# Retrospective clinical data harmonisation reporting

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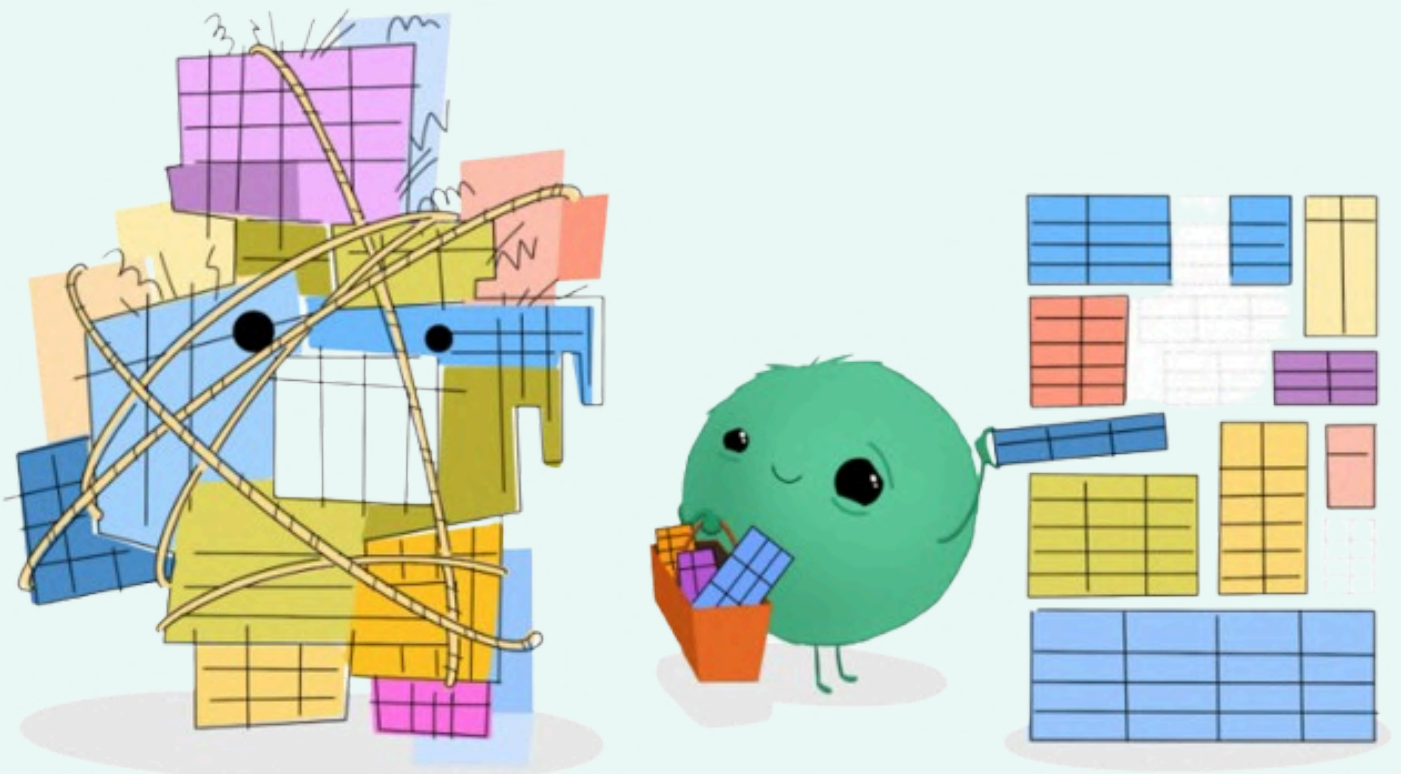
# whoami

Research Officer from National Heart Centre Singapore who collects, cleans and harmonises clinical data.



Taming the Data Beast from "Cleaning Medical Data with R" workshop by Shannon Pileggi, Crystal Lewis and Petter Higgins presented at R/Medicine 2023. Illustrated by Allison Horst.

# Outline

Data harmonisation overview strategy

Counter small but annoying issues during retrospective data harmonisation.

Suggested reports and diagram to create for different clients.

Photo by Sixteen Miles Out on Unsplash

# About Data Harmonisation

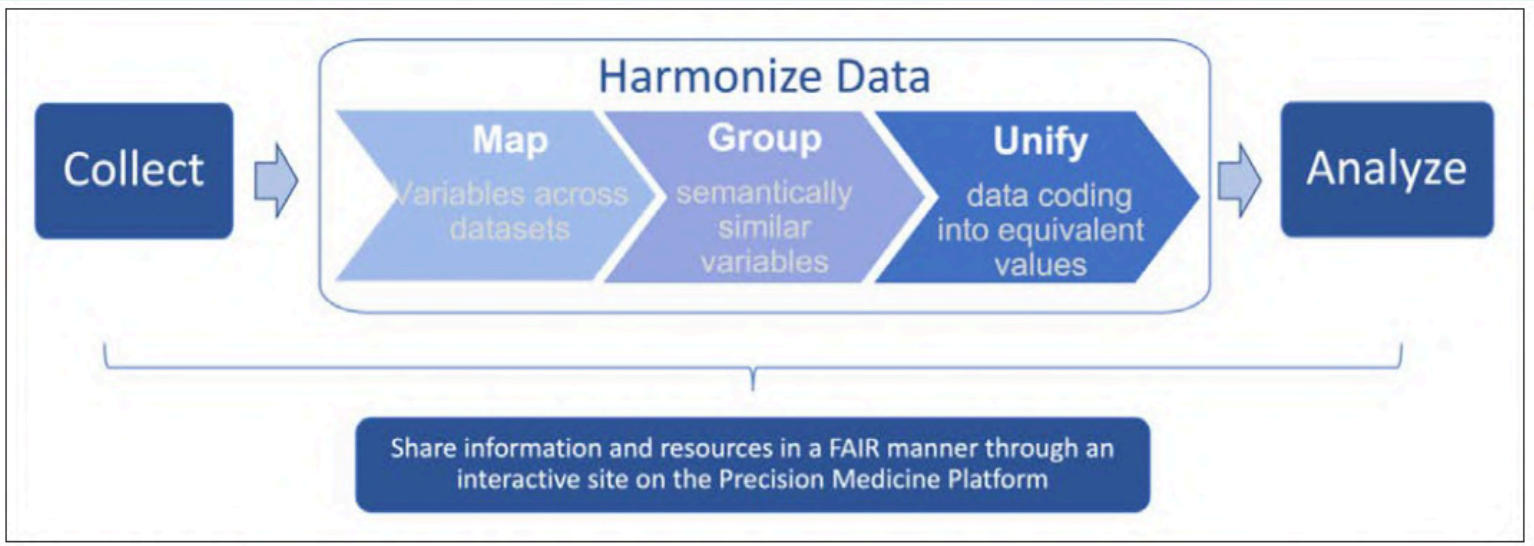
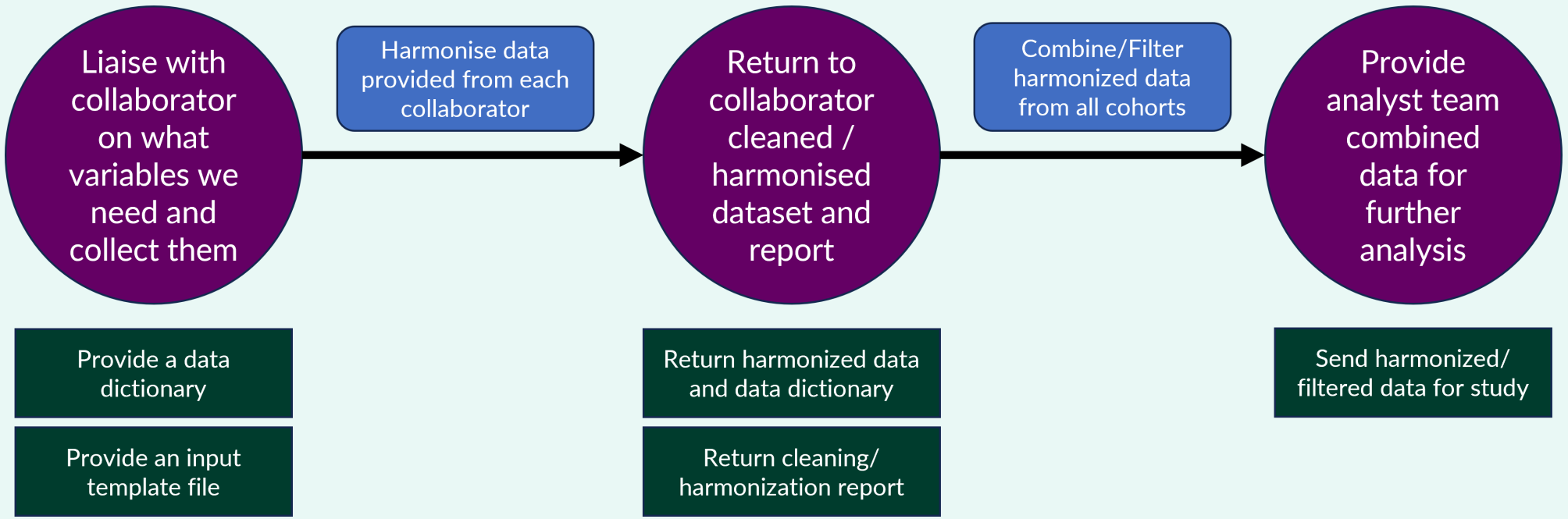



**Figure 1. The data harmonization process.**
Study data variables collected from different sources need to be mapped to one another (step 1), classified into the generalized concepts they represent (step 2), and transformed into unified harmonized variables (step 3) for analysis.

Image from Mallya et al. Circ Cardiovasc Qual Outcomes. 2023 Nov; 16(11):e009938 doi: 10.1161/CIRCOUTCOMES.123.009938.

# Tasks

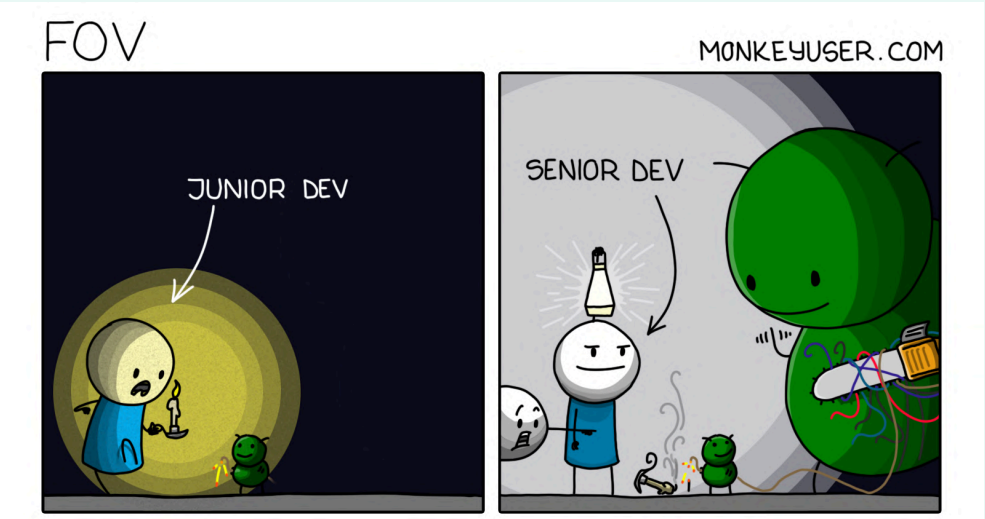
Here is a summary of my task for an international study.



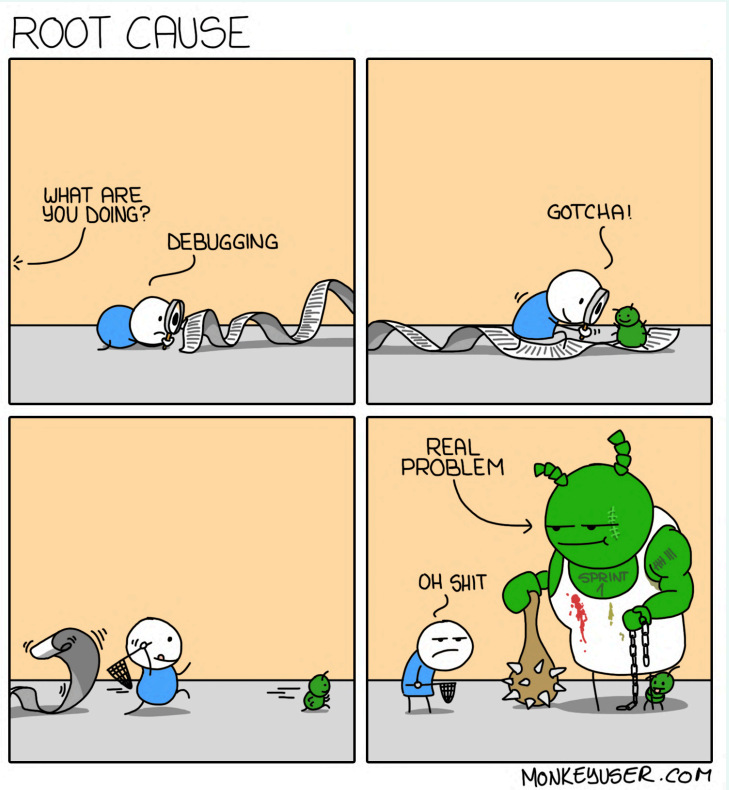
# Why Retropective Data Harmonisation ?

Collaborators may not have resources (time/funding) to match their data to the data dictionary and input template provided.

Data provided may have issues that needs relevant experience and may be hard to solve.




