import\_data\_toR\_amedits.R

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#Use read.vcf.markerstats3 for STACKS v1.44  
  
setwd("C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics")  
  
##### For reading attributes from a VCF where only MAF is recorded (no entry for major allele frequency)  
read.vcf.markerstats3 <- function(filename,max.marker) {  
 con <- file(filename,"r") #open file for reading  
 temp <- readLines(con,1) #read one line  
 comment.line <- 0  
 while(substr(temp,1,2)=="##") { #skip comment lines  
 temp <- readLines(con,1)  
 comment.line <- comment.line+1  
 }  
 header <- strsplit(temp,split="\t",fixed=TRUE)[[1]]  
   
 #FORMAT is position 9  
 n.sample <- length(header) - 9  
 sample.names <- apply(array(header[-c(1:9)]),1,function(x){y=strsplit(x,split="\t",fixed=TRUE)[[1]][1];return(y)})  
 close(con)  
   
 marker.stats <- data.frame(Chrom=rep("",max.marker),Pos=rep(0,max.marker),Name=rep("",max.marker),NSamp=rep(0,max.marker),MAF=rep(0.0,max.marker),stringsAsFactors=F,Allele1=rep("",max.marker),Allele2=rep("",max.marker))  
 GT <- matrix(0,max.marker,n.sample)  
 colnames(GT) <- sample.names  
 DP <- matrix(0,max.marker,n.sample)  
 colnames(DP) <- sample.names  
   
 con <- file(filename,"r")  
 temp <- readLines(con,comment.line+1)  
 m <- 0  
   
 while ((m < max.marker) & (length(temp)>0)) {  
 temp <- readLines(con,1)  
 if (length(temp) > 0) {  
 temp2 <- strsplit(temp,split="\t",fixed=TRUE)[[1]]  
 if ((length(grep("/",temp2[5],fixed=TRUE))==0)&(temp2[5]!="-")&(temp2[4]!="-")&(length(grep(",",temp2[4],fixed=TRUE))==0)) {  
 #only process bi-allelic SNPs (remove tri-allelic and indels)  
 #for MAF  
 temp3 <- strsplit(temp2[8],split=";",fixed=T)[[1]]  
 #for NSamp  
 temp4 <- strsplit(temp2[8],split=";",fixed=TRUE)[[1]]  
 m <- m + 1  
 marker.stats[m,"Chrom"] <- temp2[1]  
 marker.stats[m,"Pos"] <- as.integer(temp2[2])  
 marker.stats[m,"Name"] <- paste(temp2[2],temp2[3],sep=".")  
 marker.stats[m,"NSamp"] <- as.integer(strsplit(temp4[1],split="=",fixed=T)[[1]][2])  
 marker.stats[m,"MAF"] <- as.numeric(strsplit(temp3[2],split="=",fixed=T)[[1]][2])  
 marker.stats[m,"Allele1"] <- temp2[4]  
 marker.stats[m,"Allele2"] <- temp2[5]  
 }  
 }  
 print(paste("Marker",m,"done"))  
 }  
 close(con)   
   
 marker.stats <- marker.stats[1:m,]  
 rownames(marker.stats) <- marker.stats$Name  
   
 return(marker.stats)  
} #end read.vcf  
  
  
##command for Parnassius clodius data file, number is arbitrary but large  
dat3 <- read.vcf.markerstats3(filename='SNPdata/parnassius\_clodius\_unfiltered\_imputed.vcf',10000)

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read.vcf.genotypes <- function(filename,max.marker) {  
   
 get\_counts <- function(x,GT.pos) {  
 if (length(grep(":",x,fixed=TRUE))>0) {  
 y <- strsplit(x,split=":",fixed=TRUE)[[1]][GT.pos]  
 z <- strsplit(y,split="/",fixed=TRUE)[[1]]  
 return(as.numeric(z))  
 } else {  
 return(c(0,0))  
 }  
 }  
   
 con <- file(filename,"r") #open file for reading  
 temp <- readLines(con,1) #read one line  
 comment.line <- 0  
 while(substr(temp,1,2)=="##") { #skip comment lines  
 temp <- readLines(con,1)  
 comment.line <- comment.line+1  
 }  
 header <- strsplit(temp,split="\t",fixed=TRUE)[[1]]  
   
