

# Harmonisation Template for Cohort A

My Name

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# Preface

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

## Acknowledgement

Layout of this page is inspired from R package [rcompendium](#).

## File Structure

Here is the file structure of this project.

```
harmonisation_template/                                # Root of the compendium
|
|   harmonisation_template.Rproj                        # RStudio project file
|   |
|   |   .quarto/                                       # Intermediate files/folders
|   |   generated
|   |   |
|   |   |   documents.                                # Quarto renders to the
|   |   |   |
|   |   |   |   archive/                             # Folder to keep previous books
|   |   |   |   and harmonised data
|   |   |   |   |   reports/                         # Folder containing previous
|   |   |   |   |   |   documentation
|   |   |   |   |   |   |
|   |   |   |   |   |   |   # of data harmonisation
|   |   |   |   |   |   |   # Folder containing previous
|   |   |   |   |   |   |   GPS-CAD harmonised data
|   |   |   |   |   |   |   |
|   |   |   |   |   |   |   |   reports/            # Documentation of data
|   |   |   |   |   |   |   |   harmonisation
|   |   |   |   |   |   |   |   |
|   |   |   |   |   |   |   |   |   data-raw/       # Cohort raw data (.csv, .gpkg,
|   |   |   |   |   |   |   |   |   etc.)
|   |   |   |   |   |   |   |   |   {cohort name}/  # Folder containing cohort raw
|   |   |   |   |   |   |   |   |   data,
|   |   |   |   |   |   |   |   |   |
|   |   |   |   |   |   |   |   |   |   # and data dictionary
```

	data-dictionary/	# Data dictionary for harmonised
data		
	data-input/	# Data input file from
collaborators		
	docs/	# R functions documentation
generating using		
		# pkgdown:::build_site_external()
	inst/	# Arbitrary additional files to
include in the		
		# package.
	WORDLIST	# File generating by
spelling::update_wordlist()		
	man/	# R functions helps (automatically
updated)		
	{fun-demo}.Rd	# Documentation of the demo R
function		
	harmonisation-template.Rd	# High-level documentation
	quarto-yaml-template/	# Folder containing template files
for quarto book generation		
	_quarto_{cohort name}.yaml	# Quarto book generation for each
cohort		
	_quarto_all.yaml	# Quarto book generation for all
cohorts		
	R/	# R functions location
	{fun-demo}.R	# Example of an R function
	harmonisation-template-package.R	# Dummy R file for high-level
documentation		
	renv/	# Folder that contains all
packages		
		# installed in the renv
environment.		
	codes/	# R/Quarto scripts to run data
harmonisation		
	quarto_script.R	# R script to render each {cohort
name}_Cleaning/ folder.		
		# folder into html, pdf and word
document.		

<pre>       {cohort name}_Cleaning/ harmonisation      cohort.      Combine/ harmonised data   criteria,      preliminary analysis.       tests/ package testthat      .lintr   linter       .Rbuildignore ignored while        .renvignore ignored when        _pkgdown.yml documentation   pkgdown:::build_site_external()       _quarto.yml generation   file       custom-reference.docx harmonisation         DESCRIPTION       index.qmd       LICENSE generated via </pre>	<pre> # Quarto scripts to run data  # and output them for each  # Quarto scripts to filter  # based on inclusion/exclusion  # combined the filtered data for  # Test units file created by R  # Configuration for linting # R projects and packages using  # List of files/folders to be  # checking/installing the package  # List of files/folders to be  # renv is doing its snapshot  # Configuration for R package  # using  # Configuration for Quarto book  # Also the project configuration  # Microsoft word template for data  # documentation to Word  # Project metadata[*]  # Home page of Quarto book content  # Content of the MIT license </pre>
---	--

	# usethis::use_mit_license()
LICENSE.md	# Content of the MIT license
generated via	
	# usethis::use_mit_license()
NAMESPACE	# Automatically generated
README.md	# GitHub README (automatically
generated)	
README.Rmd	# GitHub README (ignore for now)
references.bib	# Bibtex file for Quarto book
references.qmd	# Reference document for Quarto
book	
renv.lock	# Metadata of R packages installed
generated	
	# using renv::snapshot
csl_file.csl	# Citation Style Language (CSL)
file to ensure	
	# citations follows the Lancet
journal	

[\*] These files are automatically created but user needs to manually add some information.

## Installation

### Installing R

Go to <https://cran.rstudio.com/>. Choose a version of R that matches the computer's operating system.

### Installing RStudio

Go to <https://posit.co/download/rstudio-desktop/>. Scroll down and choose a version of RStudio that matches the computer's operating system.



