

sNMF

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Additional Manual

<http://membres-timc.imag.fr/Olivier.Francois/snmf/files/note.pdf> (<http://membres-timc.imag.fr/Olivier.Francois/snmf/files/note.pdf>)

Installation of LEA

```
install.packages(c("fields", "RColorBrewer", "mapplots"))
```

```
if (!require("BiocManager", quietly = TRUE)) install.packages("BiocManager")
```

```
BiocManager::install("LEA")
```

```
library(knitr)
```

```
## Warning: package 'knitr' was built under R version 4.3.2
```

```
opts_chunk$set(  
  concordance=TRUE,  
  cache=TRUE  
)
```

```
library(LEA)  
library(here)
```

```
## here() starts at C:/Users/lipo0001/Documents/slubi/3bs/pop_struc
```

```
library(tidyverse)
```

```
## Warning: package 'tidyr' was built under R version 4.3.2
```

```
## Warning: package 'readr' was built under R version 4.3.2
```

```
## Warning: package 'dplyr' was built under R version 4.3.2
```

```
## Warning: package 'stringr' was built under R version 4.3.2
```

```
## — Attaching core tidyverse packages — tidyverse 2.0.0 —
## ✓ dplyr      1.1.4    ✓ readr      2.1.5
## ✓ forcats    1.0.0    ✓ stringr   1.5.1
## ✓ ggplot2    3.4.4    ✓ tibble    3.2.1
## ✓ lubridate  1.9.3    ✓ tidyr     1.3.1
## ✓ purrr      1.0.2
```

```
## — Conflicts — tidyverse_conflicts() —
## ✗ dplyr::filter() masks stats::filter()
## ✗ dplyr::lag()     masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to be
come errors
```

```
here::i_am("lea.Rmd")
```

```
## here() starts at C:/Users/lipo0001/Documents/slubi/3bs/pop_struct
```

```
# Creation of a genotype matrix data file: "genotypes.lfmm"
# The data include 400 SNPs for 50 individuals.
data("tutorial")
# Write genotypes in the lfmm format
write.lfmm(tutorial.R, "genotypes.lfmm")
```

```
## [1] "genotypes.lfmm"
```

```
# Write genotypes in the geno format
write.geno(tutorial.R, "genotypes.geno")
```

```
## [1] "genotypes.geno"
```

```
# creation of an environment gradient file: gradient.env.
# The .env file contains a single ecological variable
# for each individual.
write.env(tutorial.C, "gradients.env")
```

```
## [1] "gradients.env"
```

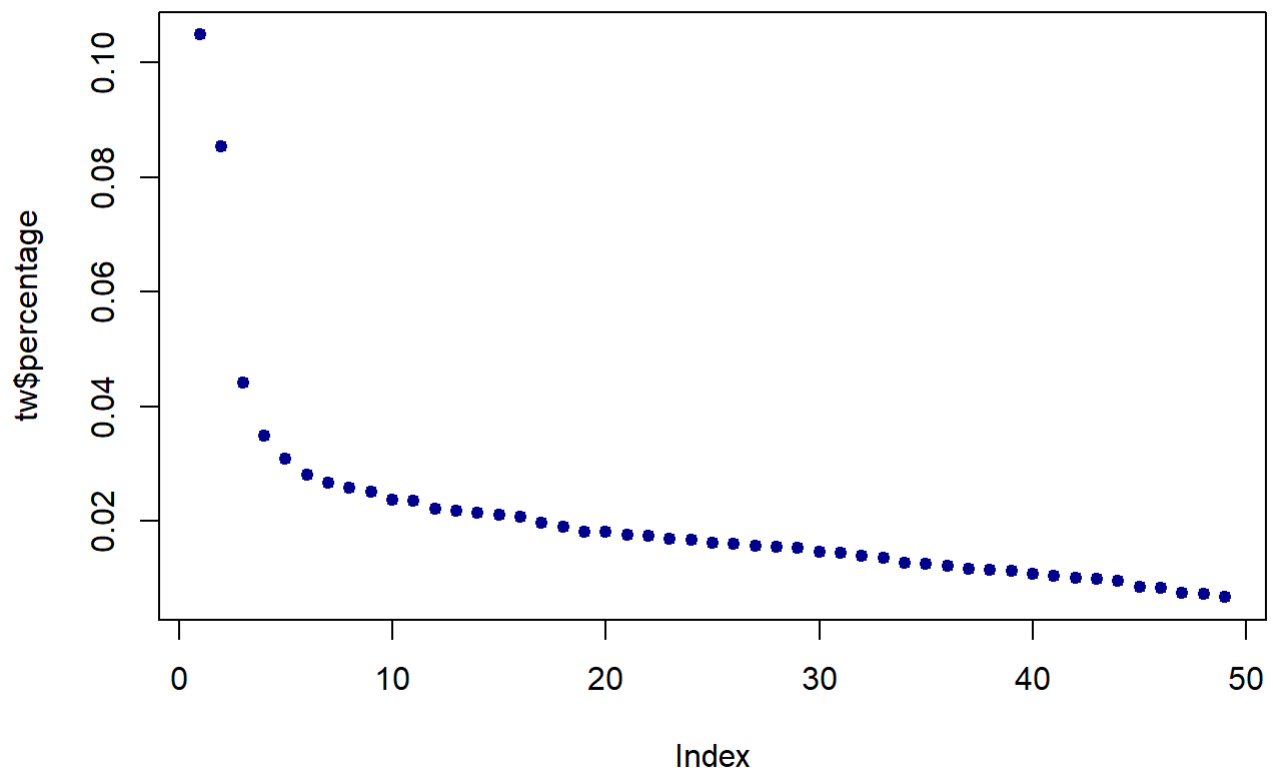
```
# run of pca
# Available options, K (the number of PCs),
#               center and scale.
# Create files: genotypes.eigenvalues - eigenvalues,
#               genotypes.eigenvectors - eigenvectors,
#               genotypes.sdev - standard deviations,
#               genotypes.projections - projections,
# Create a pcaProject object: pc.
pc <- pca("genotypes.lfmm", scale = TRUE)
```

```
## [1] "*****"
## [1] " Principal Component Analysis "
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of principal components) 50
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_stru
c\genotypes.lfmm
##      -a (eigenvalue file)            C:\Users\llpo0001\Documents\slubi\3bs\pop_stru
c\genotypes.pca/genotypes.eigenvalues
##      -e (eigenvector file)          C:\Users\llpo0001\Documents\slubi\3bs\pop_stru
c\genotypes.pca/genotypes.eigenvectors
##      -d (standard deviation file)    C:\Users\llpo0001\Documents\slubi\3bs\pop_stru
c\genotypes.pca/genotypes.sdev
##      -p (projection file)            C:\Users\llpo0001\Documents\slubi\3bs\pop_stru
c\genotypes.pca/genotypes.projections
##      -s data centered and scaled
```

```
tw <- tracy.widom(pc)
```

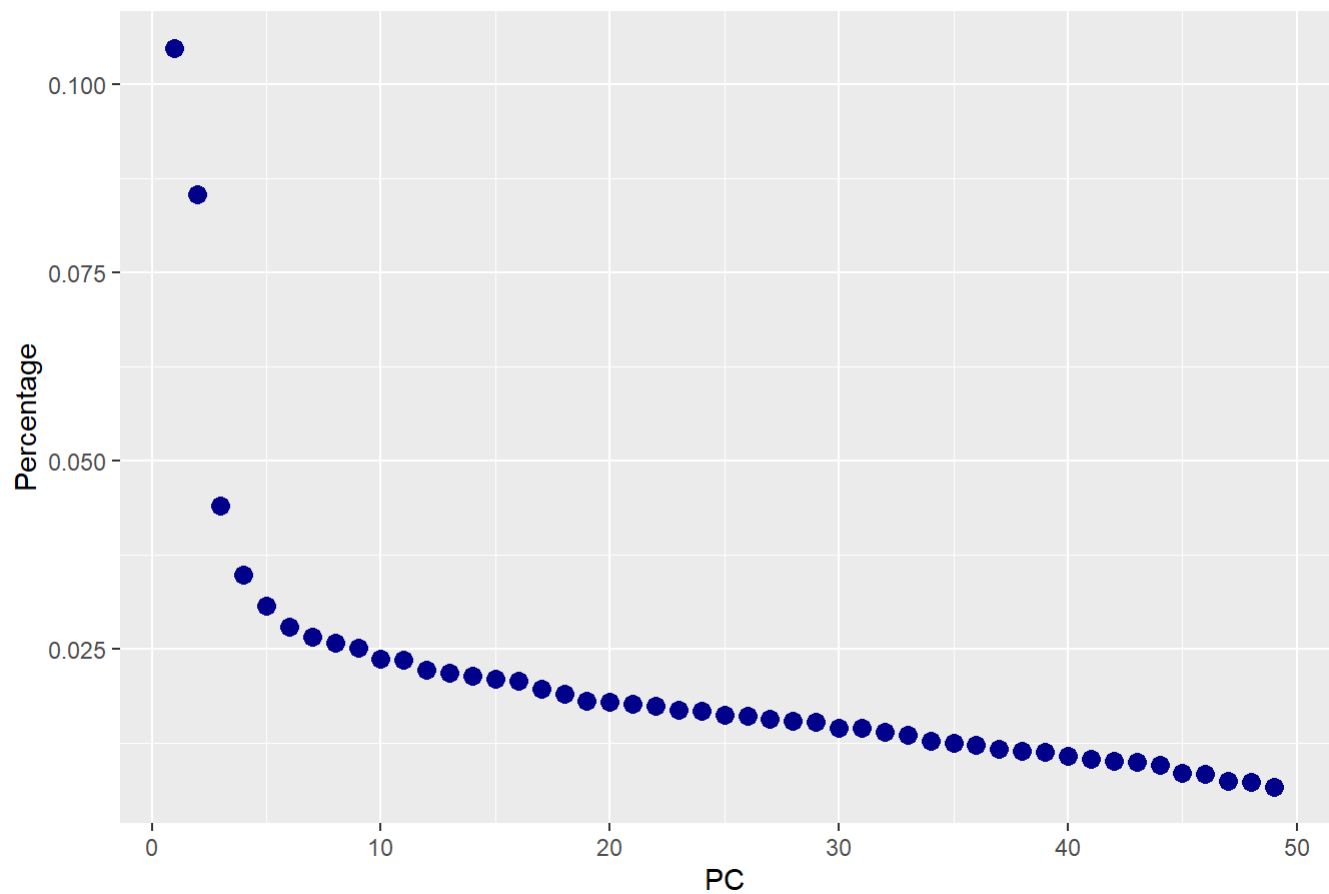
```
## [1] "*****"
## [1] " Tracy-Widom tests "
## [1] "*****"
## summary of the options:
##
##      -n (number of eigenvalues)      50
##      -i (input file)                  C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.pca/genotypes.eigenvalues
##      -o (output file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.pca/genotypes.tracywidom
```

```
# plot the percentage of variance explained by each component
plot(tw$percentage, pch = 19, col = "darkblue", cex = .8)
```



