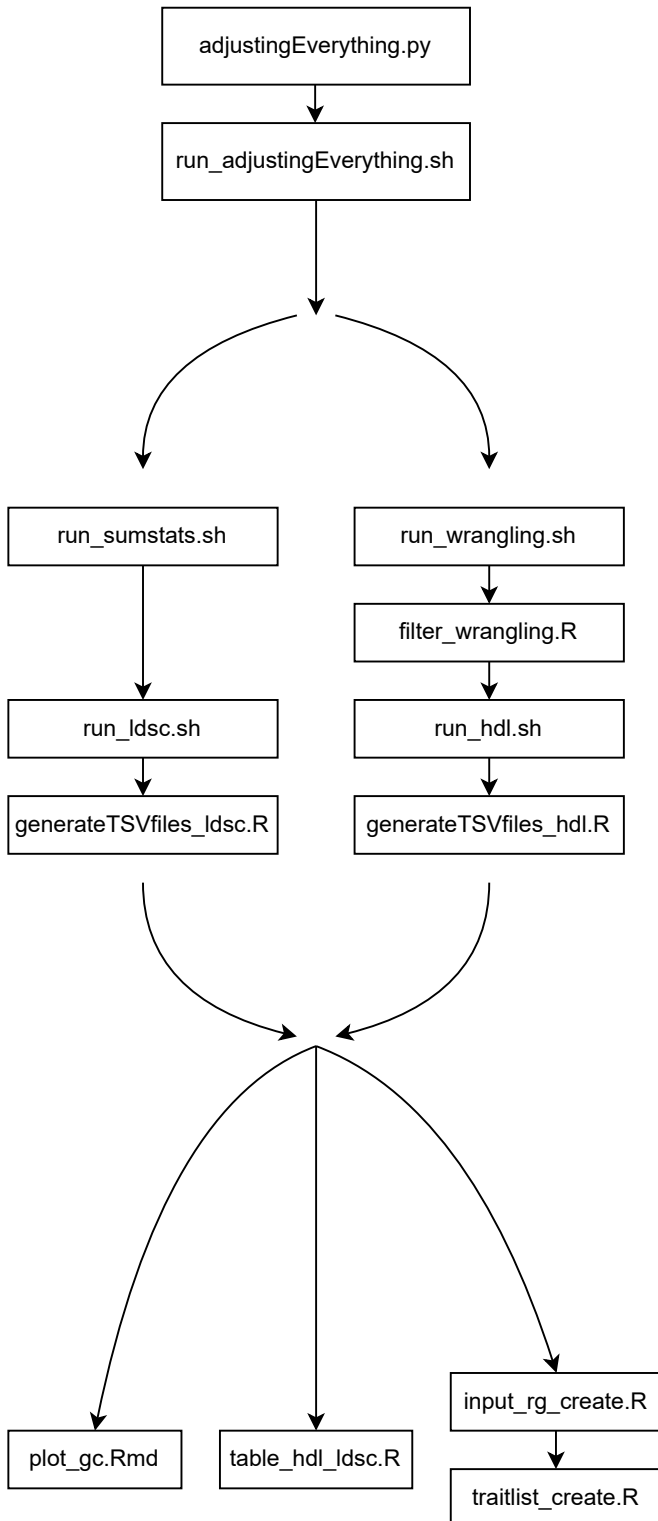# Scripts

In order to be able to use and work with the scripts, please familiarize yourself with the prerequisites listed on the GitHub page. Additionally, pay attention to the folder structure as specified on GitHub.

```
adjustingEverything.py
        │
        ▼
run_adjustingEverything.sh
```

```
run_sumstats.sh              run_wrangling.sh
      │                            │
      ▼                            ▼
  run_ldsc.sh               filter_wrangling.R
      │                            │
      ▼                            ▼
generateTSVfiles_ldsc.R        run_hdl.sh
                                   │
                                   ▼
                        generateTSVfiles_hdl.R
```

```
plot_gc.Rmd     table_hdl_ldsc.R     input_rg_create.R
                                            │
                                            ▼
                                     traitlist_create.R
```

Explained Steps

Check whether the SNPs have the same amount of columns as the header row of the data

Cut the SNPs with EAF=. or EAF=NA and if sample size is missing, include sample size (sample_size and pvalue columns should be numeric)

Run both techniques with GWAS data

Input files are stored in: /input_files/single_GWAS_cytokines_filtered

LDSC

HDL

Convert output of LDSC and HDL to readable tsv files

Filter for significance and correct all genetic correlation values that are outside of [-1,1] to 0

Visualize and analyze genetic correlations between the GWAS studies

via

Heatmaps

Tables including correlation values

Network Plots