import_data_toR_amedits.R

Audrey McCombs

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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]
  close(con)

  marker.stats <- data.frame(Chrom=rep("",max.marker),Pos=rep(0,max.marker),Name=rep("",max.marker),NSa
  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(",",t
        #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]

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 numb
    if ((length(grep(",",temp2[5],fixed=TRUE))==0)&(temp2[5]!="-")&(temp2[4]!="-")&(length(grep(",",t

      #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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## [1] "Marker 959 done"
## [1] "Marker 960 done"
## [1] "Marker 961 done"
## [1] "Marker 962 done"
## [1] "Marker 963 done"
## [1] "Marker 964 done"
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## [1] "Marker 967 done"
## [1] "Marker 968 done"
## [1] "Marker 969 done"
## [1] "Marker 970 done"
## [1] "Marker 971 done"
## [1] "Marker 972 done"
## [1] "Marker 973 done"
## [1] "Marker 974 done"
## [1] "Marker 975 done"
## [1] "Marker 976 done"
## [1] "Marker 977 done"
## [1] "Marker 978 done"
## [1] "Marker 979 done"
## [1] "Marker 980 done"
## [1] "Marker 981 done"
## [1] "Marker 982 done"
## [1] "Marker 983 done"
## [1] "Marker 984 done"
## [1] "Marker 985 done"
## [1] "Marker 986 done"
## [1] "Marker 987 done"
## [1] "Marker 988 done"
## [1] "Marker 989 done"
## [1] "Marker 990 done"
## [1] "Marker 991 done"
## [1] "Marker 992 done"
## [1] "Marker 993 done"
## [1] "Marker 994 done"
## [1] "Marker 995 done"
## [1] "Marker 996 done"
## [1] "Marker 997 done"
## [1] "Marker 998 done"
## [1] "Marker 999 done"
## [1] "Marker 1000 done"
```

```
## [1] "Marker 1001 done"
```

```
geno <- t(geno)

apply(geno[,1:5],2,table)
```

```
## $NA.12243.152_10
##
##   0   1
## 137   9
##
## $NA.13515.167_67
##
##   0   1   2
## 126  16   4
##
## $NA.13830.171_58
##
##   0   1
## 132  14
##
## $NA.17517.217_19
##
##  0  1
## 94 52
##
## $NA.17529.217_31
##
##  0  1
## 92 54
```

```
table(sapply(apply(geno,2,table), length))
```

```
##
##   2   3
## 674 327
```

```
#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]
rm(colzeros)
```

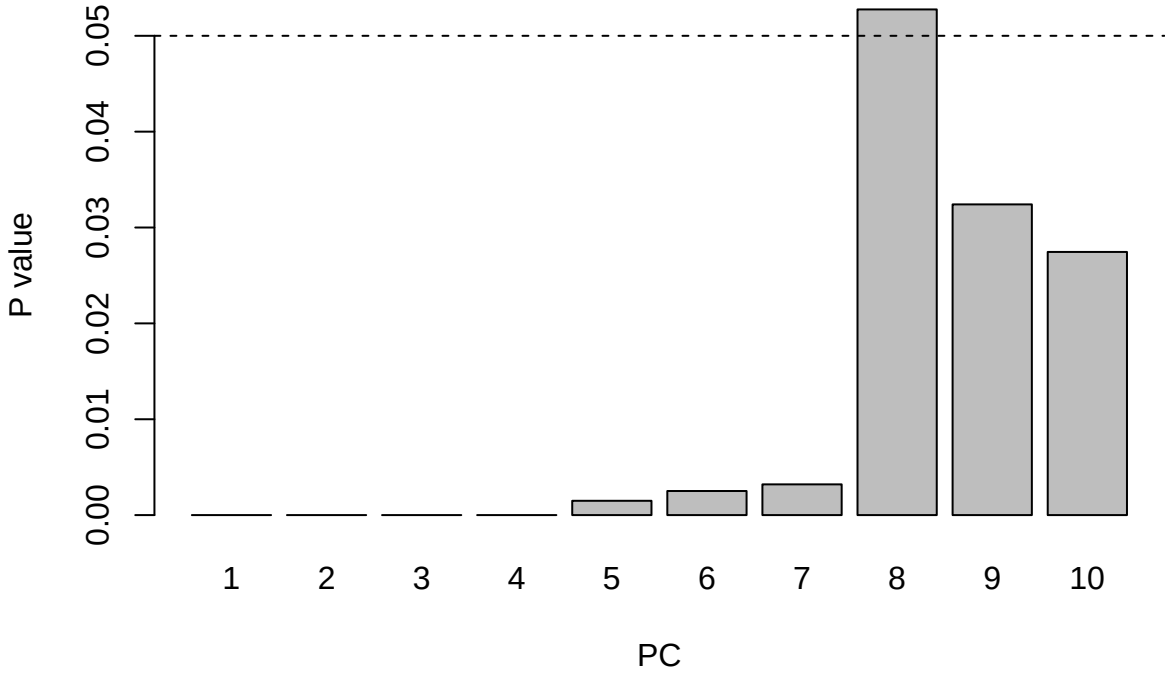
```
#Commenting this out because every time you run this it takes forever to commit. They should be good as
#write.geno(mark,"analysis/LEA_analysis/ParaFiles/para.geno")
#write.lfmm(mark,"analysis/LEA_analysis/ParaFiles/para.lfmm")

