Lab 3: Genetic Diversity

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Section 6.3 Worked Example

https://bookdown.org/hhwagner1/LandGenCourse_book/WE_3.html

Load libraries

```
require(adegenet)
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    0.027
## 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    0.009
## 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")
```

```r
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
```

```r
# 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 permuation test (p-values):", "\n")
round(HWE.test.MC,3)}
```

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

##                A     B     C     D     E F     G     H
## Airplane   0.011 1.000 1.000 0.382 0.630 1 0.250 0.011
## Bachelor   1.000 0.476 1.000 1.000 0.856 1 0.490 0.611
## BarkingFox 1.000 0.225 0.072 1.000 0.749 1 1.000 0.178
## Bob        1.000 1.000 1.000 1.000 0.012 1 1.000 0.271
## Cache      1.000 0.436 0.138 1.000 1.000 1 1.000 0.605
## Egg        1.000 1.000 1.000 1.000 0.079 1 0.526 0.441
## Frog       1.000 1.000 0.085 1.000 0.443 1 1.000 0.163
## GentianL   1.000 0.063 1.000 0.065 0.647 1 0.643 0.151
## ParagonL   1.000 0.163 1.000 1.000 1.000 1 0.339 0.076
## Pothole    1.000 1.000 1.000 1.000 0.552 1 0.546 1.000
## ShipIsland 1.000 0.624 1.000 0.692 0.142 1 0.523 0.450
## Skyhigh    1.000 0.366 0.162 0.093 0.117 1 0.078 0.036
```

```r
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 0.00000000
## 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 0.000
## 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
```

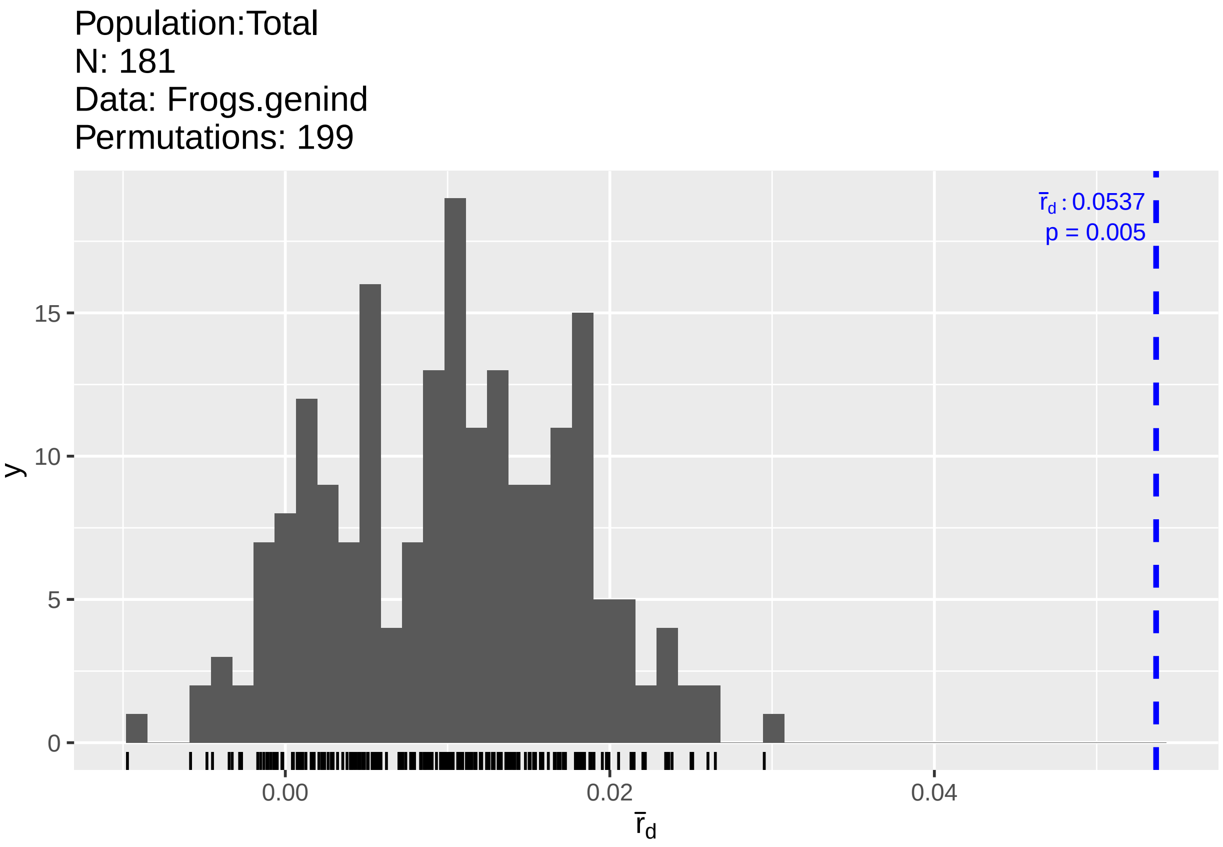
```
Chisq.fdr <- matrix(p.adjust(HWE.test.chisq,method="fdr"),
                    nrow=nrow(HWE.test.chisq))
MC.fdr <- matrix(p.adjust(HWE.test.MC, method="fdr"),
                    nrow=nrow(HWE.test.MC))