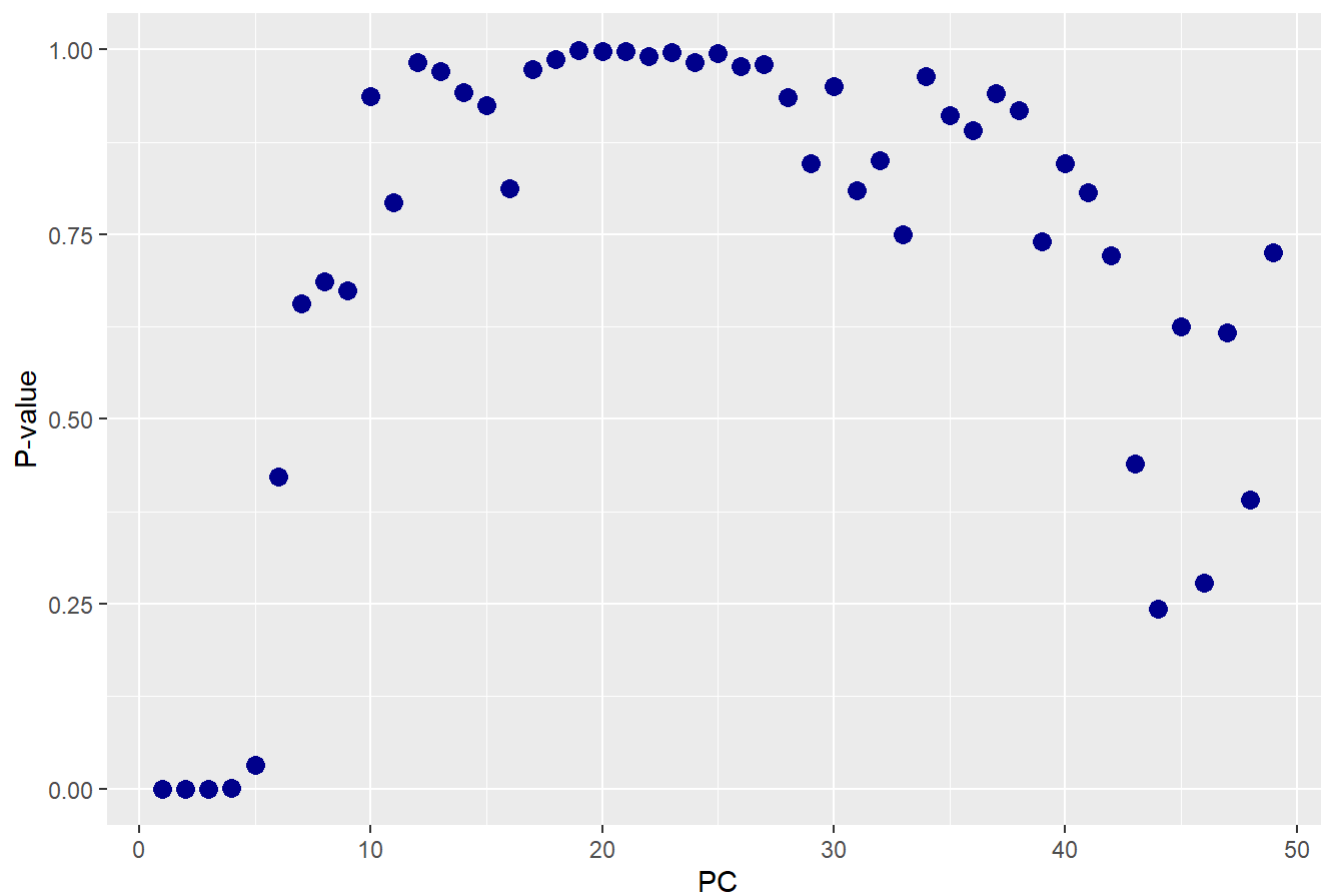
```
#And in ggplot
ggplot(tw, aes(x=N, y=percentage)) +
  geom_point(colour = "darkblue", size = 3) +
  labs(title = "Tracy-Widom Test variance in each component",
        x = "PC",
        y = "Percentage")
```

Tracy-Widom Test variance in each component



```
#Here we can also plot p-values
ggplot(tw, aes(x=N, y=pvalues)) +
  geom_point(colour = "darkblue", size = 3) +
  labs(title = "Tracy-Widom Test p-value for each component",
       x = "PC",
       y = "P-value")
```

Tracy-Widom Test p-value for each component



```
# main options
# K = number of ancestral populations
# entropy = TRUE computes the cross-entropy criterion,
# CPU = 4 is the number of CPU used (hidden input)
project = NULL
project = snmf("genotypes.geno",
               K = 1:10,
               entropy = TRUE,
               ploidy = 2,
               repetitions = 10,
               project = "new")
```

```

## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] 81522939
## [1] "*****"
## [1] "*"          create.dataset          "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -s (seed random init)              81522939
##      -r (percentage of masked data)      0.05
##      -x (genotype file in .geno format)  C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genotypes.geno
##      -o (output file in .geno format)    C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genotypes.snmf/masked/genotypes_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
otypes.snmf/masked/genotypes_I.geno:      OK.
##
## [1] "*****"
## [1] "*" sNMF K = 1  repetition 1          "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      1
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run1/genotypes_r1.1.Q
##      -g (ancestral frequencies file)    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run1/genotypes_r1.1.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              81522939
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##
## Least-square error: 6695.400084

```

```

## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run1/genotypes_r1.1.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K1/run1/genotypes_r1.1.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   1
##      -x (genotype file)              C:/Users/llpo0001/Documents/slubi/3bs/pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run1/genotypes_r1.1.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run1/genotypes_r1.1.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.579894
## Cross-Entropy (masked data):  0.607784
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 2  repetition 1      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   2
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run1/genotypes_r1.2.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run1/genotypes_r1.2.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           81522939
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g

```



```

enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 51
##
## Least-square error: 6137.698602
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/K2/run1/genotypes_r1.2.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/K2/run1/genotypes_r1.2.G:      OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   2
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/K2/run1/genotypes_r1.2.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/K2/run1/genotypes_r1.2.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.520974
## Cross-Entropy (masked data):  0.572071
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*"   sNMF K = 3  repetition 1   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   3
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/K3/run1/genotypes_r1.3.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/K3/run1/genotypes_r1.3.G

```

```

truc/genotypes.snmf/K3/run1/genotypes_r1.3.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              81522939
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##      [ ]
##      [=====]
## Number of iterations: 84
##
## Least-square error: 5714.325539
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run1/genotypes_r1.3.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K3/run1/genotypes_r1.3.G:      OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                 400
##      -K (number of ancestral pops)       3
##      -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run1/genotypes_r1.3.Q
##      -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run1/genotypes_r1.3.G
##      -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.479434
## Cross-Entropy (masked data):  0.549351
## The project is saved into :
##      genotypes.snmfProject
##
## To load the project, use:
##      project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##      remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 4  repetition 1      *"
## [1] "*****"
## summary of the options:

```

```

##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      4
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run1/genotypes_r1.4.Q
##      -g (ancestral frequencies file)    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run1/genotypes_r1.4.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              81522939
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 79
##
## Least-square error: 5458.997744
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run1/genotypes_r1.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K4/run1/genotypes_r1.4.G:      OK.
##
## [1] "*****"
## [1] "*"      cross-entropy estimation      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      4
##      -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run1/genotypes_r1.4.Q
##      -g (ancestral frequencies)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run1/genotypes_r1.4.G
##      -i (with masked genotypes)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.454383
## Cross-Entropy (masked data):  0.552288
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:

```

```

## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 5  repetition 1      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   5
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run1/genotypes_r1.5.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run1/genotypes_r1.5.G
##      -i (number max of iterations)    200
##      -a (regularization parameter)    10
##      -s (seed random init)            81522939
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                     ]
## [=====]
## Number of iterations: 136
##
## Least-square error: 5305.996072
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run1/genotypes_r1.5.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K5/run1/genotypes_r1.5.G:   OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   5
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run1/genotypes_r1.5.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run1/genotypes_r1.5.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru

```

```

c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.43563
## Cross-Entropy (masked data):  0.535118
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 6  repetition 1      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)      50
##          -L (number of loci)             400
##          -K (number of ancestral pops)   6
##          -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run1/genotypes_r1.6.Q
##          -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run1/genotypes_r1.6.G
##          -i (number max of iterations)   200
##          -a (regularization parameter)   10
##          -s (seed random init)           81522939
##          -e (tolerance error)            1E-05
##          -p (number of processes)        1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                                 ]
## [=====]
## Number of iterations: 70
##
## Least-square error: 5110.933071
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run1/genotypes_r1.6.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K6/run1/genotypes_r1.6.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)      50

```

```

##          -L (number of loci)                400
##          -K (number of ancestral pops)       6
##          -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run1/genotypes_r1.6.Q
##          -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run1/genotypes_r1.6.G
##          -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.42031
## Cross-Entropy (masked data):  0.562352
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 7  repetition 1      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                400
##          -K (number of ancestral pops)       7
##          -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)       C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run1/genotypes_r1.7.Q
##          -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run1/genotypes_r1.7.G
##          -i (number max of iterations)       200
##          -a (regularization parameter)       10
##          -s (seed random init)              81522939
##          -e (tolerance error)               1E-05
##          -p (number of processes)           1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [                                                                 ]
##   [=====]
## Number of iterations: 171
##
## Least-square error: 4984.605291
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run1/genotypes_r1.7.Q:      OK.

```

```

## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop
p_struc/genotypes.snmf/K7/run1/genotypes_r1.7.G: OK.
##
## [1] "*****"
## [1] "*" cross-entropy estimation "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   7
##      -x (genotype file)              C:/Users/llpo0001/Documents/slubi/3bs/pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run1/genotypes_r1.7.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run1/genotypes_r1.7.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.408821
## Cross-Entropy (masked data):  0.578173
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*" sNMF K = 8  repetition 1      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   8
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run1/genotypes_r1.8.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run1/genotypes_r1.8.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           81522939
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno: OK.
##

```

```

##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 44
##
## Least-square error: 4830.871411
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run1/genotypes_r1.8.Q: OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K8/run1/genotypes_r1.8.G: OK.
##
## [1] "*****"
## [1] "* cross-entropy estimation *"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 8
## -x (genotype file) C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
## -q (individual admixture) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run1/genotypes_r1.8.Q
## -g (ancestral frequencies) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run1/genotypes_r1.8.G
## -i (with masked genotypes) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
## - diploid
##
## Cross-Entropy (all data): 0.39545
## Cross-Entropy (masked data): 0.584585
## The project is saved into :
## genotypes.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 9 repetition 1 *"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 9
## -x (input file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
## -q (individual admixture file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run1/genotypes_r1.9.Q
## -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run1/genotypes_r1.9.G
## -i (number max of iterations) 200

```



```

##      -a (regularization parameter)      10
##      -s (seed random init)             81522939
##      -e (tolerance error)              1E-05
##      -p (number of processes)          1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 64
##
## Least-square error: 4639.321703
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run1/genotypes_r1.9.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K9/run1/genotypes_r1.9.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)         50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      9
##      -x (genotype file)                 C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run1/genotypes_r1.9.Q
##      -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run1/genotypes_r1.9.G
##      -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.378688
## Cross-Entropy (masked data):  0.61346
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 10  repetition 1      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)         50

```

```

##          -L (number of loci)                400
##          -K (number of ancestral pops)       10
##          -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run1/genotypes_r1.10.Q
##          -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run1/genotypes_r1.10.G
##          -i (number max of iterations)      200
##          -a (regularization parameter)       10
##          -s (seed random init)              81522939
##          -e (tolerance error)               1E-05
##          -p (number of processes)           1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                    ]
## [=====]
## Number of iterations: 102
##
## Least-square error: 4511.932736
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run1/genotypes_r1.10.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K10/run1/genotypes_r1.10.G: OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                400
##          -K (number of ancestral pops)       10
##          -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run1/genotypes_r1.10.Q
##          -g (ancestral frequencies)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run1/genotypes_r1.10.G
##          -i (with masked genotypes)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.369177
## Cross-Entropy (masked data):  0.625394
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##

```

```

## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] 1067302846
## [1] "*****"
## [1] "*"          create.dataset          "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -s (seed random init)              1067302846
##      -r (percentage of masked data)      0.05
##      -x (genotype file in .geno format)  C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genotypes.geno
##      -o (output file in .geno format)    C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genotypes.snmf/masked/genotypes_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
otypes.snmf/masked/genotypes_I.geno:      OK.
##
## [1] "*****"
## [1] "*" sNMF K = 1  repetition 2          "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      1
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run2/genotypes_r2.1.Q
##      -g (ancestral frequencies file)    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run2/genotypes_r2.1.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              1067302846
##      -e (tolerance error)                1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##
## Least-square error: 6677.640085
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run2/genotypes_r2.1.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K1/run2/genotypes_r2.1.G:  OK.
##
## [1] "*****"
## [1] "*"          cross-entropy estimation          "*"

```

```

## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   1
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run2/genotypes_r2.1.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run2/genotypes_r2.1.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.577602
## Cross-Entropy (masked data):  0.647511
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 2  repetition 2      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   2
##      -x (input file)                  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run2/genotypes_r2.2.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run2/genotypes_r2.2.G
##      -i (number max of iterations)    200
##      -a (regularization parameter)    10
##      -s (seed random init)            1067302846
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [
##   [=====]
##   Number of iterations: 38

```

```

##
## Least-square error: 6116.267446
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run2/genotypes_r2.2.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K2/run2/genotypes_r2.2.G:   OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   2
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run2/genotypes_r2.2.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run2/genotypes_r2.2.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.518456
## Cross-Entropy (masked data):  0.647693
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 3  repetition 2      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   3
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run2/genotypes_r2.3.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run2/genotypes_r2.3.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           1067302846
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid

```

```

##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                                 ]
## [=====]
## Number of iterations: 54
##
## Least-square error: 5710.594810
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run2/genotypes_r2.3.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K3/run2/genotypes_r2.3.G:   OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   3
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run2/genotypes_r2.3.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run2/genotypes_r2.3.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.478439
## Cross-Entropy (masked data):  0.602557
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 4  repetition 2      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s

