

# **Collaborative exercise**

#### **Christian Werner**

(Quantitative geneticist and biostatistician) EiB, CIMMYT, Texcoco (Mexico)

### Filippo Biscarini



(Biostatistician, bioinformatician and quantitative geneticist) CNR-IBBA, Milan (Italy)

#### Oscar González-Recio

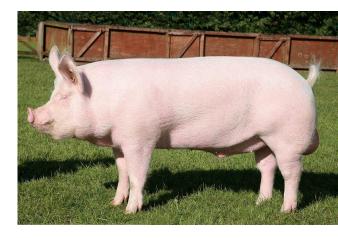


(Computational biologist and quantitative geneticist) INIA-UPM, Madrid (Spain)



- Build your own workflow!
  - a. Download the data
  - b. Prepare the data (look at the phenotypes and genotypes!)
  - c. Filter the data
  - d. Impute missing genotypes
  - e. Run the GWAS
- Data on stump tail sperm defect of Swiss Large
   White boars

(https://zenodo.org/record/4081475#.YKPfmnUzZhE)



from: https://petpigworld.com/large-white-pigs-the-essential-guide/



- Build your own workflow!
  - Download the data



- b. Prepare the data (look at the phenotypes and genotypes!)
- c. Filter the data
- d. Impute missing genotypes
- e. Run the GWAS
- Data on stump tail sperm defect of Swiss Large
   White boars
- (https://zenodo.org/record/4081475#.YKPfmnUzZhE)

!! beware !! no missing SNP
genotypes (data already filtered
and imputed)

get data with missing SNP genotypes from here:
<a href="http://www.jackdellequerce.com/data/GWAS\_cohort.tar.gz">http://www.jackdellequerce.com/data/GWAS\_cohort.tar.gz</a>





- Build your own workflow!
  - Download the data



- b. Prepare the data (look at the phenotypes and genotypes!)
- c. Filter the data
- d. Impute missing genotypes
- e. Run the GWAS
- Data on stump tail sperm defect of Swiss Large White boars
- (https://zenodo.org/record/4081475#.YKPfmnUzZhE)

take a **subset of the SNPs** (to make calculations -and trial/errors- quicker), **e.g. chromosomes 10-14** (the mutation is on chromosome 12)



- Build your own workflow!
  - a. Download the data
  - b. Prepare the data (look at the phenotypes and genotypes!)
  - c. Filter the data
  - d. Impute missing genotypes
  - e. Run the GWAS
- 1. Try on your own (individually, groups)
- 2. Let's do it all together!