Lab 3

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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

```r
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)
```

```r
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:

```r
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    0.030
## C 136.522  6       0.000    0.000
## D  83.338  6       0.000    0.000
## E 226.803 36       0.000    0.001
## F   0.024  3       0.999    1.000
## G  12.349  6       0.055    0.004
## H  76.813 28       0.000    0.000
```

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

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

##                 A     B     C     D     E F     G     H
## Airplane   0.018 1.000 1.000 0.415 0.616 1 0.256 0.012
## Bachelor   1.000 0.430 1.000 1.000 0.850 1 0.489 0.596
## BarkingFox 1.000 0.221 0.067 1.000 0.772 1 1.000 0.154
## Bob        1.000 1.000 1.000 1.000 0.017 1 1.000 0.279
## Cache      1.000 0.376 0.149 1.000 1.000 1 1.000 0.618
## Egg        1.000 1.000 1.000 1.000 0.078 1 0.546 0.415
## Frog       1.000 1.000 0.085 1.000 0.452 1 1.000 0.161
## GentianL   1.000 0.067 1.000 0.071 0.685 1 0.647 0.143
## ParagonL   1.000 0.185 1.000 1.000 1.000 1 0.306 0.071
## Pothole    1.000 1.000 1.000 1.000 0.554 1 0.520 1.000
## ShipIsland 1.000 0.603 1.000 0.685 0.141 1 0.569 0.448
## Skyhigh    1.000 0.336 0.183 0.081 0.131 1 0.081 0.038
```

```
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
```

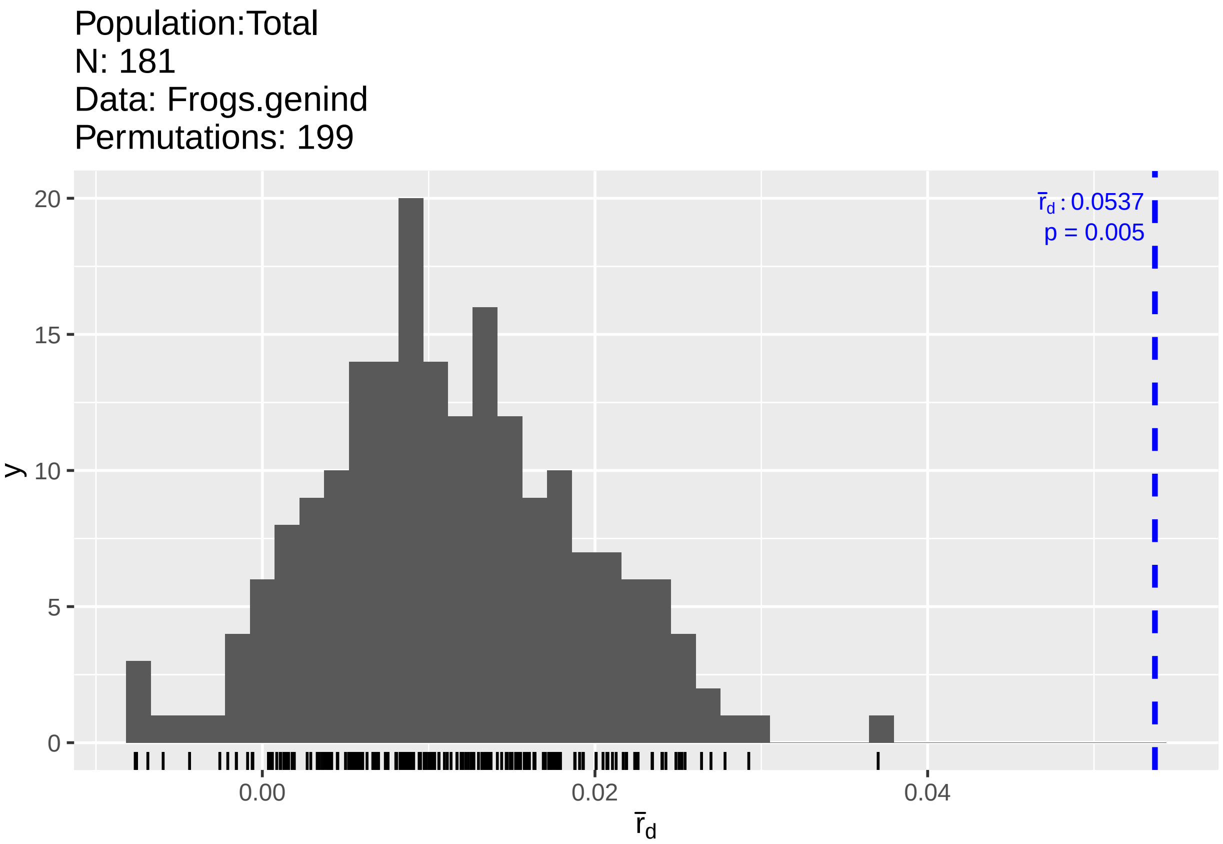
```
Chisq.fdr <- matrix(p.adjust(HWE.test.chisq,method="fdr"),
                    nrow=nrow(HWE.test.chisq))
MC.fdr <- matrix(p.adjust(HWE.test.MC, method="fdr"),
                    nrow=nrow(HWE.test.MC))

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
```