Fov from MonkeyUser.com




Root Cause from MonkeyUser.com

# Why Retropective Data Harmonisation ?

Collaborator wants transparency on how the data is processed.

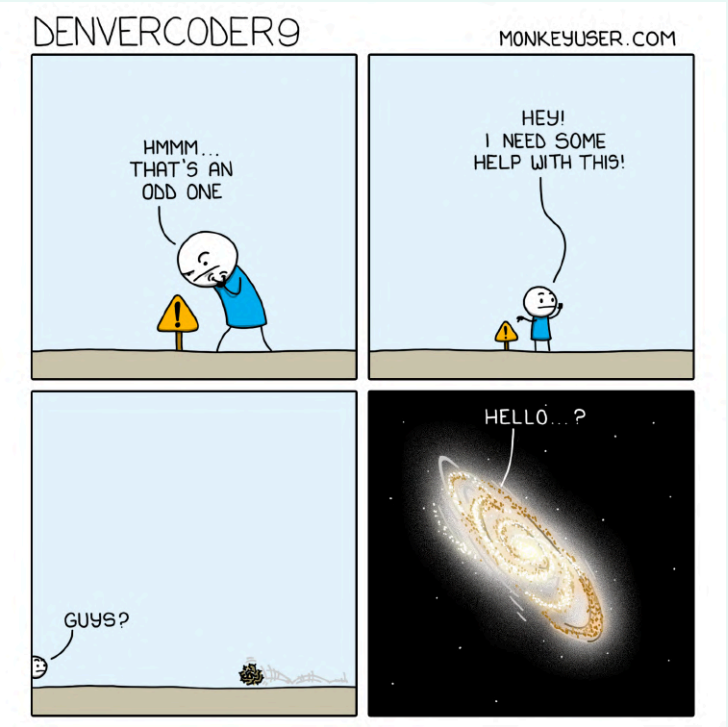
High risk of getting blame should things don't go well.


Joy from MonkeyUser.com

Businessman kneel on floor with pointing finger to him by Amonrat Rungreangfangsai

# Issues

Limited resources on how to do data harmonisation and to make a report.




R packages related to data harmonisation

- `retroharmonize` for survey data.
- `Rmonize` for epidemiological data.
- `psHarmonize` for health and education data.

Denvercoder9 from MonkeyUser.com

# Issues

`retroharmonize` works with categorical but not continuous data variables.

`Rmonize` documentation has too much jargon and difficult for me (and people with limited data science background) to understand.

`psHarmonize` variable harmonisation process is reported in a Microsoft Excel file. Works for variables with simple harmonisation process.

**A** Harmonization instructions for height

| | study | visit | item | source_dataset | source_item | code1 | code_type | coding_notes | id_var | possible_ran | domain | subdomain | final_units | source_units | label | notes | source_labels |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2 | AGES | 1 | Height | ages733_drrp_first_visit_additional | HEIGHT | | | | ID | | Clinical Risk F | Height | cm | n/a | | | |
| 3 | ARIC | 1 | Height | VISIT_1 | ANTA01 | | | No change needed | ID | | Clinical Risk F | Height | cm | cm | | | STANDING HEIGHT TO NEAR |
| 4 | ARIC | 3 | Height | VISIT_3 | ANTC1 | | | No change needed | ID | | Clinical Risk F | Height | cm | cm | | | STANDING HEIGHT TO NEAR |
| 5 | ARIC | 4 | Height | VISIT_4 | ANTD1 | | | No change needed | ID | | Clinical Risk F | Height | cm | cm | | | STANDING HEIGHT TO NEAR |
| 6 | ARIC | 5 | Height | VISIT_5 | ANT3 | | | No change needed | ID | | Clinical Risk F | Height | cm | cm | | | Standing height (cm) |
| 7 | ARIC | 6 | Height | VISIT_6 | ANT3 | | | No change needed | ID | | Clinical Risk F | Height | cm | cm | | | Standing Height (cm) |
| 8 | ARIC | 7 | Height | VISIT_7 | ANT3 | | | No change needed | ID | | Clinical Risk F | Height | cm | cm | | | Standing Height (cm) |
| 9 | CHS | 2 | Height | CHS_main | stht_y2 | | | Imputed 2 height values on visit 18 per CHS instruct | idno | | Clinical Risk F | Height | cm | cm | | | STANDING HEIGHT - CM |
| 10 | CHS | 5 | Height | CHS_main | stht_y5 | | | Imputed 2 height values on visit 18 per CHS instruct | idno | | Clinical Risk F | Height | cm | cm | | | STANDING HEIGHT - CM |
| 11 | CHS | 9 | Height | CHS_main | stht_y9 | | | Imputed 2 height values on visit 18 per CHS instruct | idno | | Clinical Risk F | Height | cm | cm | | | STANDING HEIGHT - CM |
| 12 | CHS | 18 | Height | chs_height_v18 | stht_y18 | | | Imputed 2 height values on visit 18 per CHS instruct | idno | | Clinical Risk F | Height | cm | cm | | | STANDING HEIGHT - CM |
| 13 | FHS - Cohort | 1 | Height | vr_wkthru_ex32_0_0997s_19 | HGT1 | x * 2.54 | function | Converted from inches to cm. | shareid | | Clinical Risk F | Height | cm | in | | | Height, Exam 1 |
| 14 | FHS - Cohort | 4 | Height | vr_wkthru_ex32_0_0997s_19 | HGT4 | x * 2.54 | function | Converted from inches to cm. | shareid | | Clinical Risk F | Height | cm | in | | | Height, Exam 4 |
| 15 | FHS - Cohort | 5 | Height | vr_wkthru_ex32_0_0997s_19 | HGT5 | x * 2.54 | function | Converted from inches to cm. | shareid | | Clinical Risk F | Height | cm | in | | | Height, Exam 5 |
| 16 | FHS - Cohort | 10 | Height | vr_wkthru_ex32_0_0997s_19 | HGT10 | x * 2.54 | function | Converted from inches to cm. | shareid | | Clinical Risk F | Height | cm | in | | | Height, Exam 10 |
| 17 | FHS - Cohort | 11 | Height | vr_wkthru_ex32_0_0997s_19 | HGT11 | x * 2.54 | function | Converted from inches to cm. | shareid | | Clinical Risk F | Height | cm | in | | | Height, Exam 11 |
| 18 | FHS - Cohort | 12 | Height | vr_wkthru_ex32_0_0997s_19 | HGT12 | x * 2.54 | function | Converted from inches to cm. | shareid | | Clinical Risk F | Height | cm | in | | | Height, Exam 12 |
| 19 | FHS - Cohort | 13 | Height | vr_wkthru_ex32_0_0997s_19 | HGT13 | x * 2.54 | function | Converted from inches to cm. | shareid | | Clinical Risk F | Height | cm | in | | | Height, Exam 13 |

Image from Stephen et al. Patterns (N Y). 2024 Jun; 5(8):101003 doi: 10.1016/j.patter.2024.101003.

# Harmonisation Project Template

https://jauntyjjs.github.io/harmonisation/



# Data Harmonisation Project Template

## Table of Content



### Links

Browse source code

Report a bug

### License

Full license

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### Citation

Citing harmonisation

### Developers

Jeremy Selva

Author, maintainer

# Automated capture of warnings (csv)

When reading files in batches or the same file but in a different version, is there an automated way to catch warnings/issues when reading csv files ?

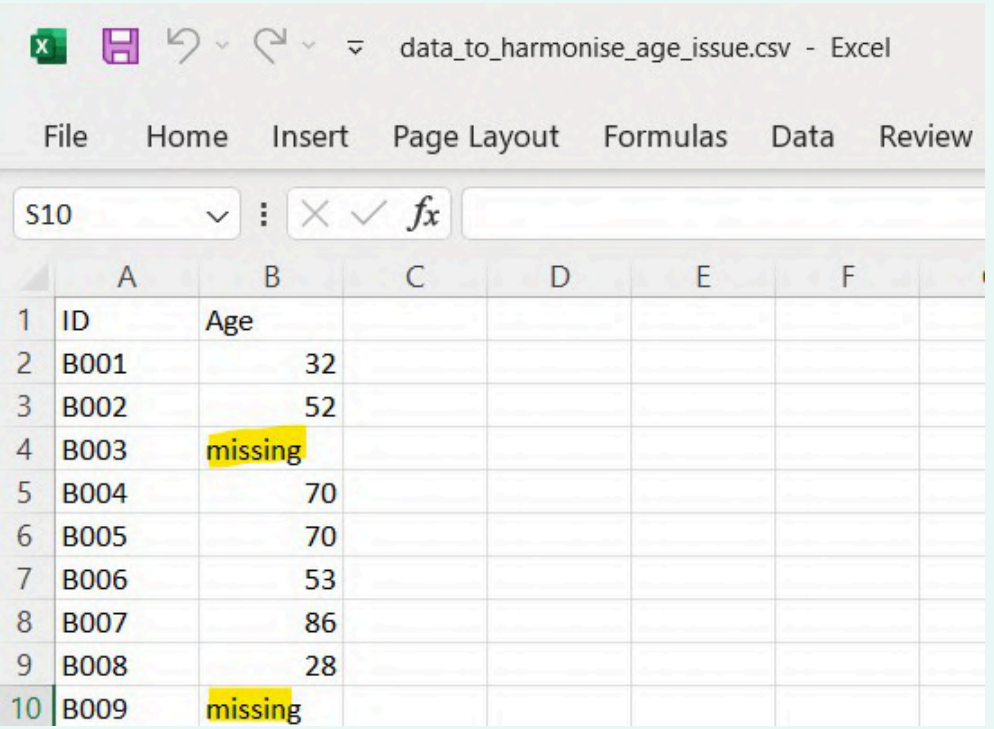
```r
cohort_data_csv <- vroom::vroom(
  file = here::here("data-raw", "Cohort_csv",
    "data_to_harmonise_age_issue.csv"),
  delim = ",",
  col_select = 1:2,
  show_col_types = FALSE,
  col_types = list(
    ID = vroom::col_character(),
    Age = vroom::col_integer()
  )
)

head(cohort_data_csv, n = 3)
```

```
# A tibble: 3 × 2

Warning: One or more parsing issues, call `problems()` on your data frame for
details,
e.g.:
  dat <- vroom(...)
  problems(dat)

  ID      Age
  <chr> <int>
1 B001     32
2 B002     52
3 B003     NA
```



# Automated capture of warnings (csv)

If there are issues with the data, the output of `vroom::problems` will be a tibble.

```
cohort_data_csv |>
  vroom::problems()
```

```
# A tibble: 4 × 5
    row   col expected   actual  file
  <int> <int> <chr>      <chr>   <chr>
1     2     2 an integer missing D:/Jeremy/PortableR/RPortableWorkDirectory/RMe…
2     4     2 an integer missing D:/Jeremy/PortableR/RPortableWorkDirectory/RMe…
3    10     2 an integer missing D:/Jeremy/PortableR/RPortableWorkDirectory/RMe…
4    17     2 an integer missing D:/Jeremy/PortableR/RPortableWorkDirectory/RMe…
```

To check for this automatically, we can use `pointblank::expect_row_count_match`.

```
cohort_data_csv |>
  vroom::problems() |>
  pointblank::expect_row_count_match(count = 0)
```

```
Error: Row counts for the two tables did not match.
The `expect_row_count_match()` validation failed beyond the absolute threshold level (1).
* failure level (1) >= failure threshold (1)
```

# Automated capture of warnings (csv)

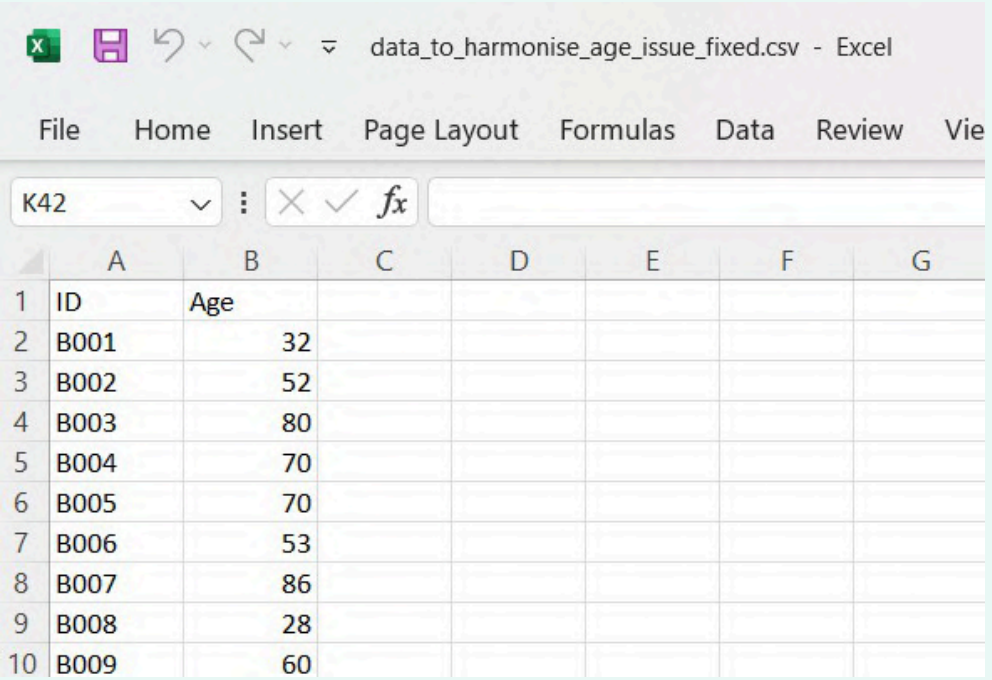
Here is a case with no issues.

```
cohort_data_csv <- vroom::vroom(
  file = here::here("data-raw", "Cohort_csv",
    "data_to_harmonise_age_issue_fixed.csv"),
  delim = ",",
  col_select = 1:2,
  show_col_types = FALSE,
  col_types = list(
    ID = vroom::col_character(),
    Age = vroom::col_integer()
  )
)

cohort_data_csv |>
  vroom::problems()
```

```
# A tibble: 0 × 5
# i 5 variables: row <int>, col <int>, expected <chr>, actual <chr>, file <chr>
```

```
cohort_data_csv |>
  vroom::problems() |>
  pointblank::expect_row_count_match(count = 0)
```




| | A | B | C | D | E | F | G |
|---|---|---|---|---|---|---|---|
| 1 | ID | Age | | | | | |
| 2 | B001 | 32 | | | | | |
| 3 | B002 | 52 | | | | | |
| 4 | B003 | 80 | | | | | |
| 5 | B004 | 70 | | | | | |
| 6 | B005 | 70 | | | | | |
| 7 | B006 | 53 | | | | | |
| 8 | B007 | 86 | | | | | |
| 9 | B008 | 28 | | | | | |
| 10 | B009 | 60 | | | | | |

