Peelii Larval Structure - Sites and Years

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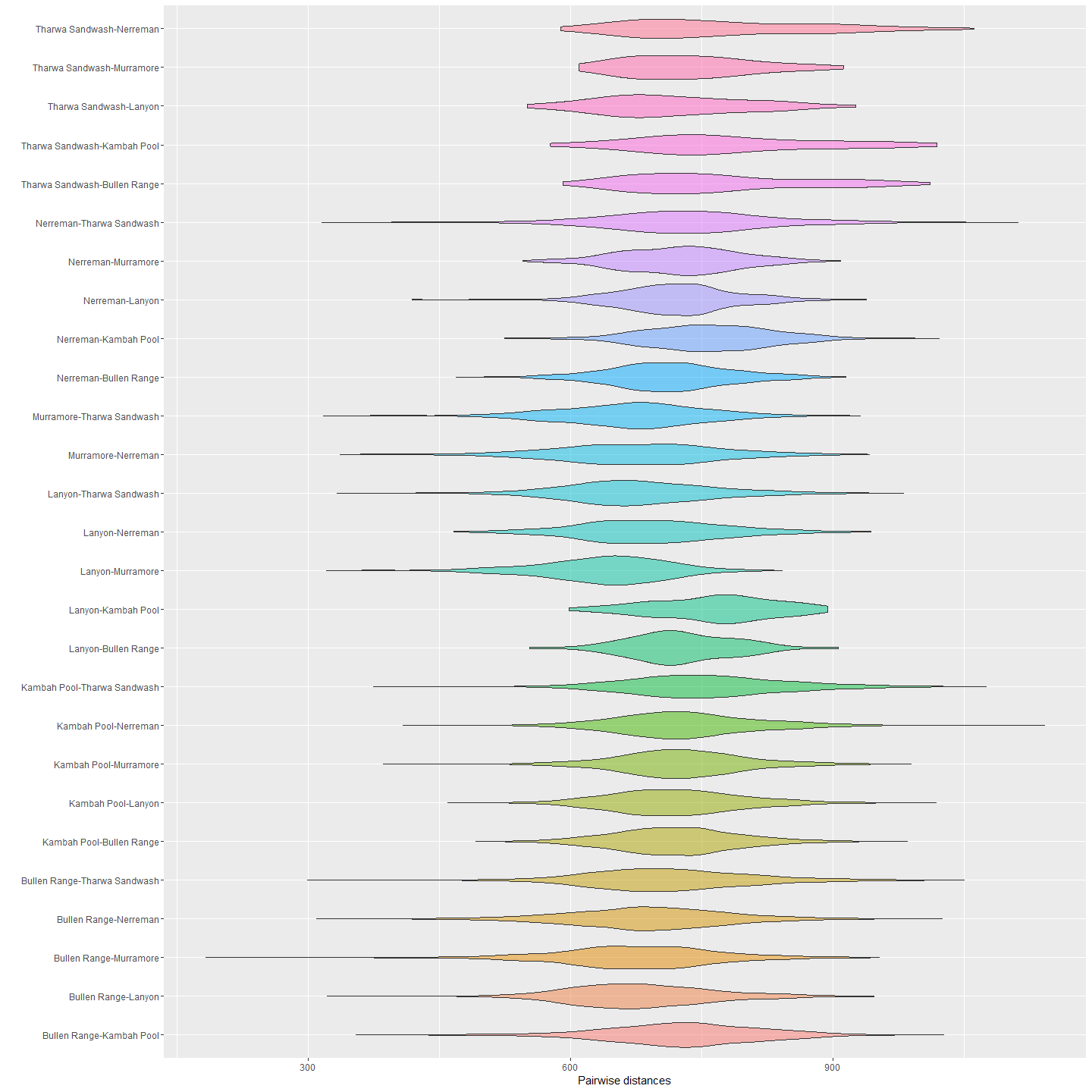
Wed Sep 21 11:30:42 AM 2016

a<-suppressPackageStartupMessages({  
library(plyr)  
library(dplyr)  
library(ggplot2)  
library(dart)  
library(tsne)  
library(adegenet)   
library(pegas)  
library(hierfstat)  
library(ade4)  
library(mmod)  
library(poppr)  
})

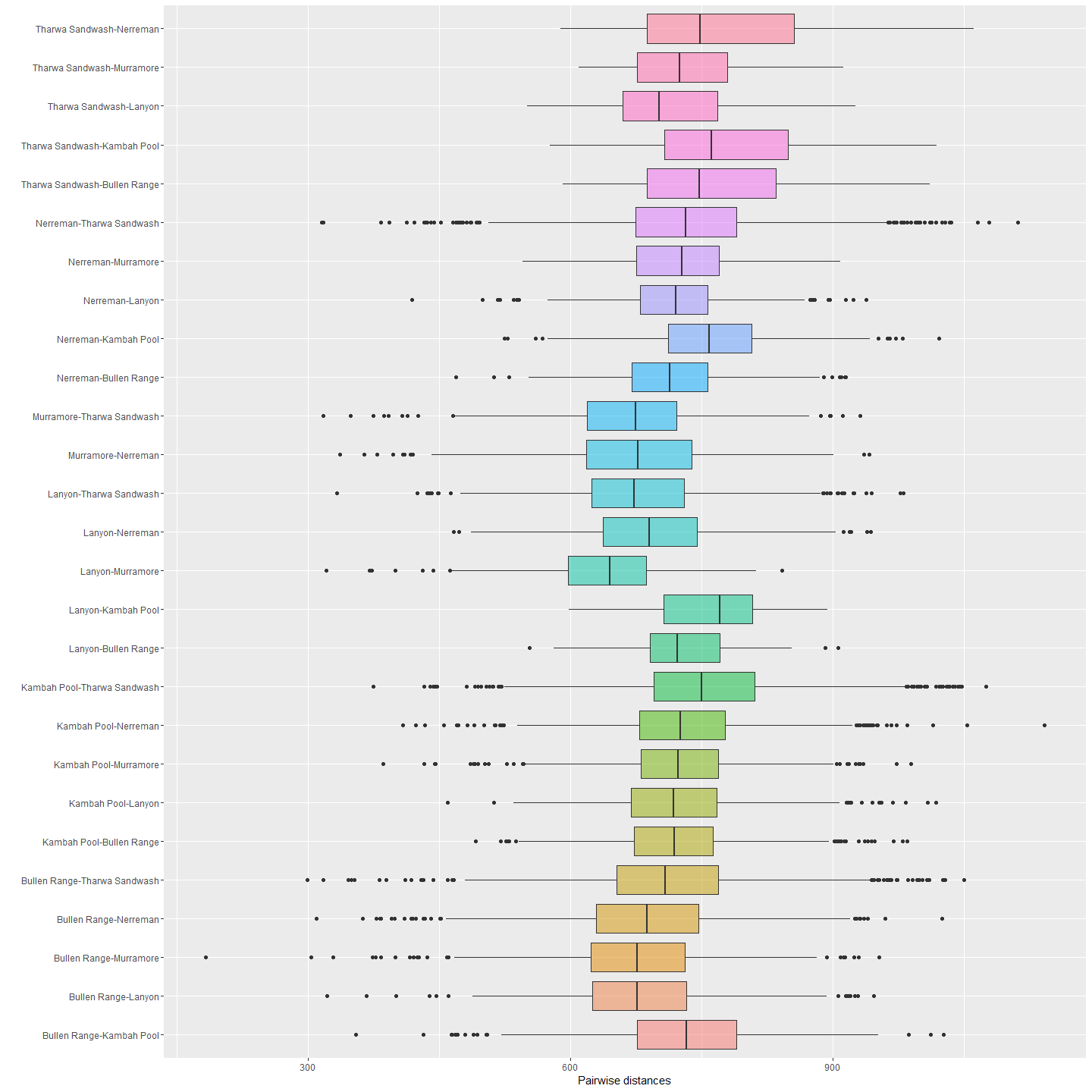
# Basic PopGen

pairDistPlot(gi, gi$pop, within=FALSE, sep="-", data=FALSE,violin=TRUE, boxplot=TRUE, jitter=TRUE)

