Lab 1: Intro to l data analysis

Practice session covering top discussed in Lecture 1

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GOAL OF TODAY'S PRACTI

Motivate the choice of learning/using R for scientific quant
out some fundamental concepts in biostatistics with concr

Lecture 1: topics

- **Introduction to R and R-studio**
  - Why R?
  - Principles of reproducible analysis with R + RStudio
- **R objects, functions, packages**
- **Understanding different types of variables**
  - Principles of "tidy data"
- **Descriptive statistics**
  - Measures of central tendency, measures of variability (or sprea
- **Visual data exploration**
  - {`ggplot2`}

INTRO TO R AN
RSTUDIO

R version

If you have previously installed R on your machine, you can
are running by executing this command in R:

```
# check your R version
R.Version()
```

```
$platform
[1] "x86_64-apple-darwin17.0"

$arch
[1] "x86_64"

$os
[1] "darwin17.0"

$system
[1] "x86_64, darwin17.0"

$status
[1] ""

$major
[1] "4"

$minor
[1] "2.2"
```

```
# or just
#R.version.string
```

Install R

R is available for free for Windows  , GNU/Linux  , and m

- To install **R**, go to this link **https://cloud.r-project.org/**.
  release is **R 4.3.3 "Angel Food Cake" released on 20**
  recent) version will do.

Install RStudio IDE

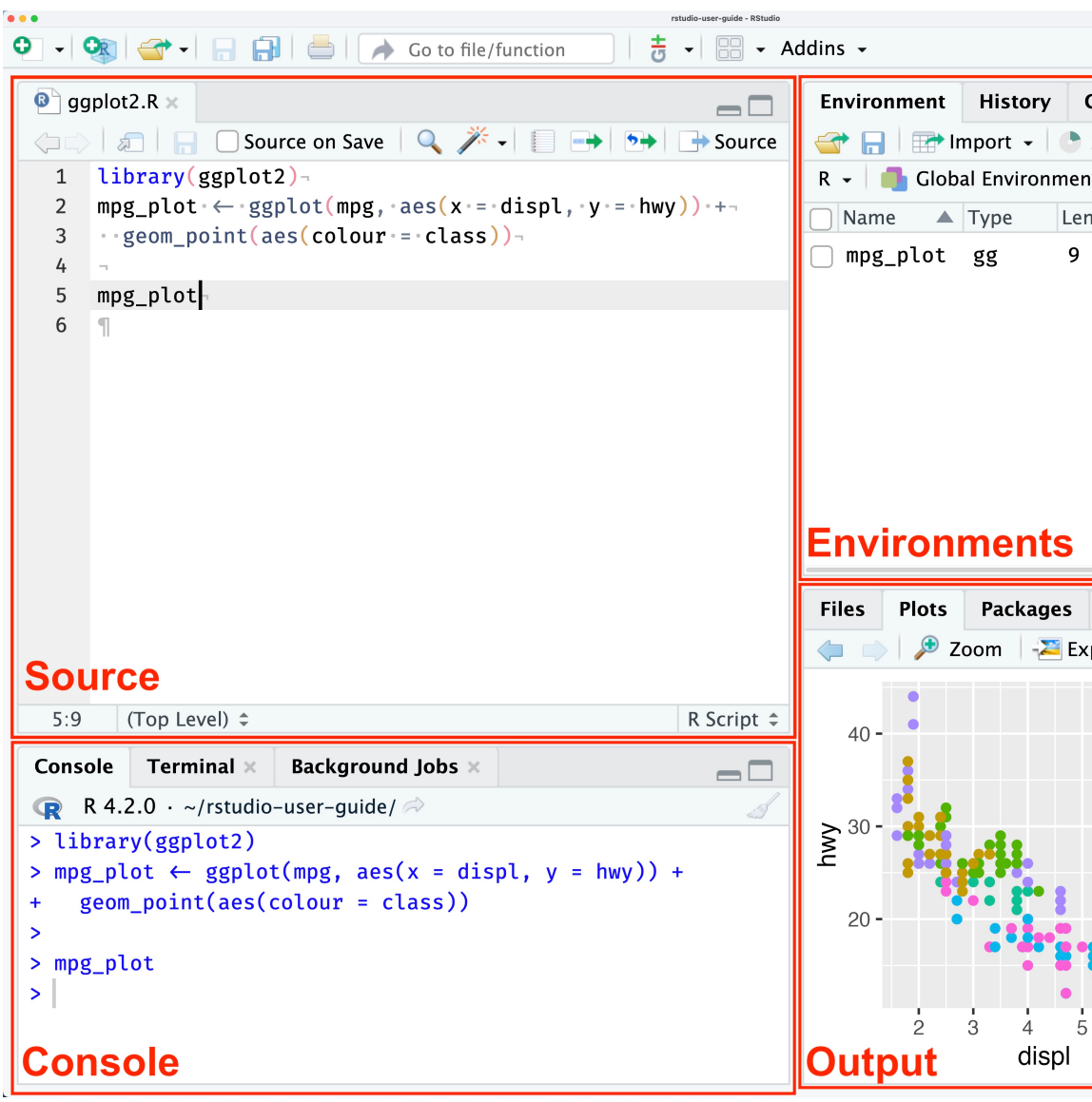
RStudio Desktop is an Integrated Development Editor (ID
interface wrapping and interfacing R (which needs to be in

Besides RStudio, R (which is a command line driven progra

- via its native interface (**R GUI**)
- from many other code editors, like **VS Code**, **Sublime Te**

To install **RStudio**, go to this link **https://posit.co/downlo**
free-version contains everything you need.

Use RStudio IDE



RStudio Pane Layout Source: Posit's RStudio User Guide

Creating an R Project [in Rs

An **R Project** will keep all the files associated with a projec
ones!) organized together – input data, R scripts, analytical
being common practice, this has the advantage of implicitl
directory", which is incredibly important when you need to
specifying their file path.

In Figure 1 you can see how easy it is just following RStudi

- Create a new directory for each project
- Select parent folder

Creating an R Project

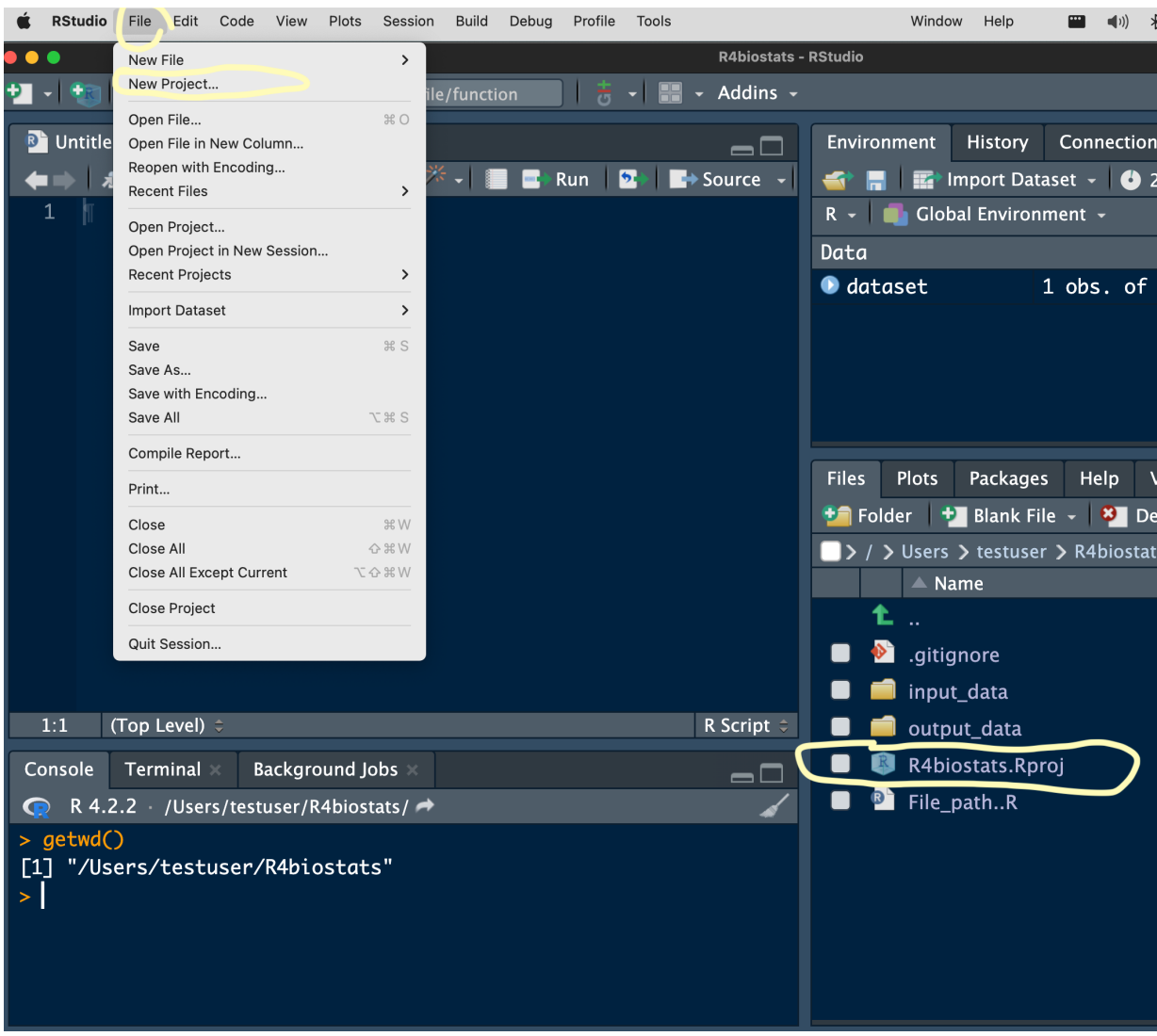


Figure 1: Creating an R project

Install R packages from CR
version)

An **R package*** is a shareable bundle of functions. Besides functions already contained in the program (i.e. the `base` p functions come in free libraries of code (or *packages*) writt find them in different repositories:

To install a package use `utils` function `install.packa`

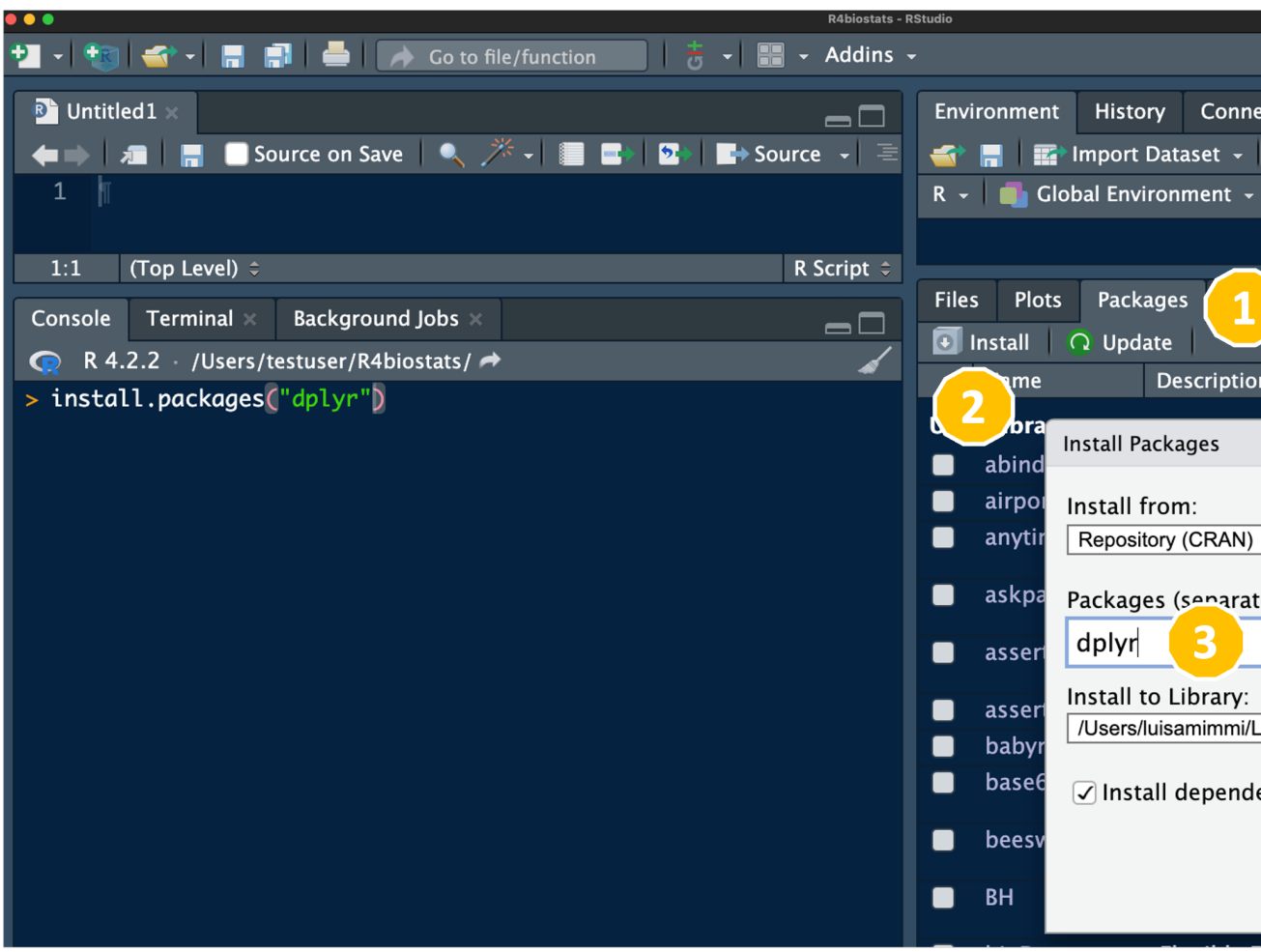
```
# Installing (ONLY the 1st time)
utils::install.packages('here')

# OR (same)
install.packages('here')
```

Here you are actually using a ***function*** (`install.packages`) of a pre-installed ***pa*** `packagename::function_name`. This prevents any ambiguity in case of duplicat what you are using.

Install R packages RStudio

In alternative, you can install/update packages using the P
right pane of RStudio.



Screenshot Install/Update pckgs from RStudio

Install R packages from G

Use `install_github` from the package `devtools`.

EXAMPLE: let's install a little package `paint` (which color
when printing).

Code

```
1 # Installing devtools (ONLY the 1st time)
2 utils::install.packages('devtools')
3
4 # Installing paint from GitHub
5 library(devtools)
6 devtools::install_github("MilesMcBain/paint
7
8 # test paint out
9 library(paint)
```

Output {p

```
1
2
```

```
> # it will show me
> paint(mtcars)
data.frame [32, 11]
mpg  dbl 21 21 22.8
cyl  dbl 6 6 4 6 8
disp dbl 160 160 10
hp   dbl 110 110 93
drat dbl 3.9 3.9 3.
wt   dbl 2.62 2.875
qsec dbl 16.46 17.0
vs   dbl 0 0 1 1 0
am   dbl 1 1 1 0 0
gear dbl 4 4 4 3 3
carb dbl 4 4 1 1 2
```


[After `devtools::install_github("MilesMcBain/paint")`, R asks me if I

Use R Packages

- We will be using {base} & {utils} (pre-installed and pre-lo
- We will also use the packages below (specifying `packag`

```
# Load them for this R session
library(here)      # tools find your project's files, base
library(janitor)   # tools for examining and cleaning data
library(skimr)     # tools for summary statistics
library(dplyr)     # {tidyverse} tools for manipulating an
library(ggplot2)   # {tidyverse} tools for plotting
library(forcats)   # {tidyverse} tool for handling factors
library(ggridges)  # alternative to plot density functions
library(fs)        # file/directory interactions
```

Help on R package/functio

To inquire about a package and/or its functions, you can a
`?package_name` or `??package_name` and RStudio will
the lower right pane.

```
1 # Opening Help page on package/function
2 ?here
3
4 ??here
```

File paths logistics

It is never good practice to “hard code” the file’s *absolute* break your code as soon as you (or someone else) need to computer, let alone within a different OS.

Let’s look at this example code using function `readr::re` `*.csv` data file into the R workspace)

```
# [NOT REPRODUCIBLE] hard coding your file path  ---------

# File path on Mac:
dataset <- readr::read_csv("/Users/testuser/R4biostats/inp
# Same file path on Windows:
dataset <- readr::read_csv("C:\Users\testuser\R4biostats\i
```

🙄...it won’t work on any other computer since it won’t hav

(Reproducible) file paths w

The `here` package lets you reference file paths in a **reproducible** ma
Project's folder as the **root**).