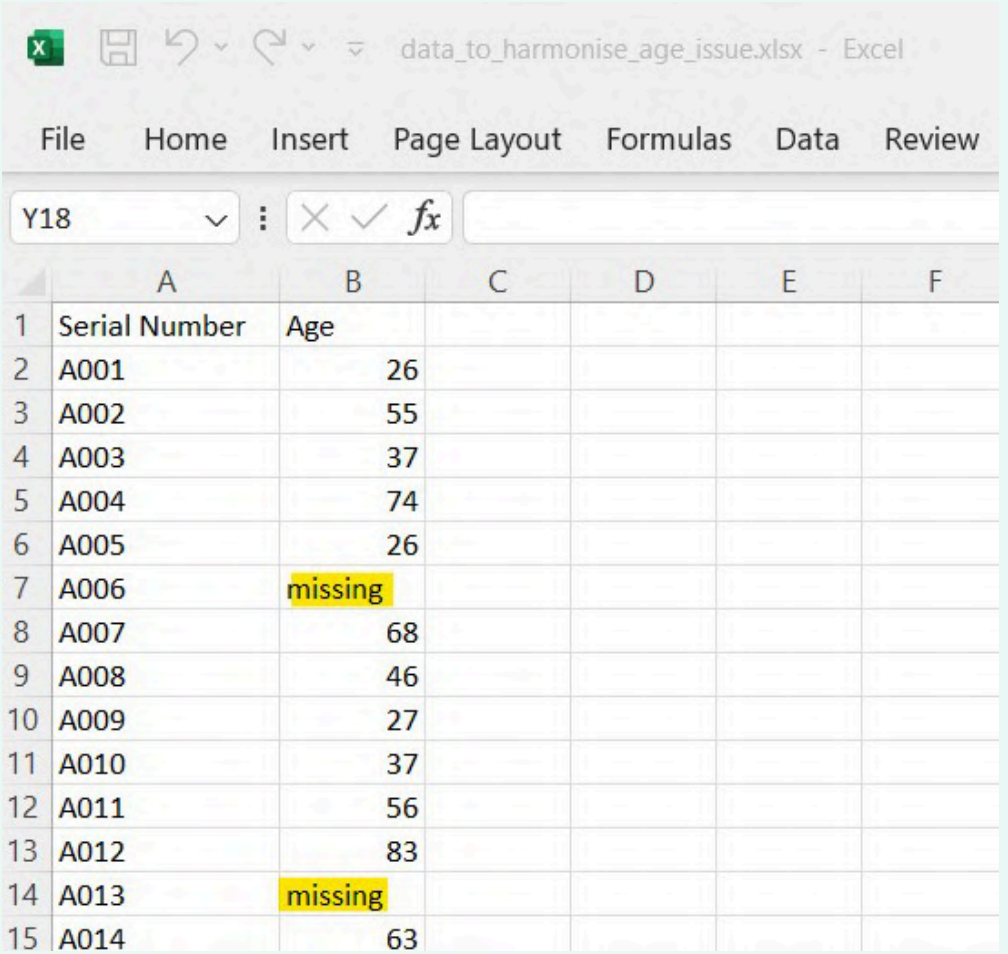
# Automated capture of warnings (Excel)

Is there an automated way to catch warnings/issues when reading Excel files ?

```r
cohort_data_excel <- readxl::read_excel(
  path = here::here("data-raw", "Cohort_Excel",
    "data_to_harmonise_age_issue.xlsx"),
  sheet = "Sheet1",
  col_types = c(
    "text", "numeric"
    )
  )
```

```
Warning: Expecting numeric in B7 / R7C2: got 'missing'

Warning: Expecting numeric in B14 / R14C2: got 'missing'
```



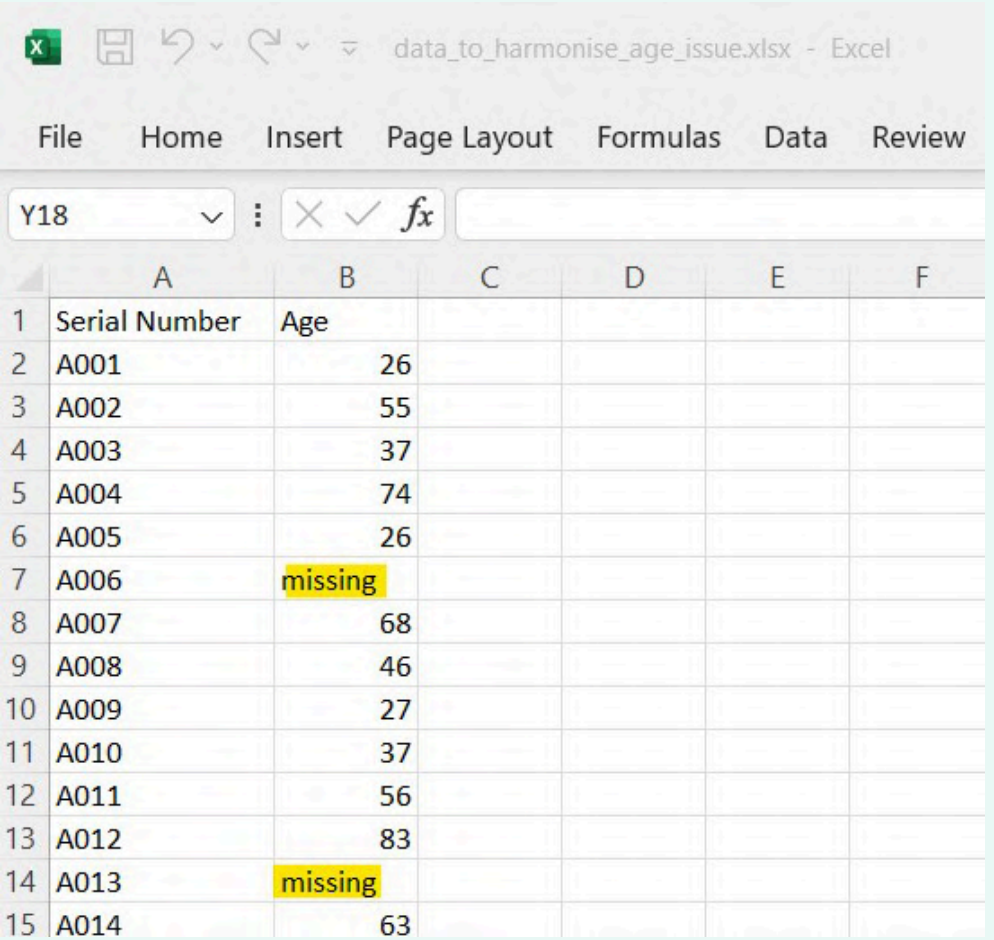

| | A | B | C | D | E | F |
|---|---|---|---|---|---|---|
| 1 | Serial Number | Age | | | | |
| 2 | A001 | 26 | | | | |
| 3 | A002 | 55 | | | | |
| 4 | A003 | 37 | | | | |
| 5 | A004 | 74 | | | | |
| 6 | A005 | 26 | | | | |
| 7 | A006 | missing | | | | |
| 8 | A007 | 68 | | | | |
| 9 | A008 | 46 | | | | |
| 10 | A009 | 27 | | | | |
| 11 | A010 | 37 | | | | |
| 12 | A011 | 56 | | | | |
| 13 | A012 | 83 | | | | |
| 14 | A013 | missing | | | | |
| 15 | A014 | 63 | | | | |

# Automated capture of warnings (Excel)

We can read the Excel file with `testthat::expect_no_condition`.

```
testthat::expect_no_condition(
  cohort_data_excel <- readxl::read_excel(
    path = here::here("data-raw", "Cohort_Excel",
      "data_to_harmonise_age_issue.xlsx"),
    sheet = "Sheet1",
    col_types = c("text", "numeric")
  )
)
```

```
Error: Expected `... <- NULL` to run without any conditions.
ℹ Actually got a <simpleWarning> with text:
  Expecting numeric in B7 / R7C2: got 'missing'
```



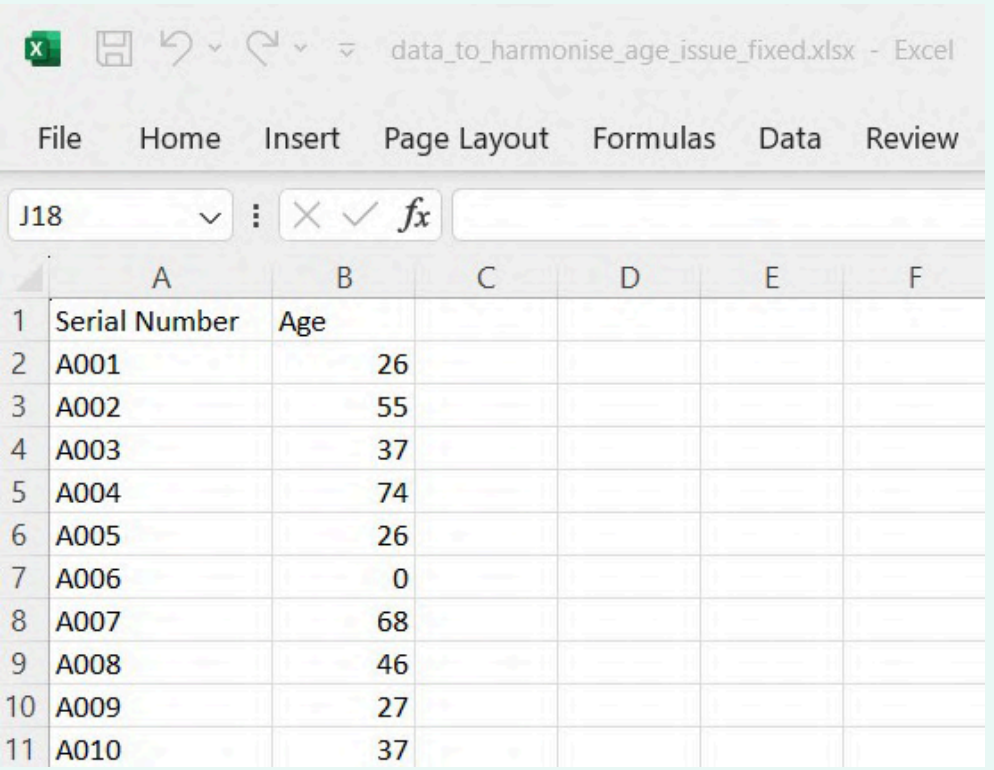

| | A | B | C | D | E | F |
|---|---|---|---|---|---|---|
| 1 | Serial Number | Age | | | | |
| 2 | A001 | 26 | | | | |
| 3 | A002 | 55 | | | | |
| 4 | A003 | 37 | | | | |
| 5 | A004 | 74 | | | | |
| 6 | A005 | 26 | | | | |
| 7 | A006 | missing | | | | |
| 8 | A007 | 68 | | | | |
| 9 | A008 | 46 | | | | |
| 10 | A009 | 27 | | | | |
| 11 | A010 | 37 | | | | |
| 12 | A011 | 56 | | | | |
| 13 | A012 | 83 | | | | |
| 14 | A013 | missing | | | | |
| 15 | A014 | 63 | | | | |

# Automated capture of warnings (Excel)

However, this method means that you will lose the pipe workflow.

```
testthat::expect_no_condition(
  cohort_data_excel <- readxl::read_excel(
    path = here::here("data-raw", "Cohort_Excel",
      "data_to_harmonise_age_issue_fixed.xlsx"),
    sheet = "Sheet1",
    col_types = c("text", "numeric")
  )
)

cohort_data_excel <- cohort_data_excel |>
  # Check if Serial Number is unique
  pointblank::rows_distinct(
    columns = "Serial Number",
  )
```




| | A | B | C | D | E | F |
|---|---|---|---|---|---|---|
| 1 | Serial Number | Age | | | | |
| 2 | A001 | 26 | | | | |
| 3 | A002 | 55 | | | | |
| 4 | A003 | 37 | | | | |
| 5 | A004 | 74 | | | | |
| 6 | A005 | 26 | | | | |
| 7 | A006 | 0 | | | | |
| 8 | A007 | 68 | | | | |
| 9 | A008 | 46 | | | | |
| 10 | A009 | 27 | | | | |
| 11 | A010 | 37 | | | | |

# Automated capture of warnings (Excel)

We can use the tee pipe operator `%T>%`.

