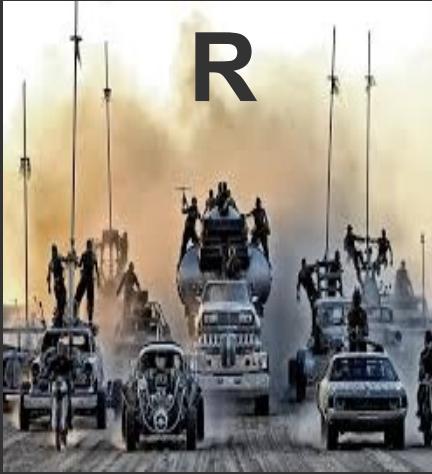


# Introduktion til R/R-studio

**Jacob Mesot Liljehult**  
Klinisk sygeplejespecialist  
cand.scient.san, PhD

# Hvorfor vælge R/RStudio



## Fordeler

- Open-source og gratis (kræver ikke licens)
- Meget fleksibel – alle analyser er tilgængelige i et program
- Simplere kodning end i SAS
- Let at få hjælp – mange ressourcer tilgængelige

## Ulemper

- Man skal lære at kode
- Kodningen kan være inkonsistent

NFAMstart.R × NFAM\_2025.Rmd × NFAM\_figures.Rmd × Udskrivelse.Rmd\* × NFAM\_rapport.Rmd ×

Source on Save Run Source

```

1 # Load all libraries used and set options
2 library(tidyverse)
3 library(lubridate)
4 library(ggtext)
5 library(pander)
6 library(patchwork)
7 panderOptions("table.style", "multiline")
8
9 ### Data input ###
10 nfamRAW <- read.csv(file = "L:\\AuditData\\NFAM data\\NFAM_raw.csv", sep = ";")
11
12
13 ### Data formatting ###
14 nfamData <- data.frame(id = 1:length(nfamRAW$ ID)) # Löbenummer
15 # Tilfældig transformering af CPR. Anvendes til identifikation af genindlæggelse
16 nfamData$ hashid <- as.numeric(nfamRAW$ hashid )
17 nfamData$ birth_year <- nfamRAW$ birth_year # Fødselsår
18 nfamData$ age <- nfamRAW$ age #Alder
19 nfamData$ gender <- factor(nfamRAW$ gender, levels = c("F","M")) # Køn (Admin)
20 # Angiver om forløbet er en genindlæggelse indenfor data perioden
21 nfamData$ readmission <- factor(nfamRAW$ x, levels = c("G"),
22                                 labels = c("Genindlagt"))
23 # Ankomst til AKA
24 nfamData$ arrival <- as.POSIXct(paste(nfamRAW$ arrival_date,
25                                     nfamRAW$ arrival_time),
26

```

16:35 (Top Level) ↴

Console Terminal × Background Jobs ×

```
R 4.3.2 - L:\AuditData\NFAM data\NFAMdata
geom_sengetransfer(aes(x = firsthospital, alpha = 0.5, color = gray))
+ geom_stratum(aes(fill = firsthospital)) +
+ geom_text(stat = "stratum",
+           aes(label = paste0(after_stat(stratum)," (n = ", after_stat(count),")")), size = 5) +
+ labs(title = "Patientflow fra senge i NFAM til destination", subtitle = "...",
+       caption = paste0("Jacob Liljehult | R/R-studio | ",format(Sys.Date(), "%d %B %Y"))) +
+ scale_fill_manual(values = c(colorLight,colorLight)) +
+ theme_void() +
+ theme(plot.title = element_textbox_simple(color = "white", size = 25, hjust = 0, face = "bold",
+                                             margin = margin(10,0,1,-0), padding = margin(10,5,10,10),
+                                             fill = "#002555"),
+       plot.subtitle = element_textbox_simple(color = "#0a5275", size = 11, hjust = 0,
+                                             margin = margin(5,0,5,0), padding = margin(5,5,5,10),
+                                             fill = "#f2f2f2"),
+       plot.caption = element_text(size = 8, color = "#a6a6a6", hjust = 1),
+       panel.background = element_rect(fill="white"),
+       axis.line = element_blank(),
+       axis.text.x = element_blank(),
+       axis.text.y = element_blank(),
+       panel.grid = element_blank(),
+       plot.margin = margin(t = 10, r = 20, b = 20, l = 10), legend.position = "none")
`summarise()` has grouped output by `firsthospital`. You can override using the `.groups` argument.
>
> # ggsave(paste0("Figur_sengeflow ",format(Sys.Date(), "%d%m%y"),".png"), width = 25.5, height = 18, units = "cm")
> |
```

Environment History Connections Tutorial

Import Dataset 85 MB

Data

- df 6 obs. of 3 variables
- nfamData 7132 obs. of 47 variables
- npath 2384 obs. of 9 variables
- pathwayRAW 2384 obs. of 8 variables
- udsksr 406 obs. of 3 variables
- udsksrRAW 406 obs. of 2 variables

Values

- colordark chr [1:8] "#006AB3" "#E11621" "#00A8AB" "#...
- colorLight chr [1:8] "#C2CDEB" "#F8C6B5" "#CAE7E7" "#D...
- colorReps 14
- Formatvalid TRUE
- slutdato "2025-09-30 23:59:59"

Functions

- flowprdiagnose Large function ( 982 kB)
- nfamdesc function (x)
- nfamdescstrata function (x, strata)
- patientDensity function (output = "table", timeperiod)

Files Plots Packages Help Viewer Presentation

Install Update

Name	Description	Version
googleAuthR	Access Google Sheets using the Sheets API v4	0.0.1
gridExtra	Miscellaneous Functions for "Grid" Graphics	2.3
gridtext	Improved Text Rendering Support for 'Grid' Graphics	0.1.5
gttable	Arrange 'Grobs' in Tables	0.3.4
haven	Import and Export 'SPSS', 'Stata' and 'SAS' Files	2.5.4
HelpersMG	Tools for Environmental Analyses, Ecotoxicology and Various R Functions	6.5
highr	Syntax Highlighting for R Source Code	0.10
hms	Pretty Time of Day	1.1.3
htmltools	Tools for HTML	0.5.7
htmlwidgets	HTML Widgets for R	1.6.4
httpuv	HTTP and WebSocket Server Library	1.6.15
httr	Tools for Working with URLs and HTTP	1.4.7
httr2	Perform HTTP Requests and Process the Responses	1.2.1
ids	Generate Random Identifiers	1.0.1
ini	Read and Write '.ini' Files	0.3.1
isoband	Generate Isolines and Isobands from Regularly Spaced Elevation Grids	0.2.7

```

1 # Load all libraries used and set options
2 library(tidyverse)
3 library(lubridate)
4 library(ggtext)
5 library(pander)
6 library(patchwork)
7 panderOptions("table.style", "multiline")
8
9 ### Data input ###
10 nfamRAW <- read.csv(file = "L:\\AuditData\\NFAM data\\NFAM_raw.csv", sep = ";")
11
12
13 ### Data formatting ###
14 nfamData <- data.frame(id = 1:length(nfamRAW$ ID)) # Löbenummer
15 # Tilfældig transformering af CPR. Anvendes til identifikation af genindlæggelse
16 nfamData$ hashid <- as.numeric(nfamRAW$ hashid )
17 nfamData$ birth_year <- nfamRAW$ birth_year # Fødselsår
18 nfamData$ age <- nfamRAW$ age #Alder
19 nfamData$ gender <- factor(nfamRAW$ gender, levels = c("F","M")) # Køn (Admin)
20 # Angiver om forløbet er en genindlæggelse indenfor data perioden
21 nfamData$ readmission <- factor(nfamRAW$ x, levels = c("G"),
22                                 labels = c("Genindlagt"))
23 # Ankomst til AKA
24 nfamData$ arrival <- as.POSIXct(paste(nfamRAW$ arrival_date,
25                                     nfamRAW$ arrival_time),
26

```

16:35 (Top Level) ▾

Console Terminal × Background Jobs ×

```

R 4.3.2 · L:/AuditData/NFAM data/auditdata.R
geom_text(stat = "stratum",
aes(label = paste0(after_stat(stratum)," (n =", after_stat(count),")")), size = 5) +
labs(title = "Patientflow fra senge i NFAM til destination", subtitle = "...",
caption = paste0("Jacob Liljehult | R/R-studio | ",format(Sys.Date(), "%d %B %Y"))) +
scale_fill_manual(values = c(colorLight,colorLight)) +
theme_void() +
theme(plot.title = element_textbox_simple(color = "white", size = 25, hjust = 0, face = "bold",
margin = margin(10,0,1,-0), padding = margin(10,5,10,10),
fill = "#002555"),
plot.subtitle = element_textbox_simple(color = "#0a5275", size = 11, hjust = 0,
margin = margin(5,0,5,0), padding = margin(5,5,5,10),
fill = "#f2f2f2"),
plot.caption = element_text(size = 8, color = "#a6a6a6", hjust = 1),
panel.background = element_rect(fill="white"),
axis.line = element_blank(),
axis.text.x = element_blank(),
axis.text.y = element_blank(),
panel.grid = element_blank(),
plot.margin = margin(t = 10, r = 20, b = 20, l = 10), legend.position = "none")
`summarise()` has grouped output by 'firsthospital'. You can override using the `.groups` argument.
>
> # ggsave(paste0("Figur_sengeflow ",format(Sys.Date(), "%d%m%y"),".png"), width = 25.5, height = 18, units = "cm")
|
```

Environment History Connections Tutorial

df	6 obs. of 3 variables
nfamData	7132 obs. of 47 variables
npath	2384 obs. of 9 variables
pathwayRAW	2384 obs. of 8 variables
udskr	406 obs. of 3 variables
udskrRAW	406 obs. of 2 variables

## Values

colordark	chr [1:8] "#006AB3" "#E11621" "#00A8AB" "#5...
colorLight	chr [1:8] "#C2CDEB" "#F8C6B5" "#CAE7E7" "#D...
colorReps	14
Formatvalid	TRUE
slutdato	"2025-09-30 23:59:59"

## Functions

flowprdiagnose	Large function ( 982 kB)
nfamdesc	function (x)
nfamdescstrata	function (x, strata)
patientDensity	function (output = "table", timeperiod)

