trueMean1 <- 5

trueSD1 <- 5

population1 <- rnorm(1e6, trueMean1, trueSD1)

trueMean2 <- 4

trueSD2 <- 5

population2 <- rnorm(1e6, trueMean2, trueSD2)

Size <-50

Sample1 <- sample(population1 , Size)

Sample2 <- sample(population2 , Size)

# yes they are different and so were the populations

boxplot(Sample1, Sample2)

source("http://jonsmitchell.com/code/simFxn04.R")

MatGrandma <- makeFounder("grandma\_mom")

MatGrandpa <- makeFounder("grandpa\_mom")

PatGrandma <- makeFounder("grandma\_da")

PatGrandpa <- makeFounder("grandpa\_da")

Alan <- makeBaby(PatGrandma, PatGrandpa)

Brenda <- makeBaby(MatGrandma, MatGrandpa)

Focus <- makeBaby(Brenda, Alan)

# Should be 50% or .5

ToMom <- length( grep("mom", Focus))/ length(Focus)

# 0.3076 and .1924. Doesn’t match my prediction

ToMomMom<- length( grep( "grandma\_mom", Focus))/ length(Focus)

ToMomDad <- length( grep( "granpa\_mom", Focus))/ length(Focus)

# Focus inst equal with relation to the maternal grandparents and the paternal grandparents. Average relatedness was 0.25.

Sibling\_01<-makeBaby(Brenda, Alan)

# I would expect 50%, a ctual was 47%.

ToSib <- length(intersect( Focus, Sibling\_01))/ length(Focus)

ManySiblings <- replicate( 1e3, length( intersect( Focus, makeBaby(Brenda, Alan)))/length( Focus))

#Shares different numbers of genes with each 1000 siblings.

quantile(ManySiblings)

mean(ManySiblings)

plot(density(ManySiblings), main="", xlab="proportion shared genes")

HWE <- function(p) {

aa<-p^2

ab<-2\*p\*(1-p)

bb<-(1-p)^2

return(c(aa=aa, ab=ab, bb=bb))

}

HWE(0.5)

plot(1, 1, type="n", xlim=c(0,1), xlab="freq. allele a", ylab="geno. freq")

p<- seq(from = 0, to = 1, by = 0.01)

GenoFreq<- t(sapply(p, HWE))

lines(p, GenoFreq[,"aa"], lwd=2, col="red")

# Frequency of aa increases as the frequency of alleles a aincrease in the population. As it decreases, frequency does too. Time is not shown in the plot. Geographical space is not as well.

lines(p, GenoFreq[,"ab"], lwd=2, col="purple")

lines(p, GenoFreq[,"bb"], lwd=2, col="blue")

legend("top", legend=c("aa","ab","bb"), col=c("red","purple","blue"), lty=1, lwd=2, bty="n")

Pop<- simPop(500)

points(Pop[,"freqa"], Pop[,"Genotypes.aa"]/500, pch=21, bg="red")

#Does not match the Hardy Weinberg expectation

Pop<-simPop(50)

points(Pop[,"freqa"], Pop[,"Genotypes.aa"]/50, pch=22, bg="red")

# More points on the graph.

install.packages("learnPopGen")

library(learnPopGen)

x<-genetic.drift(Ne=200, nrep=5, pause=0.01)

PopSizes<-5:50

Samples<- rep(PopSizes, 5)

tExt<- sapply(Samples, function(x) nrow(simPop(x, 500)))

Line<- lm(tExt ~ Samples)

summary(Line)

Line$coef

plot(Samples, tExt)

abline(Line)

# as population increases, the distance from the line increases. Population size increases, there is more extinction for alleles.