## With Issues

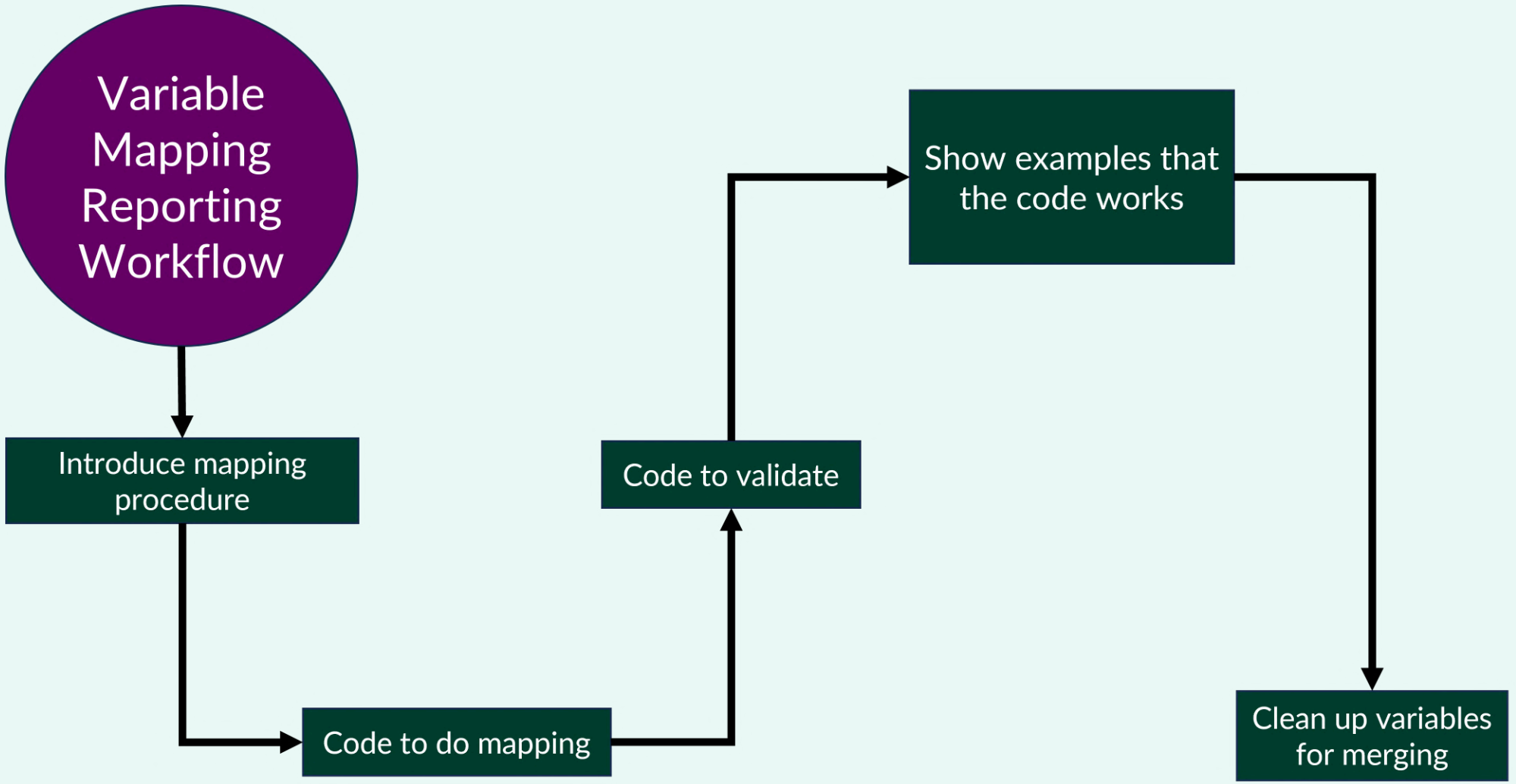
```
cohort_data_excel <- readxl::read_excel(
  path = here::here("data-raw", "Cohort_Excel",
    "data_to_harmonise_age_issue.xlsx"),
  sheet = "Sheet1",
  col_types = c(
    "text", "numeric"
    )
  ) %T>%
  testthat::expect_no_condition()
```

```
Error: Expected `.` to run without any conditions.
i Actually got a <simpleWarning> with text:
  Expecting numeric in B7 / R7C2: got 'missing'
```

## No Issues

```
cohort_data_excel_2 <- readxl::read_excel(
  path = here::here("data-raw", "Cohort_Excel",
    "data_to_harmonise_age_issue_fixed.xlsx"),
  sheet = "Sheet1",
  col_types = c("text", "numeric")
) %T>%
testthat::expect_no_condition() |>
# Check if Serial Number is unique
  pointblank::rows_distinct(
    columns = "Serial Number",
)
```

# Variable Mapping



# Variable Mapping

Let take this data set as an example.

```r
cohort_csv_data <- vroom::vroom(
  file = here::here("data-raw",
                    "Cohort_csv",
                    "data_to_harmonise.csv"),
  delim = ",",
  col_select = 1:8,
  show_col_types = FALSE,
  col_types = list(
    ID = vroom::col_character(),
    Age = vroom::col_integer(),
    Sex = vroom::col_character(),
    Height = vroom::col_double(),
    Weight = vroom::col_double(),
    `Smoke History` = vroom::col_character(),
    `Chest Pain Character` = vroom::col_character(),
    Dyspnea = vroom::col_character()
    )
  ) |>
  dplyr::rename(cohort_unique_id = "ID") |>
  # Remove rows when the ID value is NA
  dplyr::filter(!is.na(.data[["cohort_unique_id"]])) |>
  # Remove white spaces in column names
  dplyr::rename_all(stringr::str_trim) |>
  # Check if cohort id is unique
  pointblank::rows_distinct(
    columns = "cohort_unique_id",
```

| cohort_unique_id | Age | Sex | Height | Weight | S H |
|---|---|---|---|---|---|
| | | All | | | |
| B001 | 32 | Female | 170 | 63 | n |
| B002 | 52 | Female | 167 | 71 | c s |
| B003 | 80 | Male | 184 | 77 | n |
| B004 | 70 | Male | 160 | 83 | p |
| B005 | 70 | Female | 155 | 61 | c s |

1–5 of 20 rows Previous 1 of 4 Next

Download as CSV

# Variable Mapping

Let the reader know how the collaborator's data `Smoke History` is going to be mapped.

Introduce mapping procedure

````
### Smoking History

`smoke_current` is grouped as follows:

```{r}
#| label: smoke current table
#| echo: false
#| message: false
#| warnings: false
#| results: asis

tabl <- "

+----------------------+----------------------+
| Smoke History        | smoke_current        |
+:=====================+:=====================+
| non-smoker           | 0                    |
+----------------------+----------------------+
| past smoker          | 0                    |
+----------------------+----------------------+
| current smoker       | 1                    |
+----------------------+----------------------+
| NA                   | -1                   |
+----------------------+----------------------+

"
cat(tabl)
```
````

## 2.3 Smoking History

`smoke_current` is grouped as follows:

| Smoke History | smoke_current |
|---|---|
| non-smoker | 0 |
| past smoker | 0 |
| current smoker | 1 |
| NA | -1 |

`smoke_past` is grouped as follows:

| Smoke History | smoke_past |
|---|---|
| non-smoker | 0 |
| past smoker | 1 |
| current smoker | 0 |
| NA | -1 |

We do a check to ensure that we can only have these scenarios

- `smoke_current` as 1 and `smoke_past` as 0 for current smokers
- `smoke_current` as 0 and `smoke_past` as 1 for past smokers
- `smoke_current` as 0 and `smoke_past` as 0 for non-smokers
- `smoke_current` as -1 and `smoke_past` as -1 for unknown

# Variable Mapping

## Code to do mapping

```r
smoking_data <- cohort_csv_data |>
  dplyr::select(c("cohort_unique_id",
                  "Smoke History")) |>
  dplyr::mutate(
    smoke_current = dplyr::case_when(
      is.na(.data[["Smoke History"]]) ~ "-1",
      .data[["Smoke History"]] == "non-smoker" ~ "0",
      .data[["Smoke History"]] == "past smoker" ~ "0",
      .data[["Smoke History"]] == "current smoker" ~ "1",
      .default = NA_character_
    ),
    smoke_current = forcats::fct_relevel(
      .data[["smoke_current"]],
      c("0", "1")),
    smoke_past = dplyr::case_when(
      is.na(.data[["Smoke History"]]) ~ "-1",
      .data[["Smoke History"]] == "non-smoker" ~ "0",
      .data[["Smoke History"]] == "past smoker" ~ "1",
      .data[["Smoke History"]] == "current smoker" ~ "0",
      .default = NA_character_
    ),
    smoke_past = forcats::fct_relevel(
      .data[["smoke_past"]],
      c("0", "1")),
    `Smoke History` = forcats::fct(
      .data[["Smoke History"]]
```

### 2.3 Smoking History

`smoke_current` is grouped as follows:

| Smoke History | smoke_current |
|---|---|
| non-smoker | 0 |
| past smoker | 0 |
| current smoker | 1 |
| NA | -1 |

`smoke_past` is grouped as follows:

| Smoke History | smoke_past |
|---|---|
| non-smoker | 0 |
| past smoker | 1 |
| current smoker | 0 |
| NA | -1 |

# Variable Mapping

## Code to validate

```
smoking_data <- smoking_data |>
  pointblank::col_vals_in_set(
    columns = c("smoke_current", "smoke_past"),
    set = c("0", "1", "-1")
  ) |>
  pointblank::col_vals_expr(
    expr = pointblank::expr(
      (.data[["smoke_current"]] == "1" & .data[["smoke_past"]] == "0") |
      (.data[["smoke_current"]] == "-1" & .data[["smoke_past"]] == -"1") |
      (.data[["smoke_current"]] == "0" & .data[["smoke_past"]] %in% c("0", "
    )
  )
```

We do a check to ensure that we can only have these scenarios

- `smoke_current` as 1 and `smoke_past` as 0 for current smokers
- `smoke_current` as 0 and `smoke_past` as 1 for past smokers
- `smoke_current` as 0 and `smoke_past` as 0 for non-smokers
- `smoke_current` as -1 and `smoke_past` as -1 for unknown

Reference: https://github.com/rstudio/pointblank/issues/578

# Variable Mapping

## Show examples that the code works

```
::: {.content-visible when-format="html"}

```{r}
#| label: smoking data html
#| eval: !expr out_type == "html"

if (params$show_table && knitr::is_html_output()) {
  smoking_data |>
    harmonisation::reactable_with_download_csv_button()
}

```

:::
```

Html Output

| cohort_unique_id | Smoke History | smoke_current | smoke_past |
|---|---|---|---|
| | All | All | All |
| B001 | non-smoker | 0 | 0 |
| B002 | current smoker | 1 | 0 |
| B003 | non-smoker | 0 | 0 |
| B004 | past smoker | 0 | 1 |
| B005 | current smoker | 1 | 0 |

1–5 of 20 rows Previous 1 of 4 Next

Download as CSV

# Variable Mapping

## Show examples that the code works

````
::: {.content-visible unless-format="html"}

```{r}
#| label: smoking data not html
#| eval: !expr out_type != "html"

if (params$show_table) {
  smoking_data |>
    dplyr::distinct(.data[["Smoke History"]],
                    .keep_all = TRUE) |>
    knitr::kable()
}

```

:::
````

**Pdf Output**

```
if (params$show_table) {
  smoking_data |>
    dplyr::distinct(.data[["Smoke History"]],
                    .keep_all = TRUE) |>
    knitr::kable()
}
```

| cohort_unique_id | Smoke History | smoke_current | smoke_past |
|---|---|---|---|
| B001 | non-smoker | 0 | 0 |
| B002 | current smoker | 1 | 0 |
| B004 | past smoker | 0 | 1 |
| B017 | NA | -1 | -1 |

# Variable Mapping

## Clean up variables for merging

```
smoking_data <- smoking_data |>
  dplyr::select(-c("Smoke History"))
```

| cohort_unique_id | smoke_current | smoke_past |
|---|---|---|
| | All | All |
| B001 | 0 | 0 |
| B002 | 1 | 0 |
| B003 | 0 | 0 |
| B004 | 0 | 1 |
| B005 | 1 | 0 |

1–5 of 20 rows Previous 1 of 4 Next

Download as CSV

# Merging Harmonised Data

Suppose we have completed harmonising a batch of clinical data.

```
age_gender_data |>
  reactable_with_download_csv_button(
    defaultPageSize = 5,
    paginationType = "jump",
    style = list(fontSize = "1rem"),
  )
```

| cohort_unique_id | age_years | sex |
|---|---|---|
| | | All |
| B001 | 32 | 0 |
| B002 | 52 | 0 |
| B003 | 80 | 1 |
| B004 | 70 | 1 |
| B005 | 70 | 0 |

1–5 of 20 rows Previous 1 of 4 Next

Download as CSV

```
body_measurement_data |>
  reactable_with_download_csv_button(
    defaultPageSize = 5,
    paginationType = "jump",
    style = list(fontSize = "1rem"),
  )
```

| cohort_unique_id | height_cm | weight_kg | bsa_m2 | bmi |
|---|---|---|---|---|
| B001 | 170 | 63 | 1.72 | 21.8 |
| B002 | 167 | 71 | 1.81 | 25.46 |
| B003 | 184 | 77 | 1.98 | 22.74 |
| B004 | 160 | 83 | 1.92 | 32.42 |
| B005 | 155 | 61 | 1.62 | 25.39 |

1–5 of 20 rows Previous 1 of 4 Next

Download as CSV

How can we merge them without issues of missing rows or additional columns ?

