totalt",pop_collapse,"collapsade
      ↪ populationer."))
  }

  lines( # Addera linje för ett försök
        x = t,
        y = n,
        lwd = 1,
        col = "blue"
      )
}
```



```
[1] "Försök 2 dog ut. Totalt 1 kollapsade populationer."
[1] "Försök 8 dog ut. Totalt 2 kollapsade populationer."
[1] "Försök 10 dog ut. Totalt 3 kollapsade populationer."
```

För att beräkna utdöenderisk i procent.

```
extinction_rate <- (pop_collapse / attempts) * 100
print(paste("Utdöenderisken är", extinction_rate, "%"))
```

```
[1] "Utdöenderisken är 30 %"
```

4.5 Lesliematriser

För användning av en livstabell översätts den till en Leslie/Lefkovitch matris.

Livstabell för *Caretta caretta*

Stage #	Class	Size (cm)	Approx. Age	P(Survival)	P(Growth)	Fecundity
1	eggs, hatchlings	<10,0	<1	0	0,6747	0
2	small juveniles	10,1-58,0	1-7	0,737	0,0486	0
3	large juveniles	58,1-80,0	8-15	0,661	0,0147	0
4	subadults	80,0-87,0	16-21	0,6907	0,0518	0
5	novice breeders	>87,0	22	0	0,8091	127
6	1st-yr remigrants	>87,0	23	0	0,8091	4
7	mature breeders	>87,0	24-54	0,8091	0	80



En Leslie-matris använder åldersklasser där ingen kan “stanna” i klassen, alltså är diagonalen 0.

En Lefkovitch-matris använder ontogenetiska stadier där en individ kan antingen “stanna” i samma klass eller “gå vidare” till nästa klass, alltså kan diagonalen vara >0.

Leslie/Lefkovich-matrisen

Nästa år (t+1) Händer under året I år (t)

$$\begin{bmatrix} N_0(t+1) \\ N_1(t+1) \\ N_2(t+1) \\ N_3(t+1) \end{bmatrix} = \begin{bmatrix} s_0 & f_1 & f_2 & f_3 \\ g_0 & s_1 & 0 & 0 \\ 0 & g_1 & s_2 & 0 \\ 0 & 0 & g_2 & s_3 \end{bmatrix} \begin{bmatrix} N_0(t) \\ N_1(t) \\ N_2(t) \\ N_3(t) \end{bmatrix}$$

$$\begin{bmatrix} s_0 & f_1 & f_2 & f_3 \\ g_0 & s_1 & 0 & 0 \\ 0 & g_1 & s_2 & 0 \\ 0 & 0 & g_2 & s_3 \end{bmatrix}$$

s_i = P(överleva och stanna i samma klass)

g_i = P(överleva och tillväxa till nästa klass/ålder)

f_i = fekunditet i klassen/åldern

```
caretta_matris <- rbind( # En Lefkovitch matris
  r1 = c(c1 = 0, c2 = 0, c3 = 0, c4 = 0, c5 = 127, c6 = 4, c7 = 80),
  r2 = c(0.6747, 0.737, 0, 0, 0, 0, 0),
  r3 = c(0, 0.0486, 0.661, 0, 0, 0, 0),
  r4 = c(0, 0, 0.0147, 0.6907, 0, 0, 0),
  r5 = c(0, 0, 0, 0.0518, 0, 0, 0),
  r6 = c(0, 0, 0, 0, 0.8091, 0, 0),
  r7 = c(0, 0, 0, 0, 0, 0.8091, 0.8091)
)
caretta_matris
```

	c1	c2	c3	c4	c5	c6	c7
r1	0.0000	0.0000	0.0000	0.0000	127.0000	4.0000	80.0000
r2	0.6747	0.7370	0.0000	0.0000	0.0000	0.0000	0.0000
r3	0.0000	0.0486	0.6610	0.0000	0.0000	0.0000	0.0000
r4	0.0000	0.0000	0.0147	0.6907	0.0000	0.0000	0.0000
r5	0.0000	0.0000	0.0000	0.0518	0.0000	0.0000	0.0000
r6	0.0000	0.0000	0.0000	0.0000	0.8091	0.0000	0.0000
r7	0.0000	0.0000	0.0000	0.0000	0.0000	0.8091	0.8091

För att få ut egenvärdet (r-värdet) och egenvektorn (stabil stadiefördelning). Om λ är 0.90 innebär det att populationen minskar med 10% (förändrings faktor för populationen). Den relativa fördelningen ($\frac{\text{egenvektor}}{\text{sum(egenvektor)}} \cdot 100$) indikerar hur många procent av den totala populationen bör finnas i varje klass. Kan användas som `p = relativ_dist` i `chisq.test()` för att göra ett anpassningstest med en observerad population.

