

# Lab 3: Spatial Data

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2024-09-17

## Section 6.3 Worked Example

[https://bookdown.org/hhwagner1/LandGenCourse\\_book/WE\\_3.html](https://bookdown.org/hhwagner1/LandGenCourse_book/WE_3.html)

Load libraries

```
require(adeigenet)
require(LandGenCourse)
require(pegas)
require(PopGenReport)
require(dplyr)
require(poppr)
require(here)
```

### 1. Overview

The data set we will use is ralu.loci

### 2. Import straight from the package after library is loaded

```
data(ralu.loci, package="LandGenCourse")
Frogs <- data.frame(FrogID = paste(substr(ralu.loci$Pop, 1, 3),
                                     row.names(ralu.loci), sep="."), ralu.loci)
Frogs.genind <- adegenet::df2genind(X=Frogs[,c(4:11)], sep=":", ncode=NULL,
                                   ind.names= Frogs$FrogID, loc.names=NULL,
                                   pop=Frogs$Pop, NA.char="NA", ploidy=2,
                                   type="codom", strata=NULL, hierarchy=NULL)

Frogs.genind

## /// GENIND OBJECT ///////////
##
## // 181 individuals; 8 loci; 39 alleles; size: 55.5 Kb
##
## // Basic content
##   @tab: 181 x 39 matrix of allele counts
##   @loc.n.all: number of alleles per locus (range: 3-9)
##   @loc.fac: locus factor for the 39 columns of @tab
##   @all.names: list of allele names for each locus
##   @ploidy: ploidy of each individual (range: 2-2)
##   @type: codom
##   @call: adegenet::df2genind(X = Frogs[, c(4:11)], sep = ":", ncode = NULL,
##     ind.names = Frogs$FrogID, loc.names = NULL, pop = Frogs$Pop,
##     NA.char = "NA", ploidy = 2, type = "codom", strata = NULL,
```

```
##      hierarchy = NULL)
##
## // Optional content
##      @pop: population of each individual (group size range: 7-23)

Get info on genind object, check that they are polymorphic
Frogs.genind

## /// GENIND OBJECT ///////////
##
## // 181 individuals; 8 loci; 39 alleles; size: 55.5 Kb
##
## // Basic content
##      @tab: 181 x 39 matrix of allele counts
##      @loc.n.all: number of alleles per locus (range: 3-9)
##      @loc.fac: locus factor for the 39 columns of @tab
##      @all.names: list of allele names for each locus
##      @ploidy: ploidy of each individual (range: 2-2)
##      @type: codom
##      @call: adegenet::df2genind(X = Frogs[, c(4:11)], sep = ":", ncode = NULL,
##      ind.names = Frogs$FrogID, loc.names = NULL, pop = Frogs$Pop,
##      NA.char = "NA", ploidy = 2, type = "codom", strata = NULL,
##      hierarchy = NULL)
##
## // Optional content
##      @pop: population of each individual (group size range: 7-23)
```

```
summary(Frogs.genind)
```

```
##
## // Number of individuals: 181
## // Group sizes: 21 8 14 13 7 17 9 20 19 13 17 23
## // Number of alleles per locus: 3 4 4 4 9 3 4 8
## // Number of alleles per group: 21 21 20 22 20 19 19 25 18 14 18 26
## // Percentage of missing data: 10.64 %
## // Observed heterozygosity: 0.1 0.4 0.09 0.36 0.68 0.02 0.38 0.68
## // Expected heterozygosity: 0.17 0.47 0.14 0.59 0.78 0.02 0.48 0.74
```

Test for HWE with pegas:

```
round(pegas::hw.test(Frogs.genind, B = 1000), digits = 3)
```

```
##      chi^2 df Pr(chi^2 >) Pr.exact
## A  40.462  3      0.000    0.000
## B  17.135  6      0.009    0.025
## C 136.522  6      0.000    0.000
## D  83.338  6      0.000    0.000
## E 226.803 36      0.000    0.000
## F   0.024  3      0.999    1.000
## G  12.349  6      0.055    0.007
## H  76.813 28      0.000    0.000
```

```
# Chi-squared test: p-value
```

```
HWE.test <- data.frame(sapply(seppop(Frogs.genind),
                             function(ls) pegas::hw.test(ls, B=0)[,3]))
HWE.test.chisq <- t(data.matrix(HWE.test))
{cat("Chi-squared test (p-values):", "\n")
```

```
round(HWE.test.chisq,3)}
```

```
## Chi-squared test (p-values):
```

```
##           A      B      C      D      E      F      G      H
## Airplane  0.092 0.359 1.000 0.427 0.680 1.000 0.178 0.051
## Bachelor  1.000 0.557 0.576 0.686 0.716 1.000 0.414 0.609
## BarkingFox 0.890 0.136 0.005 0.533 0.739 0.890 0.708 0.157
## Bob       0.764 0.864 0.362 0.764 0.033 1.000 0.860 0.287
## Cache     1.000 0.325 0.046 0.659 0.753 1.000 0.709 0.402
## Egg       1.000 0.812 1.000 1.000 0.156 1.000 0.477 0.470
## Frog      1.000 0.719 0.070 0.722 0.587 1.000 0.564 0.172
## GentianL  0.809 0.059 1.000 0.028 0.560 0.717 0.474 0.108
## ParagonL  1.000 0.054 0.885 0.709 0.868 1.000 0.291 0.000
## Pothole   1.000 1.000 1.000 0.488 0.248 1.000 0.296 0.850
## ShipIsland 0.807 0.497 1.000 0.521 0.006 1.000 0.498 0.403
## Skyhigh   0.915 0.493 0.063 0.001 0.155 1.000 0.126 0.078
```

```
# Monte Carlo: p-value
```

```
HWE.test <- data.frame(sapply(seppop(Frogs.genind),
                             function(ls) pegas::hw.test(ls, B=1000)[,4]))
HWE.test.MC <- t(data.matrix(HWE.test))
{cat("MC permutation test (p-values):", "\n")
round(HWE.test.MC,3)}
```

```
## MC permutation test (p-values):
```

```
##           A      B      C      D      E F      G      H
## Airplane  0.023 1.000 1.000 0.387 0.633 1 0.259 0.015
## Bachelor  1.000 0.418 1.000 1.000 0.863 1 0.470 0.601
## BarkingFox 1.000 0.196 0.047 1.000 0.756 1 1.000 0.173
## Bob       1.000 1.000 1.000 1.000 0.016 1 1.000 0.270
## Cache     1.000 0.373 0.139 1.000 1.000 1 1.000 0.608
## Egg       1.000 1.000 1.000 1.000 0.088 1 0.541 0.439
## Frog      1.000 1.000 0.076 1.000 0.454 1 1.000 0.176
## GentianL  1.000 0.057 1.000 0.057 0.635 1 0.618 0.135
## ParagonL  1.000 0.181 1.000 1.000 1.000 1 0.299 0.060
## Pothole   1.000 1.000 1.000 1.000 0.517 1 0.539 1.000
## ShipIsland 1.000 0.617 1.000 0.665 0.122 1 0.533 0.455
## Skyhigh   1.000 0.387 0.178 0.101 0.106 1 0.071 0.030
```

```
alpha=0.05 # /96
```

```
Prop.loci.out.of.HWE <- data.frame(Chisq=apply(HWE.test.chisq<alpha, 2, mean),
                                   MC=apply(HWE.test.MC<alpha, 2, mean))
Prop.loci.out.of.HWE # Type this line again to see results table
```

```
##           Chisq      MC
## A 0.00000000 0.08333333
## B 0.00000000 0.00000000
## C 0.16666667 0.08333333
## D 0.16666667 0.00000000
## E 0.16666667 0.08333333
## F 0.00000000 0.00000000
## G 0.00000000 0.00000000
## H 0.08333333 0.16666667
```

```
Prop.pops.out.of.HWE <- data.frame(Chisq=apply(HWE.test.chisq<alpha, 1, mean),
  MC=apply(HWE.test.MC<alpha, 1, mean))
Prop.pops.out.of.HWE
```

```
##           Chisq    MC
## Airplane  0.000 0.250
## Bachelor  0.000 0.000
## BarkingFox 0.125 0.125
## Bob       0.125 0.125
## Cache     0.125 0.000
## Egg       0.000 0.000
## Frog      0.000 0.000
## GentianL  0.125 0.000
## ParagonL  0.125 0.000
## Pothole   0.000 0.000
## ShipIsland 0.125 0.000
## Skyhigh   0.125 0.125
```

```
Chisq.fdr <- matrix(p.adjust(HWE.test.chisq,method="fdr"),
  nrow=nrow(HWE.test.chisq))
MC.fdr <- matrix(p.adjust(HWE.test.MC, method="fdr"),
  nrow=nrow(HWE.test.MC))
```