# Merging Harmonised Data

`unmatched = "error"` in `dplyr::inner_join` helps to avoid patients with no match.

```
join_specification <- dplyr::join_by("cohort_unique_id")

demo_behave_data <- cohort_csv_data |>
  dplyr::select(c("cohort_unique_id")) |>
  dplyr::inner_join(age_gender_data,
                    by = join_specification,
                    unmatched = "error",
                    relationship = "one-to-one") |>
  dplyr::inner_join(body_measurement_data,
                    by = join_specification,
                    unmatched = "error",
                    relationship = "one-to-one") |>
  dplyr::inner_join(smoking_data,
                    by = join_specification,
                    unmatched = "error",
                    relationship = "one-to-one") |>
  dplyr::relocate(c("bsa_m2", "bmi"),
                  .after = "sex")
```

```
three_penguins <- tibble::tribble(
  ~samp_id, ~species,    ~island,
  1,        "Adelie",    "Torgersen",
  2,        "Gentoo",    "Biscoe",
  3,        "Chinstrap", "Dream"
)

weight_extra <- tibble::tribble(
  ~samp_id,  ~body_mass_g,
  1,         3220,
  2,         4730,
  4,         4725
)

three_penguins |>
  dplyr::inner_join(
    y = weight_extra,
    by = dplyr::join_by("samp_id"),
    unmatched = "error"
 )
```

```
Error in `dplyr::inner_join()`:
! Each row of `x` must have a match in `y`.
ℹ Row 3 of `x` does not have a match.
```

Reference: https://www.tidyverse.org/blog/2023/08/teach-tidyverse-23/#improved-and-expanded-_join-functionality

# Merging Harmonised Data

`unmatched = "error"` in `dplyr::inner_join` helps to avoid patients with no match.

```r
join_specification <- dplyr::join_by("cohort_unique_id")

demo_behave_data <- cohort_csv_data |>
  dplyr::select(c("cohort_unique_id")) |>
  dplyr::inner_join(age_gender_data,
                    by = join_specification,
                    unmatched = "error",
                    relationship = "one-to-one") |>
  dplyr::inner_join(body_measurement_data,
                    by = join_specification,
                    unmatched = "error",
                    relationship = "one-to-one") |>
  dplyr::inner_join(smoking_data,
                    by = join_specification,
                    unmatched = "error",
                    relationship = "one-to-one") |>
  dplyr::relocate(c("bsa_m2", "bmi"),
                  .after = "sex")
```

```r
three_penguins <- tibble::tribble(
  ~samp_id, ~species,    ~island,
  1,        "Adelie",    "Torgersen",
  2,        "Gentoo",    "Biscoe",
  3,        "Chinstrap", "Dream"
)

weight_extra <- tibble::tribble(
  ~samp_id,  ~body_mass_g,
  1,         3220,
  3,         4725
)

three_penguins |>
  dplyr::inner_join(
    y = weight_extra,
    by = dplyr::join_by("samp_id"),
    unmatched = "error"
 )
```

```
Error in `dplyr::inner_join()`:
! Each row of `x` must have a match in `y`.
ℹ Row 2 of `x` does not have a match.
```

Reference: https://www.tidyverse.org/blog/2023/08/teach-tidyverse-23/#improved-and-expanded-_join-functionality

# Merging Harmonised Data

`relationship = "one-to-one"` in `dplyr::inner_join` helps to avoid patients with multiple match.

```r
join_specification <- dplyr::join_by("cohort_unique_id")

demo_behave_data <- cohort_csv_data |>
  dplyr::select(c("cohort_unique_id")) |>
  dplyr::inner_join(age_gender_data,
                    by = join_specification,
                    unmatched = "error",
                    relationship = "one-to-one") |>
  dplyr::inner_join(body_measurement_data,
                    by = join_specification,
                    unmatched = "error",
                    relationship = "one-to-one") |>
  dplyr::inner_join(smoking_data,
                    by = join_specification,
                    unmatched = "error",
                    relationship = "one-to-one") |>
  dplyr::relocate(c("bsa_m2", "bmi"),
                  .after = "sex")
```

```r
three_penguins <- tibble::tribble(
  ~samp_id, ~species,    ~island,
  1,        "Adelie",    "Torgersen",
  2,        "Gentoo",    "Biscoe",
  3,        "Chinstrap", "Dream"
)

weight_extra <- tibble::tribble(
  ~samp_id,  ~body_mass_g,
  1,         3220,
  2,         4730,
  2,         4725,
  3,         4000
)

three_penguins |>
  dplyr::inner_join(
    y = weight_extra,
    by = dplyr::join_by("samp_id"),
    relationship = "one-to-one"
 )
```

```
Error in `dplyr::inner_join()`:
! Each row in `x` must match at most 1 row in `y`.
ℹ Row 2 of `x` matches multiple rows in `y`.
```

Reference: https://www.tidyverse.org/blog/2023/08/teach-tidyverse-23/#improved-and-expanded-_join-functionality

# Merging Harmonised Data

Use `pointblank::has_columns` to ensure we only have harmonised variables.

```
testthat::expect_false(
  pointblank::has_columns(
    demo_behave_data,
    columns = c(
      dplyr::ends_with(".x"),
      dplyr::ends_with(".y")
    )
  )
)

testthat::expect_equal(
  ncol(demo_behave_data), 9
)

testthat::expect_true(
  pointblank::has_columns(
    demo_behave_data,
    columns = c(
      "age_years", "sex",
      "height_cm", "weight_kg", "bsa_m2", "bmi",
      "smoke_current", "smoke_past"
    )
  )
)
```

```
three_penguins <- tibble::tribble(
  ~samp_id, ~species,    ~island,
  1,        "Adelie",    "Torgersen",
  2,        "Gentoo",    "Biscoe",
  3,        "Chinstrap", "Dream"
)

weight_extra <- tibble::tribble(
  ~samp_id,  ~island,
  1,         "Torgersen",
  2,         "Biscoe",
  3,         "Dream"
)

three_penguins <- three_penguins |>
  dplyr::inner_join(
    y = weight_extra,
    by = dplyr::join_by("samp_id"),
    unmatched = "error",
    relationship = "one-to-one"
 )

three_penguins |>
  pointblank::has_columns(
    columns = c(
      dplyr::ends_with(".x"),
```

```
[1] TRUE
```

```
colnames(three_penguins)
```

```
[1] "samp_id"  "species"  "island.x" "island.y"
```

# Automated Report Challenge

One variable mapping report takes at least one page.

On average, a clinical trial will have a few hundred variables.

- One hundred columns for clinical and demographics.
- Two hundred columns for medication.

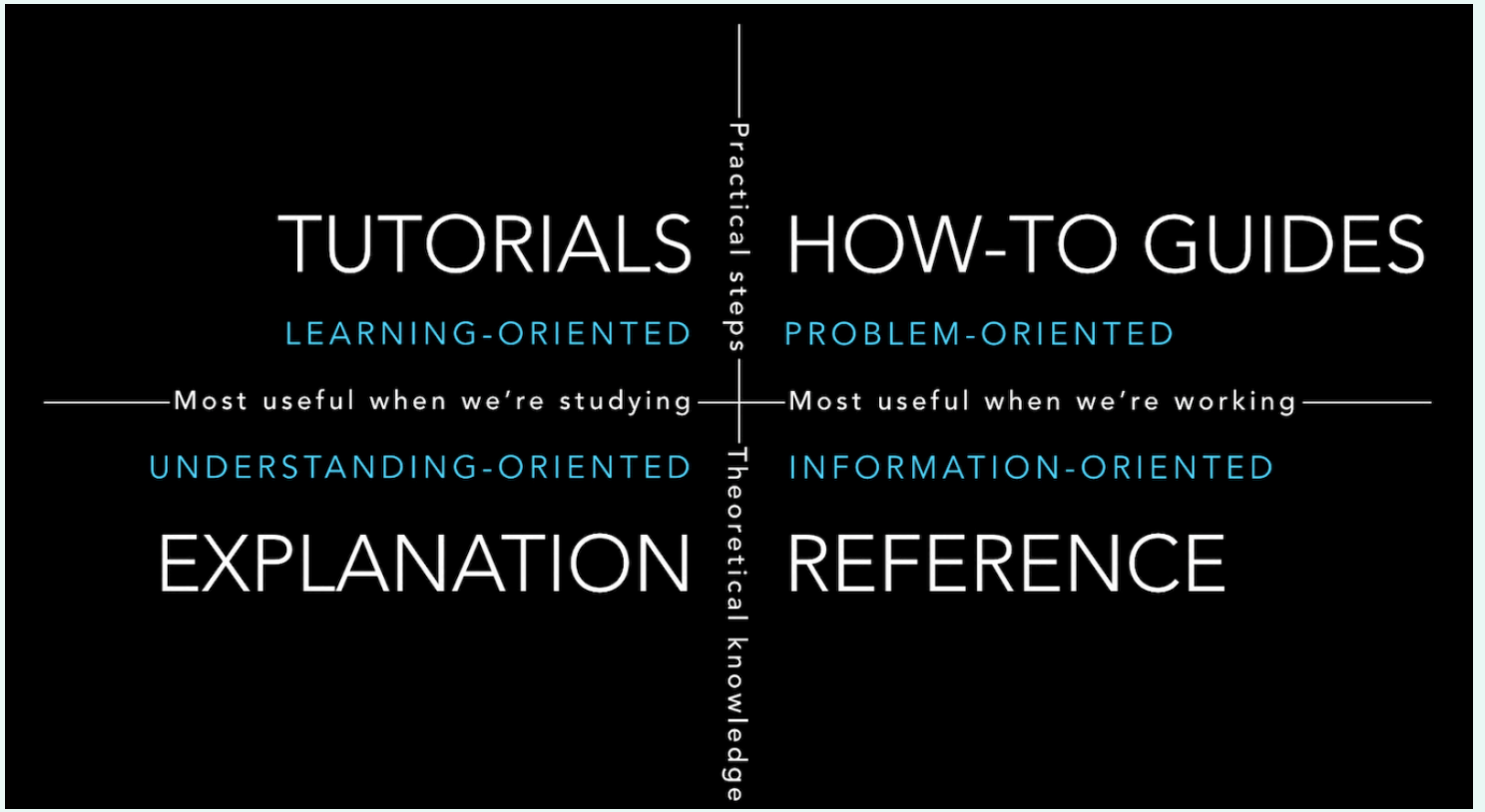
Harmonisation report can have at least a few hundreds pages for each cohort.

There is a need to automate the creation of these reports.


Businessman in pile of documents asking for help by Amonrat Rungreangfangsai

# Automated Report Challenge

Collaborator wants different ways to report how data harmonisation is done.




The documentation system by Divio

# Quarto Books

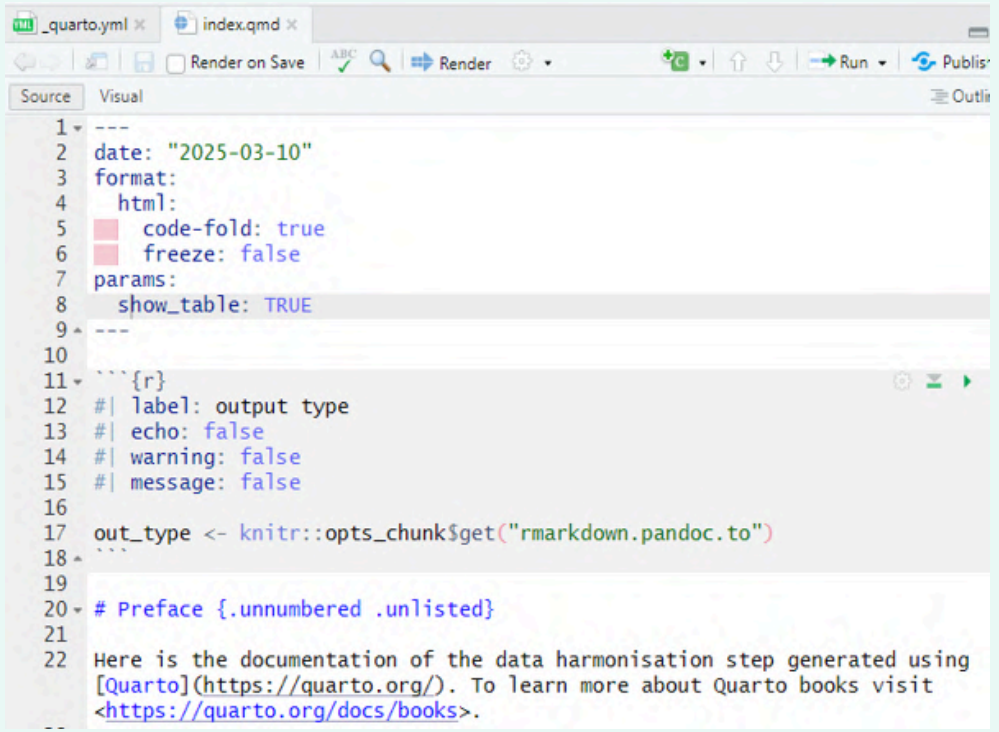
To make a Quarto book or website, we need a `_quarto.yml` and `index.qmd` file