## Installing Rtools

Go to <https://cran.r-project.org/bin/windows/Rtools/>. Choose a version of Rtools that matches the R version that was installed.

## Quarto

Quarto converts R scripts into a technical report or notebook in html, pdf, Microsoft Word, *etc.* It is installed together with RStudio. User can also go to <https://quarto.org/docs/get-started/> to install it separately. For Quarto to be able to create pdf files, a [pdf engine](#) must be installed as well. For ease, it is suggested to install [TinyTex](#) using the terminal command `quarto install tinytex`.

## R Package Installation

Use Posit Public Package Manager [PPM](#) to set up your repository environment to install R packages from [CRAN](#). This is because PPM allows installation of frozen R package versions based on a snapshot date.

One way to do that is to set in the `.Rprofile` file with the code `options(repos = c(P3M = "{link to repository url form Posit Public Package Manager}"))`

R packages can be installed using the package [pak](#) as an alternative to `install.packages()` and `remotes::install_github()` ([https://remotes.r-lib.org/reference/install\\_github.html](https://remotes.r-lib.org/reference/install_github.html)). [Benefits of using \[pak\]](#) can be found [here](#)

You can also view your repository environment using the command `pak::repo_get()`

R package can be loaded using the command `library({package_name})`. You can use the R package [annotater](#) to add additional information on what the loaded package does.

## Using renv

You can increase reproducibility by using the package [renv](#). Install `renv` from CRAN with `pak::pak("renv")`. If this is your first time using `renv`, start with the [Introduction to renv vignette](#). Use `renv::init(bare = TRUE)` to start with an empty `renv` environment.

`renv` will freeze the exact package versions you depend on (in `renv.lock`). This ensures that each collaborator (or you in the future) will use the exact same versions of these packages. Moreover `renv` provides to each project its own private package library making each project isolated from others.

Install required dependencies locally with `install.packages()` or `renv::install()` from CRAN, Bioconductor, Github, explicit file path, etc.

Sometimes the right `downloader` (libcurl or others) needs to be set for installation of R packages inside the `renv` environment to be successful. Setting the R environmental variable `RENV_DOWNLOAD_FILE_METHOD = "libcurl"` may help.

Save the local environment with `renv::snapshot()` to create the `renv.lock` file.

## R Functions Management

R functions heavily used in this project can be found in the `R` folder. Documentation (`man` folder), test units (`test` folder) corresponding to these functions are structured the same as creating an R package. Relevant R packages required for R package development (and available on Posit Public Package Manager [PPM](#)) are

```
library("usethis")
library("devtools")
library("roxygen2")
library("testthat")
library("covr")
library("spelling")
library("lintr")
library("sinew")
library("pkgdown")
```

Here is an example of the command to use `pak::pak("{package name}")` to install packages from [PPM](#).

There is no need to source the functions in the `R` folder. Use `devtools::load_all()` instead. `devtools::load_all()` will load required dependencies listed in `DESCRIPTION` and R functions stored in `R/`. Prior installation of these dependencies is required for the load to be successful.

After loading, R functions can be documented (using `devtools::document()`), tested (using `devtools::test()` and then `devtools::check()`) and even installed as an R package (using `devtools::install`).

More information of this workflow can be found in [Chapter 1: The Whole Game](#) of the R Packages (2e) book.

## R Packages

R packages installed from Posit Public Package Manager [PPM](#) using command `pak::pak("{package name}")` are

```
library("renv")
library("sessioninfo")
library("knitr")
library("rmarkdown")
library("quarto")
library("rlang")
library("cli")

library("fs")
library("here")
library("fst")
library("readxl")
library("vroom")

library("dplyr")
library("tidyr")
library("magrittr")
library("stringr")
library("forcats")
library("purrr")
library("lubridate")
library("tibble")
library("glue")

library("collateral")
library("pointblank")
library("testthat")

library("htmltools")
library("htmlwidgets")
library("fontawesome")
library("reactable")
library("flextable")

library("openxlsx")

library("harmonisation")
```

Here are all the R packages used in this analysis.

```
harmonisation::get_r_package_info() |>
  knitr::kable()
```