```

```

truc/genotypes.snmf/K4/run2/genotypes_r2.4.Q
##      -g (ancestral frequencies file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run2/genotypes_r2.4.G
##      -i (number max of iterations)        200
##      -a (regularization parameter)        10
##      -s (seed random init)                1067302846
##      -e (tolerance error)                 1E-05
##      -p (number of processes)             1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 87
##
## Least-square error: 5412.142042
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run2/genotypes_r2.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K4/run2/genotypes_r2.4.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)            50
##      -L (number of loci)                  400
##      -K (number of ancestral pops)        4
##      -x (genotype file)                   C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)             C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run2/genotypes_r2.4.Q
##      -g (ancestral frequencies)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run2/genotypes_r2.4.G
##      -i (with masked genotypes)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.451558
## Cross-Entropy (masked data):  0.608677
## The project is saved into :
## genotypes.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 5  repetition 2      *"

```

```

## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   5
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run2/genotypes_r2.5.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run2/genotypes_r2.5.G
##      -i (number max of iterations)    200
##      -a (regularization parameter)    10
##      -s (seed random init)            1067302846
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 65
##
## Least-square error: 5221.771317
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run2/genotypes_r2.5.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K5/run2/genotypes_r2.5.G:   OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   5
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run2/genotypes_r2.5.Q
##      -g (ancestral frequencies)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run2/genotypes_r2.5.G
##      -i (with masked genotypes)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.432261
## Cross-Entropy (masked data):  0.643295
## The project is saved into :
## genotypes.snmfProject

```



```

##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 6 repetition 2      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   6
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run2/genotypes_r2.6.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run2/genotypes_r2.6.G
##      -i (number max of iterations)  200
##      -a (regularization parameter)  10
##      -s (seed random init)          1067302846
##      -e (tolerance error)           1E-05
##      -p (number of processes)       1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                     ]
## [=====]
## Number of iterations: 64
##
## Least-square error: 5092.418263
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run2/genotypes_r2.6.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K6/run2/genotypes_r2.6.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   6
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run2/genotypes_r2.6.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru

```

```

c/genotypes.snmf/K6/run2/genotypes_r2.6.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.421862
## Cross-Entropy (masked data):  0.643027
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 7  repetition 2      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   7
##      -x (input file)                C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run2/genotypes_r2.7.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run2/genotypes_r2.7.G
##      -i (number max of iterations)  200
##      -a (regularization parameter)   10
##      -s (seed random init)           1067302846
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 128
##
## Least-square error: 4902.899549
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run2/genotypes_r2.7.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K7/run2/genotypes_r2.7.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:

```

```

##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      7
##      -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run2/genotypes_r2.7.Q
##      -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run2/genotypes_r2.7.G
##      -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.401761
## Cross-Entropy (masked data):  0.652018
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 8  repetition 2      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      8
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run2/genotypes_r2.8.Q
##      -g (ancestral frequencies file)    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run2/genotypes_r2.8.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              1067302846
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [ ]
##   [=====]
## Number of iterations: 97
##
## Least-square error: 4762.181717

```

```

## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run2/genotypes_r2.8.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K8/run2/genotypes_r2.8.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   8
##      -x (genotype file)              C:/Users/llpo0001/Documents/slubi/3bs/pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run2/genotypes_r2.8.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run2/genotypes_r2.8.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.390403
## Cross-Entropy (masked data):  0.711183
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 9  repetition 2      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   9
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run2/genotypes_r2.9.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run2/genotypes_r2.9.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           1067302846
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g

```

```

enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                                ]
## [=====]
## Number of iterations: 32
##
## Least-square error: 4658.707455
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run2/genotypes_r2.9.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K9/run2/genotypes_r2.9.G:  OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   9
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run2/genotypes_r2.9.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run2/genotypes_r2.9.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.381651
## Cross-Entropy (masked data):  0.722622
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*" sNMF K = 10  repetition 2   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   10
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run2/genotypes_r2.10.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s

```

```

truc/genotypes.snmf/K10/run2/genotypes_r2.10.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              1067302846
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##      [ ]
##      [=====]
## Number of iterations: 122
##
## Least-square error: 4493.610688
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run2/genotypes_r2.10.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K10/run2/genotypes_r2.10.G: OK.
##
## [1] "*****"
## [1] "*"      cross-entropy estimation      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                 400
##      -K (number of ancestral pops)       10
##      -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run2/genotypes_r2.10.Q
##      -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run2/genotypes_r2.10.G
##      -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.367913
## Cross-Entropy (masked data):  0.747001
## The project is saved into :
##      genotypes.snmfProject
##
## To load the project, use:
##      project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##      remove.snmfProject("genotypes.snmfProject")
##
## [1] 1916587767
## [1] "*****"
## [1] "*"      create.dataset      "*"
## [1] "*****"

```

```

## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -s (seed random init)          1916587767
##      -r (percentage of masked data) 0.05
##      -x (genotype file in .geno format) C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genotypes.geno
##      -o (output file in .geno format)  C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genotypes.snmf/masked/genotypes_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
otypes.snmf/masked/genotypes_I.geno:      OK.
##
## [1] "*****"
## [1] "* sNMF K = 1  repetition 3      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   1
##      -x (input file)                  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run3/genotypes_r3.1.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run3/genotypes_r3.1.G
##      -i (number max of iterations)    200
##      -a (regularization parameter)    10
##      -s (seed random init)            1916587767
##      -e (tolerance error)              1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##
## Least-square error: 6666.960083
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run3/genotypes_r3.1.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K1/run3/genotypes_r3.1.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   1
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc

```

```

\genotypes.geno
##      -q (individual admixture)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run3/genotypes_r3.1.Q
##      -g (ancestral frequencies)    C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run3/genotypes_r3.1.G
##      -i (with masked genotypes)    C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.577209
## Cross-Entropy (masked data):  0.651023
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 2  repetition 3      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   2
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run3/genotypes_r3.2.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run3/genotypes_r3.2.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           1916587767
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##  [                                     ]
##  [=====]
## Number of iterations: 47
##
## Least-square error: 6125.282091
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run3/genotypes_r3.2.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K2/run3/genotypes_r3.2.G:  OK.
##

```



```

## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   2
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run3/genotypes_r3.2.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run3/genotypes_r3.2.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.518498
## Cross-Entropy (masked data):  0.619026
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*" sNMF K = 3  repetition 3   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   3
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run3/genotypes_r3.3.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run3/genotypes_r3.3.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           1916587767
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [

```

]

```

## [=====]
## Number of iterations: 69
##
## Least-square error: 5697.266661
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run3/genotypes_r3.3.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K3/run3/genotypes_r3.3.G:   OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   3
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run3/genotypes_r3.3.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run3/genotypes_r3.3.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.478521
## Cross-Entropy (masked data):  0.591795
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*" sNMF K = 4  repetition 3      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run3/genotypes_r3.4.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run3/genotypes_r3.4.G
##      -i (number max of iterations)  200
##      -a (regularization parameter)  10
##      -s (seed random init)          1916587767
##      -e (tolerance error)            1E-05

```

```

##          -p (number of processes)          1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                                                      ]
## [=====]
## Number of iterations: 109
##
## Least-square error: 5449.702610
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run3/genotypes_r3.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K4/run3/genotypes_r3.4.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                 400
##          -K (number of ancestral pops)       4
##          -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run3/genotypes_r3.4.Q
##          -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run3/genotypes_r3.4.G
##          -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.451954
## Cross-Entropy (masked data):  0.574716
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 5  repetition 3      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                 400
##          -K (number of ancestral pops)       5
##          -x (input file)                     C:/Users/llpo0001/Documents/slubi/3bs/pop_s

```

```

truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run3/genotypes_r3.5.Q
##      -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run3/genotypes_r3.5.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              1916587767
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 79
##
## Least-square error: 5265.731791
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run3/genotypes_r3.5.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K5/run3/genotypes_r3.5.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                 400
##      -K (number of ancestral pops)       5
##      -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run3/genotypes_r3.5.Q
##      -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run3/genotypes_r3.5.G
##      -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.433363
## Cross-Entropy (masked data):  0.588901
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##

```

```

## [1] "*****"
## [1] "* sNMF K = 6  repetition 3      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   6
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run3/genotypes_r3.6.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run3/genotypes_r3.6.G
##      -i (number max of iterations)  200
##      -a (regularization parameter)  10
##      -s (seed random init)          1916587767
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                     ]
## [=====]
## Number of iterations: 126
##
## Least-square error: 5095.972878
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run3/genotypes_r3.6.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K6/run3/genotypes_r3.6.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   6
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run3/genotypes_r3.6.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run3/genotypes_r3.6.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.418647
## Cross-Entropy (masked data):  0.612017

```

```

## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 7  repetition 3      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   7
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run3/genotypes_r3.7.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run3/genotypes_r3.7.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)    10
##      -s (seed random init)           1916587767
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [                                                                ]
##   [=====]
## Number of iterations: 163
##
## Least-square error: 4951.111234
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run3/genotypes_r3.7.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K7/run3/genotypes_r3.7.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   7
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru

```

```

c/genotypes.snmf/K7/run3/genotypes_r3.7.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run3/genotypes_r3.7.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.405335
## Cross-Entropy (masked data):  0.663812
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 8  repetition 3      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   8
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run3/genotypes_r3.8.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run3/genotypes_r3.8.G
##      -i (number max of iterations)  200
##      -a (regularization parameter)   10
##      -s (seed random init)           1916587767
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [ ]
##   [=====]
## Number of iterations: 43
##
## Least-square error: 4753.576276
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run3/genotypes_r3.8.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K8/run3/genotypes_r3.8.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"

```

```

## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   8
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run3/genotypes_r3.8.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run3/genotypes_r3.8.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):    0.3887
## Cross-Entropy (masked data): 0.687119
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 9  repetition 3      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   9
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run3/genotypes_r3.9.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run3/genotypes_r3.9.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           1916587767
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:    OK.
##
##
## Main algorithm:
##   [
##   [=====]
##   Number of iterations: 70

```



```

##
## Least-square error: 4636.311459
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run3/genotypes_r3.9.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K9/run3/genotypes_r3.9.G:   OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   9
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run3/genotypes_r3.9.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run3/genotypes_r3.9.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.379255
## Cross-Entropy (masked data):  0.689188
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 10  repetition 3      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   10
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run3/genotypes_r3.10.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run3/genotypes_r3.10.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           1916587767
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid

```

```

##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                                 ]
## [=====]
## Number of iterations: 28
##
## Least-square error: 4493.102299
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run3/genotypes_r3.10.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K10/run3/genotypes_r3.10.G: OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   10
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run3/genotypes_r3.10.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run3/genotypes_r3.10.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.368104
## Cross-Entropy (masked data):  0.737845
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] 616161579
## [1] "*****"
## [1] "*      create.dataset      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -s (seed random init)           616161579
##      -r (percentage of masked data)   0.05
##      -x (genotype file in .geno format) C:\Users\llpo0001\Documents\slubi\3bs\p

```

```

op_struc\genotypes.geno
##      -o (output file in .geno format)          C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genotypes.snmf/masked/genotypes_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
otypes.snmf/masked/genotypes_I.geno:      OK.
##
## [1] "*****"
## [1] "* sNMF K = 1  repetition 4      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      1
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run4/genotypes_r4.1.Q
##      -g (ancestral frequencies file)    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run4/genotypes_r4.1.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              616161579
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##
## Least-square error: 6673.920081
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run4/genotypes_r4.1.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K1/run4/genotypes_r4.1.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      1
##      -x (genotype file)                 C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run4/genotypes_r4.1.Q
##      -g (ancestral frequencies)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run4/genotypes_r4.1.G
##      -i (with masked genotypes)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno

```

```

##          - diploid
##
## Cross-Entropy (all data):      0.577061
## Cross-Entropy (masked data):  0.645173
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 2  repetition 4      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)      50
##          -L (number of loci)             400
##          -K (number of ancestral pops)   2
##          -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run4/genotypes_r4.2.Q
##          -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run4/genotypes_r4.2.G
##          -i (number max of iterations)   200
##          -a (regularization parameter)   10
##          -s (seed random init)           616161579
##          -e (tolerance error)            1E-05
##          -p (number of processes)        1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                     ]
## [=====]
## Number of iterations: 51
##
## Least-square error: 6134.903126
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run4/genotypes_r4.2.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K2/run4/genotypes_r4.2.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)      50
##          -L (number of loci)             400

```

```

##          -K (number of ancestral pops)      2
##          -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run4/genotypes_r4.2.Q
##          -g (ancestral frequencies)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run4/genotypes_r4.2.G
##          -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.519625
## Cross-Entropy (masked data):  0.605794
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 3  repetition 4      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                 400
##          -K (number of ancestral pops)       3
##          -x (input file)                     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)       C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run4/genotypes_r4.3.Q
##          -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run4/genotypes_r4.3.G
##          -i (number max of iterations)       200
##          -a (regularization parameter)       10
##          -s (seed random init)              616161579
##          -e (tolerance error)               1E-05
##          -p (number of processes)           1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [ ]
##   [=====]
## Number of iterations: 71
##
## Least-square error: 5705.225237
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run4/genotypes_r4.3.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po