Where is my Working Directory?

```
here::here()
```

You should get: **"/Users/YourName/RProj_Dir"**

Now, you can embed `here(dir,subdir)` specifications in other fu
For example, create sub-directories (for saving input data and output

```
## --- [check the function documentation]
?fs::dir_create
# with `here` I simply add subfolder names relative to my wd
fs::dir_create(here("practice", "data","data_input"))
# ...and a subfolder to put output files at the end
fs::dir_create(here("practice", "data","data_output"))

## --- [if I need to remove it (I have them already)]
fs::dir_delete(here("practice", "data"))
```

R OBJECTS, FUNCTIONS, PACKAGES

Importing data into R work

We are using real data provided by Thabtah,Fadi. (2017). A
Machine Learning Repository. https://doi.org/10.24432/C5

We use `utils::read.csv` to load a csv file

```
1 ?read.csv # to learn about function and arguments
```

Option 1: Importing from a

```r
autism_data_url <- read.csv(
  file = "https://raw.githubusercontent.com/Sydney-Informa
  header = TRUE, # 1st line is the name of the variables
  sep = ",", # which is the field separator character.
  na.strings = c("?") # specific values R should interpret
)
```

Option 2: Importing from m you previously downloaded

- `here` lets me specify the complete path of the destinati

> **Tip**
>
> Make sure to match your own folder structure the file path `here(...)`!

```
# Check my working directory location
# here::here()

# Use `here` in specifying all the subfolders AFTER the wo
autism_data_file <- read.csv(
  file = here("practice", "data_input", "01_datasets", "au
  header = TRUE, # 1st line is the name of the variables
  sep = ",", # which is the field separator character.
  na.strings = c("?"),# specific values R should interpret
  row.names = NULL)
```

DATA OBSERVA
& MANIPULATI

Viewing the dataset and va

```
View(autism_data_file)
```

- Or click on the object in Environment tab (upper right pa

```
# What data type is this data?
class(autism_data_file)
```

```
[1] "data.frame"
```

```
# What variables are included in this dataset?
base::colnames(autism_data_file)
```

```
 [1] "id"              "A1_Score"        "A2_Score"        "A3_Score"
 [5] "A4_Score"        "A5_Score"        "A6_Score"        "A7_Score"
 [9] "A8_Score"        "A9_Score"        "A10_Score"       "age"
[13] "gender"          "ethnicity"       "jaundice"        "autism"
[17] "contry_of_res"   "used_app_before" "result"          "age_desc"
[21] "relation"        "Class.ASD"
```

- Notice the var name formatting inconsistency: `Class.A`

Manipulate / clean the data

I want consistent name formatting for variables: no "`.`", on
a very handy function `clean_names` from the `janitor` p

```
autism_data <- janitor::clean_names(autism_data_file,
                                    case = "none")
# check change
colnames(autism_data)
```

```
 [1] "id"              "A1_Score"        "A2_Score"        "A3_Score"
 [5] "A4_Score"        "A5_Score"        "A6_Score"        "A7_Score"
 [9] "A8_Score"        "A9_Score"        "A10_Score"       "age"
[13] "gender"          "ethnicity"       "jaundice"        "autism"
[17] "contry_of_res"   "used_app_before" "result"          "age_desc"
[21] "relation"        "Class_ASD"
```

```
dim(autism_data)
```

```
[1] 704  22
```

- By default `clean_names` renames cols into **"snake"** fo
- The option `case` is for capitalization preferences
  - `case = "none"` leaves the case as is, but only uses

Isolate a variable (column)

You can use the $ sign to extract a variable (column name)

```
autism_data$id
autism_data$A1_Score
autism_data$gender
autism_data$autism
```

Add a new column

(I prefer to rename the dataframe when I make changes)

```
# rename dataframe
autism_pids <- autism_data
```

Create a **new column**, using `paste` (function to concatena

```
# create a new column
autism_pids$pids <- paste("PatientID_" , autism_data$id, s
```

Check results:

```
# check change in df structure
base::colnames(autism_pids)
```

```
 [1] "id"              "A1_Score"        "A2_Score"        "A3_Score"
 [5] "A4_Score"        "A5_Score"        "A6_Score"        "A7_Score"
 [9] "A8_Score"        "A9_Score"        "A10_Score"       "age"
[13] "gender"          "ethnicity"       "jaundice"        "autism"
[17] "contry_of_res"   "used_app_before" "result"          "age_desc"
[21] "relation"        "Class_ASD"       "pids"
```

```
dim(autism_data)
```

```
[1] 704  22
```

```
dim(autism_pids)
```

```
[1] 704  23
```

(optional) Clean up my wor

```
# what do I have in the environment?
ls()
```

```
[1] "autism_data"      "autism_data_file" "autism_pids"
```

```
# remove all EXCEPT for "autism_pids"
rm("autism_data", "autism_data_file", "autism_data_url" )
```


(Warning: mind that after `rm()`, you will not have these objects in your workspace a

Different ways t
select rows &/c
columns (from

Option 1 Extrac

- (head only specifies to take the first 6 observations of t

```
# With the `$` sign I extract a variable (column name)
head(autism_pids$id)
```

```
[1] 1 2 3 4 5 6
```

```
head(autism_pids$pids)
```

```
[1] "PatientID_1" "PatientID_2" "PatientID_3" "PatientID_4" "PatientID_
[6] "PatientID_6"
```

```
head(autism_pids$A1_Score)
```

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

```
head(autism_pids$ethnicity)
```

```
[1] "White-European" "Latino"         "Latino"         "White-European"
[5] NA               "Others"
```

Option 2a Extract co

- This is called “indexing”

```
# Indexing to pick `[ , #col]`
head(autism_pids[ ,1] )# empty rows means all
```

```
[1] 1 2 3 4 5 6
```

```
head(autism_pids[ ,23])
```

```
[1] "PatientID_1" "PatientID_2" "PatientID_3" "PatientID_4" "PatientID_
[6] "PatientID_6"
```

```
head(autism_pids[ ,2])
```

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

```
head(autism_pids[ ,14])
```

```
[1] "White-European" "Latino"         "Latino"         "White-European"
[5] NA               "Others"
```

Option 2b Extract ro

```
# Indexing to pick `[#row, ]`
head(autism_pids[1 , ] ) # empty cols means all
```

```
  id A1_Score A2_Score A3_Score A4_Score A5_Score A6_Score A7_Score A8_
1  1        1        1        1        1        0        0        1
  A9_Score A10_Score age gender      ethnicity jaundice autism contry_o
1        0         0  26      f White-European       no     no United S
  used_app_before result    age_desc relation Class_ASD        pids
1              no      6 18 and more     Self        NO PatientID_1
```

```
head(autism_pids[50,])
```

```
   id A1_Score A2_Score A3_Score A4_Score A5_Score A6_Score A7_Score A8
50 50        1        1        0        0        0        1        1
   A9_Score A10_Score age gender ethnicity jaundice autism contry_of_re
50        0         1  30      f     Asian       no     no    Bangades
   used_app_before result    age_desc relation Class_ASD         pids
50              no      6 18 and more     Self        NO PatientID_50
```

```
head(autism_pids[25:26 ,])
```

```
   id A1_Score A2_Score A3_Score A4_Score A5_Score A6_Score A7_Score A8
25 25        1        1        1        1        0        0        0
26 26        0        1        1        0        0        0        0
   A9_Score A10_Score age gender ethnicity jaundice autism contry_of_re
25        0         0  43      m      <NA>       no     no       Lebanc
26        0         0  24      f      <NA>      yes     no   Afghanista
   used_app_before result    age_desc relation Class_ASD         pids
25              no      5 18 and more     <NA>        NO PatientID_25
26              no      3 18 and more     <NA>        NO PatientID_26
```

Option 3 Extract rows & co

```
# Indexing to pick `[#row, #col]`
autism_pids[1:3,1]
```

```
[1] 1 2 3
```

```
autism_pids[1:3,23]
```

```
[1] "PatientID_1" "PatientID_2" "PatientID_3"
```

```
autism_pids[1:3,2]
```

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

```
autism_pids[1:3,14]
```

```
[1] "White-European" "Latino"         "Latino"
```

What are the da types of the variables?

Option 1 using base functio

- on the whole dataset

```
# What are the data types of the variables? --------------
str(autism_pids) # integer and character
```

```
'data.frame':   704 obs. of  23 variables:
 $ id              : int  1 2 3 4 5 6 7 8 9 10 ...
 $ A1_Score        : int  1 1 1 1 1 1 0 1 1 1 ...
 $ A2_Score        : int  1 1 1 1 0 1 1 1 1 1 ...
 $ A3_Score        : int  1 0 0 0 0 1 0 1 0 1 ...
 $ A4_Score        : int  1 1 1 1 0 1 0 1 0 1 ...
 $ A5_Score        : int  0 0 1 0 0 1 0 0 1 0 ...
 $ A6_Score        : int  0 0 0 0 0 0 0 0 0 1 ...
 $ A7_Score        : int  1 0 1 1 0 1 0 0 0 1 ...
 $ A8_Score        : int  1 1 1 1 1 1 1 0 1 1 ...
 $ A9_Score        : int  0 0 1 0 0 1 0 1 1 1 ...
 $ A10_Score       : int  0 1 1 1 0 1 0 0 1 0 ...
 $ age             : int  26 24 27 35 40 36 17 64 29 17 ...
 $ gender          : chr  "f" "m" "m" "f" ...
 $ ethnicity       : chr  "White-European" "Latino" "Latino" "White-Euro
 $ jaundice        : chr  "no" "no" "yes" "no" ...
 $ autism          : chr  "no" "yes" "yes" "yes" ...
 $ contry_of_res   : chr  "United States" "Brazil" "Spain" "United State
 $ used_app_before: chr  "no" "no" "no" "no" ...
 $ result          : int  6 5 8 6 2 9 2 5 6 8 ...
```

Option 1 using base functio

- on specific columns

```
# What values can the variables take? --------------------
summary(autism_pids$pids)
```

```
   Length     Class      Mode
      704 character character
```

```
length(unique(autism_pids$pids)) # N unique values
```

```
[1] 704
```

```
sum(is.na(autism_pids$pids)) # N missing values
```

```
[1] 0
```

```
summary(autism_pids$ethnicity)
```

```
   Length     Class      Mode
      704 character character
```

```
length(unique(autism_pids$ethnicity)) # N unique values
```

```
[1] 12
```

```
sum(is.na(autism_pids$ethnicity)) # N missing values
```

```
[1] 95
```

Option 2 using skimr funct

- on specific columns

```
autism_pids %>%
  skimr::skim(pids, ethnicity) %>%
  dplyr::select(#skim_variable,
                skim_type,
                complete_rate,
                n_missing,
                character.n_unique)
```

```
# A tibble: 2 × 4
  skim_type complete_rate n_missing character.n_unique
  <chr>             <dbl>     <int>               <int>
1 character         1             0                 704
2 character         0.865        95                  11
```

Option 2 using `skimr` fu

- on the whole dataset

```
autism_pids %>%
  skimr::skim()
```

```
── Variable type: character ──────────────────────────────────────────────
   skim_variable   n_missing complete_rate min max empty n_unique white
 1 gender                  0          1       1   1     0        2
 2 ethnicity              95          0.865   5  15     0       11
 3 jaundice                0          1       2   3     0        2
 4 autism                  0          1       2   3     0        2
 5 contry_of_res           0          1       4  20     0       67
 6 used_app_before         0          1       2   3     0        2
 7 age_desc                0          1      11  11     0        1
 8 relation               95          0.865   4  24     0        5
 9 Class_ASD               0          1       2   3     0        2
10 pids                    0          1      11  13     0      704

── Variable type: numeric ────────────────────────────────────────────────
   skim_variable n_missing complete_rate    mean      sd p0  p25  p50
 1 id                    0          1     352.    203.     1 177. 352. 5
 2 A1_Score              0          1       0.722   0.449  0   0    1
 3 A2_Score              0          1       0.453   0.498  0   0    0
 4 A3_Score              0          1       0.457   0.499  0   0    0
```

Recoding varia

From character to factor us

```
#### char 2 factor ----------------------------------------
# Say I want to treat some variables as factors
autism_pids$gender <- as.factor(autism_pids$gender)
autism_pids$ethnicity <- as.factor(autism_pids$ethnicity)
autism_pids$contry_of_res <- as.factor(autism_pids$contry_
autism_pids$relation <- as.factor(autism_pids$relation)

# check
class(autism_pids$gender)
```

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

```
class(autism_pids$ethnicity)
```

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

```
class(autism_pids$contry_of_res)
```

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

```
class(autism_pids$relation)
```

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

From character to factor us (n cols)

```r
autism_pids_temp <- autism_pids # copy df for test

to_factor <- c("gender", "ethnicity", "contry_of_res", "re
autism_pids_temp[ ,to_factor] <-  lapply(X =  autism_pids[

# check
class(autism_pids_temp$gender)
```

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

```r
class(autism_pids_temp$ethnicity)
```

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

```r
class(autism_pids_temp$contry_of_res)
```

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

```r
class(autism_pids_temp$relation)
```

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

```r
# now I have Variable type: factor
```

Inspect factors levels (3 di ways)

- using `base::levels` function

```
levels(autism_pids$ethnicity)
```

```
[1] "Asian"           "Black"           "Hispanic"        "Latino"
[5] "Middle Eastern " "others"          "Others"          "Pasifika"
[9] "South Asian"     "Turkish"         "White-European"
```

- using `base::table` function

```
table(autism_pids$ethnicity,useNA = "ifany")
```

```
          Asian           Black        Hispanic          Latino Middle
            123              43              13              20
         others          Others        Pasifika    South Asian
              1              30              12              36
White-European            <NA>
            233              95
```

Inspect factors levels – 3 d ways (cont.)

- using `janitor` function `tabyl`, which uses the “pipe” o the output of a function as input of the next one

```
janitor::tabyl(autism_pids$ethnicity) %>%
  adorn_totals() %>%
  adorn_pct_formatting()
```

autism_pids$ethnicity	n	percent	valid_percent
Asian	123	17.5%	20.2%
Black	43	6.1%	7.1%
Hispanic	13	1.8%	2.1%
Latino	20	2.8%	3.3%
Middle Eastern	92	13.1%	15.1%
others	1	0.1%	0.2%
Others	30	4.3%	4.9%
Pasifika	12	1.7%	2.0%
South Asian	36	5.1%	5.9%
Turkish	6	0.9%	1.0%
White-European	233	33.1%	38.3%
<NA>	95	13.5%	-
Total	704	100.0%	100.0%

Identify missing values

Use `is.na` to check if the 95 missing obs are the same m
`relation`

```
1 which(is.na(autism_pids$ethnicity)) # indices of TRUE elem
```

```
 [1]   5  13  14  15  20  21  25  26  63  80  81  82  92 217 222 239 25
[20] 278 286 307 316 325 338 339 340 341 342 343 344 345 346 347 348 34
[39] 352 353 354 355 356 362 366 370 371 373 379 380 381 382 383 384 38
[58] 388 389 391 396 400 401 402 404 424 428 429 430 433 439 454 486 50
[77] 535 536 537 538 557 565 572 573 589 594 637 643 646 652 653 659 66
```

```
1 which(is.na(autism_pids$relation))  # indices of TRUE elem
```

```
 [1]   5  13  14  15  20  21  25  26  63  80  81  82  92 217 222 239 25
[20] 278 286 307 316 325 338 339 340 341 342 343 344 345 346 347 348 34
[39] 352 353 354 355 356 362 366 370 371 373 379 380 381 382 383 384 38
[58] 388 389 391 396 400 401 402 404 424 428 429 430 433 439 454 486 50
[77] 535 536 537 538 557 565 572 573 589 594 637 643 646 652 653 659 66
```

...indeed they are the same IDs!

From character to logical

I may prefer to code a variable as logical. For example, ag
explicit if coded as logical.

- I create a new column `age_desc_log`

```
# observe a subset of some columns
autism_subset <- autism_pids [1:5, c("gender","jaundice",
                                     "Class_ASD","pids")]
# View(autism_subset)

# recode "age_desc" as LOGICAL new var "age_desc_log"
autism_pids$age_desc_log <- ifelse(autism_pids$age_desc ==
class(autism_pids$age_desc)
```

```
[1] "character"
```

```
class(autism_pids$age_desc_log)
```

```
[1] "logical"
```

From character to dummy [

I also may need binary variables expressed as [0,1] (e.g. to
variables into regression analysis). Let's recode `autism`.

```
autism_pids$autism_dummy <- ifelse(autism_pids$autism == '
class(autism_pids$autism)
```

```
[1] "character"
```

```
class(autism_pids$autism_dummy)
```

```
[1] "numeric"
```

Subsetting the data for furt investigation

Recall how to view the names of columns / variables

```
colnames(autism_pids)
```

```
 [1] "id"              "A1_Score"        "A2_Score"        "A3_Score"
 [5] "A4_Score"        "A5_Score"        "A6_Score"        "A7_Score"
 [9] "A8_Score"        "A9_Score"        "A10_Score"       "age"
[13] "gender"          "ethnicity"       "jaundice"        "autism"
[17] "contry_of_res"   "used_app_before" "result"          "age_desc"
[21] "relation"        "Class_ASD"       "pids"            "age_desc_lo
[25] "autism_dummy"
```

using `head` or `tail` from u

- `head` or `tail` return the first or last parts of an object

```
head(autism_pids)   #return fist 6 obs
tail(autism_pids)   #return last 6 obs
```

using head or tail from u

```r
head(autism_pids, n = 2) #return fist 2 obs
```

```
  id A1_Score A2_Score A3_Score A4_Score A5_Score A6_Score A7_Score A8_
1  1        1        1        1        1        0        0        1
2  2        1        1        0        1        0        0        0
  A9_Score A10_Score age gender      ethnicity jaundice autism contry_o
1        0         0  26      f White-European       no      no United S
2        0         1  24      m         Latino       no     yes        P
  used_app_before result    age_desc relation Class_ASD        pids
1              no      6 18 and more     Self        NO PatientID_1
2              no      5 18 and more     Self        NO PatientID_2
  age_desc_log autism_dummy
1         TRUE            0
2         TRUE            1
```

```r
tail(autism_pids, n = 2) #return last 2 obs
```

```
     id A1_Score A2_Score A3_Score A4_Score A5_Score A6_Score A7_Score
703 703        1        0        0        1        1        0        1
704 704        1        0        1        1        1        0        1
    A9_Score A10_Score age gender      ethnicity jaundice autism contry
703        1         1  35      m    South Asian       no      no       P
704        1         1  26      f White-European       no      no
    used_app_before result    age_desc relation Class_ASD          pids
703              no      6 18 and more     Self        NO PatientID_703
704              no      8 18 and more     Self       YES PatientID_704
    age_desc_log autism_dummy
703         TRUE            0
704         TRUE            0
```

Investigating a subset of o

E.g. I learned that some patients have missing age... how m

```
# run...
sum(is.na(autism_pids$age))
```

```
[1] 2
```

```
# or
skimr::n_missing(autism_pids$age)
```

```
[1] 2
```

So, next, I want to ID those patients with missing age.