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 0.000     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
```

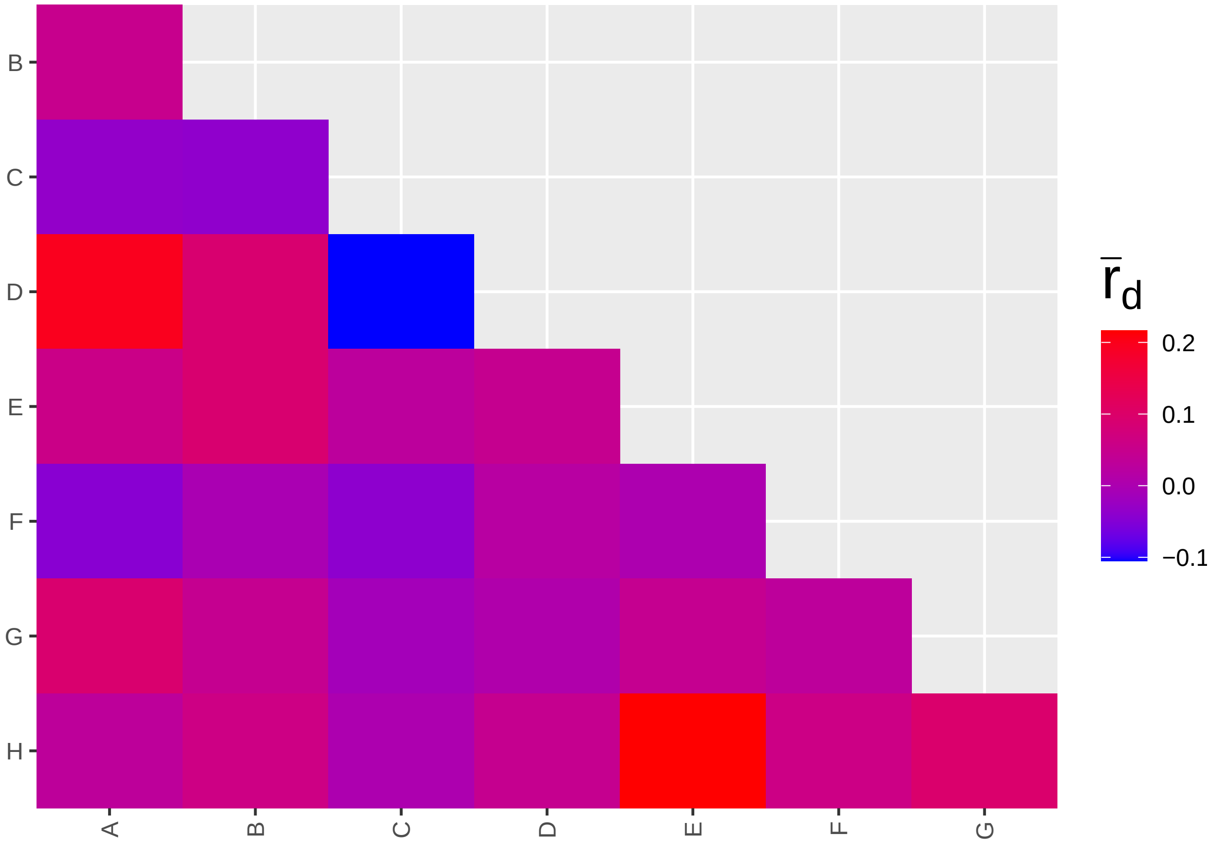
Linkage Disequilibrium

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