package	version	date	source
cli	3.6.4	2025-02-13	RSPM
collateral	0.5.2	2021-10-25	RSPM
covr	3.6.4	2023-11-09	RSPM
devtools	2.4.5	2022-10-11	RSPM
dplyr	1.1.4	2023-11-17	RSPM
flextable	0.9.7	2024-10-27	RSPM
fontawesome	0.5.3	2024-11-16	RSPM
forcats	1.0.0	2023-01-29	RSPM
fs	1.6.5	2024-10-30	RSPM
fst	0.9.8	2022-02-08	RSPM
glue	1.8.0	2024-09-30	RSPM
harmonisation	0.0.0.9999	2025-03-09	local
here	1.0.1	2020-12-13	RSPM
htmltools	0.5.8.1	2024-04-04	RSPM
htmlwidgets	1.6.4	2023-12-06	RSPM
knitr	1.49	2024-11-08	RSPM
lintr	3.2.0	2025-02-12	RSPM
lubridate	1.9.4	2024-12-08	RSPM
magrittr	2.0.3	2022-03-30	RSPM
openxlsx	4.2.8	2025-01-25	RSPM
pkgdown	2.1.1	2024-09-17	RSPM
pointblank	0.12.2	2024-10-23	RSPM
purrr	1.0.4	2025-02-05	RSPM
quarto	1.4.4	2024-07-20	RSPM
reactable	0.4.4	2023-03-12	RSPM
readxl	1.4.4	2025-02-27	RSPM
renv	1.1.0	2025-01-29	RSPM (R 4.4.0)
rlang	1.1.5	2025-01-17	RSPM
rmarkdown	2.29	2024-11-04	RSPM
roxygen2	7.3.2	2024-06-28	RSPM
sessioninfo	1.2.2	2021-12-06	CRAN (R 4.4.2)
sinew	0.4.0	2022-03-31	RSPM
spelling	2.3.1	2024-10-04	RSPM
stringr	1.5.1	2023-11-14	RSPM
testthat	3.2.3	2025-01-13	RSPM
tibble	3.2.1	2023-03-20	RSPM
tidyr	1.3.1	2024-01-24	RSPM
usethis	3.1.0	2024-11-26	RSPM
vroom	1.6.5	2023-12-05	RSPM

## R Platform Information

Here are the R platform environment used in this analysis.

```
harmonisation::get_r_platform_info() |>  
  knitr::kable()
```

setting	value
version	R version 4.4.2 (2024-10-31 ucrt)
os	Windows 11 x64 (build 26100)
system	x86_64, mingw32
ui	RTerm
language	(EN)
collate	English_Singapore.utf8
ctype	English_Singapore.utf8
tz	Asia/Singapore
date	2025-03-12
pandoc	3.2 @ C:/Program Files/RStudio/resources/app/bin/quarto/bin/tools/ (via rmarkdown)
quarto	1.6.37 @ C:/Program Files/Quarto/bin/quarto.exe/ (via quarto)
knitr	1.49 from RSPM

## DESCRIPTION

The DESCRIPTION file contains important compendium metadata. Though DESCRIPTION file is specific to R package, it can be used to work with research compendia (see below). For further information on how to edit this file, please read <https://r-pkgs.org/description.html>.

## Data Harmonisation

To start the harmonisation of data, run the R script `quarto_script.R` in `reports` folder.

For each cohort, the script will clean the raw data and create a Quarto book for each cohort in html, word and pdf.

This involves copying a specific yaml file (`_quarto_{cohort name}.yaml`) from the `quarto-yaml-template` folder to the project folder `harmonisation_template` and rename it as `_quarto.yaml`, overwriting any existing `_quarto.yaml` file. Using the `_quarto.yaml` file. Quarto will then start running the Quarto scripts in the `reports/{cohort_name}_Cleaning` folder. This involves reading the raw data in the `data-raw/{cohort_name}` folder, placing preprocessing data in the

reports/{cohort\_name}\_Cleaning/preprocessed\_data folder, outputting the harmonised data as excel file called `cleaned_{cohort_name}.xlsx` in the `reports` folder. Also, the data harmonisation process documentation will be created in the `books/{cohort_name}` folder as a Quarto book in html, word and pdf.

After data harmonisation, data combining for all cohorts, data filtering and preliminary analysis will be done by copying `_quarto_Prelim.yml` file from the `quarto-yaml-template` folder to the project folder `harmonisation_template` and rename it as `_quarto.yml`, overwriting any existing `_quarto.yml` file. Using the `_quarto.yml` file, Quarto runs the Quarto scripts in the `reports/Combine` folder. Results will be outputted as excel files called `harmonised.xlsx`, `harmonised_batch1.xlsx`, `harmonised_batch2.xlsx` in the `reports` folder. In addition, the preliminary results will be created in the `books/Prelim` folder as a Quarto book in html, word and pdf.

After doing this for each cohort, the script will then create a combined data harmonisation process documentation (for all the cohorts) as a Quarto book in html. The specific `yml` file (`_quarto_all.yml`) in the `quarto-yaml-template` folder will be used and the documentation will be created in the `books/all` folder. Data combining for all cohorts, data filtering and preliminary analysis will also be done by running Quarto scripts in the `reports/Combine` folder.