```

```

p_struc/genotypes.snmf/K3/run4/genotypes_r4.3.G: OK.
##
## [1] "*****"
## [1] "*   cross-entropy estimation   *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   3
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run4/genotypes_r4.3.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run4/genotypes_r4.3.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.476959
## Cross-Entropy (masked data):  0.608314
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 4  repetition 4      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run4/genotypes_r4.4.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run4/genotypes_r4.4.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)    10
##      -s (seed random init)           616161579
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##

```

```

## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 33
##
## Least-square error: 5462.653045
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run4/genotypes_r4.4.Q: OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K4/run4/genotypes_r4.4.G: OK.
##
## [1] "*****"
## [1] "* cross-entropy estimation *"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 4
## -x (genotype file) C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
## -q (individual admixture) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run4/genotypes_r4.4.Q
## -g (ancestral frequencies) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run4/genotypes_r4.4.G
## -i (with masked genotypes) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
## - diploid
##
## Cross-Entropy (all data): 0.450828
## Cross-Entropy (masked data): 0.608801
## The project is saved into :
## genotypes.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 5 repetition 4 *"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 5
## -x (input file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
## -q (individual admixture file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run4/genotypes_r4.5.Q
## -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run4/genotypes_r4.5.G
## -i (number max of iterations) 200
## -a (regularization parameter) 10

```

```

##          -s (seed random init)                616161579
##          -e (tolerance error)                  1E-05
##          -p (number of processes)              1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                                 ]
## [=====]
## Number of iterations: 61
##
## Least-square error: 5232.072809
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run4/genotypes_r4.5.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K5/run4/genotypes_r4.5.G:  OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)            50
##          -L (number of loci)                   400
##          -K (number of ancestral pops)         5
##          -x (genotype file)                    C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)             C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run4/genotypes_r4.5.Q
##          -g (ancestral frequencies)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run4/genotypes_r4.5.G
##          -i (with masked genotypes)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.43012
## Cross-Entropy (masked data):  0.627947
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*" sNMF K = 6  repetition 4   "*"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)            50
##          -L (number of loci)                   400

```



```

##          -K (number of ancestral pops)          6
##          -x (input file)                        C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)          C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run4/genotypes_r4.6.Q
##          -g (ancestral frequencies file)         C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run4/genotypes_r4.6.G
##          -i (number max of iterations)          200
##          -a (regularization parameter)           10
##          -s (seed random init)                  616161579
##          -e (tolerance error)                   1E-05
##          -p (number of processes)               1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                    ]
## [=====]
## Number of iterations: 134
##
## Least-square error: 5079.151054
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run4/genotypes_r4.6.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K6/run4/genotypes_r4.6.G:  OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)              50
##          -L (number of loci)                    400
##          -K (number of ancestral pops)          6
##          -x (genotype file)                     C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)              C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run4/genotypes_r4.6.Q
##          -g (ancestral frequencies)            C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run4/genotypes_r4.6.G
##          -i (with masked genotypes)            C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.416272
## Cross-Entropy (masked data):  0.644425
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:

```

```

## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 7  repetition 4      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   7
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run4/genotypes_r4.7.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run4/genotypes_r4.7.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)    10
##      -s (seed random init)           616161579
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                                ]
## [=====]
## Number of iterations: 167
##
## Least-square error: 4910.880560
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run4/genotypes_r4.7.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K7/run4/genotypes_r4.7.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   7
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run4/genotypes_r4.7.Q
##      -g (ancestral frequencies)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run4/genotypes_r4.7.G
##      -i (with masked genotypes)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##

```

```

## Cross-Entropy (all data):      0.400153
## Cross-Entropy (masked data):  0.676186
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 8  repetition 4      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   8
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run4/genotypes_r4.8.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run4/genotypes_r4.8.G
##      -i (number max of iterations)  200
##      -a (regularization parameter)  10
##      -s (seed random init)          616161579
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 200
##
## Least-square error: 4796.034552
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run4/genotypes_r4.8.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K8/run4/genotypes_r4.8.G:  OK.
##
## [1] "*****"
## [1] "*   cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   8
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc

```

```

\genotypes.geno
##      -q (individual admixture)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run4/genotypes_r4.8.Q
##      -g (ancestral frequencies)    C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run4/genotypes_r4.8.G
##      -i (with masked genotypes)    C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.39047
## Cross-Entropy (masked data):  0.695881
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 9  repetition 4      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   9
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run4/genotypes_r4.9.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run4/genotypes_r4.9.G
##      -i (number max of iterations)  200
##      -a (regularization parameter)   10
##      -s (seed random init)           616161579
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [                                     ]
##   [=====]
## Number of iterations: 78
##
## Least-square error: 4617.028576
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run4/genotypes_r4.9.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K9/run4/genotypes_r4.9.G:  OK.
##

```

```

## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   9
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run4/genotypes_r4.9.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run4/genotypes_r4.9.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.37598
## Cross-Entropy (masked data):  0.72144
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*" sNMF K = 10  repetition 4   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   10
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run4/genotypes_r4.10.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run4/genotypes_r4.10.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           616161579
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [

```

```

## [=====]
## Number of iterations: 39
##
## Least-square error: 4479.912632
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run4/genotypes_r4.10.Q: OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K10/run4/genotypes_r4.10.G: OK.
##
## [1] "*****"
## [1] "*" cross-entropy estimation "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   10
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run4/genotypes_r4.10.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run4/genotypes_r4.10.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data): 0.367098
## Cross-Entropy (masked data): 0.801997
## The project is saved into :
## genotypes.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] 25949788
## [1] "*****"
## [1] "*" create.dataset "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -s (seed random init)          25949788
##      -r (percentage of masked data)  0.05
##      -x (genotype file in .geno format) C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genotypes.geno
##      -o (output file in .geno format) C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genotypes.snmf/masked/genotypes_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
otypes.snmf/masked/genotypes_I.geno: OK.
##

```

```

## [1] "*****"
## [1] "* sNMF K = 1  repetition 5      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   1
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run5/genotypes_r5.1.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run5/genotypes_r5.1.G
##      -i (number max of iterations)  200
##      -a (regularization parameter)  10
##      -s (seed random init)          25949788
##      -e (tolerance error)            1E-05
##      -p (number of processes)       1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##
## Least-square error: 6726.080083
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run5/genotypes_r5.1.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K1/run5/genotypes_r5.1.G:   OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   1
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run5/genotypes_r5.1.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run5/genotypes_r5.1.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.57987
## Cross-Entropy (masked data):  0.590883
## The project is saved into :
##  genotypes.snmfProject
##

```

```

## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 2  repetition 5      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   2
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run5/genotypes_r5.2.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run5/genotypes_r5.2.G
##      -i (number max of iterations)  200
##      -a (regularization parameter)   10
##      -s (seed random init)           25949788
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                     ]
## [=====]
## Number of iterations: 44
##
## Least-square error: 6162.027685
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run5/genotypes_r5.2.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K2/run5/genotypes_r5.2.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   2
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run5/genotypes_r5.2.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run5/genotypes_r5.2.G

```



```

##          -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.521537
## Cross-Entropy (masked data):  0.550827
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 3  repetition 5      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)      50
##          -L (number of loci)            400
##          -K (number of ancestral pops)   3
##          -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run5/genotypes_r5.3.Q
##          -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run5/genotypes_r5.3.G
##          -i (number max of iterations)   200
##          -a (regularization parameter)   10
##          -s (seed random init)           25949788
##          -e (tolerance error)            1E-05
##          -p (number of processes)        1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [ ]
##   [=====]
## Number of iterations: 67
##
## Least-square error: 5723.371610
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run5/genotypes_r5.3.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K3/run5/genotypes_r5.3.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##

```

```

##          -n (number of individuals)          50
##          -L (number of loci)                400
##          -K (number of ancestral pops)       3
##          -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)            C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run5/genotypes_r5.3.Q
##          -g (ancestral frequencies)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run5/genotypes_r5.3.G
##          -i (with masked genotypes)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.480184
## Cross-Entropy (masked data):  0.53079
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 4  repetition 5      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                400
##          -K (number of ancestral pops)       4
##          -x (input file)                     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)       C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run5/genotypes_r5.4.Q
##          -g (ancestral frequencies file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run5/genotypes_r5.4.G
##          -i (number max of iterations)        200
##          -a (regularization parameter)        10
##          -s (seed random init)                25949788
##          -e (tolerance error)                 1E-05
##          -p (number of processes)             1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [ ]
##   [=====]
## Number of iterations: 128
##
## Least-square error: 5486.705607
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru

```

```

c/genotypes.snmf/K4/run5/genotypes_r5.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop
p_struc/genotypes.snmf/K4/run5/genotypes_r5.4.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run5/genotypes_r5.4.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run5/genotypes_r5.4.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.454087
## Cross-Entropy (masked data):  0.555278
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 5  repetition 5      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   5
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run5/genotypes_r5.5.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run5/genotypes_r5.5.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           25949788
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.

```

```

##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 52
##
## Least-square error: 5285.882019
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run5/genotypes_r5.5.Q: OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K5/run5/genotypes_r5.5.G: OK.
##
## [1] "*****"
## [1] "* cross-entropy estimation *"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 5
## -x (genotype file) C:/Users/llpo0001/Documents/slubi/3bs/pop_struc
\genotypes.geno
## -q (individual admixture) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run5/genotypes_r5.5.Q
## -g (ancestral frequencies) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run5/genotypes_r5.5.G
## -i (with masked genotypes) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
## - diploid
##
## Cross-Entropy (all data): 0.43642
## Cross-Entropy (masked data): 0.559291
## The project is saved into :
## genotypes.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 6 repetition 5 *"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 6
## -x (input file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
## -q (individual admixture file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run5/genotypes_r5.6.Q
## -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run5/genotypes_r5.6.G

```

```

##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)             25949788
##      -e (tolerance error)              1E-05
##      -p (number of processes)          1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 43
##
## Least-square error: 5116.251473
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run5/genotypes_r5.6.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K6/run5/genotypes_r5.6.G:      OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      6
##      -x (genotype file)                 C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run5/genotypes_r5.6.Q
##      -g (ancestral frequencies)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run5/genotypes_r5.6.G
##      -i (with masked genotypes)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.421875
## Cross-Entropy (masked data):  0.570622
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 7  repetition 5      *"
## [1] "*****"
## summary of the options:
##

```

```

##          -n (number of individuals)          50
##          -L (number of loci)                 400
##          -K (number of ancestral pops)        7
##          -x (input file)                     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)       C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run5/genotypes_r5.7.Q
##          -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run5/genotypes_r5.7.G
##          -i (number max of iterations)       200
##          -a (regularization parameter)       10
##          -s (seed random init)               25949788
##          -e (tolerance error)                 1E-05
##          -p (number of processes)             1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 87
##
## Least-square error: 4970.566191
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run5/genotypes_r5.7.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K7/run5/genotypes_r5.7.G:  OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                 400
##          -K (number of ancestral pops)        7
##          -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run5/genotypes_r5.7.Q
##          -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run5/genotypes_r5.7.G
##          -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.405447
## Cross-Entropy (masked data):  0.582305
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")

```

```

##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 8  repetition 5      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   8
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run5/genotypes_r5.8.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run5/genotypes_r5.8.G
##      -i (number max of iterations)    200
##      -a (regularization parameter)    10
##      -s (seed random init)            25949788
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 122
##
## Least-square error: 4819.417669
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run5/genotypes_r5.8.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K8/run5/genotypes_r5.8.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   8
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run5/genotypes_r5.8.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run5/genotypes_r5.8.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno

```

```

##          - diploid
##
## Cross-Entropy (all data):      0.393468
## Cross-Entropy (masked data):  0.613487
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 9  repetition 5      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)      50
##          -L (number of loci)             400
##          -K (number of ancestral pops)   9
##          -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run5/genotypes_r5.9.Q
##          -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run5/genotypes_r5.9.G
##          -i (number max of iterations)   200
##          -a (regularization parameter)   10
##          -s (seed random init)           25949788
##          -e (tolerance error)            1E-05
##          -p (number of processes)        1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                                ]
## [=====]
## Number of iterations: 131
##
## Least-square error: 4668.291259
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run5/genotypes_r5.9.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K9/run5/genotypes_r5.9.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)      50
##          -L (number of loci)             400

