An introduction to tidy R programming with the OMOP common data model

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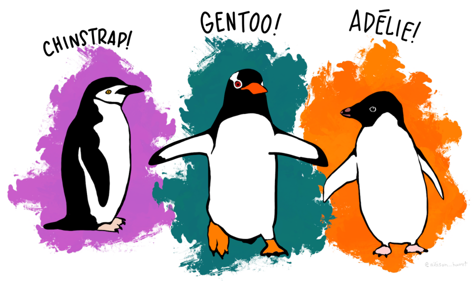
Preface

The source code for the book can be found at this Github repository Please open an issue there if you have a question or suggestion. Pull requests with suggested changes and additions are also most welcome.

1 Getting started

1.1 A first data analysis in R with a database



Artwork by @allison_horst

Before we start thinking about working with health care data spread across the OMOP common data model, let's first do a quick data analysis using a simpler dataset. For this we'll use data data from palmerpenguins package, which contains data on penguins collected from the Palmer Station in Antarctica.

1.2 Getting set up

Assuming that you have R and RStudio already set up, first we need to install a few packages not included in base R if we don´t already have them.

```
install.packages("dplyr")
install.packages("ggplot2")
install.packages("DBI")
install.packages("duckdb")
install.packages("palmerpenguins")
```

Once installed, we can load them like so.

```r
library(dplyr)
library(ggplot2)
library(DBI)
library(duckdb)
library(palmerpenguins)
```

1.3 Taking a peek at the data

We can get an overview of the data using the `glimpse()` command.

```r
glimpse(penguins)
```

```
Rows: 344
Columns: 8
$ species           <fct> Adelie, Adelie, Adelie, Adelie, Adelie, Adelie, Adel~
$ island            <fct> Torgersen, Torgersen, Torgersen, Torgersen, Torgerse~
$ bill_length_mm    <dbl> 39.1, 39.5, 40.3, NA, 36.7, 39.3, 38.9, 39.2, 34.1, ~
$ bill_depth_mm     <dbl> 18.7, 17.4, 18.0, NA, 19.3, 20.6, 17.8, 19.6, 18.1, ~
$ flipper_length_mm <int> 181, 186, 195, NA, 193, 190, 181, 195, 193, 190, 186~
$ body_mass_g       <int> 3750, 3800, 3250, NA, 3450, 3650, 3625, 4675, 3475, ~
$ sex               <fct> male, female, female, NA, female, male, female, male~
$ year              <int> 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007~
```

Or we could take a look at the first rows of the data using `head()`

```r
head(penguins, 5)
```

```
# A tibble: 5 x 8
  species island    bill_length_mm bill_depth_mm flipper_l~1 body_~2 sex    year
  <fct>   <fct>              <dbl>         <dbl>       <int>   <int> <fct> <int>
1 Adelie  Torgersen           39.1          18.7         181    3750 male   2007
2 Adelie  Torgersen           39.5          17.4         186    3800 fema~  2007
3 Adelie  Torgersen           40.3          18           195    3250 fema~  2007
4 Adelie  Torgersen           NA            NA            NA      NA <NA>   2007
5 Adelie  Torgersen           36.7          19.3         193    3450 fema~  2007
# ... with abbreviated variable names 1: flipper_length_mm, 2: body_mass_g
```

1.4 Inserting data into a database

Let's put our penguins data into a duckdb database. We create the duckdb database, add the penguins data, and then create a reference to the table containing the data.

```r
db<-dbConnect(duckdb::duckdb(), dbdir=":memory:")
dbWriteTable(db, "penguins", penguins)
penguins_db<-tbl(db, "penguins")
```

Now the data is in a database we could use SQL to get the first rows that we saw before

```r
dbGetQuery(db, "SELECT * FROM penguins LIMIT 5")
```

```
  species    island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
1  Adelie Torgersen           39.1          18.7               181        3750
2  Adelie Torgersen           39.5          17.4               186        3800
3  Adelie Torgersen           40.3          18.0               195        3250
4  Adelie Torgersen             NA            NA                NA          NA
5  Adelie Torgersen           36.7          19.3               193        3450
     sex year
1   male 2007
2 female 2007
3 female 2007
4   <NA> 2007
5 female 2007
```

But we could also use the same R code as before

```r
head(penguins_db, 5)
```

```
# Source:   SQL [5 x 8]
# Database: DuckDB 0.5.0 [eburn@Windows 10 x64:R 4.2.1/:memory:]
  species island    bill_length_mm bill_depth_mm flipper_l~1 body_~2 sex    year
  <fct>   <fct>              <dbl>         <dbl>       <int>   <int> <fct> <int>
1 Adelie  Torgersen           39.1          18.7         181    3750 male   2007
2 Adelie  Torgersen           39.5          17.4         186    3800 fema~  2007
3 Adelie  Torgersen           40.3          18           195    3250 fema~  2007
4 Adelie  Torgersen           NA            NA            NA      NA <NA>   2007
5 Adelie  Torgersen           36.7          19.3         193    3450 fema~  2007
# ... with abbreviated variable names 1: flipper_length_mm, 2: body_mass_g
```

