

sNMF analysis - S. botryophora

```
# Load library with sNMF function
library(LEA)
# Set input filenames
inputs <- c("bo6_10_ingroup", "bo6_30_ingroup", "bo6_50_ingroup", "bo6_70_ingroup", "bo6_90_ingroup")

# Read in sample names from vcf file
library(vcfR)

## Warning: package 'vcfR' was built under R version 3.6.3

##
##      *****      ***   vcfR   ***      *****
##      This is vcfR 1.10.0
##      browseVignettes('vcfR') # Documentation
##      citation('vcfR') # Citation
##      *****      *****      *****      *****

vcf <- read.vcfR(paste(inputs[1], ".vcf", sep=""))
samples <- colnames(vcf@gt)[-1]

# Convert vcf file to .geno format for sNMF
for(i in 1:length(inputs)){
  vcf2geno(paste(inputs[i], ".vcf", sep=""))
}

##
## - number of detected individuals: 42
## - number of detected loci: 882
##
## For SNP info, please check ./bo6_10_ingroup.vcfsnp.
##
## 13 line(s) were removed because these are not SNPs.
## Please, check ./bo6_10_ingroup.removed file, for more informations.
##
##
## - number of detected individuals: 42
## - number of detected loci: 5545
##
## For SNP info, please check ./bo6_30_ingroup.vcfsnp.
##
## 138 line(s) were removed because these are not SNPs.
## Please, check ./bo6_30_ingroup.removed file, for more informations.
##
##
```

```

## - number of detected individuals: 42
## - number of detected loci: 17597
##
## For SNP info, please check ./bo6_50_ingroup.vcfsnp.
##
## 423 line(s) were removed because these are not SNPs.
## Please, check ./bo6_50_ingroup.removed file, for more informations.
##
##
## - number of detected individuals: 42
## - number of detected loci: 65236
##
## For SNP info, please check ./bo6_70_ingroup.vcfsnp.
##
## 1347 line(s) were removed because these are not SNPs.