## General Recommendations

- Ensure the workspace is always in a blank state. Use `usethis::use_blank_slate(scope = c("user", "project"))` to create this setting.
- Keep the root of the project as clean as possible
- Store your raw data in `data-raw`
- Document raw data modifications. See `Flowchart.xlsx`.
- Export modified raw data in `reports/{cohort_name}_Cleaning/preprocessed_data`
- Store only **R functions** in `R/`
- Store only **R scripts** and/or **qmd** in `reports/{cohort_name}_Cleaning`
- Built relative paths using `here::here()`
- Call external functions as `{package_name}::{function()}`
- Use `devtools::document()` to update the `NAMESPACE`
- Use `rcompendium::add_dependencies` to update the list of required dependencies in `DESCRIPTION`
- Do not source your functions but use instead `devtools::load_all()`. `devtools::load_all()` will load required dependencies listed in `DESCRIPTION` and R functions stored in `R/`

**Part I**

**Cohort A Cleaning**

# 1 R Package And Environment

## 1.1 R Packages Used

Here are the R packages used in this analysis.

```
harmonisation::get_r_package_info() |>  
  knitr::kable()
```

package	version	date	source
dplyr	1.1.4	2023-11-17	RSPM
fontawesome	0.5.3	2024-11-16	RSPM
forcats	1.0.0	2023-01-29	RSPM
glue	1.8.0	2024-09-30	RSPM
harmonisation	0.0.0.9999	2025-03-09	local
here	1.0.1	2020-12-13	RSPM
htmltools	0.5.8.1	2024-04-04	RSPM
magrittr	2.0.3	2022-03-30	RSPM
openxlsx	4.2.8	2025-01-25	RSPM
pointblank	0.12.2	2024-10-23	RSPM
purrr	1.0.4	2025-02-05	RSPM
quarto	1.4.4	2024-07-20	RSPM
reactable	0.4.4	2023-03-12	RSPM
readxl	1.4.4	2025-02-27	RSPM
sessioninfo	1.2.2	2021-12-06	CRAN (R 4.4.2)
stringr	1.5.1	2023-11-14	RSPM
testthat	3.2.3	2025-01-13	RSPM
tibble	3.2.1	2023-03-20	RSPM
tidyr	1.3.1	2024-01-24	RSPM

## 1.2 R Platform Information

Here are the R platform environment used in this analysis.



```
harmonisation::get_r_platform_info() |>
  knitr::kable()
```

setting	value
version	R version 4.4.2 (2024-10-31 ucrt)
os	Windows 11 x64 (build 26100)
system	x86_64, mingw32
ui	RTerm
language	(EN)
collate	English_Singapore.utf8
ctype	English_Singapore.utf8
tz	Asia/Singapore
date	2025-03-12
pandoc	3.2 @ C:/Program Files/RStudio/resources/app/bin/quarto/bin/tools/ (via rmarkdown)
quarto	1.6.37 @ C:/Program Files/Quarto/bin/quarto.exe/ (via quarto)
knitr	1.49 from RSPM

## 1.3 Data dictionary

Check to see if the data dictionary 20250310\_data\_dictionary.xlsx exists.

```
dict_relative_path <- fs::path(
  "data-raw",
  "data_dictionary",
  params$data_dictionary
)

dict_path <- here::here(dict_relative_path)

if (!file.exists(dict_path)) {
  stop(glue::glue("Input data dictionary {dict_path} cannot be found"))
}
```

## 2 Read Cohort A Data

### 2.1 Read Data

We read the data and have the following warnings

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

This warning occurs because we expect the second column **Age** to be numeric but there exists some text columns.

Suppose we ask the collaborator to fix the age column and the collaborator returns a new file. To ensure that there are no messages, we can use `testthat::expect_no_condition`.

Here is an example when it gives an error with the old file

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

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

We can read the new file in the following way. However, this method means that you will need to read the file twice.

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

To read the file only once, we can use the tee pipe operator `%T>%`.

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

## 2.2 Check for unique patient id

We can use `pointblank::rows_distinct` to check if the column Serial Number has unique values.

```

cohort_A_data <- readxl::read_excel(
  path = here::here("data-raw",
                    "Cohort_A",
                    "data_to_harmonise_age_issue_fixed.xlsx"),
  sheet = "Sheet1",
  col_types = c(
    "text", "numeric"
  )
) %T>%
testthat::expect_no_condition() |>
dplyr::rename(cohort_unique_id = "Serial Number") |>
# Remove rows when the ID value is NA
dplyr::filter(!is.na(.data[["cohort_unique_id"]])) |>
dplyr::mutate(
  cohort_unique_id = as.character(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",
)

```

## 2.3 Clean Weight columns

Sometimes the collaborator will not give you a new file and will only respond with an email acknowledging that it is an error.

