

# Collaborative **exercise**

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# GWAS workflow/pipeline - collaborative exercise

- Build your own workflow/pipeline!
  - 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

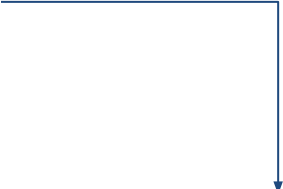
(<https://zenodo.org/record/4081475#.YKPfmnUzZhE>)



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

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

→ [software/injectMissing.R](#)



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- 
1. Try on your own (individually, groups)
  2. Let's do it all together!

