# Workflow disease profiles

Distiller setting

Folder names

File names (file names in R)

## Data cleaning

SLR objective names:

* ExperimentalInfections

Steps:

1. Run SAVED REPORTS in **Distiller** to download CSV reports as CSV:
   1. DATA\_EXTRACT\_STORYMAPS
   2. REF\_extract
2. Place CSVs (2) on “data/DistillerData\_raw” and **remove date/time stamps**
3. Run \*\_data\_cleaning.R. Depends on: \*\_columnNames.csv

Result: saved cleaned files in “data/FilesDownload”

## Right side

If setting up the disease profile for the first time, make sure to use the scripts in **RUN-pathogen-first-time.R** to set up folders.

All disease and workflow setting are set in RUN-list-header.r. This is where any new diseases should be added.

All individual tabs are generated within the file RUN-list.r.

The current list of files associated with each section of the disease profiles are:

|  |  |
| --- | --- |
| Basic functions/multiple sections | Functions.R  Metanalysis\_functions.R |
| Geographical distribution |  |
| Field studies |  |
| Disease | 1impact\_MA.r (meta analyses)  1impact.Rmd (flexdashboard)  1impact-NOPAPER.Rmd (runs when no references available for the paper)  1impact-onlyREF.Rmd (runs when there is one reference, but not enough data for any plots) |
| Agent |  |
| Transmission |  |
| Diagnosis |  |
| Vectors |  |
| Vector Control |  |
| Vaccination |  |
| Treatments |  |

## Left side

If setting up the disease profile for the first time, make sure to use the scripts in **RUN-pathogen-first-time.R** to create an Excel skeleton.

Update the left side by editing the Excel files manually.

To change them in bulk, use the scripts in excel\_text\_correction.r.