You will need to edit the values yourself. It is best not to edit the file as you may forget to make the manual change if the collaborator gives you a new version a few months later with the same error.

It is also advised to record such changes before data harmonisation.

We read the data with the some issues with the weight.

```

cohort_A_data <- readxl::read_excel(
  path = here::here("data-raw",
                    "Cohort_A",
                    "data_to_harmonise.xlsx"),
  sheet = "Sheet1",
  col_types = c(
    "text", # unique id
    "numeric", "text", # age and sex
    "numeric", "numeric", # height and weight
  )
)

```

```

    "numeric", "numeric", "numeric", "numeric", # smoking history
    "numeric", "numeric" # symptoms
  )
) %T>%
testthat::expect_no_condition() |>
dplyr::rename(cohort_unique_id = "Serial Number") |>
# Remove rows when the ID value is NA
dplyr::filter(!is.na(.data[["cohort_unique_id"]])) |>
dplyr::mutate(
  cohort_unique_id = as.character(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",
)

```

## 2.4 Update Weight

Here are the following patient's height that needs to be updated.

- A018 has a weight of 215.4kg. Value is changed to 90 kg.

```

weight_data <- cohort_A_data |>
dplyr::select(c("cohort_unique_id", "weight")) |>
# Check if these patient IDs are present
pointblank::col_vals_make_subset(
  columns = c("cohort_unique_id"),
  set = c("A018")
) |>
dplyr::mutate(
  updated_weight = dplyr::case_when(
    .data[["cohort_unique_id"]] == "A018" & .data[["weight"]] == 215.4 ~
↪ 90.1,
    .default = .data[["weight"]]
  ),
)

```

Remove unnecessary columns so that we can merge with the other fields.

```

weight_data <- weight_data |>
dplyr::select(-c("weight"))

```

## 2.5 Merge updated weight

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

cohort_A_data <- cohort_A_data |>
  dplyr::left_join(weight_data,
                    by = join_specification,
                    unmatched = "error",
                    relationship = "one-to-one") |>
  dplyr::mutate(
    `weight` = .data[["updated_weight"]]
  ) |>
  dplyr::select(-c("updated_weight"))
```

## 2.6 Check corrections

We check if the corrections are made based on the collaborator request. Changes are made manually on the excel file as the collaborator is no longer providing newer version of the data.

- weight changed from 215.4kg to 90.1kg for patient A018

```
cohort_A_data |>
  # Check if these patient IDs are present
  pointblank::expect_col_vals_make_subset(
    columns = c("cohort_unique_id"),
    set = c("A018")
  ) |>
  pointblank::expect_col_vals_expr(
    expr = pointblank::expr(
      dplyr::case_when(
        .data[["cohort_unique_id"]] %in% "A018" ~
          isTRUE(all.equal(
            target = 90.1,
            current =
              ↪ cohort_A_data[["weight"]][which(cohort_A_data[["cohort_unique_id"]]
              ↪ == "A018")],
            tolerance = 0.0001)
          ))
    )
  )
```

## 2.7 Write Preprocessed File

We output data to be used for the next session.

```
cohort_A_data |>
  fst::write_fst(
    path = here::here(params$analysis_folder,
                      params$harmonisation_folder,
                      params$preprocessing_folder,
                      "01_Cohort_A_cleaned.fst")
  )
```

## 3 Extract Demographic

### 3.1 Read Preprocessed File

We read output data from the previous section.

### 3.2 Check for integer vector

We have a function that checks if the numeric vector has integers.

```
non_integer_data <- data.frame(  
  non_integer_col = c(-1, 0, NA, 2.0000,  
                     3.010, pi, exp(1)  
)  
)  
  
non_integer_data |>  
  pointblank::col_vals_expr(  
    expr = ~ harmonisation::is_integer_vector(  
      input_vector = non_integer_data[["non_integer_col"]],  
      allow_na = TRUE)  
  )
```

```
Error: The `col_vals_expr()` validation failed beyond the absolute  
threshold level (1).  
* failure level (3) >= failure threshold (1)
```

### 3.3 Demographics and Behavioral parameters

#### 3.3.1 Age and Sex

`age_years` will be mapped from the column `age`. `age` value of 0 is set as missing.

`sex` is grouped as follows:



sex before	sex
F	0
M	1