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\analys
##         -a (eigenvalue file)                C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analys
##         -e (eigenvector file)               C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analys
##         -d (standard deviation file)        C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analys
##         -p (projection file)                C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analys
##         -s data centered and scaled
```

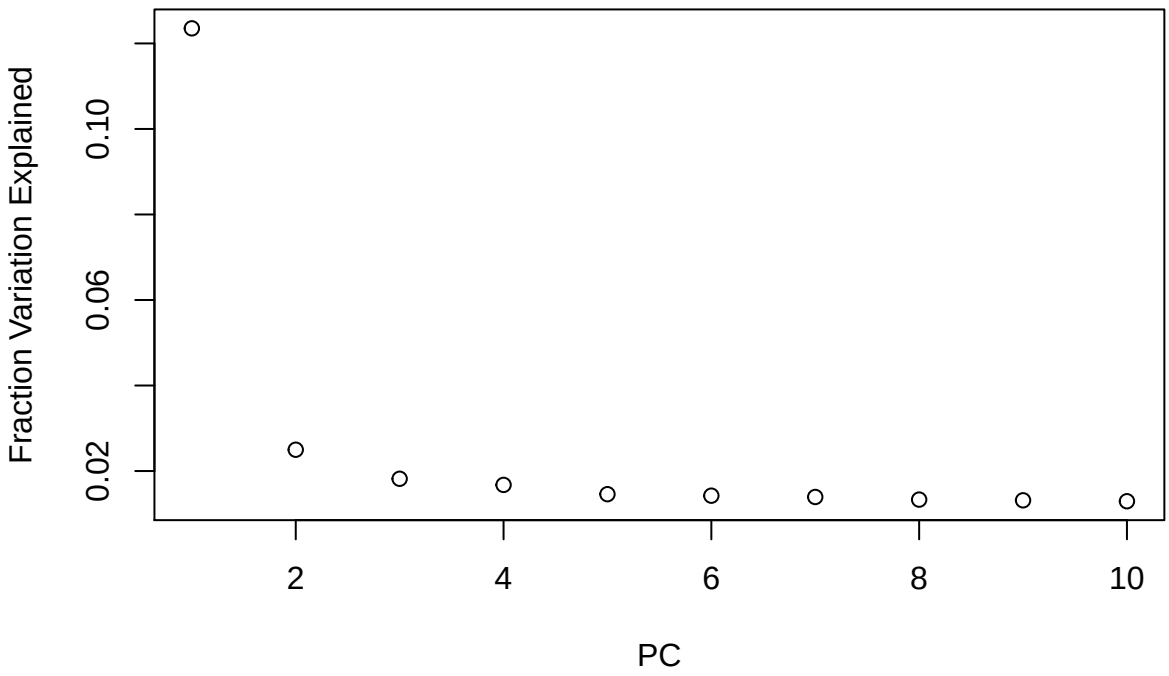
```
#Tracey Widom test.  From R doc: Perform tracy-widom tests on a set of eigenvalues to determine the num