```
##          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)
```

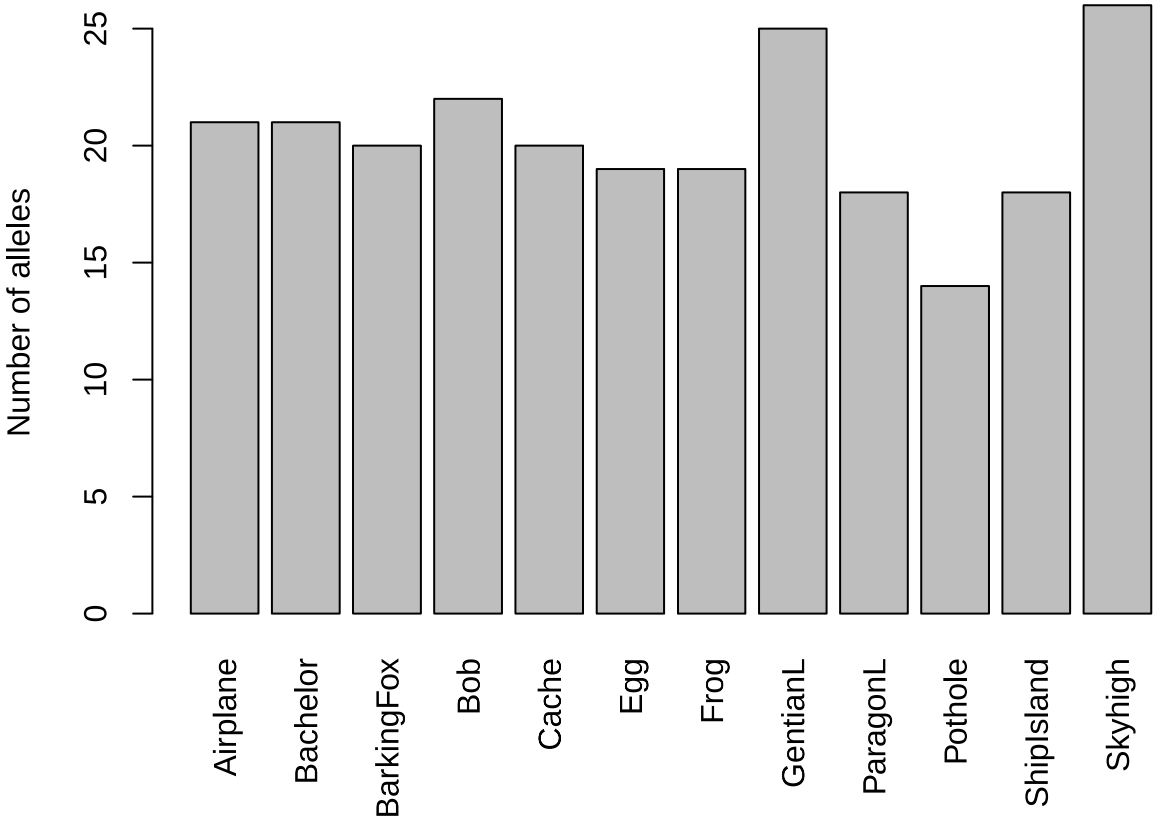
Genetic Diversity

allelic richness

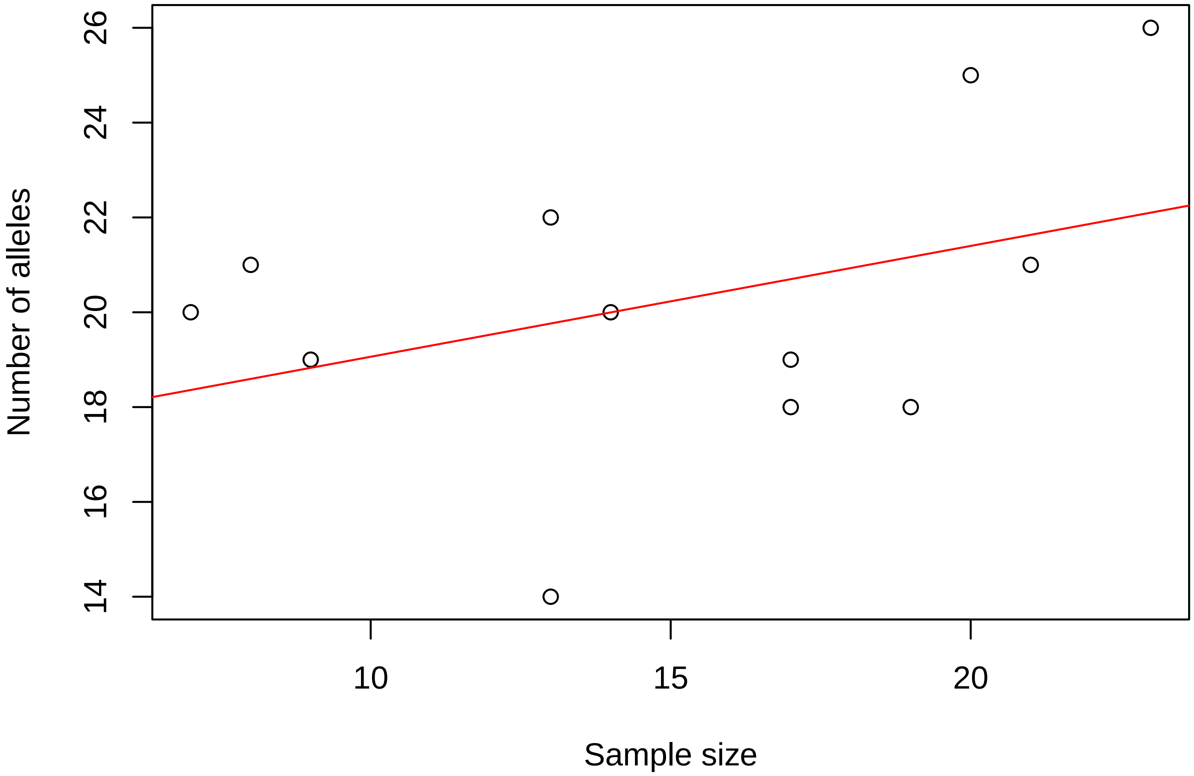
```
Sum <- adegenet::summary(Frogs.genind)
names(Sum)
```