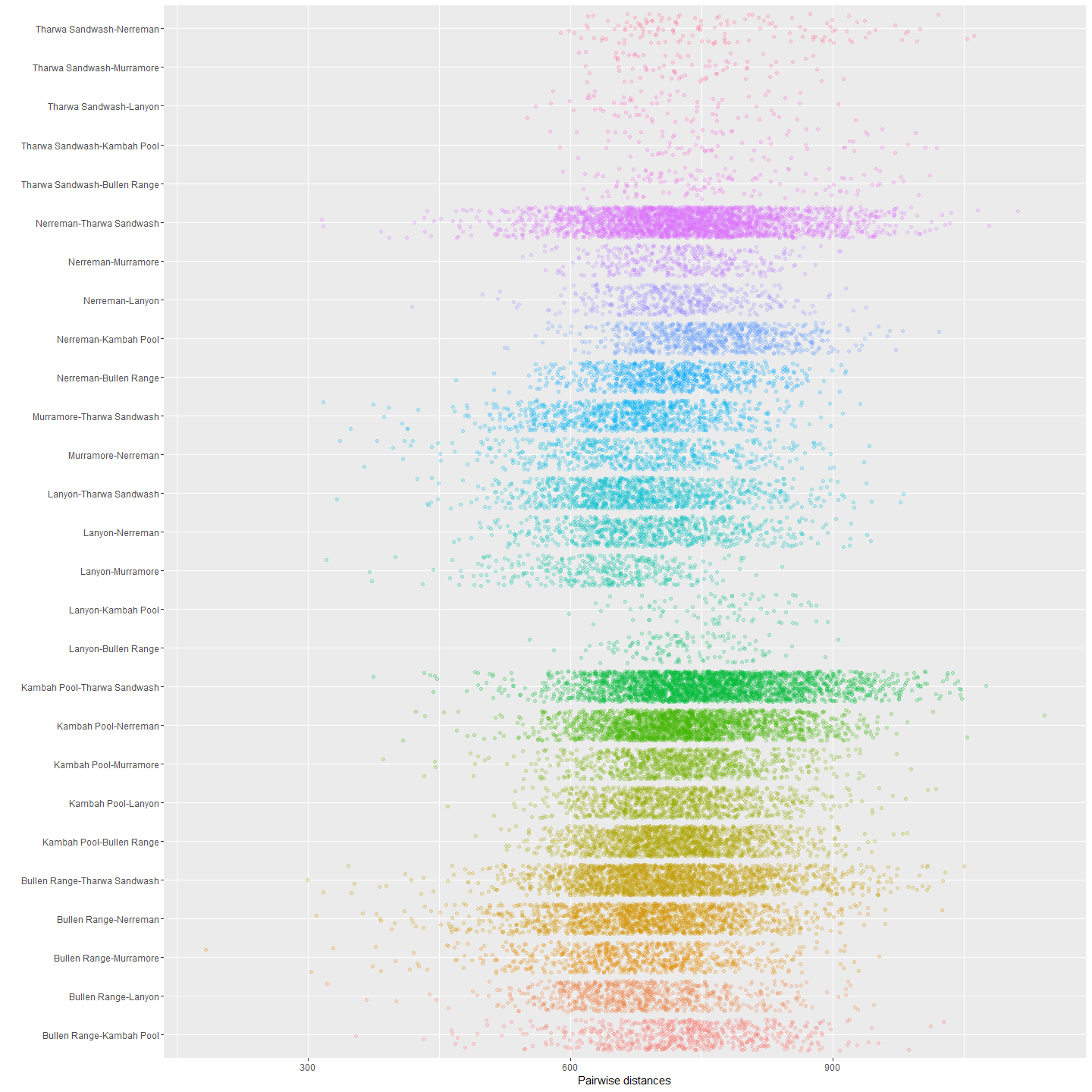
## $violin



##   
## $boxplot



##   
## $jitter



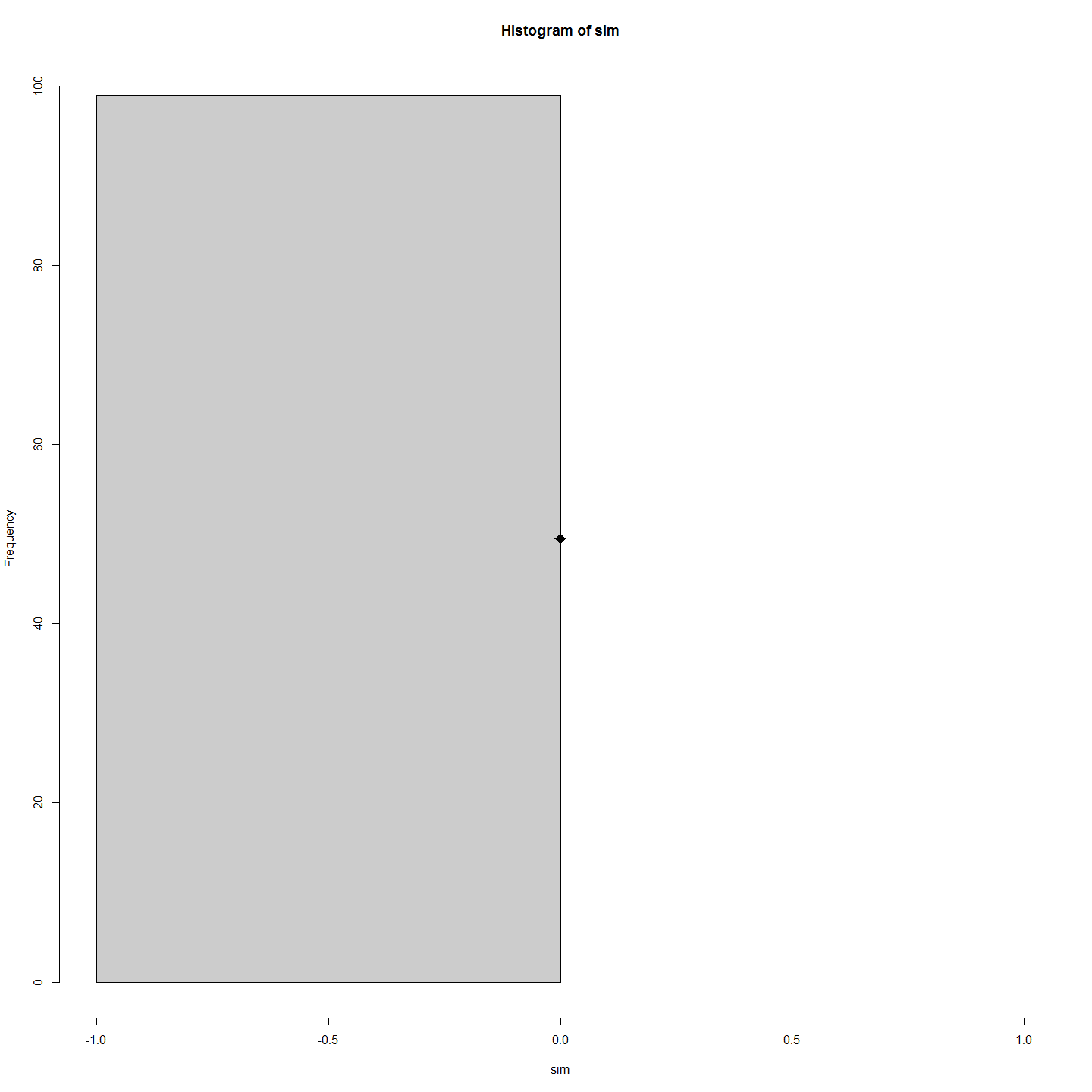
## fstat(gi)

## pop Ind  
## Total 0.01827464 -0.1371021  
## pop 0.00000000 -0.1582691

## Is the structure between populations significant? popStrSig<- gstat.randtest(gi, nsim = 99) popStrSig

## Monte-Carlo test  
## Call: gstat.randtest(x = gi, nsim = 99)  
##   
## Observation: 0   
##   
## Based on 99 replicates  
## Simulated p-value: 1   
## Alternative hypothesis: greater   
##   
## Std.Obs Expectation Variance   
## NaN 0 0

plot(popStrSig)



giHs <- genind2hierfstat(gi)  
#head(giHs)  
varglob<-varcomp.glob(giHs$pop, giHs[, -1])  
varglob$overall

## Pop Ind Error   
## 3.93667 -33.47080 244.95118

varglob$F

## Pop Ind  
## Total 0.01827464 -0.1371021  
## Pop 0.00000000 -0.1582691

## Pairwise Fst (populations)

matFst <- pairwise.fst(gi[1:50, treatOther = FALSE])  
matFst

## 1 2 3  
## 2 -0.3540884   
## 3 -0.6989234 -0.1901033   
## 4 -0.9214085 -0.4227752 -0.5910064

Thus there is no significant difference between populations.  
is.euclid(matFst)

## [1] FALSE

## Summary GI Object

div <- summary(gi)

### Total number of genotypes: 243 Population sample sizes: Bullen Range Kambah Pool Lanyon Murramore Nerreman Tharwa 42 54 21 18 55 53 Number of alleles per population

## Bullen Range Kambah Pool Lanyon Murramore Nerreman Tharwa Sandwash   
## 7177 7130 7024 7059 7365 7465   
##   
## # Percentage of missing data:   
## [1] 22.73779  
##   
## # Observed heterozygosity:

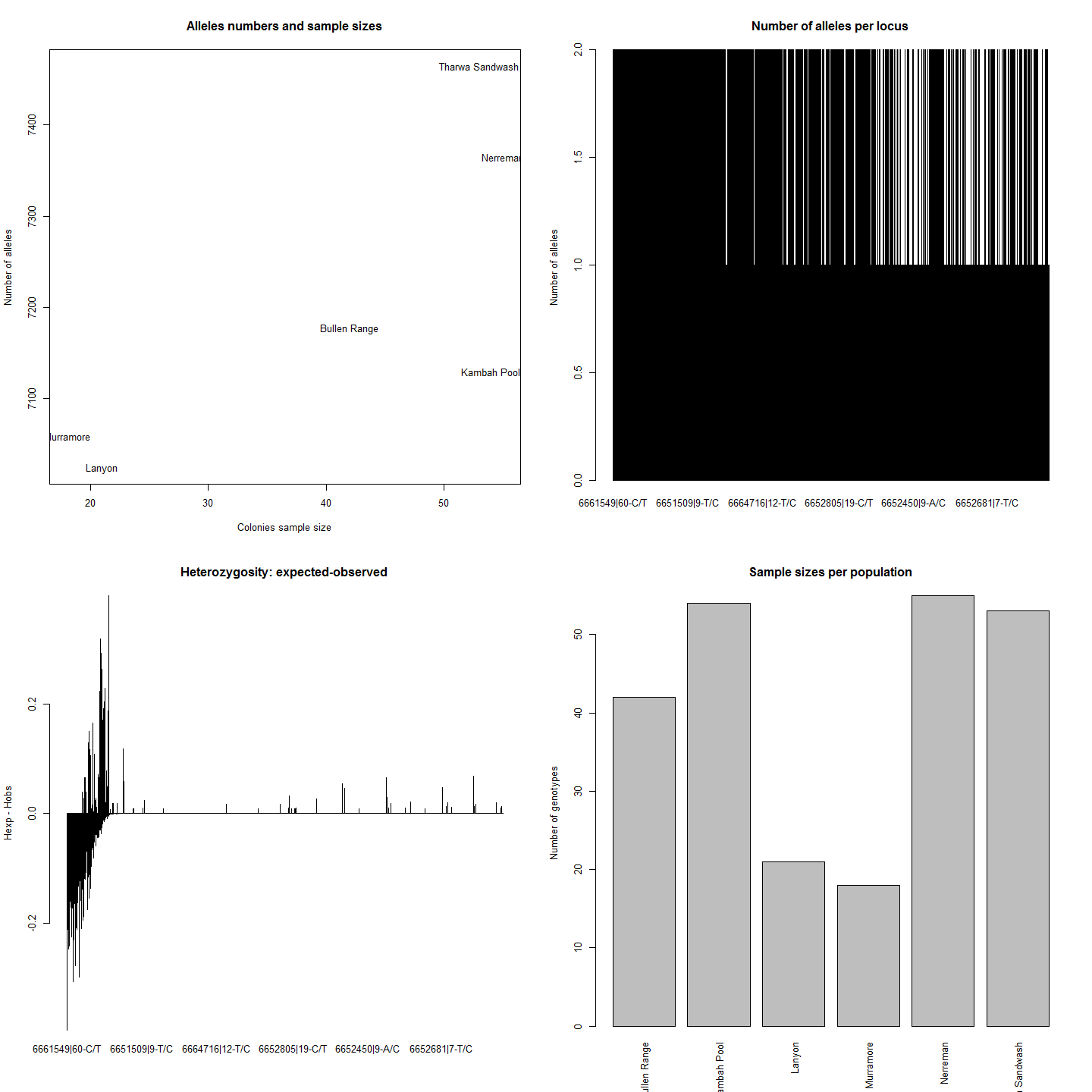
### div$pop.eff

## Bullen Range Kambah Pool Lanyon Murramore Nerreman Tharwa Sandwash   
## 42 54 21 18 55 53

names(div)