1.5 Translation from R to SQL

The magic here is provided by dbplyr which takes the R code and converts it into SQL, which is this case looks like

```
head(penguins_db, 1) %>%
  show_query()
```

```
<SQL>
SELECT *
FROM penguins
LIMIT 1
```

More complicated SQL can also be written in what might be familiar dplyr code, for example

```
penguins_db %>%
  group_by(species) %>%
  summarise(min_bill_length_mm=min(bill_length_mm),
            median_bill_length_mm=median(bill_length_mm),
            max_bill_length_mm=max(bill_length_mm)) %>%
  mutate(min_max_bill_length_mm=paste0(min_bill_length_mm,
                                       " to ",
                                       max_bill_length_mm)) %>%
  select("species",
         "median_bill_length_mm",
         "min_max_bill_length_mm")
```

```
# Source:   SQL [3 x 3]
# Database: DuckDB 0.5.0 [eburn@Windows 10 x64:R 4.2.1/:memory:]
  species   median_bill_length_mm min_max_bill_length_mm
  <fct>                     <dbl> <chr>
1 Adelie                     38.8 32.1 to 46.0
2 Gentoo                     47.3 40.9 to 59.6
3 Chinstrap                  49.6 40.9 to 58.0
```

with the corresponding SQL looking like

```
penguins_db %>%
  group_by(species) %>%
  summarise(min_bill_length_mm=min(bill_length_mm),
            median_bill_length_mm=median(bill_length_mm),
            max_bill_length_mm=max(bill_length_mm)) %>%
  mutate(min_max_bill_length_mm=paste0(min, " to ", max)) %>%
  select("species",
         "median_bill_length_mm",
         "min_max_bill_length_mm") %>%
  show_query()
```

```
<SQL>
SELECT
  species,
  median_bill_length_mm,
  CONCAT_WS('', .Primitive("min"), ' to ', .Primitive("max")) AS min_max_bill_length_mm
FROM (
  SELECT
    species,
    MIN(bill_length_mm) AS min_bill_length_mm,
    PERCENTILE_CONT(0.5) WITHIN GROUP (ORDER BY bill_length_mm) AS median_bill_length_mm,
    MAX(bill_length_mm) AS max_bill_length_mm
  FROM penguins
  GROUP BY species
) q01
```

1.6 Example analysis

Let´s start by getting a count by species

```
penguins_db %>%
  group_by(species) %>%
  count()
```

```
# Source:   SQL [3 x 2]
# Database: DuckDB 0.5.0 [eburn@Windows 10 x64:R 4.2.1/:memory:]
  species       n
  <fct>     <dbl>
1 Adelie      152
2 Gentoo      124
3 Chinstrap    68
```

Now suppose we are particularly interested in the body mass variable. We can first notice that there are a couple of missing records for this.

```
penguins_db %>%
  mutate(missing_body_mass_g=if_else(
    is.na(body_mass_g),1,0
  )) %>%
  group_by(species, missing_body_mass_g) %>%
  tally()
```

```
# Source:   SQL [5 x 3]
# Database: DuckDB 0.5.0 [eburn@Windows 10 x64:R 4.2.1/:memory:]
# Groups:   species
  species   missing_body_mass_g     n
  <fct>                   <dbl> <dbl>
1 Adelie                      0   151
2 Adelie                      1     1
3 Gentoo                      0   123
4 Gentoo                      1     1
5 Chinstrap                   0    68
```