_quarto.yml | index.qmd

```yaml
project:
  type: book
  output-dir: reports/Cohort_B

book:
  downloads: [pdf, docx]
  title: "Harmonisation Template for Cohort B"
  author: "My Name"
  navbar:
    search: true
  sidebar:
    collapse-level: 1

  chapters:
    - index.qmd
    - part: Cohort B Cleaning
      chapters:
        - codes/Cohort_B/00_R_Package_And_Environment.qmd
        - codes/Cohort_B/01_Read_Cohort_B_Data.qmd
        - codes/Cohort_B/02_Extract_Demographic.qmd
        - codes/Cohort_B/03_Export_To_Excel.qmd
```




```yaml
---
date: "2025-03-10"
format:
  html:
    code-fold: true
    freeze: false
params:
  show_table: TRUE
---
```

```{r}
#| label: output type
#| echo: false
#| warning: false
#| message: false

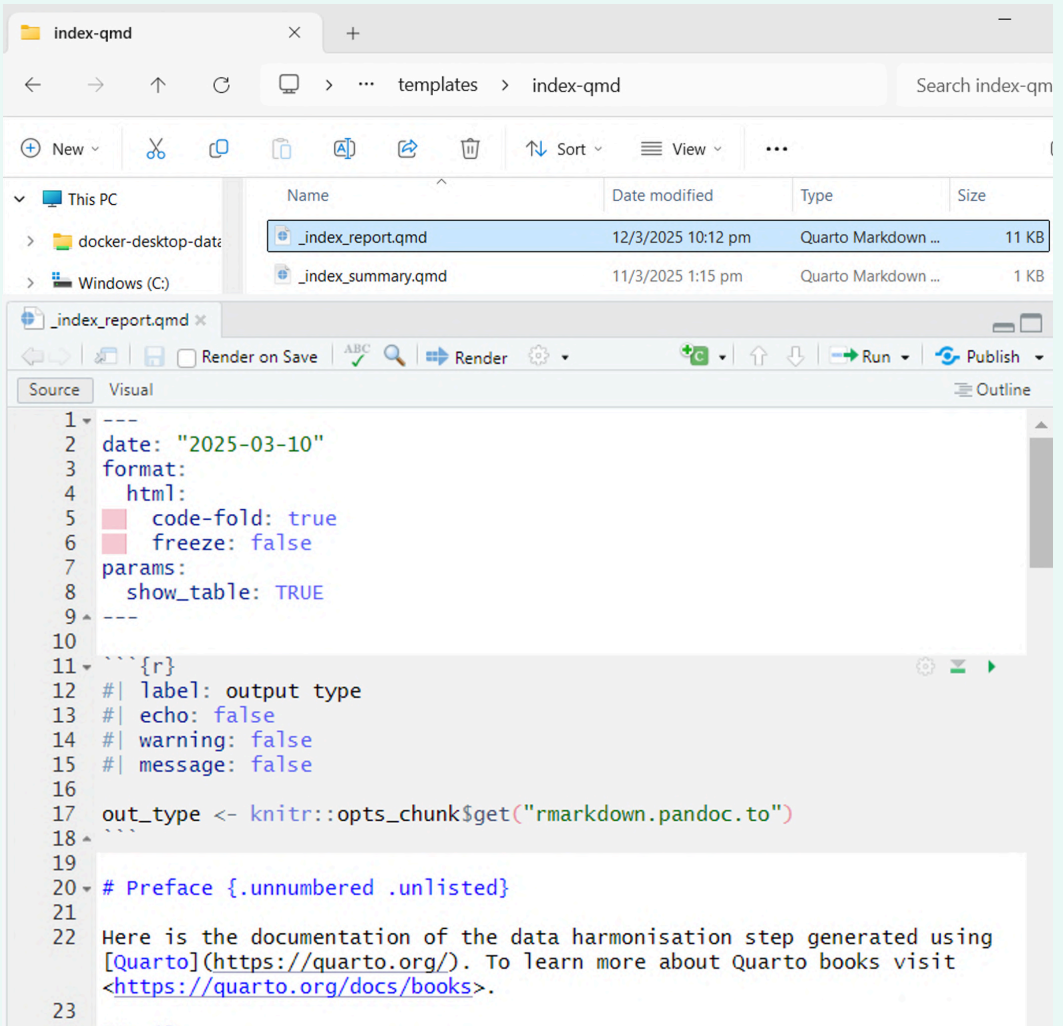
out_type <- knitr::opts_chunk$get("rmarkdown.pandoc.to")
```

```
# Preface {.unnumbered .unlisted}

Here is the documentation of the data harmonisation step generated using
[Quarto](https://quarto.org/). To learn more about Quarto books visit
<https://quarto.org/docs/books>.
```

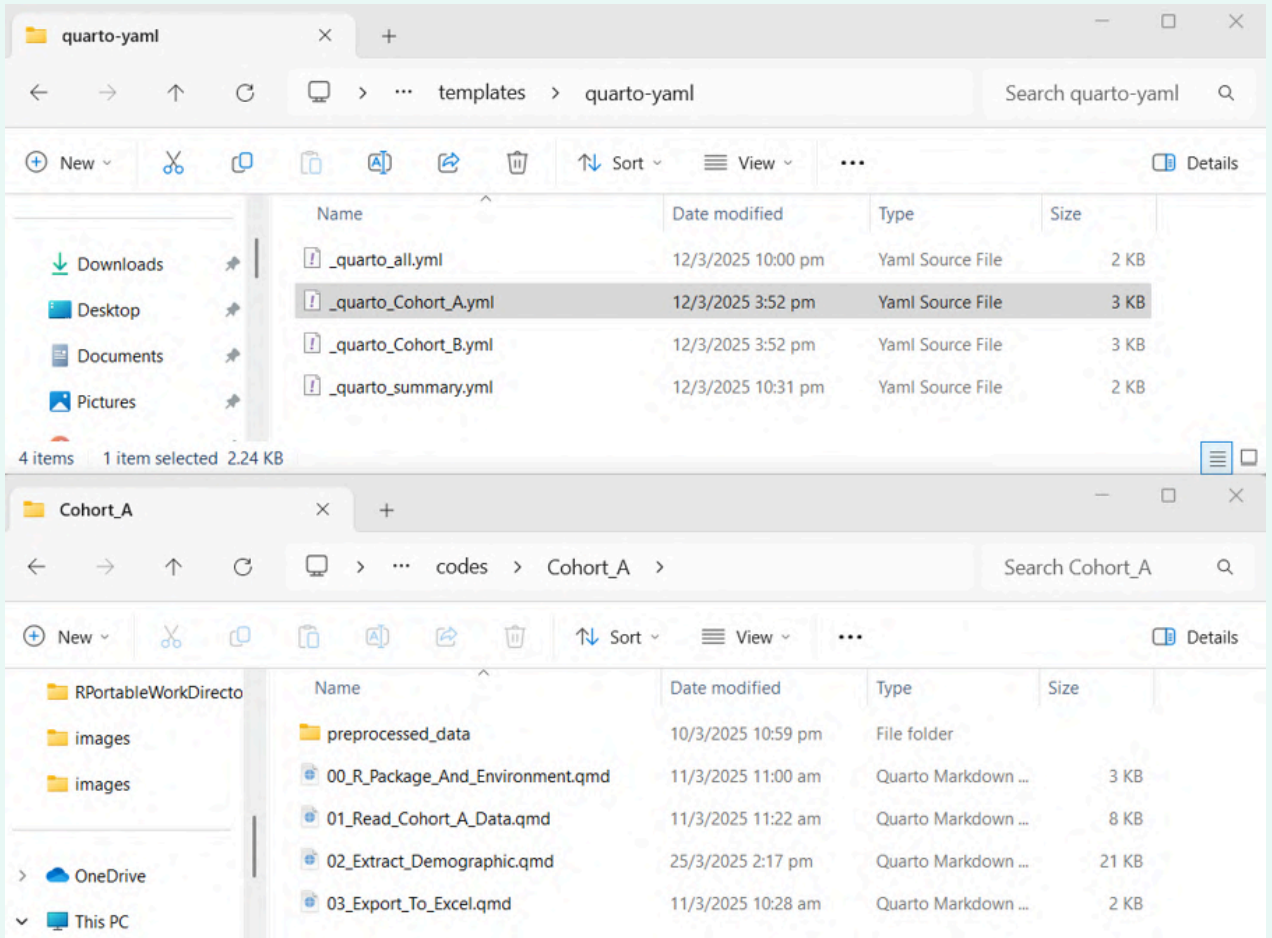
# Automated Technical Report (Reference)

We create an `index.qmd` file for technical report generation.



# Automated Technical Report (Reference)

We create a `_quarto.yml` file and relevant Quarto files for each cohort.



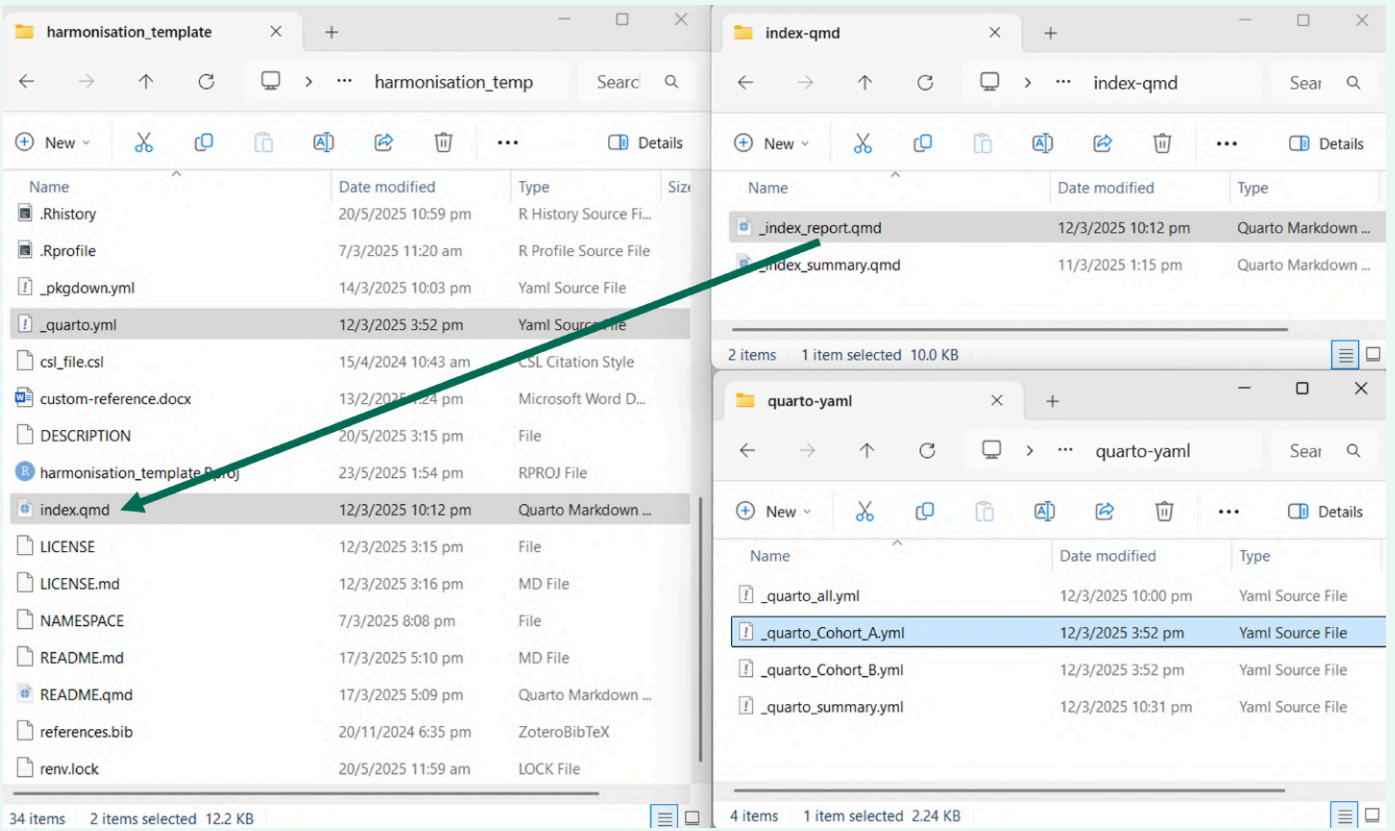
# Automated Technical Report (Reference)

Create an automated script to generate a technical report in pdf, word and html for each cohort

```r
# Copy the right index.qmd
# file

index_qmd_file <- paste0(
  "_index_",
  "report",
  ".qmd"
)

fs::file_copy(
  path = here::here(
    "templates",
    "index-qmd",
    index_qmd_file),
  new_path = here::here(
    "index.qmd"
  ),
  overwrite = TRUE
)
```



# Automated Technical Report (Reference)

Create an automated script to generate a technical report in pdf, word and html for each cohort

