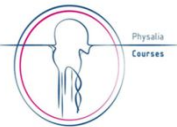


Towards the GWAS pipeline: revising the steps



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the stand-alone **GWAS** scripts

- Run GWAS programmatically
 - gwas_rrblup.R
 - gwas_statgengwas.R



step 1 - getting the data

- **1.get_data.sh**
 - Download the data
 - Prepare the data



step 2 - filter the data

- **2.steps_filtering.sh**
 - Filter genotype data:
 - MAF
 - Missing rate



step 3 - **imputing** missing genotypes

- **3.step_imputation.sh**
 - Impute missing genotype data:
 - LHCI



step 4 - run the GWAS

- **4.gwas.sh**
 - Run GWAS through the stand-alone script
 - (try both gwas_rrblup.R and gwas_statgengwas.R)



NEXT LECTURE

A bioinformatic **pipeline** for GWAS