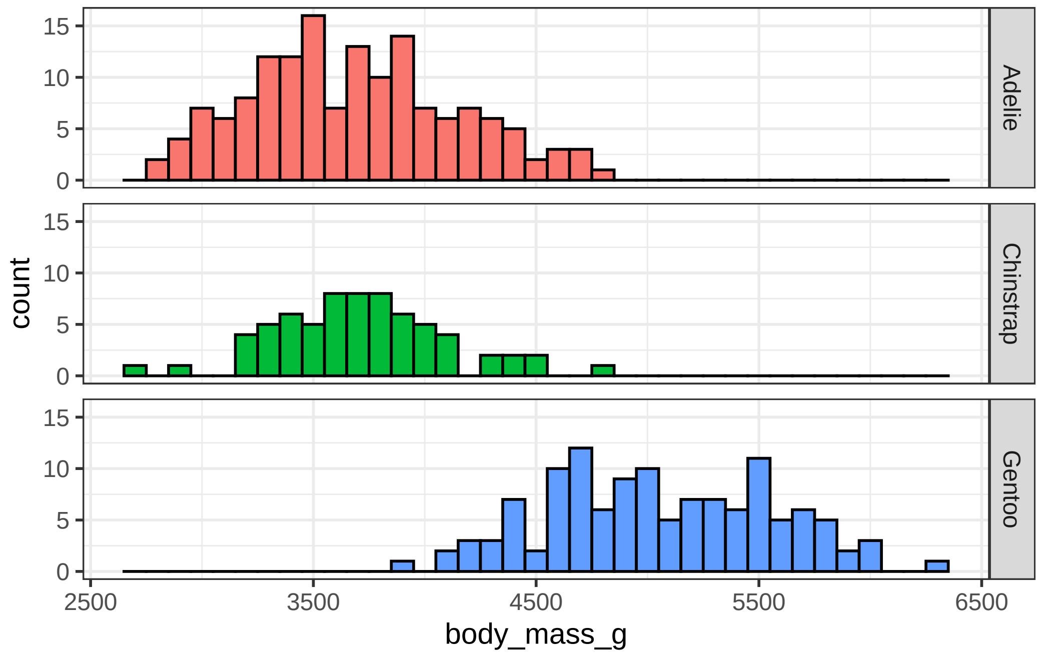
We can get the mean for each of the species (dropping those two missing records).

```
penguins_db %>%
  group_by(species) %>%
  summarise(mean_body_mass_g=round(mean(body_mass_g, na.rm=TRUE),0))
```

```
# Source:   SQL [3 x 2]
# Database: DuckDB 0.5.0 [eburn@Windows 10 x64:R 4.2.1/:memory:]
  species   mean_body_mass_g
  <fct>                <dbl>
1 Adelie                3701
2 Gentoo                5076
3 Chinstrap             3733
```

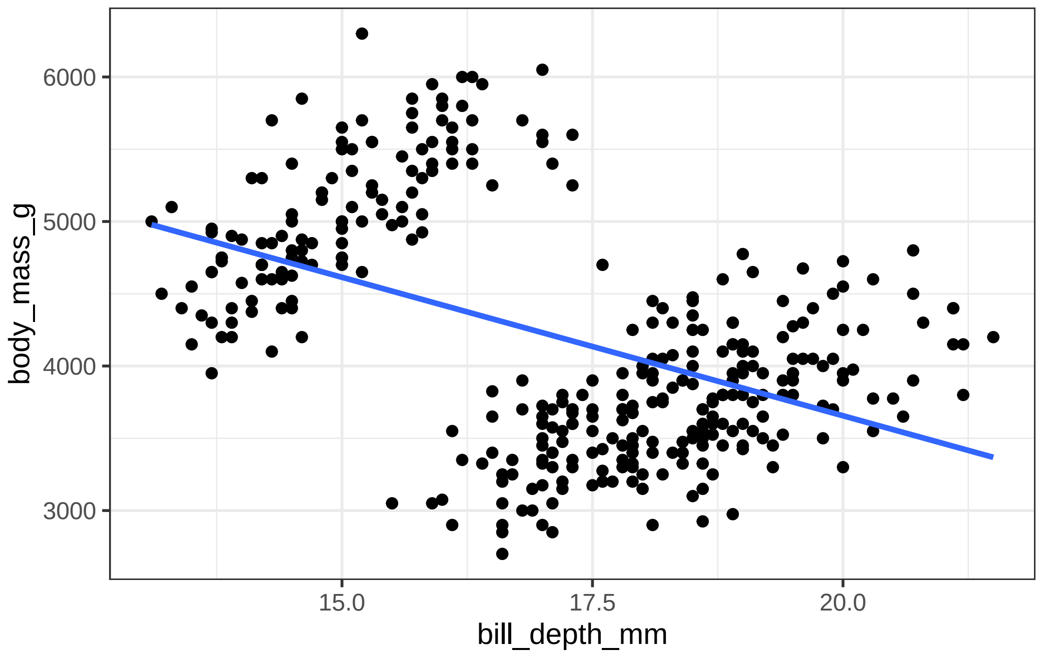
We can then also do a histogram for each of the species. For this we need to bring the data into R so that we can work with `ggplot()`, and we use `collect()` to do this.

```
penguins_db %>%
  collect() %>%
  ggplot(aes(group=species, fill=species))+
  facet_grid(species~ .) +
  geom_histogram(aes(body_mass_g), colour="black", binwidth = 100)+
  theme_bw()+
  theme(legend.position = "none")
```