Files Plots Packages Help Viewer Presentation

Name	Description	Version
ggsheets4	Access Google Sheets using the Sheets API v4	0.6.1
gridExtra	Miscellaneous Functions for "Grid" Graphics	2.3
gridtext	Improved Text Rendering Support for 'Grid' Graphics	0.1.5
gttable	Arrange 'Grobs' in Tables	0.3.4
haven	Import and Export 'SPSS', 'Stata' and 'SAS' Files	2.5.4
HelpersMG	Tools for Environmental Analyses, Ecotoxicology and Various R Functions	6.5
highr	Syntax Highlighting for R Source Code	0.10
hms	Pretty Time of Day	1.1.3
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httr2	Perform HTTP Requests and Process the Responses	1.2.1
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ini	Read and Write '.ini' Files	0.3.1
isoband	Generate Isolines and Isobands from Regularly Spaced Elevation Grids	0.2.7

NFAMdata - RStudio

File Edit Code View Plots Session Build Debug Profile Tools Help

Go to file/function Addins

```

10 nfamRAW <- read.csv(file = "L:\\AuditData\\NFAM data\\NFAM_raw.csv", sep = ";")
11
12
13 ##### Data formatting #####
14 nfamData <- data.frame(id = 1:length(nfamRAW$ ID)) # Löbenummer
15 # Tilfældig transformering af CPR. Anvendes til identifikation af genindlæggelse
16 nfamData$ hashid <- as.numeric(nfamRAW$ hashid )
17 nfamData$ birth_year <- nfamRAW$ birth_year # Fødselsår
18 nfamData$ age <- nfamRAW$ age #Alder
19 nfamData$ gender <- factor(nfamRAW$ gender, levels = c("F","M")) # Køn (Admin)
20 # Angiver om forløbet er en genindlæggelse indenfor data perioden
21 nfamData$ readmission <- factor(nfamRAW$ x, levels = c("G"),
22                                 labels = c("Genindlagt"))
23 # Ankomst til AKA
24 nfamData$ arrival <- as.POSIXct(paste(nfamRAW$ arrival_date,
25                                     nfamRAW$ arrival_time),
26

```

164:35 (Top Level) R Script

Console Terminal Background Jobs

```

R 4.3.2 - L:/AuditData/NFAM data/
geom_text(aes(label = paste0(after_stat(stratum), " (n = ", after_stat(count), ")")), size = 5) +
  geom_text(stat = "stratum",
            aes(label = paste0(after_stat(stratum), " (n = ", after_stat(count), ")")), size = 5) +
  labs(title = "Patientflow fra senge i NFAM til destination", subtitle = "...",
       caption = paste0("Jacob Liljehult | R/R-studio | ", format(Sys.Date(), "%d %B %Y"))) +
  scale_fill_manual(values = c(colorLight, colorLight)) +
  theme_void() +
  theme(plot.title = element_textbox_simple(color = "white", size = 25, hjust = 0, face = "bold",
                                             margin = margin(10,0,1,-0), padding = margin(10,5,10,10),
                                             fill = "#002555"),
        plot.subtitle = element_textbox_simple(color = "#0a5275", size = 11, hjust = 0,
                                               margin = margin(5,0,5,0), padding = margin(5,5,5,10),
                                               fill = "#f2f2f2"),
        plot.caption = element_text(size = 8, color = "#a6a6a6", hjust = 1),
        panel.background = element_rect(fill="white"),
        axis.line = element_blank(),
        axis.text.x = element_blank(),
        axis.text.y = element_blank(),
        panel.grid = element_blank(),
        plot.margin = margin(t = 10, r = 20, b = 20, l = 10), legend.position = "none")
  summarise() has grouped output by 'firsthospital'. You can override using the '.groups' argument.
>
> # ggsave(paste0("Figur_sengeflow ",format(Sys.Date(), "%d%m%y"), ".png"), width = 25.5, height = 18, units = "cm")
> |

```

Files Plots Packages Help Viewer Presentation

udskrRAW	406 obs. of 2 variables
values	
colordark	chr [1:8] "#006AB3" "#E11621" "#00A8AB" "#5...
colorLight	chr [1:8] "#C2CDEB" "#F8C6B5" "#CAE7E7" "#D...
colorReps	14
Formatvalid	TRUE
slutdato	"2025-09-30 23:59:59"
Functions	
flowprdiagnose	Large function ( 982 kB)
nfamdesc	function (x)
nfamdescstrata	function (x, strata)
patientDensity	function (output = "table", timeperiod)

Jacob Mesot Liljehult 7

NFAMstart.R NFAM\_2025.Rmd NFAM\_figures.Rmd Udkrivelser.Rmd NFAM\_raport.Rmd

Environment History Connections Tutorial

```

1 # Load all libraries used and set options
2 library(tidyverse)
3 library(lubridate)
4 library(ggtext)
5 library(pander)
6 library(patchwork)
7 panderOptions("table.style", "multiline")
8
9 ### Data input ###
10 nfamRAW <- read.csv(file = "L:\\AuditData\\NFAM data\\NFAM_raw.csv", sep = ";")
11
12
13 ### Data formatting ###
14 nfamData <- data.frame(id = 1:length(nfamRAW$ ID)) # Løbenummer
15 # Tilfældig transformering af CPR. Anvendes til identifikation af genindlæggelse
16 nfamData$ hashid <- as.numeric(nfamRAW$ hashid )
17 nfamData$ birth_year <- nfamRAW$ birth_year # Fødselsår
18 nfamData$ age <- nfamRAW$ age #Alder
19 nfamData$ gender <- factor(nfamRAW$ gender, levels = c("F","M")) # Køn (Admin)
20 # Angiver om forløbet er en genindlæggelse indenfor data perioden
21 nfamData$ readmission <- factor(nfamRAW$ X, levels = c("G"),
22                                 labels = c("Genindlagt"))
23 # Ankomst til AKA
24 nfamData$ arrival <- as.POSIXct(paste(nfamRAW$ arrival_date,
25                                     nfamRAW$ arrival_time),
26                                     fill = "#f2f2f2"),
27                                     plot.caption = element_text(size = 8, color = "#a6a6a6", hjust = 1),
28                                     panel.background = element_rect(fill="white"),
29                                     axis.line = element_blank(),
30                                     axis.text.x = element_blank(),
31                                     axis.text.y = element_blank(),
32                                     panel.grid = element_blank(),
33                                     plot.margin = margin(t = 10, r = 20, b = 20, l = 10), legend.position = "none")
34 summarise() has grouped output by 'firsthospital'. You can override using the '.groups' argument.
>
> # ggsave(paste0("Figur_sengeflow ",format(sys.date(), "%d%m%y"),".png"), width = 25.5, height = 18, units = "cm")
> |

```

164:35 (Top Level) ▾ R Script

hms	Pretty Time of Day	1.1.5
htmltools	Tools for HTML	0.5.7
htmlwidgets	HTML Widgets for R	1.6.4
httpuv	HTTP and WebSocket Server Library	1.6.15
httr	Tools for Working with URLs and HTTP	1.4.7
httr2	Perform HTTP Requests and Process the Responses	1.2.1
ids	Generate Random Identifiers	1.0.1
ini	Read and Write '.ini' Files	0.3.1
isoband	Generate Isolines and Isobands from Regularly Spaced Elevation Grids	0.2.7

```
NFAMstart.R  NFAM_2025.Rmd  NFAM_figures.Rmd  Udskrivelse.Rmd*  NFAM_rapport.Rmd
1 # Load all libraries used and set options
2 library(tidyverse)
3 library(lubridate)
4 library(ggtext)
5 library(pander)
6 library(patchwork)
7 panderOptions("table.style", "multiline")
```

Run Source

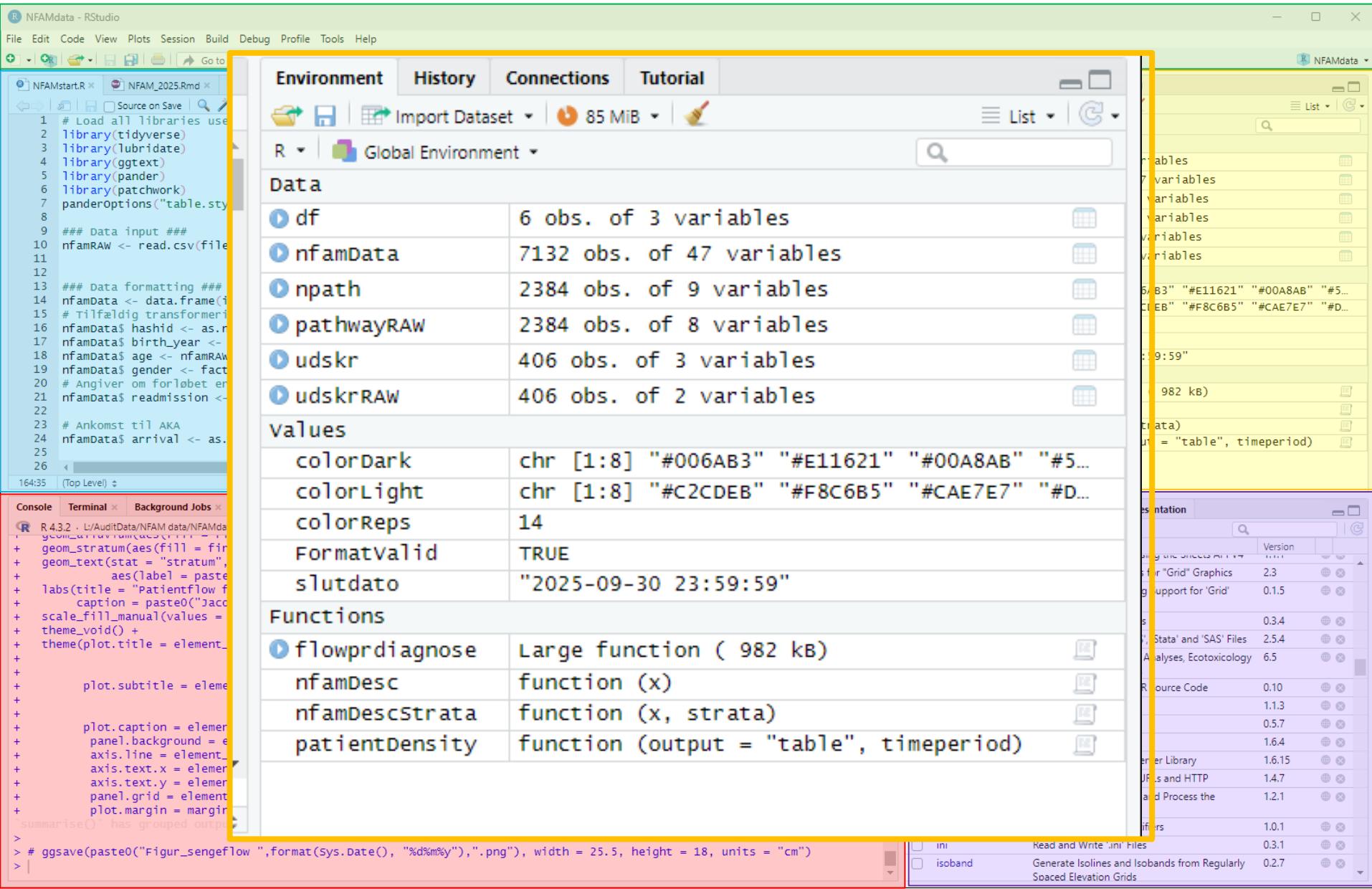
Environment History Connections Tutorial

df	6 obs. of 3 variables
nfamData	7132 obs. of 47 variables
npath	2384 obs. of 9 variables