New df (patients missing age)

I want to extract only the obs (*rows*) of interest with a few u

Option 1) using [ ] from base

```
missing_age_subset <- autism_pids[is.na(autism_pids$age),
                                  c("pids", "age", "autism
missing_age_subset
```

```
           pids age autism_dummy
63 PatientID_63  NA            0
92 PatientID_92  NA            0
```

New df (patients missing age)

I want to extract only the obs (*rows*) of interest with a few u

Option 2) using `which` from `base`

```
missing_age_subset2 <- autism_pids[which(is.na(autism_pids
                                         c("pids", "age", "autis
missing_age_subset2
```

```
           pids age autism_dummy
63 PatientID_63  NA            0
92 PatientID_92  NA            0
```

New df (patients missing age)

I want to extract only the obs (*rows*) of interest with a few u

Option 3) using subset from base

```
# arguments allow me to specify rows and cols
missing_age_subset3 <- subset(x = autism_pids,
                              subset = is.na(autism_pids$a
                              select = c("pids", "age", "a
                              )
missing_age_subset3
```

```
           pids age autism_dummy
63 PatientID_63  NA            0
92 PatientID_92  NA            0
```

New df (filtering on 2 conditions

Option 1) using `base::subset`

```r
# Creates a SUBSET based on MORE conditions (`age` and `et
twocond_base_subset <- subset(x = autism_pids,
                              # 2 logical conditions
                              subset = age < 25 & contry_of_res =
                              # pick a few cols
                              select = c("pids", "age", "contry_o
                                         "autism_dummy"))

twocond_base_subset
```

```
             pids age contry_of_res autism_dummy
2     PatientID_2  24        Brazil            1
54   PatientID_54  21        Brazil            1
94   PatientID_94  19        Brazil            1
429 PatientID_429  20        Brazil            0
587 PatientID_587  21        Brazil            0
588 PatientID_588  21        Brazil            0
```

New df (filtering on 2 conditions

Option 2) using `dplyr` (`filter` + `select`)

Switching to the package `dplyr` and embracing the "pipe
which the filtering (rows) and selecting (columns) is done i

```
## here the filtering (rows) and selecting (columns) is do
twocond_dplyr_subset <- autism_pids %>%
  dplyr::filter(age < 25 & contry_of_res == "Brazil") %>%
  dplyr::select (pids, age, contry_of_res, autism_dummy)

twocond_dplyr_subset
```

```
           pids age contry_of_res autism_dummy
1   PatientID_2  24        Brazil            1
2  PatientID_54  21        Brazil            1
3  PatientID_94  19        Brazil            1
4 PatientID_429  20        Brazil            0
5 PatientID_587  21        Brazil            0
6 PatientID_588  21        Brazil            0
```

Dealing with m
data

Input values where missing

⚠️WARNING: This is a very delicate & risky step ⚠️

- any modified/imputed data (beyond the *original collection*) can
  and statistical modeling
- it will be necessary to document and justify whichever approac
  data.

  Let's assume we can get the missing data by cross-checking re

```
# 1/2 create a new variable
autism_pids$age_inputed <- autism_pids$age
# 2/2 replace value (presumably taken from other source) of `aged_
  # CONDITIONAL on `pids`
autism_pids$age_inputed[autism_pids$pids == "PatientID_63"] <-  65
autism_pids$age_inputed[autism_pids$pids == "PatientID_92"] <-  45

# check
skimr::n_missing(autism_pids$age)
```

```
[1] 2
```

```
skimr::n_missing(autism_pids$age_inputed)
```

```
[1] 0
```

DESCRIPTIVE STATISTICS

Summarizing all variables

Try these 2 options:

base::c

```
summary(autism_pids)
```

skimr

```
skim
```

Notice `summary` different b
according to the variable's

The function's results depend on the class of the object

- look at the output in case of `integer` (e.g. A1_Score)

```
summary(autism_pids$A1_Score)     # min, max quartiles, me
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.0000  0.0000  1.0000  0.7216  1.0000  1.0000
```

- look at the output in case of `factor` (e.g. ethnicity)

```
summary(autism_pids$ethnicity)    # counts of levels' freq
```

```
          Asian           Black        Hispanic          Latino Middle
            123              43              13              20
         others          Others        Pasifika     South Asian
              1              30              12              36
White-European            NA's
            233              95
```

Notice `summary` different b
according to the variable's

- look at the output in case of `logical` (e.g. age_desc_log

```
1 summary(autism_pids$age_desc_log) # counts of TRUE
```

```
   Mode    TRUE
logical     704
```

Frequency distributions wit

- Frequency distributions can be used for nominal, ordina variables

```
1 table(autism_pids$gender)
```

```
  f   m
337 367
```

```
1 table(autism_pids$age) # automatically drops missing...
```

```
17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40
18 31 35 46 49 37 37 34 27 28 31 24 27 30 21 18 16 12 17 13 17 13  7 16
43 44 45 46 47 48 49 50 51 52 53 54 55 56 58 59 60 61 64
11 10  4  6  8  4  3  5  1  5  6  2  6  2  2  1  1  2  1
```

```
1 table(autism_pids$age, useNA = "ifany") #...unless specifi
```

```
  17   18   19   20   21   22   23   24   25   26   27   28   29   30
  18   31   35   46   49   37   37   34   27   28   31   24   27   30
  33   34   35   36   37   38   39   40   41   42   43   44   45   46
  16   12   17   13   17   13    7   16    3   15   11   10    4    6
  49   50   51   52   53   54   55   56   58   59   60   61   64 <NA>
   3    5    1    5    6    2    6    2    2    1    1    2    1    2
```

Cross tabulation with `tabl`

- Cross tabulation

```
1 table(autism_pids$gender, autism_pids$age_inputed)
```

```
  17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 3
f  7 11 22 22 18 14 17 10 11 14 18 15 16 13  8 14  6  7 12  7 11  6
m 11 20 13 24 31 23 20 24 16 14 13  9 11 17 13  4 10  5  5  6  6  7

  42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 58 59 60 61 64 65
f  6  5  4  5  4  3  2  2  2  0  2  4  1  1  0  1  0  1  1  0  0
m  9  6  6  0  2  5  2  1  3  1  3  2  1  5  2  1  1  0  1  1  1
```

```
1 table(autism_pids$ethnicity, autism_pids$autism_dummy)
```

```
                  0   1
Asian           118   5
Black            38   5
Hispanic         12   1
Latino           12   8
Middle Eastern   83   9
others            1   0
Others           28   2
Pasifika         10   2
South Asian      34   2
Turkish           5   1
White-European  183  50
```

Grouping and summarizing R

E.g. I want to know the average age of men and women sub

Option 1) using by

```r
# by(data$column, data$grouping_column, mean)
by(data = autism_pids$age_inputed, INDICES = autism_pids$g
```

```
autism_pids$gender: f
[1] 29.60237
------------------------------------------------------------
autism_pids$gender: m
[1] 28.98365
```

Grouping and summarizing in R

Option 2) using `tapply`

```r
# i.e. apply a function to subsets of a vector or array, s
tapply(X = autism_pids$age_inputed, INDEX = autism_pids$ge
```

```
       f        m
29.60237 28.98365
```

Option 3) using `split` + `sapply`

```r
# sapply(split(data$column, data$grouping_column), mean)
sapply(X = split(autism_pids$age_inputed, autism_pids$gend
```

```
       f        m
29.60237 28.98365
```

Grouping and summarizing

```
autism_pids %>%
  dplyr::group_by(gender) %>%
  dplyr::summarise(mean(age_inputed))  # returns a datafra
```

```
# A tibble: 2 × 2
  gender `mean(age_inputed)`
  <fct>                <dbl>
1 f                     29.6
2 m                     29.0
```

I could add more statistics to the grouped summary...

```
autism_pids %>%
  dplyr::group_by(gender) %>%
  dplyr::summarise(mean_age = mean(age_inputed),
                   N_obs = n(),
                   N_with_autism = sum(autism_dummy == 1)
  )
```

```
# A tibble: 2 × 4
  gender mean_age N_obs N_with_autism
  <fct>     <dbl> <int>         <int>
1 f          29.6   337            54
2 m          29.0   367            37
```

Measures of ce tendency

Mean and median

Recall that:

Population MEAN $\mu = \frac{\sum_{i=1}^{n} x_i}{n}$

Sample MEAN $\bar{x} = \frac{\sum_{i=1}^{n} x_i}{n}$

Sample MEDIAN

For uneven n: $Mdn = \frac{x_{(n+1)}}{2}$

For even n: $Mdn = \frac{x_{(n/2)} + x_{(n/2+1)}}{2}$

Mean/Median using base R

- Important to specify the argument `na.rm = TRUE` or th

```
## Let's use `age` and `age_inputed` to see what inputed m
mean(autism_pids$age)
```

```
[1] NA
```

```
median(autism_pids$age)
```

```
[1] NA
```

```
mean(autism_pids$age, na.rm = TRUE)
```

```
[1] 29.20655
```

```
median(autism_pids$age, na.rm = TRUE)
```

```
[1] 27
```

```
mean(autism_pids$age_inputed)
```

```
[1] 29.27983
```

```
median(autism_pids$age_inputed)
```

```
[1] 27
```

Create custom function to c statistical mode 1/2

R doesn't have a built-in function for the statistical mode, s one: `f_calc_mode`

Define the custom function

```
f_calc_mode  <- function(x) {
  # `unique` returns a vector of unique values
  uni_x <- unique(x)
  # `match` returns the index positions of 1st vector agai
  match_x <- match(x, uni_x)
  # `tabulate` count the occurrences of integer values in
  tab_x  <-  tabulate(match_x)
  # returns element of uni_x that corresponds to max occur
  uni_x[tab_x == max(tab_x)]
}
```

Create custom function to c
statistical mode 2/2

Call the custom function

```
1 f_calc_mode(autism_pids$age)
```

```
[1] 21
```

```
1 f_calc_mode(autism_pids$age_inputed)
```

```
[1] 21
```

```
1 f_calc_mode(autism_pids$ethnicity)
```

```
[1] White-European
11 Levels: Asian Black Hispanic Latino Middle Eastern  others ... White
```

Measures of variability (or s

Variance and Standard devi

Recall that:

Population Variance $\sigma^2 = \frac{\sum_{i=1}^{n}(x_i - \mu)^2}{n}$

Sample Variance $s^2 = \frac{\sum (x_i - \bar{x})^2}{n-1}$

Population Standard deviation $\sigma = \sqrt{\frac{\sum_{i=1}^{n}(x_i - \mu)^2}{n}}$

Sample Standard deviation $s = \sqrt{\frac{\sum (x_i - \bar{x})^2}{n-1}}$

Variance and Standard devi

base R

- Important to specify the argument `na.rm = TRUE` or th use the `age_inputed` variable)

```
1 var(autism_pids$age, na.rm = TRUE)
```

```
[1] 94.28966
```

```
1 var(autism_pids$age_inputed)
```

```
[1] 96.19328
```

```
1 sd(autism_pids$age, na.rm = TRUE)
```

```
[1] 9.710286
```

```
1 sd(autism_pids$age_inputed)
```

```
[1] 9.807817
```

VISUAL DATA EXPLORATION

Plotting with ggplot2

`ggplot2` provides a set of tools to map data to visual elements o
of plot you want, and then subsequently to control the fine details
basically allows to build a plot layer by layer (Figure 2).

- **data** -> specify what the dataset is
- **aesthetic mappings** (or just *aesthetics*) -> specify which datas
  the plot elements (e.g. x and y values, or categorical variable in
- **geom** -> the overall type of plot, e.g. `geom_point()` makes sc
  makes barplots, `geom_boxplot()` makes boxplots.

Additional (optional) pieces:

- information about the **scales**,
- the labels of **legends** and axes
- other **guides** that help people to read the plot,

Plotting with ggplot2 (cont

a layered approach!

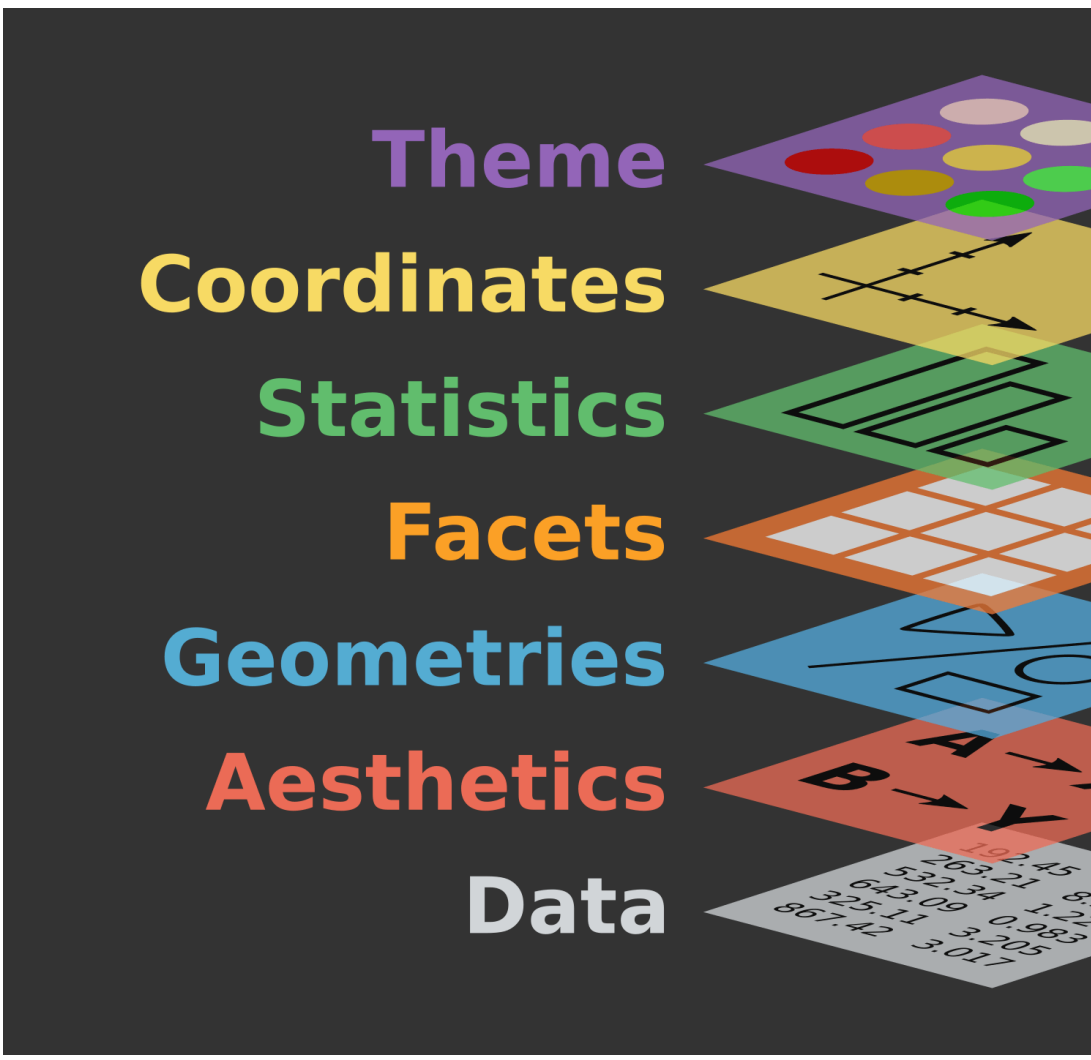


Figure 2: ggplot2 layers Source: Mine Çetinkaya-Rundel' Data Viz class

Save some colors (for custo plots)

- Colors are defined in the form of **Hexadecimal color va**

```
two_col_palette <-  c("#9b2339", "#005ca1")

contrast_cols_palette <- c("#E7B800","#239b85", "#85239b",
                "#d8e600", "#0084e6", "#399B23", "#e60066"
                "#00d8e6", "#e68000")
```

Distribution of continuous var

Histograms

Histograms (and density plots) are often used to show the continuous variable.