```
age_gender_data <- cohort_A_data |>
  dplyr::select(c("cohort_unique_id",
                 "age",
                 "sex")) |>
  pointblank::col_vals_expr(
    expr = ~ harmonisation::is_integer_vector(
      cohort_A_data[["age"]],
      allow_na = TRUE)
  ) |>
  dplyr::mutate(
    # Convert age to type integer
    age_years = as.integer(.data[["age"]]),
    # Convert age of 0 to NA
    age_years = dplyr::case_when(
      .data[["age_years"]] == 0 ~ NA_integer_,
      .default = .data[["age_years"]]
    ),
    sex_before = .data[["sex"]],
    # Convert categorical columns to factors
    sex = dplyr::case_when(
      .data[["sex_before"]] == "F" ~ "0",
      .data[["sex_before"]] == "M" ~ "1",
      .default = as.character(.data[["sex_before"]])
    ),
    `sex_before` = forcats::fct_relevel(
      .data[["sex_before"]],
      c("F", "M")
    ),
    sex = forcats::fct_relevel(
      .data[["sex"]],
      c("0", "1")),
  ) |>
  dplyr::relocate(
    "sex",
    .before = "sex_before"
  ) |>
  pointblank::col_vals_in_set(
    columns = "sex",
    set = c("0", "1")
  ) |>
  pointblank::col_vals_between(
```

```

    columns = "age_years",
    left = 0,
    right = 100,
    inclusive = c(FALSE, TRUE),
    na_pass = TRUE
  )

```

Remove unnecessary columns so that we can merge with the other fields.

```

age_gender_data <- age_gender_data |>
  dplyr::select(-c("age", "sex_before"))

```

### 3.3.2 Height, Weight, BMI and BSA

`height_cm` will be mapped from the column `height`. `weight_kg` will be mapped from the column `weight`.

`bsa_m2` in  $m^2$  will be calculated as  $\sqrt{(\text{Height(cm)} \times \text{Weight(kg)})/3600}$  `bmi` will be calculated as  $\text{Weight(kg)} / ((\text{Height(m)})^2)$

All values are then converted to two decimal places.

To date, only patient A010 has a bmi greater than 50.

```

body_measurement_data <- cohort_A_data |>
  dplyr::select(c("cohort_unique_id",
                  "weight", "height")) |>
  dplyr::mutate(
    height_cm = .data[["height"]],
    weight_kg = .data[["weight"]],
    bsa_m2 = sqrt((.data[["height_cm"]] * .data[["weight_kg"]]) / 3600),
    bsa_m2 = harmonisation::round_to_nearest_digit(.data[["bsa_m2"]],
      ↪ digits = 2),
    bmi = .data[["weight_kg"]] / ((.data[["height_cm"]] / 100)^2),
    bmi = harmonisation::round_to_nearest_digit(.data[["bmi"]], digits =
      ↪ 2),
    height_cm = harmonisation::round_to_nearest_digit(.data[["height_cm"]],
      ↪ digits = 2),
    weight_kg = harmonisation::round_to_nearest_digit(.data[["weight_kg"]],
      ↪ digits = 2)
  ) |>
  pointblank::col_vals_gt(
    columns = "bmi",
    preconditions = ~ . %>%
      dplyr::filter(

```

```

      .data[["cohort_unique_id"]] %in% c("A010")
    ),
    value = 50,
    na_pass = TRUE
  ) |>
pointblank::col_vals_between(
  columns = "bmi",
  preconditions = ~ . %>%
    dplyr::filter(
      !.data[["cohort_unique_id"]] %in% c("A010")
    ),
  left = 15,
  right = 50,
  inclusive = c(TRUE, TRUE),
  na_pass = TRUE
)

```

Remove unnecessary columns so that we can merge with the other fields.

```

body_measurement_data <- body_measurement_data |>
  dplyr::select(-c("height", "weight"))

```

### 3.3.3 Smoking History

`smoke_current` will be mapped from the column `smoke_current_good`. `smoke_past` will be mapped from the column `smoke_past_good`.

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

```

smoking_data <- cohort_A_data |>
  dplyr::select(c("cohort_unique_id",
                  "smoke_current_good", "smoke_past_good")) |>
  dplyr::mutate(
    smoke_current = as.character(.data[["smoke_current_good"]]),
    smoke_current_good = forcats::fct_relevel(
      as.character(.data[["smoke_current_good"]]),
      c("0", "1")),
    smoke_current = forcats::fct_relevel(
      .data[["smoke_current"]],

```

```

      c("0", "1")),
    smoke_past = as.character(.data[["smoke_past_good"]]),
    smoke_past_good = forcats::fct_relevel(
      as.character(.data[["smoke_past_good"]]),
      c("0", "1")),
    smoke_past = forcats::fct_relevel(
      .data[["smoke_past"]],
      c("0", "1")),
  ) |>
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",
↪ "1"))
  )
)

```

Remove unnecessary columns so that we can merge with the other fields.