Console Terminal Background Jobs

```
R 4.3.2 · L/AuditData/NFAM data/NFAMdata/ ↵
+ geom_label(aes(label = paste0(after_stat(stratum), " (n = ", after_stat(count), ")")), size = 5) +
+ labs(title = "Patientflow fra senge i NFAM til destination", subtitle = "...",
+       caption = paste0("Jacob Liljehult | R/R-studio | ", format(Sys.Date(), "%d %B %Y")))) +
+ scale_fill_manual(values = c(colorLight,colorLight)) +
+ theme_void() +
+ theme(plot.title = element_textbox_simple(color = "white", size = 25, hjust = 0, face = "bold",
+                                             margin = margin(10,0,1,-0), padding = margin(10,5,10,10),
+                                             fill = "#002555"),
+       plot.subtitle = element_textbox_simple(color = "#0a5275", size = 11, hjust = 0,
+                                             margin = margin(5,0,5,0), padding = margin(5,5,5,10),
+                                             fill = "#f2f2f2"),
+       plot.caption = element_text(size = 8, color = "#a6a6a6", hjust = 1),
+       panel.background = element_rect(fill="white"),
+       axis.line = element_blank(),
+       axis.text.x = element_blank(),
+       axis.text.y = element_blank(),
+       panel.grid = element_blank(),
+       plot.margin = margin(t = 10, r = 20, b = 20, l = 10), legend.position = "none")
"summarise()" has grouped output by 'firsthospital'. You can override using the '.groups' argument.
>
> # ggsave(paste0("Figur_sengeflow ",format(Sys.Date(), "%d%m%y"),".png"), width = 25.5, height = 18, units = "cm")
> 2+2
[1] 4
> |
```

<input type="checkbox"/> httr2	Perform HTTP Requests and Process the Responses	1.2.1
<input type="checkbox"/> ids	Generate Random Identifiers	1.0.1
<input type="checkbox"/> ini	Read and Write '.ini' Files	0.3.1
<input type="checkbox"/> isoband	Generate Isolines and Isobands from Regularly Spaced Elevation Grids	0.2.7



```
1 # Load all libraries
2 library(tidyverse)
3 library(lubridate)
4 library(ggtext)
5 library(pander)
6 library(patchwork)
7 panderOptions("table.collapse", TRUE)
8
9 ### Data input ####
10 nfamRAW <- read.csv(f
11
12
13 ### Data formatting #
14 nfamData <- data.frame(
15   # Tilfeldig transform
16   nfamData$ hashid <- a
17   nfamData$ birth_year
18   nfamData$ age <- nfam
19   nfamData$ gender <- f
20   # Angiver om forløbet
21   nfamData$ readmission
22
23 # Ankomst til AKA
24 nfamData$ arrival <-
25
26
```

16:35 (Top Level) ▾

Console Terminal × Background Jobs

```
R 4.3.2 - L/AuditData/NFAM data/NFAM_2025.Rmd
geom_rect(aes(xmin = 0, xmax = 100, ymin = 0, ymax = 100), fill = "#E1E1E1")
+ geom_rect(aes(xmin = 0, xmax = 100, ymin = 0, ymax = 100), fill = "#E1E1E1")
+ geom_text(stat = "stratify", aes(label = paste0("Ankomst", timeperiod)))
+ labs(title = "Patientflow", subtitle = "Arrival", caption = paste0("Tidspunkt", timeperiod))
+ scale_fill_manual(values = c("#E1E1E1", "#E1E1E1"))
+ theme_void() +
+ theme(plot.title = element_text(size = 14, color = "black", font = "bold"),
+       plot.subtitle = element_text(size = 12, color = "black", font = "bold"),
+       plot.caption = element_text(size = 10, color = "black", font = "italic"),
+       panel.background = element_rect(fill = "#E1E1E1", color = "#E1E1E1"),
+       axis.line = element_line(color = "#E1E1E1"),
+       axis.text.x = element_text(size = 10, color = "black", font = "bold"),
+       axis.text.y = element_text(size = 10, color = "black", font = "bold"),
+       panel.grid = element_rect(color = "#E1E1E1"),
+       plot.margin = margin(10, 10, 10, 10))
+ summarise() has grouped output by 'timeperiod'. You can override using the 'groups' argument.
>
> # ggsave(paste0("Figur_sengeflow ",format(sys.date(), "%d%m%y"), ".png"), width = 25.5, height = 18, units = "cm")
> |
```

**Files Plots Packages Help Viewer Presentation**

**Install Update**

Name	Description	Version
<b>User Library</b>		
<input type="checkbox"/> <b>abind</b>	Combine Multidimensional Arrays	1.4-5
<input type="checkbox"/> <b>askpass</b>	Password Entry Utilities for R, Git, and SSH	1.2.0
<input type="checkbox"/> <b>assertthat</b>	Easy Pre and Post Assertions	0.2.1
<input type="checkbox"/> <b>backports</b>	Reimplementations of Functions Introduced Since R-3.0.0	1.4.1
<input type="checkbox"/> <b>base64enc</b>	Tools for base64 encoding	0.1-3
<input type="checkbox"/> <b>bit</b>	Classes and Methods for Fast Memory-Efficient Boolean Selections	4.0.5
<input type="checkbox"/> <b>bit64</b>	A S3 Class for Vectors of 64bit Integers	4.0.5
<input type="checkbox"/> <b>blob</b>	A Simple S3 Class for Representing Vectors of Binary Data ('BLOBS')	1.2.4
<input type="checkbox"/> <b>brew</b>	Templating Framework for Report Generation	1.0-10
<input type="checkbox"/> <b>brio</b>	Basic R Input Output	1.1.4
<input type="checkbox"/> <b>broom</b>	Convert Statistical Objects into Tidy Tibbles	1.0.5
<input type="checkbox"/> <b>bslib</b>	Custom 'Bootstrap' 'Sass' Themes for 'shiny' and 'rmarkdown'	0.6.1
<input type="checkbox"/> <b>cachem</b>	Cache R Objects with Automatic Pruning	1.1.0
<input type="checkbox"/> <b>callr</b>	Call R from R	3.7.5

<input type="checkbox"/> <b>ids</b>	Generate Random Identifiers	1.0.1
<input type="checkbox"/> <b>ini</b>	Read and Write '.ini' Files	0.3.1
<input type="checkbox"/> <b>isoband</b>	Generate Isolines and Isobands from Regularly Spaced Elevation Grids	0.2.7

**Variables**

variables variables variables variables variables variables

AB" "#E11621" "#00A8AB" "#5...  
DEB" "#F8C6B5" "#CAE7E7" "#D...

59:59"

( 982 kB)

rata)  
t = "table", timeperiod)

**Presentation**

Version

ing the Sheets API v4

for "Grid" Graphics

Support for 'Grid'