- Option 1) `data` inside the `ggplot()` function

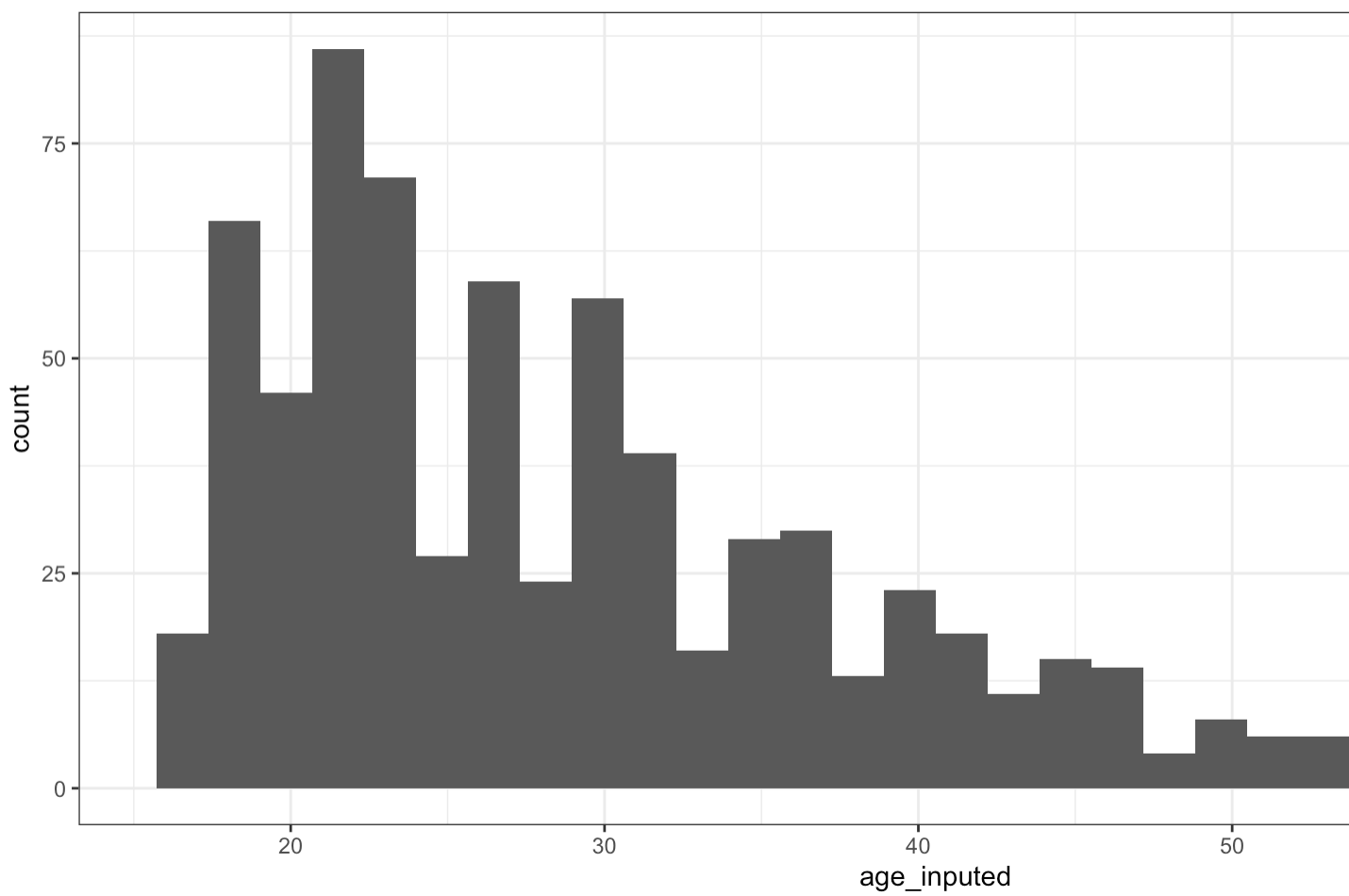
```
ggplot(data = autism_pids, mapping = aes(x=age_inputed)) +
  geom_histogram() +
  theme_bw()
```

- Option 2) `data` before the pipe `%>%`

```
autism_pids %>%
  ggplot(aes(x = age_inputed )) +
  geom_histogram() +
  theme_bw()
```


notice that after calling `ggplot()`, subsequent layers are added with `+`

Histograms



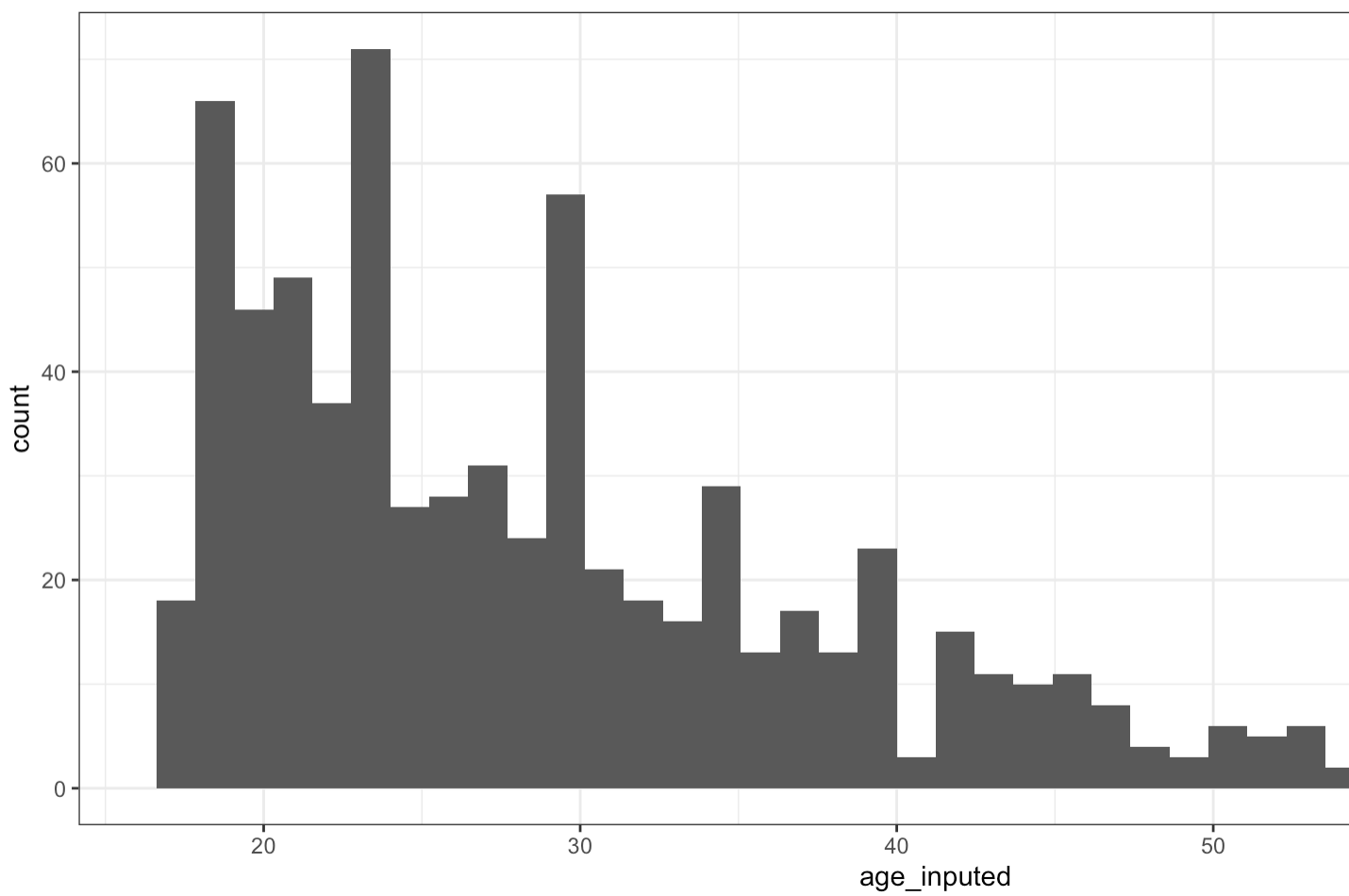
... define bin width

Histograms split the data into ranges (bins) and show the r
each. Hence, it's important to pick widths that represents t

- The default value is 30
- We can change it using the argument `bins = #`

```
autism_pids %>%
  ggplot(aes(x = age_inputed )) +
  # specify to avoid warning if we fail to specify the num
  geom_histogram(bins=40) +
  theme_bw()
```

... define bin width

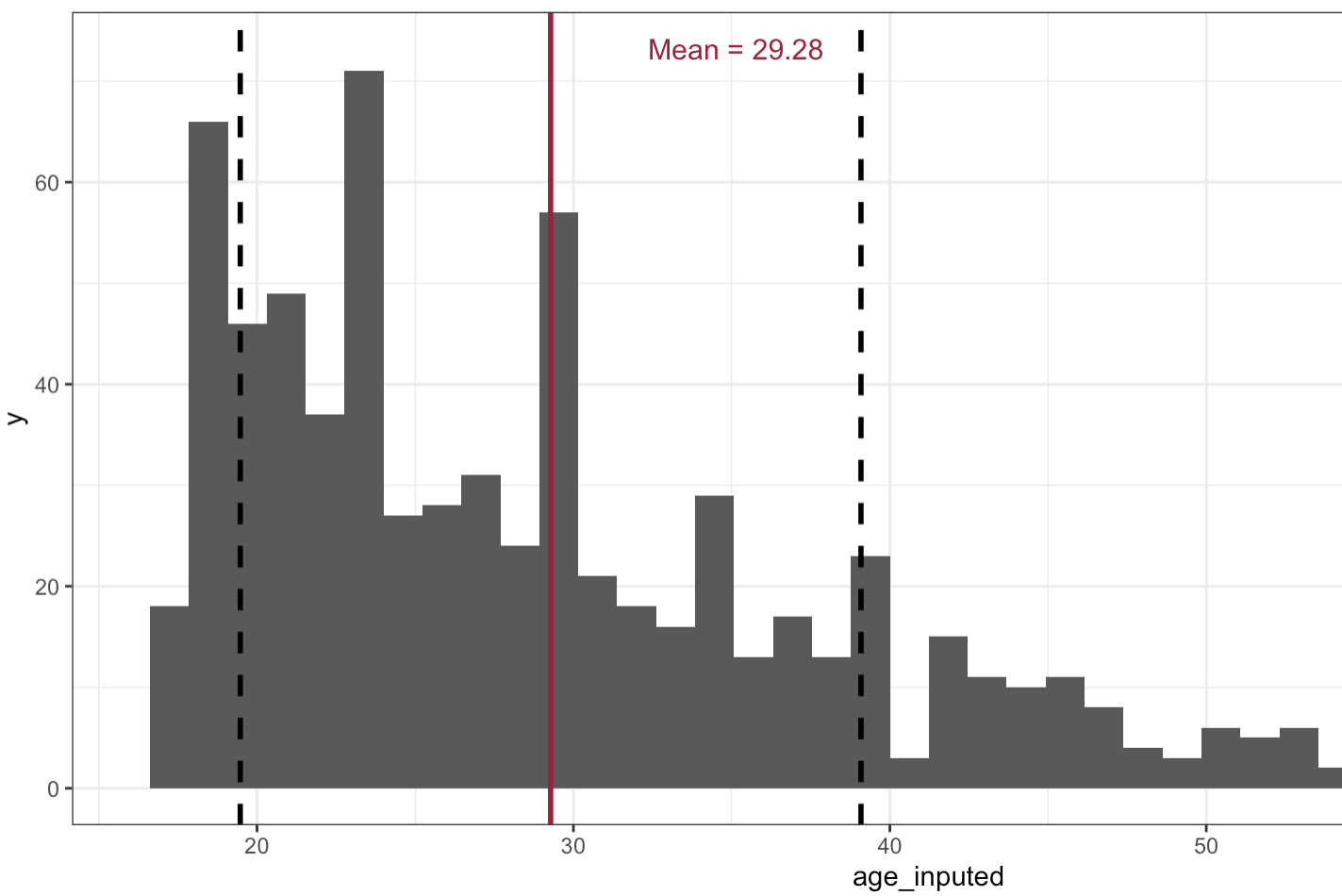


... add mean and std dev ve

- using `geom_vline()` to add a vertical line for the *mean* -1 and +1 *sd* from the mean.
- using `annotate()` for adding small annotations (such a

```
autism_pids %>%
  ggplot(aes(x = age_inputed )) +
  geom_histogram(bins=40) +
  # add mean vertical line
  geom_vline(xintercept = mean(autism_pids$age_inputed),
             na.rm = FALSE,
             lwd=1,
             color="#9b2339") +
  # add annotations with the mean value
  annotate("text",
           x = mean(autism_pids$age_inputed) * 1.2, # coor
           y = mean(autism_pids$age_inputed) * 2.5,
           label = paste("Mean =", round(mean(autism_pids$
           col = "#9b2339",
           size = 4)+
  # add also sd +1 and -1
  geom_vline(aes(xintercept = mean(autism_pids$age_inputed
             color = "#000000", size = 1, linetype = "dash
  geom_vline(aes(xintercept = mean(autism_pids$age_inputed
             color = "#000000", size = 1, linetype = "dash
  theme_bw()
```

... add mean and std dev ve

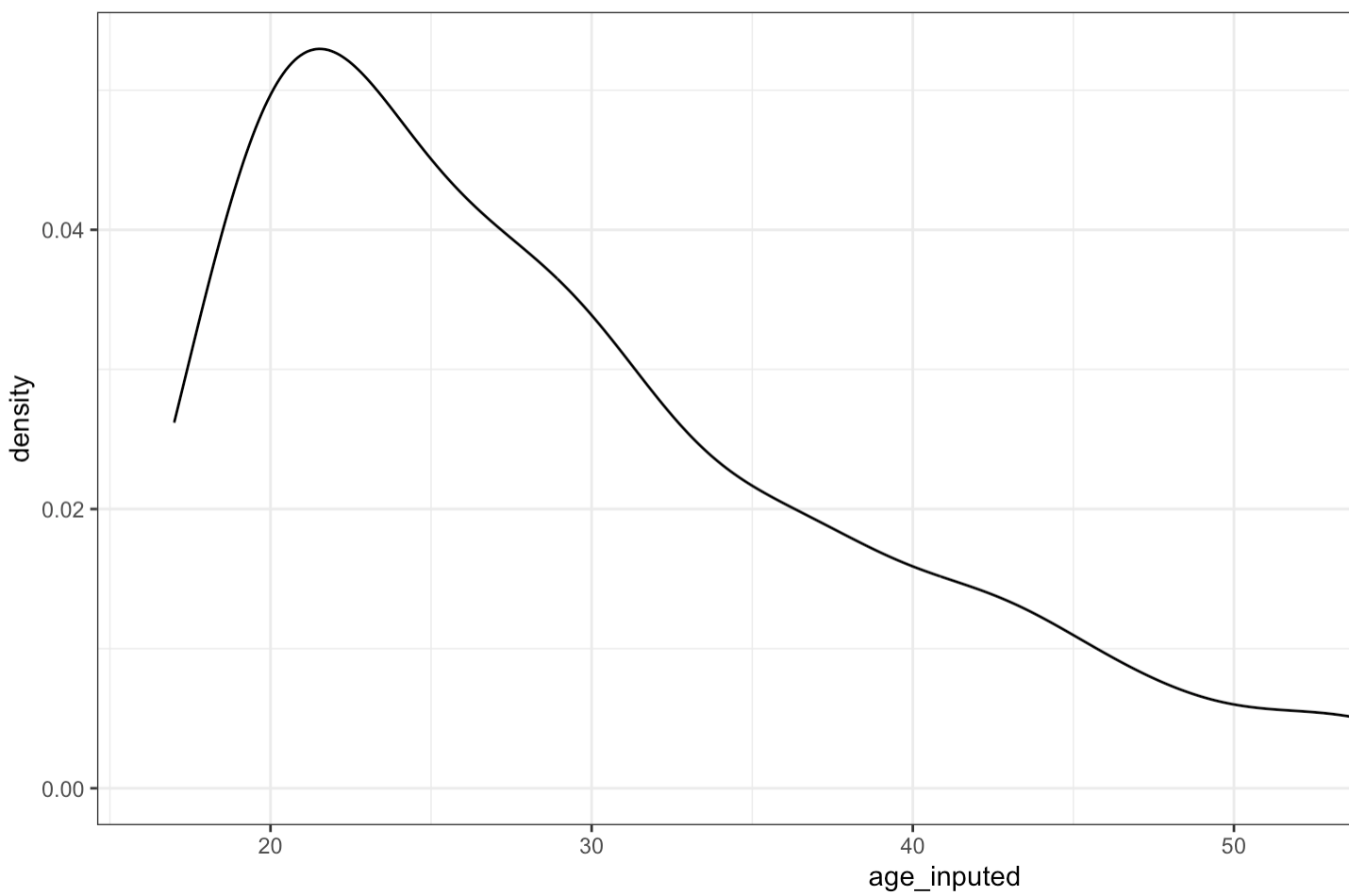


Density plot

- specifying `x` (the continuous variable)
- using `geom_density()`, in which we

```
autism_pids %>%
  ggplot(aes(x = age_inputed)) +
  geom_density()+
  theme_bw()
```

Density plot

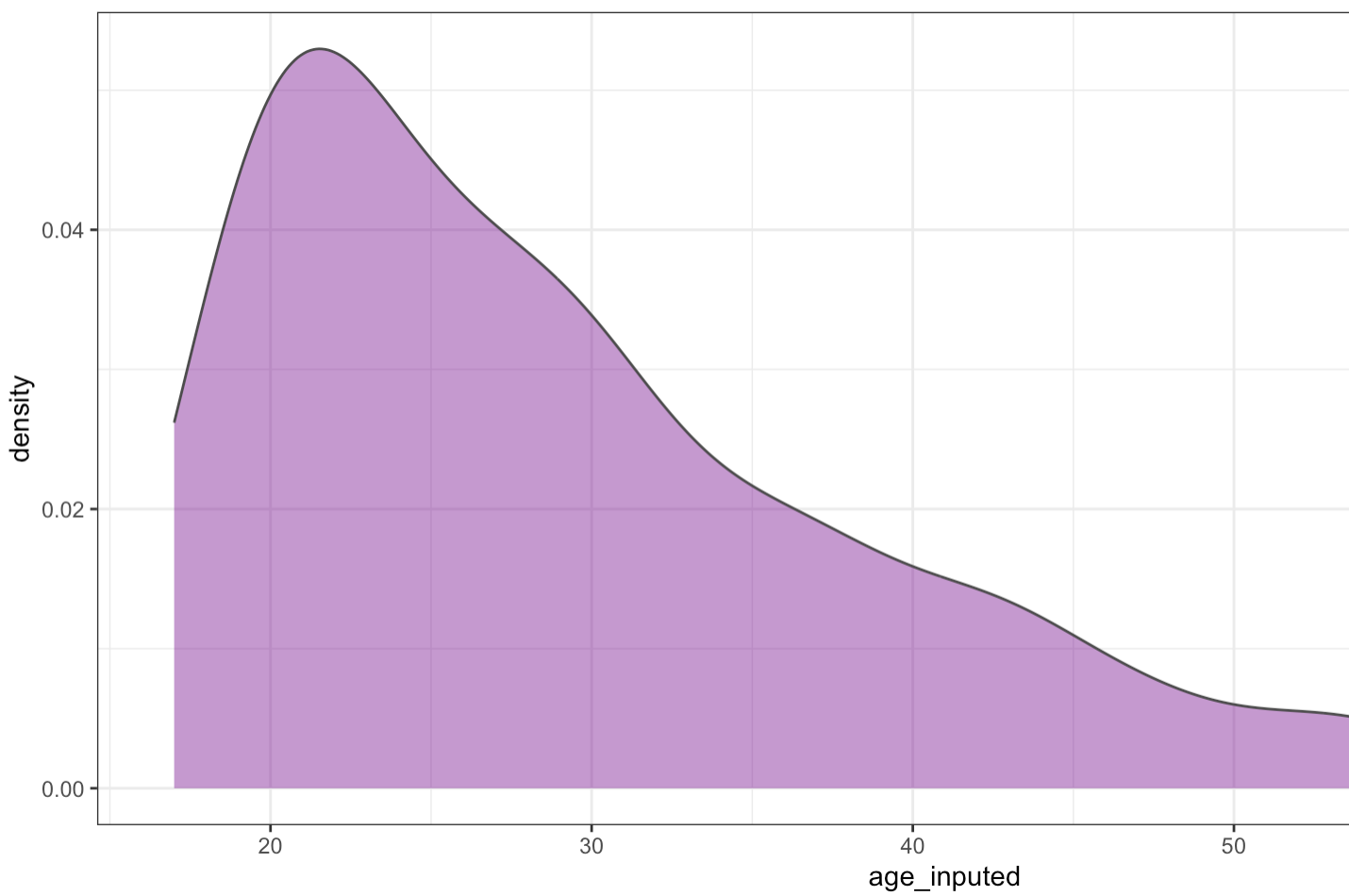


Density plot (cont.)