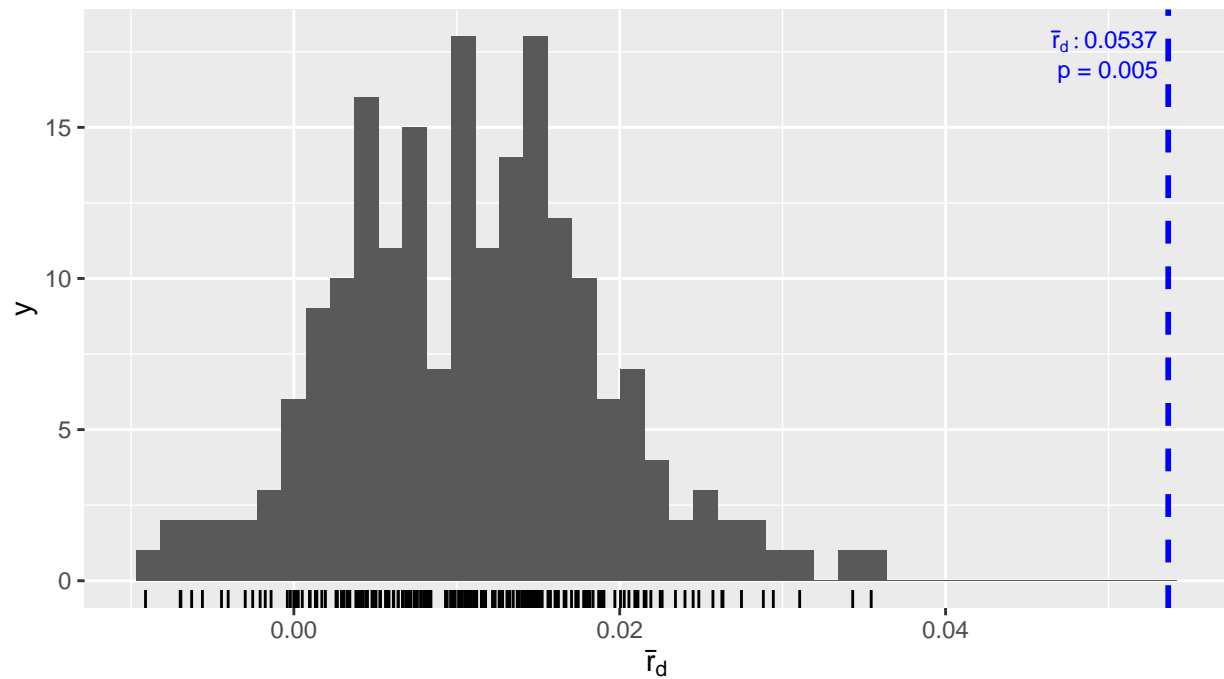
```
Prop.pops.out.of.HWE <- data.frame(Chisq=apply(HWE.test.chisq<alpha, 1, mean),
  MC=apply(HWE.test.MC<alpha, 1, mean),
  Chisq.fdr=apply(Chisq.fdr<alpha, 1, mean),
  MC.fdr=apply(MC.fdr<alpha, 1, mean))
Prop.pops.out.of.HWE
```

```
##           Chisq    MC Chisq.fdr MC.fdr
## Airplane  0.000 0.250    0.000    0
## Bachelor  0.000 0.000    0.000    0
## BarkingFox 0.125 0.125    0.000    0
## Bob       0.125 0.125    0.000    0
## Cache     0.125 0.000    0.000    0
## Egg       0.000 0.000    0.000    0
## Frog      0.000 0.000    0.000    0
## GentianL  0.125 0.000    0.000    0
## ParagonL  0.125 0.000    0.125    0
## Pothole   0.000 0.000    0.000    0
## ShipIsland 0.125 0.000    0.000    0
## Skyhigh   0.125 0.125    0.125    0
```