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/analys
##         -o (output file)                    C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analys
```

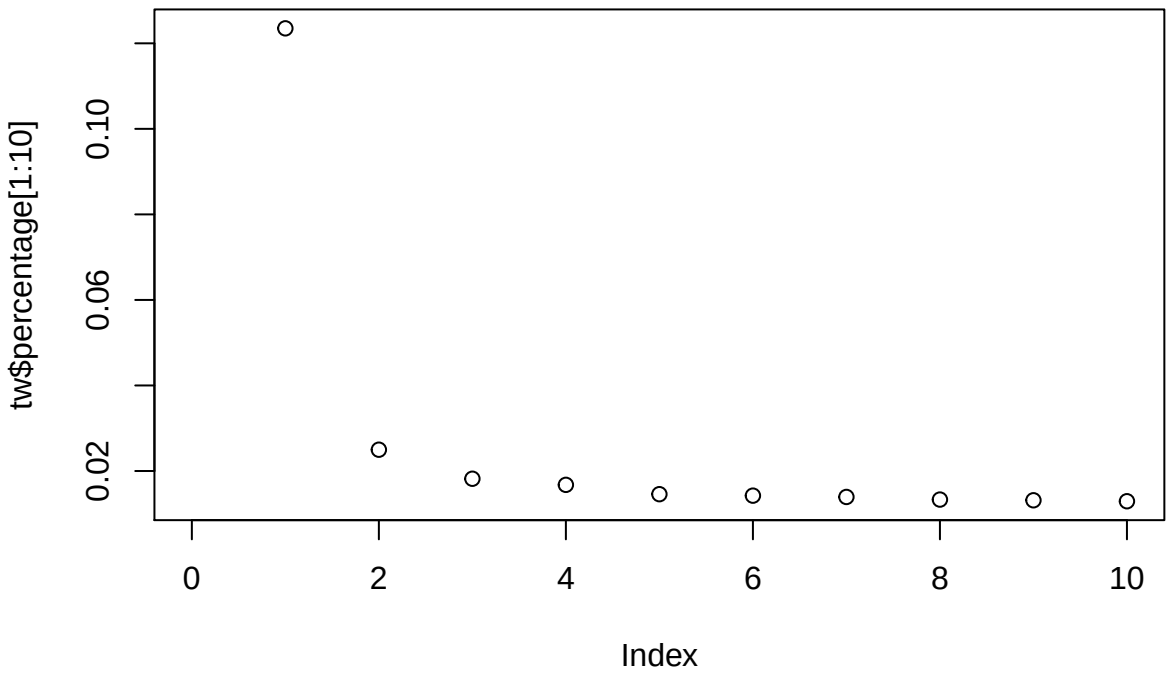
```
barplot(tw$pvalues[1:10],ylab="P value",xlab="PC",names.arg=1:10)
abline(h=0.05,lty=2)
```



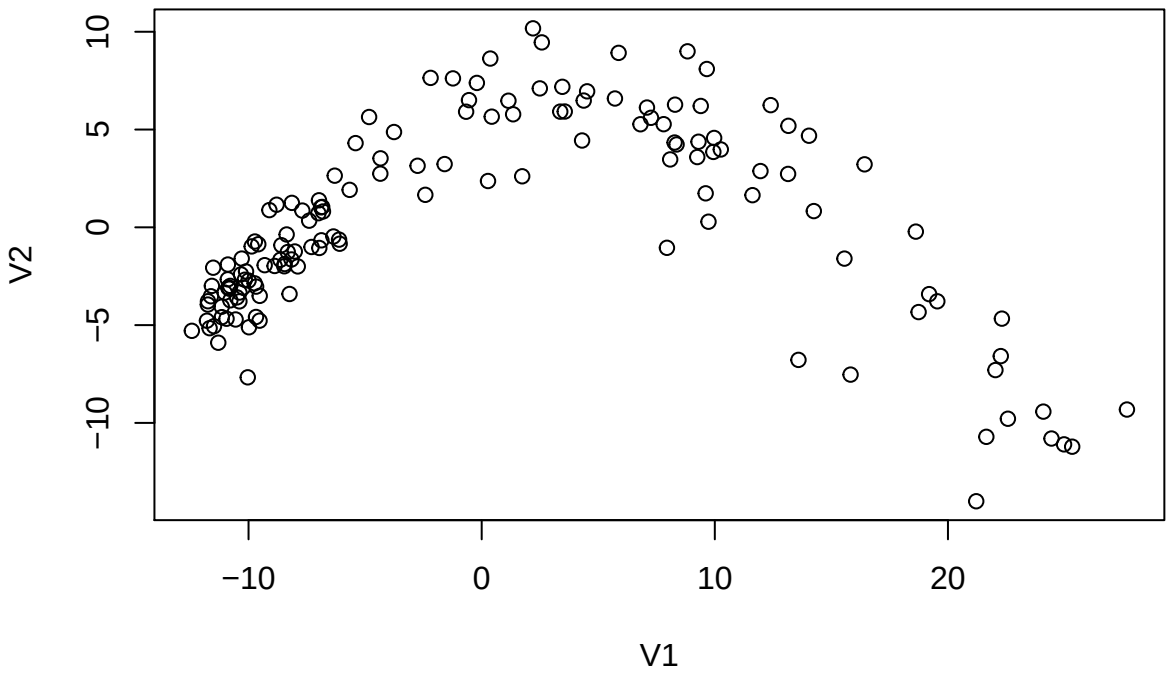