```



```

##          -K (number of ancestral pops)      9
##          -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run5/genotypes_r5.9.Q
##          -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run5/genotypes_r5.9.G
##          -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.3835
## Cross-Entropy (masked data):  0.633362
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 10  repetition 5      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                 400
##          -K (number of ancestral pops)       10
##          -x (input file)                     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)       C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run5/genotypes_r5.10.Q
##          -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run5/genotypes_r5.10.G
##          -i (number max of iterations)       200
##          -a (regularization parameter)       10
##          -s (seed random init)               25949788
##          -e (tolerance error)                1E-05
##          -p (number of processes)            1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [ ]
##   [=====]
## Number of iterations: 84
##
## Least-square error: 4532.377039
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run5/genotypes_r5.10.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po

```

```

p_struc/genotypes.snmf/K10/run5/genotypes_r5.10.G: OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   10
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run5/genotypes_r5.10.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run5/genotypes_r5.10.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.369526
## Cross-Entropy (masked data):  0.634232
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] 90550749
## [1] "*****"
## [1] "*"   create.dataset   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -s (seed random init)          90550749
##      -r (percentage of masked data)  0.05
##      -x (genotype file in .geno format) C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genotypes.geno
##      -o (output file in .geno format) C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genotypes.snmf/masked/genotypes_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
otypes.snmf/masked/genotypes_I.geno:      OK.
##
## [1] "*****"
## [1] "*" sNMF K = 1 repetition 6   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400

```

```

##          -K (number of ancestral pops)          1
##          -x (input file)                        C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)          C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run6/genotypes_r6.1.Q
##          -g (ancestral frequencies file)         C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run6/genotypes_r6.1.G
##          -i (number max of iterations)          200
##          -a (regularization parameter)          10
##          -s (seed random init)                  90550749
##          -e (tolerance error)                   1E-05
##          -p (number of processes)               1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##
## Least-square error: 6680.840083
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run6/genotypes_r6.1.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K1/run6/genotypes_r6.1.G:  OK.
##
## [1] "*****"
## [1] "*"      cross-entropy estimation      "*"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)              50
##          -L (number of loci)                    400
##          -K (number of ancestral pops)          1
##          -x (genotype file)                     C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)               C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run6/genotypes_r6.1.Q
##          -g (ancestral frequencies)              C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run6/genotypes_r6.1.G
##          -i (with masked genotypes)              C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.577057
## Cross-Entropy (masked data):  0.658358
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"

```

```

## [1] "*" sNMF K = 2  repetition 6      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   2
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run6/genotypes_r6.2.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run6/genotypes_r6.2.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           90550749
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##      [ ]
##      [=====]
## Number of iterations: 66
##
## Least-square error: 6107.407816
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run6/genotypes_r6.2.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K2/run6/genotypes_r6.2.G:  OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   2
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run6/genotypes_r6.2.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run6/genotypes_r6.2.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.517381
## Cross-Entropy (masked data):  0.654636
## The project is saved into :

```

```

## genotypes.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 3 repetition 6      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      3
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run6/genotypes_r6.3.Q
##      -g (ancestral frequencies file)    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run6/genotypes_r6.3.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              90550749
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                     ]
## [=====]
## Number of iterations: 65
##
## Least-square error: 5698.864621
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run6/genotypes_r6.3.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K3/run6/genotypes_r6.3.G:   OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      3
##      -x (genotype file)                 C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run6/genotypes_r6.3.Q

```

```

##          -g (ancestral frequencies)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run6/genotypes_r6.3.G
##          -i (with masked genotypes)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.477246
## Cross-Entropy (masked data):  0.617489
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 4  repetition 6          *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                400
##          -K (number of ancestral pops)       4
##          -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run6/genotypes_r6.4.Q
##          -g (ancestral frequencies file)    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run6/genotypes_r6.4.G
##          -i (number max of iterations)      200
##          -a (regularization parameter)      10
##          -s (seed random init)              90550749
##          -e (tolerance error)               1E-05
##          -p (number of processes)           1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [
##   [=====]
##   Number of iterations: 75
##
##   Least-square error: 5465.668251
##   Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run6/genotypes_r6.4.Q:      OK.
##   Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K4/run6/genotypes_r6.4.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation          *"
## [1] "*****"

```

```

## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run6/genotypes_r6.4.Q
##      -g (ancestral frequencies)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run6/genotypes_r6.4.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.451412
## Cross-Entropy (masked data):  0.628992
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 5  repetition 6      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   5
##      -x (input file)                  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run6/genotypes_r6.5.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run6/genotypes_r6.5.G
##      -i (number max of iterations)    200
##      -a (regularization parameter)    10
##      -s (seed random init)            90550749
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##  [
##  [=====]
##  Number of iterations: 52
##

```

```

## Least-square error: 5254.394982
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run6/genotypes_r6.5.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K5/run6/genotypes_r6.5.G:   OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   5
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run6/genotypes_r6.5.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run6/genotypes_r6.5.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.432306
## Cross-Entropy (masked data):  0.631633
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 6  repetition 6      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   6
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run6/genotypes_r6.6.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run6/genotypes_r6.6.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)    10
##      -s (seed random init)            90550749
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##

```



```

## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                                 ]
## [=====]
## Number of iterations: 48
##
## Least-square error: 5076.435319
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run6/genotypes_r6.6.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K6/run6/genotypes_r6.6.G:   OK.
##
## [1] "*****"
## [1] "*   cross-entropy estimation   *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   6
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run6/genotypes_r6.6.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run6/genotypes_r6.6.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.417586
## Cross-Entropy (masked data):  0.643564
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 7  repetition 6      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   7
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run6/genotypes_r6.7.Q

```

```

##      -g (ancestral frequencies file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run6/genotypes_r6.7.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              90550749
##      -e (tolerance error)                1E-05
##      -p (number of processes)            1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 47
##
## Least-square error: 4927.610307
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run6/genotypes_r6.7.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K7/run6/genotypes_r6.7.G:      OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                 400
##      -K (number of ancestral pops)       7
##      -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run6/genotypes_r6.7.Q
##      -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run6/genotypes_r6.7.G
##      -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.404281
## Cross-Entropy (masked data):  0.65742
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 8  repetition 6      *"
## [1] "*****"

```

```

## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   8
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run6/genotypes_r6.8.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run6/genotypes_r6.8.G
##      -i (number max of iterations)    200
##      -a (regularization parameter)    10
##      -s (seed random init)            90550749
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##      [                                     ]
##      [=====]
## Number of iterations: 91
##
## Least-square error: 4765.805481
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run6/genotypes_r6.8.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K8/run6/genotypes_r6.8.G:  OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   8
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run6/genotypes_r6.8.Q
##      -g (ancestral frequencies)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run6/genotypes_r6.8.G
##      -i (with masked genotypes)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.388251
## Cross-Entropy (masked data):  0.711539
## The project is saved into :
##   genotypes.snmfProject
##

```

```

## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 9  repetition 6      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      9
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run6/genotypes_r6.9.Q
##      -g (ancestral frequencies file)    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run6/genotypes_r6.9.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              90550749
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 104
##
## Least-square error: 4659.375655
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run6/genotypes_r6.9.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K9/run6/genotypes_r6.9.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      9
##      -x (genotype file)                 C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run6/genotypes_r6.9.Q
##      -g (ancestral frequencies)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run6/genotypes_r6.9.G

```

```

##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.38096
## Cross-Entropy (masked data):  0.719044
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 10  repetition 6      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   10
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run6/genotypes_r6.10.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run6/genotypes_r6.10.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)    10
##      -s (seed random init)           90550749
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [ ]
##   [=====]
## Number of iterations: 58
##
## Least-square error: 4515.492703
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run6/genotypes_r6.10.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K10/run6/genotypes_r6.10.G: OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##

```

```

##          -n (number of individuals)          50
##          -L (number of loci)                400
##          -K (number of ancestral pops)      10
##          -x (genotype file)                 C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run6/genotypes_r6.10.Q
##          -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run6/genotypes_r6.10.G
##          -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.369749
## Cross-Entropy (masked data):  0.735509
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] 400924082
## [1] "*****"
## [1] "*"          create.dataset          "*"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                400
##          -s (seed random init)              400924082
##          -r (percentage of masked data)      0.05
##          -x (genotype file in .geno format)  C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genotypes.geno
##          -o (output file in .geno format)    C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genotypes.snmf/masked/genotypes_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
otypes.snmf/masked/genotypes_I.geno:      OK.
##
## [1] "*****"
## [1] "* sNMF K = 1  repetition 7          *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                400
##          -K (number of ancestral pops)      1
##          -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)       C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run7/genotypes_r7.1.Q
##          -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run7/genotypes_r7.1.G

```

```

##          -i (number max of iterations)          200
##          -a (regularization parameter)          10
##          -s (seed random init)                  400924082
##          -e (tolerance error)                    1E-05
##          -p (number of processes)                1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##
## Least-square error: 6647.280082
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run7/genotypes_r7.1.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K1/run7/genotypes_r7.1.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)              50
##          -L (number of loci)                     400
##          -K (number of ancestral pops)           1
##          -x (genotype file)                      C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)               C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run7/genotypes_r7.1.Q
##          -g (ancestral frequencies)              C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run7/genotypes_r7.1.G
##          -i (with masked genotypes)              C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.575458
## Cross-Entropy (masked data):  0.677823
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 2  repetition 7      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)              50
##          -L (number of loci)                     400
##          -K (number of ancestral pops)           2

```

```

##      -x (input file)                C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run7/genotypes_r7.2.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run7/genotypes_r7.2.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           400924082
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                     ]
## [=====]
## Number of iterations: 20
##
## Least-square error: 6094.062672
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run7/genotypes_r7.2.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K2/run7/genotypes_r7.2.G:  OK.
##
## [1] "*****"
## [1] "*   cross-entropy estimation   *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)       50
##      -L (number of loci)              400
##      -K (number of ancestral pops)    2
##      -x (genotype file)               C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run7/genotypes_r7.2.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run7/genotypes_r7.2.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.516833
## Cross-Entropy (masked data):  0.639999
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")

```



```

##
## [1] "*****"
## [1] "* sNMF K = 3  repetition 7      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   3
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run7/genotypes_r7.3.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run7/genotypes_r7.3.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)    10
##      -s (seed random init)           400924082
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                     ]
## [=====]
## Number of iterations: 34
##
## Least-square error: 5680.265703
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run7/genotypes_r7.3.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K3/run7/genotypes_r7.3.G:   OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   3
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run7/genotypes_r7.3.Q
##      -g (ancestral frequencies)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run7/genotypes_r7.3.G
##      -i (with masked genotypes)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.476073

```

```

## Cross-Entropy (masked data): 0.630063
## The project is saved into :
## genotypes.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 4 repetition 7      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run7/genotypes_r7.4.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run7/genotypes_r7.4.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           400924082
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 93
##
## Least-square error: 5416.213966
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run7/genotypes_r7.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K4/run7/genotypes_r7.4.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno

```

```

##          -q (individual admixture)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run7/genotypes_r7.4.Q
##          -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run7/genotypes_r7.4.G
##          -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.450067
## Cross-Entropy (masked data):  0.630828
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 5  repetition 7      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                 400
##          -K (number of ancestral pops)       5
##          -x (input file)                     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)       C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run7/genotypes_r7.5.Q
##          -g (ancestral frequencies file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run7/genotypes_r7.5.G
##          -i (number max of iterations)       200
##          -a (regularization parameter)       10
##          -s (seed random init)               400924082
##          -e (tolerance error)                 1E-05
##          -p (number of processes)            1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [ ]
##   [=====]
## Number of iterations: 107
##
## Least-square error: 5206.336293
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run7/genotypes_r7.5.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K5/run7/genotypes_r7.5.G:  OK.
##
## [1] "*****"

```

```

## [1] "*"      cross-entropy estimation      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   5
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run7/genotypes_r7.5.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run7/genotypes_r7.5.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.431167
## Cross-Entropy (masked data):  0.641326
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*" sNMF K = 6  repetition 7      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   6
##      -x (input file)                C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run7/genotypes_r7.6.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run7/genotypes_r7.6.G
##      -i (number max of iterations)  200
##      -a (regularization parameter)  10
##      -s (seed random init)          400924082
##      -e (tolerance error)           1E-05
##      -p (number of processes)       1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##  [
##  [=====]

```

```

## Number of iterations: 121
##
## Least-square error: 5061.953718
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run7/genotypes_r7.6.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K6/run7/genotypes_r7.6.G:  OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   6
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run7/genotypes_r7.6.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run7/genotypes_r7.6.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.416741
## Cross-Entropy (masked data):  0.678735
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*" sNMF K = 7  repetition 7      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   7
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run7/genotypes_r7.7.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run7/genotypes_r7.7.G
##      -i (number max of iterations)  200
##      -a (regularization parameter)  10
##      -s (seed random init)          400924082
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1

