First Estimates

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```r
library ( dplyr )
library ( ggplot2 )

tempDir = "/scratch/genevol/users/lucas/"
saveDir = "/raid/genevol/users/lucas/heritability/plots/"
```

Introduction

Step 1

After the removal of monomorphisms, filtration of the desired samples and after obtaining the list of non-correlated genes per chromosome (considering correlation value of $\sqrt{0.1}$), it is now desired to calculate the GRM matrix.

```r
# Read file with all chromosomes
allChrFile = SeqArray::seqOpen ( paste0 ( tempDir , "allChr.gds" ) )
# List of all genes of interest (after pruning)
listGenes = readRDS ( paste0 ( tempDir , "fullPrunedList.rds" ) )

# GRM - calculated as defined in CGTA
grm_obj = SNPRelate::snpgdsGRM( allChrFile , snp.id = listGenes , method = "GCTA")
```

```
## Genetic Relationship Matrix (GRM, GCTA):
## Calculating allele counts/frequencies ...
## [...................................................]  0%, ETC: ---    [===========================
## # of selected variants: 532,105
##      # of samples: 445
##      # of SNVs: 532,105
##      using 1 thread
## CPU capabilities: Double-Precision SSE2
## Wed Oct 21 12:36:15 2020    (internal increment: 8752)
## [...................................................]  0%, ETC: ---      [===========================
## Wed Oct 21 12:38:45 2020    Done.
```