## [1] "N" "pop.eff" "loc.n.all" "pop.nall" "NA.perc" "Hobs" "Hexp"

par(mfrow = c(2, 2))  
plot(div$pop.eff, div$pop.nall, xlab = "Colonies sample size", ylab = "Number of alleles", main = "Alleles numbers and sample sizes", type = "n")  
text(div$pop.eff, div$pop.nall, lab = names(div$pop.eff))  
barplot(div$loc.n.all, ylab = "Number of alleles", main ="Number of alleles per locus")  
barplot(div$Hexp - div$Hobs, main = "Heterozygosity: expected-observed",ylab = "Hexp - Hobs")  
barplot(div$pop.eff, main = "Sample sizes per population", ylab = "Number of genotypes", las = 3)



plot(div$Hobs, xlab="Loci number", ylab="Observed Heterozygosity",main="Observed heterozygosity per locus")

### Number of alleles per locus

mean(nAll(gi)) # Number of alleles per locus

## [1] 1.309554

### plot(div$Hobs,div$Hexp, xlab="Hobs", ylab="Hexp", main="Expected heterozygosity as a function of observed heterozygosity per locus")

### bartlett.test(list(div$Hexp, div$Hobs)) # a test : H0: Hexp = Hobs

Bartlett test of homogeneity of variances  
##   
## data: list(div$Hexp, div$Hobs)  
## Bartlett's K-squared = 198.48, df = 1, p-value < 2.2e-16

basicstat <- basic.stats(gi, diploid = TRUE, digits = 2)   
names(basicstat)

## [1] "n.ind.samp" "pop.freq" "Ho" "Hs" "Fis" "perloc" "overall"

### basicstat$overall

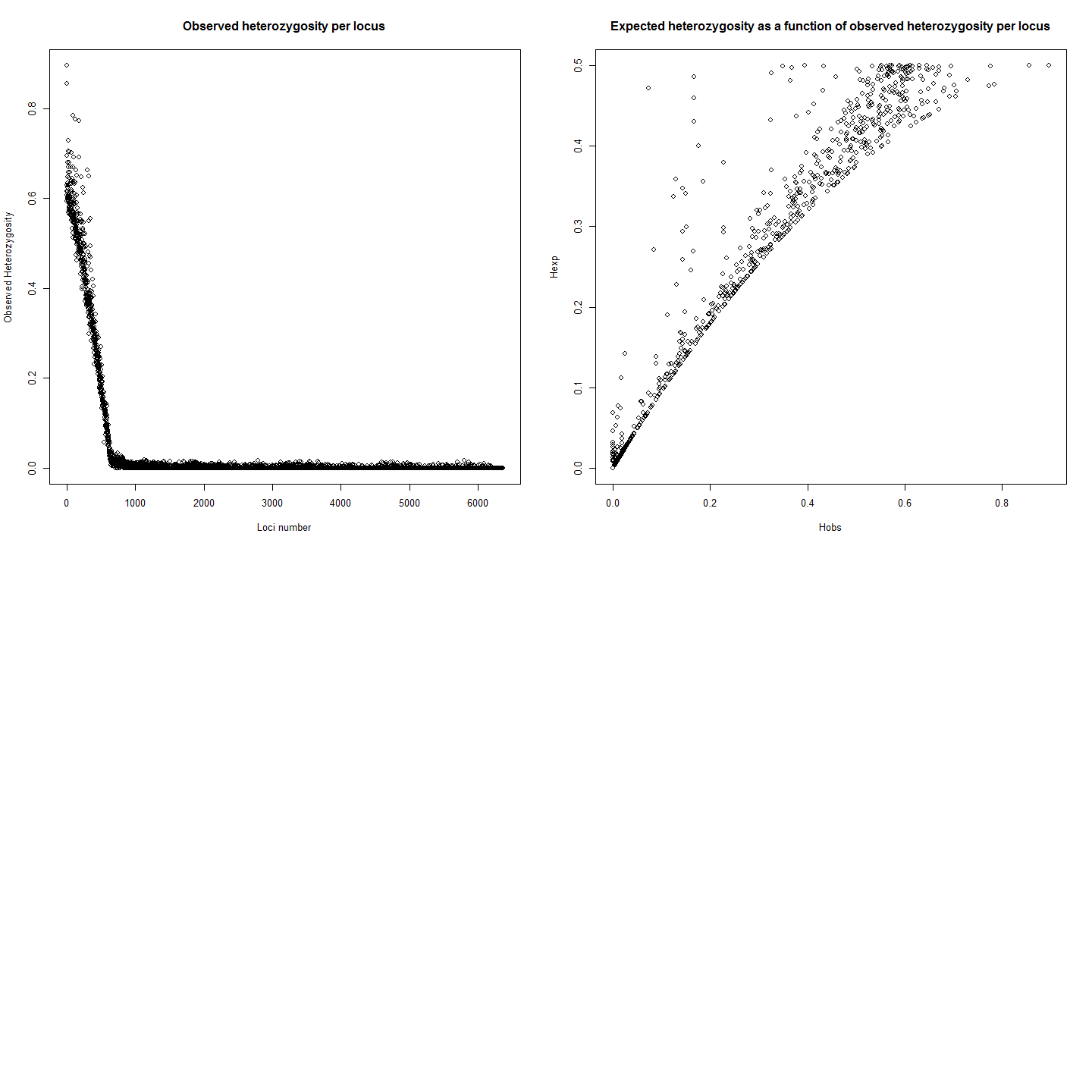
## Ho Hs Ht Dst Htp Dstp Fst Fstp Fis Dest   
## 0.04 0.03 0.03 0.00 0.03 0.00 0.01 0.02 -0.17 0.00

#mmod outputs  
diff\_stats(gi, phi\_st = FALSE)

## $per.locus  
## Hs Ht Gst Gprime\_st D  
##   
## $global  
## Hs Ht Gst\_est Gprime\_st D\_het D\_mean   
## 0.0334095095 0.0337786260 0.0109275164 0.0135366773 0.0004582497 NA

pairwise\_Gst\_Hedrick(gi, linearized = FALSE)

## Bullen Range Kambah Pool Lanyon Murramore Nerreman  
## Kambah Pool 0.0170039267   
## Lanyon 0.0215351522 0.0254476655   
## Murramore 0.0097138889 0.0222876343 -0.0061221781   
## Nerreman 0.0043467943 0.0127127101 0.0158470560 0.0057630683   
## Tharwa Sandwash 0.0220704982 0.0263026441 0.0064427734 0.0008349941 0.0189271318



#poppr functions  
library(poppr)   
mlg(gi)

## #############################  
## # Number of Individuals: 243   
## # Number of MLG: 243   
## #############################

## [1] 243

## **poppr**(gi)

## | Bullen Range   
## | Kambah Pool   
## | Lanyon   
## | Murramore   
## | Nerreman   
## | Tharwa Sandwash   
## | Total

## Pop N MLG eMLG SE H G lambda E.5 Hexp Ia rbarD File  
## 1 Bullen Range 42 42 18 NaN 3.74 42 0.976 1 0.0335 4.71 0.00672 gi  
## 2 Kambah Pool 54 54 18 1.49e-06 3.99 54 0.981 1 0.0305 7.66 0.01225 gi  
## 3 Lanyon 21 21 18 NaN 3.04 21 0.952 1 0.0319 5.94 0.00997 gi  
## 4 Murramore 18 18 18 0.00e+00 2.89 18 0.944 1 0.0357 7.57 0.01196 gi  
## 5 Nerreman 55 55 18 NaN 4.01 55 0.982 1 0.0347 6.95 0.00855 gi  
## 6 Tharwa Sandwash 53 53 18 1.76e-06 3.97 53 0.981 1 0.0343 9.78 0.01107 gi  
## 7 Total 243 243 18 NaN 5.49 243 0.996 1 0.0337 6.97 0.00689 gi