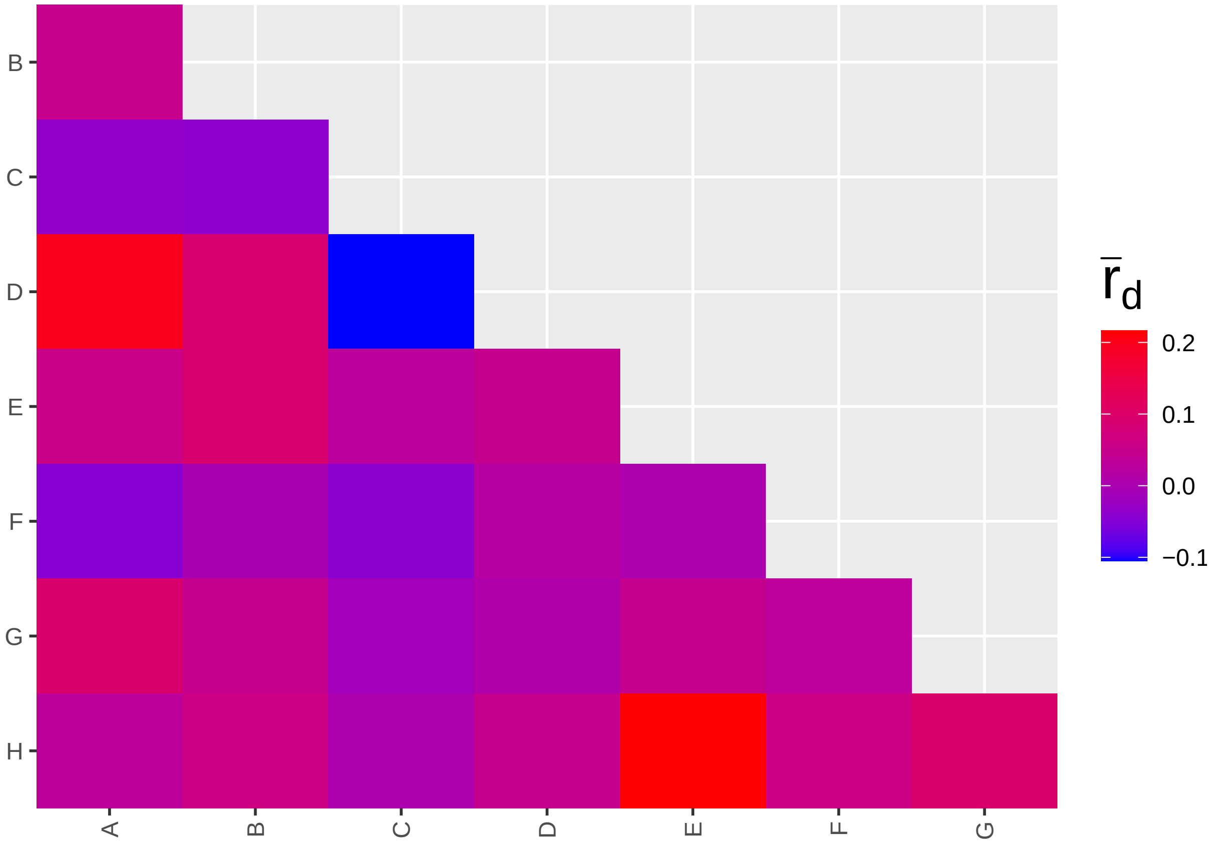
Linkage Disequilibrium

```
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)
```