## Linkage Disequilibrium

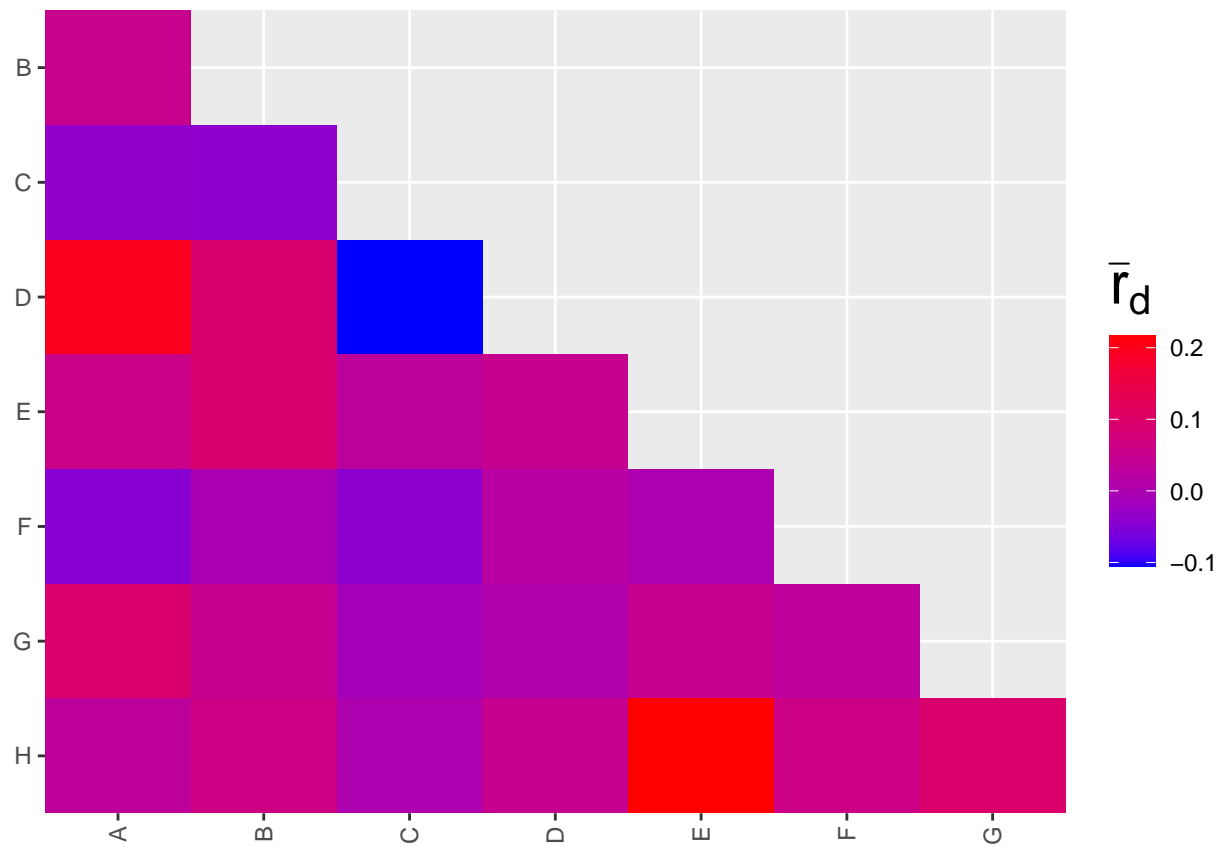
```
poppr::ia(Frogs.genind, sample=199)
```

Population: Total  
 N: 181  
 Data: Frogs.genind  
 Permutations: 199



```
##      Ia      p.Ia      rbarD      p.rD
## 0.33744318 0.00500000 0.05366542 0.00500000
```

```
LD.pair <- poppr::pair.ia(Frogs.genind)
```



LD.pair

```
##          Ia  rbarD
## A:B  0.0485  0.0492
## A:C -0.0314 -0.0335
## A:D  0.1886  0.1966
## A:E  0.0560  0.0569
## A:F -0.0272 -0.0452
## A:G  0.0931  0.0935
## A:H  0.0294  0.0304
## B:C -0.0329 -0.0375
## B:D  0.0903  0.0911
## B:E  0.0910  0.0910
## B:F -0.0013 -0.0025
## B:G  0.0451  0.0452
## B:H  0.0621  0.0623
## C:D -0.0859 -0.1049
## C:E  0.0247  0.0284
## C:F -0.0311 -0.0397
## C:G -0.0107 -0.0118
## C:H  0.0012  0.0015
## D:E  0.0455  0.0458
## D:F  0.0094  0.0199
## D:G  0.0069  0.0070
## D:H  0.0461  0.0462
## E:F  0.0013  0.0025
## E:G  0.0453  0.0454
```

```
## E:H  0.2153  0.2159
## F:G  0.0167  0.0299
## F:H  0.0296  0.0606
## G:H  0.0942  0.0953
```

## Null Alleles

```
# Null alleles: depends on method! See help file.
Null.alleles <- PopGenReport::null.all(Frogs.genind)
```