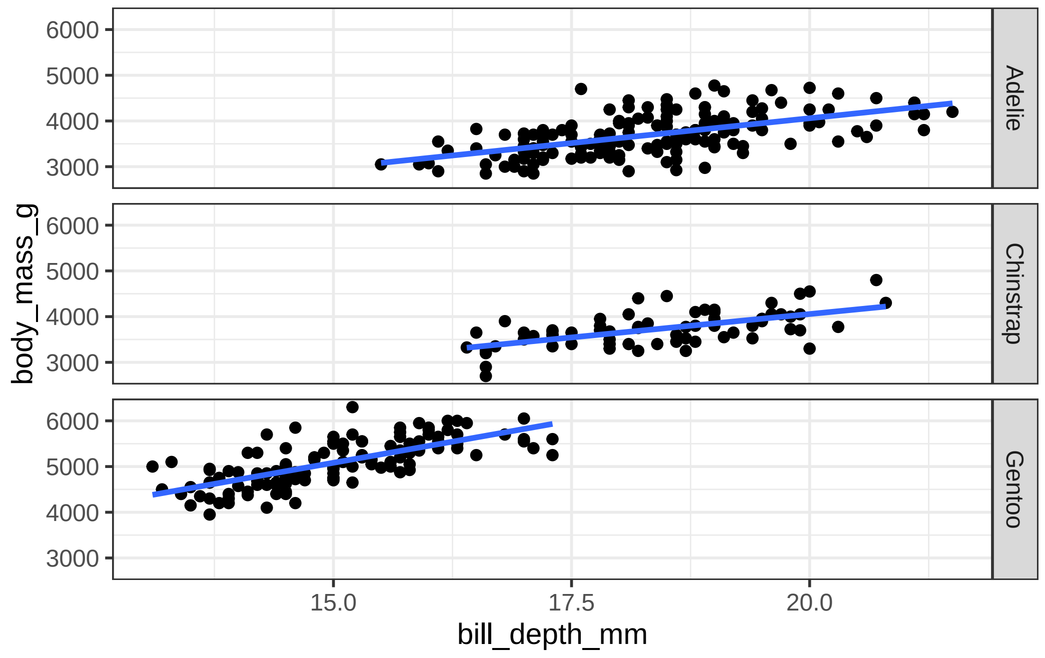
How about the relationship between body mass and bill depth?

```
penguins %>%
  collect() %>%
  ggplot(aes(x=bill_depth_mm,y=body_mass_g))+
  geom_point()+
  geom_smooth(method="lm",se=FALSE )+
  theme_bw()+
  theme(legend.position = "none")
```



But what about by species?

```
penguins %>%
  collect() %>%
  ggplot(aes(x=bill_depth_mm,y=body_mass_g))+
  facet_grid(species~ .) +
  geom_point()+
  geom_smooth(method="lm",se=FALSE )+
  theme_bw()+
  theme(legend.position = "none")
```



As well as having an example of working with data in database from R, you also have an example of Simpson´s paradox! And now we've reached the end of this example, we can close the database like so

1.7 Further reading

- R for Data Science (Chapter 13: Relational data)
- Writing SQL with dbplyr
- Data Carpentry: SQL databases and R

2 Creating a reference to a database using the OMOP common data model

2.1 Connecting to a database from R using DBI

Database connections from R can be made using the DBI package. The back-end for `DBI` is facilitated by database specific driver packages. As an example, lets say we want to work with a local duckdb from R. In this case the we can use the duckdb R package as the driver.

```
library(DBI)
db<-dbConnect(duckdb::duckdb(), dbdir=":memory:")
```

If we instead wanted to connect to other database management systems, these connections would be supported by the associated back-end packages and could look something like the below example for Postgres:

```
# Postgres
db <- DBI::dbConnect(RPostgres::Postgres(),
                      dbname = Sys.getenv("CDM5_POSTGRESQL_DBNAME"),
                      host = Sys.getenv("CDM5_POSTGRESQL_HOST"),
                      user = Sys.getenv("CDM5_POSTGRESQL_USER"),
                      password = Sys.getenv("CDM5_POSTGRESQL_PASSWORD"))
```

2.2 Creating a reference to the OMOP common data model

As seen in the previous chapter, once a connection to the database has been created then we could create references to the various tables in the database and build queries using in a familiar dplyr style. However, as we already know what the structure of the OMOP CDM looks like, we can avoid the overhead of building *ad hoc* references by instead using the `CDMConnector` package to quickly create a reference to the OMOP CDM data as a whole.

If you don't already have it installed, the first step would be to install `CDMConnector` from CRAN.

```r
install.packages("CDMConnector")
```

Once we have it installed, we can then load it as with other R packages.

```r
library(CDMConnector)
```

For this example, we'll use the Eunomia example data contained in a duckdb database. First we need to download the data. And once downloaded, make sure to add the path to your Renviron.

```r
# change pathToData to the location you want to save the data
CDMConnector::downloadEunomiaData(
  pathToData = here::here(),
  overwrite = TRUE
)
# once downloaded, save your pathToData to your Renviron (and then restart R)
# EUNOMIA_DATA_FOLDER="......"
```

```r
db <- DBI::dbConnect(duckdb::duckdb(),
                     dbdir = CDMConnector::eunomia_dir())
cdm <- CDMConnector::cdm_from_con(con = db,
                                  cdm_schema = "main")
cdm
```

```
# OMOP CDM reference (tbl_duckdb_connection)

Tables: person, observation_period, visit_occurrence, visit_detail, condition_occurrence, dru
```