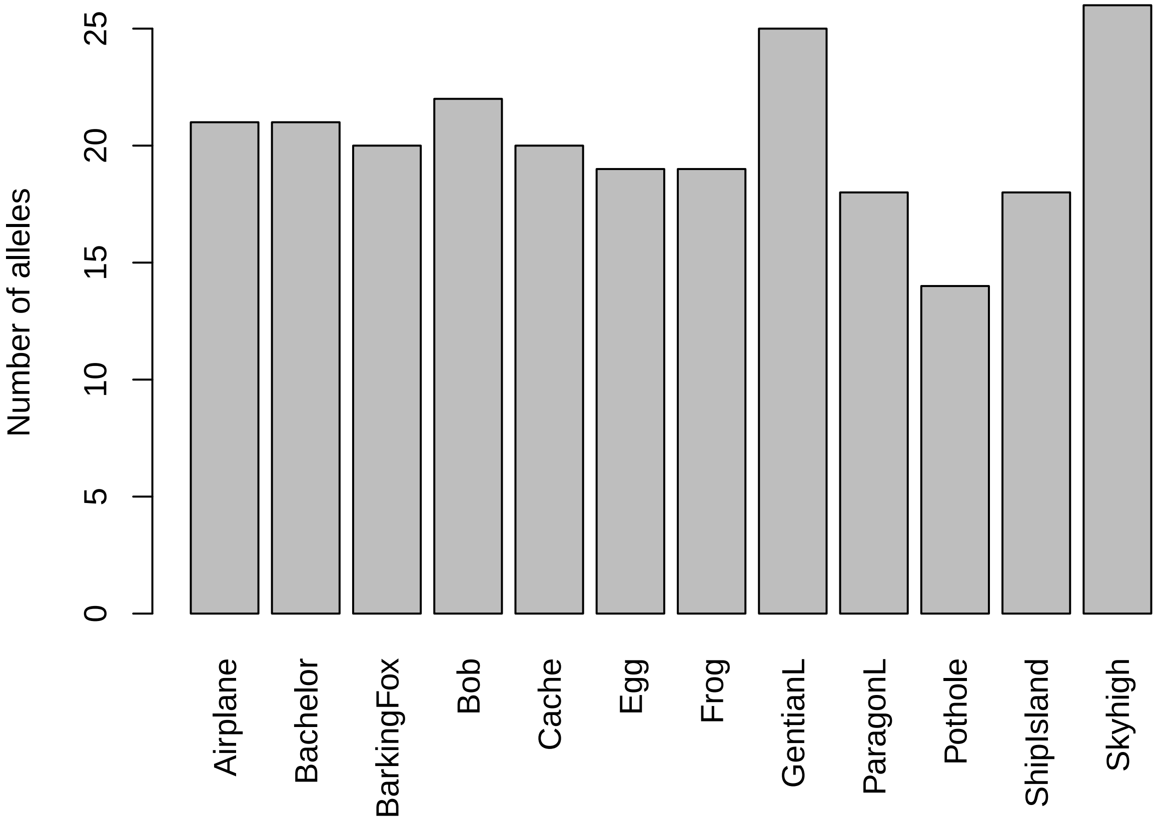
Genetic Diversity

allelic richness

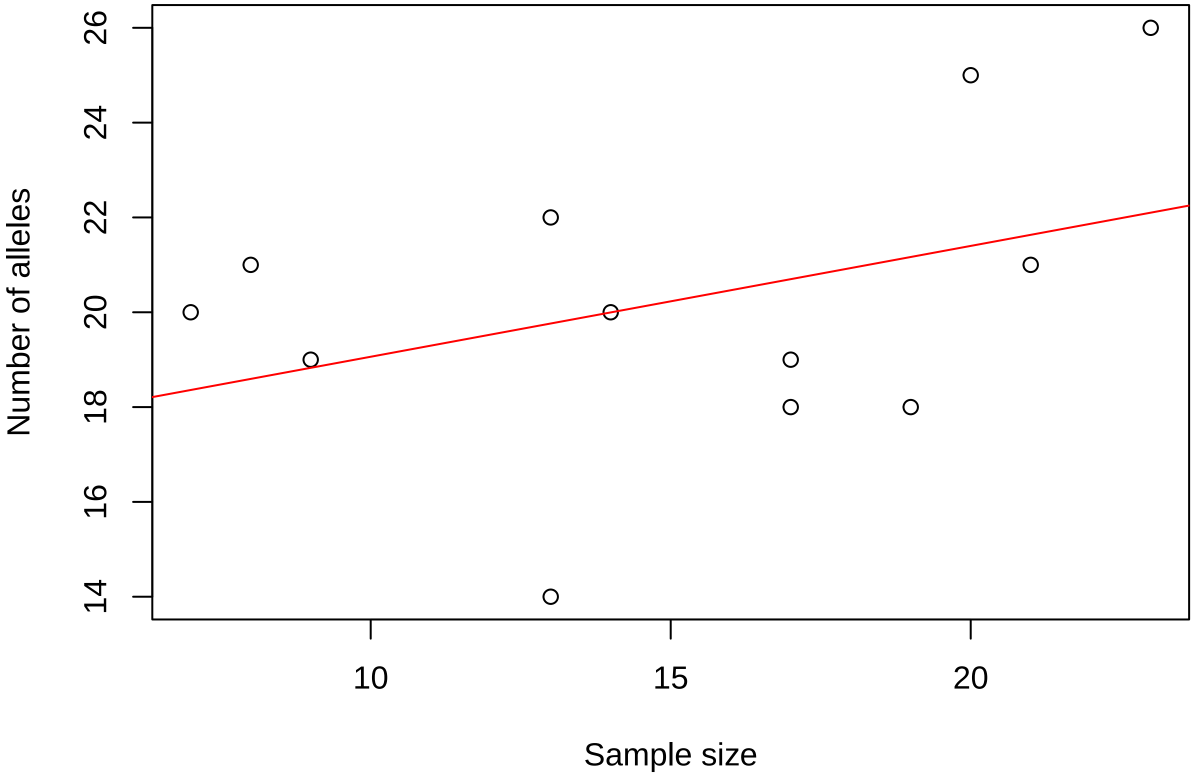
```
Sum <- adegenet::summary(Frogs.genind)
names(Sum)
```

```
## [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")
```