```
plot(pc$sdev[1:10]^2/sum(pc$sdev^2),xlab="PC",ylab="Fraction Variation Explained")
```




```
plot(tw$percentage[1:10], xlim = c(0,10))  #3 major genetic clusters in the data
```




```
plot(pc$projections)
```




```
#Compute admixture
snmf2 <- snmf("analysis/LEA_analysis/ParaFiles/para.geno",K=1:10,ploidy=2,entropy=T,alpha=100,project="
```

```
## 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] 790300450
## [1] "***********************************"
## [1] "*          create.dataset           *"
## [1] "***********************************"
## summary of the options:
##
##         -n (number of individuals)                146
##         -L (number of loci)                       1001
##         -s (seed random init)                     790300450
##         -r (percentage of masked data)            0.05
##         -x (genotype file in .geno format)        C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics
##         -o (output file in .geno format)          C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics
##
##  Write genotype file with masked data, C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LE
```

```
##
## [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/ana
##         -q (individual admixture file)        C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -g (ancestral frequencies file)       C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -i (number max of iterations)         200
##         -a (regularization parameter)         100
##         -s (seed random init)                 790300450
##         -e (tolerance error)                  1E-05
##         -p (number of processes)              1
##         - diploid
##
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA_analysis/ParaFiles
##
##
## Main algorithm:
##
## Least-square error: 42898.096882
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/
##
## [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\analysi
##         -q (individual admixture)          C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -g (ancestral frequencies)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -i (with masked genotypes)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         - diploid
##
## Cross-Entropy (all data):     0.479848
## Cross-Entropy (masked data):  0.497293
## 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/ana
##         -q (individual admixture file)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -g (ancestral frequencies file)        C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -i (number max of iterations)          200
##         -a (regularization parameter)          100
##         -s (seed random init)                  790300450
##         -e (tolerance error)                   1E-05
##         -p (number of processes)               1
##         - diploid
##
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA_analysis/ParaFiles
##
##
## Main algorithm:
##  [                                                                                ]
##  [========]
## Number of iterations: 22
##
## Least-square error: 37197.099460
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/
##
## [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\analysi
##         -q (individual admixture)          C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -g (ancestral frequencies)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -i (with masked genotypes)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         - diploid
##
## Cross-Entropy (all data):     0.417168
## Cross-Entropy (masked data):  0.445996
## 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/ana
##         -q (individual admixture file)        C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -g (ancestral frequencies file)       C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -i (number max of iterations)         200
##         -a (regularization parameter)         100
##         -s (seed random init)                 790300450
##         -e (tolerance error)                  1E-05
##         -p (number of processes)              1
##         - diploid
##
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA_analysis/ParaFiles
##
##
## Main algorithm:
##  [                                                                                ]
##  [==================]
## Number of iterations: 49
##
## Least-square error: 36333.804001
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/