```

```

##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##      [
##      [=====]
## Number of iterations: 51
##
## Least-square error: 4898.502111
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run7/genotypes_r7.7.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K7/run7/genotypes_r7.7.G:      OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)      400
##      -K (number of ancestral pops)      7
##      -x (genotype file)      C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run7/genotypes_r7.7.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run7/genotypes_r7.7.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.399949
## Cross-Entropy (masked data): 0.70632
## The project is saved into :
##      genotypes.snmfProject
##
## To load the project, use:
##      project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##      remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 8  repetition 7      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)      400
##      -K (number of ancestral pops)      8
##      -x (input file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno

```

```

##      -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run7/genotypes_r7.8.Q
##      -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run7/genotypes_r7.8.G
##      -i (number max of iterations)       200
##      -a (regularization parameter)       10
##      -s (seed random init)               400924082
##      -e (tolerance error)                 1E-05
##      -p (number of processes)             1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##      [                                     ]
##      [=====]
## Number of iterations: 43
##
## Least-square error: 4763.023717
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run7/genotypes_r7.8.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K8/run7/genotypes_r7.8.G:  OK.
##
## [1] "*****"
## [1] "*"      cross-entropy estimation      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)           50
##      -L (number of loci)                  400
##      -K (number of ancestral pops)        8
##      -x (genotype file)                   C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)            C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run7/genotypes_r7.8.Q
##      -g (ancestral frequencies)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run7/genotypes_r7.8.G
##      -i (with masked genotypes)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.387656
## Cross-Entropy (masked data):  0.710577
## The project is saved into :
##      genotypes.snmfProject
##
## To load the project, use:
##      project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##      remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"

```

```

## [1] "*" sNMF K = 9  repetition 7      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   9
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run7/genotypes_r7.9.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run7/genotypes_r7.9.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           400924082
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##      [ ]
##      [=====]
## Number of iterations: 106
##
## Least-square error: 4616.009996
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run7/genotypes_r7.9.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K9/run7/genotypes_r7.9.G:  OK.
##
## [1] "*****"
## [1] "*"  cross-entropy estimation      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   9
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run7/genotypes_r7.9.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run7/genotypes_r7.9.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.379305
## Cross-Entropy (masked data):  0.752653
## The project is saved into :

```



```

## genotypes.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 10 repetition 7      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      10
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run7/genotypes_r7.10.Q
##      -g (ancestral frequencies file)    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run7/genotypes_r7.10.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              400924082
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                                ]
## [=====]
## Number of iterations: 84
##
## Least-square error: 4485.816697
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run7/genotypes_r7.10.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K10/run7/genotypes_r7.10.G: OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      10
##      -x (genotype file)                 C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run7/genotypes_r7.10.Q

```

```

##          -g (ancestral frequencies)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run7/genotypes_r7.10.G
##          -i (with masked genotypes)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.366862
## Cross-Entropy (masked data):  0.781038
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] 1154283607
## [1] "*****"
## [1] "*"          create.dataset          "*"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                 400
##          -s (seed random init)               1154283607
##          -r (percentage of masked data)       0.05
##          -x (genotype file in .geno format)   C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genotypes.geno
##          -o (output file in .geno format)     C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genotypes.snmf/masked/genotypes_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
otypes.snmf/masked/genotypes_I.geno:      OK.
##
## [1] "*****"
## [1] "* sNMF K = 1  repetition 8          *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                 400
##          -K (number of ancestral pops)       1
##          -x (input file)                     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)       C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run8/genotypes_r8.1.Q
##          -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run8/genotypes_r8.1.G
##          -i (number max of iterations)       200
##          -a (regularization parameter)       10
##          -s (seed random init)               1154283607
##          -e (tolerance error)                1E-05
##          -p (number of processes)            1
##          - diploid
##

```

```

## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##
## Least-square error: 6677.920081
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run8/genotypes_r8.1.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K1/run8/genotypes_r8.1.G:  OK.
##
## [1] "*****"
## [1] "*   cross-entropy estimation   *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   1
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run8/genotypes_r8.1.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run8/genotypes_r8.1.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.576092
## Cross-Entropy (masked data):  0.664462
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 2  repetition 8   *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   2
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run8/genotypes_r8.2.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run8/genotypes_r8.2.G
##      -i (number max of iterations)   200

```

```

##      -a (regularization parameter)      10
##      -s (seed random init)             1154283607
##      -e (tolerance error)              1E-05
##      -p (number of processes)          1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 50
##
## Least-square error: 6108.156892
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run8/genotypes_r8.2.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K2/run8/genotypes_r8.2.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   2
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run8/genotypes_r8.2.Q
##      -g (ancestral frequencies)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run8/genotypes_r8.2.G
##      -i (with masked genotypes)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.517608
## Cross-Entropy (masked data):  0.630157
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 3  repetition 8      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50

```

```

##          -L (number of loci)                400
##          -K (number of ancestral pops)       3
##          -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run8/genotypes_r8.3.Q
##          -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run8/genotypes_r8.3.G
##          -i (number max of iterations)      200
##          -a (regularization parameter)      10
##          -s (seed random init)              1154283607
##          -e (tolerance error)               1E-05
##          -p (number of processes)           1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                    ]
## [=====]
## Number of iterations: 62
##
## Least-square error: 5685.205986
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run8/genotypes_r8.3.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K3/run8/genotypes_r8.3.G:  OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                400
##          -K (number of ancestral pops)       3
##          -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run8/genotypes_r8.3.Q
##          -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run8/genotypes_r8.3.G
##          -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.475913
## Cross-Entropy (masked data):  0.60689
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##

```

```

## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 4  repetition 8      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (input file)                C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run8/genotypes_r8.4.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run8/genotypes_r8.4.G
##      -i (number max of iterations)  200
##      -a (regularization parameter)  10
##      -s (seed random init)          1154283607
##      -e (tolerance error)            1E-05
##      -p (number of processes)       1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                     ]
## [=====]
## Number of iterations: 60
##
## Least-square error: 5410.508711
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run8/genotypes_r8.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K4/run8/genotypes_r8.4.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run8/genotypes_r8.4.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run8/genotypes_r8.4.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid

```

```

##
## Cross-Entropy (all data):      0.448936
## Cross-Entropy (masked data):  0.624406
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 5  repetition 8      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   5
##      -x (input file)                  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run8/genotypes_r8.5.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run8/genotypes_r8.5.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)            1154283607
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [                                                                    ]
##   [=====]
## Number of iterations: 159
##
## Least-square error: 5221.915844
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run8/genotypes_r8.5.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K5/run8/genotypes_r8.5.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   5

```

```

##      -x (genotype file)                C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run8/genotypes_r8.5.Q
##      -g (ancestral frequencies)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run8/genotypes_r8.5.G
##      -i (with masked genotypes)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.42979
## Cross-Entropy (masked data):  0.646064
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 6  repetition 8      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)        50
##      -L (number of loci)              400
##      -K (number of ancestral pops)    6
##      -x (input file)                  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run8/genotypes_r8.6.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run8/genotypes_r8.6.G
##      -i (number max of iterations)    200
##      -a (regularization parameter)    10
##      -s (seed random init)            1154283607
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [ ]
##   [=====]
## Number of iterations: 78
##
## Least-square error: 5050.594747
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run8/genotypes_r8.6.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K6/run8/genotypes_r8.6.G:  OK.

```



```

##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   6
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run8/genotypes_r8.6.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run8/genotypes_r8.6.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):    0.416677
## Cross-Entropy (masked data): 0.667024
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*" sNMF K = 7  repetition 8   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   7
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run8/genotypes_r8.7.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run8/genotypes_r8.7.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           1154283607
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:    OK.
##
##
## Main algorithm:

```

```

## [
## [=====]
## Number of iterations: 50
##
## Least-square error: 4925.507684
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run8/genotypes_r8.7.Q: OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K7/run8/genotypes_r8.7.G: OK.
##
## [1] "*****"
## [1] "* cross-entropy estimation *"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 7
## -x (genotype file) C:/Users/llpo0001/Documents/slubi/3bs/pop_struc
\genotypes.geno
## -q (individual admixture) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run8/genotypes_r8.7.Q
## -g (ancestral frequencies) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run8/genotypes_r8.7.G
## -i (with masked genotypes) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
## - diploid
##
## Cross-Entropy (all data): 0.399759
## Cross-Entropy (masked data): 0.661013
## The project is saved into :
## genotypes.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 8 repetition 8 *"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 8
## -x (input file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
## -q (individual admixture file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run8/genotypes_r8.8.Q
## -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run8/genotypes_r8.8.G
## -i (number max of iterations) 200
## -a (regularization parameter) 10
## -s (seed random init) 1154283607

```

```

##          -e (tolerance error)                1E-05
##          -p (number of processes)            1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                                 ]
## [=====]
## Number of iterations: 62
##
## Least-square error: 4783.986168
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run8/genotypes_r8.8.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K8/run8/genotypes_r8.8.G:   OK.
##
## [1] "*****"
## [1] "*   cross-entropy estimation   *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                 400
##          -K (number of ancestral pops)       8
##          -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run8/genotypes_r8.8.Q
##          -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run8/genotypes_r8.8.G
##          -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.394295
## Cross-Entropy (masked data):  0.703338
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 9  repetition 8   *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                 400
##          -K (number of ancestral pops)       9

```

```

##          -x (input file)                C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run8/genotypes_r8.9.Q
##          -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run8/genotypes_r8.9.G
##          -i (number max of iterations)   200
##          -a (regularization parameter)   10
##          -s (seed random init)           1154283607
##          -e (tolerance error)             1E-05
##          -p (number of processes)         1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 67
##
## Least-square error: 4618.627293
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run8/genotypes_r8.9.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K9/run8/genotypes_r8.9.G:  OK.
##
## [1] "*****"
## [1] "*   cross-entropy estimation   *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)       50
##          -L (number of loci)              400
##          -K (number of ancestral pops)    9
##          -x (genotype file)               C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run8/genotypes_r8.9.Q
##          -g (ancestral frequencies)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run8/genotypes_r8.9.G
##          -i (with masked genotypes)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.376311
## Cross-Entropy (masked data):  0.720425
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")

```

```

##
## [1] "*****"
## [1] "* sNMF K = 10  repetition 8      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   10
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run8/genotypes_r8.10.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run8/genotypes_r8.10.G
##      -i (number max of iterations)    200
##      -a (regularization parameter)    10
##      -s (seed random init)            1154283607
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                     ]
## [=====]
## Number of iterations: 147
##
## Least-square error: 4523.703151
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run8/genotypes_r8.10.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K10/run8/genotypes_r8.10.G: OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   10
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run8/genotypes_r8.10.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run8/genotypes_r8.10.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.366624

```

```

## Cross-Entropy (masked data): 0.77745
## The project is saved into :
## genotypes.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] 889644157
## [1] "*****"
## [1] "*"          create.dataset          "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -s (seed random init)              889644157
##      -r (percentage of masked data)      0.05
##      -x (genotype file in .geno format)  C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genotypes.geno
##      -o (output file in .geno format)    C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genotypes.snmf/masked/genotypes_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
otypes.snmf/masked/genotypes_I.geno:      OK.
##
## [1] "*****"
## [1] "* sNMF K = 1 repetition 9          *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      1
##      -x (input file)                   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run9/genotypes_r9.1.Q
##      -g (ancestral frequencies file)    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run9/genotypes_r9.1.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              889644157
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##
## Least-square error: 6687.080082

```

```

## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run9/genotypes_r9.1.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K1/run9/genotypes_r9.1.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   1
##      -x (genotype file)              C:/Users/llpo0001/Documents/slubi/3bs/pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run9/genotypes_r9.1.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run9/genotypes_r9.1.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.577568
## Cross-Entropy (masked data):  0.630714
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 2  repetition 9      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   2
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run9/genotypes_r9.2.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run9/genotypes_r9.2.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           889644157
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g

```

```

enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 52
##
## Least-square error: 6114.436414
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run9/genotypes_r9.2.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K2/run9/genotypes_r9.2.G:  OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   2
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run9/genotypes_r9.2.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run9/genotypes_r9.2.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.519637
## Cross-Entropy (masked data):  0.593889
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*" sNMF K = 3  repetition 9      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   3
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run9/genotypes_r9.3.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s

```



```

truc/genotypes.snmf/K3/run9/genotypes_r9.3.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              889644157
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##      [ ]
##      [=====]
## Number of iterations: 45
##
## Least-square error: 5707.717188
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run9/genotypes_r9.3.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K3/run9/genotypes_r9.3.G:      OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                 400
##      -K (number of ancestral pops)       3
##      -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run9/genotypes_r9.3.Q
##      -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run9/genotypes_r9.3.G
##      -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.477136
## Cross-Entropy (masked data):  0.572696
## The project is saved into :
##      genotypes.snmfProject
##
## To load the project, use:
##      project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##      remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 4  repetition 9      *"
## [1] "*****"
## summary of the options:

```

```

##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      4
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run9/genotypes_r9.4.Q
##      -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run9/genotypes_r9.4.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              889644157
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 59
##
## Least-square error: 5443.635296
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run9/genotypes_r9.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K4/run9/genotypes_r9.4.G:   OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      4
##      -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run9/genotypes_r9.4.Q
##      -g (ancestral frequencies)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run9/genotypes_r9.4.G
##      -i (with masked genotypes)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.452122
## Cross-Entropy (masked data):  0.560987
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:

```

```

## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 5 repetition 9      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   5
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run9/genotypes_r9.5.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run9/genotypes_r9.5.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           889644157
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                     ]
## [=====]
## Number of iterations: 135
##
## Least-square error: 5259.692635
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run9/genotypes_r9.5.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K5/run9/genotypes_r9.5.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   5
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run9/genotypes_r9.5.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run9/genotypes_r9.5.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru

```

```

c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.432375
## Cross-Entropy (masked data):  0.558871
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 6  repetition 9      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)      50
##          -L (number of loci)             400
##          -K (number of ancestral pops)   6
##          -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run9/genotypes_r9.6.Q
##          -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run9/genotypes_r9.6.G
##          -i (number max of iterations)   200
##          -a (regularization parameter)   10
##          -s (seed random init)           889644157
##          -e (tolerance error)            1E-05
##          -p (number of processes)        1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                                 ]
## [=====]
## Number of iterations: 115
##
## Least-square error: 5093.455769
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run9/genotypes_r9.6.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K6/run9/genotypes_r9.6.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)      50

```

```

##          -L (number of loci)                400
##          -K (number of ancestral pops)       6
##          -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run9/genotypes_r9.6.Q
##          -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run9/genotypes_r9.6.G
##          -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.417993
## Cross-Entropy (masked data):  0.593041
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 7  repetition 9      *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                400
##          -K (number of ancestral pops)       7
##          -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)       C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run9/genotypes_r9.7.Q
##          -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run9/genotypes_r9.7.G
##          -i (number max of iterations)       200
##          -a (regularization parameter)       10
##          -s (seed random init)              889644157
##          -e (tolerance error)               1E-05
##          -p (number of processes)           1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [
##   [=====]
## Number of iterations: 102
##
## Least-square error: 4944.898623
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run9/genotypes_r9.7.Q:      OK.

```

```

## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop
p_struc/genotypes.snmf/K7/run9/genotypes_r9.7.G: OK.
##
## [1] "*****"
## [1] "*" cross-entropy estimation "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   7
##      -x (genotype file)              C:/Users/llpo0001/Documents/slubi/3bs/pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run9/genotypes_r9.7.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run9/genotypes_r9.7.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.406664
## Cross-Entropy (masked data):  0.654065
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*" sNMF K = 8  repetition 9      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   8
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run9/genotypes_r9.8.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run9/genotypes_r9.8.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           889644157
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno: OK.
##

```

```

##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 54
##
## Least-square error: 4760.410147
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run9/genotypes_r9.8.Q: OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K8/run9/genotypes_r9.8.G: OK.
##
## [1] "*****"
## [1] "* cross-entropy estimation *"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 8
## -x (genotype file) C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
## -q (individual admixture) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run9/genotypes_r9.8.Q
## -g (ancestral frequencies) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run9/genotypes_r9.8.G
## -i (with masked genotypes) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
## - diploid
##
## Cross-Entropy (all data): 0.391225
## Cross-Entropy (masked data): 0.641756
## The project is saved into :
## genotypes.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 9 repetition 9 *"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 9
## -x (input file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
## -q (individual admixture file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run9/genotypes_r9.9.Q
## -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run9/genotypes_r9.9.G
## -i (number max of iterations) 200

```

```

##      -a (regularization parameter)      10
##      -s (seed random init)             889644157
##      -e (tolerance error)              1E-05
##      -p (number of processes)          1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##      [                                     ]
##      [=====]
## Number of iterations: 37
##
## Least-square error: 4660.770826
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run9/genotypes_r9.9.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K9/run9/genotypes_r9.9.G:  OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   9
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run9/genotypes_r9.9.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run9/genotypes_r9.9.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.379864
## Cross-Entropy (masked data):  0.678157
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*" sNMF K = 10  repetition 9      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50

```



```

##          -L (number of loci)                400
##          -K (number of ancestral pops)       10
##          -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##          -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run9/genotypes_r9.10.Q
##          -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run9/genotypes_r9.10.G
##          -i (number max of iterations)      200
##          -a (regularization parameter)       10
##          -s (seed random init)              889644157
##          -e (tolerance error)               1E-05
##          -p (number of processes)           1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                                                      ]
## [=====]
## Number of iterations: 177
##
## Least-square error: 4527.584975
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run9/genotypes_r9.10.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K10/run9/genotypes_r9.10.G: OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   *"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                400
##          -K (number of ancestral pops)       10
##          -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##          -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run9/genotypes_r9.10.Q
##          -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run9/genotypes_r9.10.G
##          -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.367868
## Cross-Entropy (masked data):  0.688749
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##

```

```

## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] 1902266605
## [1] "*****"
## [1] "*"          create.dataset          "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -s (seed random init)              1902266605
##      -r (percentage of masked data)     0.05
##      -x (genotype file in .geno format) C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genotypes.geno
##      -o (output file in .geno format)   C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genotypes.snmf/masked/genotypes_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
otypes.snmf/masked/genotypes_I.geno:      OK.
##
## [1] "*****"
## [1] "*" sNMF K = 1  repetition 10          "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      1
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run10/genotypes_r10.1.Q
##      -g (ancestral frequencies file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K1/run10/genotypes_r10.1.G
##      -i (number max of iterations)     200
##      -a (regularization parameter)     10
##      -s (seed random init)              1902266605
##      -e (tolerance error)              1E-05
##      -p (number of processes)          1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##
## Least-square error: 6693.480082
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run10/genotypes_r10.1.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K1/run10/genotypes_r10.1.G: OK.
##
## [1] "*****"
## [1] "*"          cross-entropy estimation          "*"

```

```

## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   1
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run10/genotypes_r10.1.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K1/run10/genotypes_r10.1.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.578455
## Cross-Entropy (masked data):  0.621724
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 2  repetition 10      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   2
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run10/genotypes_r10.2.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K2/run10/genotypes_r10.2.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           1902266605
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [
##   [=====]
##   Number of iterations: 34

```

```

##
## Least-square error: 6144.193299
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run10/genotypes_r10.2.Q: OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K2/run10/genotypes_r10.2.G: OK.
##
## [1] "*****"
## [1] "* cross-entropy estimation *"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 2
## -x (genotype file) C:/Users/llpo0001/Documents/slubi/3bs/pop_struc
\genotypes.geno
## -q (individual admixture) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run10/genotypes_r10.2.Q
## -g (ancestral frequencies) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K2/run10/genotypes_r10.2.G
## -i (with masked genotypes) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
## - diploid
##
## Cross-Entropy (all data): 0.519113
## Cross-Entropy (masked data): 0.618338
## The project is saved into :
## genotypes.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 3 repetition 10 *"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 3
## -x (input file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
## -q (individual admixture file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run10/genotypes_r10.3.Q
## -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K3/run10/genotypes_r10.3.G
## -i (number max of iterations) 200
## -a (regularization parameter) 10
## -s (seed random init) 1902266605
## -e (tolerance error) 1E-05
## -p (number of processes) 1
## - diploid

```

```

##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                                                                      ]
## [=====]
## Number of iterations: 79
##
## Least-square error: 5691.642419
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run10/genotypes_r10.3.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K3/run10/genotypes_r10.3.G: OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   3
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run10/genotypes_r10.3.Q
##      -g (ancestral frequencies)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K3/run10/genotypes_r10.3.G
##      -i (with masked genotypes)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.47843
## Cross-Entropy (masked data):  0.577485
## The project is saved into :
## genotypes.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 4  repetition 10      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   4
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s

```

```

truc/genotypes.snmf/K4/run10/genotypes_r10.4.Q
##      -g (ancestral frequencies file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K4/run10/genotypes_r10.4.G
##      -i (number max of iterations)        200
##      -a (regularization parameter)        10
##      -s (seed random init)                1902266605
##      -e (tolerance error)                 1E-05
##      -p (number of processes)             1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 39
##
## Least-square error: 5467.525380
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run10/genotypes_r10.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K4/run10/genotypes_r10.4.G: OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)            50
##      -L (number of loci)                  400
##      -K (number of ancestral pops)        4
##      -x (genotype file)                   C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)             C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run10/genotypes_r10.4.Q
##      -g (ancestral frequencies)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K4/run10/genotypes_r10.4.G
##      -i (with masked genotypes)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.454538
## Cross-Entropy (masked data):  0.591372
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 5  repetition 10      *"

```

```

## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   5
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run10/genotypes_r10.5.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K5/run10/genotypes_r10.5.G
##      -i (number max of iterations)    200
##      -a (regularization parameter)    10
##      -s (seed random init)            1902266605
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 127
##
## Least-square error: 5261.247707
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run10/genotypes_r10.5.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K5/run10/genotypes_r10.5.G: OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   5
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run10/genotypes_r10.5.Q
##      -g (ancestral frequencies)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K5/run10/genotypes_r10.5.G
##      -i (with masked genotypes)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.43236
## Cross-Entropy (masked data):  0.586515
## The project is saved into :
## genotypes.snmfProject

```

```

##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 6  repetition 10      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   6
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run10/genotypes_r10.6.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K6/run10/genotypes_r10.6.G
##      -i (number max of iterations)  200
##      -a (regularization parameter)  10
##      -s (seed random init)          1902266605
##      -e (tolerance error)           1E-05
##      -p (number of processes)       1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [                                     ]
## [=====]
## Number of iterations: 53
##
## Least-square error: 5068.771195
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run10/genotypes_r10.6.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K6/run10/genotypes_r10.6.G: OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   6
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K6/run10/genotypes_r10.6.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru

```



```

c/genotypes.snmf/K6/run10/genotypes_r10.6.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.418886
## Cross-Entropy (masked data):  0.617251
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 7  repetition 10      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   7
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run10/genotypes_r10.7.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K7/run10/genotypes_r10.7.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           1902266605
##      -e (tolerance error)            1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [ ]
##   [=====]
## Number of iterations: 74
##
## Least-square error: 4910.779488
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run10/genotypes_r10.7.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K7/run10/genotypes_r10.7.G: OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:

```

```

##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      7
##      -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run10/genotypes_r10.7.Q
##      -g (ancestral frequencies)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K7/run10/genotypes_r10.7.G
##      -i (with masked genotypes)         C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.403071
## Cross-Entropy (masked data):  0.637498
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "* sNMF K = 8  repetition 10      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      8
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run10/genotypes_r10.8.Q
##      -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K8/run10/genotypes_r10.8.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              1902266605
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
##   [
##   [=====]
##   Number of iterations: 116
##
##   Least-square error: 4792.773949

```

```

## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run10/genotypes_r10.8.Q: OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K8/run10/genotypes_r10.8.G: OK.
##
## [1] "*****"
## [1] "*" cross-entropy estimation "*"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 8
## -x (genotype file) C:/Users/llpo0001/Documents/slubi/3bs/pop_struc
\genotypes.geno
## -q (individual admixture) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run10/genotypes_r10.8.Q
## -g (ancestral frequencies) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K8/run10/genotypes_r10.8.G
## -i (with masked genotypes) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
## - diploid
##
## Cross-Entropy (all data): 0.391138
## Cross-Entropy (masked data): 0.628946
## The project is saved into :
## genotypes.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*" sNMF K = 9 repetition 10 "*"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 9
## -x (input file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
## -q (individual admixture file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run10/genotypes_r10.9.Q
## -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K9/run10/genotypes_r10.9.G
## -i (number max of iterations) 200
## -a (regularization parameter) 10
## -s (seed random init) 1902266605
## -e (tolerance error) 1E-05
## -p (number of processes) 1
## - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g

```

```

enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 120
##
## Least-square error: 4655.651874
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run10/genotypes_r10.9.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K9/run10/genotypes_r10.9.G: OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   9
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run10/genotypes_r10.9.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K9/run10/genotypes_r10.9.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.381007
## Cross-Entropy (masked data):  0.671067
## The project is saved into :
##  genotypes.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genotypes.snmfProject")
##
## [1] "*****"
## [1] "*" sNMF K = 10  repetition 10  "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   10
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/masked/genotypes_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genotypes.snmf/K10/run10/genotypes_r10.10.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s