Once we have created the our reference to the overall OMOP CDM, we can reference specific tables using the "$" operator or [[" "]].

```r
cdm$observation_period
```

```
# Source:   table<main.observation_period> [?? x 5]
# Database: DuckDB 0.5.0 [eburn@Windows 10 x64:R 4.2.1/C:\Users\eburn\AppData\Local\Temp\Rtmp
   observation_period_id person_id observation_period_start~1 observat~2 perio~3
                   <dbl>     <dbl> <date>                     <date>       <dbl>
 1                     6         6 1963-12-31                 2007-02-06  4.48e7
 2                    13        13 2009-04-26                 2019-04-14  4.48e7
 3                    27        27 2002-01-30                 2018-11-21  4.48e7
 4                    16        16 1971-10-14                        2017-11-02  4.48e7
 5                    55        55 2009-05-30                        2019-03-23  4.48e7
 6                    60        60 1990-11-21                        2019-01-23  4.48e7
 7                    42        42 1909-11-03                        2019-03-13  4.48e7
 8                    33        33 1986-05-12                        2018-09-10  4.48e7
 9                    18        18 1965-11-17                        2018-11-07  4.48e7
10                    25        25 2007-03-18                        2019-04-07  4.48e7
# ... with more rows, and abbreviated variable names
#   1: observation_period_start_date, 2: observation_period_end_date,
#   3: period_type_concept_id
```

```
cdm[["observation_period"]]
```

```
# Source:   table<main.observation_period> [?? x 5]
# Database: DuckDB 0.5.0 [eburn@Windows 10 x64:R 4.2.1/C:\Users\eburn\AppData\Local\Temp\Rtm
   observation_period_id person_id observation_period_start~1 observat~2 perio~3
                   <dbl>     <dbl> <date>                     <date>       <dbl>
 1                     6         6 1963-12-31                 2007-02-06  4.48e7
 2                    13        13 2009-04-26                 2019-04-14  4.48e7
 3                    27        27 2002-01-30                 2018-11-21  4.48e7
 4                    16        16 1971-10-14                 2017-11-02  4.48e7
 5                    55        55 2009-05-30                 2019-03-23  4.48e7
 6                    60        60 1990-11-21                 2019-01-23  4.48e7
 7                    42        42 1909-11-03                 2019-03-13  4.48e7
 8                    33        33 1986-05-12                 2018-09-10  4.48e7
 9                    18        18 1965-11-17                 2018-11-07  4.48e7
10                    25        25 2007-03-18                 2019-04-07  4.48e7
# ... with more rows, and abbreviated variable names
#   1: observation_period_start_date, 2: observation_period_end_date,
#   3: period_type_concept_id
```

When we created our reference we could have also specified a subset of cdm tables that we want to read:

```
cdm <- CDMConnector::cdm_from_con(db,
                                  cdm_tables = c("person","observation_period"))
cdm
```

```
# OMOP CDM reference (tbl_duckdb_connection)

Tables: person, observation_period
```

Moreover, we can also specify a write schema and the tables that we are interested in it when creating our reference. For example, if we wanted to create a reference to the person and observation period tables in the common data model along with cohort tables in a schema we have write access to, we could do this like so:

```
cdm <- CDMConnector::cdm_from_con(db,
  cdm_schema = "main",
  cdm_tables = c("person","observation_period"),
  write_schema = "results",
  cohort_tables = c("exposure_cohort", "outcome_cohort"))
```

2.3 Database snapshot

We can also use `CDMConnector` to provide a summary of the metadata for the OMOP CDM data we have connected to

```
cdm_from_con(con = db,
             cdm_schema = "main") %>%
  snapshot() %>%
  glimpse()
```

```
List of 7
 $ cdm_source_name       : chr "Synthea synthetic health database"
 $ cdm_version           : chr "v5.3.1"
 $ cdm_holder            : chr "OHDSI Community"
 $ cdm_release_date      : Date[1:1], format: "2019-05-25"
 $ vocabulary_version    : chr "v5.0 18-JAN-19"
 $ person_cnt            : num 2694
 $ observation_period_cnt: num 5343
 - attr(*, "class")= chr "cdm_snapshot"
```

2.4 Further reading

- CDMConnector package

3 Exploring the CDM

Let's first connect again to our Eunomia data and create the reference to the common data model.

```r
library(dbplyr)
library(dplyr)
library(CDMConnector)
library(ggplot2)
```