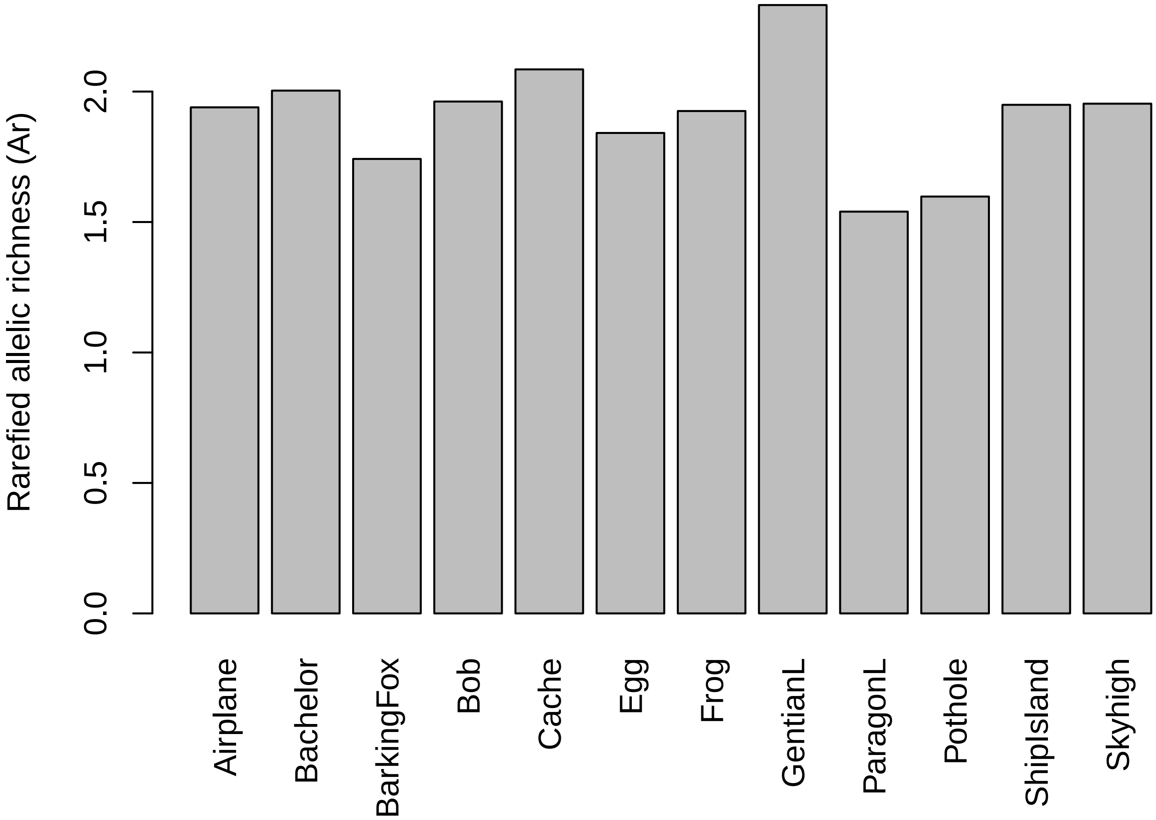
```
plot(Sum$n.by.pop, Sum$pop.n.all,
       xlab = "Sample size", ylab = "Number of alleles")
abline(lm(Sum$pop.n.all ~ Sum$n.by.pop), col = "red")
```