0.3.4

'Stata' and 'SAS' Files

Analyses, Ecotoxicology

Source Code

1.1.3

0.5.7

1.6.4

ver Library

RLs and HTTP

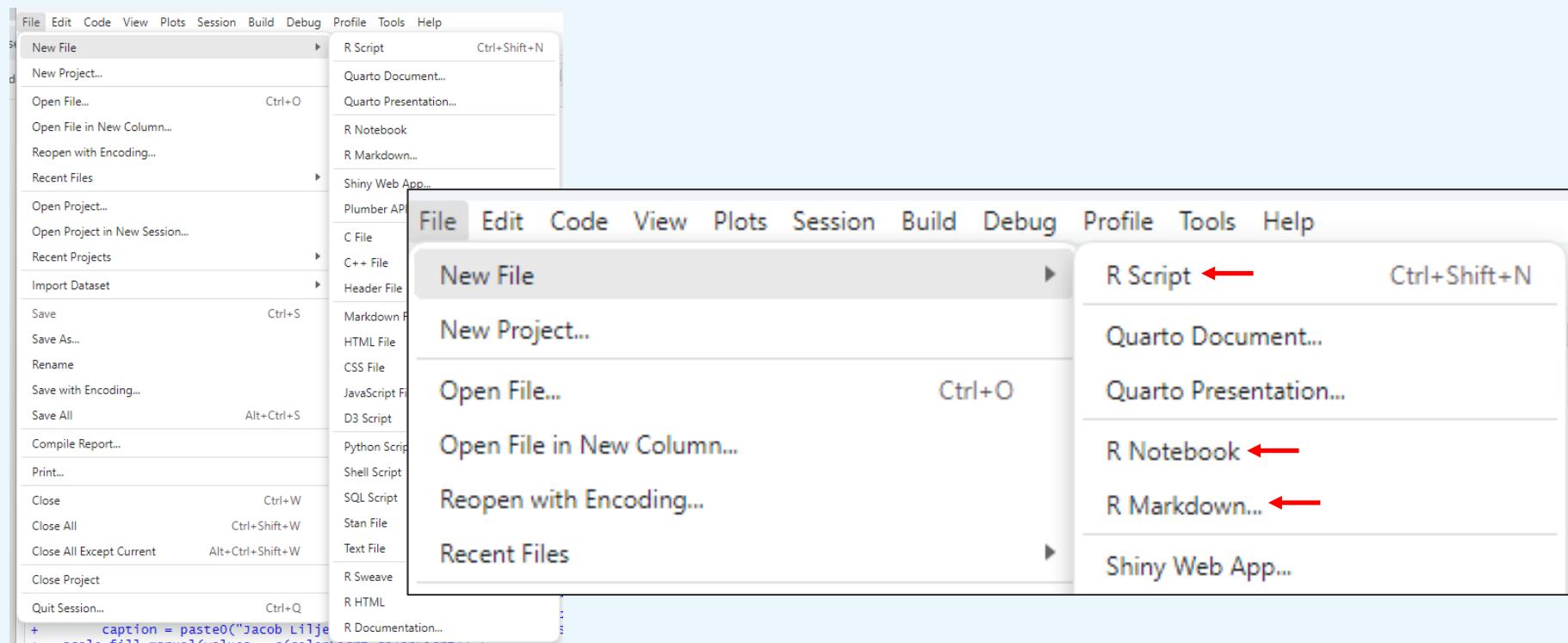
and Process the

ids

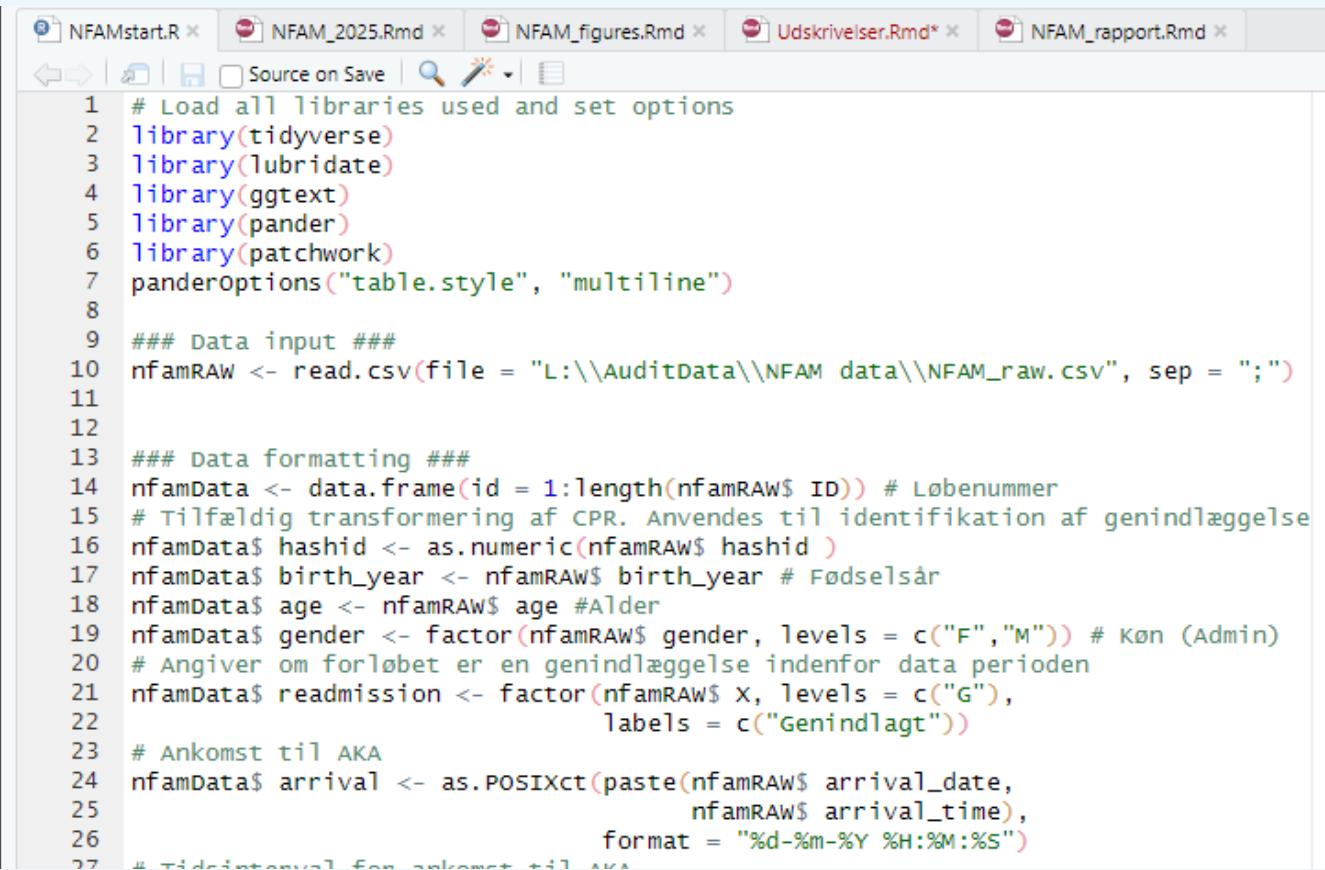
ini

isoband

# Projekter og filer



# R-script fil

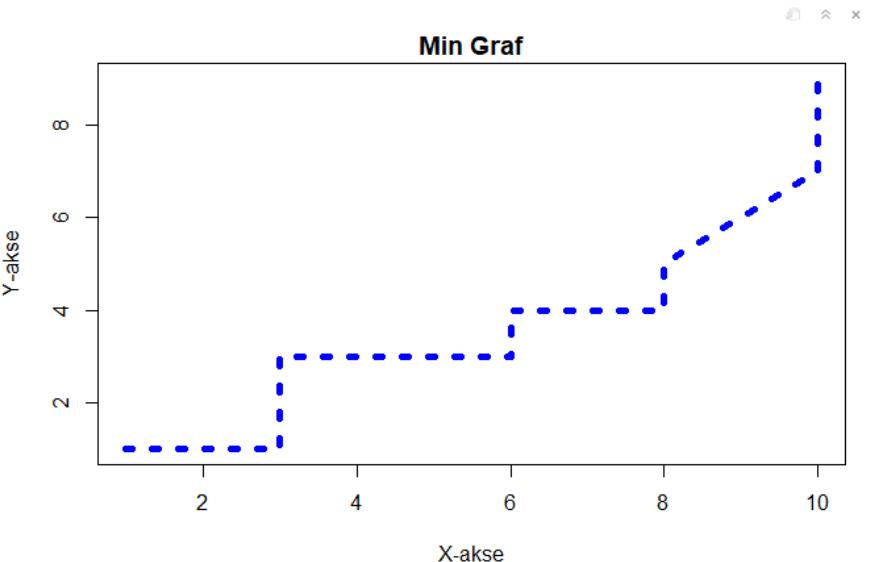


```
1 # Load all libraries used and set options
2 library(tidyverse)
3 library(lubridate)
4 library(ggtext)
5 library(pander)
6 library(patchwork)
7 panderoptions("table.style", "multiline")
8
9 ### Data input #####
10 nfamRAW <- read.csv(file = "L:\\AuditData\\NFAM data\\NFAM_raw.csv", sep = ";")
11
12
13 ### Data formatting #####
14 nfamData <- data.frame(id = 1:length(nfamRAW$ ID)) # Løbenummer
15 # Tilfældig transformering af CPR. Anvendes til identifikation af genindlæggelse
16 nfamData$ hashid <- as.numeric(nfamRAW$ hashid )
17 nfamData$ birth_year <- nfamRAW$ birth_year # Fødselsår
18 nfamData$ age <- nfamRAW$ age #Alder
19 nfamData$ gender <- factor(nfamRAW$ gender, levels = c("F","M")) # Køn (Admin)
20 # Angiver om forløbet er en genindlæggelse indenfor data perioden
21 nfamData$ readmission <- factor(nfamRAW$ x, levels = c("G"),
22                                 labels = c("Genindlagt"))
23 # Ankomst til AKA
24 nfamData$ arrival <- as.POSIXct(paste(nfamRAW$ arrival_date,
25                                     nfamRAW$ arrival_time),
26                                     format = "%d-%m-%Y %H:%M:%S")
27 # Tiddefintionsvalg for ankomst +11 min
```

- Ren kode
- Koden køres i *Console* (*Ctrl+Enter* eller 'Run') 
- Tekst kan sættes ind som kommentar, men *køres* ikke
- Kan anvendes i andre dokumenter via funktionen *source()*

# R-Markdown fil

```
1062 På linjer kan vi ændre tykkelse af linjen med `lwd` og typen med `lty`.
1063
1064
1065 ``{r}
1066 # Farve på plottet
1067 par(mar = c(4, 4, 1.5, 1)) # Laver mindre magniner omkring figur
1068 plot(c(1,3,3,6,6,8,8,9,10,10), c(1,1,3,3,4,4,5,6,7,9), type="l", col = "blue",
1069   lwd = 5, # tykkere linje
1070   lty = 3, # linjetype = stiplet linje
1071   main="Min Graf", xlab="X-akse", ylab="Y-akse")
1072 ...
1073
1074 ## De forskellige linjetyper
1075
```



The sidebar on the right contains a navigation menu with various R-related topics:

- Introduktion
- R/RStudio
- RMarkdown
- Hvordan bruger man R?
- Regler for mellemrum og linjeskift
- Kommentarer
- Data og variable
- Regler for input
- Navngivning af variable
- Scope af data
- Fjernelse af variable
- Datatyper
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- Date/time
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- Skiv din egen funktion
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- Flow control i funktioner
- Import og export af data
- Plain text filer (csv og txt)
- Indlæsning af fil i samme bibliotek
- Indlæsning af fil fra andet bibliotek
- Indlæsning af fil fra internettet
- Indlæsning af andre formatter
- Export af data
- Plots
- Punkter med plot()
- De forskellige shapes
- Linjer
- De forskellige linjetyper
- Titler og akse labels

- Kombineret kode og tekst
- Kode indsættes i ‘chunks’
- Outputtet vises i samme vindue
- Kan knittes til et dokument

# Syntaks

Funktioner består af et navn og en række argumenter, som skrives inde i parentesen

```
functionName(argument1, argument2, ...)
```

```
sample(x = 1:10, size = 100, replace=TRUE)  
sample(1:10, 100, TRUE)  
sample(replace=TRUE, size = 100, x = 1:10)
```

```
sample(TRUE, 100, 1:10)  
Fejl i sample.int(length(x), size, replace,  
prob): ugyldigt 'replace'-argument
```

```
# Uden mellemrum  
seq(from=10,to=100,by=10)  
## [1] 10 20 30 40 50 60 70 80 90 100  
  
# Med mellemrum  
seq ( from = 10, to = 100, by = 10 )  
## [1] 10 20 30 40 50 60 70 80 90 100  
  
# Med linjeskift  
seq(  
  from=10,  
  to=100,  
  by=10)  
## [1] 10 20 30 40 50 60 70 80 90 100
```

```
se q( from = 10, to = 100, by = 10)  
Fejl: uventet symbol in "se q"
```

# Pakker og biblioteker

R indeholder allerede en lang række basisfunktioner, som er klar til brug (kaldes *BaseR*)

Derudover findes der forskellige **biblioteker** (*Libraries*) med funktioner, som kan installeres via **pakker** (*packages*)

Pakker skal kun installeres én gang.