- specifying shape colors with the arguments inside `geom`
- `color` for the line color
- `fill` for area color
- `alpha` to specify the degree of transparency in the dens

```
autism_pids %>%
  ggplot(aes( x=age_inputed)) +
  geom_density(fill="#85239b", color="#4c4c4c", alpha=0.5)
  theme_bw()
```

Density plot (cont.)

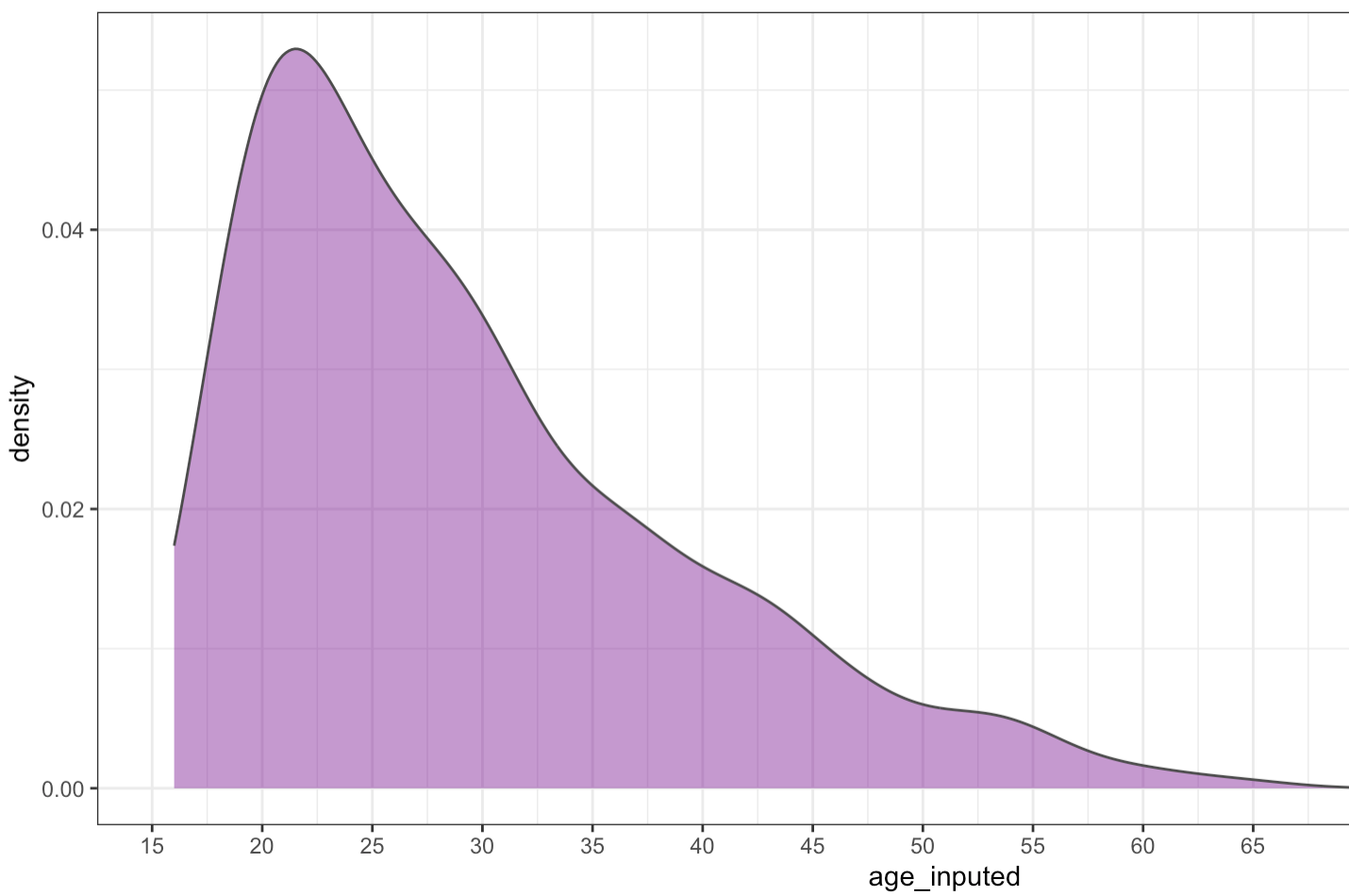


... increase # of x-axis tick

- specifying the amount of breaks inside `scale_x_cont`

```
autism_pids %>%
  ggplot(aes( x=age_inputed)) +
  geom_density(fill="#85239b", color="#4c4c4c", alpha=0.5)
  theme_bw() +
  # increase number of x axis ticks
  scale_x_continuous(breaks = seq(10, 100,5 ), limits = c(
```

… increase # of x-axis ticks



Distribution of continuous var by categorical v

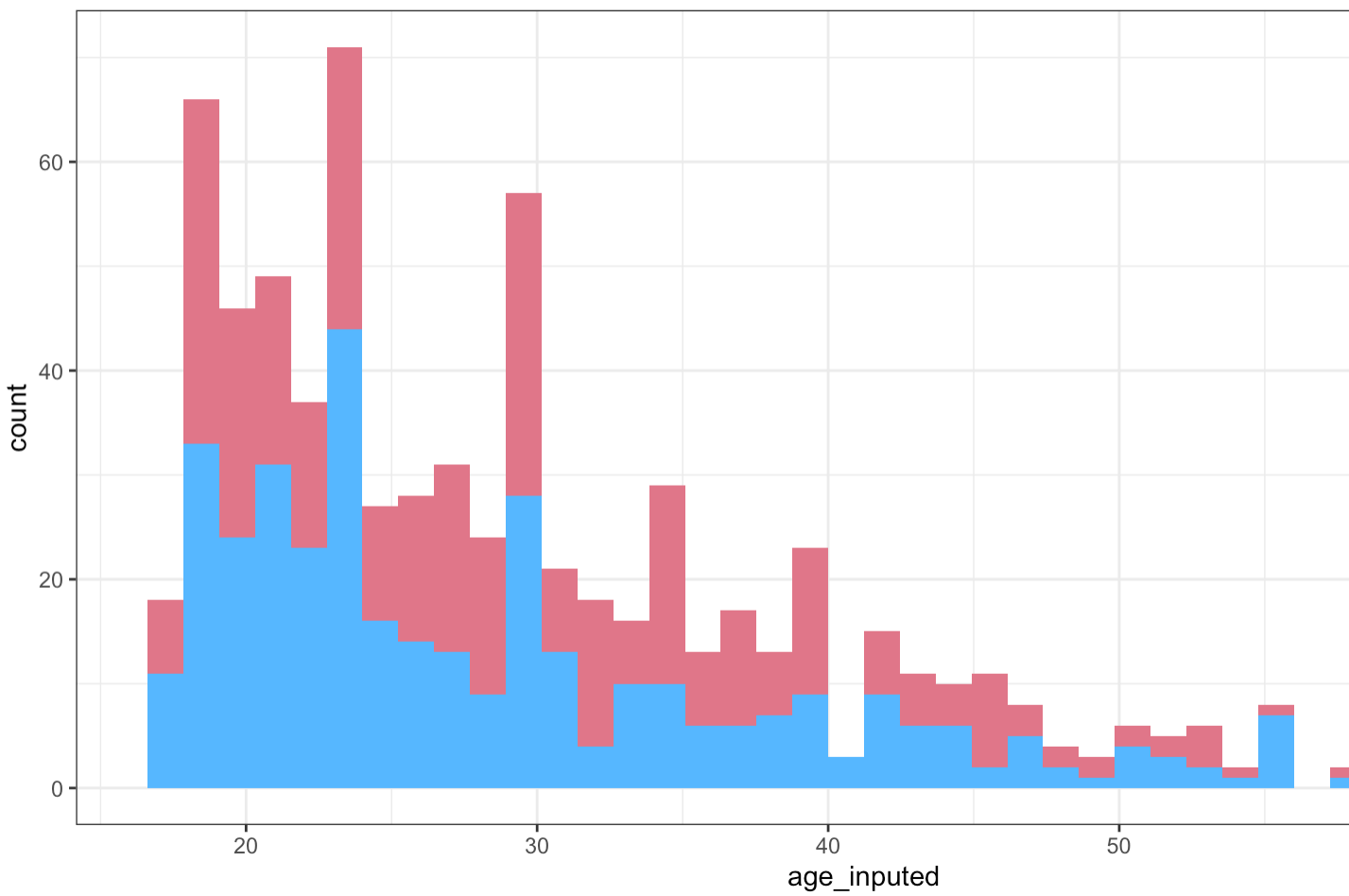
Histograms with `fill = c`

1. indicate the categorical group as `fill =` in the aesthet
2. specify custom colors for each group:

- use `scale_color_manual()` for changing line color
- use `scale_fill_manual()` for changing area fill colo

```
autism_pids %>%
  # specifying `fill` = gender
  ggplot(mapping = aes(x = age_inputed, fill = gender )) +
  geom_histogram(bins=40) +
  scale_fill_manual(values = c("#e07689","#57b7ff")) +
  scale_color_manual(values = c("#9b2339","#005ca1")) +
  theme_bw()
```

Histograms with `fill = c`

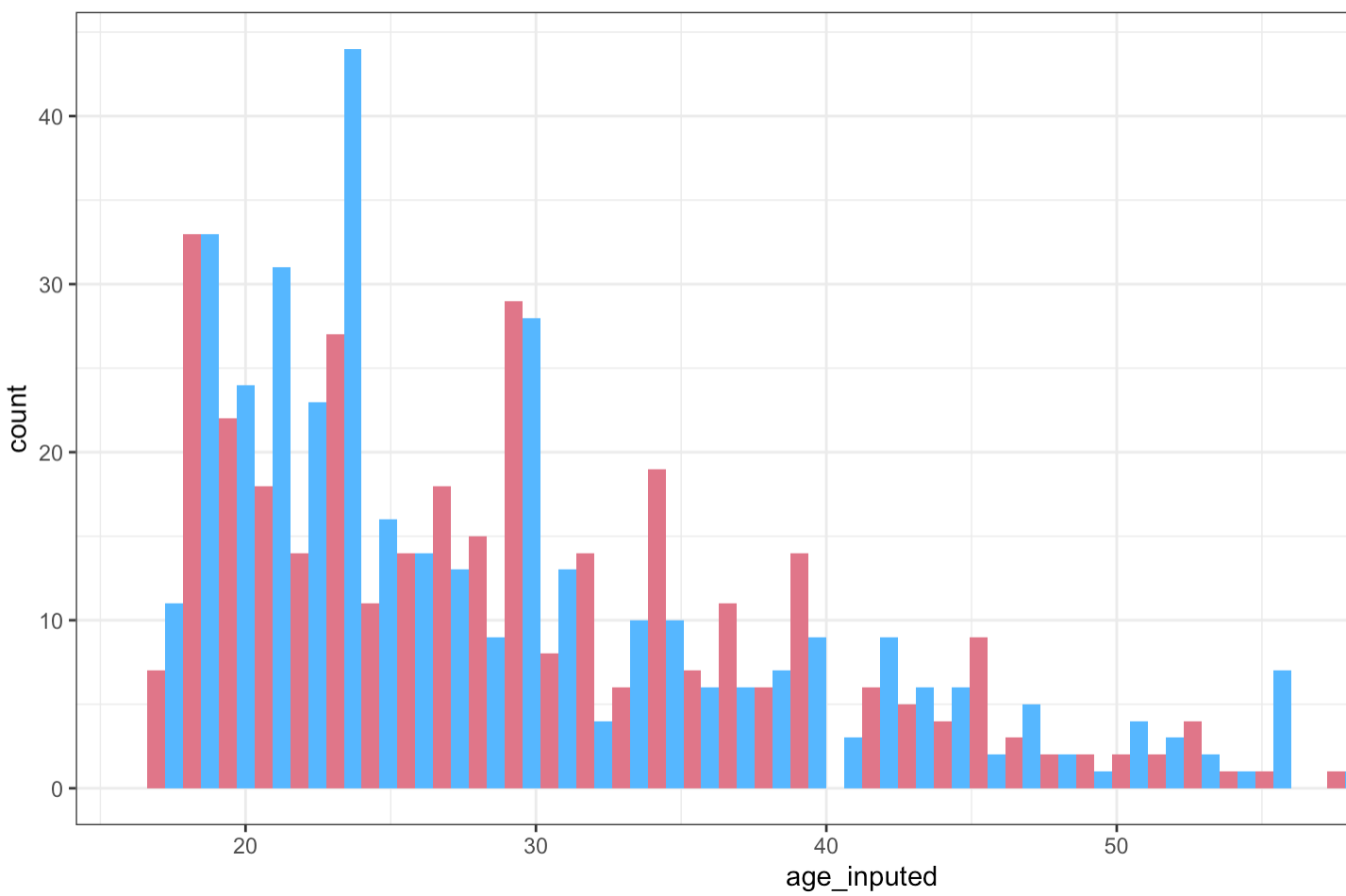


... shifting bars by group

- using the specification `position = 'dodge'` inside g

```
# trying to improve readability
autism_pids %>%
  ggplot(mapping = aes(x = age_inputed, fill = gender )) +
  # bars next to each other with `position = 'dodge'`
  geom_histogram(bins=40, position = 'dodge')  +
  scale_fill_manual(values = c("#e07689","#57b7ff")) +
  scale_color_manual(values = c("#9b2339","#005ca1")) +
  theme_bw()
```

… shifting bars by group



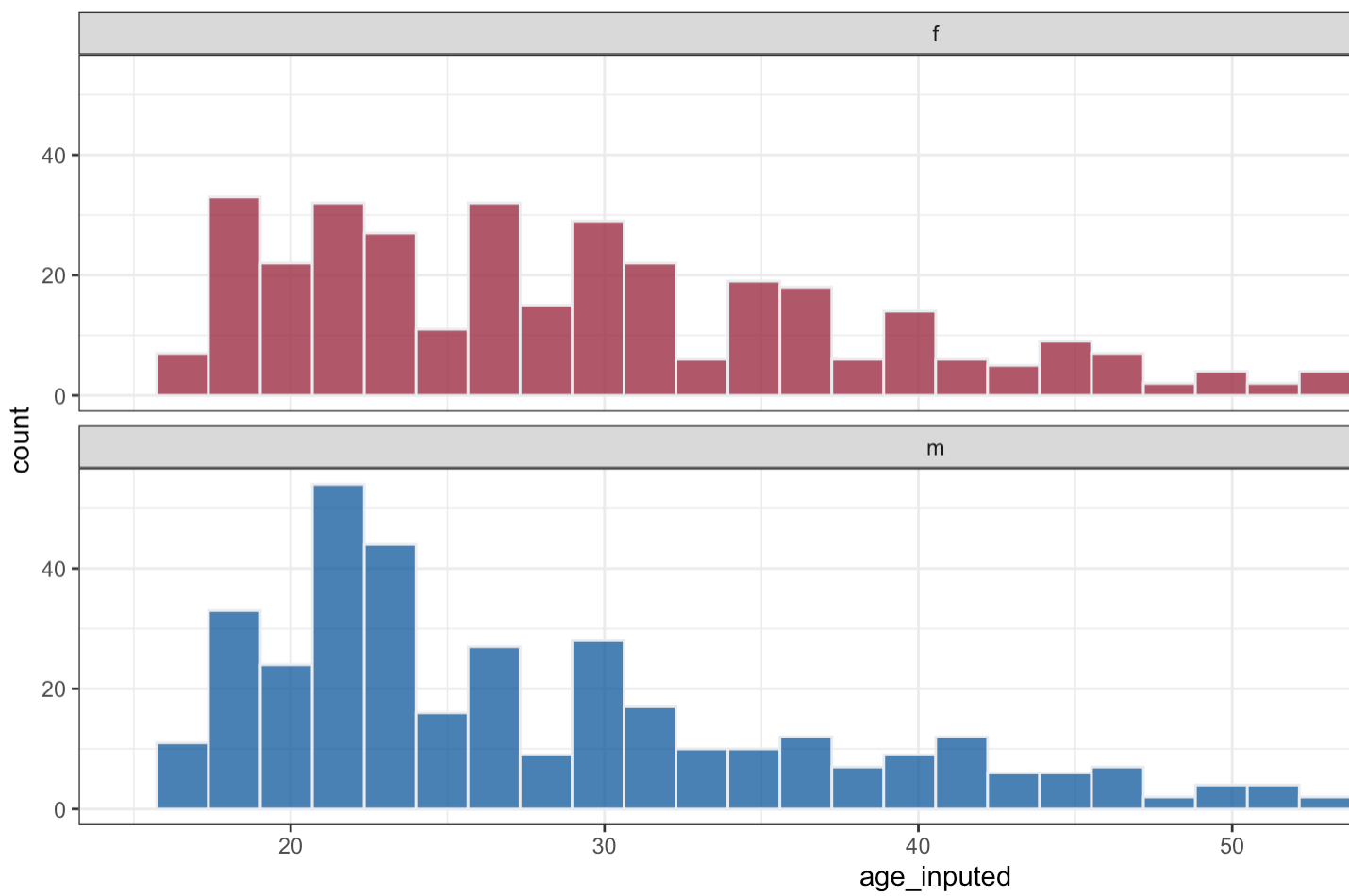
...facet by gender

That's still not very easy to digest. Instead of only filling, yo
into multiple plots to improve readability

- adding `facet_wrap()` with the the specification of `~c`
- also `ncol = 1` requires the subplot to be in 1 column

```
autism_pids %>%
  ggplot(aes(x = age_inputed, fill = gender )) +
  geom_histogram(color="#e9ecef", alpha=0.8, position = 'd
  theme_bw() +
  # splitting the gender groups, specifying `ncol` to see
  facet_wrap(~gender, ncol = 1)  +
  scale_fill_cyclical(values = c("#9b2339","#005ca1"))
```

...facet by gender



… adding 2 mean/median v gender)

I want to see the mean vertical line for each of the subgrou need to create a small dataframe of summary statistics (`g`

I do so by using `dplyr` add a column `mean_age` with the

```
group_stats <- autism_pids %>%
  dplyr::group_by(gender) %>%
  dplyr::summarize(mean_age = mean(age_inputed),
                   median_age = median (age_inputed))

group_stats
```

```
# A tibble: 2 × 3
  gender mean_age median_age
  <fct>     <dbl>      <dbl>
1 f          29.6         28
2 m          29.0         26
```

(Small digression on `tid`

The new small dataframe `group_stats` offers an example of **resha** "wide" form (with each variable in its own column) to a "long" form (o *measures names* and another for both the *measures values*).