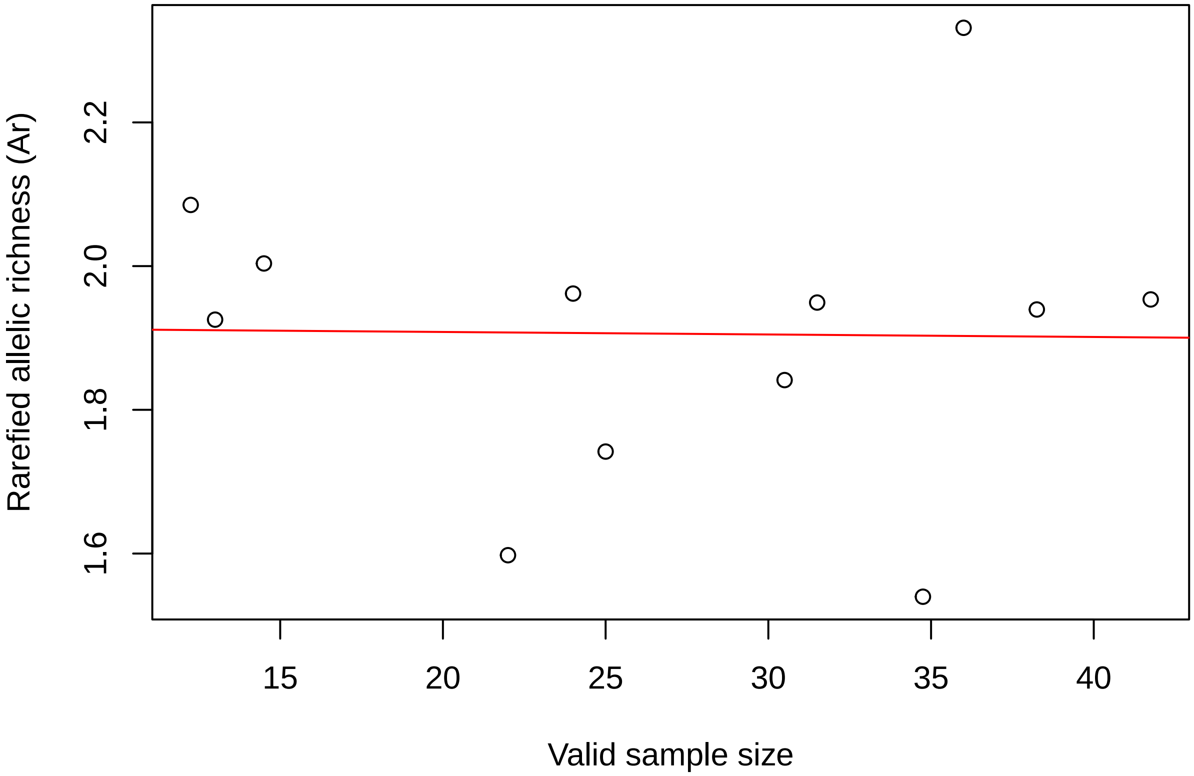
```
Richness <- PopGenReport::allel.rich(Frogs.genind, min.alleles = NULL)
Richness$alleles.sampled
```

```
## [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")
```



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.