 #format is position 9  
 n.sample <- length(header) - 9  
   
 sample.names <- apply(array(header[-c(1:9)]),1,function(x){y=strsplit(x,split=":",fixed=TRUE)[[1]][1];return(y)})  
   
 temp <- readLines(con,1)  
 temp2 <- strsplit(temp,split="\t",fixed=TRUE)[[1]]  
 temp3 <- strsplit(temp2[9],split=":",fixed=TRUE)[[1]]  
 GT.pos <- match("GT",temp3)  
 close(con)  
   
 print("Got genotype positions")  
   
 genotypes1 <- matrix(NA,max.marker,n.sample)  
 genotypes2 <- matrix(NA,max.marker,n.sample)  
 genotypes <- matrix(NA,max.marker,n.sample)  
 colnames(genotypes1) <- sample.names  
 colnames(genotypes2) <- sample.names  
 colnames(genotypes) <- sample.names  
 marker.names <- array(rep("",max.marker))  
   
 con <- file(filename,"r")  
 temp <- readLines(con,comment.line+1)  
 m <- 0  
   
 while ((m < max.marker) & (length(temp)>0)) {  
 temp <- readLines(con,1)  
 if (length(temp) > 0) {  
 temp2 <- strsplit(temp,split="\t",fixed=TRUE)[[1]]  
 temp3 <- strsplit(temp2[1],split="d",fixed=TRUE)[[1]] #splitting by "d" because the scaffold number is preceded by "scaffold"  
 if ((length(grep(",",temp2[5],fixed=TRUE))==0)&(temp2[5]!="-")&(temp2[4]!="-")&(length(grep(",",temp2[4],fixed=TRUE))==0)) {  
   
 #only process bi-allelic SNPs (remove tri-allelic and indels)  
 counts <- apply(array(temp2[-c(1:9)]),1,get\_counts,GT.pos)  
 m <- m + 1  
 genotypes1[m,] <- counts[1,]  
 genotypes2[m,] <- counts[2,]  
 marker.names[m] <- paste(temp3[2],temp2[2],temp2[3],sep=".")  
 }  
 }  
 print(paste("Marker",m,"done",sep=" "))  
 }  
 close(con)   
   
 i <- seq(1,n.sample,by=1)  
 j <- seq(1,max.marker,by=1)  
 for (i in 1:n.sample){  
 for (j in 1:max.marker){  
 genotypes[j,i] <- sum(genotypes1[j,i],genotypes2[j,i])  
 }  
 }  
 genotypes[1:m,]  
 rownames(genotypes) <- marker.names  
   
 return(genotypes)  
   
} #end read.vcf  
  
  
  
#command for Parnassius clodius, number refers to loci  
geno <- read.vcf.genotypes(filename="SNPdata/parnassius\_clodius\_unfiltered\_imputed.vcf",1001)

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geno <- t(geno)  
  
#Conduct PCA and SNMF clustering  
source("http://bioconductor.org/biocLite.R")

## Bioconductor version 3.5 (BiocInstaller 1.26.1), ?biocLite for help

## A newer version of Bioconductor is available for this version of R,  
## ?BiocUpgrade for help

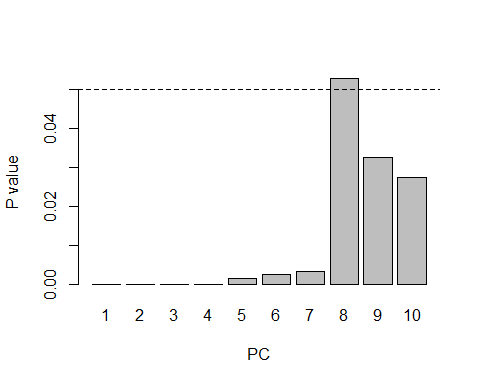
#biocLite("LEA")  
library('LEA')  
library('maps')  
#install.packages('RColorBrewer')  
library('RColorBrewer')  
colors <- brewer.pal(5,"Accent")  
  
#Remove invariant SNPs  
colzeros <- apply(geno,2,sd)==0  
mark <- geno[,colzeros==F]  
  