### Private Alleles

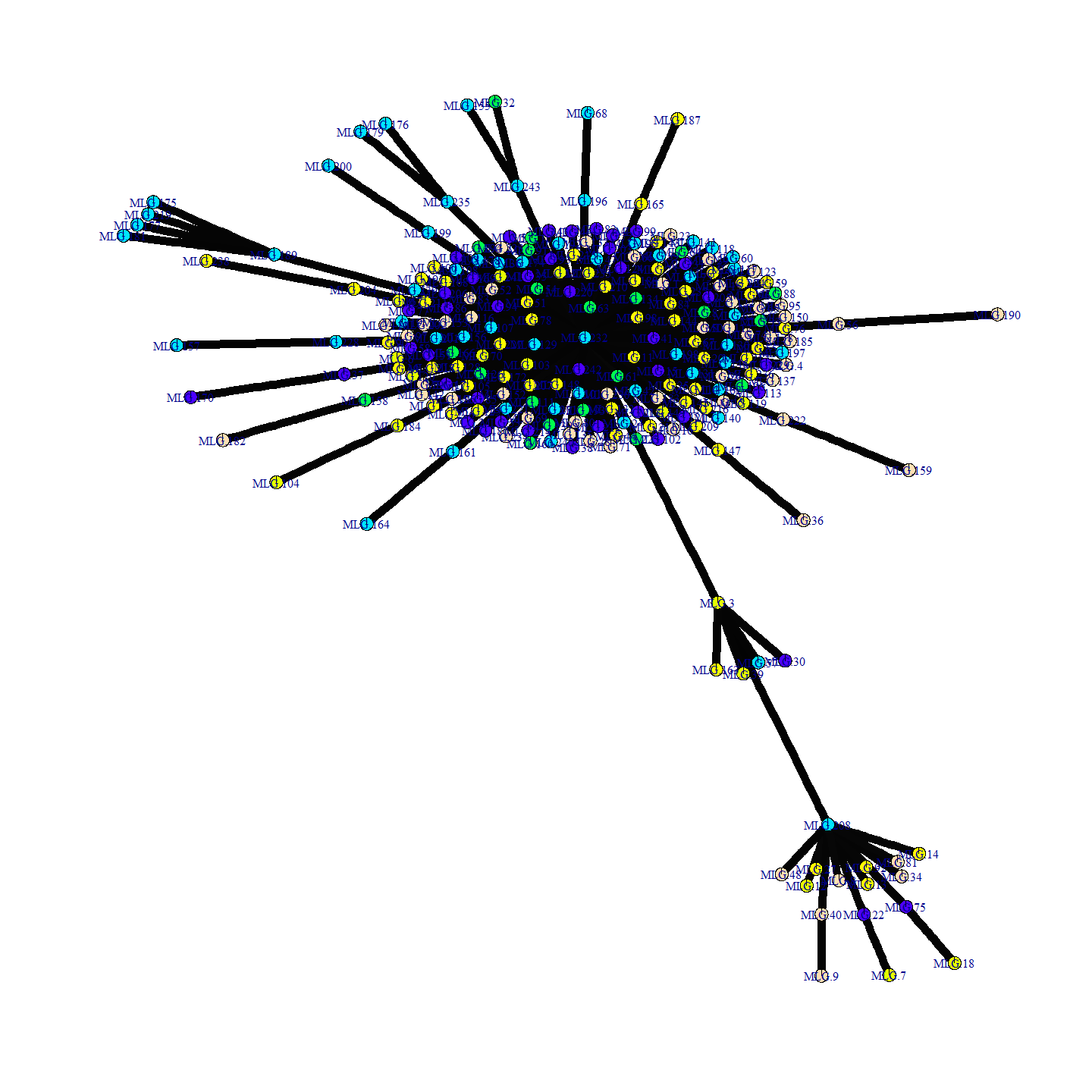
pa<-data.frame(private\_alleles(gi))  
pa<-data.frame(t(pa))  
summary(pa)

## Bullen.Range Kambah.Pool Lanyon Murramore Nerreman Tharwa.Sandwash   
## Min. :0.0000 Min. :0.00000 Min. :0.00000 Min. :0.0000 Min. :0.0000 Min. :0.0000   
## 1st Qu.:0.0000 1st Qu.:0.00000 1st Qu.:0.00000 1st Qu.:0.0000 1st Qu.:0.0000 1st Qu.:0.0000   
## Median :0.0000 Median :0.00000 Median :0.00000 Median :0.0000 Median :0.0000 Median :0.0000   
## Mean :0.1115 Mean :0.09248 Mean :0.02992 Mean :0.0417 Mean :0.2412 Mean :0.3536   
## 3rd Qu.:0.0000 3rd Qu.:0.00000 3rd Qu.:0.00000 3rd Qu.:0.0000 3rd Qu.:0.0000 3rd Qu.:1.0000   
## Max. :2.0000 Max. :5.00000 Max. :1.00000 Max. :2.0000 Max. :4.0000 Max. :4.0000

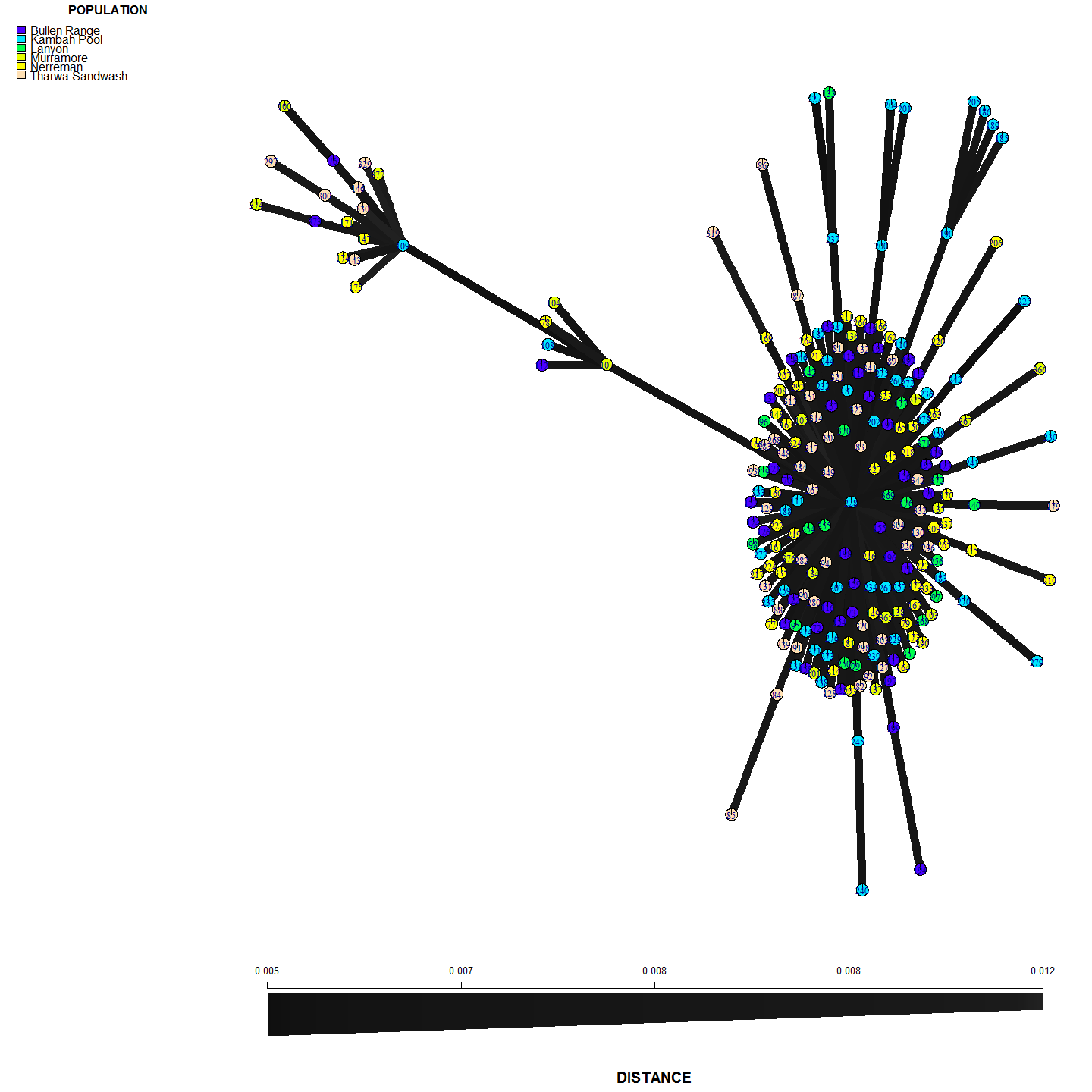
tab <- mlg.table(gi, plot = FALSE)  
diversity\_stats(tab)

## Index  
## Pop H G lambda E.5  
## Bullen Range 3.737670 42 0.9761905 1  
## Kambah Pool 3.988984 54 0.9814815 1  
## Lanyon 3.044522 21 0.9523810 1  
## Murramore 2.890372 18 0.9444444 1  
## Nerreman 4.007333 55 0.9818182 1  
## Tharwa Sandwash 3.970292 53 0.9811321 1

adist <- diss.dist(gi, percent = TRUE)  
amsn <- poppr.msn(gi, adist)



# Default  
library("igraph") # To get all the layouts.  
set.seed(500)  
plot\_poppr\_msn(gi, amsn, gadj = 15)



# Heterozygosity

Hs(gi)

## Bullen Range Kambah Pool Lanyon Murramore Nerreman Tharwa Sandwash   
## 0.04375030 0.04420646 0.04083251 0.04254215 0.04704342 0.04643666

