

Lab Notebook

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scripts Folder

00_make_directories.sh

This file creates some subdirectories under the same directory where this file is located, in the following structure:

- data
 - ambiguous_indel_snps
 - intersecting_filtered
 - kgp_filtered
 - kgp_merged
 - kgp_meta
 - ukb_filtered
 - ukb_merged
 - ukb_meta
 - ukb_populations
 - models
 - phenotypes
 - gwas_results
 - prs
 - kgp_populations
 - fst
 - LDpred
 - * prs

- * tmp-data
 - * val_prs
 - prs_comparisons
 - theory
 - theor_herit
 - theoretical
- img

For me, these directories are under \$WORK2/pgs_portability.

01_UKBB_genotypes_filtered.sh

This file filters out the indels and ambiguous variants.

I had to copy the files from /corral-repl/utexas/Recombining-sex-chro/ukb/data/genotype_calls/ into my directory for this script to work, or it will throw a `FileNotFoundError`.

I'm working on getting the .sam file from BioBank.

01a_get_ambiguous_indel_snps.py

01b_remove_ambiguous_indel_snps.py

01c_find_duplicates.py

01d_import_1KG.sh