Men de enkelte biblioteker skal indlæses `library()` eller refereres `:::` hver gang R startes op.

## Installation af pakke

Via menu:

**Tools → Install packages...**

Skriv navnet i *Packages* feltet

Via console/kode

```
install.packages("Tidyverse")
```

## Indlæsning af bibliotek

```
library(lunar)
```

```
lunar::lunar.phase(date, name=T)
```

# Tidyverse



Pakke med forskellige biblioteker til datahåndtering og fremstilling

- **readr**: Værktøjer til indlæsning af datasæt fra forskellige formater
- **dplyr**: Værktøjer til datahåndtering
- **ggplot2**: Datavisualisering
- **tidyr**: Rensning af data
- **tibble**: Tabulering af data
- **stringr**: Værktøjer til string/tekst data
- **forcats**: Værktøjer til kategorisk data
- **lubridate**: Værktøjer til tid/dato data
- **purrr**: Værktøjer til funktionel programmering

# Data-input

## Definition af data-variabel

```
myVariable <- "Hello World"  
myVariable = "Hello World"
```

- Variablen skal have et **gyldigt navn** •
- Tekst variable skal omsluttet af enkelt (' ) eller dobbelt (" ) citationstegn
- Heltal indtastes som de er
- Der kan kun bruges punktum som decimalseperator (3.14195)
- Konstanterne **TRUE** og **FALSE** bruges kun til logiske variable

Det er vigtigt at skelne mellem **NULL** og **NA**, da de håndteres meget forskelligt: **NULL** = *udefineret* element (Har ingen værdi), mens **NA** = manglende værdi.

### Tilladte navne:

```
minvariabel <- "Værdi"  
min_variabel <- "Værdi"  
minVariabel <- "Værdi"  
MINVARIABLE <- "Værdi"  
minvariabel2 <- "Værdi"  
.minvariabel <- "Værdi"
```

### Forbudte navne:

```
2minvariabel <- "Værdi"  
min-variabel <- "Værdi"  
min variabel <- "Værdi"  
_min_variabel <- "Værdi"  
minv@ariabel <- "Værdi"  
TRUE <- "Værdi"
```

# Datatyper

heltalVar <- 42	Integer	Heltal
decimalVar <- 3.14195	Numeric	Decimaltal
tekstVar <- "Tekst"	Character	Tekst
logiskVar <- TRUE	Logical	Logiske værdier; Kan være enten TRUE / FALSE
nullVar <- NULL		Udefineret data
naVar <- NA		Manglende data / tomt felt
factVar <- factor("Tekst")	Factor	Kategorisk data

navn	type	attributter	værdier
testData	10 obs. of 5 variables		
\$ id	: int	1 2 3 4 5 6 7 8 9 10	
\$ weight	: num	55.3 95 93.4 78.1 96.4 ...	
\$ diagnose	: chr	"I64" "I64" "I61" "I61" ...	
\$ ivt	: logi	FALSE FALSE TRUE TRUE TRUE ...	
\$ survival	: Factor	w/ 2 levels "Alive", "Dead":	2 2 1 2 1 1 1 1 2 1

# Datastrukturer

Datastrukturer er metoder til at organiserer data

**Vektor:** Samling af data af samme datatype i en dimension:

```
drikkevarer <- c("vand", "kaffe", "te")
```

**Lists:** Samling af data af forskellig datatype i en dimension:

```
minListe <- list("kaffe", "vand", 42,  
TRUE)
```

**Matrix:** Samling af data af samme datatype i to dimensioner:

```
minMatrix <- matrix(c(1, 2, 3, 4, 5, 6),  
nrow = 3, ncol = 2)
```

**Dataframe:** Datastruktur, der består af sammenhængende vektorer

```
minDataFrame <- data.frame (  
  patientnr = c(1, 2, 3, 4,  
  5, 6, 7, 8),  
  diagnose = c("I61", "I61",  
  "I61", "I64", "I64",  
  "I63", "I64", "I61"),  
  sysBT = c(142, 165, 153,  
  120, 145, 168,  
  165, 133),  
  køn = factor(c(1, 1, 2, 1,  
  2, 2, 2, 1),  
  labels = c("Mand", "Kvinde"))  
)
```

# Matematiske operatorer

## Simple operatorer

```
5 + 5
## [1] 10
5 - 5
## [1] 0
5 * 5
## [1] 25
5 / 5
## [1] 1
```

## Regning med elementer

```
tal <- 8
tal + 10
## [1] 18
```

## Indbyggede matematiske funktioner

```
sqrt(100)
## [1] 10
4^2
## [1] 16
log(2)
## [1] 0.6931472
exp(1)
## [1] 2.718282
sum(2,18,5)
## [1] 25
```

# Logiske operatorer

```
10 < 12 # TRUE fordi 10 er mindre end 12
## [1] TRUE

10 <= 12 # TRUE fordi 10 er mindre end ELLER lig med 12
## [1] TRUE

10 > 12 # FALSE fordi 10 ikke er større end 12
## [1] FALSE

10 >= 12 # FALSE fordi 10 ikke er større end ELLER lig med 12
## [1] FALSE

10 == 12 # FALSE fordi 10 ikke er lig med 12
## [1] FALSE

10 != 12 # TRUE fordi 10 ikke er lig med 12
## [1] TRUE
```

# If...else funktioner

```
a <- 10
b <- 12

if (a < b) {
print("a er mindre end b")
} else {
print("a er større end b") }
## [1] "a er mindre end b"
```

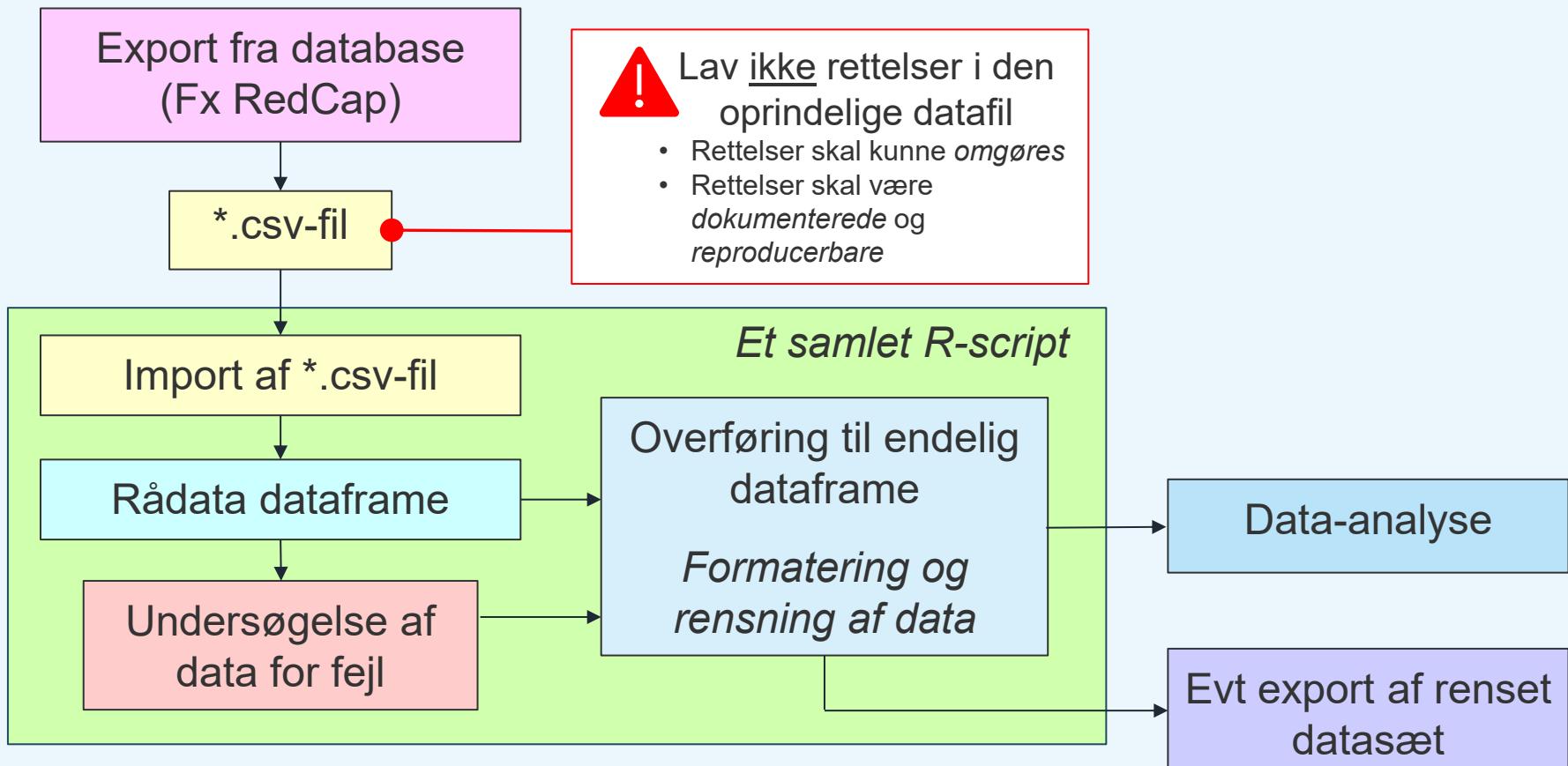
```
a <- 7562

ifelse(a > 1000, "Ja", "Nej")
## [1] "Ja"
```