- This can be done using `tidyr::pivot_longer` function, where specified:
  - `cols`: The names of the columns to pivot
  - `names_to`: The name for the new character column
  - `values_to`: The name for the new values column

```
group_stats_long <- group_stats %>%
  tidyr::pivot_longer(cols = mean_age:median_age,
                      names_to = "Stat",
                      values_to = "Value") %>%
  dplyr::mutate(label = as.character(glue::glue("{gender}_{Stat}")))

group_stats_long
```

```
# A tibble: 4 × 4
  gender Stat       Value label
  <fct>  <chr>      <dbl> <chr>
1 f      mean_age    29.6 f_mean_age
2 f      median_age  28   f_median_age
3 m      mean_age    29.0 m_mean_age
4 m      median_age  26   m_median_age
```

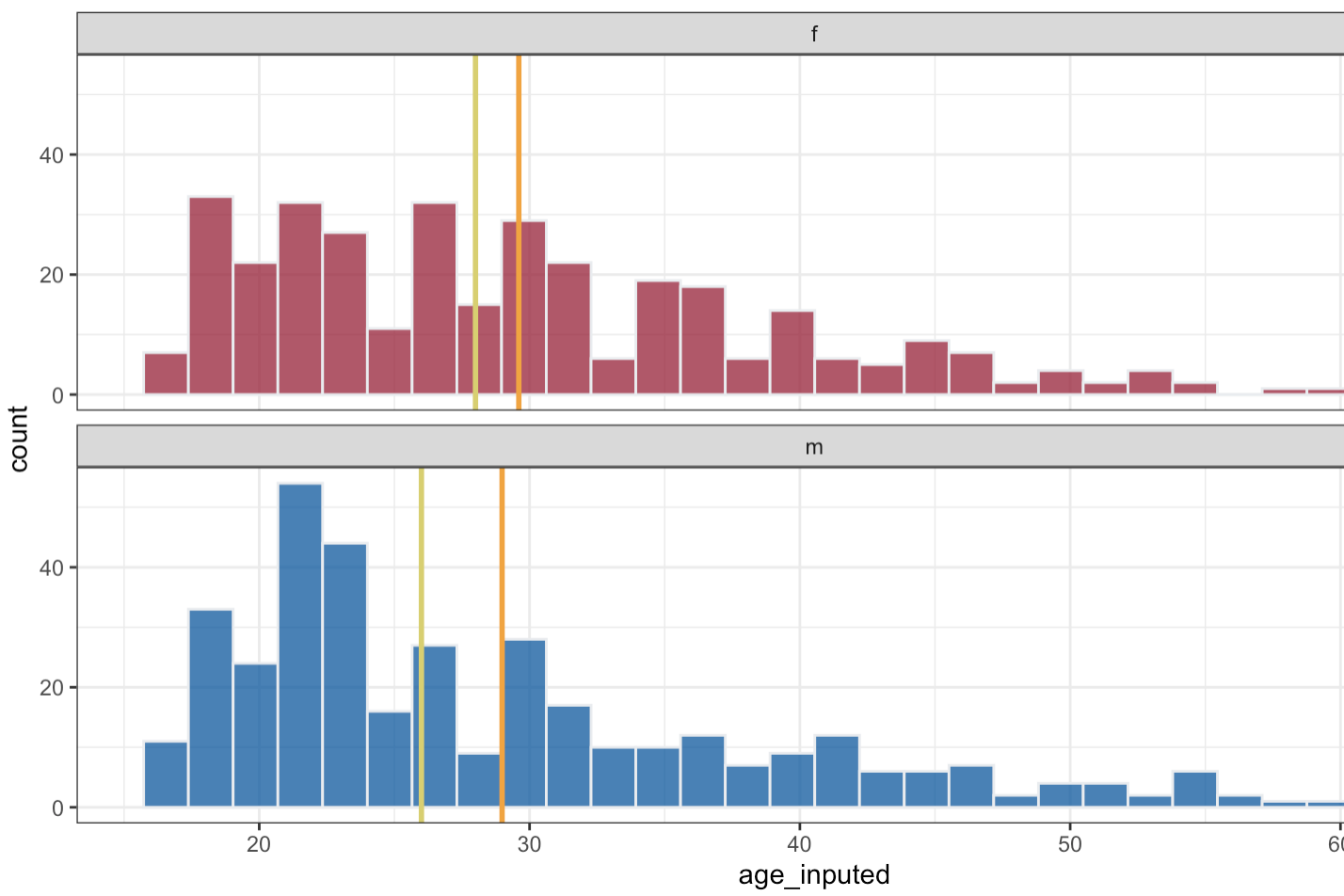
...facet by gender + vert lin

Notice that now the plot will have 2 `data` sources:

- `autism_pids`
- `group_stats_long`

```
autism_pids %>%
  ggplot(aes(x = age_inputed, fill = gender)) +
  # geom_histogram from dataframe 1
  geom_histogram(bins=30,color="#e9ecef", alpha=0.8, posit
  facet_wrap(~gender, ncol = 1) +
  scale_fill_manual(values = c("#9b2339","#005ca1"))  +
  # geom_vline from dataframe 2
  geom_vline(data = group_stats_long,
             mapping = aes(xintercept = Value, color = Sta
             lwd=1,
             linetype=1) +
  scale_color_manual(values = c( "#f0a441" , "#d8cf71")) +
  theme_bw()
```

...facet by gender + vert lin



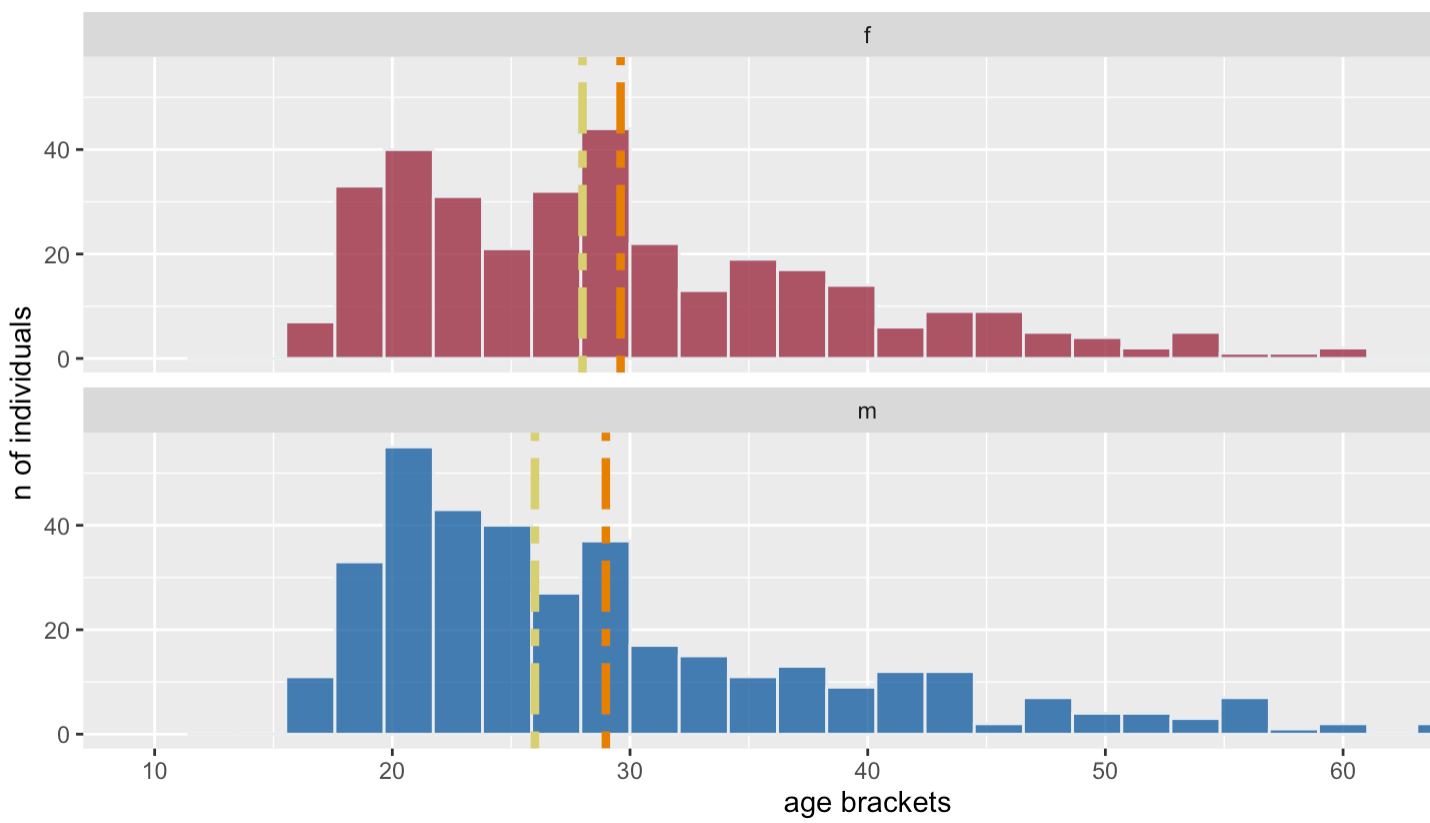
... finishing touches

- using `labs()` and `theme()` layers

```
hist_plot <- autism_pids %>%
  ggplot(aes(x = age_inputed, fill = gender)) +
  # geom_histogram from dataframe 1
  geom_histogram(bins=30,color="#e9ecef", alpha=0.8, posit
  facet_wrap(~gender, ncol = 1) +
  scale_fill_manual(values = c("#9b2339","#005ca1"))  +
  # geom_vline from dataframe 2
  geom_vline(data = group_stats_long,
             mapping = aes(xintercept = Value, color = Sta
             lwd=1.5,
             linetype=6) +
  scale_color_manual(values = c( "#e68000", "#d8cf71")) +
  # increase number of x axis ticks
  scale_x_continuous(breaks = seq(10, 100,10 ), limits = c
  # Additional theme details
  labs(x = "age brackets", y = "n of individuals",
       color = "Stats",
       title = "Distribution of observations by gender",
       subtitle = "",
       caption = "Source: Thabtah,Fadi (2017) https://doi.
  theme(legend.position = "right",
        plot.title = element_text(face = "bold"))
hist_plot
```

... finishing touches

Distribution of observations by gender



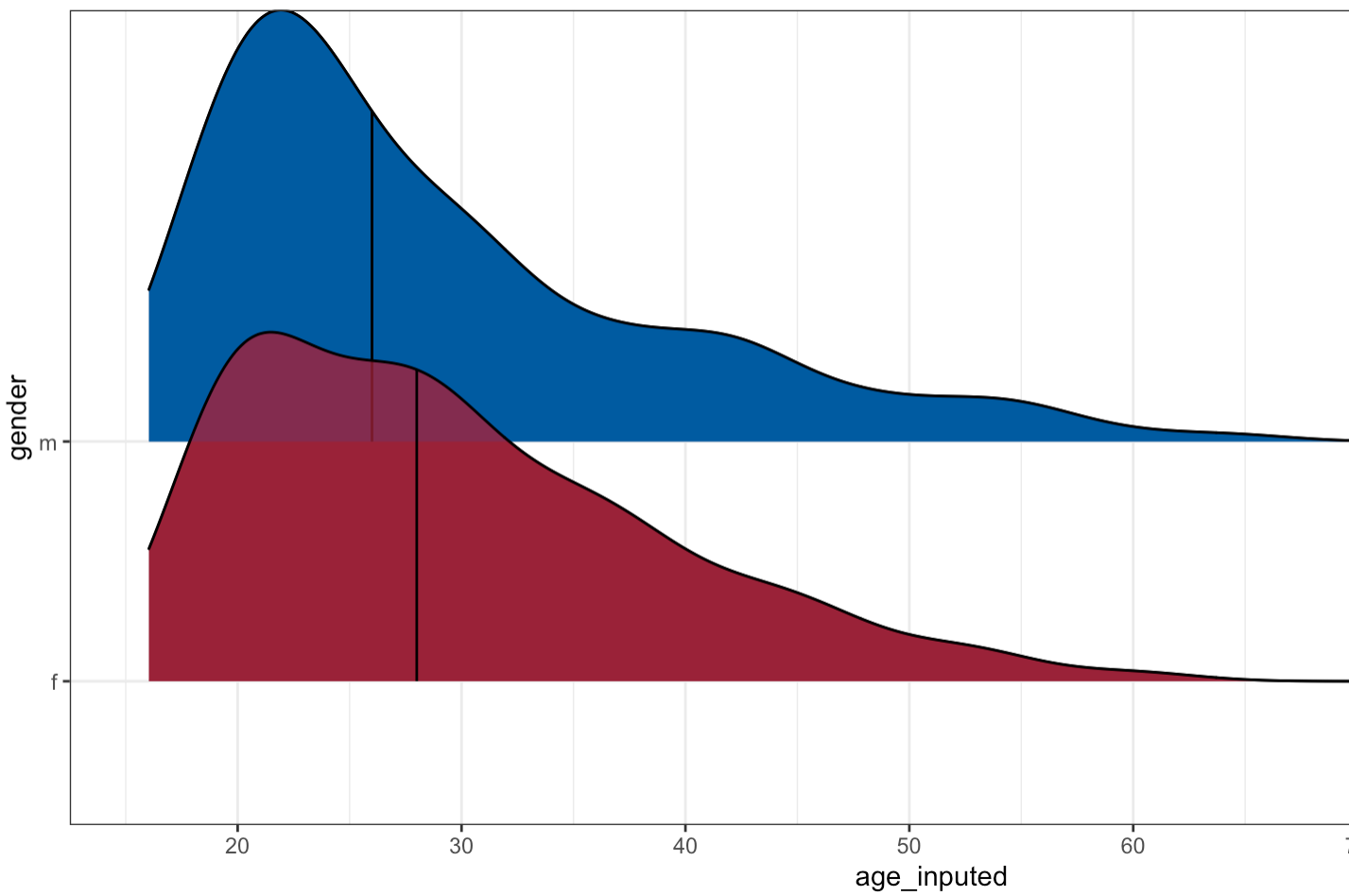
Source: Thabtah,Fadi (2017) https://doi.o

Density ggridges package

As an alternative, you can use the ggridges package to m
geom_density_ridges calculates density estimates fro
then plots those, using the ridgeline visualization. In this c
median line.

```
autism_pids %>%
  # this takes also `y` = group
  ggplot(aes(x=age_inputed, y = gender, fill = gender)) +
  ggridges::geom_density_ridges() +
  # I can add quantile lines (2 is the median)
  stat_density_ridges(quantile_lines = TRUE, quantiles = c
  # increase number of x axis ticks
  scale_x_continuous(breaks = seq(10, 100,10 ), limits = c
  scale_fill_cyclical(values = c("#9b2339","#005ca1")) +
  theme_bw()
```

Density ggridges package



Barchart

Bar charts provide a visual presentation of categorical data
(height of the bar proportional to the number of cases in e