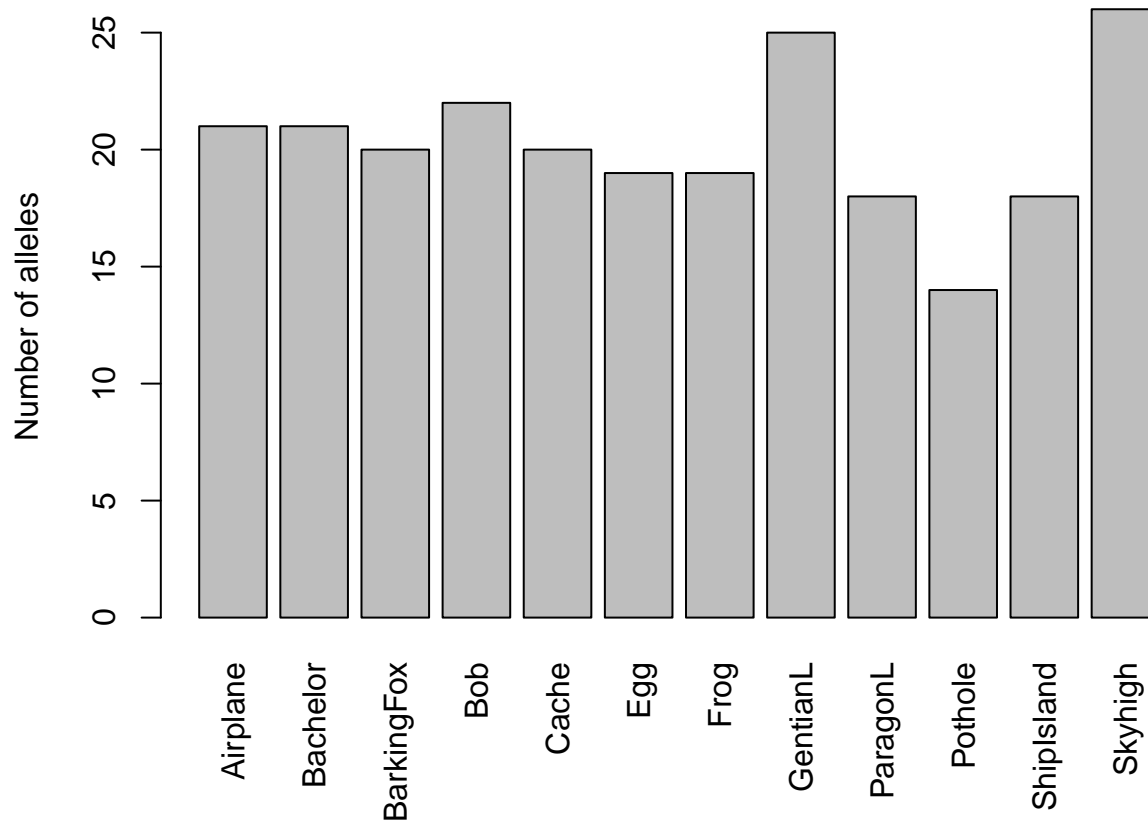
## Genetic Diversity

### allelic richness

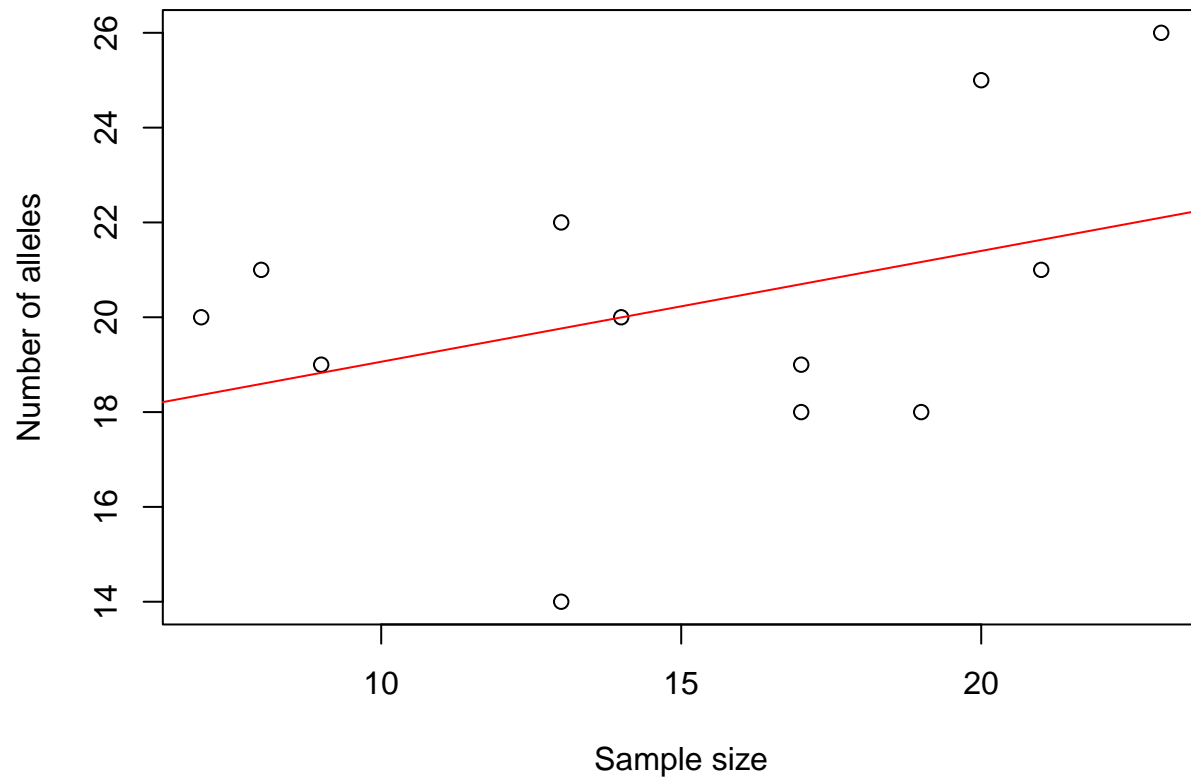
```
Sum <- adegenet::summary(Frogs.genind)
names(Sum)

## [1] "n"          "n.by.pop"  "loc.n.all" "pop.n.all" "NA.perc"   "Hobs"
## [7] "Hexp"

par(mar=c(5.5, 4.5,1,1))
barplot(Sum$pop.n.all, las=3,
        xlab = "", ylab = "Number of alleles")
```



```
plot(Sum$n.by.pop, Sum$pop.n.all,
     xlab = "Sample size", ylab = "Number of alleles")
abline(lm(Sum$pop.n.all ~ Sum$n.by.pop), col = "red")
```