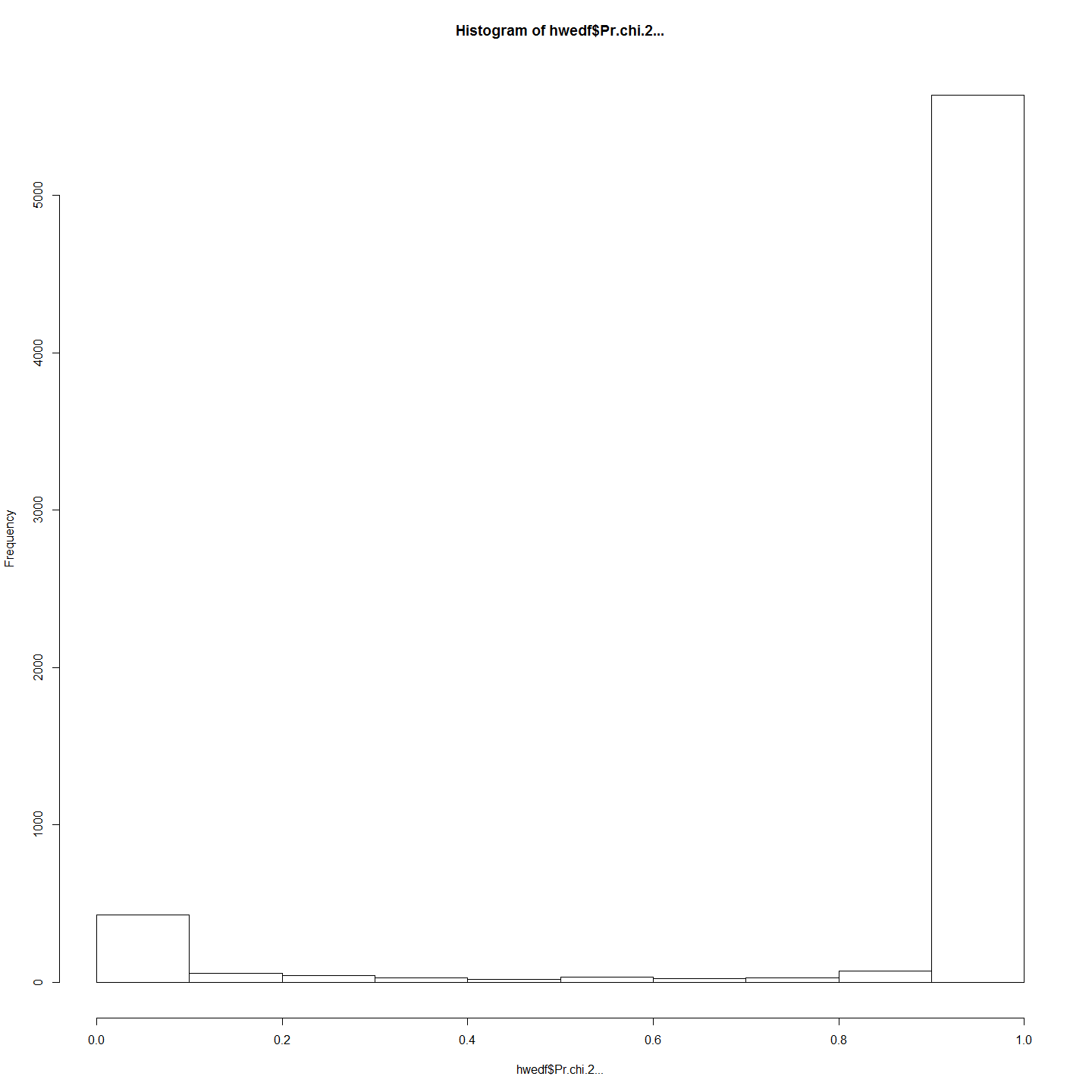
This function computes the expected heterozygosity (Hs) within populations of a genpop object. This function is available for codominant markers (@type="codom") only. Hs is commonly used for measuring within population genetic diversity (and as such, it still has sense when computed from haploid data).

# Hardy Weinberg and Genotypic Disequilibrium

#Analysis on genInd object (individuals)  
#Hardy Weinberg  
source("genlight2genInd.R")  
gI<-genlight2genind(gl.dart)

## Start conversion....  
## Please note conversion of bigger data sets will take some time!  
## Once finished, we recommend to save the object using >save(object, file="object.rdata")  
##   
## Matrix converted.. Prepare genind object...  
## Finished! Took 72 seconds.

hwe<-hw.test(gI, B=0)  
hwedf<-data.frame(hwe)  
hist(hwedf$Pr.chi.2...)



hwdf<-hw.test(gi, B=0)  
hwdf<-data.frame(hwdf)  
names(hwdf)[names(hwdf)=="Pr.chi.2..."] <- "p"  
  
p.adjust.M <- p.adjust.methods[p.adjust.methods != "fdr"]  
p.adj <- sapply(p.adjust.M, function(meth) p.adjust(hwdf$p, meth))  
corrected<-data.frame(p.adj)  
  
#Before Bonferroni correction  
nrow(subset(corrected, none<0.05))

## [1] 369

#Only   
nrow(subset(corrected, bonferroni<0.05))

## [1] 104

### After bonferroni correction

#and with BY  
nrow(subset(corrected, BY<0.05))

## [1] 141

corrected<-apply(p.adj, 2, format.pval, digits = 3)  
corrected<-data.frame(corrected)  
corrected<-corrected[order(as.numeric(corrected$none)),]  
corrected[1:40,]

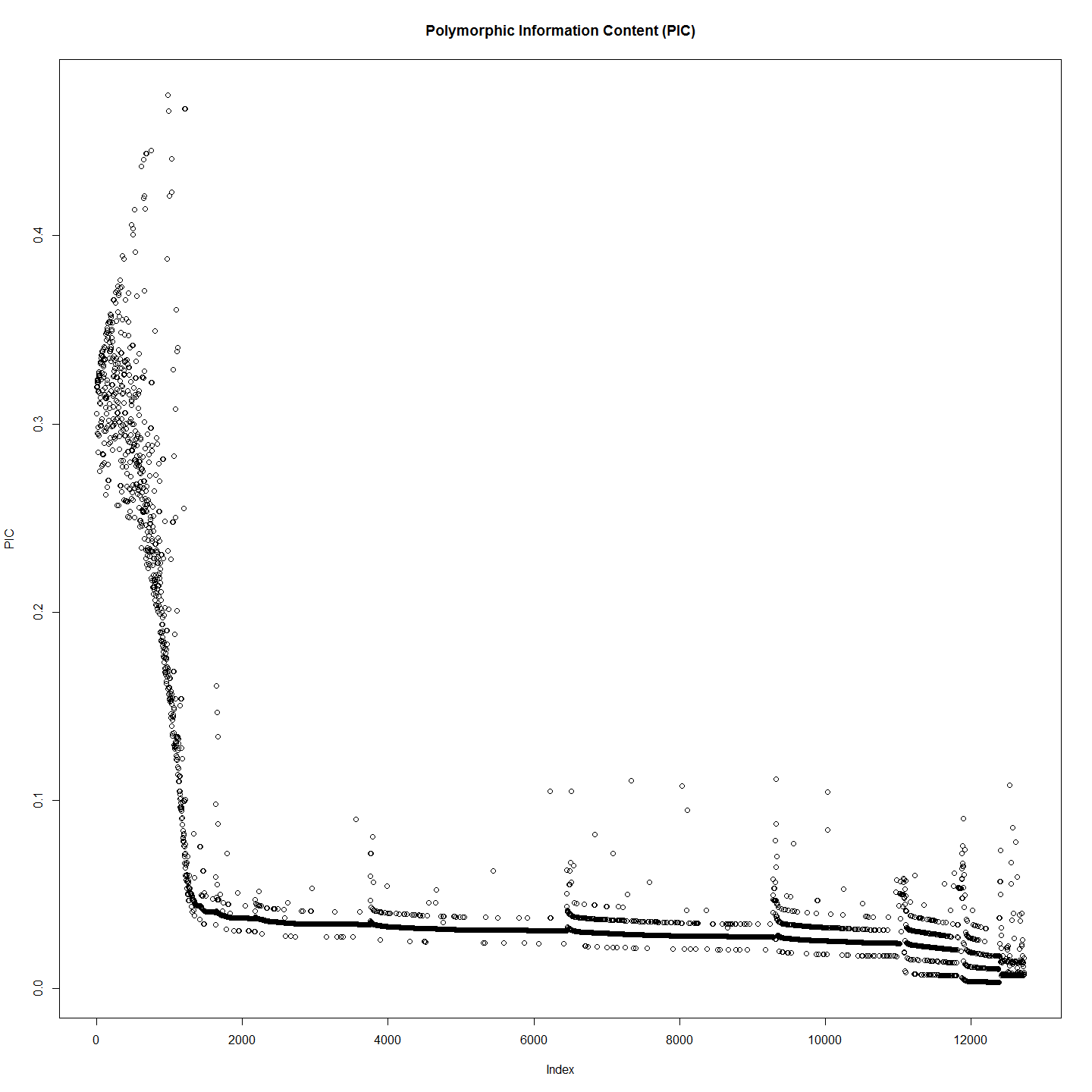
## holm hochberg hommel bonferroni BH BY none  
## 600 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 606 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 731 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 820 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 826 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 834 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 1407 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 2327 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 3234 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 3277 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 3327 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 3343 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 3643 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 4017 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 4051 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 4660 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 4661 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 4663 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 4666 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 4694 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 4731 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 4936 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 5017 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 5227 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 5482 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 5538 7.03e-13 7.03e-13 7.03e-13 7.07e-13 2.08e-14 1.94e-13 < 2e-16  
## 5552 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 5615 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 5934 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 5943 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 5965 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 6266 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 6335 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 6347 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16  
## 101 0.636925 0.636925 0.629253 0.651043 0.004684 0.043726 0.000102  
## 89 0.687874 0.687874 0.679476 0.703234 0.005023 0.046894 0.000111  
## 22 0.717811 0.717811 0.708930 0.733957 0.005205 0.048596 0.000115  
## 60 0.783510 0.783510 0.773564 0.801263 0.005643 0.052679 0.000126  
## 253 0.796375 0.796375 0.786392 0.814550 0.005696 0.053178 0.000128  
## 328 0.876017 0.876017 0.864752 0.896154 0.006220 0.058069 0.000141

# Population Structure

See: runPCAandTSNEYearsandSites.Rmd

## Polymorphic Information Content

#A script to plot all M. peelii snps average PIC (PIC of reference and PIC of alternate state allele) against index number of the data frame. This shows that using the first X number of snps is using the alleles with the highest PIC.  
  
  
df<-allPeeliSnps; main<-"All Peelii snps"  
df<-df[-c(1:4),]  
  
pic<-df[2:nrow(df),14] #check pic in order  
plot(as.character(pic),main="Polymorphic Information Content (PIC)", ylab="PIC")# to show PIC is in order (ish) ideally cut off would be 1300 or so.



## Genome Structure in Larvae by Years and Sites

### FST and Sites

library(StAMPP)  
system.time(snpfst <-stamppFst(gl,nboots=1, percent=95, nclusters=8))

## user system elapsed   
## 27.52 0.04 61.60

snpfst

## Kambah Pool Bullen Range Nerreman Tharwa Sandwash Lanyon Murramore  
## Kambah Pool NA NA NA NA NA NA  
## Bullen Range 0.01524984 NA NA NA NA NA  
## Nerreman 0.01241047 0.007348972 NA NA NA NA  
## Tharwa Sandwash 0.02727594 0.026001892 0.02273005 NA NA NA  
## Lanyon 0.02823645 0.029941074 0.02402186 0.012530020 NA NA  
## Murramore 0.02516960 0.020465393 0.01636588 0.008125193 0.004919345 NA

rm(snpfst)

Although not strong some difference in the three upper sites and the three lower sites is evident. The difference between the 3 upper and three lower sites also is greater than the difference among each of the three lower, or the three upper sites.