```

smoking_data <- smoking_data |>
dplyr::select(-c("smoke_current_good", "smoke_past_good"))

```

Here is a case when the validation has failed.

```

smoking_data_bad <- cohort_A_data |>
dplyr::select(c("cohort_unique_id",
                "smoke_current_bad", "smoke_past_bad")) |>
dplyr::filter(
  .data[["cohort_unique_id"]] %in% c("A010", "A016")
) |>
dplyr::mutate(
  smoke_current = as.character(.data[["smoke_current_bad"]]),
  smoke_past = as.character(.data[["smoke_past_bad"]]),
)

smoking_data_bad |>
pointblank::col_vals_in_set(
  columns = c("smoke_current", "smoke_past"),
  set = c("0", "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",
↵ "1"))
  )
)

```

Error: The `col\_vals\_expr()` validation failed beyond the absolute threshold level (1).  
 \* failure level (2) >= failure threshold (1)

### 3.3.4 Chest Pain

#### 3.3.4.1 Shortness of Breath

have\_sob values remained unchanged.

```

shortness_of_breath_data <- cohort_A_data |>
dplyr::select(c("cohort_unique_id", "have_sob")) |>
dplyr::mutate(
  have_sob = forcats::fct_relevel(
    as.character(.data[["have_sob"]]),
    c("0", "1"))
) |>
pointblank::col_vals_in_set(
  columns = c("have_sob"),
  set = c("0", "1", "-1")
)

```

#### 3.3.4.2 Have chest pain or not

have\_chest\_pain is grouped as follows:

chest_pain_type	have_chest_pain
0	0
1, 2 or 3	1

```

have_chest_pain_data <- cohort_A_data |>
  dplyr::select(c("cohort_unique_id", "chest_pain_type")) |>
  dplyr::mutate(
    have_chest_pain = dplyr::case_when(
      .data[["chest_pain_type"]] %in% c(0) ~ "0",
      .data[["chest_pain_type"]] %in% c(1, 2, 3) ~ "1",
      .default = NA_character_
    ),
    have_chest_pain = forcats::fct_relevel(
      .data[["have_chest_pain"]],
      c("0", "1")
    ),
    chest_pain_type = forcats::fct_relevel(
      as.character(.data[["chest_pain_type"]]),
      c("0", "1", "2", "3", "4", "-1")
    )
  ) |>
  pointblank::col_vals_in_set(
    columns = c("have_chest_pain"),
    set = c("0", "1")
  )

```

Remove unnecessary columns so that we can merge with the other fields.

```

have_chest_pain_data <- have_chest_pain_data |>
  dplyr::select(-c("chest_pain_type"))

```

### 3.3.4.3 Symptomatic or Asymptomatic

symptoms is grouped as follows:

have_sob	have_chest_pain	symptoms
-1	-1	-1
0	0	0
0 or 1	1	1
1	0	2

```

symptoms_data <- cohort_A_data |>
  dplyr::select(c("cohort_unique_id")) |>
  dplyr::left_join(shortness_of_breath_data,
    by = dplyr::join_by("cohort_unique_id"),
    unmatched = "error",
  )

```

```

        relationship = "one-to-one") |>
dplyr::left_join(have_chest_pain_data,
                 by = dplyr::join_by("cohort_unique_id"),
                 unmatched = "error",
                 relationship = "one-to-one") |>
dplyr::mutate(
  symptoms = dplyr::case_when(
    (.data[["have_chest_pain"]] == "-1" &
     .data[["have_sob"]] == "-1"
    ) ~ "-1",
    (.data[["have_chest_pain"]] == "0" &
     .data[["have_sob"]] == "0"
    ) ~ "0",
    (.data[["have_chest_pain"]] == "1" &
     .data[["have_sob"]] %in% c("0", "1")
    ) ~ "1",
    (.data[["have_chest_pain"]] == "0" &
     .data[["have_sob"]] == "1"
    ) ~ "2",
    .default = NA_character_
  ),
  symptoms = forcats::fct_relevel(
    .data[["symptoms"]],
    c("0", "1", "2"))
) |>
pointblank::col_vals_in_set(
  columns = c("symptoms"),
  set = c("0", "1", "2")
)

```

Remove unnecessary columns so that we can merge with the other fields.