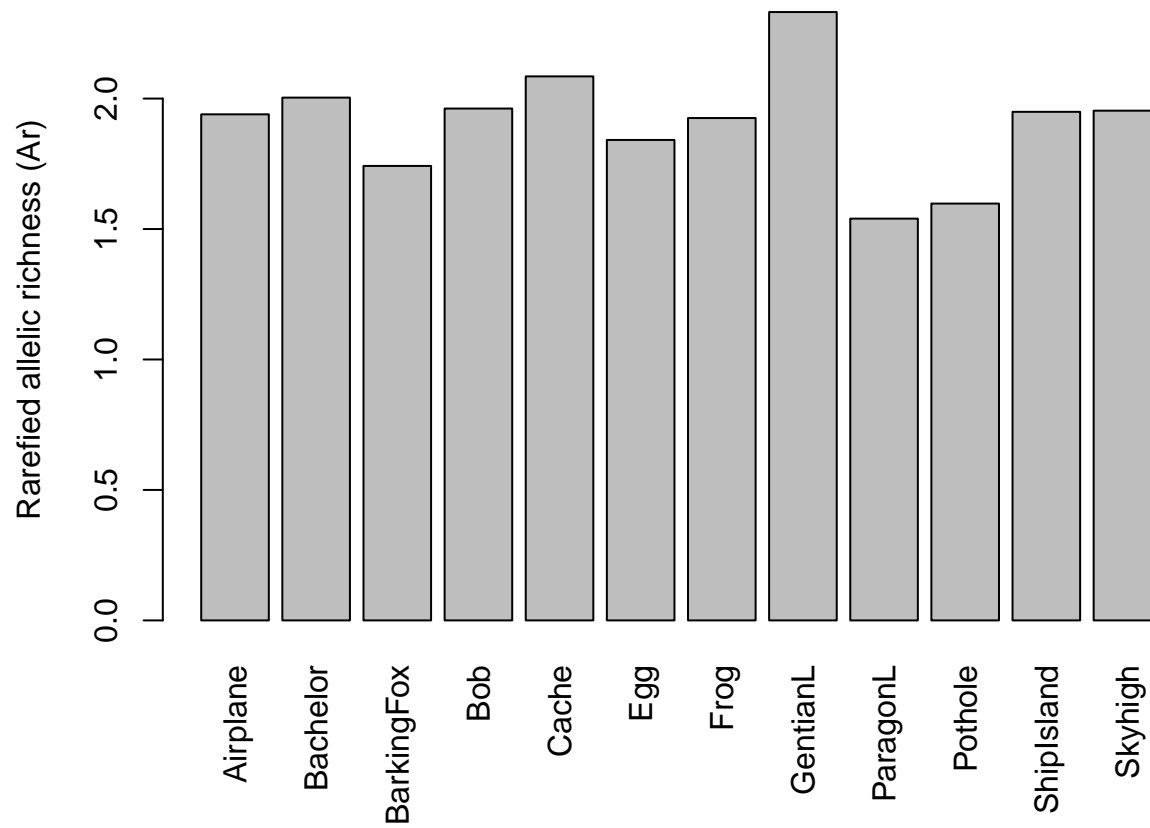


```
Richness <- PopGenReport::allel.rich(Frogs.genind, min.alleles = NULL)
Richness$alleles.sampled
```

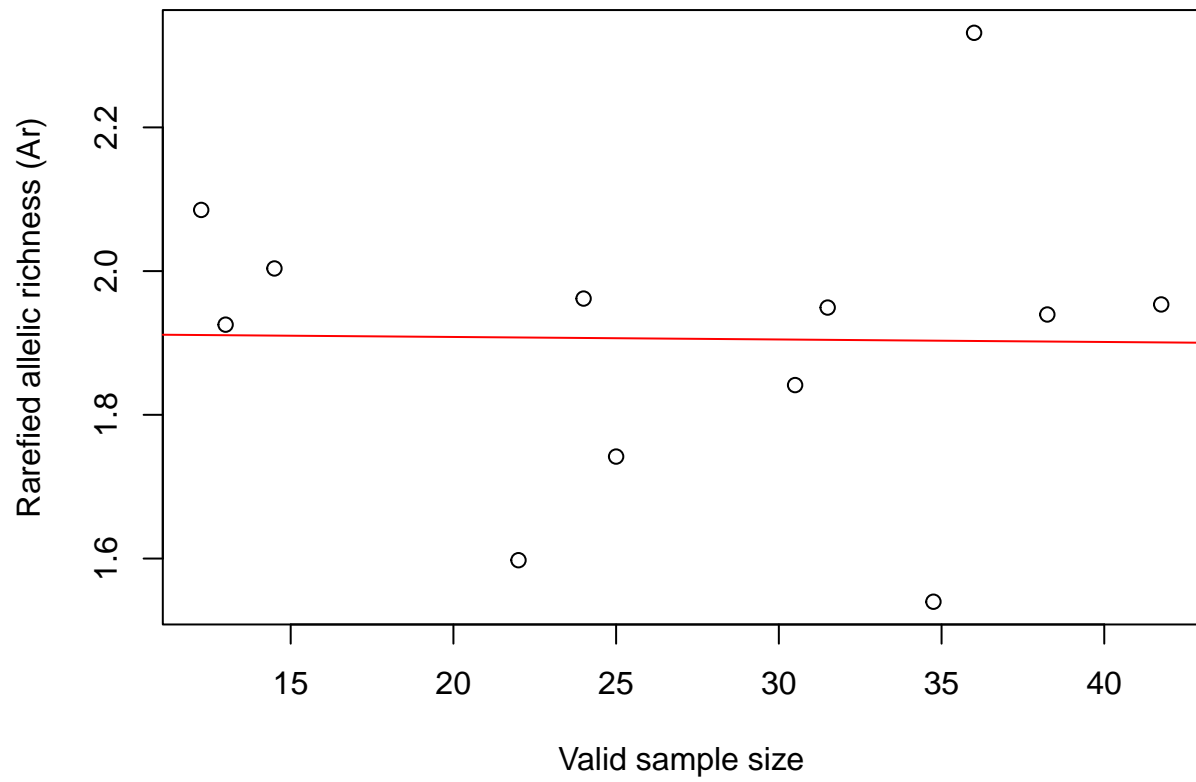
```
## [1] 6
```

```
par(mar=c(5.5, 4.5,1,1))
barplot(Richness$mean.richness, las=3, ylab="Rarefied allelic richness (Ar)")
```





```
plot(colMeans(Richness$pop.sizes), Richness$mean.richness,
     xlab="Valid sample size",
     ylab="Rarefied allelic richness (Ar)")
abline(lm(Richness$mean.richness ~ colMeans(Richness$pop.sizes)), col="red")
```



longer correlated with sample size.

No

## 6.4 Exercise

Task: Drop offspring (seeds, OffID==1) from dataset `pulsatilla_genotypes.csv`, check for HWE by site and locus and calculate Hexp for each site.

