

Software: Genetic Drift Illustration

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# Erik Otárola-Castillo June 2010

# R program to illustrate Genetic Drift in a population. "Real Time" shows the change in the
# frequency of two alleles in a population over several generations due to random sampling.

ngen<-1000
npop<-500
plot(1:ngen,seq(0,1,length.out=ngen),type="n",ylim=c(0,1))
a<-c(rep(1, npop), rep(2, npop))
prop1<-numeric(ngen)
prop2<-numeric(ngen)
#hist(a,main=paste("Frequencies of 1s and 2s at generation 0"))
t<-numeric(npop*2)
for (j in 1:ngen) {
  for (i in 1:(npop*2)) {
    t[i]<-sample(a,1,replace=FALSE)
  }
  a<-t
  prop1[j]<-(sum(t==1)/(npop*2));prop2[j]<-1-prop1[j]
  plot(1:j,prop1[1:j],col="blue",type="l",ylim=c(0,1),xlim=c(0,ngen),xlab="Generation
  Time",ylab="Relative Frequency of Alleles",main=paste("GENETIC DRIFT: Frequencies of Red
  and Blue alleles at generation",j))
  lines(1:j,prop2[1:j],col="red")
  #hist(t,main=paste("Frequencies of 1s and 2s at generation",j))
}

proportions<-cbind(prop1,prop2)

hist(t,main=paste("Frequencies of 1s and 2s at generation",j))
```