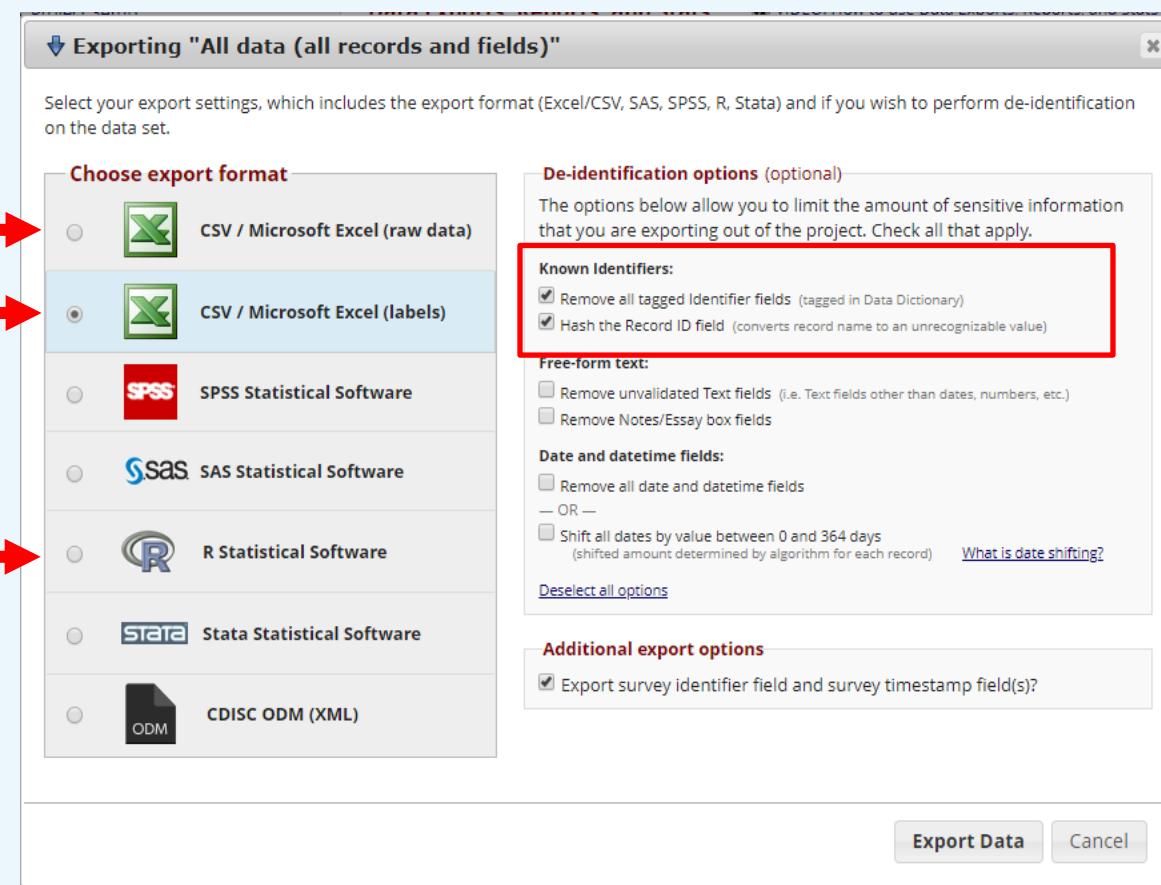
```
a <- 1000
b <- 25
c <- 756

if(a > b & a > c){ print("begge betingelser er opfyldt") }
## [1] "begge betingelser er opfyldt"
if(a > b | a > c){ print("mindst en betingelse er opfyldt") }
## [1] "mindst en betingelse er opfyldt"
```

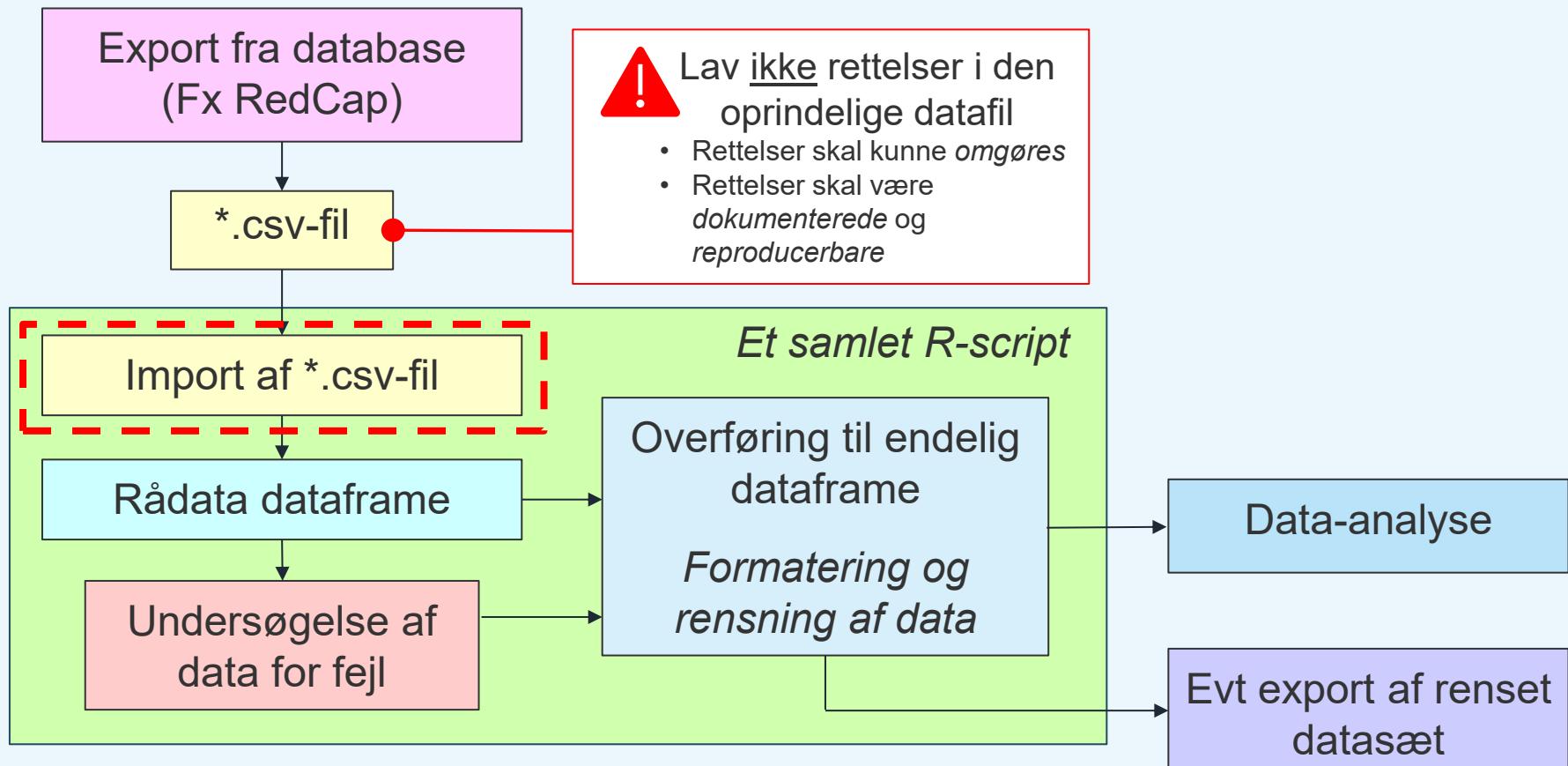
# Klargøre af data til analyse



# Export fra RedCap



# Klargøre af data til analyse



# Indlæsning af data

## Indlæsning af \*.csv-fil

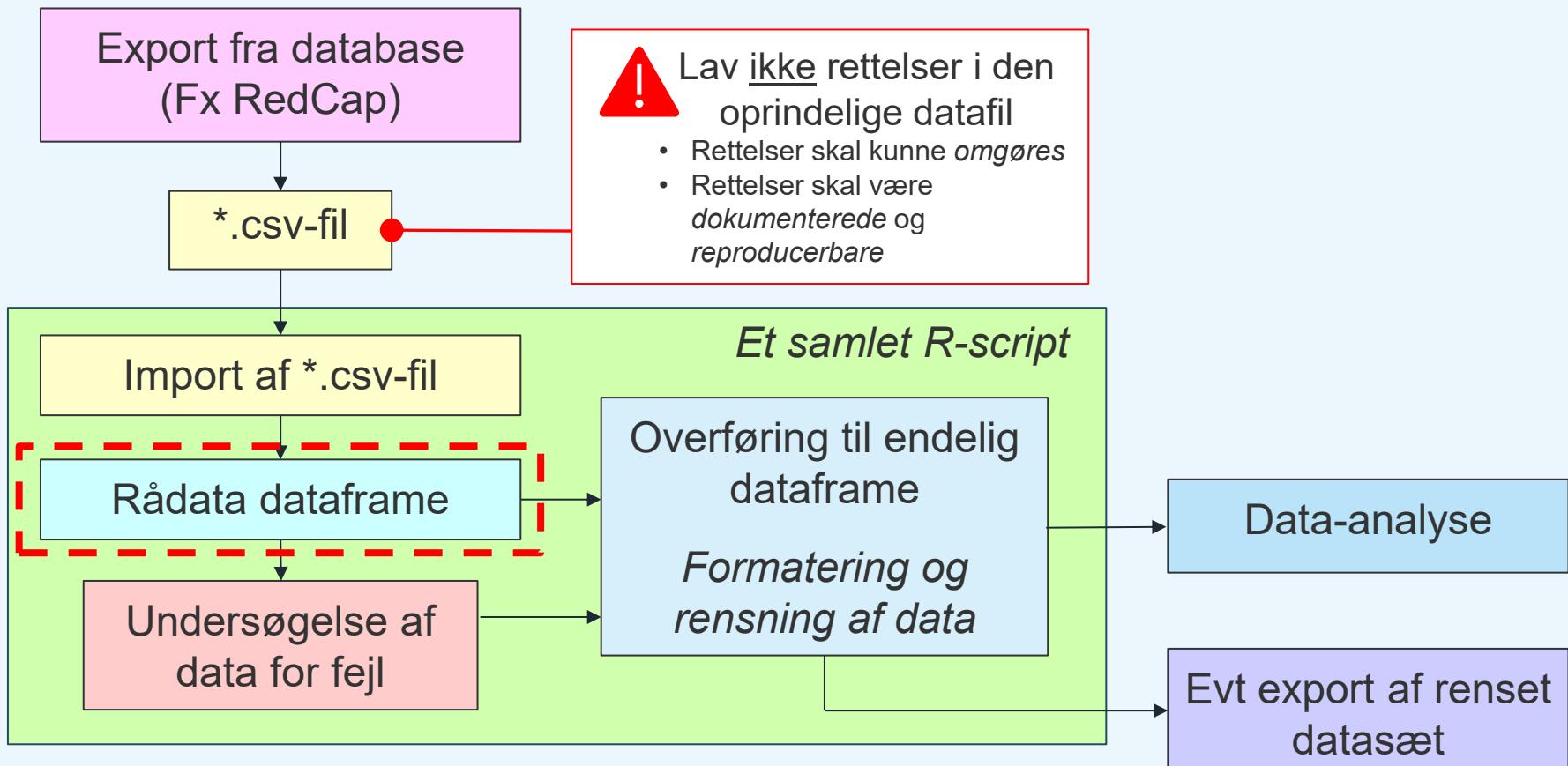
```
# Indlæsning af fil i engelsk formatering
strokedf <- read.csv("strokedata.csv")
# Indlæsning af fil i dansk formatering, altså
# semikolon mellem værdier og komma som decimal separator
strokedf <- read.csv("strokedata_dk.csv", sep=";", dec = ",")
```

```
# Indlæsning af fil fra et fælles drev
strokedf <- read.csv("L:\\AuditData\\Apodata\\strokedata.csv")
```