### Temporal Structure

glt<-gl  
glt@pop<-as.factor(gl@other$covariates)  
system.time(snpfstTemporal <-stamppFst(glt,nboots=1, percent=95, nclusters=8))

## user system elapsed   
## 13.95 0.00 17.46

snpfstTemporal

## 2013 2011 2012  
## 2013 NA NA NA  
## 2011 0.014914747 NA NA  
## 2012 0.005010593 0.01111121 NA

rm(glt); rm(npfstTemporal)

There is little difference between years.

### Genetic Distance between Sites

gi<-df2genind(data.frame(gl),ncode=1, pop=gl$pop)  
gp<-genind2genpop(gi)

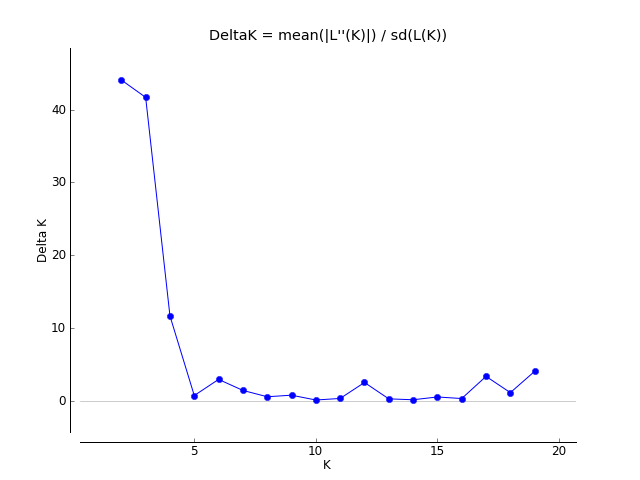
##   
## Converting data from a genind to a genpop object...   
##   
## ...done.

dist.genpop(gp)

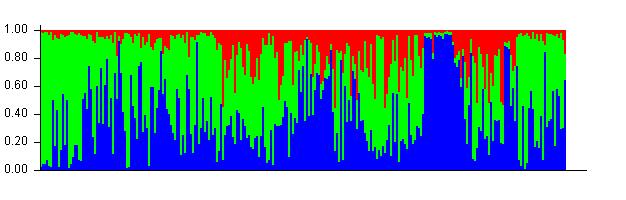
## Bullen Range Kambah Pool Lanyon Murramore Nerreman  
## Kambah Pool 0.003084083   
## Lanyon 0.004076401 0.004261646   
## Murramore 0.003632366 0.005372541 0.003149246   
## Nerreman 0.001670094 0.002379941 0.003443184 0.003267281   
## Tharwa Sandwash 0.002998878 0.003526237 0.002719802 0.002499254 0.002531829

#or Isolation by Distance (site)  
library(ade4)  
Dgen <- dist.genpop(gp, method = 2)  
Dgeo2<-select(larv, SiteName, Distance.to.Angle.Crossing..m.)  
Dgeo2<-unique(Dgeo2)  
rownames(Dgeo2)<-Dgeo2[,1]  
Dgeo2[,1]<-NULL  
Dgeo2<-dist(Dgeo2)  
ibd <- mantel.randtest(Dgen, Dgeo2)  
ibd

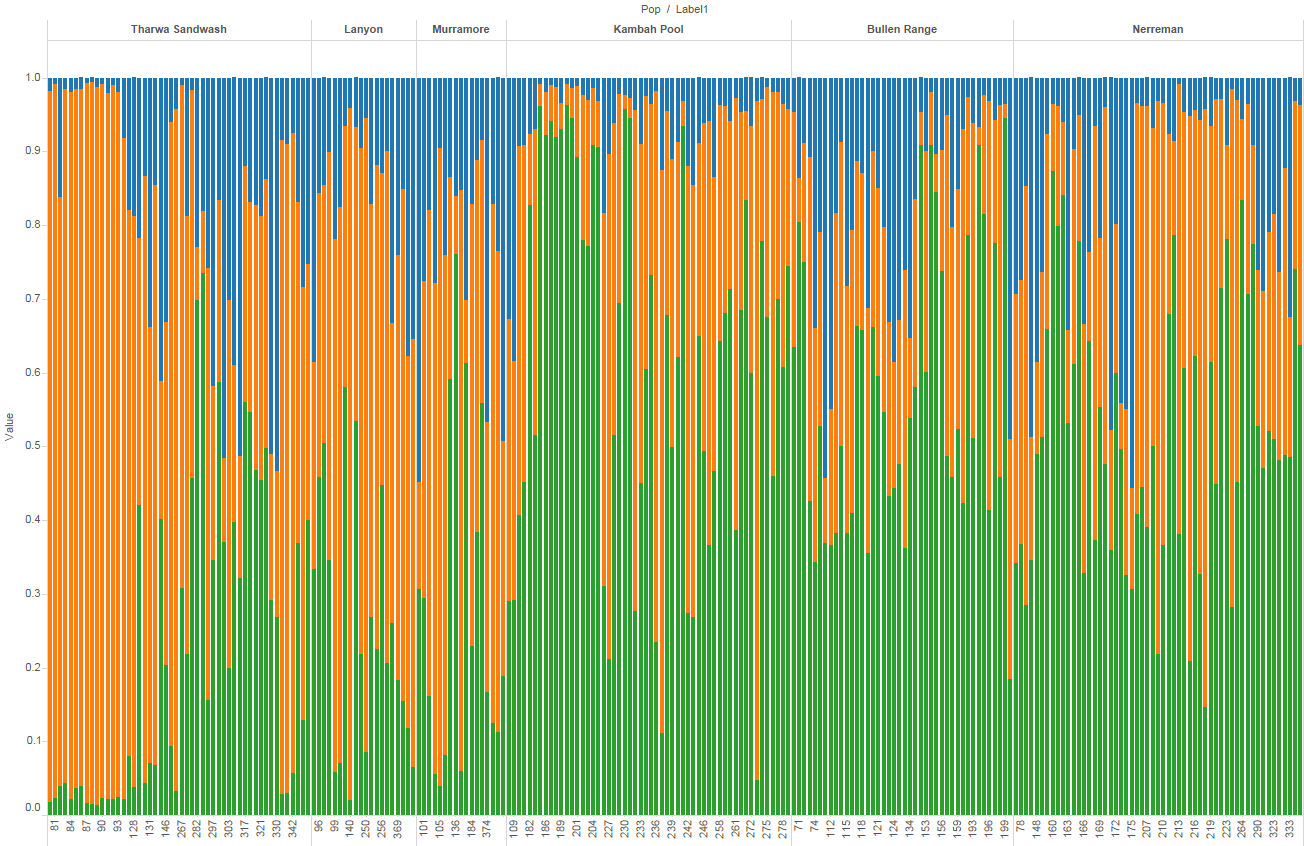
## Monte-Carlo test  
## Call: mantel.randtest(m1 = Dgen, m2 = Dgeo2)  
##   
## Observation: 0.3790073   
##   
## Based on 999 replicates  
## Simulated p-value: 0.086   
## Alternative hypothesis: greater   
##   
## Std.Obs Expectation Variance   
## 1.440281716 -0.005850301 0.071401155

Following the evanno method we settled on 3 groups. 

so with three groups.



No real structure is evident if we look at structure based on collection site



When the structure is examined based on the nest site rather than the collection site which better accounts for putative barriers and unidirectional dispersal. then:

after nests chapter is done

#Looking for DAPC, fixed differences, and Correspondence Analysis between populations.  
  
require(reshape2)  
require(dart)  
require(pegas)  
all.dart <- read.dart("otherData/larvalPeeliSnps.csv", topskip = 5)

## Added the following covmetrics:  
## CloneID SNP SnpPosition CallRate OneRatioSnp FreqHomRef FreqHomSnp FreqHets AvgCountRef AvgCountSnp RepAvg .  
## Number of rows per Clone. Should be only 2s:  
## 2  
## Recognised: 243 individuals and 6364 SNPs in otherData/larvalPeeliSnps.csv

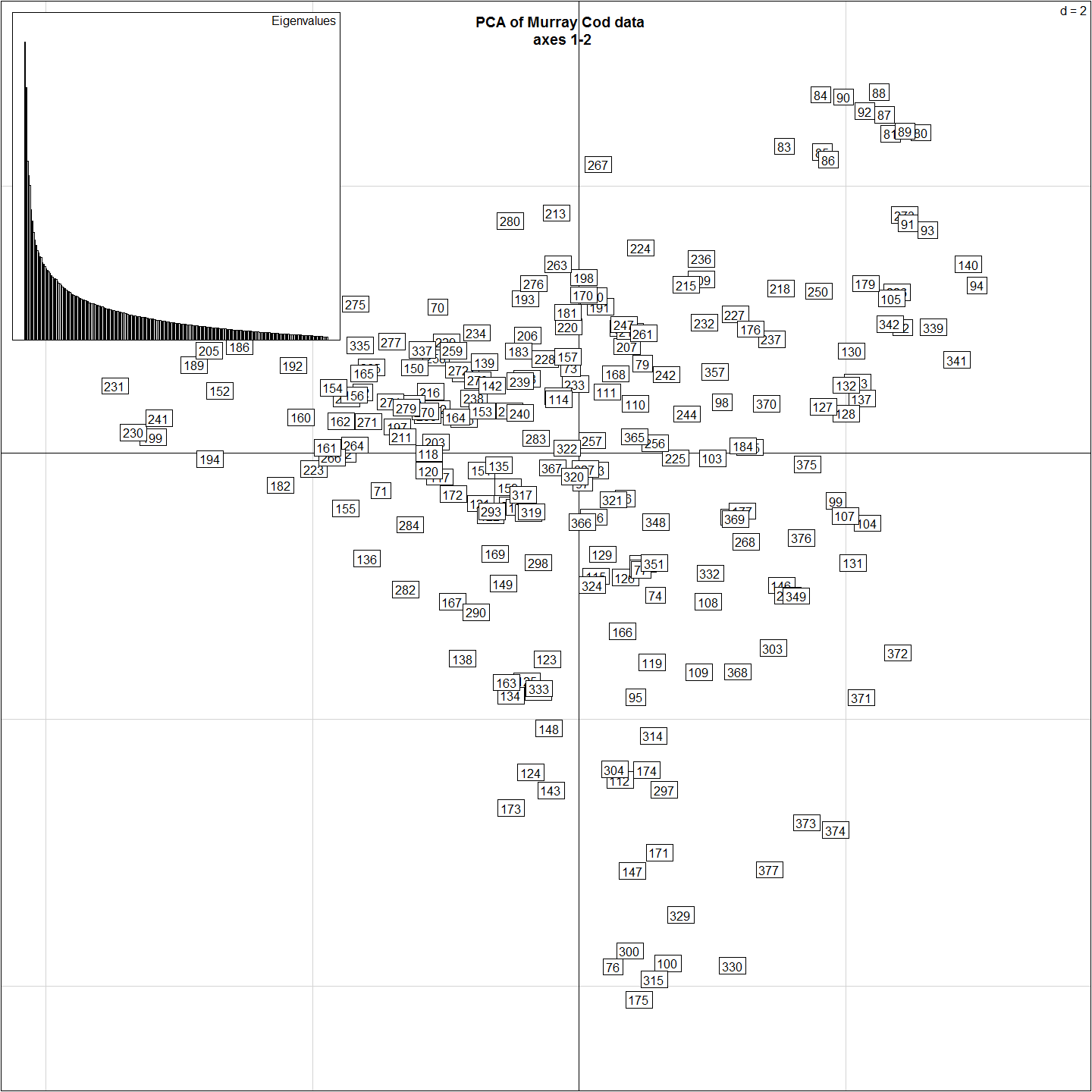
gl.dart <- dart2genlight(all.dart, covfilename = "otherData/qslLarvalPeeliiMetaForPCA.csv") # this glObject is then suitable for sharing via GitHub or such for open data as required by PeerJ etc. Need better file but.