```
## [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")
```



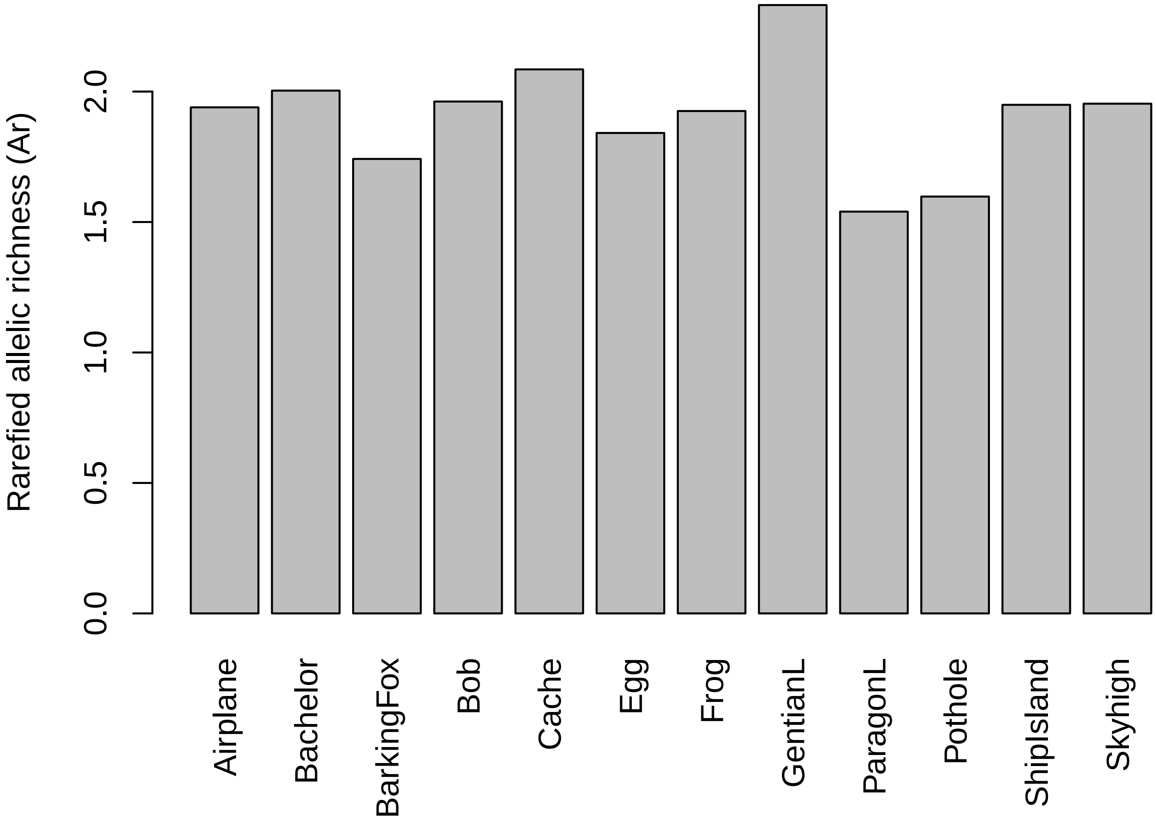
```
plot(Sum$n.by.pop, Sum$pop.n.all,
       xlab = "Sample size", ylab = "Number of alleles")
abline(lm(Sum$pop.n.all ~ Sum$n.by.pop), col = "red")