Drop offspring

```
Flowers <- read.csv("./downloads/pulsatilla_genotypes.csv", header=TRUE)
as_tibble(Flowers)
```

```
## # A tibble: 536 x 19
##       ID OffID Population        X        Y loc1_a loc1_b loc2_a loc2_b loc3_a
##    <int> <int> <chr>         <dbl>    <dbl>  <int>  <int>  <int>  <int>  <int>
##  1    62     0 A21        4426941. 5427173.    340    340    422    422    413
##  2    64     0 A21        4426933. 5427178.    334    334    424    424    417
##  3    65     0 A21        4426936. 5427173.    338    340    417    422    417
##  4    66     0 A21        4426937. 5427174.    340    344    422    422    411
##  5    68     0 A21        4426934. 5427171.    336    342    417    422    423
##  6    69     0 A21        4426933. 5427166.    336    346    422    422    417
##  7    75     0 A21        4426925. 5427175.    340    340    422    422    415
##  8    76     0 A21        4426925. 5427173.    338    340    417    422    413
##  9    77     0 A21        4426922. 5427174.    344    352    422    422    415
## 10    78     0 A21        4426922. 5427174.    342    352    417    424    425
## # i 526 more rows
## # i 9 more variables: loc3_b <int>, loc4_a <int>, loc4_b <int>, loc5_a <int>,
## #   loc5_b <int>, loc6_a <int>, loc6_b <int>, loc7_a <int>, loc7_b <int>
```

Filter offspring (seeds) from the dataset

```
Flowers <- filter(Flowers, OffID==0)
as_tibble(Flowers)
```

```
## # A tibble: 221 x 19
##       ID OffID Population       X       Y loc1_a loc1_b loc2_a loc2_b loc3_a
##    <int> <int> <chr>        <dbl>   <dbl>  <int>  <int>  <int>  <int>  <int>
##  1    62     0 A21        4426941. 5427173.    340    340    422    422    413
##  2    64     0 A21        4426933. 5427178.    334    334    424    424    417
##  3    65     0 A21        4426936. 5427173.    338    340    417    422    417
##  4    66     0 A21        4426937. 5427174.    340    344    422    422    411
##  5    68     0 A21        4426934. 5427171.    336    342    417    422    423
##  6    69     0 A21        4426933. 5427166.    336    346    422    422    417
##  7    75     0 A21        4426925. 5427175.    340    340    422    422    415
##  8    76     0 A21        4426925. 5427173.    338    340    417    422    413
##  9    77     0 A21        4426922. 5427174.    344    352    422    422    415
## 10    78     0 A21        4426922. 5427174.    342    352    417    424    425
## # i 211 more rows
## # i 9 more variables: loc3_b <int>, loc4_a <int>, loc4_b <int>, loc5_a <int>,
## #   loc5_b <int>, loc6_a <int>, loc6_b <int>, loc7_a <int>, loc7_b <int>
```

Count the number of individuals in each pop

```
table(Flowers$Population)
```

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

Dataframe with the first 5 columns, then paste loc1__a:loc1__b, etc.

```
Flowers <- data.frame(Flowers[,1:5],loc1 = paste(Flowers$loc1_a, Flowers$loc1_b, sep=":"), loc2 = paste
as_tibble(Flowers)
```

```
## # A tibble: 221 x 12
##       ID OffID Population       X       Y loc1   loc2  loc3  loc4  loc5  loc6
##    <int> <int> <chr>        <dbl>   <dbl> <chr>  <chr> <chr> <chr> <chr> <chr>
##  1    62     0 A21        4426941. 5427173. 340:3~ 422:~ 413:~ 446:~ 121:~ 155:~
##  2    64     0 A21        4426933. 5427178. 334:3~ 424:~ 417:~ 444:~ 122:~ 155:~
##  3    65     0 A21        4426936. 5427173. 338:3~ 417:~ 417:~ 446:~ 135:~ 153:~
##  4    66     0 A21        4426937. 5427174. 340:3~ 422:~ 411:~ 446:~ 122:~ 157:~
##  5    68     0 A21        4426934. 5427171. 336:3~ 417:~ 423:~ 448:~ 119:~ 155:~
##  6    69     0 A21        4426933. 5427166. 336:3~ 422:~ 417:~ 444:~ 122:~ 155:~
##  7    75     0 A21        4426925. 5427175. 340:3~ 422:~ 415:~ 442:~ 121:~ 152:~
##  8    76     0 A21        4426925. 5427173. 338:3~ 417:~ 413:~ 446:~ 126:~ 155:~
##  9    77     0 A21        4426922. 5427174. 344:3~ 422:~ 415:~ 446:~ 121:~ 155:~
## 10    78     0 A21        4426922. 5427174. 342:3~ 417:~ 425:~ 446:~ 121:~ 157:~
## # i 211 more rows
## # i 1 more variable: loc7 <chr>
```