3.1 Counting people

The OMOP CDM is person-centric, with the person table containing records to uniquely identify each person in the database. As each row refers to a unique person, we can quickly get a count of the number of individuals in the database like so

```r
cdm$person %>%
  count() %>%
  pull()
```

```
[1] 2694
```

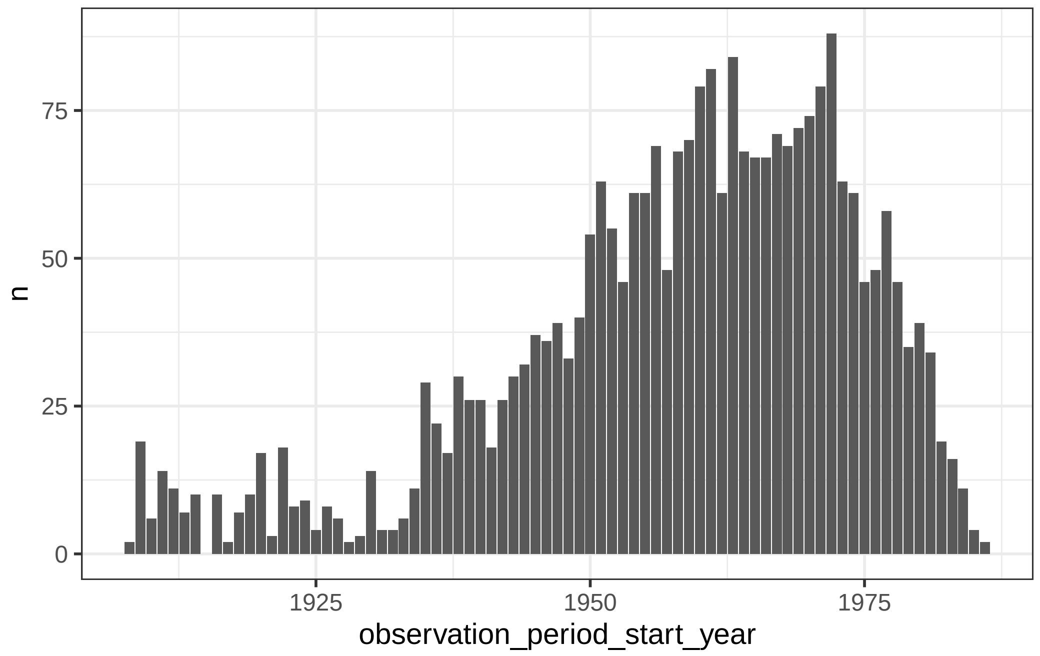
The person table also contains some demographic information, including a gender_concept_id for each person. We can get a count grouped by this variable, but as this uses a concept we'll also need to join to the concept table to get the corresponding concept name for each concept id.

```r
cdm$person %>%
  group_by(gender_concept_id) %>%
  count() %>%
  left_join(cdm$concept,
            by=c("gender_concept_id" = "concept_id")) %>%
              select("gender_concept_id", "concept_name", "n") %>%
  collect()
```

```
# A tibble: 2 x 3
  gender_concept_id concept_name     n
              <dbl> <chr>        <dbl>
1              8532 FEMALE        1373
2              8507 MALE          1321
```

The observation period table contains records indicating spans of time over which clinical events can be reliably observed for the people in the person table. Someone can potentially have multiple observation periods. So say we wanted a count of people grouped by the year during which their first observation period started. We could do this as below (note the use of compute() to store the results of the first query in a temporary table in the database)

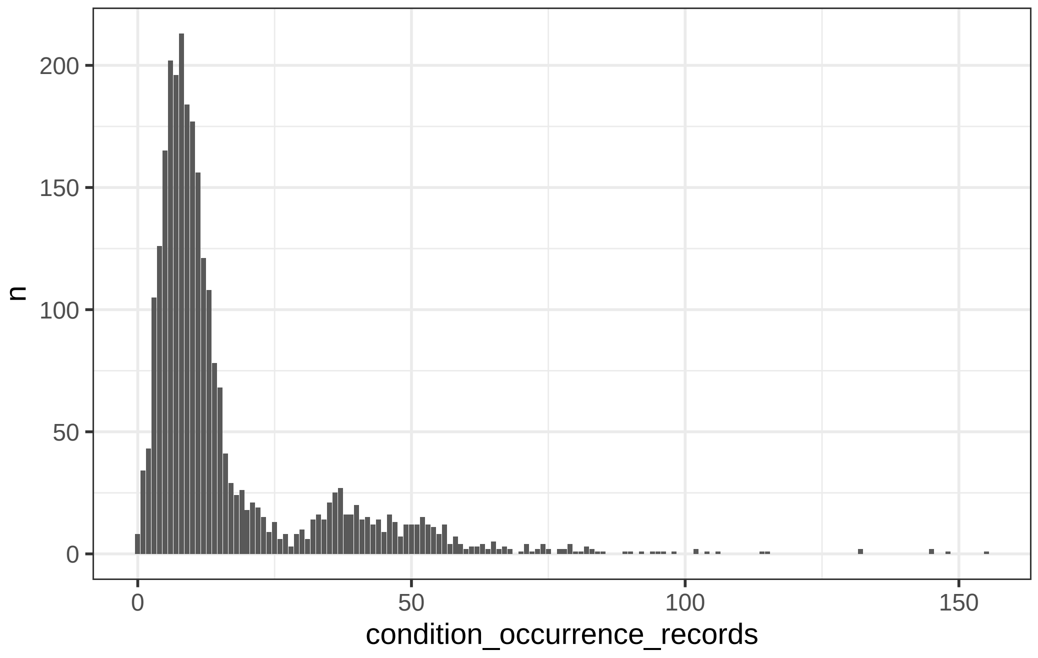
```
first_observation_period <- cdm$observation_period %>%
    group_by(person_id) %>%
    mutate(seq = dplyr::row_number()) %>%
    filter(seq==1) %>%
    compute()

cdm$person %>%
  left_join(first_observation_period,
            by = "person_id") %>%
  mutate(observation_period_start_year=year(observation_period_start_date)) %>%
  group_by(observation_period_start_year) %>%
  count() %>%
  collect() %>%
  ggplot() +
  geom_col(aes(observation_period_start_year, n)) +
  theme_bw()
```