```



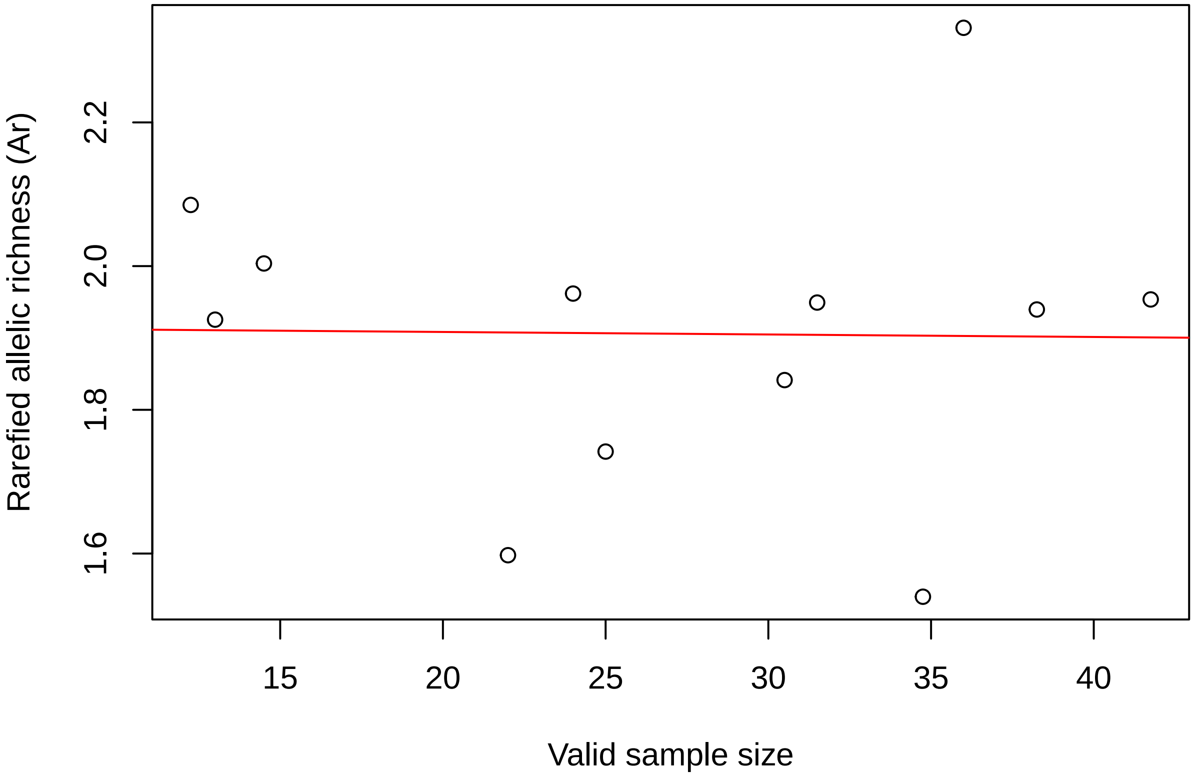
```r
Richness <- PopGenReport::allel.rich(Frogs.genind, min.alleles = NULL)
Richness$alleles.sampled
```

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