Create 'genind' object:

```
Flowers.genind <- df2genind(X=Flowers[,c(6:12)], sep=":", ncode=NULL, ind.names= Flowers$ID, loc.names=
```

Get info on genind object:

```
Flowers.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 = Flowers[, c(6:12)], sep = ":", ncode = NULL, ind.names = Flowers$ID,
##     loc.names = names(Flowers[, c(6:12)]), pop = Flowers$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(Flowers.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
```

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)

g.Flowers <- read_population("./downloads/pulsatilla_genotypes.csv",type = "column",locus.columns = c(6

g.Flowers <- g.Flowers[g.Flowers$OffID==0,] # filter() is not working

g.Flowers.genind <- df2genind(X=g.Flowers[,c(6:12)], sep=":", ncode=NULL, ind.names=g.Flowers$ID, loc.na

g.Flowers.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.Flowers[, c(6:12)], sep = ":", ncode = NULL,
##     ind.names = g.Flowers$ID, loc.names = NULL, pop = g.Flowers$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.Flowers.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.Flowers.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.Flowers.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   0.257  0.668  0.941  0.296  0.123  0.721  0.424
## A25   0.191  1.000  0.339  0.101  0.634  0.547  0.321
## A26   0.081  0.739  0.961  0.407  0.981  0.238  0.130
## A45   0.793  0.496  0.521  0.053  0.236  0.011  0.631
## A41   0.378  0.820  0.070  0.015  0.637  0.927  0.838
## A03   0.868  0.019  0.286  0.069  0.008  0.681  0.408
## G05a  0.123  0.540  0.013  0.972  0.165  0.370  0.154
```