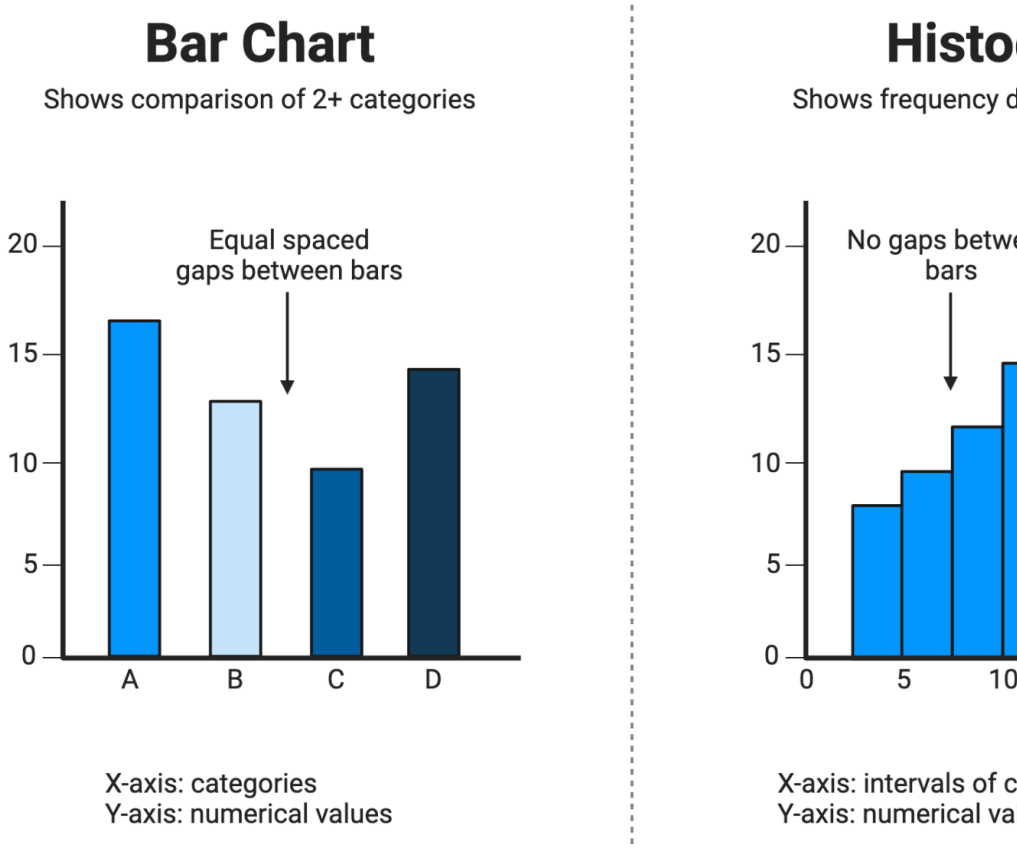


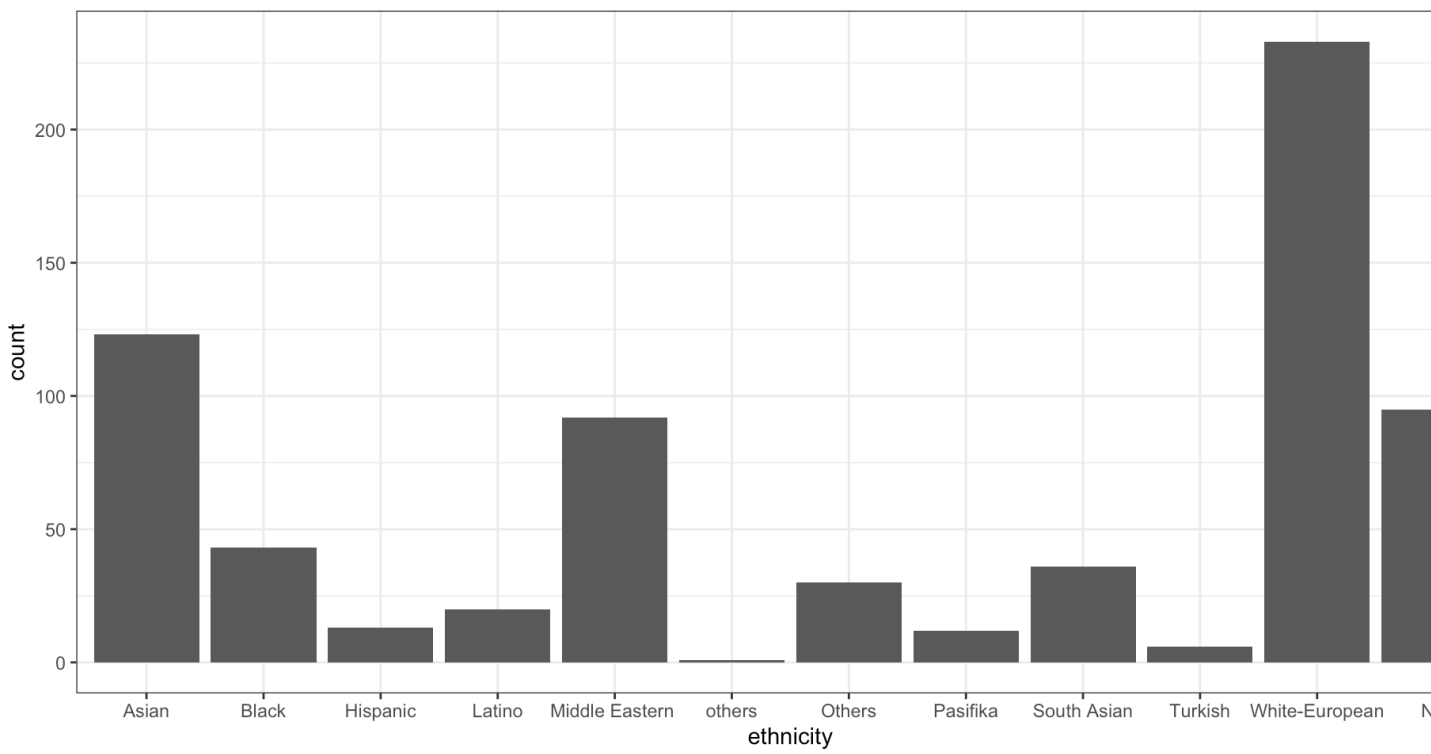
Figure 3: Difference barchart v. histogram Source: https://www.biorender.com/

Barchart (cont.)

```r
# Let's take a variable that we recoded as `factor`
class(autism_pids$ethnicity)
```

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

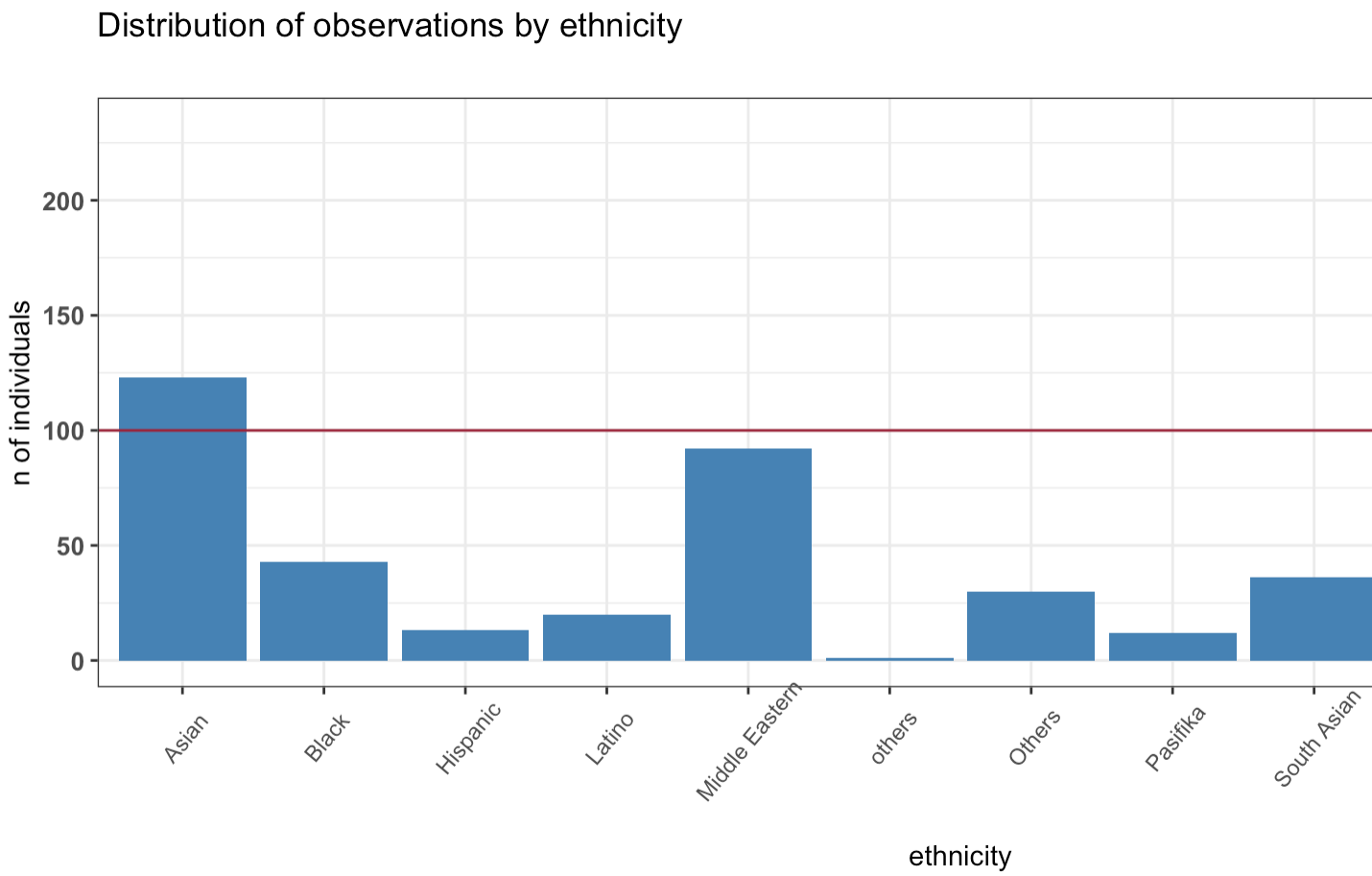
```r
#### ... no formatting ----------------------------------
autism_pids %>%
  ggplot(aes(x = ethnicity )) +
  geom_bar() +
  theme_bw()
```



...improve theme

```r
autism_pids %>%
  ggplot(aes(x = ethnicity )) +
  geom_bar(fill = "steelblue") +
  # reference line
  geom_hline(yintercept=100, color = "#9b2339", size=0.5,
  # labels, title, etc
  labs(x = "ethnicity", y = "n of individuals",
       color = "Stats",
       title = "Distribution of observations by ethnicity"
       subtitle = "",
       caption = "Autism study")  +
  theme_bw() +
  # specification son axis labels
  theme(axis.text.x = element_text(angle=50, vjust=0.75),
        axis.text.y = element_text(size=10,face="bold"))
```

...improve theme



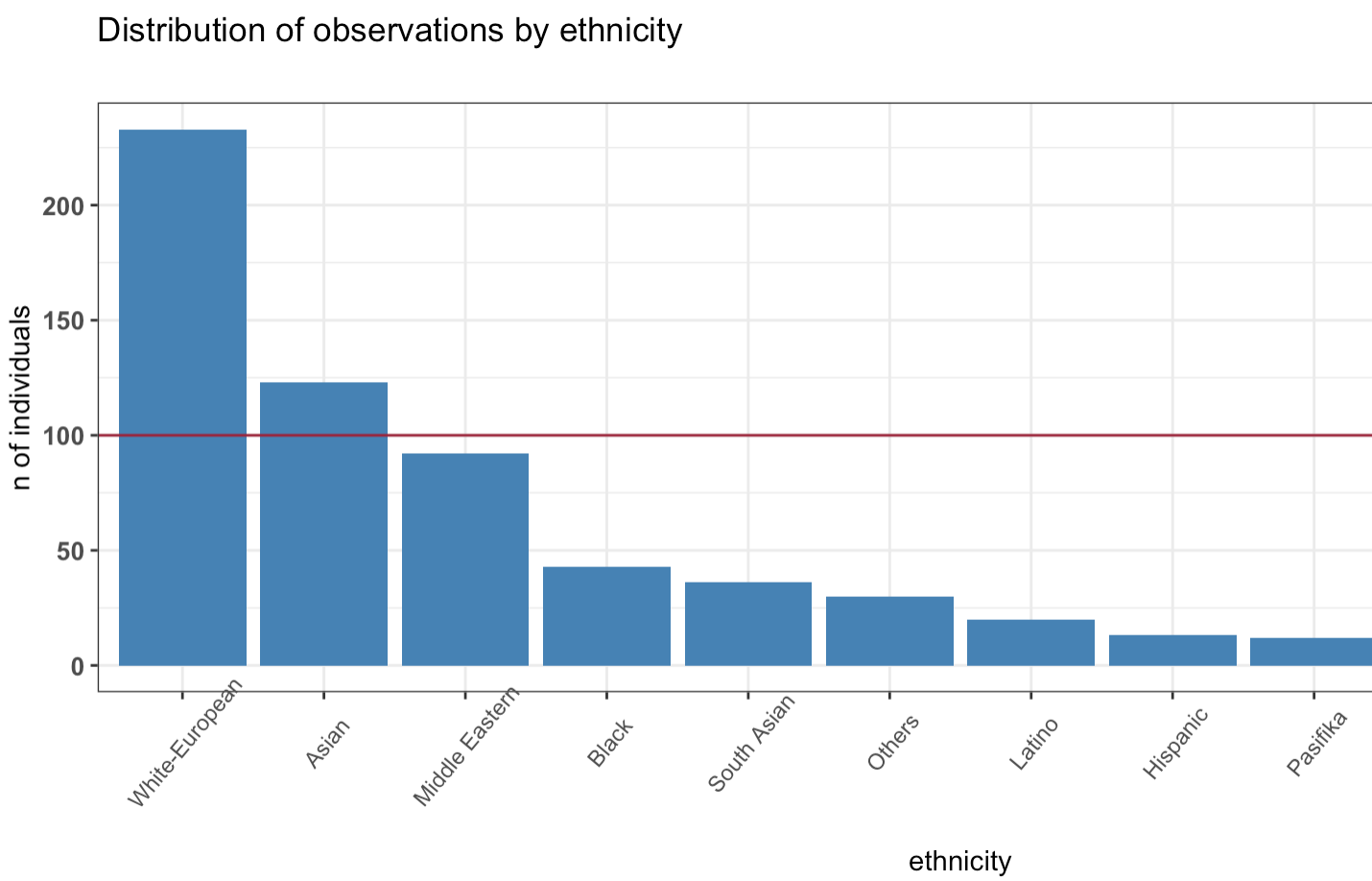
...improve readability (reorc

Reordering the bars by count using the package `forcats` `fct_infreq`

- (which we can do because ethnicity was recoded as `fac`

```
autism_pids %>%
    # we modify our x like so
    ggplot(aes(x = forcats::fct_infreq(ethnicity ))) +
    geom_bar(fill = "steelblue") +
    geom_hline(yintercept=100, color = "#9b2339", size=0.5
    labs(x = "ethnicity", y = "n of individuals",
         color = "Stats",
         title = "Distribution of observations by ethnicit
         subtitle = "",
         caption = "Autism study")  +
    # --- wrap long x labels (flipped ) !!!
    #  scale_x_discrete(labels = function(x) stringr::str_
    theme_bw() +
    theme(axis.text.x = element_text(angle=50, vjust=0.75)
          axis.text.y = element_text(size=10,face="bold"))
```

...improve readability (reorc



...improve readability (high

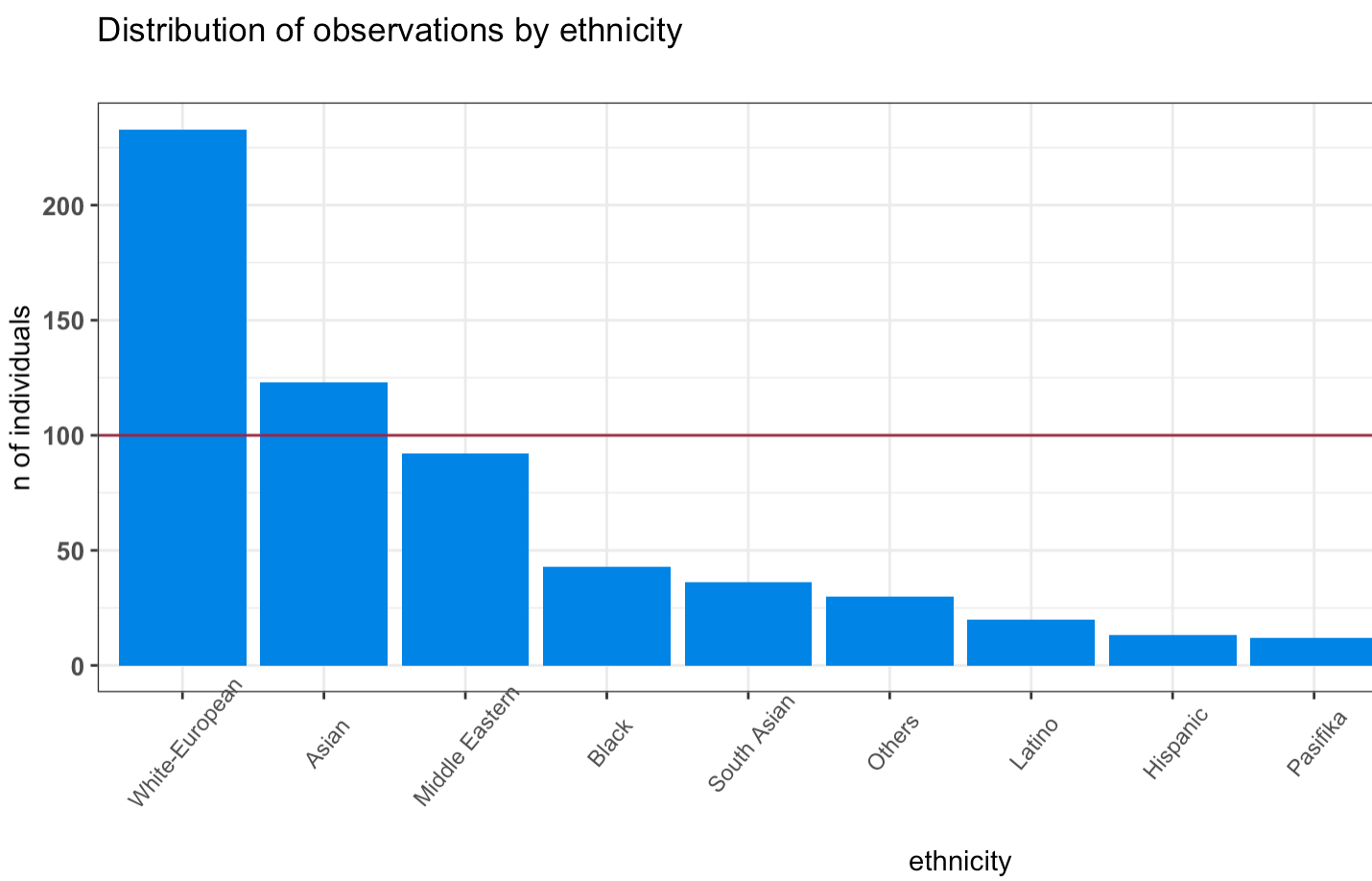
Let's highlight the fact that the last column (NA) represents