```r
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")
```



No longer correlated with sample size.

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:

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

```
##  [1] FALSE FALSE  TRUE FALSE FALSE  TRUE FALSE FALSE FALSE FALSE
```

```r
vec[vec == 3 | vec == 6]
```

```
## [1] 3 6
```

Drop offspring

Using adegenet and base R

```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

# 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)
```

```r
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

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

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

With Gstudio this time

```r
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
```

```r
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, po

# 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)
```

```r
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

```r
# 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 permuation test (p-values):", "\n")
round(HWE.test.MC,3)}
```

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

```
##      loc1_a loc2_a loc3_a loc4_a loc5_a loc6_a loc7_a
## A21   0.259  0.640  0.945  0.334  0.105  0.707  0.429
## A25   0.195  1.000  0.342  0.097  0.621  0.538  0.293
## A26   0.074  0.718  0.953  0.370  0.984  0.281  0.158
## A45   0.784  0.521  0.555  0.068  0.249  0.010  0.662
## A41   0.345  0.821  0.078  0.025  0.618  0.932  0.803
## A03   0.862  0.024  0.262  0.058  0.002  0.691  0.397
## G05a  0.102  0.566  0.010  0.961  0.137  0.393  0.148
```

```
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
```

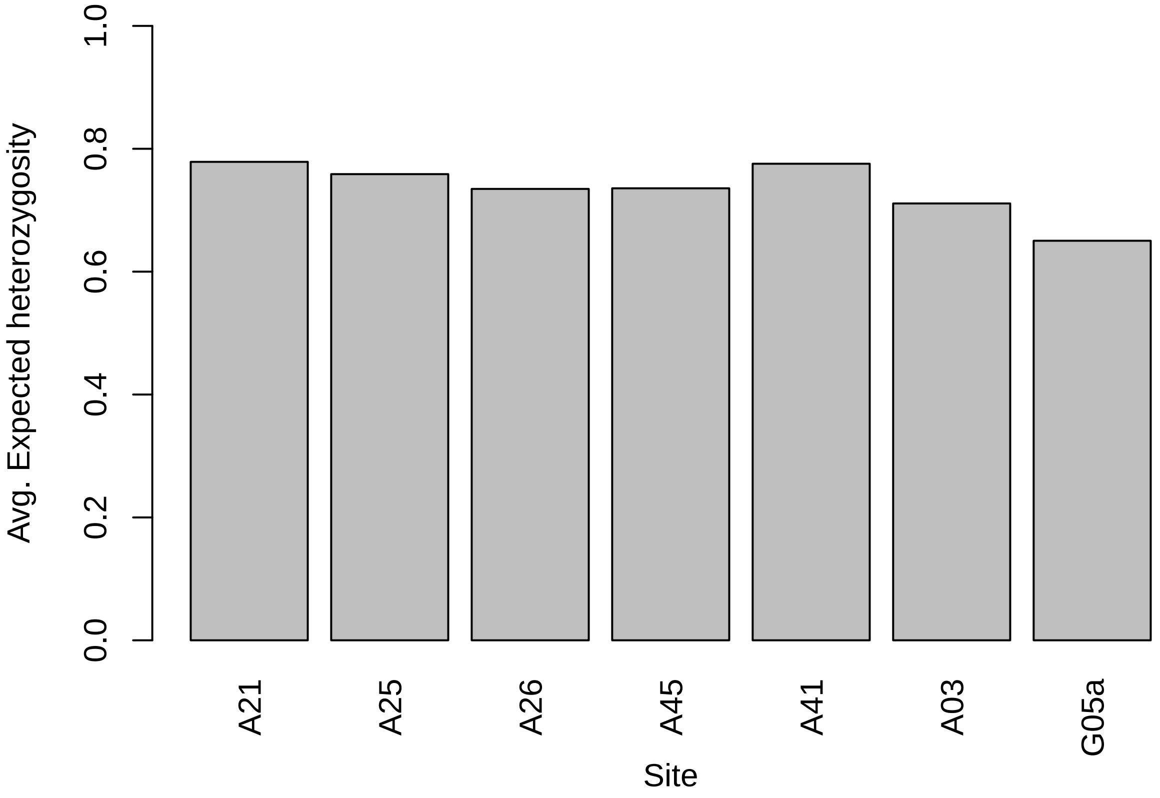
Hexp for each site

