# GD Notebook

## DATACLEANING FOR GD

#### Load the libraries

#### Data loading

```
barometer_dt_raw <- readxl::read_excel("../Data/GD_opgeschoond/221122_data_RGD_DECIDE_nw.xlsx")</pre>
```

#### Data manipulation

```
barometer_dt <- barometer_dt_raw %>%
  dplyr::rename(
   Filenumber = Dossier_ID,
   Samplenumber = sample_id,
   Farm_ID = farm_ID,
   Project = project,
   Date = date
   ) %>%
  dplyr::mutate(
   Country ='The Netherlands',
   Lab_reference ='2',
   Sample_type = case_when(
      reason_of_sampling == 'Autopsy' ~ 'Autopsy',
      sample == 'BAL' ~ 'BAL',
      sample == 'SWABS' ~ 'Swab',
      sample == 'OTHER' ~ 'Unknown',
      TRUE ~ 'Missing'
```

```
Diagnostic_test = case_when(
      test == 'PCR' ~ 'PCR',
      test == 'Kweek' ~ "Culture",
      TRUE ~ 'Missing'
   ),
   Breed = case_when(
     breed == "beef" ~ 'Beef',
      breed == "dairy" ~'Dairy',
      breed == "mixed" ~ 'Mixed',
      breed == "veal" ~ 'Veal',
      breed %in% c("other", "rearing", "unknown") ~ 'Unknown',
      TRUE ~ 'Unknown'
   ),
   Province = case_when(
      provincie == "DR" ~ 'Drenthe',
      provincie == "FL" ~'Flevoland',
      provincie == "FR" ~'Friesland',
      provincie == "GL" ~'Gelderland',
      provincie == "GR" ~'Groningen',
      provincie == "LB" ~'Limburg',
      provincie == "NB" ~'North Brabant',
      provincie == "NH" ~'North Holland',
     provincie == "OV" ~'Overijssel',
      provincie == "UT" ~'Utrecht',
      provincie == "ZH" ~'South Holland',
      provincie == "ZL" ~'Zeeland',
      TRUE ~ 'Missing'
   )
  )%>%
  dplyr::select(
   Filenumber,
   Diagnostic_test,
   Samplenumber,
   Country,
   Lab_reference,
   Sample_type,
   Breed,
   PM,
   MH,
   HS,
   MB,
   BRSV,
   PI3,
   BCV,
   Date,
   Province,
   Project,
   Farm_ID
  ) %>%
  dplyr::distinct() %>%
dplyr::mutate(
   Filenumber = sha256_hash(as.character(Filenumber)),
```

```
Samplenumber = sha256_hash(as.character(Samplenumber)),
Farm_ID = sha256_hash(as.character(Farm_ID))
)
```

## Filter data for 'monitoring' and 'no projects'

```
barometer_dt_filtered <- filter(barometer_dt, Project == 'monitoring' | Project == 'no project')</pre>
```

#### Floor date to 1st of the month

```
barometer_dt_filtered$Floored_date <- lubridate::floor_date(barometer_dt_filtered$Date, "month")</pre>
```

### Aggregate data based on farm\_ID and month (WIDE)

```
barometer_groupby <- barometer_dt_filtered %>%
  group_by(Lab_reference, Country, Breed, Floored_date, Province, Farm_ID, Diagnostic_test, Sample_type
  summarise(across(c(PM, MH, HS, MB, BRSV, PI3, BCV), max))
```

#### Convert to LONG

```
barometer_long <- barometer_groupby %>%
  tidyr::pivot_longer(
    cols = c('PM', 'MH', 'HS', 'MB', 'BRSV', 'PI3', 'BCV'),
    names_to = 'Pathogen',
    values_to = 'Result',
)
```

#### Save file to csv (long version)

```
write.csv(barometer_long, "../Data/CleanedData/barometer_GD.csv", row.names=TRUE)
```

#### Write to excel

```
writexl::write_xlsx(barometer_dt, "barometer_long_GD.xlsx")
```