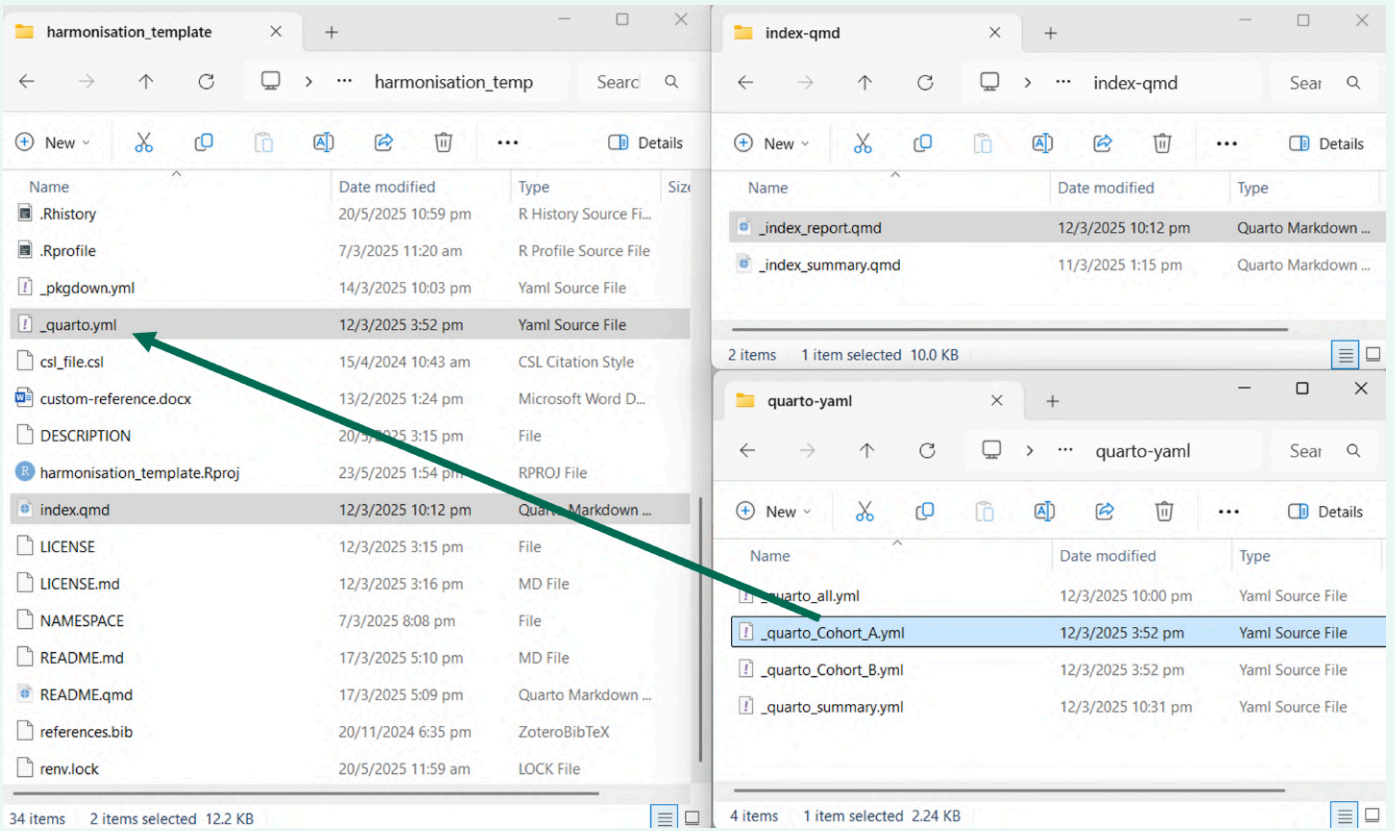
```r
copy_and_render <- function(
    cohort
) {

  # Copy quarto.yml file
  # for each cohort

  quarto_yml_file <- paste0(
    "_quarto_",
    cohort,
    ".yml"
  )

  fs::file_copy(
    path = here::here(
      "templates",
      "quarto-yaml",
      quarto_yml_file),
    new_path = here::here("_quarto.yml"),
    overwrite = TRUE
  )

  # Render each cohort
  quarto::quarto_render(
    as_job = FALSE
  )
```

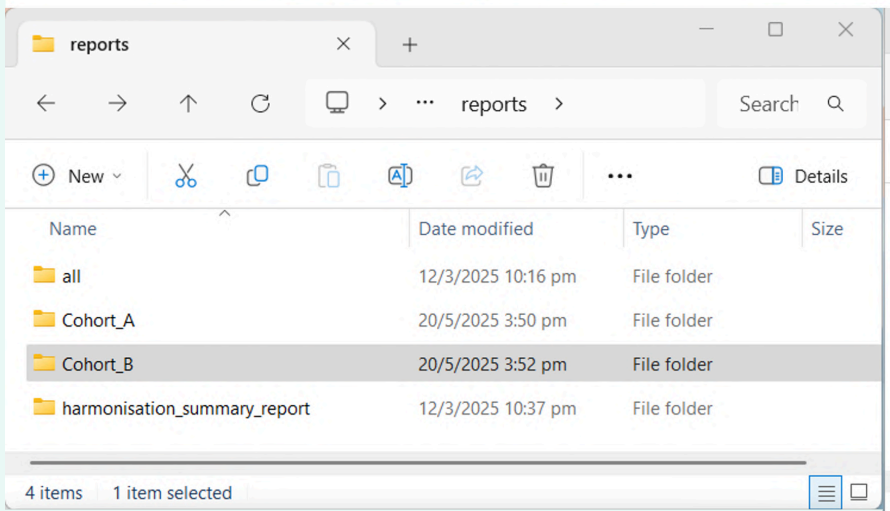


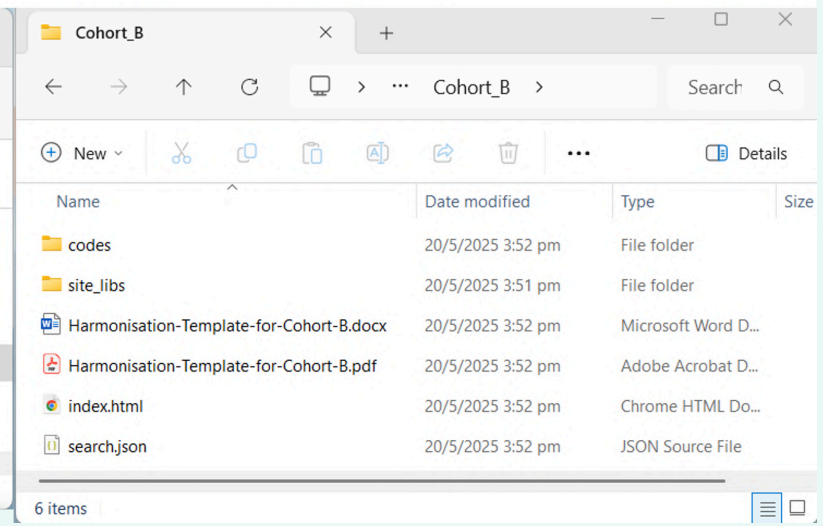
# Automated Technical Report (Reference)

Output of these reports are as follows:

Run the R script `cohort_harmonisation_script.R` in `codes` folder to generate:

- Cohort_A Harmonisation Report:
  - 🌐 HTML: https://jauntyjjs-harmonisation-cohort-a.netlify.app
  - 📕 PDF : https://jauntyjjs-harmonisation-cohort-a.netlify.app/Harmonisation-Template-for-Cohort-A.pdf
  - 📘 Word: https://jauntyjjs-harmonisation-cohort-a.netlify.app/Harmonisation-Template-for-Cohort-A.docx
- Cohort_B Harmonisation Report:
  - 🌐 HTML: https://jauntyjjs-harmonisation-cohort-b.netlify.app
  - 📕 PDF : https://jauntyjjs-harmonisation-cohort-b.netlify.app/Harmonisation-Template-for-Cohort-B.pdf
  - 📘 Word: https://jauntyjjs-harmonisation-cohort-b.netlify.app/Harmonisation-Template-for-Cohort-B.docx



# Automated Summary Report (How-to-Guide)

A similar method is done to create a summary report in word using `flextable`.

### 2.4 Smoking History

*smoke_current* is the harmonised data field to denote if the patient is a current smoker during the time of the CT scan. *smoke_past* is the harmonised data field to denote if the patient is a past smoker during the time of the CT scan.

They hold the following values:

*Table S6: Harmonised values of smoke_current and smoke_past.*

| Value | Description |
|---|---|
| 0 | no |
| 1 | yes |
| -1 | unknown |

They are harmonised as follows:

*Table S7: Harmonised process of smoke_current and smoke_past.*

| Cohort ID | Original Response | Harmonisation Response |
|---|---|---|
| Cohort A | Column *smoke_current_good* with<br><br>*0* as no.<br><br>*1* as yes.<br><br>*-1* as unknown.<br><br>Column *smoke_past_good* with<br><br>*0* as no.<br><br>*1* as yes.<br><br>*-1* as unknown. | *smoke_current* will take the values of *smoke_current_good*.<br><br>*smoke_past* will take the values of *smoke_past_good*. |
| Cohort B | Column *Smoke History* with<br><br>*non-smoker* as non-smoker.<br><br>*past smoker* as a past smoker.<br><br>*current smoker* as a current smoker.<br><br>*NA* as unknown. | Map the values of *Smoke History* to *smoke_current* as follows:<br><br>*non-smoker* and *past smoker* as 0.<br><br>*current smoker* as 1.<br><br>*NA* as -1.<br><br>Map the values of *Smoke History* to *smoke_past* as follows:<br><br>*non-smoker* and *current smoker* as 0.<br><br>*past smoker* as 1.<br><br>*NA* as -1. |

After harmonisation, we validate the values of *smoke_current* and *smoke_past* to ensure that there can only be the following cases:

*Table S8: Valid values of smoke_current and smoke_past.*

| Description | *smoke_current* | *smoke_past* |
|---|---|---|
| Non-smoker | 0 | 0 |
| Past smoker | 0 | 1 |
| Current smoker | 1 | 0 |
| Unknown | -1 | -1 |

# Data Variable Justfication Report (Explanation)

Initially we have `smoke_history` with values 0 (Non-smoker), 1 (Current smoker), 2 (Past smoker) and -1 (Unknown).

However, in the early stage of the study, some collaborators could only provide if the patient has a smoking history but could not specify if the patient is a current or past smoker.

| Patient | smoke_history | Problem |
|---|---|---|
| Non-smoker | 0 | No smoking history |
| Current smoker | 1 | Have smoking history |
| Past smoker | 2 | |
| Missing | -1 | Missing |

# Data Variable Justfication Report (Explanation)

To deal with this case, we have `smoke_history`, `smoke_current` and `smoke_past` to hold values 1 (Yes), 0 (No) and -1 (Unknown).

| Patient | smoke_history | smoke_current | smoke_past |
|---|---|---|---|
| Current smoker | 1 | 1 | 0 |
| Past smoker | 1 | 0 | 1 |
| Non-smoker | 0 | 0 | 0 |
| Have smoking history | 1 | -1 | -1 |
| Missing | -1 | -1 | -1 |

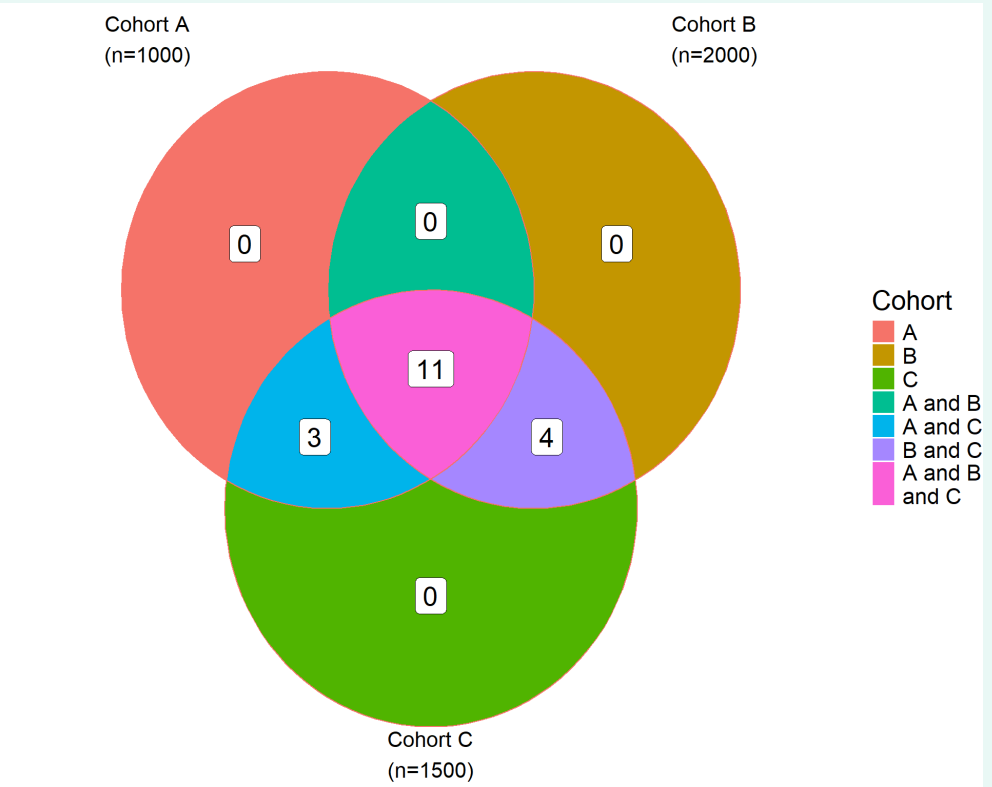
# Overview Diagrams

How many variables can each cohort provide ?