1. Create the `highlight` variable
2. Map color to a variable (`fill = highlight`)

...improve readability (

```
autism_pids %>%
  ## --- prep the dataframe
  dplyr::mutate(# Add a factor variable with two levels
    highlight = forcats::fct_other(ethnicity,
                                   keep = "NA",
                                   other_level = "All Grou
  ## --- now plot
  # In `aes mapping` we map color to a variable (`fill = h
  ggplot(aes(x = forcats::fct_infreq(ethnicity), fill = hi
  geom_bar()+
  # Use custom color palettes
  scale_fill_manual(values=c("#0084e6")) +
  # Add a line at a significant level
  geom_hline(yintercept=100, color = "#9b2339", size=0.5,
  theme_bw() +
  # make some more theme specifications
  labs(x = "ethnicity", y = "n of individuals",
       color = "Stats",
       title = "Distribution of observations by ethnicity"
       subtitle = "",
       caption = "Autism study")  +
  theme(axis.text.x = element_text(angle=50, vjust=0.75),
        axis.text.y = element_text(size=10,face="bold"))
  theme(legend.position = "none")
```

...improve readability (



Boxplot

The boxplot is one of the simplest ways of representing a c
variable and it is packed with information. It consists of tw

- **Box** — Extending from the 1st to the 3rd quartile (Q1 to Q
middle that represents the median.
- **Whiskers** — Lines extending from both ends of the box
whisker values are calculated as Q1/Q3 -/+ 1.5 * IQR)
- Everything outside is represented as an **outlier**

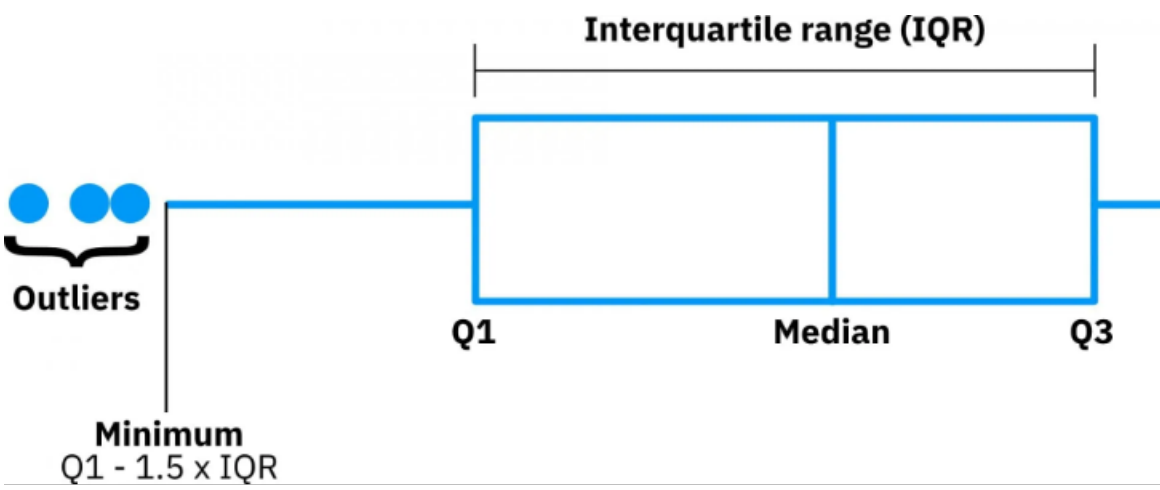


Figure 4: Boxplot Source: https://www.appsilon.com/post/ggplot2-boxplots

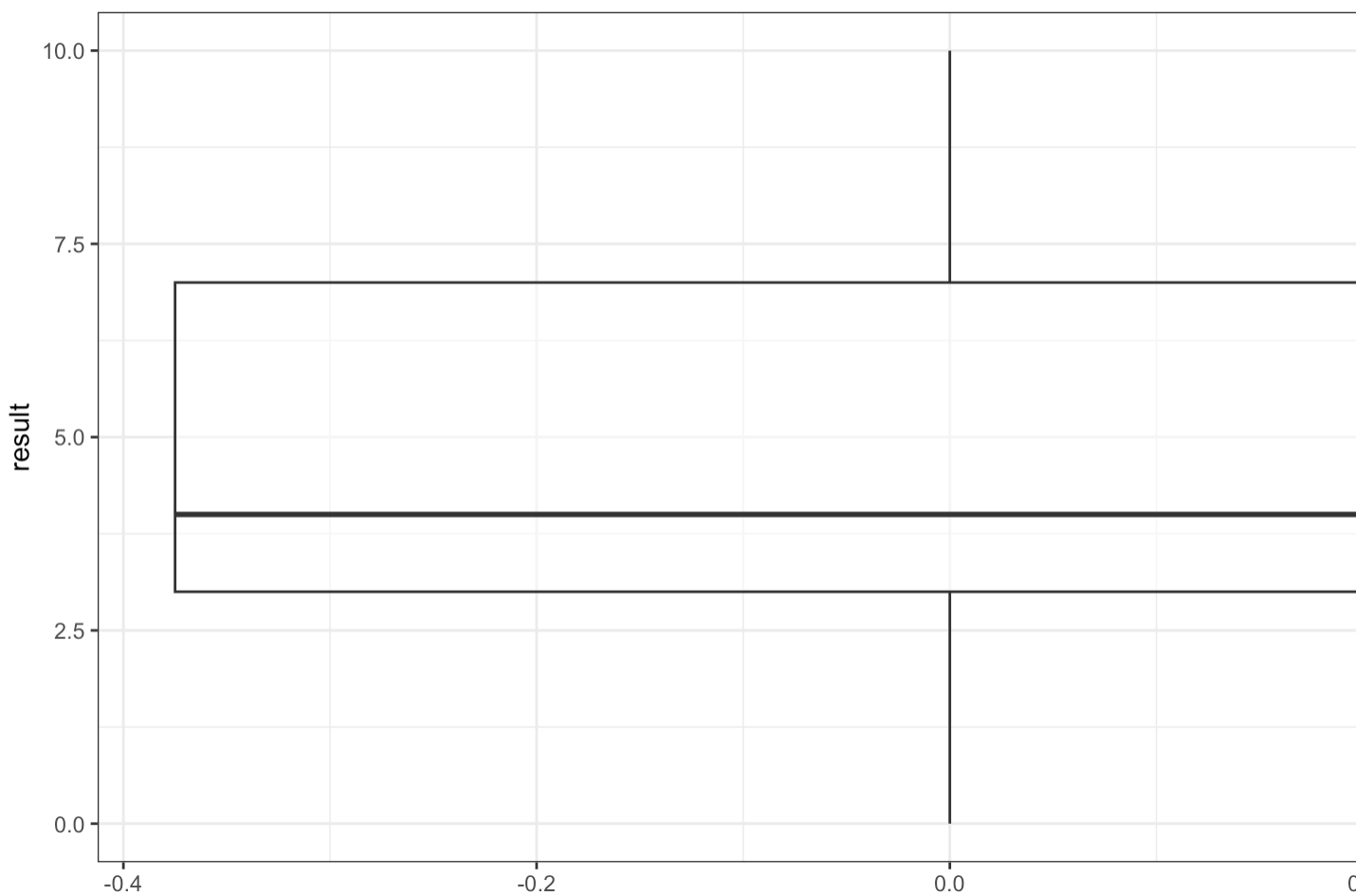
Boxplot example 1

Let's use a boxplot to explore how the continuous variable
the autism dataset.

- in the aesthetic mapping we specify only `x` (continuous v
- switch to vertical orientation with `coord_flip()`

```
autism_pids %>%
  ggplot(aes(x = result )) +
  geom_boxplot(alpha=0.5)+
  # switch to vertical orientation
  coord_flip() +
  theme_bw()
```

Boxplot example 1



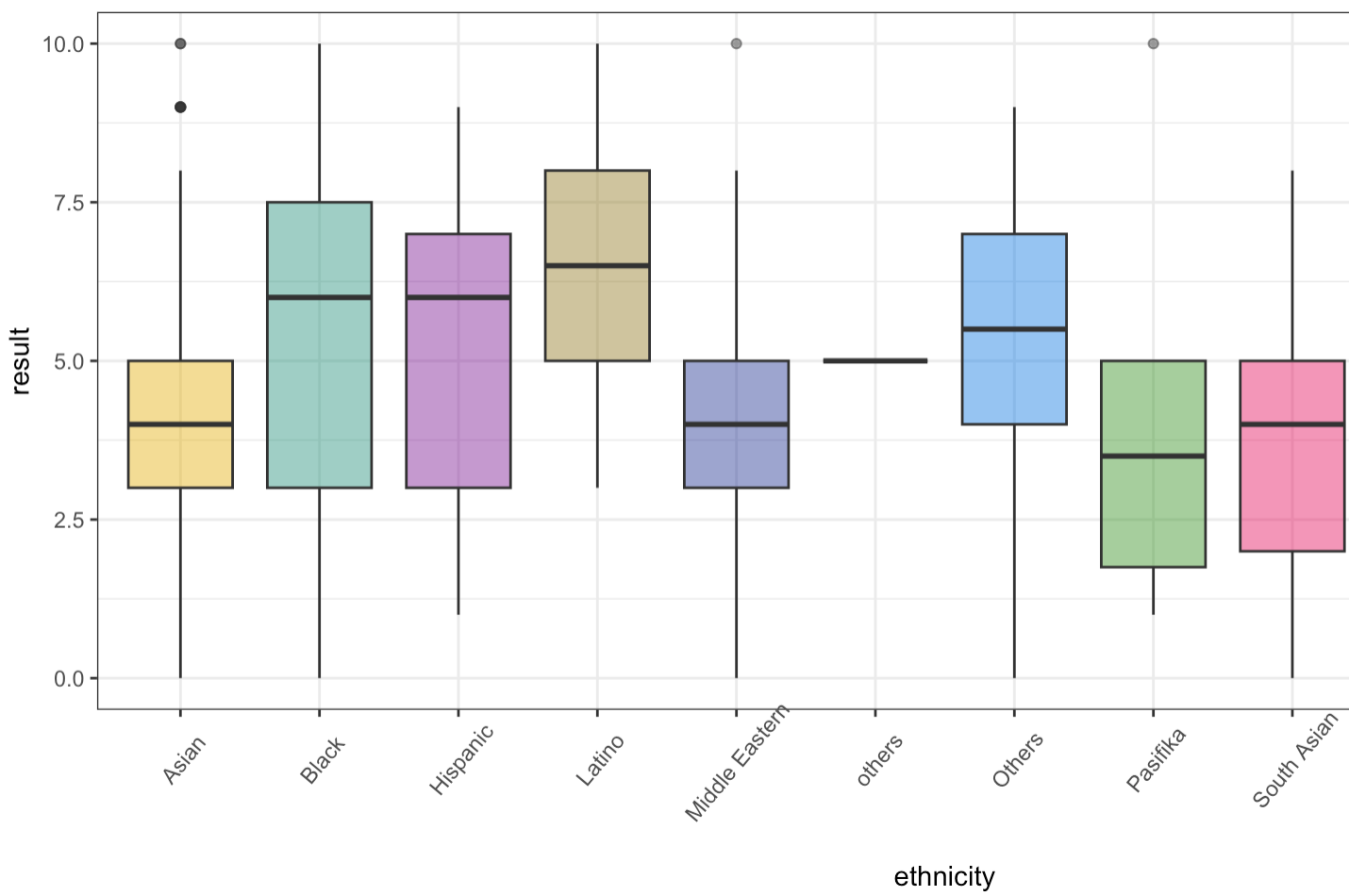
Boxplot example 2

Let's also explore how the continuous variable `result` is c
categorical variable (factor) `ethnicity`.

- in the aesthetic mapping we specify `y` (continuous variab
(categorical variable)
- make x axis labels readable with `theme(axis.text.x`
- I specify colors that I had previously saved in a color pa
`contrast_cols_palette`

```
autism_pids %>%
  ggplot(aes(x = ethnicity,  y= result, fill = ethnicity))
  geom_boxplot(alpha=0.5)+
  scale_fill_manual(values =  contrast_cols_palette)   +
  theme_bw()+
  # make x axis labes readable
  theme(axis.text.x = element_text(angle=50, vjust=0.75))
  # drop legend and Y-axis title
  theme(legend.position = "none")
```

Boxplot example 2



Violin plot

Similarly, the violin plot is an interesting alternative to sho
continuous variable along one or more categorical variable
plot shows the smoothed curve of the **probability density**
data.

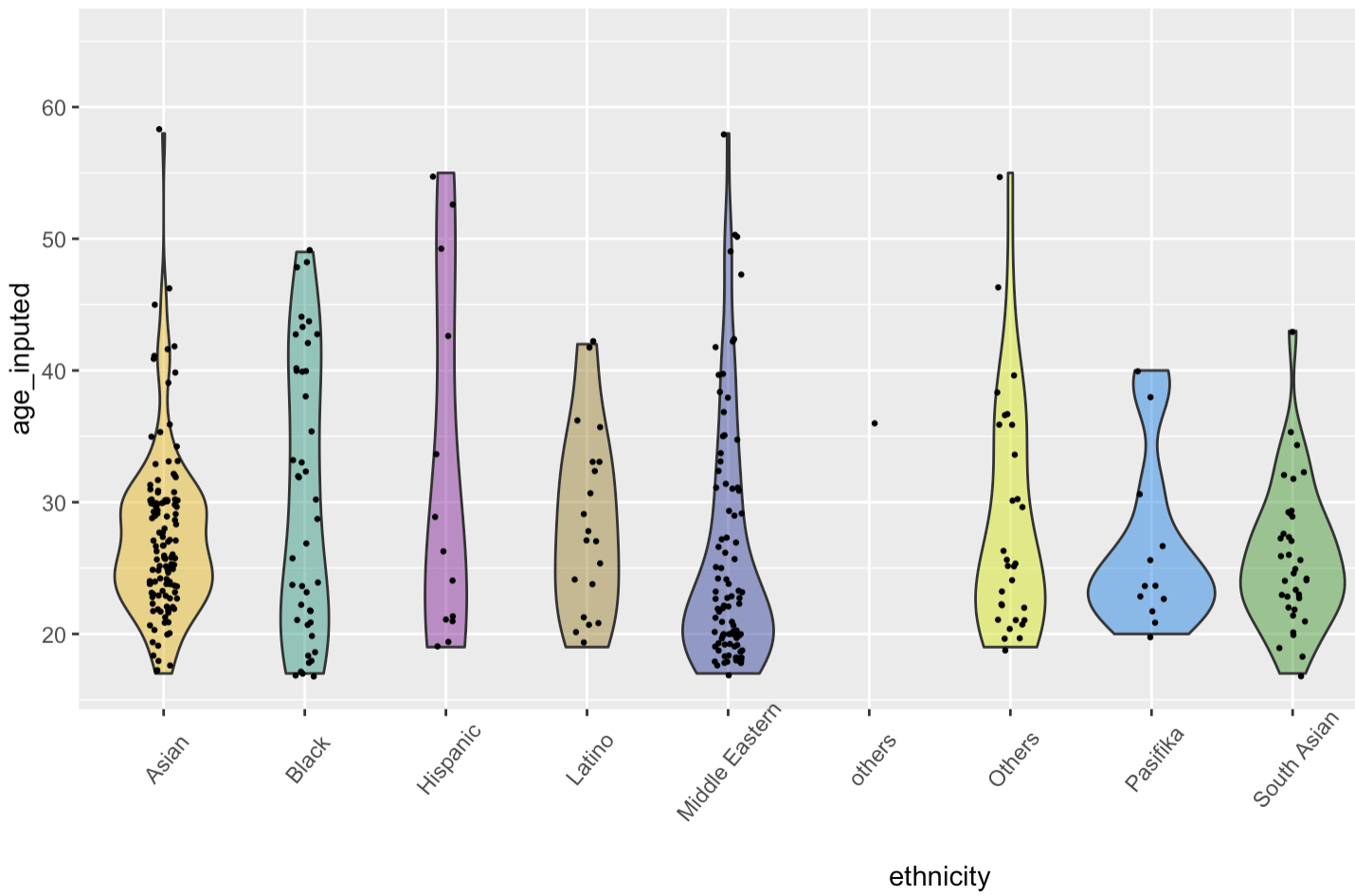
Compared to the box plot, a violin plot provides more infor
only the summary statistics but also the shape and variabil
to identify any **skewness** or **multimodality** in the data).

Violin plot example

- it requires the `geom_violin` function
- it can be enriched by adding with other `geoms`, such as to create more complex and informative plots
- let's add points with the `geom_point` layer

```
autism_pids %>%
  ggplot(mapping = aes(y = age_inputed, x = ethnicity, fil
  geom_violin(alpha=0.5) +
  geom_point(position = position_jitter(width = 0.1), size
  scale_fill_manual(values =  contrast_cols_palette)  +
  # make x axis labes readable
  theme(axis.text.x = element_text(angle=50, vjust=0.75))
  # drop legend and Y-axis title
  theme(legend.position = "none")
```

Violin plot example



SAVING & EXPORTING OU ARTIFACTS

Saving one plot

If I want to use these output files later, I can easily save in
at the beginning.

- save a plot with `ggplot2::ggsave`
- specifying the output directory with `here::here(...)`

```
ggsave (hist_plot,
        filename = here::here("practice",  "data_output",
```

Saving a .Rds data file.

- save a dataframe with `base::saveRDS`
- specifying the output directory with `here::here(...)`

```
saveRDS (object = autism_pids,
         file =  here::here("practice",  "data_output", "a
```

- (later) load a saved dataframe with `base::readRDS`

```
# to load it later I will use
readRDS(here::here("practice",  "data_output", "autism_pid
```


notice I renamed while saving: next time I load it it will be called “autism_pids_v2”

Final thoughts/recommend

- Always **read the documentation** (`?package::functi` examples at the bottom)
- Always **inspect the data** / variables **before** and **after** m
- **Better rename** (i.e. create a new R object) when you rec or a dataset
    - *(this promotes reproducibility, since you will be able steps)*
- Always plot distributions for **visual data exploration**
- Make changes in **small increments** (like we saw in build subsequent layers)