```
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
```

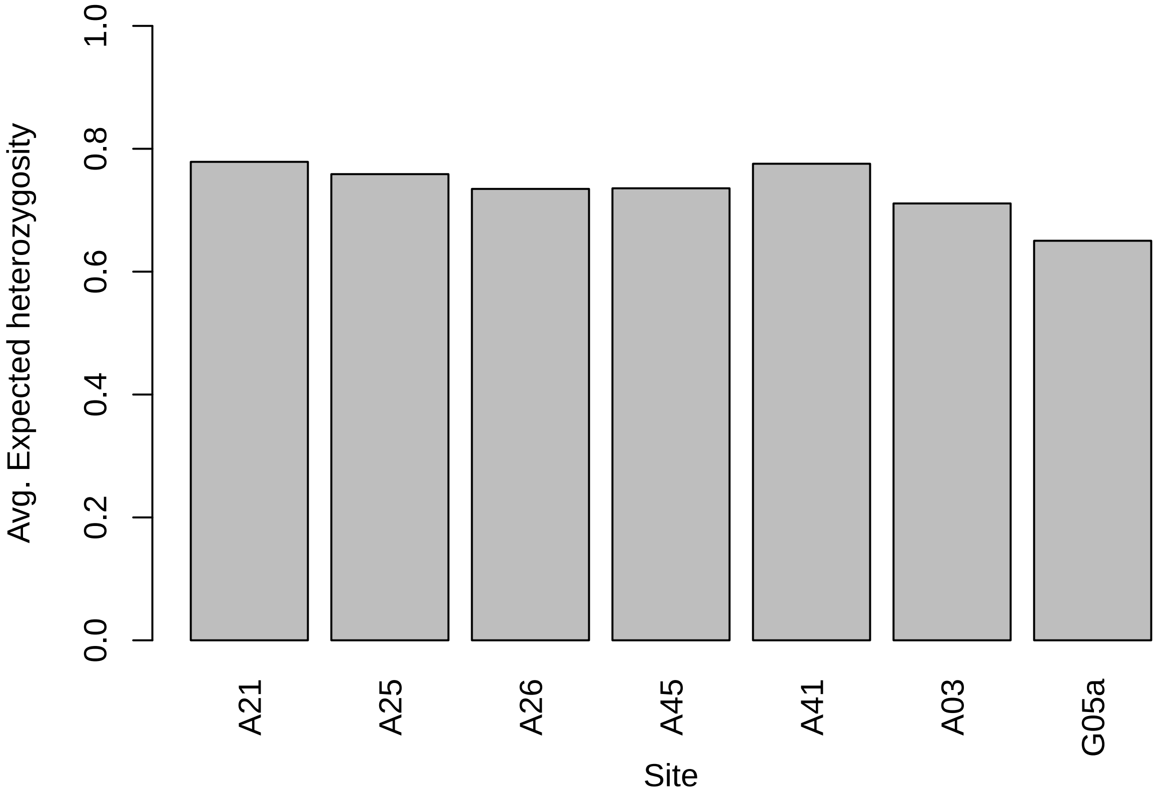
Hexp for each site

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

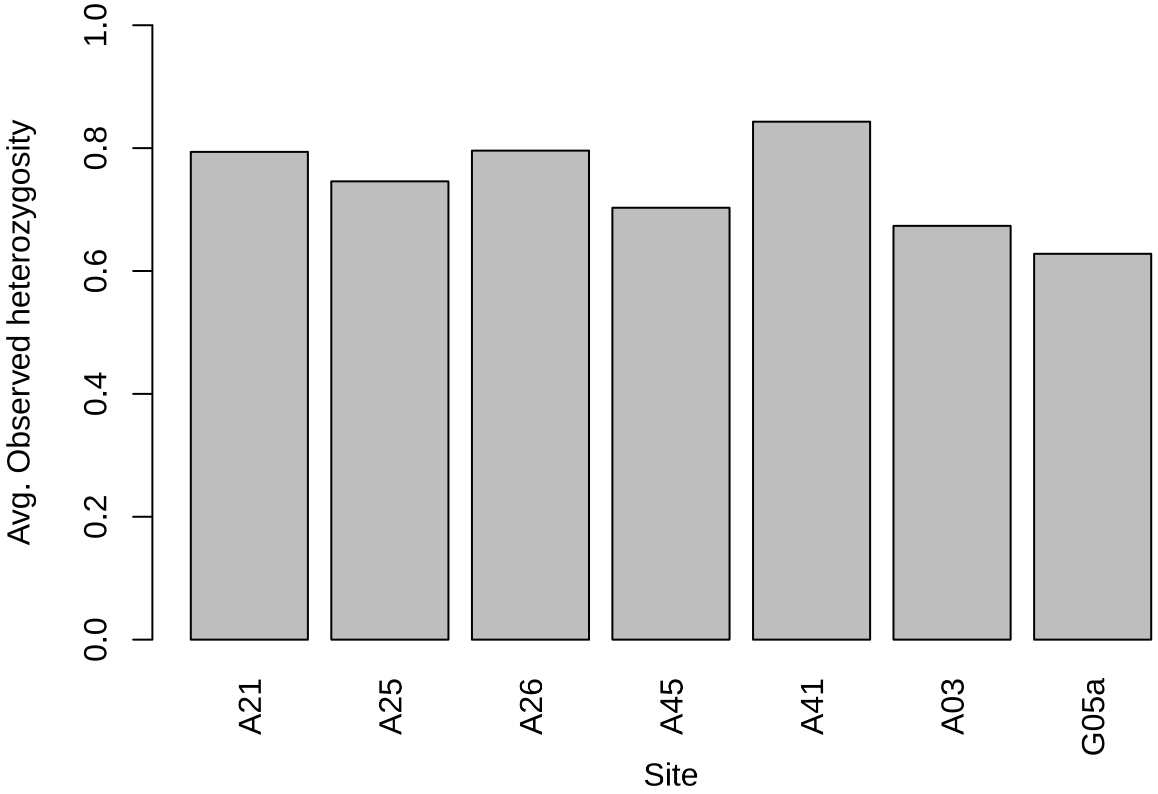
```
## Expected heterozygosity (Hexp):
```

```
##      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.Flowers.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.