#Commenting this out because every time you run this it takes forever to commit. They should be good as is, unless we're analyzing a new dataset.  
#write.geno(mark,"analysis/LEA\_analysis/ParaFiles/para.geno")  
#write.lfmm(mark,"analysis/LEA\_analysis/ParaFiles/para.lfmm")  
  
pc <- pca("analysis/LEA\_analysis/ParaFiles/para.lfmm",scale=TRUE)

## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] " Principal Component Analysis "  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of principal components) 146  
## -x (genotype file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.lfmm  
## -a (eigenvalue file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.pca\/para.eigenvalues  
## -e (eigenvector file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.pca\/para.eigenvectors  
## -d (standard deviation file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.pca\/para.sdev  
## -p (projection file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.pca\/para.projections  
## -s data centered and scaled

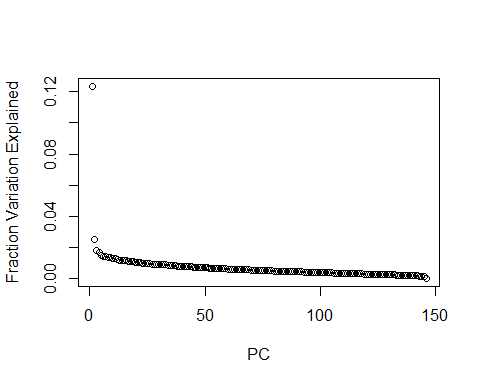
tw = tracy.widom(pc)

## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] " Tracy-Widom tests "  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of eigenvalues) 146  
## -i (input file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.pca/para.eigenvalues  
## -o (output file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.pca/para.tracywidom

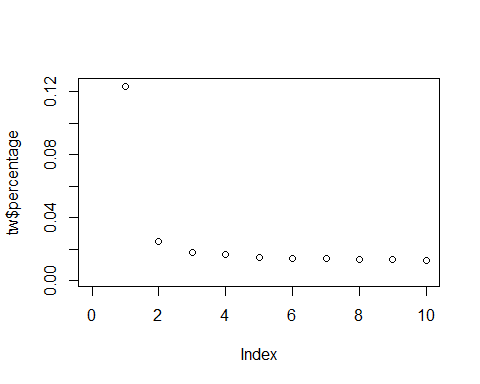
barplot(tw$pvalues[1:10],ylab="P value",xlab="PC",names.arg=1:10)  
abline(h=0.05,lty=2)



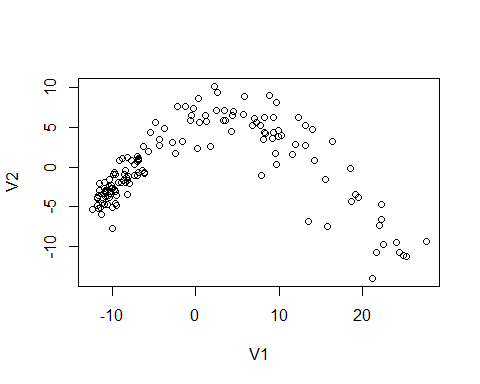
plot(pc$sdev^2/sum(pc$sdev^2),xlab="PC",ylab="Fraction Variation Explained")



plot(tw$percentage, xlim = c(0,10)) #3 major genetic clusters in the data



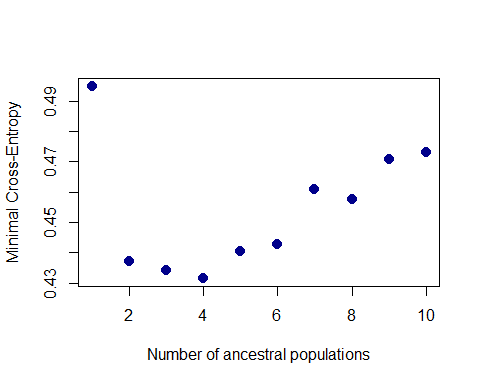
plot(pc$projections)



snmf2 <- snmf("analysis/LEA\_analysis/ParaFiles/para.geno",K=1:10,ploidy=2,entropy=T,alpha=100,project="new")