How many variables can be harmonised ?

```r
demographic_list <- list(
  A = c("Age", "Sex",
        "Hypertension", "Dyslipidemia", "Family Hx CAD", "Diabetes",
        "Smoke Current", "Smoke Past",
        "Have Chest Pain", "Chest Pain Character",
        "Dyspnea",
        "BMI", "Height", "Weight"),
  B = c("Age", "Sex",
        "Hypertension", "Dyslipidemia", "Family Hx CAD", "Diabetes",
        "Smoke Current", "Smoke Past",
        "Have Chest Pain", "Chest Pain Character",
        "Dyspnea",
        "HDL", "Total Cholesterol",
        "Triglyceride", "LDL"),
  C = c("Age", "Sex",
        "Hypertension", "Dyslipidemia", "Family Hx CAD", "Diabetes",
        "Smoke Current", "Smoke Past",
        "Have Chest Pain", "Chest Pain Character",
        "Dyspnea",
        "BMI", "Height", "Weight",
        "HDL", "Total Cholesterol",
        "Triglyceride", "LDL")
)

cohort_a_label_name <- "Cohort A\n(n=1000)"
cohort_b_label_name <- "Cohort B\n(n=2000)"
```

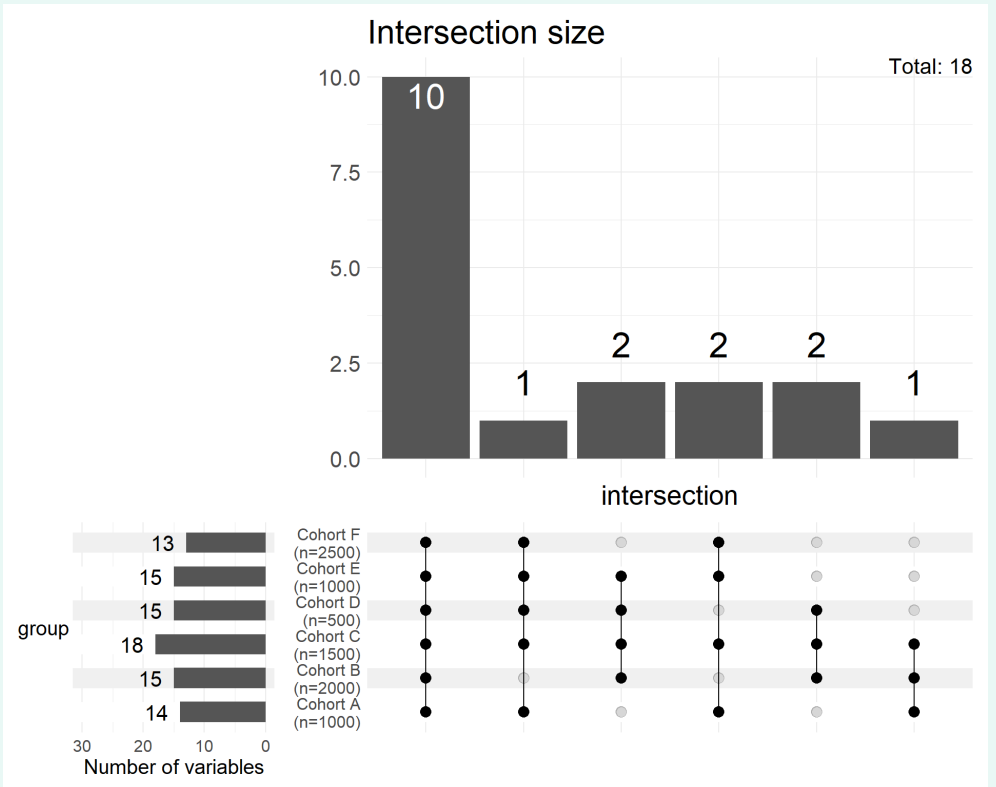



But it does not work for many (> 10) cohorts.

# Overview Diagrams

Upset plots are too complicated for clinicians.

```r
demographic_venn <- tibble::tibble(
  column_name = c("Age", "Sex",
                  "Hypertension", "Dyslipidemia", "Family Hx CAD", "Diabetes
                  "Smoke Current", "Smoke Past",
                  "Have Chest Pain", "Chest Pain Character",
                  "Dyspnea",
                  "BMI", "Height", "Weight",
                  "HDL", "Total Cholesterol",
                  "Triglyceride", "LDL"),
  `Cohort A` = c(1, 1,
                 1, 1, 1, 1,
                 1, 1,
                 1, 1,
                 1,
                 1, 1, 1,
                 0, 0,
                 0, 0),
  `Cohort B` = c(1, 1,
                 1, 1, 1, 1,
                 1, 1,
                 1, 1,
                 1,
                 0, 0, 0,
                 1, 1,
                 1, 1),
  `Cohort C` = c(1, 1,
```




Cannot answer follow-up questions:

How many cohorts provide patient's blood lipid information and how many patients have this information ?

# Overview Diagrams

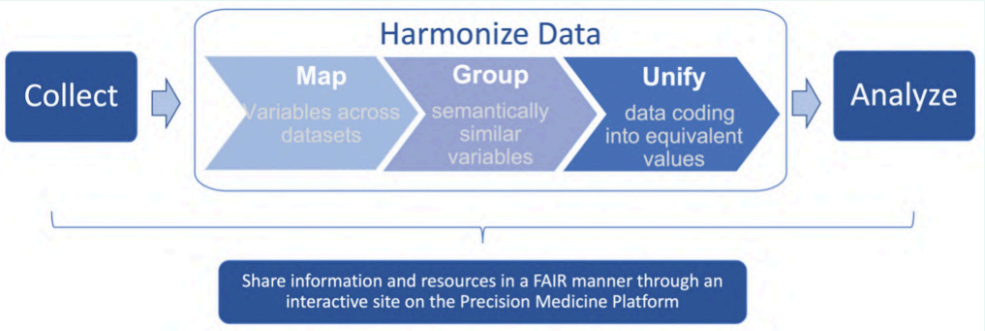
Create a “heatmap”using Microsoft PowerPoint.

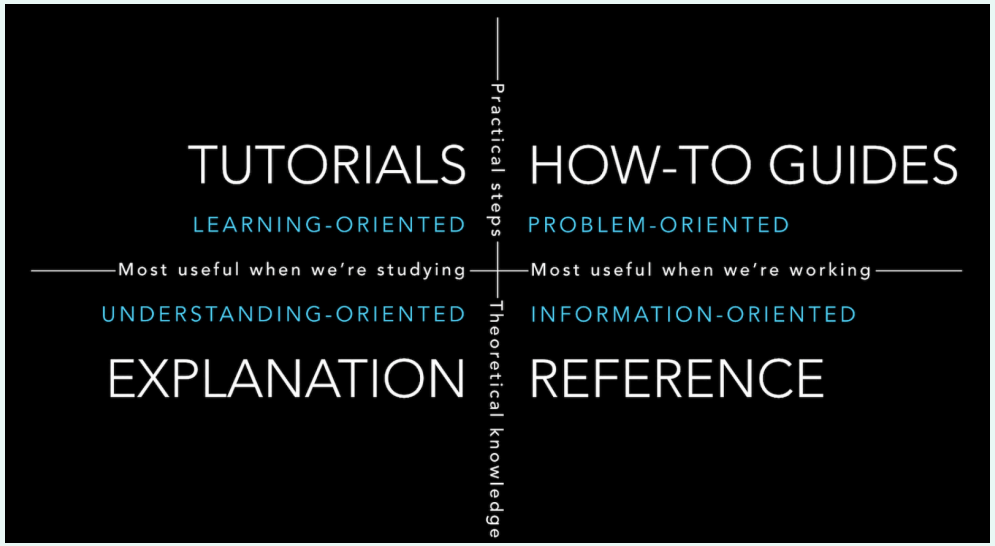
| Country | Cohort | N | Variables | Age<br>Sex<br>Hypertension<br>Dyslipidemia<br>Family Hx CAD<br>Diabetes<br>Smoke Current<br>Smoke Past<br>Have Chest Pain<br>Chest Pain Character | Dyspnea | BMI | Height<br>Weight | HDL<br>Total Cholesterol | Triglyceride<br>LDL |
|---|---|---|---|---|---|---|---|---|---|
| | | | | 10 | 1 | 1 | 2 | 2 | 2 |
| Country A | Cohort A | 1000 | 15 | ✓ | ✓ | ✓ | ✓ | × | × |
| | Cohort B | 2000 | 16 | ✓ | ✓ | × | × | ✓ | ✓ |
| Country B | Cohort C | 1500 | 18 | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Country C | Cohort D | 500 | 16 | ✓ | × | ✓ | × | ✓ | ✓ |
| Country D | Cohort E | 1000 | 16 | ✓ | × | ✓ | ✓ | ✓ | × |
| | Cohort F | 2500 | 14 | ✓ | × | ✓ | ✓ | | |
| **Total** | | | | **8500** | **4500** | **6500** | **6000** | **5000** | **4000** |

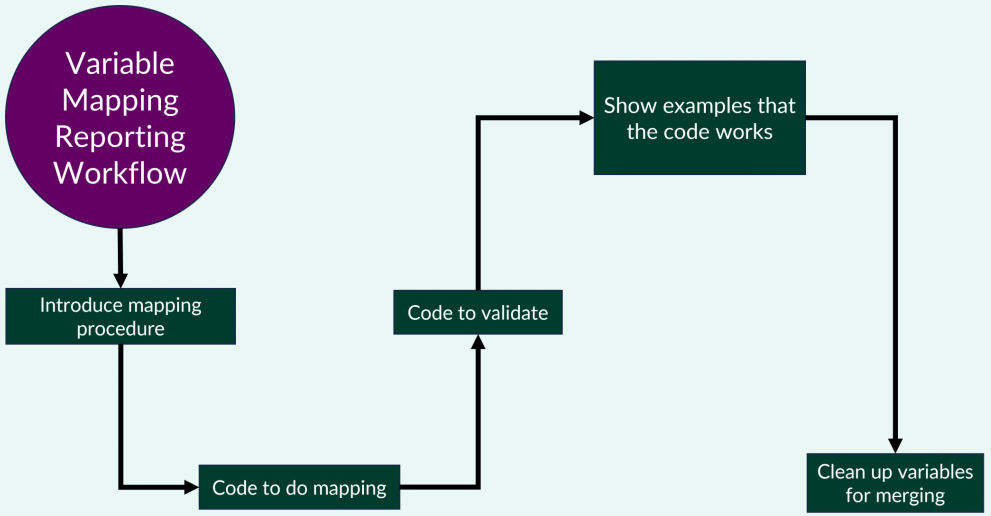
| Variable Colour Legend | |
|---|---|
| | Age |
| | Sex |
| | Comorbidity |
| | Smoking history |
| | Symptoms |
| | Obesity |
| | Blood lipid |

| Table Legend | |
|---|---|
| ✓ | Available |
| × | Not available |
| | Pending arrival |

# Summary




| | | | | 10 | | | 2 | 2 | 2 |
|---|---|---|---|---|---|---|---|---|---|
| | | | | Age | | | Height | HDL | Triglyceride |
| | | | | Sex | | | | | |
| | | | | Hypertension | | | | | |
| | | | | Dyslipidemia | | | | | |
| | | | | Family Hx CAD | | | | | |
| | | | | Diabetes | | | | | |
| | | | | Smoke Current | | | | | |
| | | | | Smoke Past | | | | | |
| | | | | Have Chest Pain | 1 | 1 | | | |
| **Country** | **Cohort** | **N** | **Variables** | Chest Pain Character | Dyspnea | BMI | Weight | Total Cholesterol | LDL |
| Country A | Cohort A | 1000 | 15 | ✓ | ✓ | ✓ | ✓ | × | × |
| | Cohort B | 2000 | 16 | ✓ | ✓ | × | × | ✓ | ✓ |
| Country B | Cohort C | 1500 | 18 | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| Country C | Cohort D | 500 | 16 | ✓ | × | ✓ | × | ✓ | ✓ |
| Country D | Cohort E | 1000 | 16 | ✓ | × | ✓ | ✓ | ✓ | × |
| | Cohort F | 2500 | 14 | ✓ | × | ✓ | ✓ | | |
| **Total** | | | | **8500** | **4500** | **6500** | **6000** | **5000** | **4000** |

| Variable Colour Legend | |
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| | Age |
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| Table Legend | |
|---|---|
| ✓ | Available |
| × | Not available |
| | Pending arrival |

# Thank you

Harmonisation project template on GitHub: https://github.com/JauntyJJS/harmonisation/

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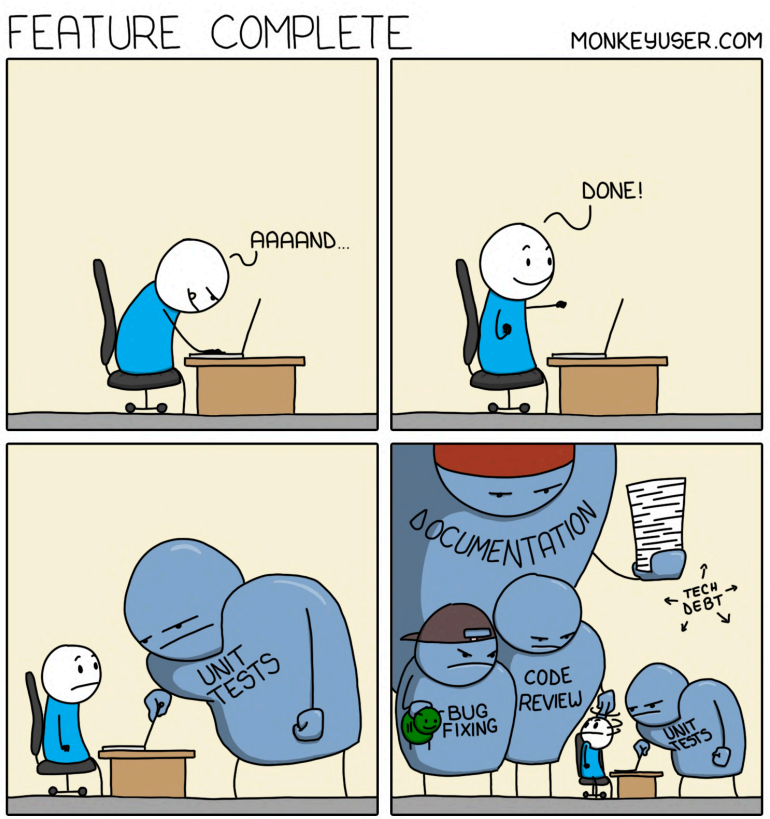
## Data Harmonisation Project Template

R-CMD-check.yaml passing

### Table of Content



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