## Please, check ./bo6_70_ingroup.removed file, for more informations.
##
##
## - number of detected individuals: 42
## - number of detected loci: 234664
##
## For SNP info, please check ./bo6_90_ingroup.vcfsnp.
##
## 4046 line(s) were removed because these are not SNPs.
## Please, check ./bo6_90_ingroup.removed file, for more informations.

```

```
#Run sNMF with k from 1 to 1+number of populations
```

```
k <- c(1:12)
```

```

for(i in 1:length(inputs)){
  snmf(paste(inputs[i],".geno",sep=""), K = k, repetitions = 5, CPU=6,
        project = "new", entropy = TRUE, iterations = 2000, alpha = 1)

  snmf(paste(inputs[i],".geno",sep=""), K = k, repetitions = 5, CPU=6,
        project = "continue", entropy = TRUE, iterations = 2000, alpha = 10)

  snmf(paste(inputs[i],".geno",sep=""), K = k, repetitions = 5, CPU=6,
        project = "continue", entropy = TRUE, iterations = 2000, alpha = 100)
}

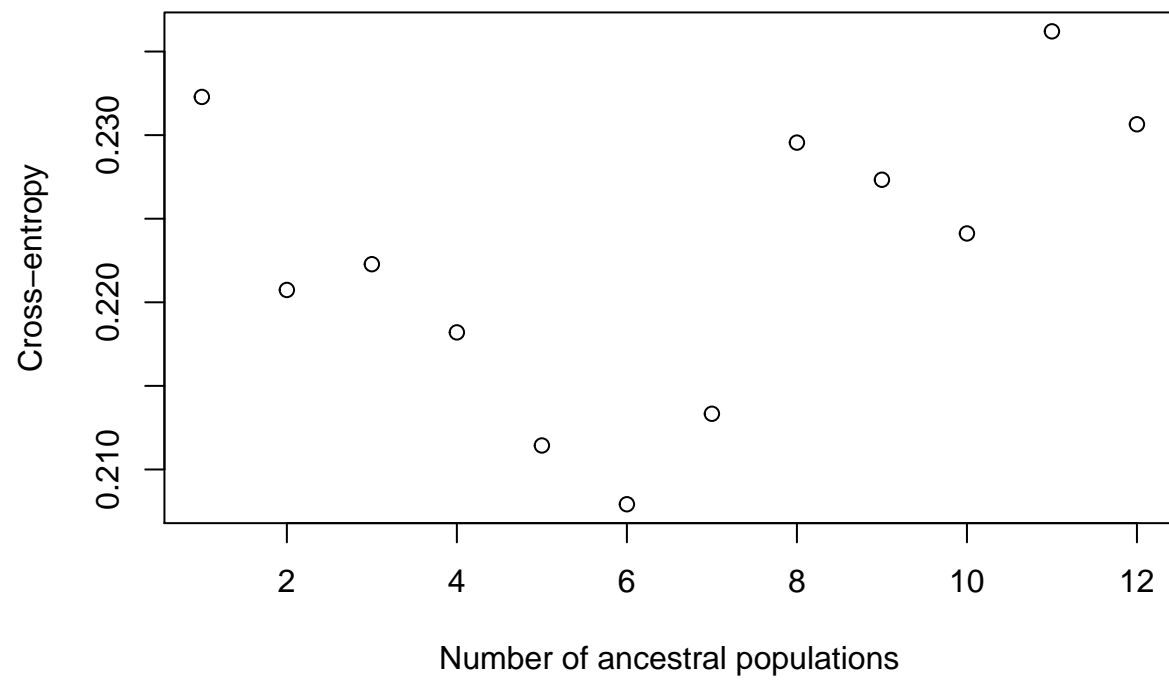
```

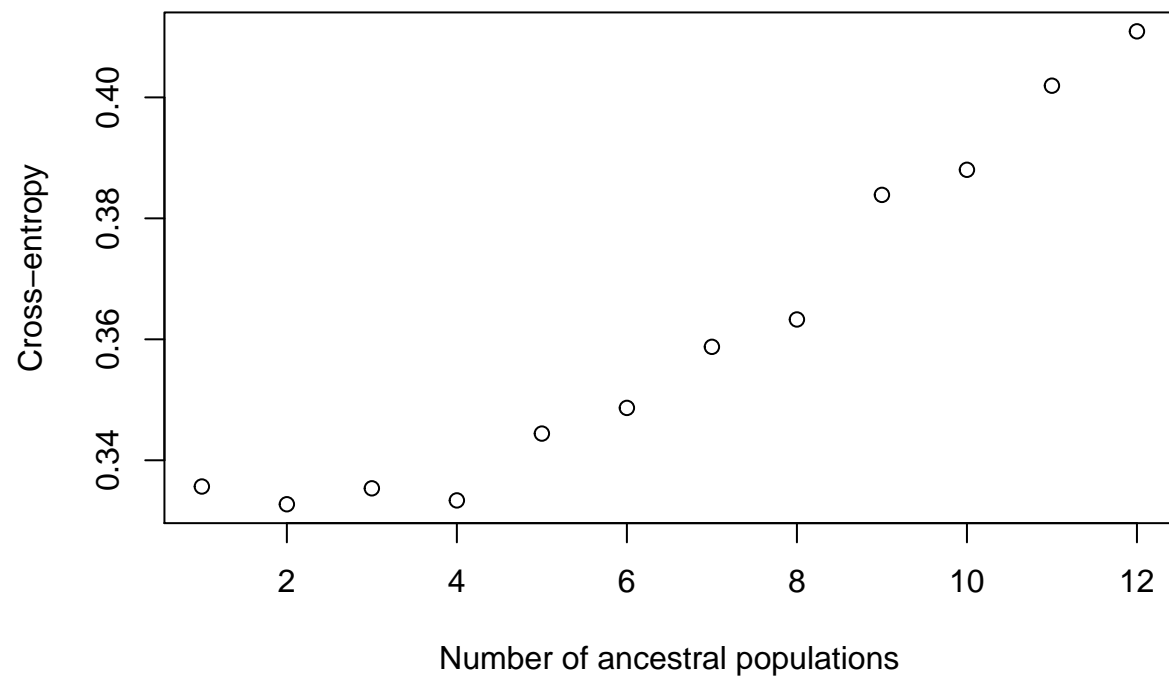
```
# Plot the cross entropy
```

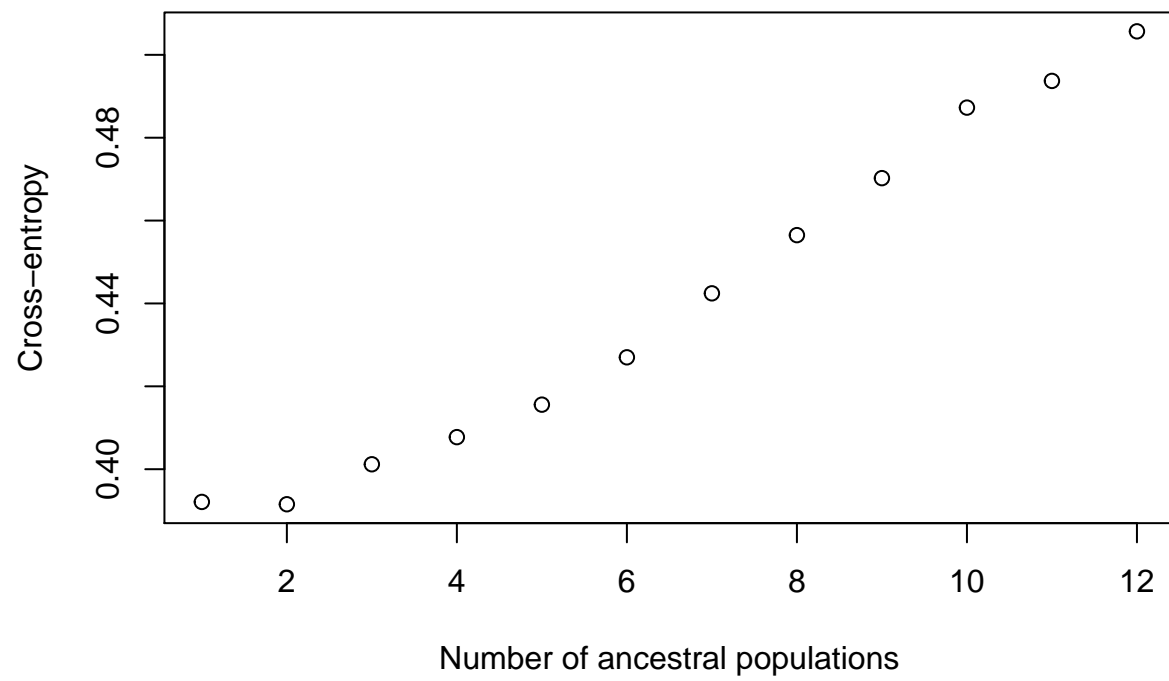
```

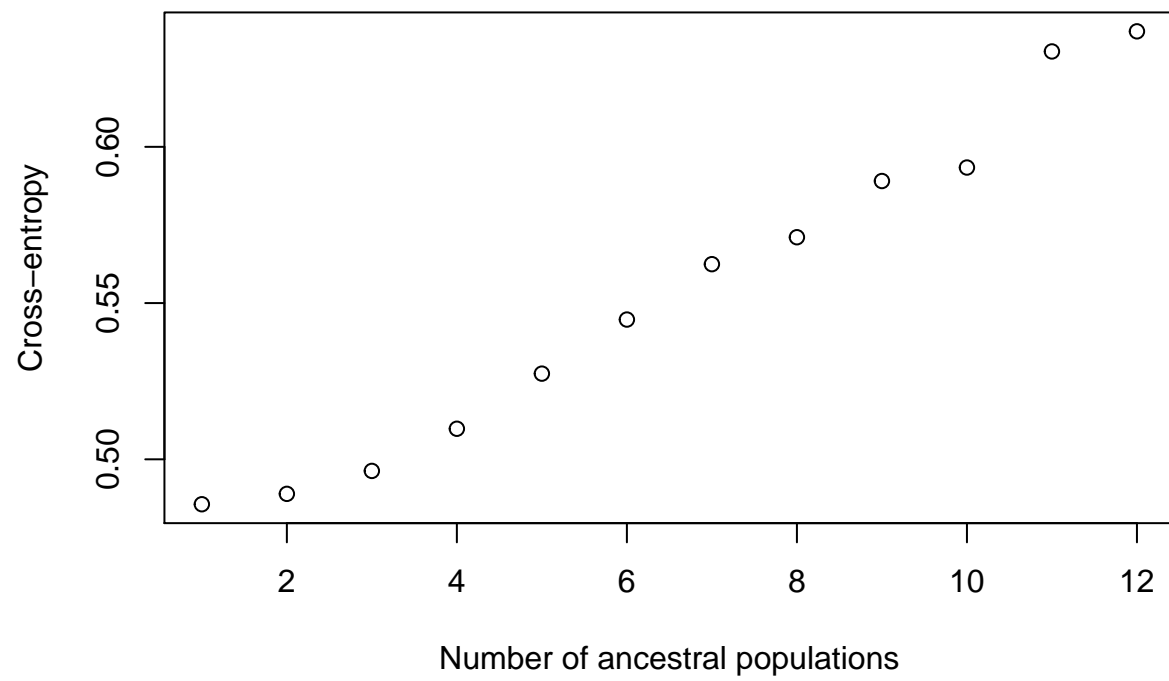
for(i in 1:length(inputs)){
  snmf <- load.snmfProject(paste(inputs[i],".snmfProject",sep=""))
  plot(snmf)
  summary(snmf)
}

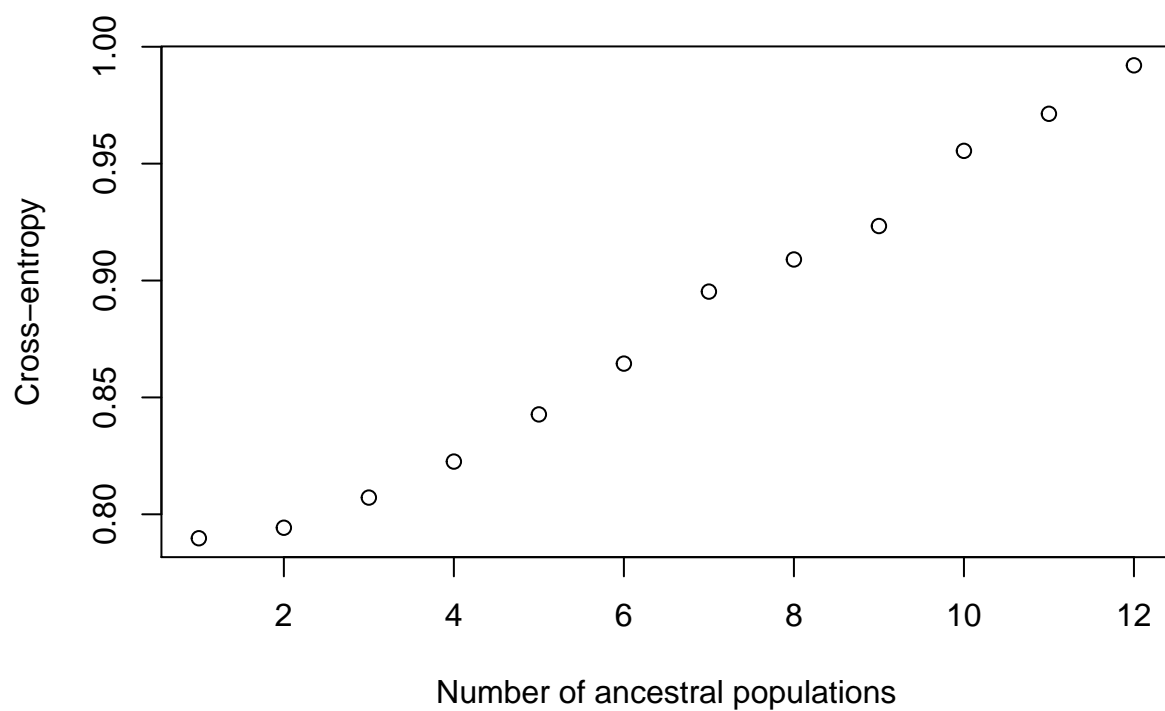
```











```
# Plot barplots
for(i in 1:length(inputs)){
  snmf <- load.snmfProject(paste(inputs[i], ".snmfProject", sep=""))
  for(j in 2:5){
    ce <- cross.entropy(snmf, K = j)
    best <- which.min(ce)

    qmatrix = Q(snmf, K = j, run = best)

    barplot(t(qmatrix), border = NA, space = 0, xlab = "", ylab = "Admixture coefficients",
            names.arg=samples, las=2)
    mtext("Individuals", side=1, line=4)
  }
}
```