```

symptoms_data <- symptoms_data |>
dplyr::select(-c("have_chest_pain", "have_sob"))

```

### 3.3.4.4 Chest Pain Type

chest\_pain\_type is grouped as follows:

have_sob	chest_pain_type before	chest_pain_type
-1	-1	-1
0	0	0
0 or 1	1	1

have_sob	chest_pain_type before	chest_pain_type
0 or 1	2	2
0 or 1	3	2
1	0	4

```

chest_pain_type_data <- cohort_A_data |>
  dplyr::select(c("cohort_unique_id", "chest_pain_type")) |>
  dplyr::left_join(shortness_of_breath_data,
    by = dplyr::join_by("cohort_unique_id"),
    unmatched = "error",
    relationship = "one-to-one") |>
  dplyr::mutate(
    chest_pain_type_before = .data[["chest_pain_type"]],
    chest_pain_type = dplyr::case_when(
      (.data[["chest_pain_type_before"]] == "-1" &
        .data[["have_sob"]] == "-1"
      ) ~ "-1",
      (.data[["chest_pain_type_before"]] == "0" &
        .data[["have_sob"]] == "0"
      ) ~ "0",
      (.data[["chest_pain_type_before"]] == "1" &
        .data[["have_sob"]] %in% c("0", "1")
      ) ~ "1",
      (.data[["chest_pain_type_before"]] == "2" &
        .data[["have_sob"]] %in% c("0", "1")
      ) ~ "2",
      (.data[["chest_pain_type_before"]] == "3" &
        .data[["have_sob"]] %in% c("0", "1")
      ) ~ "3",
      (.data[["chest_pain_type_before"]] == "0" &
        .data[["have_sob"]] == "1"
      ) ~ "4",
      .default = NA_character_
    ),
    chest_pain_type_before = forcats::fct_relevel(
      as.character(.data[["chest_pain_type_before"]]),
      c("0", "1", "2", "3")),
    chest_pain_type = forcats::fct_relevel(
      .data[["chest_pain_type"]],
      c("0", "1", "2", "3"))
  ) |>
  dplyr::relocate(
    "chest_pain_type_before",
    .before = "cohort_unique_id"
  ) |>

```



```
pointblank::col_vals_in_set(
  columns = c("chest_pain_type"),
  set = c("0", "1", "2", "3", "4")
)
```

Remove unnecessary columns so that we can merge with the other fields.

```
chest_pain_type_data <- chest_pain_type_data |>
  dplyr::select(-c("have_sob", "chest_pain_type_before"))
```

### 3.3.4.5 Combined chest pain related tables

We combine all chest related tables together

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

chest_pain_data <- cohort_A_data |>
  dplyr::select(c("cohort_unique_id")) |>
  dplyr::left_join(have_chest_pain_data,
    by = join_specification,
    unmatched = "error",
    relationship = "one-to-one") |>
  dplyr::left_join(chest_pain_type_data,
    by = join_specification,
    unmatched = "error",
    relationship = "one-to-one") |>
  dplyr::left_join(shortness_of_breath_data,
    by = join_specification,
    unmatched = "error",
    relationship = "one-to-one") |>
  dplyr::left_join(symptoms_data,
    by = join_specification,
    unmatched = "error",
    relationship = "one-to-one")

testthat::expect_true(
  pointblank::has_columns(
    chest_pain_data,
    columns = c("have_sob", "have_chest_pain", "symptoms",
      ↪ "chest_pain_type")
  )
)

testthat::expect_equal(
```

```
ncol(chest_pain_data), 5
)
```

### 3.3.5 Combine Demographics

We combine all the data to give the `demo_behave_data`.

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

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

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",
      "have_sob", "have_chest_pain",
      "symptoms", "chest_pain_type"
    )
  )
)
```

```
testthat::expect_equal(  
  ncol(demo_behave_data), 13  
)
```

### 3.4 Write Preprocessed File

We output data to be used for the next session.

```
demo_behave_data |>  
  fst::write_fst(  
    path = here::here(  
      params$analysis_folder,  
      params$harmonisation_folder,  
      params$preprocessing_folder,  
      "02_demographic_data.fst"),  
  )
```

## 4 Export To Excel

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

### 4.1 Read all tabular data

We read all tabular data from the previous section.

### 4.2 Export Data as Excel

We export the standardised data to an excel file called harmonised\_\_Cohort\_\_A.xlsx

```
# Create a new workbook
my_workbook <- openxlsx::createWorkbook()

sheet_name = c("demographics")

output_data = list(demo_behave_data) |>
  purrr::map(
    .f = harmonisation::add_cohort_name,
    cohort_name = params$cohort_name,
    cohort_name_column = "cohort_name"
  )

purrr::walk2(
  .x = sheet_name,
  .y = output_data,
  .f = harmonisation::write_to_sheet,
  workbook = my_workbook
)

# Save workbook
openxlsx::saveWorkbook(
  wb = my_workbook,
  file = here::here(params$analysis_folder,
    params$output_folder,
```

```
        params$cleaned_folder,  
        params$output_excel_file),  
  overwrite = TRUE  
)
```