3.2 Counting records

Number of drug exposure records per person

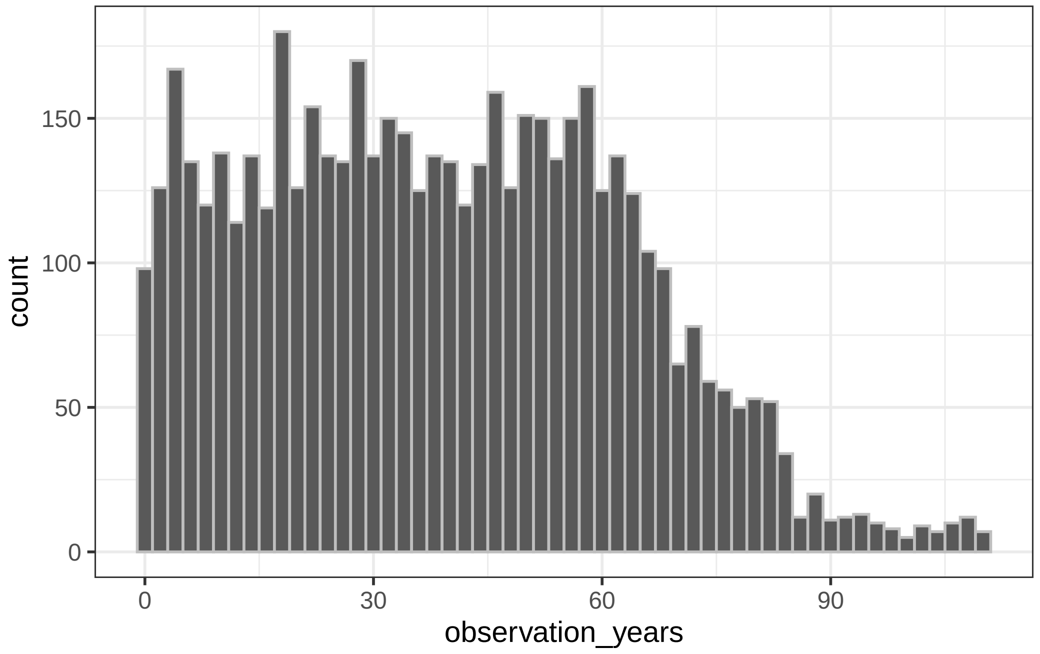
```
cdm$person %>%
  left_join(cdm$measurement %>%
  group_by(person_id) %>%
  count(name = "condition_occurrence_records"),
          by="person_id") %>%
  mutate(condition_occurrence_records = if_else(
    is.na(condition_occurrence_records), 0,
    condition_occurrence_records)) %>%
  group_by(condition_occurrence_records) %>%
  count() %>%
  collect() %>%
  ggplot() +
  geom_col(aes(condition_occurrence_records, n)) +
  theme_bw()
```



3.3 Working with dates

Dates are supported somewhat inconsistently by dbplyr, but CDMConnector provides some functions that provide more general support. We can use the datediff function from CDMConnector for example to calculate the difference between two dates. We can use this, for example, to get the number of years people's observation period last for.

```
cdm$observation_period %>%
  dplyr::mutate(observation_years =
                  !!CDMConnector::datediff("observation_period_start_date",
                                           "observation_period_end_date",
                                           interval = "year"))  %>%
  collect() %>%
  ggplot() +
  geom_histogram(aes(observation_years),
                 binwidth=2, colour="grey") +
  theme_bw()
```