Practice indexing:

```
vec <- 1:10
vec == 3 | vec == 6

## [1] FALSE FALSE TRUE FALSE FALSE TRUE FALSE FALSE FALSE
vec[vec == 3 | vec == 6]

## [1] 3 6
```

### Drop offspring

Using `adegenet` and base R

```
library(adegenet)

# 1. CSV file "./downloads/pulsatilla_genotypes.csv" --> data frame
# with base R function read.csv()
Flr <- read.csv("./downloads/pulsatilla_genotypes.csv", header=TRUE)

# 2. Select only adults with base R indexing of data frame
# rows where OffID==0, all columns
Flr <- Flr[Flr$OffID==0,]

# 3. Combine columns with base R function paste()
Flr <- data.frame(Flr[,1:5], loc1 = paste(Flr[,6], Flr[,7], sep=":"),
                  loc2 = paste(Flr[,8], Flr[,9], sep=":"),
                  loc3 = paste(Flr[,10], Flr[,11], sep=":"),
                  loc4 = paste(Flr[,12], Flr[,13], sep=":"),
                  loc5 = paste(Flr[,14], Flr[,15], sep=":"),
                  loc6 = paste(Flr[,16], Flr[,17], sep=":"),
                  loc7 = paste(Flr[,18], Flr[,19], sep=":"))

# 4. Create genind object with "adegenet" function df2genind()
# using NA.char = "NA"
Flr.genind <- df2genind(X=Flr[,c(6:12)], sep=":", ncode=NULL, ind.names= Flr$ID, loc.names=names(Flr[,c(6:12)]))

# 5. Check genind object
Flr.genind

## /// GENIND OBJECT ///////////
##
## // 221 individuals; 7 loci; 105 alleles; size: 130.8 Kb
##
## // Basic content
## @tab: 221 x 105 matrix of allele counts
## @loc.n.all: number of alleles per locus (range: 8-25)
## @loc.fac: locus factor for the 105 columns of @tab
## @all.names: list of allele names for each locus
## @ploidy: ploidy of each individual (range: 2-2)
## @type: codom
## @call: df2genind(X = Flr[, c(6:12)], sep = ":", ncode = NULL, ind.names = Flr$ID,
```

```
## loc.names = names(Flr[, c(6:12)]), pop = Flr$Population,
## NA.char = "NA", ploidy = 2, type = "codom", strata = NULL,
## hierarchy = NULL)
##
## // Optional content
## @pop: population of each individual (group size range: 14-56)
```

```
summary(Flr.genind)
```

```
##
## // Number of individuals: 221
## // Group sizes: 21 56 21 22 14 42 45
## // Number of alleles per locus: 18 8 25 8 19 14 13
## // Number of alleles per group: 63 68 54 50 51 73 53
## // Percentage of missing data: 0.9 %
## // Observed heterozygosity: 0.74 0.54 0.89 0.71 0.74 0.68 0.74
## // Expected heterozygosity: 0.83 0.57 0.89 0.74 0.81 0.76 0.83
```

## Count the number of individuals in each pop

```
table(Flr$Population)
```

```
##
## A03 A21 A25 A26 A41 A45 G05a
## 42 21 56 21 14 22 45
```

## With Gstudio this time

```
library(gstudio)
```

```
## Warning: replacing previous import 'dplyr::union' by 'raster::union' when
## loading 'gstudio'

## Warning: replacing previous import 'dplyr::intersect' by 'raster::intersect'
## when loading 'gstudio'

## Warning: replacing previous import 'dplyr::select' by 'raster::select' when
## loading 'gstudio'

## Registered S3 method overwritten by 'gstudio':
## method from
## print.locus genetics

##
## Attaching package: 'gstudio'

## The following object is masked from 'package:pegas':
##
## Fst

## The following objects are masked from 'package:adegenet':
##
## alleles, ploidy
```

```
library(adegenet)
```

```
# 1. CSV file "./downloads/pulsatilla_genotypes.csv" --> data frame
```

```

# with "gstudio" function read_population()
g.Flr <- read_population("./downloads/pulsatilla_genotypes.csv",
                        type = "column", locus.columns = c(6:19))

# 2. Select only adults with base R indexing of data frame
# rows where OffID==0, all columns
g.Flr <- g.Flr[g.Flr$OffID==0,]

# 3. Nothing to do here

# 4. Create genind object with "adegenet" function df2genind()
# using NA.char = ""
g.Flr.genind <- df2genind(X=g.Flr[,c(6:12)], sep=":", ncode=NULL, ind.names=g.Flr$ID, loc.names=NULL, pop.names=NULL)

# 5. Check genind object
g.Flr.genind

## /// GENIND OBJECT ///
##
## // 221 individuals; 7 loci; 105 alleles; size: 129.8 Kb
##
## // Basic content
## @tab: 221 x 105 matrix of allele counts
## @loc.n.all: number of alleles per locus (range: 8-25)
## @loc.fac: locus factor for the 105 columns of @tab
## @all.names: list of allele names for each locus
## @ploidy: ploidy of each individual (range: 2-2)
## @type: codom
## @call: df2genind(X = g.Flr[, c(6:12)], sep = ":", ncode = NULL, ind.names = g.Flr$ID,
## loc.names = NULL, pop = g.Flr$Population, NA.char = "", ploidy = 2,
## type = "codom", strata = NULL, hierarchy = NULL)
##
## // Optional content
## @pop: population of each individual (group size range: 14-56)

summary(g.Flr.genind)

##
## // Number of individuals: 221
## // Group sizes: 21 56 21 22 14 42 45
## // Number of alleles per locus: 18 8 25 8 19 14 13
## // Number of alleles per group: 63 68 54 50 51 73 53
## // Percentage of missing data: 0.9 %
## // Observed heterozygosity: 0.74 0.54 0.89 0.71 0.74 0.68 0.74
## // Expected heterozygosity: 0.83 0.57 0.89 0.74 0.81 0.76 0.83

```

## Check for HWE by site and locus and calculate Hexp for each site

Test for HWE with pegas by site

```

# Chi-squared test: p-value
HWE.test <- data.frame(sapply(seppop(g.Flr.genind),
                             function(ls) pegas::hw.test(ls, B=0)[,3]))
HWE.test.chisq <- t(data.matrix(HWE.test))
{cat("Chi-squared test (p-values):", "\n")}