## Start conversion....  
## Please note conversion of bigger data sets will take some time!  
## Once finished, we recommend to save the object using save(object, file="object.rdata")  
##   
 |   
   
## Try to add covariate file: otherData/qslLarvalPeeliiMetaForPCA.csv .  
## Ids of covariate file does not match the number of ids in the genetic file. Maybe this is fine if a subset matches.  
## Ids of covariate file (at least a subset of) are matching!  
## Found 243 matching ids out of 251 ids provided in the covariate file.  
## Added pop factor.  
## Added latlon data.  
## Added YearOnly to the other$covariates slot.  
## Added estimatedAge to the other$covariates slot.  
## Added Day.of.Year to the other$covariates slot.  
## Added hatchedDoY to the other$covariates slot.  
## Added Delta13C to the other$covariates slot.  
## Added Delta15N to the other$covariates slot.  
## Added CNRatio to the other$covariates slot.  
## Added Distance.to.Angle.Crossing..m. to the other$covariates slot.  
## Added raceCladeName to the other$covariates slot.  
## Added cladeGoTName to the other$covariates slot.  
## Added mumPulldown to the other$covariates slot.  
## Added Fathers to the other$covariates slot.  
## Added inbredCoeff to the other$covariates slot.

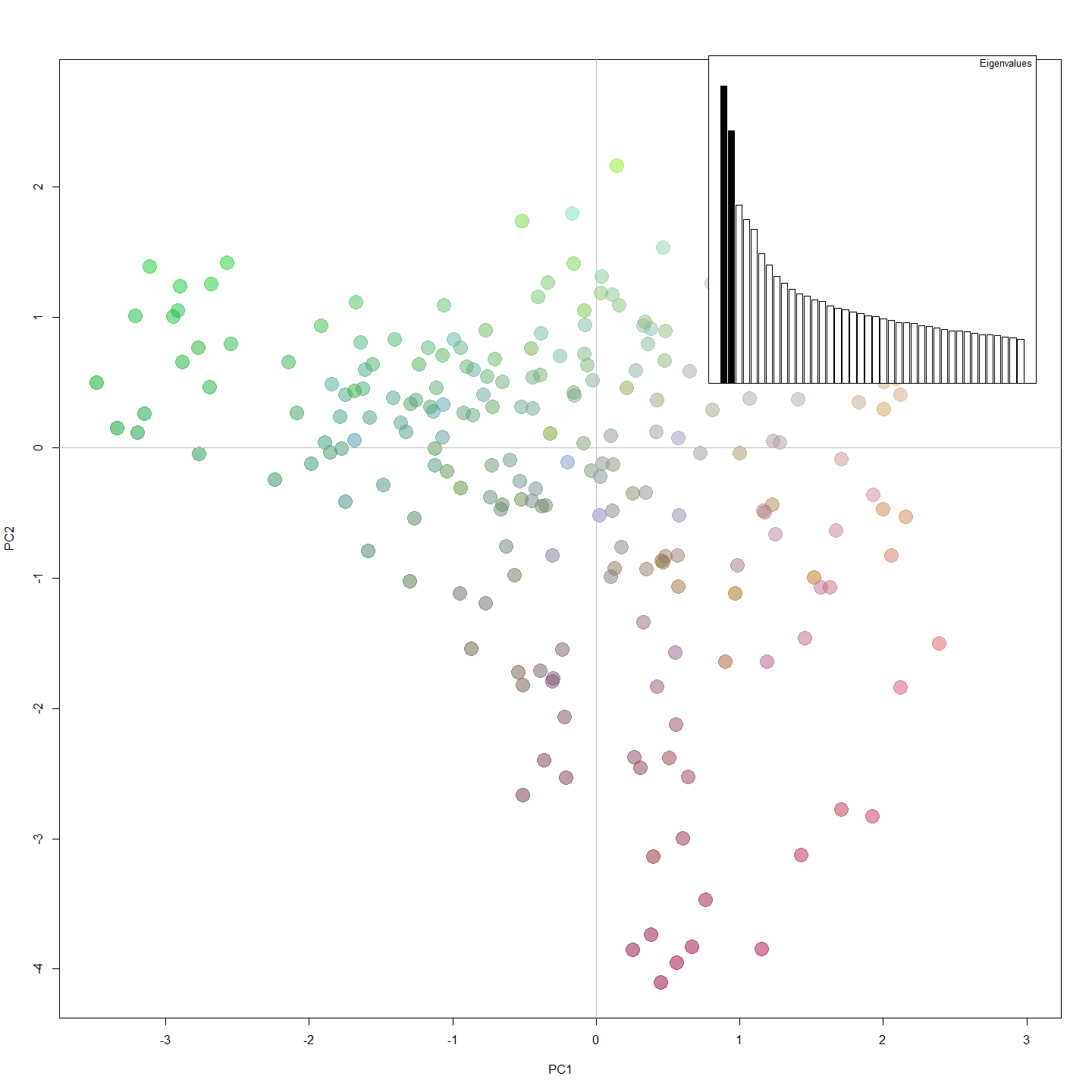
# cant work gl.fixed.diff(gl.dart, t=0)  
  
#PCA  
pca1 <- glPca(gl.dart, nf = 3 ,parallel = FALSE)  
pca1

## === PCA of genlight object ===  
## Class: list of type glPca  
## Call ($call):glPca(x = gl.dart, nf = 3, parallel = FALSE)  
##   
## Eigenvalues ($eig):  
## 2.077 1.762 1.245 1.144 1.078 0.908 ...  
##   
## Principal components ($scores):  
## matrix with 243 rows (individuals) and 3 columns (axes)   
##   
## Principal axes ($loadings):  
## matrix with 6364 rows (SNPs) and 3 columns (axes)

scatter(pca1, posi="topleft")  
title("PCA of Murray Cod data\n axes 1-2")



myCol <- colorplot(pca1$scores,pca1$scores, transp=TRUE, cex=4)  
abline(h=0,v=0, col="grey")  
add.scatter.eig(pca1$eig[1:40],2,1,2, posi="topright", inset=.05, ratio=.3)



#There are   
sum(is.na(gI$tab)) #missing values in the data

## [1] 30511

forPCOA<-scaleGen(gI, NA.method="mean") #scale the data  
forPCOA[1:5,1:5]

## 6661549-60-C/T.A 6661549-60-C/T.B 6650588-15-C/T.A 6650588-15-C/T.B 6661794-21-A/G.A  
## 185 2.006758 -2.006758 1.499011 -1.499011 0.1184337  
## 186 2.006758 -2.006758 1.499011 -1.499011 1.7172889  
## 187 0.289708 -0.289708 1.499011 -1.499011 0.1184337  
## 188 0.289708 -0.289708 1.499011 -1.499011 1.7172889  
## 189 0.289708 -0.289708 1.499011 -1.499011 0.1184337