3.4 Statistical summaries

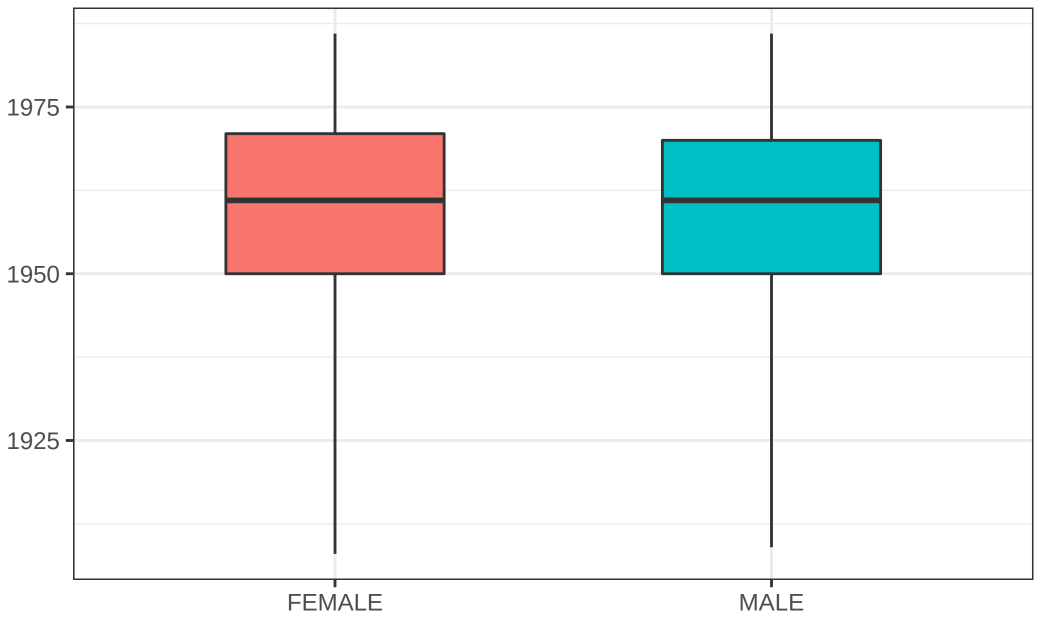
We can also use summarise for various other calculations

```
cdm$person %>%
  summarise(min_year_of_birth = min(year_of_birth, na.rm=TRUE),
            q05_year_of_birth = quantile(year_of_birth, 0.05, na.rm=TRUE),
            mean_year_of_birth = round(mean(year_of_birth, na.rm=TRUE),0),
            median_year_of_birth = median(year_of_birth, na.rm=TRUE),
            q95_year_of_birth = quantile(year_of_birth, 0.95, na.rm=TRUE),
            max_year_of_birth = max(year_of_birth, na.rm=TRUE)) %>%
  glimpse()
```

```
Rows: ??
Columns: 6
Database: DuckDB 0.5.0 [eburn@Windows 10 x64:R 4.2.1/C:\Users\eburn\AppData\Local\Temp\RtmpA
$ min_year_of_birth    <dbl> 1908
$ q05_year_of_birth    <dbl> 1922
$ mean_year_of_birth   <dbl> 1958
$ median_year_of_birth <dbl> 1961
$ q95_year_of_birth    <dbl> 1979
$ max_year_of_birth    <dbl> 1986
```

As we've seen before, we can also quickly get results for various groupings or restrictions

```
cdm$person %>%
   group_by(gender_concept_id) %>%
   summarise(min_year_of_birth = min(year_of_birth, na.rm=TRUE),
            q25_year_of_birth = quantile(year_of_birth, 0.25, na.rm=TRUE),
            median_year_of_birth = median(year_of_birth, na.rm=TRUE),
            q75_year_of_birth = quantile(year_of_birth, 0.75, na.rm=TRUE),
            max_year_of_birth = max(year_of_birth, na.rm=TRUE)) %>%
  left_join(cdm$concept,
            by=c("gender_concept_id" = "concept_id")) %>%
   collect() %>%
  ggplot(aes(x = concept_name, group = concept_name,
             fill = concept_name)) +
  geom_boxplot(aes(
    lower = q25_year_of_birth,
    upper = q75_year_of_birth,
    middle = median_year_of_birth,
    ymin = min_year_of_birth,
    ymax = max_year_of_birth),
    stat = "identity", width = 0.5) +
  theme_bw()+
  theme(legend.position = "none") +
  xlab("")
```


1975
1950
1925
FEMALE
MALE

4 Adding a cohort

4.1 Defining a cohort definition

capr - defining json ….

4.2 Adding a cohort to the CDM

via cdm connector

4.3 Cohort summary

Attributes: Cohort count, settings, attrition …..

5 Dscribing a cohort

5.1 CohortProfiles

5.2

References