```

```
round(HWE.test.chisq,3)}
```

```
## Chi-squared test (p-values):
```

```
##      loc1_a loc2_a loc3_a loc4_a loc5_a loc6_a loc7_a
## A21    0.296  0.730  0.555  0.457  0.068  0.858  0.530
## A25    0.069  0.992  0.404  0.076  0.018  0.930  0.587
## A26    0.000  0.576  0.998  0.508  0.846  0.180  0.354
## A45    0.983  0.828  0.442  0.178  0.359  0.120  0.244
## A41    0.586  0.733  0.179  0.038  0.468  0.956  0.717
## A03    1.000  0.193  0.040  0.047  0.000  0.970  0.490
## G05a   0.436  0.672  0.121  0.954  0.394  0.973  0.104
```

```
# Monte Carlo: p-value
```

```
HWE.test <- data.frame(sapply(seppop(g.Flr.genind),
                             function(ls) pegas::hw.test(ls, B=1000)[,4]))
HWE.test.MC <- t(data.matrix(HWE.test))
{cat("MC permutation test (p-values):", "\n")
round(HWE.test.MC,3)}
```

```
## MC permutation test (p-values):
```

```
##      loc1_a loc2_a loc3_a loc4_a loc5_a loc6_a loc7_a
## A21    0.237  0.639  0.958  0.302  0.119  0.731  0.441
## A25    0.218  1.000  0.348  0.097  0.624  0.558  0.326
## A26    0.095  0.746  0.964  0.397  0.982  0.270  0.152
## A45    0.813  0.491  0.565  0.064  0.267  0.010  0.675
## A41    0.373  0.815  0.072  0.014  0.659  0.945  0.835
## A03    0.886  0.029  0.297  0.063  0.002  0.686  0.402
## G05a   0.109  0.520  0.004  0.964  0.149  0.403  0.152
```

```
alpha=0.05 # /96
```

```
Prop.loci.out.of.HWE <- data.frame(Chisq=apply(HWE.test.chisq<alpha, 2, mean),
                                   MC=apply(HWE.test.MC<alpha, 2, mean))
Prop.loci.out.of.HWE # Type this line again to see results table
```

```
##      Chisq      MC
## loc1_a 0.1428571 0.0000000
## loc2_a 0.0000000 0.1428571
## loc3_a 0.1428571 0.1428571
## loc4_a 0.2857143 0.1428571
## loc5_a 0.2857143 0.1428571
## loc6_a 0.0000000 0.1428571
## loc7_a 0.0000000 0.0000000
```

```
Prop.pops.out.of.HWE <- data.frame(Chisq=apply(HWE.test.chisq<alpha, 1, mean),
                                   MC=apply(HWE.test.MC<alpha, 1, mean))
Prop.pops.out.of.HWE
```

```
##      Chisq      MC
## A21 0.0000000 0.0000000
## A25 0.1428571 0.0000000
## A26 0.1428571 0.0000000
## A45 0.0000000 0.1428571
## A41 0.1428571 0.1428571
## A03 0.4285714 0.2857143
## G05a 0.0000000 0.1428571
```

```

Chisq.fdr <- matrix(p.adjust(HWE.test.chisq,method="fdr"),
                    nrow=nrow(HWE.test.chisq))
MC.fdr <- matrix(p.adjust(HWE.test.MC, method="fdr"),
                 nrow=nrow(HWE.test.MC))

Prop.pops.out.of.HWE <- data.frame(Chisq=apply(HWE.test.chisq<alpha, 1, mean),
                                   MC=apply(HWE.test.MC<alpha, 1, mean),
                                   Chisq.fdr=apply(Chisq.fdr<alpha, 1, mean),
                                   MC.fdr=apply(MC.fdr<alpha, 1, mean))
Prop.pops.out.of.HWE

```

```

##           Chisq           MC Chisq.fdr MC.fdr
## A21  0.0000000 0.0000000 0.0000000      0
## A25  0.1428571 0.0000000 0.0000000      0
## A26  0.1428571 0.0000000 0.1428571      0
## A45  0.0000000 0.1428571 0.0000000      0
## A41  0.1428571 0.1428571 0.0000000      0
## A03  0.4285714 0.2857143 0.1428571      0
## G05a 0.0000000 0.1428571 0.0000000      0

```

## Hexp for each site

```

Hobs <- t(sapply(seppop(g.Flr.genind), function(ls) summary(ls)$Hobs))
Hexp <- t(sapply(seppop(g.Flr.genind), function(ls) summary(ls)$Hexp))
{cat("Expected heterozygosity (Hexp):", "\n")
round(Hexp, 2)}

```

```
## Expected heterozygosity (Hexp):
```

```

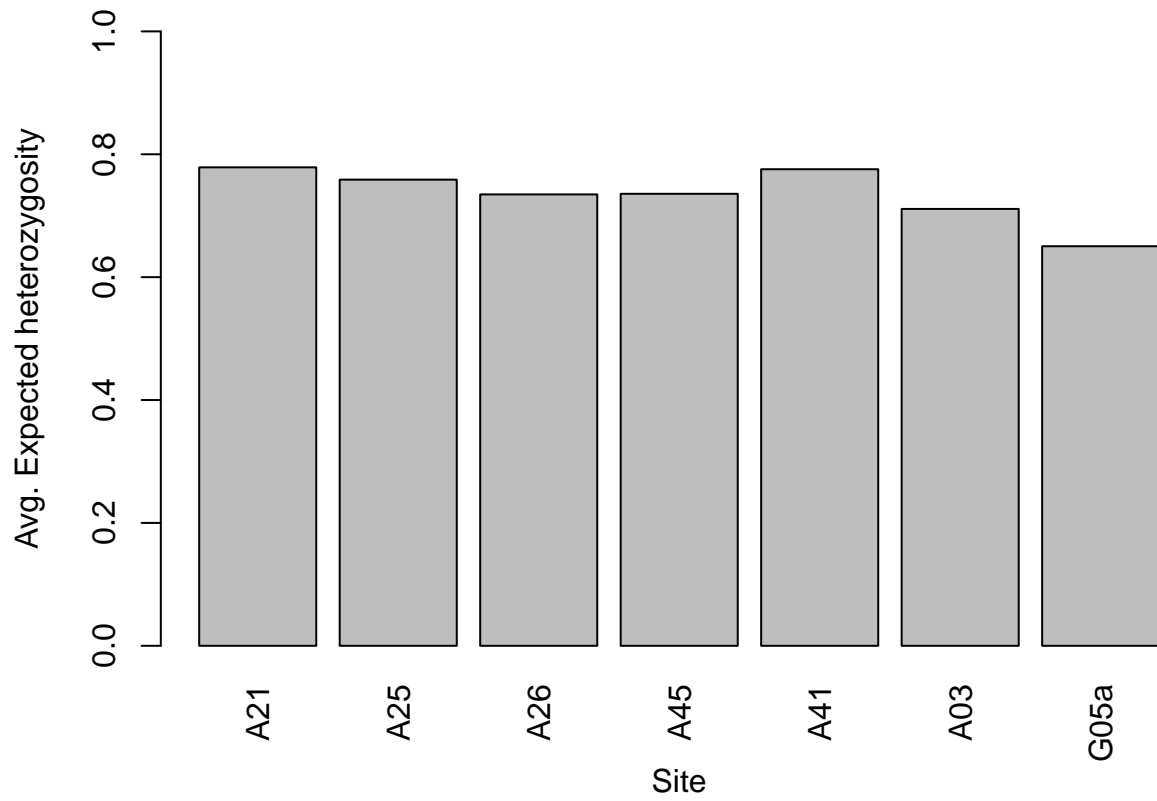
##      loc1_a loc2_a loc3_a loc4_a loc5_a loc6_a loc7_a
## A21    0.82   0.59   0.92   0.74   0.81   0.73   0.83
## A25    0.87   0.59   0.87   0.70   0.64   0.77   0.86
## A26    0.56   0.65   0.78   0.81   0.76   0.80   0.78
## A45    0.78   0.56   0.86   0.67   0.73   0.74   0.80
## A41    0.76   0.68   0.77   0.81   0.82   0.77   0.83
## A03    0.67   0.60   0.89   0.58   0.85   0.67   0.72
## G05a    0.85   0.33   0.83   0.75   0.82   0.50   0.48

