Basic Animal Simulation

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2017-11-27

This document provides

(2015)

```r
# Basic animal breeding simulation
# Based on "historical breeding" portion of Jenko et al., 2015
# https://gsejournal.biomedcentral.com/articles/10.1186/s12711-015-0135-3
library(AlphaSimR)
# Generate initial haplotypes
FOUNDERPOP = runMacs(nInd=1000,nChr=10,segSites=1000,
                     inbred=FALSE,species="TEST") #Using TEST instead of CATTLE for speed

# Set simulation parameters
SIMPARAM = createSimulation(FOUNDERPOP,maxQtl=1000,maxSnp=0,gender="yes_sys")
# Add a trait with additive effects
SIMPARAM = addTraitA(FOUNDERPOP,nQtlPerChr=1000,meanG=0,varG=1)

calves = newPop(FOUNDERPOP)
popMean = meanG(calves)
popVar = varG(calves)
for(i in 1:20){
  bulls = selectMale(calves,25,use="gv")
  cows = selectFemale(calves,500,use="gv")
  calves = randCross2(cows,bulls,nCrosses=1000)
  popMean = c(popMean,meanG(calves))
  popVar = c(popVar,varG(bulls))
}
plot(0:20,popMean,type="l",xlab="Generation",ylab="GV",main="Genetic Gain")
plot(0:20,popVar,type="l",xlab="Generation",ylab="GV",main="Genetic Variance")
```

References

Jenko, Janez, Gregor Gorjanc, Matthew A. Cleveland, Rajeev K. Varshney, C. Bruce A. Whitelaw, John A. Woolliams, and John M. Hickey. 2015. "Potential of Promotion of Alleles by Genome Editing to Improve Quantitative Traits in Livestock Breeding Programs." *Genetics Selection Evolution* 47 (55). https://doi.org/10.1186/s12711-015-0135-3.