## Indlæsning fra web-side

```
strokedf <-
read.csv("https://jacobliljehult.github.io/research/strokedata.csv",
sep=",", header=T, stringsAsFactors = TRUE)
```

# Klargøre af data til analyse



# Dataflow

## NFAMstart.R

```
# Load all libraries used
library(tidyverse)
library(lubridate)
### Data input ###
nfamRAW <- read.csv(file =
  "L:\\AuditData\\NFAM data\\NFAM_raw.csv",
  sep = ";")

### Data formatting ###
nfamData <- data.frame(id =
  1:length(nfamRAW$ ID)) # Løbenummer
nfamData$ age <- nfamRAW$ age #Alder
nfamData$ gender <- factor(nfamRAW$ gender,
  levels = c("F", "M")) # Køn (Admin)
# Ankomst til AKA
nfamData$ arrival <-
  as.POSIXct(paste(nfamRAW$ arrival_date,
    nfamRAW$ arrival_time),
  format = "%d-%m-%Y %H:%M:%S")
rm(nfamRAW) # Fjerner rádata
```

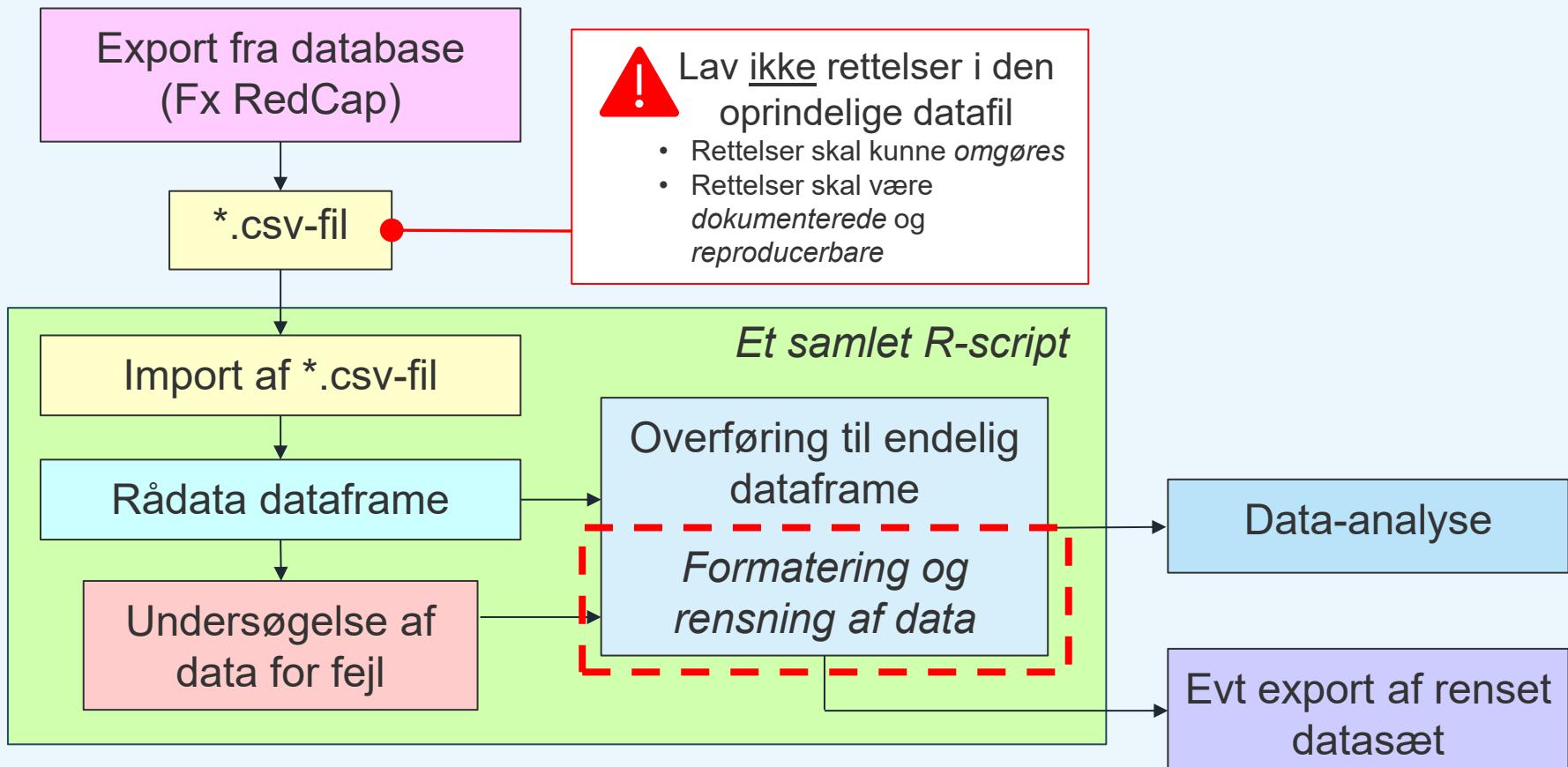
## NFAM\_rapport.Rmd

```
```{r}
source ("NFAMstart.R")
```

# Patientgrundlag
Siden 4. september har der været `r
length(nfamData$id)` neurologiske
patientforløb i AKA.

```{r}
nfamData %>% select(npAthway_bed,
  destination,destination_ward) %>%
  filter(!is.na(npAthway_bed) &
  !is.na(destination_ward)) %>%
  mutate(grp = factor(paste(npAthway_bed,
  "|",destination_ward))) %>%
  group_by(grp) %>% summarise(Antal = n())
%>% mutate(Procent = paste(round(
  Antal/sum(Antal)*100,1), "%"))
```
```

# Klargøre af data til analyse



# Struktur af datasæt

```
str(testData)
```

```
## 'data.frame': 100 obs. of 11 variables:  
## $ id : int 1 2 3 4 5 6 7 8 9 10 ...  
## $ hospital : Factor w/ 5 levels "NOH", "BBH", "HGH", ...: 2 4 3 1 4 3 3 3 5 2 ...  
## $ admission : POSIXct, format: "2024-01-04 15:02:00" "2024-01-18 13:50:00" ...  
## $ discharge : POSIXct, format: "2024-01-12 16:35:00" "2024-01-26 15:44:00" ...  
## $ gender : Factor w/ 2 levels "F", "M": 2 2 1 1 2 2 1 1 1 1 ...  
## $ age : num 66 65 60 53 88 55 68 69 59 72 ...  
## $ height : num 183 169 173 184 177 191 162 162 163 155 ...  
## $ weight : num 86.6 72.5 34.7 53.2 76 ...  
## $ allocation: Factor w/ 2 levels "Control", "Treatment": 2 2 2 2 2 1 1 2 1 1 ...  
## $ sbp_pre : num 151 127 146 137 141 152 148 122 144 137 ...  
## $ sbp_post : num 144 120 144 128 137 151 151 119 146 135 ...
```

navn type

værdier

# Formatering af datatyper

```
# Formattering af numeriske værdier
testData$age <- as.numeric(testDataRaw$age)

# Formattering af heltal
testData$age <- as.integer(testDataRaw$age)

# Formattering af tekst
testData$hospital <- as.character(testDataRaw$hospital)

# Formattering af factor fra tekstvariabel
testData$gender <- as.factor(testDataRaw$gender)

# Formattering af factor med labels
testData$hospital <- as.factor(testDataRaw$hospital,
  levels = c(1,2,3,4,5),
  labels = c("NOH", "BBH", "HGH", "AHH", "RH"))
```

## Dato

Tekstformat: "2024-01-04"

```
as.POSIXct(testDataRaw$admission_date, format = "%Y-%m-%d")
```

```
lubridate::ymd(testDataRaw$admission_date)
```

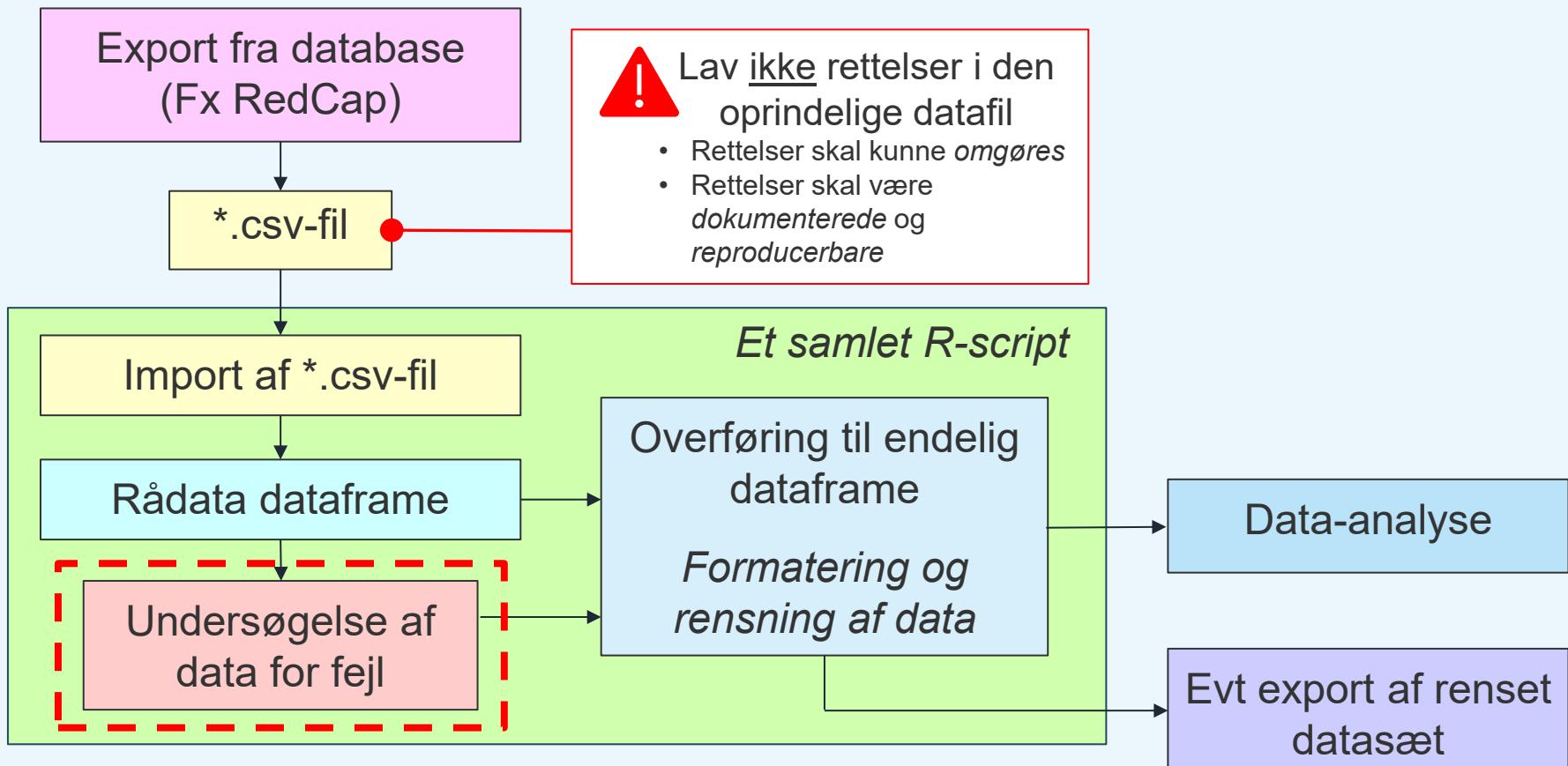
## Dato + tid

Tekstformat: "2024-01-04 10:35"

```
as.POSIXct(testDataRaw$admission, format = "%Y-%m-%d %H:%M")
```

```
lubridate::ymd_hm(testDataRaw$admission)
```