##
## [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\analysi
##         -q (individual admixture)          C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -g (ancestral frequencies)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -i (with masked genotypes)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         - diploid
##
## Cross-Entropy (all data):     0.403695
## Cross-Entropy (masked data):  0.442493
## 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/ana
##         -q (individual admixture file)        C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -g (ancestral frequencies file)       C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -i (number max of iterations)         200
##         -a (regularization parameter)         100
##         -s (seed random init)                 790300450
##         -e (tolerance error)                  1E-05
##         -p (number of processes)              1
##         - diploid
##
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA_analysis/ParaFiles
##
##
## Main algorithm:
##  [                                                                                ]
##  [====================]
## Number of iterations: 57
##
## Least-square error: 35658.325877
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/
##
## [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\analysi
##         -q (individual admixture)          C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -g (ancestral frequencies)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -i (with masked genotypes)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         - diploid
##
## Cross-Entropy (all data):     0.396182
## Cross-Entropy (masked data):  0.443527
## 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/ana
##         -q (individual admixture file)        C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -g (ancestral frequencies file)       C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -i (number max of iterations)         200
##         -a (regularization parameter)         100
##         -s (seed random init)                 790300450
##         -e (tolerance error)                  1E-05
##         -p (number of processes)              1
##         - diploid
##
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA_analysis/ParaFiles
##
##
## Main algorithm:
##  [                                                                              ]
##  [================================================================================]
## Number of iterations: 200
##
## Least-square error: 35165.149677
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/
##
## [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\analysi
##         -q (individual admixture)          C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -g (ancestral frequencies)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -i (with masked genotypes)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         - diploid
##
## Cross-Entropy (all data):     0.389602
## Cross-Entropy (masked data):  0.450664
## 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/ana
##         -q (individual admixture file)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -g (ancestral frequencies file)        C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -i (number max of iterations)          200
##         -a (regularization parameter)          100
##         -s (seed random init)                  790300450
##         -e (tolerance error)                   1E-05
##         -p (number of processes)               1
##         - diploid
##
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA_analysis/ParaFiles
##
##
## Main algorithm:
##  [                                                                              ]
##  [==============================================================================]
## Number of iterations: 181
##
## Least-square error: 34679.831934
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/
##
## [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\analysi
##         -q (individual admixture)          C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -g (ancestral frequencies)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -i (with masked genotypes)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         - diploid
##
## Cross-Entropy (all data):     0.384667
## Cross-Entropy (masked data):  0.458368
## 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/ana
##         -q (individual admixture file)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -g (ancestral frequencies file)        C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -i (number max of iterations)          200
##         -a (regularization parameter)          100
##         -s (seed random init)                  790300450
##         -e (tolerance error)                   1E-05
##         -p (number of processes)               1
##         - diploid
##
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA_analysis/ParaFiles
##
##
## Main algorithm:
##  [                                                                                ]
##  [==========]
## Number of iterations: 28
##
## Least-square error: 34299.595025
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/