## The project is saved into :  
## analysis/LEA\_analysis/ParaFiles/para.snmfProject   
##   
## To load the project, use:  
## project = load.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## To remove the project, use:  
## remove.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## [1] 1314405036  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* create.dataset \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -s (seed random init) 1314405036  
## -r (percentage of masked data) 0.05  
## -x (genotype file in .geno format) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.geno  
## -o (output file in .geno format) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
##   
## Write genotype file with masked data, C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno: OK.  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* sNMF K = 1 repetition 1 \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 1  
## -x (input file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## -q (individual admixture file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K1/run1/para\_r1.1.Q  
## -g (ancestral frequencies file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K1/run1/para\_r1.1.G  
## -i (number max of iterations) 200  
## -a (regularization parameter) 100  
## -s (seed random init) 1314405036  
## -e (tolerance error) 1E-05  
## -p (number of processes) 1  
## - diploid  
##   
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno: OK.  
##   
##   
## Main algorithm:  
##   
## Least-square error: 43016.357163  
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K1/run1/para\_r1.1.Q: OK.  
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K1/run1/para\_r1.1.G: OK.  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* cross-entropy estimation \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 1  
## -x (genotype file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.geno  
## -q (individual admixture) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K1/run1/para\_r1.1.Q  
## -g (ancestral frequencies) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K1/run1/para\_r1.1.G  
## -i (with masked genotypes) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## - diploid  
##   
## Cross-Entropy (all data): 0.480082  
## Cross-Entropy (masked data): 0.494831  
## The project is saved into :  
## analysis/LEA\_analysis/ParaFiles/para.snmfProject   
##   
## To load the project, use:  
## project = load.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## To remove the project, use:  
## remove.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* sNMF K = 2 repetition 1 \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 2  
## -x (input file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## -q (individual admixture file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K2/run1/para\_r1.2.Q  
## -g (ancestral frequencies file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K2/run1/para\_r1.2.G  
## -i (number max of iterations) 200  
## -a (regularization parameter) 100  
## -s (seed random init) 1314405036  
## -e (tolerance error) 1E-05  
## -p (number of processes) 1  
## - diploid  
##   
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno: OK.  
##   
##   
## Main algorithm:  
## [ ]  
## [========]  
## Number of iterations: 22  
##   
## Least-square error: 37355.944290  
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K2/run1/para\_r1.2.Q: OK.  
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K2/run1/para\_r1.2.G: OK.  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* cross-entropy estimation \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 2  
## -x (genotype file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.geno  
## -q (individual admixture) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K2/run1/para\_r1.2.Q  
## -g (ancestral frequencies) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K2/run1/para\_r1.2.G  
## -i (with masked genotypes) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## - diploid  
##   
## Cross-Entropy (all data): 0.41763  
## Cross-Entropy (masked data): 0.437138  
## The project is saved into :  
## analysis/LEA\_analysis/ParaFiles/para.snmfProject   
##   
## To load the project, use:  
## project = load.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## To remove the project, use:  
## remove.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* sNMF K = 3 repetition 1 \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 3  
## -x (input file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## -q (individual admixture file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K3/run1/para\_r1.3.Q  
## -g (ancestral frequencies file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K3/run1/para\_r1.3.G  
## -i (number max of iterations) 200  
## -a (regularization parameter) 100  
## -s (seed random init) 1314405036  
## -e (tolerance error) 1E-05  
## -p (number of processes) 1  
## - diploid  
##   
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno: OK.  
##   
##   
## Main algorithm:  
## [ ]  
## [====================]  
## Number of iterations: 53  
##   
## Least-square error: 36318.811956  
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K3/run1/para\_r1.3.Q: OK.  
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K3/run1/para\_r1.3.G: OK.  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* cross-entropy estimation \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 3  
## -x (genotype file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.geno  
## -q (individual admixture) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K3/run1/para\_r1.3.Q  
## -g (ancestral frequencies) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K3/run1/para\_r1.3.G  
## -i (with masked genotypes) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## - diploid  
##   
## Cross-Entropy (all data): 0.40434  
## Cross-Entropy (masked data): 0.434273  
## The project is saved into :  
## analysis/LEA\_analysis/ParaFiles/para.snmfProject   
##   
## To load the project, use:  
## project = load.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## To remove the project, use:  
## remove.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* sNMF K = 4 repetition 1 \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 4  
## -x (input file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## -q (individual admixture file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K4/run1/para\_r1.4.Q  
## -g (ancestral frequencies file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K4/run1/para\_r1.4.G  
## -i (number max of iterations) 200  
## -a (regularization parameter) 100  
## -s (seed random init) 1314405036  
## -e (tolerance error) 1E-05  
## -p (number of processes) 1  
## - diploid  
##   
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno: OK.  