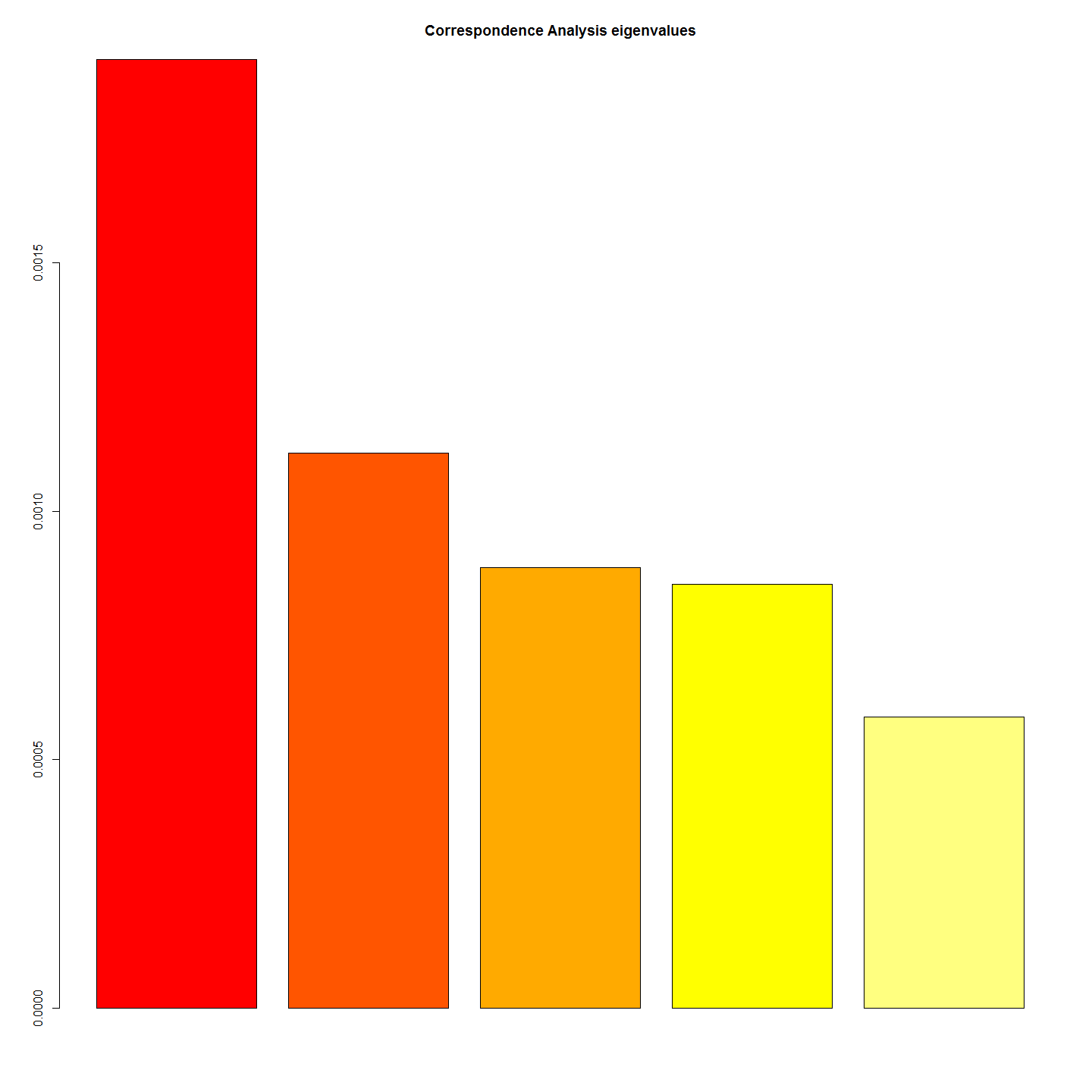
pca1 <- dudi.pca(forPCOA,cent=FALSE,scale=FALSE,scannf=FALSE,nf=3)  
barplot(pca1$eig[1:50],main="PCA eigenvalues", col=heat.colors(50))

### Correspondance Analysis

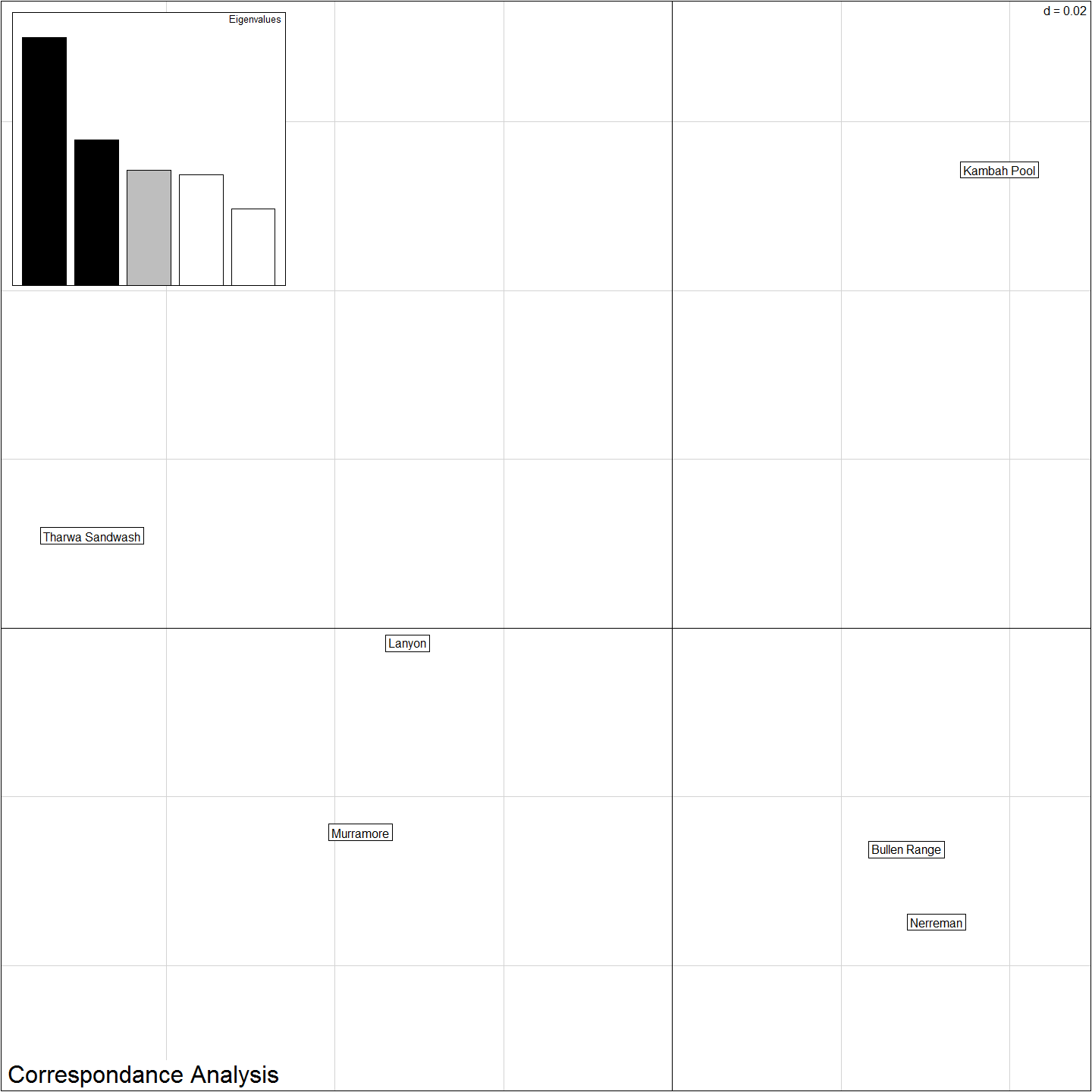
#Correspondance Analysis (genepop object)  
obj <- genind2genpop(gI)

##   
## Converting data from a genind to a genpop object...   
##   
## ...done.

ca1 <- dudi.coa(tab(obj),scannf=FALSE,nf=3)  
barplot(ca1$eig,main="Correspondence Analysis eigenvalues",  
 col=heat.colors(length(ca1$eig)))



s.label(ca1$li, sub="Correspondance Analysis",csub=2)  
add.scatter.eig(ca1$eig,nf=3,xax=1,yax=2,posi="topleft")



#Isolation By Distance  
# Dgen <- dist.genpop(obj,method=2)  
# Dgeo <- dist(gI$other$latlong) #need xys for sites in gI for this to work.  
# ibd <- mantel.randtest(Dgen,Dgeo)  
# ibd

all\_labels()

## [1] "Project\_Template\_and\_Knitr" "Set\_Global\_Options" "unnamed-chunk-1" "unnamed-chunk-2"   
## [5] "unnamed-chunk-3" "unnamed-chunk-4" "unnamed-chunk-5" "poppr functions"   
## [9] "unnamed-chunk-6" "unnamed-chunk-7" "unnamed-chunk-8" "unnamed-chunk-9"   
## [13] "unnamed-chunk-10" "unnamed-chunk-11" "PCAtSNEStructure" "unnamed-chunk-12"   
## [17] "dapcCorrespondence" "Include\_Chunk\_Labels\_and\_Session Information" "averagePIC" "dapcCorroStructure"

proc.time()-ptm

## user system elapsed   
## 3712.95 13.85 3921.54

#Session Information  
sessionInfo()

## R version 3.3.0 (2016-05-03)  
## Platform: x86\_64-w64-mingw32/x64 (64-bit)  
## Running under: Windows 7 x64 (build 7601) Service Pack 1  
##   
## locale:  
## [1] LC\_COLLATE=English\_Australia.1252 LC\_CTYPE=English\_Australia.1252 LC\_MONETARY=English\_Australia.1252 LC\_NUMERIC=C LC\_TIME=English\_Australia.1252   
##   
## attached base packages:  
## [1] stats graphics grDevices utils datasets methods base   
##   
## other attached packages:  
## [1] reshape2\_1.4.1 StAMPP\_1.4 igraph\_1.0.1 poppr\_2.2.1 mmod\_1.3.1 hierfstat\_0.04-22 pegas\_0.9 ape\_3.5 tsne\_0.1-3   
## [10] dart\_0.3 adegenet\_2.0.1 ade4\_1.7-4 ggplot2\_2.1.0 plyr\_1.8.4 dplyr\_0.5.0 ProjectTemplate\_0.7 knitr\_1.13   
##   
## loaded via a namespace (and not attached):  
## [1] Rcpp\_0.12.6 lattice\_0.20-33 deldir\_0.1-12 gtools\_3.5.0 assertthat\_0.1 digest\_0.6.10 foreach\_1.4.3 mime\_0.5 R6\_2.1.2 nnls\_1.4   
## [11] evaluate\_0.9 coda\_0.18-1 lazyeval\_0.2.0 spdep\_0.6-6 gdata\_2.17.0 vegan\_2.4-0 phangorn\_2.0.4 gmodels\_2.16.2 Matrix\_1.2-6 rmarkdown\_1.0   
## [21] labeling\_0.3 splines\_3.3.0 stringr\_1.0.0 munsell\_0.4.3 shiny\_0.13.2 httpuv\_1.3.3 mgcv\_1.8-13 htmltools\_0.3.5 tibble\_1.1 quadprog\_1.5-5   
## [31] codetools\_0.2-14 permute\_0.9-0 MASS\_7.3-45 grid\_3.3.0 nlme\_3.1-128 xtable\_1.8-2 gtable\_0.2.0 DBI\_0.5 magrittr\_1.5 formatR\_1.4   
## [41] scales\_0.4.0 KernSmooth\_2.23-15 stringi\_1.1.1 LearnBayes\_2.15 doParallel\_1.0.10 sp\_1.2-3 seqinr\_3.3-0 boot\_1.3-18 fastmatch\_1.0-4 iterators\_1.0.8   
## [51] tools\_3.3.0 parallel\_3.3.0 yaml\_2.1.13 colorspace\_1.2-6 cluster\_2.0.4