##
## [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\analysi
##         -q (individual admixture)          C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -g (ancestral frequencies)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -i (with masked genotypes)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         - diploid
##
## Cross-Entropy (all data):     0.378383
## Cross-Entropy (masked data):  0.460496
## The project is saved into :
##  analysis/LEA_analysis/ParaFiles/para.snmfProject
##
## To load the project, use:
```

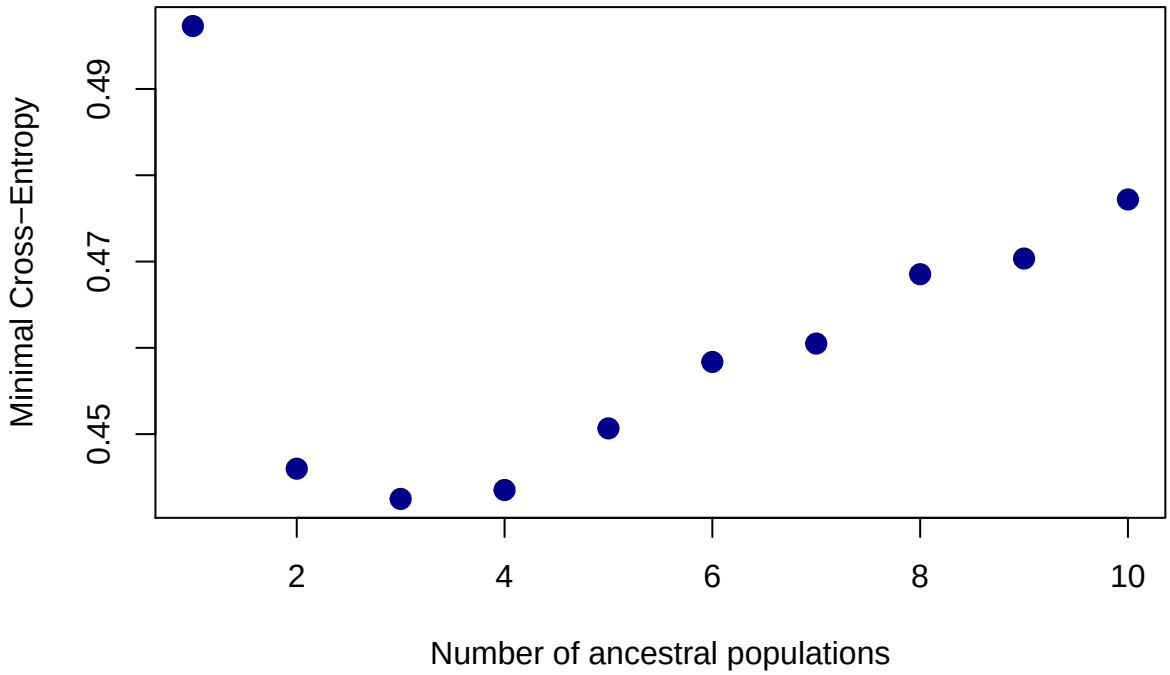
```
##  project = load.snmfProject("analysis/LEA_analysis/ParaFiles/para.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("analysis/LEA_analysis/ParaFiles/para.snmfProject")
##
## [1] "************************************"
## [1] "* sNMF K = 8  repetition 1      *"
## [1] "************************************"
## 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/ana
##         -q (individual admixture file)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -g (ancestral frequencies file)        C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -i (number max of iterations)          200
##         -a (regularization parameter)          100
##         -s (seed random init)                  790300450
##         -e (tolerance error)                   1E-05
##         -p (number of processes)               1
##         - diploid
##
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA_analysis/ParaFiles
##
##
## Main algorithm:
##  [                                                                                ]
##  [==========================]
## Number of iterations: 71
##
## Least-square error: 33917.732513
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/
##
## [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\analysi
##         -q (individual admixture)          C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -g (ancestral frequencies)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -i (with masked genotypes)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         - diploid
##
## Cross-Entropy (all data):     0.37353
## Cross-Entropy (masked data):  0.468533
## 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/ana
##         -q (individual admixture file)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -g (ancestral frequencies file)        C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -i (number max of iterations)          200
##         -a (regularization parameter)          100
##         -s (seed random init)                  790300450
##         -e (tolerance error)                   1E-05
##         -p (number of processes)               1
##         - diploid
##
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA_analysis/ParaFiles
##
##
## Main algorithm:
##  [                                                                                ]
##  [===============]
## Number of iterations: 39
##
## Least-square error: 33431.262708
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/
##
## [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\analysi
##         -q (individual admixture)          C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -g (ancestral frequencies)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -i (with masked genotypes)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         - diploid
##
## Cross-Entropy (all data):     0.368375
## Cross-Entropy (masked data):  0.47035
## 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/ana
##         -q (individual admixture file)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -g (ancestral frequencies file)        C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -i (number max of iterations)          200
##         -a (regularization parameter)          100
##         -s (seed random init)                  790300450
##         -e (tolerance error)                   1E-05
##         -p (number of processes)               1
##         - diploid
##
## Read genotype file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysis/LEA_analysis/ParaFiles
##
##
## Main algorithm:
##  [                                                                                ]
##  [==============]
## Number of iterations: 38
##
## Least-square error: 33123.736630
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/
##
## [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\analysi
##         -q (individual admixture)          C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -g (ancestral frequencies)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         -i (with masked genotypes)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
##         - diploid
##
## Cross-Entropy (all data):     0.363353
## Cross-Entropy (masked data):  0.477196
## 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
```

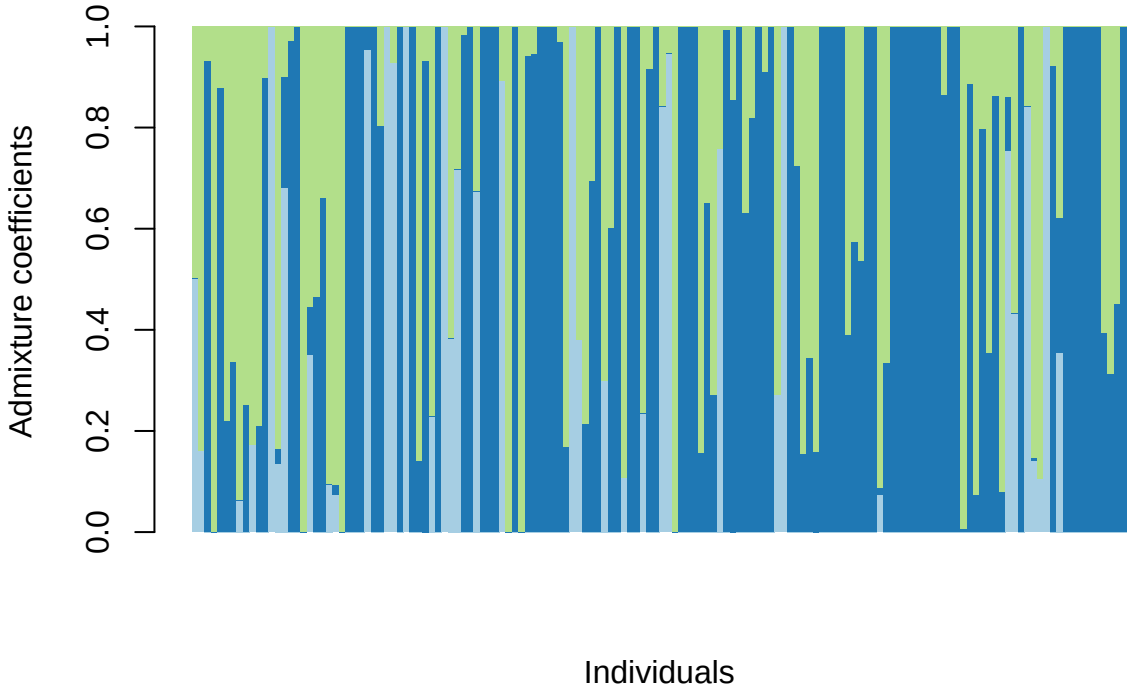