##   
##   
## Main algorithm:  
## [ ]  
## [===============================================]  
## Number of iterations: 126  
##   
## Least-square error: 35813.226113  
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K4/run1/para\_r1.4.Q: OK.  
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K4/run1/para\_r1.4.G: OK.  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* cross-entropy estimation \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 4  
## -x (genotype file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.geno  
## -q (individual admixture) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K4/run1/para\_r1.4.Q  
## -g (ancestral frequencies) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K4/run1/para\_r1.4.G  
## -i (with masked genotypes) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## - diploid  
##   
## Cross-Entropy (all data): 0.397007  
## Cross-Entropy (masked data): 0.431622  
## The project is saved into :  
## analysis/LEA\_analysis/ParaFiles/para.snmfProject   
##   
## To load the project, use:  
## project = load.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## To remove the project, use:  
## remove.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* sNMF K = 5 repetition 1 \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 5  
## -x (input file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## -q (individual admixture file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K5/run1/para\_r1.5.Q  
## -g (ancestral frequencies file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K5/run1/para\_r1.5.G  
## -i (number max of iterations) 200  
## -a (regularization parameter) 100  
## -s (seed random init) 1314405036  
## -e (tolerance error) 1E-05  
## -p (number of processes) 1  
## - diploid  
##   
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno: OK.  
##   
##   
## Main algorithm:  
## [ ]  
## [===============================]  
## Number of iterations: 84  
##   
## Least-square error: 35219.905354  
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K5/run1/para\_r1.5.Q: OK.  
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K5/run1/para\_r1.5.G: OK.  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* cross-entropy estimation \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 5  
## -x (genotype file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.geno  
## -q (individual admixture) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K5/run1/para\_r1.5.Q  
## -g (ancestral frequencies) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K5/run1/para\_r1.5.G  
## -i (with masked genotypes) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## - diploid  
##   
## Cross-Entropy (all data): 0.390267  
## Cross-Entropy (masked data): 0.440489  
## The project is saved into :  
## analysis/LEA\_analysis/ParaFiles/para.snmfProject   
##   
## To load the project, use:  
## project = load.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## To remove the project, use:  
## remove.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* sNMF K = 6 repetition 1 \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 6  
## -x (input file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## -q (individual admixture file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K6/run1/para\_r1.6.Q  
## -g (ancestral frequencies file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K6/run1/para\_r1.6.G  
## -i (number max of iterations) 200  
## -a (regularization parameter) 100  
## -s (seed random init) 1314405036  
## -e (tolerance error) 1E-05  
## -p (number of processes) 1  
## - diploid  
##   
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno: OK.  
##   
##   
## Main algorithm:  
## [ ]  
## [============================]  
## Number of iterations: 74  
##   
## Least-square error: 34758.116575  
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K6/run1/para\_r1.6.Q: OK.  
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K6/run1/para\_r1.6.G: OK.  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* cross-entropy estimation \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 6  
## -x (genotype file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.geno  
## -q (individual admixture) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K6/run1/para\_r1.6.Q  
## -g (ancestral frequencies) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K6/run1/para\_r1.6.G  
## -i (with masked genotypes) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## - diploid  
##   
## Cross-Entropy (all data): 0.383824  
## Cross-Entropy (masked data): 0.44271  
## The project is saved into :  
## analysis/LEA\_analysis/ParaFiles/para.snmfProject   
##   
## To load the project, use:  
## project = load.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## To remove the project, use:  
## remove.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* sNMF K = 7 repetition 1 \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 7  
## -x (input file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## -q (individual admixture file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K7/run1/para\_r1.7.Q  
## -g (ancestral frequencies file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K7/run1/para\_r1.7.G  
## -i (number max of iterations) 200  
## -a (regularization parameter) 100  
## -s (seed random init) 1314405036  
## -e (tolerance error) 1E-05  
## -p (number of processes) 1  
## - diploid  
##   
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno: OK.  
##   
##   
## Main algorithm:  
## [ ]  
## [=============]  
## Number of iterations: 36  
##   
## Least-square error: 34474.126472  
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K7/run1/para\_r1.7.Q: OK.  
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K7/run1/para\_r1.7.G: OK.  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* cross-entropy estimation \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 7  