```
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)}
```

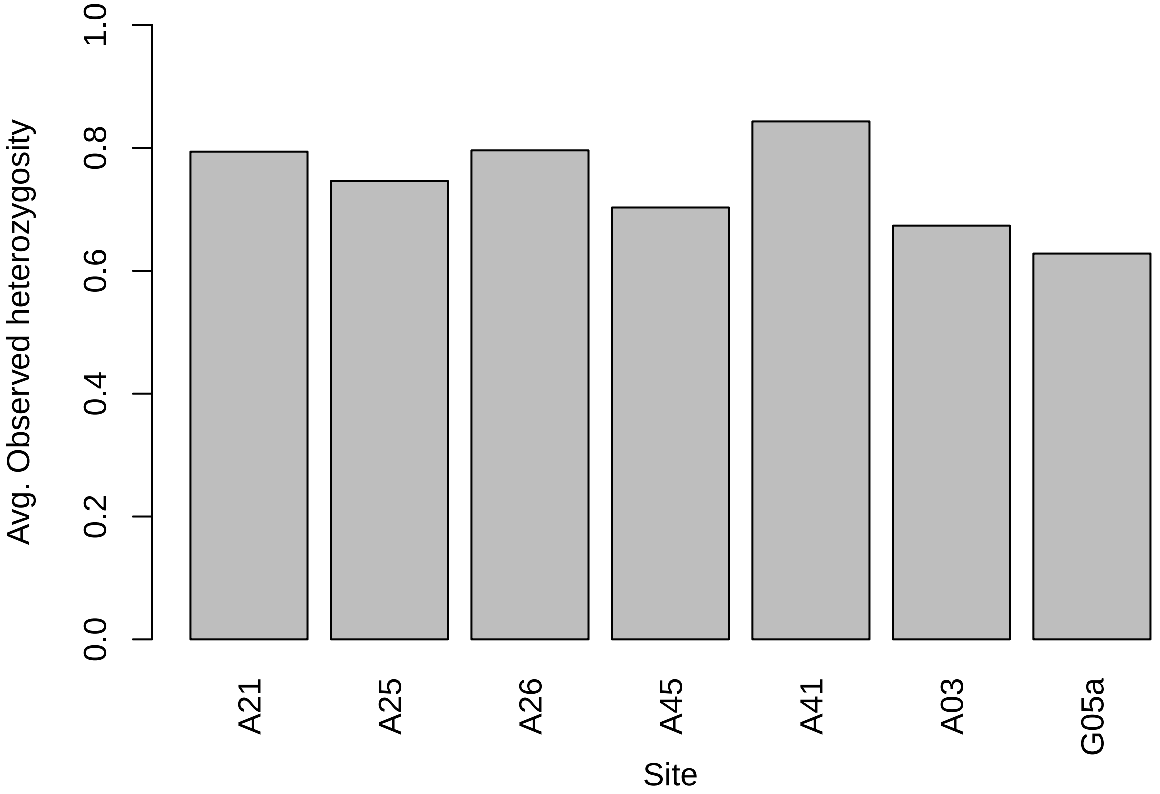
```
## Expected heterozygosity (Hexp):
```

```
##      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.