```
caretta_eigen <- eigen(caretta_matris)

# Egentligen det största egenvärdet, men det bör vara första.
Re(caretta_eigen$values[1])
```

```
[1] 0.9450846
```

```
# Samma index för egenvektor som egenvärdet.
Re(caretta_eigen$vectors[,1])
```

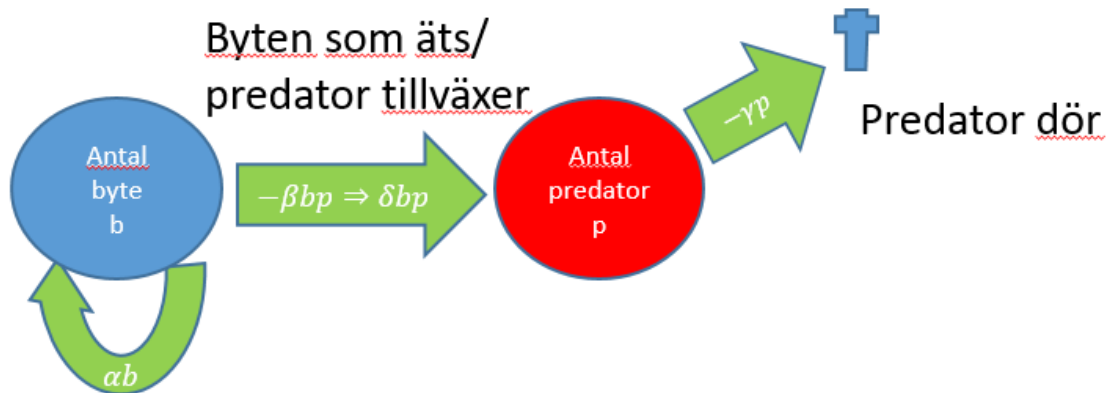
```
[1] 0.2908382596 0.9430228664 0.1613283678 0.0093226030 0.0005109710
[6] 0.0004374493 0.0026027957
```

```
# Relativ fördelning i procent
caretta_dist <- Re(caretta_eigen$vectors[,1])
caretta_dist_procent <- (caretta_dist/sum(caretta_dist))*100
caretta_dist_procent
```

```
[1] 20.65519760 66.97304431 11.45746547 0.66208692 0.03628892 0.03106745
[7] 0.18484934
```

4.6 Lotka-Volterra byte-predator modell

En specifik modell som bygger på att lösa ett ekvationssystem av differentialekvationer.



Byte tillväxer

```

# Funktion med ekvationssystemet att lösa
LV_fun <- function(times, # Intervall
                    y,      # Begynnelsevärden
                    parms   # Andra värden
) {
  # variabler att använda (från parms)
  alfa <- parms["alfa"]
  beta <- parms["beta"]
  delta <- parms["delta"]
  gamma <- parms["gamma"]
  # K <- parms["K"] # alt. där K = bärkraft

