**Purpose:** Check the master doc about why these are in two separate folders

# Key Scripts:

* [data\_prep.R](#_data_prep.R)
* [gbd\_data\_sub.R](#_gbd_data_sub.R)
* gbd\_outputs.R
* plot\_output.R
* read\_spec\_object.R

## data\_prep.R

**Created by:** Maggie Walters ([mwalte10@uw.edu](mailto:mwalte10@uw.edu))

**Documentation updated: 5/5/2020**

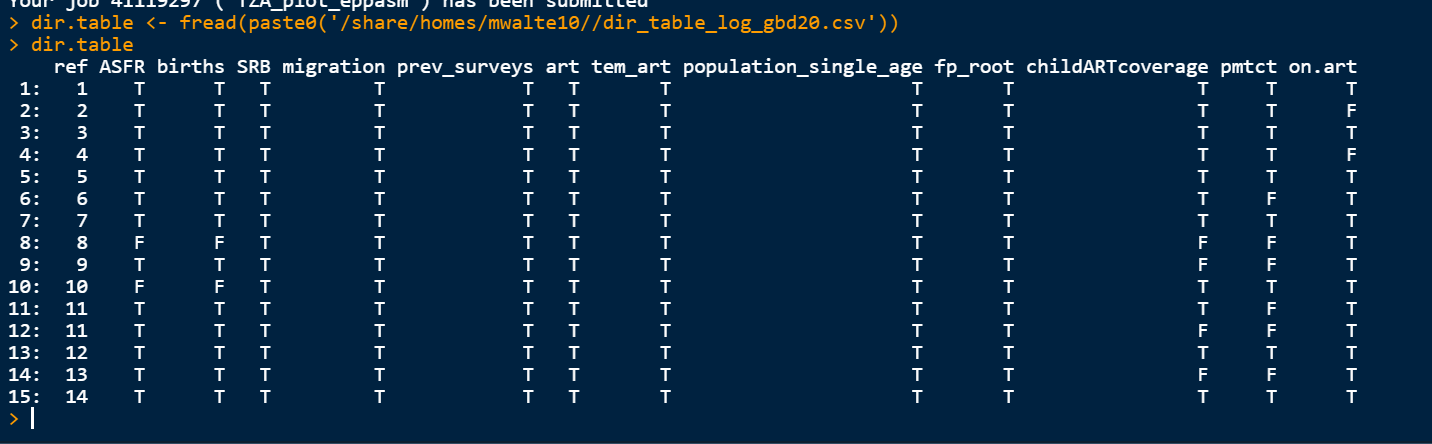
**Script updated: 5/5/2020**

**Purpose:** This script uses toggles to indicate what file paths should be used by read\_spec\_object(). Currently, T indicates the most up-to-date filepath while F pulls those used in gbd19. This file reads in the highest “ref” number to determine which toggles are true or false.

**Called by:** main.R

**Inputs:**

* /share/hiv/epp\_input/gbd20/eppasm\_run\_table.csv
* /share/homes/mwalte10/dir\_table\_log\_gbd20.csv
  + This is currently in my home directory to allow for different people to run different tests.



**Outputs:**

Outputs are the filepaths for ASFR, births, SRB, migration, prev\_surveys, art.dt (adult art, corresponds to column “art”), tem\_art (Tembisa ART estimates for ZAF), population\_single\_age, art (child ART coverage), and pmtct.

The following outputs are filepaths that are based on the fp\_root argument, which indicates where parameters for children are stored. These include: artdist (child ART distribution), artelig (child ART eligibility), percbf (percent breastfed), mort.art (child mortality on ART), prog (child progress parameters through CD4 stages), mort.offart (mortality not on ART), and dropout (dropout rates for PMTCT).

The following parameters change each year, and so will need their filepath updated:

**Future innovation:**

The structure of dir\_table\_log\_gbd20.csv could be improved so that it can be stored centrally and used by multiple people at the same time to conduct simultaneous tests. To do this I think the following columns should be added: user, run\_name, location.

## gbd\_data\_sub.R

**Created by:**

**Documentation updated: 5/5/2020**

**Script updated: 5/5/2020**

**Purpose:** This script contains the functions that are called in read\_spec\_object() to pull in the correct parameters for a given location.

**Called by:** read\_spec\_object() in main.R

**Key functions:**

* extend\_years()
  + Arguments: dt, years
* extrapolate\_years()
  + Arguments: dt, end\_year, years\_to\_average, trans\_vars, id\_vars
* append.ciba.incrr()
  + Arguments: dt, loc, run.name
* append.diag()
  + Arguments: dt, loc, run.name
* append.vr()
  + Arguments: dt, loc, run.name
* append.deaths()
  + Arguments: dt, loc, run.name, start,year, stop.year
* convert\_paed\_cd4()
  + Arguments: dt, agegr
* sub.paeds()
  + Arguments: dt, loc, k, start.year, stop.year
* sub.pop.params.specfp()
  + Arguments: fp, loc, k
* sub.prev()
  + Arguments: loc, dt
* add\_frr\_noage\_fp()
  + Arguments: obj
* sub.prev.granular()
  + Arguments: dt, loc
* sub.off.art()
  + Arguments: dt, loc, k
* sub.on.art()
  + Arguments: dt, loc, k
* sub.cd4.prog()
  + Arguments: dt, loc, k
* geo\_adj()
  + Arguments: loc, dt, i, uncertainty
* geo\_adj\_old()
* sub.art()
* sub.sexincrr()
* sub.anc.prior()

**Inputs:**

**Outputs:**

**Future innovation:**