## -x (genotype file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.geno  
## -q (individual admixture) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K7/run1/para\_r1.7.Q  
## -g (ancestral frequencies) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K7/run1/para\_r1.7.G  
## -i (with masked genotypes) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## - diploid  
##   
## Cross-Entropy (all data): 0.380558  
## Cross-Entropy (masked data): 0.460729  
## The project is saved into :  
## analysis/LEA\_analysis/ParaFiles/para.snmfProject   
##   
## To load the project, use:  
## project = load.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## To remove the project, use:  
## remove.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* sNMF K = 8 repetition 1 \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 8  
## -x (input file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## -q (individual admixture file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K8/run1/para\_r1.8.Q  
## -g (ancestral frequencies file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K8/run1/para\_r1.8.G  
## -i (number max of iterations) 200  
## -a (regularization parameter) 100  
## -s (seed random init) 1314405036  
## -e (tolerance error) 1E-05  
## -p (number of processes) 1  
## - diploid  
##   
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno: OK.  
##   
##   
## Main algorithm:  
## [ ]  
## [==============]  
## Number of iterations: 38  
##   
## Least-square error: 33974.839782  
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K8/run1/para\_r1.8.Q: OK.  
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K8/run1/para\_r1.8.G: OK.  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* cross-entropy estimation \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 8  
## -x (genotype file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.geno  
## -q (individual admixture) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K8/run1/para\_r1.8.Q  
## -g (ancestral frequencies) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K8/run1/para\_r1.8.G  
## -i (with masked genotypes) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## - diploid  
##   
## Cross-Entropy (all data): 0.374203  
## Cross-Entropy (masked data): 0.457685  
## The project is saved into :  
## analysis/LEA\_analysis/ParaFiles/para.snmfProject   
##   
## To load the project, use:  
## project = load.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## To remove the project, use:  
## remove.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* sNMF K = 9 repetition 1 \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 9  
## -x (input file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## -q (individual admixture file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K9/run1/para\_r1.9.Q  
## -g (ancestral frequencies file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K9/run1/para\_r1.9.G  
## -i (number max of iterations) 200  
## -a (regularization parameter) 100  
## -s (seed random init) 1314405036  
## -e (tolerance error) 1E-05  
## -p (number of processes) 1  
## - diploid  
##   
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno: OK.  
##   
##   
## Main algorithm:  
## [ ]  
## [====================]  
## Number of iterations: 53  
##   
## Least-square error: 33610.593154  
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K9/run1/para\_r1.9.Q: OK.  
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K9/run1/para\_r1.9.G: OK.  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* cross-entropy estimation \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 9  
## -x (genotype file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.geno  
## -q (individual admixture) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K9/run1/para\_r1.9.Q  
## -g (ancestral frequencies) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K9/run1/para\_r1.9.G  
## -i (with masked genotypes) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## - diploid  
##   
## Cross-Entropy (all data): 0.370211  
## Cross-Entropy (masked data): 0.470624  
## The project is saved into :  
## analysis/LEA\_analysis/ParaFiles/para.snmfProject   
##   
## To load the project, use:  
## project = load.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## To remove the project, use:  
## remove.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* sNMF K = 10 repetition 1 \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 10  
## -x (input file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## -q (individual admixture file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K10/run1/para\_r1.10.Q  
## -g (ancestral frequencies file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K10/run1/para\_r1.10.G  
## -i (number max of iterations) 200  
## -a (regularization parameter) 100  
## -s (seed random init) 1314405036  
## -e (tolerance error) 1E-05  
## -p (number of processes) 1  
## - diploid  
##   
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno: OK.  
##   
##   
## Main algorithm:  
## [ ]  
## [================]  
## Number of iterations: 43  
##   
## Least-square error: 33279.794076  
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K10/run1/para\_r1.10.Q: OK.  
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K10/run1/para\_r1.10.G: OK.  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* cross-entropy estimation \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 10  
## -x (genotype file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.geno  
## -q (individual admixture) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K10/run1/para\_r1.10.Q  
## -g (ancestral frequencies) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K10/run1/para\_r1.10.G  
## -i (with masked genotypes) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/masked/para\_I.geno  
## - diploid  
##   
## Cross-Entropy (all data): 0.364331  
## Cross-Entropy (masked data): 0.473073  
## The project is saved into :  
## analysis/LEA\_analysis/ParaFiles/para.snmfProject   
##   
## To load the project, use:  
## project = load.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## To remove the project, use:  
## remove.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")