  # Begynnelsevärden (från y)
  B <- y["B"]
  P <- y["P"]

  # Differentialekvationen att lösa numeriskt
  dBdt <- (alfa * B - beta * B * P)
  # dBdt <- (alpha * B(1 - B/K) - beta * B * P) # alt. där K = bärkraft

  dPdt <- (delta * B * P - gamma * P)

  # Spara & returnera resultatet
  result_vec <- c(
    dBdt,
    dPdt
  )
}

```

```

    )
    result_list <- list(result_vec)
    return(result_list)
}

# Vektor med alla tidssteg (t) att sätta in
time_span_LV <- seq(
  0,
  30,
  by = 0.1
)

# Vektor med begynnelsevärden
init_LV <- c(
  B = 200,
  P = 10
)

# Vektor med andra värden för formeln
params_LV <- c(
  alfa = 2.5,      # Tillväxt byten
  beta = 0.15,    # Byten som äts
  delta = 0.02,   # Tillväxt predator
  gamma = 1.5     # Död predator
  # K = 500 # alt. där K = bärkraft
)

# Lösa ekvationerna numeriskt
sol_LV <- ode(
  y = init_LV,          # Begynnelsevärden
  times = time_span_LV, # Intervall
  func = LV_fun,        # Funktionen
  parms = params_LV,    # Andra värden
  method = "rk4"        # Runge-Kutta version 4
)
sol_LV <- as.data.frame(sol_LV)

```

Plotta grafen.

```

# Plotta antal insekter [milljoner] respektive spindlar [tusen] mot tid
plot(

```

```

sol_LV$time,
sol_LV$B,
type = "l",

col = "blue",

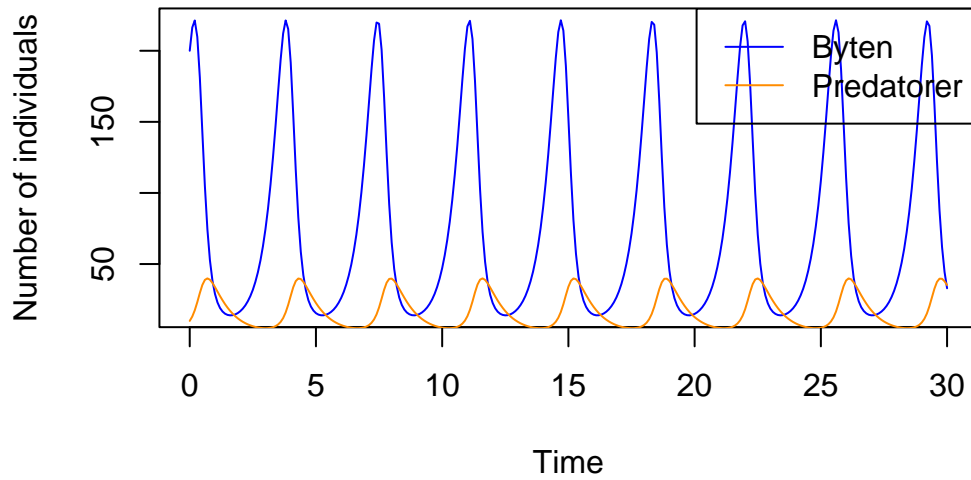
xlab = "Time",
ylab = "Number of individuals",
main = "Lotka-Volterra model"
)
lines(
  sol_LV$time,
  sol_LV$P,

  col = "darkorange"
)
legend(
  "topright",
  legend = c("Byten",
             "Predatorer"),

  lty = c(1, 1),
  col = c("blue",
          "darkorange")
)

```

Lotka–Volterra model



```
# "Fasporträtt" (två pop. mot varandra där tiden blir att följa linjen)
plot(
  sol_LV$B,
  sol_LV$P,
  type = "l",

  col = "darkgreen",

  xlab = "Byten",
  ylab = "Predatorer",
  main = "Fasporträtt"
)
```

Fasporträtt

