

Genomic Selection

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(Massman et al. 2013) (Covarrubias-Pazaran 2016) (Akdemir and Godfrey 2015)

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library(AlphaSimR)
FOUNDERPOP = runMacs(nInd=100,nChr=10,segSites=1200,
                    inbred=FALSE,species="TEST")
SIMPARAM = createSimulation(FOUNDERPOP,maxQtl=200,maxSnp=1000,gender="yes_sys")
SIMPARAM = addTraitA(FOUNDERPOP,nQtlPerChr=100,meanG=0,varG=1)
SIMPARAM = addSnpChip(1000)
pop = newPop(FOUNDERPOP)
unlink("GS",recursive=TRUE)
dir.create("GS")
writeRecords(pop,"GS",1)
for(gen in 1:9){
  pop = randCross(pop,100)
  writeRecords(pop,"GS",1)
}
#Predict
pop = randCross(pop,100)
gsModel = RRBLUP("GS",1,use="GV")
pop = setEBV(pop,gsModel)
cor(pop@gv[,1],pop@ebv[,1])
#Select on EBV
best = selectInd(pop,10,use="ebv")
meanG(best)-meanG(pop)
```

References

- Akdemir, Deniz, and Okeke Uche Godfrey. 2015. *EMMREML: Fitting Mixed Models with Known Covariance Structures*. <https://CRAN.R-project.org/package=EMMREML>.
- Covarrubias-Pazaran, Giovanni. 2016. "Genome Assisted Prediction of Quantitative Traits Using the R Package Sommer." *PLoS ONE* 11:1–15. <https://doi.org/10.1371/journal.pone.0156744>.
- Massman, Jon M., Andres Gordillo, Robenzon E. Lorenzana, and Rex Bernardo. 2013. "Genomewide Predictions from Maize Single-Cross Data." *Theoretical and Applied Genetics* 126 (1):12–22. <https://doi.org/10.1007/s00122-012-1955-y>.