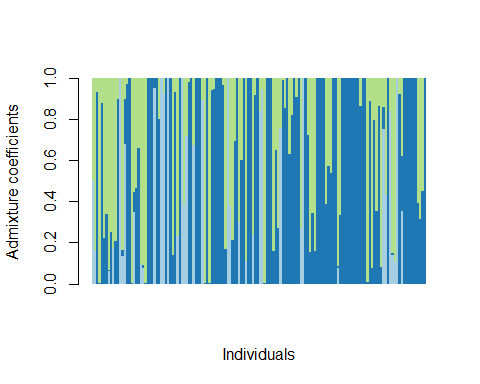
plot(snmf2,col="blue4",cex=1.4,pch=19) #minimum at K=3



K=3  
snmf = snmf("analysis/LEA\_analysis/ParaFiles/para.geno", K = K, alpha = 100, project = "new")

## The project is saved into :  
## analysis/LEA\_analysis/ParaFiles/para.snmfProject   
##   
## To load the project, use:  
## project = load.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## To remove the project, use:  
## remove.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## [1] "\* sNMF K = 3 repetition 1 \*"  
## [1] "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*"  
## summary of the options:  
##   
## -n (number of individuals) 146  
## -L (number of loci) 1001  
## -K (number of ancestral pops) 3  
## -x (input file) C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.geno  
## -q (individual admixture file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K3/run1/para\_r1.3.Q  
## -g (ancestral frequencies file) C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K3/run1/para\_r1.3.G  
## -i (number max of iterations) 200  
## -a (regularization parameter) 100  
## -s (seed random init) 660679819  
## -e (tolerance error) 1E-05  
## -p (number of processes) 1  
## - diploid  
##   
## Read genotype file C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA\_analysis\ParaFiles\para.geno: OK.  
##   
##   
## Main algorithm:  
## [ ]  
## [==================]  
## Number of iterations: 47  
##   
## Least-square error: 35713.629481  
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K3/run1/para\_r1.3.Q: OK.  
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA\_analysis/ParaFiles/para.snmf/K3/run1/para\_r1.3.G: OK.  
##   
## The project is saved into :  
## analysis/LEA\_analysis/ParaFiles/para.snmfProject   
##   
## To load the project, use:  
## project = load.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")  
##   
## To remove the project, use:  
## remove.snmfProject("analysis/LEA\_analysis/ParaFiles/para.snmfProject")

qmatrix = Q(snmf, K = K)  
barplot(t(qmatrix),col=brewer.pal(K,"Paired"),border=NA,space=0,xlab="Individuals",ylab="Admixture coefficients")



#for clodius  
source("analysis/adegenet\_analysis/PopKey.R")  
coord <- popkey[,c(1,2,4,3)]  
names(coord)[3:4] <- c("Latitude", "Longitude")  
rm(popkey)  
  
ids <- noquote(rownames(mark))  
samples\_used <- (coord$SampleID %in% ids)  
newcoord <- coord[samples\_used,]  
pops <- unique(newcoord$SiteID)  
Npop = length(unique(newcoord$SiteID))  
q3.samples <- cbind(newcoord,qmatrix)  
pop.means <- aggregate(.~SiteID, data=q3.samples, mean)  
qpop <- data.matrix(pop.means[1:29,5:ncol(pop.means)])  
coord.pop <- cbind(pop.means[,4],pop.means[,3])  
  
unique(apply(qpop,1,function(x){round(sum(x),2)==1})) #check that all pops' ancestry proportions sum to 1

## [1] TRUE

#write file for later plotting  
write.csv(x = pop.means, file = "analysis/LEA\_analysis/PopMeans.csv", sep = ",", col.names = T, row.names = F)

## Warning in write.csv(x = pop.means, file = "analysis/LEA\_analysis/  
## PopMeans.csv", : attempt to set 'col.names' ignored

## Warning in write.csv(x = pop.means, file = "analysis/LEA\_analysis/  
## PopMeans.csv", : attempt to set 'sep' ignored