# Klargøre af data til analyse

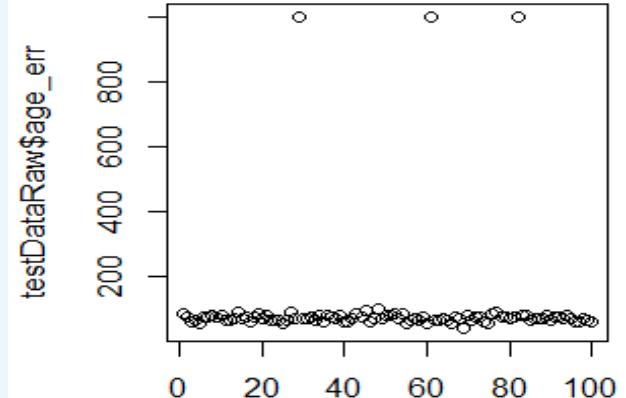


# Undersøgelse for ekstreme værdier

```
summary(testDataRaw$age_err)
```

```
## Min. 1st Qu. Median Mean 3rd Qu. Max.  
## 45.00 64.00 69.00 96.43 74.50 999.00
```

```
plot(testDataRaw$age_err)
```



Rettelse af ekstreme værdier til NA

```
ifelse(testDataRaw$age_err != 999, testDataRaw$age_err, NA)
```

# Forkerte kategorier

```
unique(testDataRaw$gender_err)
```

```
## [1] 1 0 2
```

```
table(testDataRaw$gender_err)
```

```
## 0 1 2  
## 39 53 8
```

```
table(testDataRaw$gender_err, testDataRaw$hospital)
```

```
##      NOH   BBH   HGH   AHH   RH  
## 0     8    11     7    13     0  
## 1    12     9    13     7    12  
## 2     0     0     0     0     8
```

## Betinget rettelse af værdier

```
ifelse(testDataRaw$hospital == "RH",  
       ifelse(testDataRaw$gender_err == 1, 0, 1),  
              testDataRaw$gender_err)
```

# Fejl i decimaltegn

```
testDataRaw$ weight_err  
## [1] "86,65" "72,5" "34,69" "53,17" "76,03" "100,65" "64,01" "53,79"  
  
testData$ weight_err <- as.numeric(testDataRaw$ weight_err)  
## Warning: NAs introduced by coercion
```

## Rettelse af tegn i tekst + formatering til tal

```
testData$ weight_err <- as.numeric(  
  gsub(",",".", testDataRaw$ weight_err) )
```

# Forkert kodning af NA-værdi

```
unique(testDataRaw$ height_err)
```

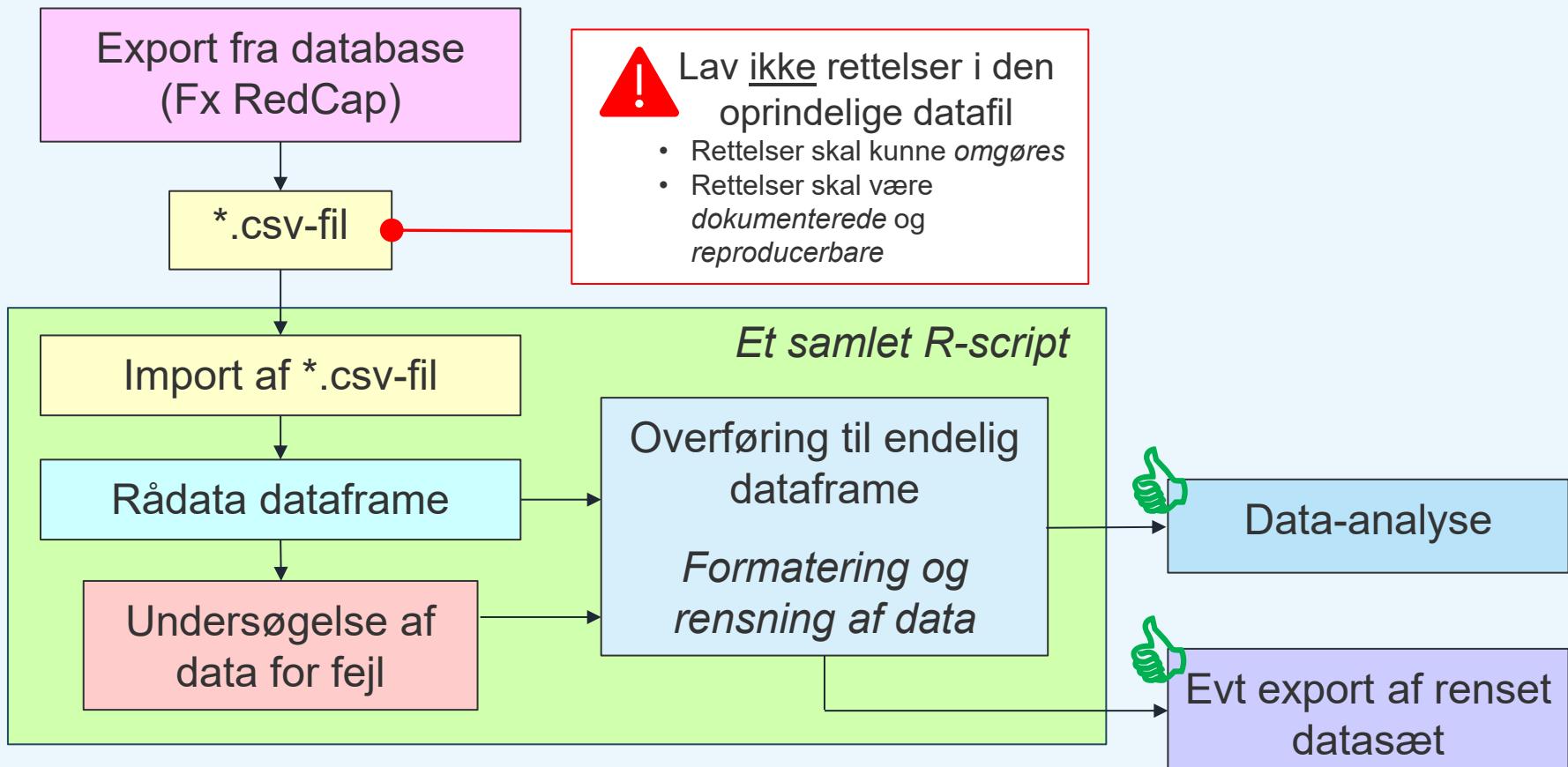
```
## [1] "183" "169" "173" "184" "177" "191" "162" "." "163" "155" "164" "189"
```

## Rettelse af manglende værdi

```
testData$ height_err <- as.numeric(testDataRaw$ height_err)
```

```
## Warning: NAs introduced by coercion
## [1] 183 169 173 184 177 191 162 NA 163 155 164 189 168 184 171
```

# Klargøre af data til analyse



# Deskriptiv statistik

## Kvantitative data

```
summary(strokedata$age)
```

|       |         |        |       |         |       |
|-------|---------|--------|-------|---------|-------|
| Min.  | 1st Qu. | Median | Mean  | 3rd Qu. | Max.  |
| 21.00 | 64.00   | 73.00  | 71.85 | 81.00   | 99.00 |

### Konfidensinterval

En nem måde at udregne et konfidensinterval for en kontinuert variable er at lave en *one-sample t-test* mod variablens eget gennemsnit

```
t.test(strokedata$age,  
       mu = mean(strokedata$age)  
       )$conf.int[1:2]  
[1] 71.09142 72.60984
```

|                |                        |
|----------------|------------------------|
| length(x)      | længden af en variabel |
| mean(x)        | gennemsnit             |
| median(x)      | median                 |
| min(x)         | mindste værdi          |
| max(x)         | maksimal værdi         |
| range(x)       | range                  |
| var(x)         | variation              |
| sd(x)          | standard deviation     |
| quantile(x, p) | percentiler            |

Argumentet na.rm = TRUE kan bruges til at ignorere NA værdier

# Deskriptiv statistik

## Kategorisk data

Enkel variabel

```
table(strokedata$inhospmors)
Alive Dead
 971   60
```

2 x 2 tabel (Absolutte tal)

```
with(strokedata,
  table(diagnosis, inhospmors))
inhospmors
diagnosis Alive Dead
  ICH     88    22
  IS      883   38
```

2 x 2 tabel (procent)

```
with(strokedata,
  prop.table(
    table(diagnosis, inhospmors)))
inhospmors
diagnosis      Alive        Dead
  ICH 0.08535403 0.02133851
  IS   0.85645005 0.03685742
```

### Konfidensinterval

Konfidensintervaller for proportioner kan udregnes med funktionerne `prop.test()` eller `binom.test()`

```
prop.test(75, 100,
  conf.level = 0.95)$conf.int[1:2]
[1] 0.6516159 0.8288245
```



```
# Procent for rækker
with(df, prop.table(table(x, y) , 1))
# Procent for koloner
with(df, prop.table(table(x, y) , 2))
```