```
K=3
snmf1 = snmf("analysis/LEA_analysis/ParaFiles/para.geno", K = K, alpha = 100, project = "new")
```

```
## 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\ana
##         -q (individual admixture file)         C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -g (ancestral frequencies file)        C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/ana
##         -i (number max of iterations)          200
##         -a (regularization parameter)          100
##         -s (seed random init)                  193289016
##         -e (tolerance error)                   1E-05
##         -p (number of processes)               1
##         - diploid
##
## Read genotype file C:\Users\Audrey McCombs\Desktop\ParnassiusGenetics\analysis\LEA_analysis\ParaFiles
##
##
## Main algorithm:
##  [                                                                              ]
##  [==============]
## Number of iterations: 38
##
## Least-square error: 35713.627796
## Write individual ancestry coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/analysi
## Write ancestral allele frequency coefficient file C:/Users/Audrey McCombs/Desktop/ParnassiusGenetics/
##
## 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(snmf1, K = K)
barplot(t(qmatrix),col=brewer.pal(K,"Paired"),border=NA,space=0,xlab="Individuals",ylab="Admixture coefi
```




```
rm(K)

# create df for clodius
source("analysis/adegenet_analysis/PopKey.R")
coord <- popkey[,c(1,2,4,3)]
names(coord)[3:4] <- c("Latitude", "Longitude")
rm(popkey)

  #make df with only the good samples
ids <- noquote(rownames(mark))
samples_used <- (coord$SampleID %in% ids)
coords <- coord[samples_used,]
rm(ids)
rm(coord)
rm(samples_used)

  #get actual sample size for each pop
samp.size.all <- as.data.frame(table(coords$SiteID))
names(samp.size.all) <- c("SiteID","n")
samp.size <- samp.size.all[samp.size.all$n != 0,]
rm(samp.size.all)

  #full df for all 146 samples: site ID, lat-long, admixture
pops <- unique(coords$SiteID)
Npop = length(unique(coords$SiteID))
Npop
```

```
## [1] 29
```

```
q3.samples <- cbind(coords,qmatrix)
rm(pops)
rm(Npop)
rm(coords)

  #reduced df, aggregated across sites
pop.means <- aggregate(.~SiteID, data=q3.samples, mean)
qpop <- data.matrix(pop.means[,5:ncol(pop.means)]) #just admixtures
coord.pop <- cbind(pop.means[,4],pop.means[,3]) #just lat-long
pop.means <- merge(pop.means, samp.size, by = "SiteID")
rm(samp.size)
pop.means <- pop.means[,c(1, 8, 3:7)]

#check that all pops' ancestry proportions sum to 1
unique(apply(qpop,1,function(x){round(sum(x),2)==1}))
```

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

```
#write file for later plotting
write.csv(x = pop.means, file = "analysis/LEA_analysis/PopMeans.csv", sep = ",", col.names = T, row.nam
```

```
## 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
```