```

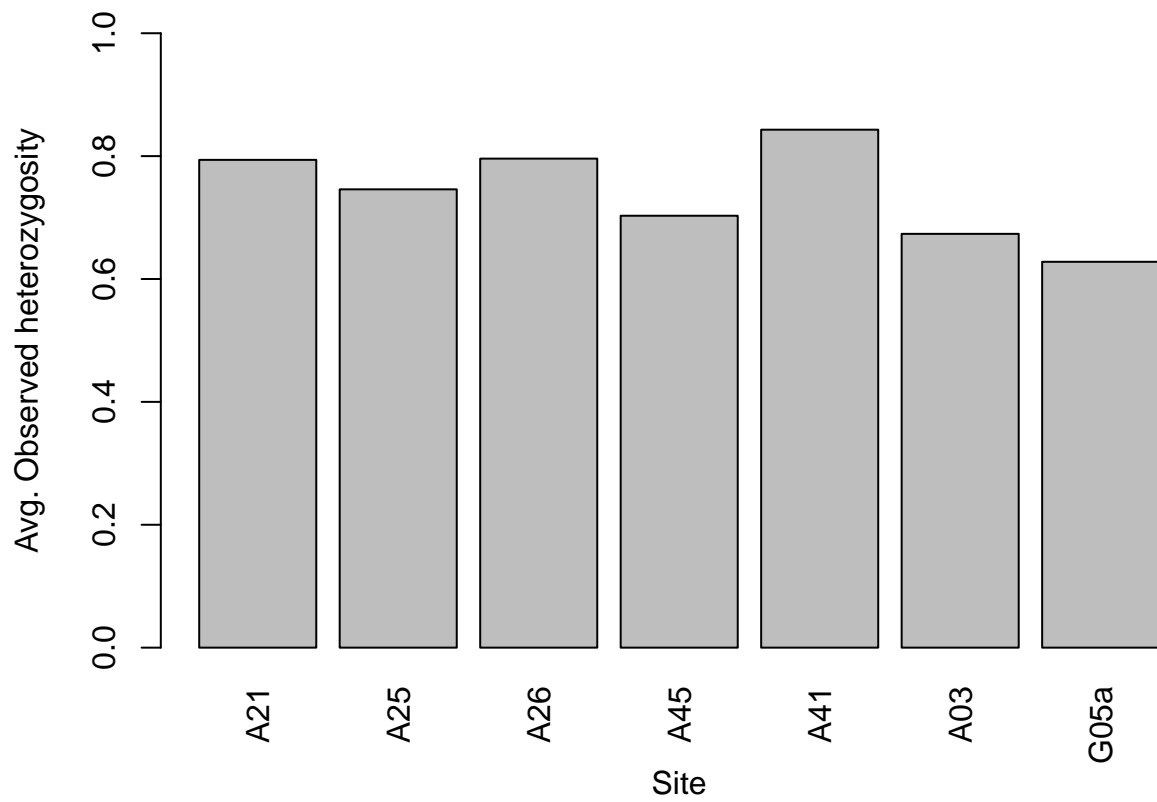
```

par(mar=c(5.5, 4.5, 1, 1))
Hobs.pop <- apply(Hobs, MARGIN = 1, FUN = mean)
Hexp.pop <- apply(Hexp, 1, mean)
barplot(Hexp.pop, ylim=c(0,1), las=3, ylab="Avg. Expected heterozygosity", xlab = "Site")

```



```
barplot(Hobs.pop, ylim=c(0,1), las=3, ylab="Avg. Observed heterozygosity", xlab = "Site")
```



Data frame of summary statistics



```

Sum <- summary(g.Flr.genind)
H.pop <- data.frame(Pop = names(Hobs.pop),
                    n = Sum[2]$n.by.pop,
                    Hobs = Hobs.pop,
                    Hexp = Hexp.pop)
H.pop

```

```

##      Pop  n      Hobs      Hexp
## A21  A21  21  0.7938776 0.7787476
## A25  A25  56  0.7459098 0.7587271
## A26  A26  21  0.7959184 0.7346939
## A45  A45  22  0.7029375 0.7356625
## A41  A41  14  0.8430141 0.7756482
## A03  A03  42  0.6734694 0.7110058
## G05a G05a  45  0.6279942 0.6503175

```

Save “H.pop” for later in output file (eval = FALSE so that it doesn’t do this every time I knit)

```

saveRDS(H.pop, file = "./output/H.pop.rds")

```

**Question: Which site had the lowest expected heterozygosity?**

Site G05a had the lowest average expected heterozygosity, at 0.6503175.