```

```

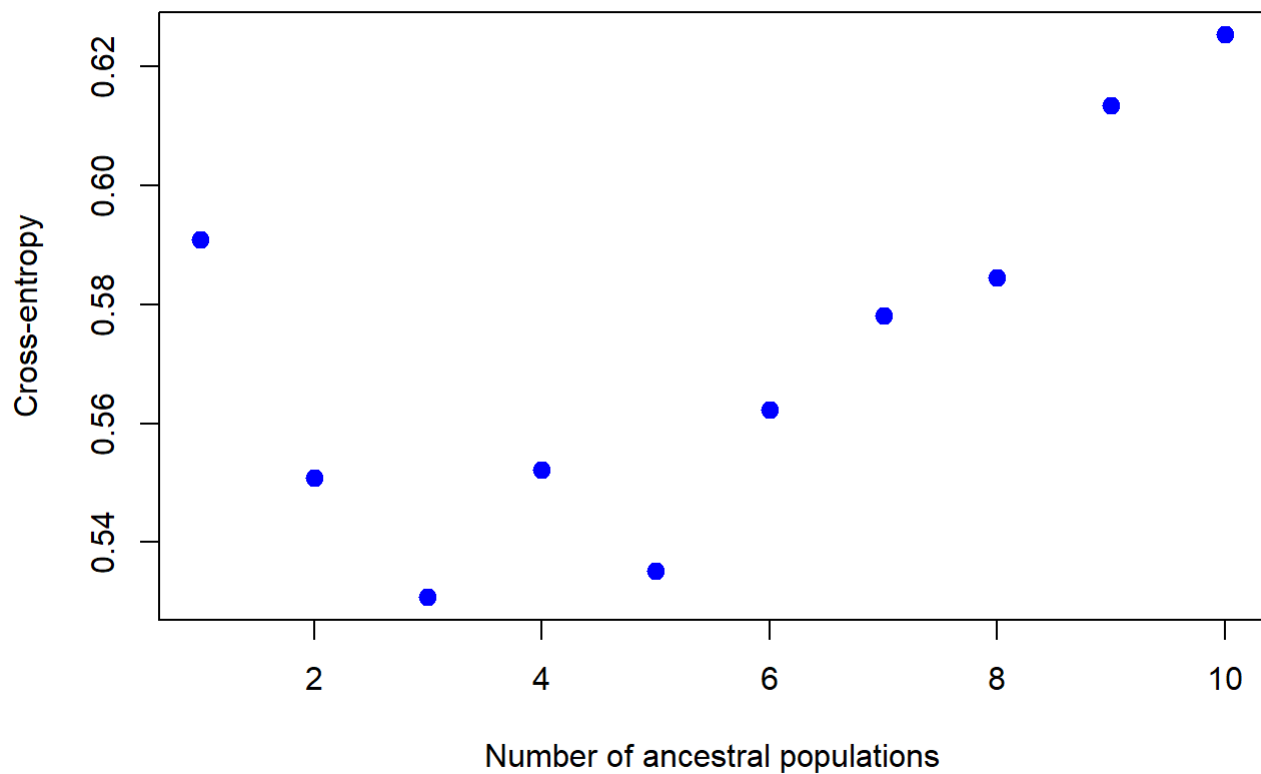
truc/genotypes.snmf/K10/run10/genotypes_r10.10.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              1902266605
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genotypes.snmf/masked/g
enotypes_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 29
##
## Least-square error: 4545.831967
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run10/genotypes_r10.10.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genotypes.snmf/K10/run10/genotypes_r10.10.G:      OK.
##
## [1] "*****"
## [1] "*"      cross-entropy estimation      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      10
##      -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genotypes.geno
##      -q (individual admixture)           C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run10/genotypes_r10.10.Q
##      -g (ancestral frequencies)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/K10/run10/genotypes_r10.10.G
##      -i (with masked genotypes)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genotypes.snmf/masked/genotypes_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.371091
## Cross-Entropy (masked data):  0.707609
## The project is saved into :
##   genotypes.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genotypes.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genotypes.snmfProject")

```

```

# plot cross-entropy criterion for all runs in the snmf project
plot(project, col = "blue", pch = 19, cex = 1.2)

```

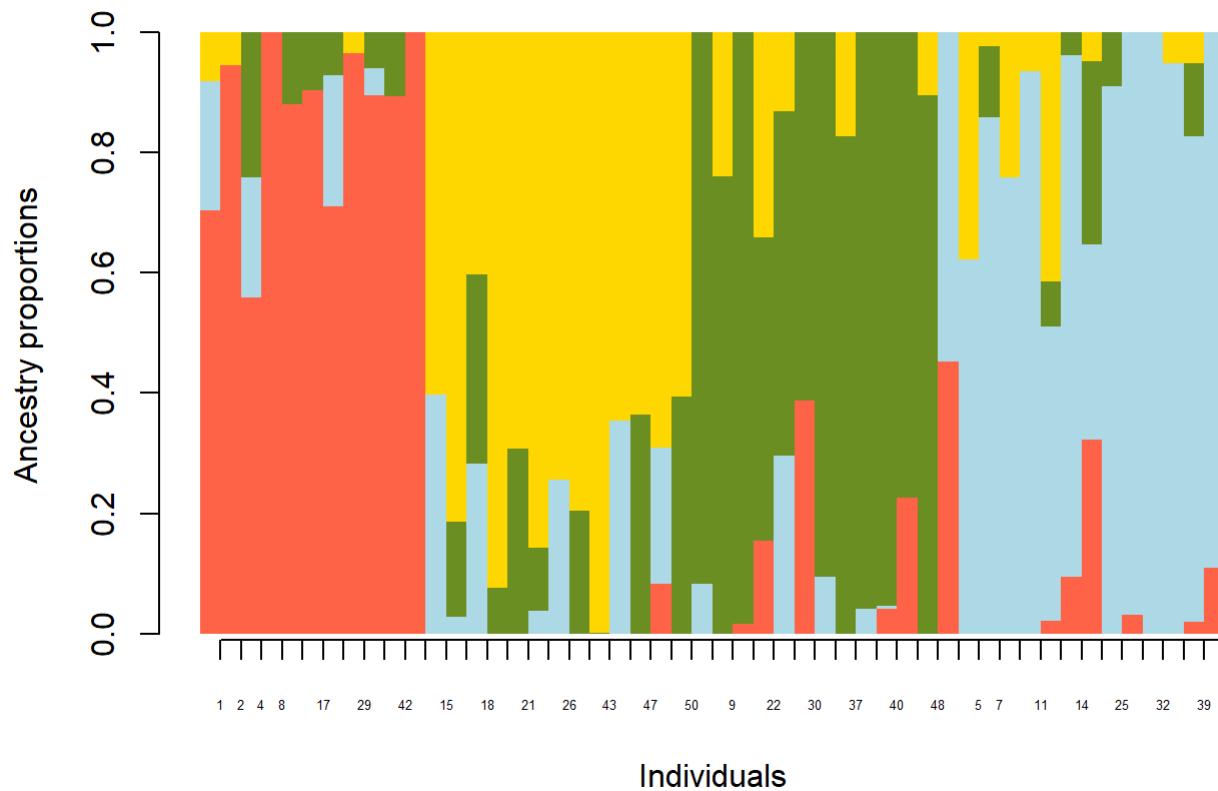


```
ce <- cross.entropy(project, K = 4)
best <- which.min(ce)
```

```
# select the best run for K = 4 clusters
best = which.min(cross.entropy(project, K = 4))
my.colors <- c("tomato", "lightblue",
               "olivedrab", "gold")
barchart(project, K = 4, run = best,
          border = NA, space = 0,
          col = my.colors,
          xlab = "Individuals",
          ylab = "Ancestry proportions",
          main = "Ancestry matrix") -> bp

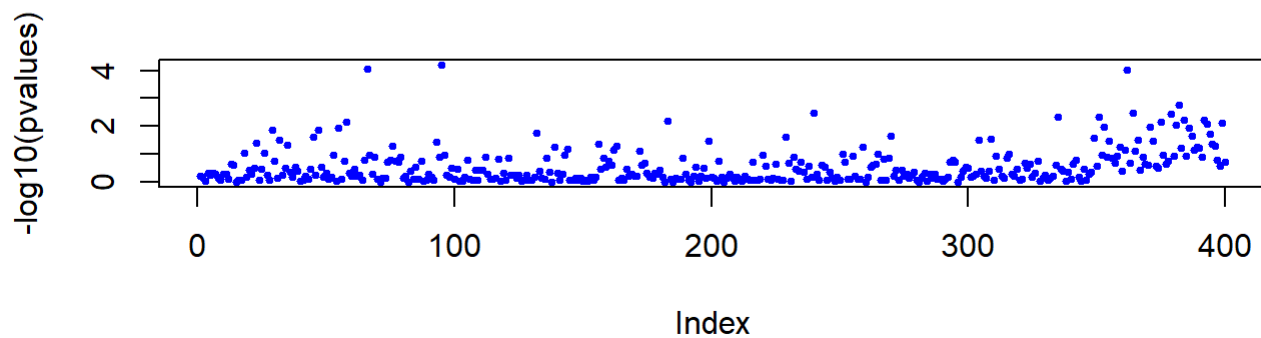
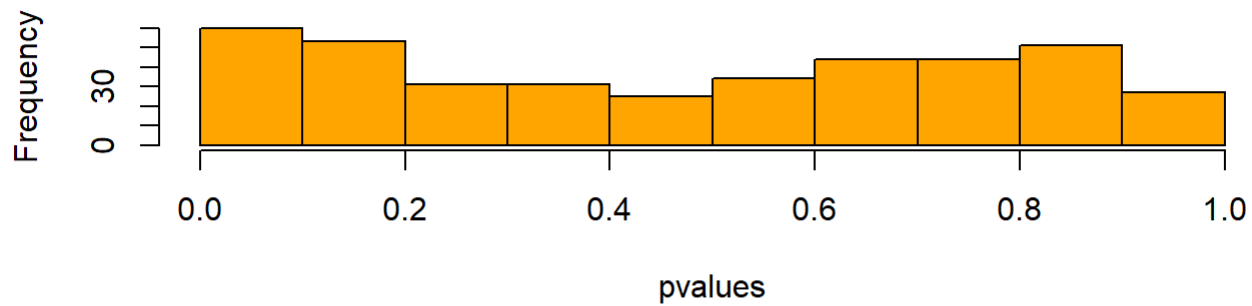
axis(1, at = 1:length(bp$order),
     labels = bp$order, las=1,
     cex.axis = .4)
```

Ancestry matrix



```
# Genome scan for selection: opulation differentiation tests
p = snmf.pvalues(project,
                  entropy = TRUE,
                  ploidy = 2,
                  K = 4)
pvalues = p$pvalues
par(mfrow = c(2,1))
hist(pvalues, col = "orange")
plot(-log10(pvalues), pch = 19, col = "blue", cex = .5)
```

Histogram of pvalues



```
# creation of a genotype matrix with missing genotypes
dat = as.numeric(tutorial.R)
dat[sample(1:length(dat), 100)] <- 9
dat <- matrix(dat, nrow = 50, ncol = 400)
write.lfmm(dat, "genoM.lfmm")
```

```
## [1] "genoM.lfmm"
```

```
project.missing = snmf("genoM.lfmm", K = 4,
  entropy = TRUE, repetitions = 10,
  project = "new")
```



```

## [1] "*****"
## [1] " Conversion from the lfmm format to the geno format"
## [1] "*****"
## The project is saved into :
##   genoM.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genoM.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genoM.snmfProject")
##
## [1] 217405619
## [1] "*****"
## [1] "*"          create.dataset          "*"
## [1] "*****"
## summary of the options:
##
##           -n (number of individuals)           50
##           -L (number of loci)                 400
##           -s (seed random init)                217405619
##           -r (percentage of masked data)        0.05
##           -x (genotype file in .geno format)    C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genoM.geno
##           -o (output file in .geno format)      C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genoM.snmf/masked/genoM_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
oM.snmf/masked/genoM_I.geno:      OK.
##
## [1] "*****"
## [1] "*" sNMF K = 4  repetition 1      "*"
## [1] "*****"
## summary of the options:
##
##           -n (number of individuals)           50
##           -L (number of loci)                 400
##           -K (number of ancestral pops)        4
##           -x (input file)                     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/masked/genoM_I.geno
##           -q (individual admixture file)        C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run1/genoM_r1.4.Q
##           -g (ancestral frequencies file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run1/genoM_r1.4.G
##           -i (number max of iterations)        200
##           -a (regularization parameter)        10
##           -s (seed random init)                217405619
##           -e (tolerance error)                 1E-05
##           -p (number of processes)             1
##           - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genoM.snmf/masked/genoM
_I.geno:      OK.
##
##

```

```

## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 66
##
## Least-square error: 5465.042330
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run1/genoM_r1.4.Q: OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genoM.snmf/K4/run1/genoM_r1.4.G: OK.
##
## [1] "*****"
## [1] "* cross-entropy estimation *"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -K (number of ancestral pops) 4
## -x (genotype file) C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genoM.geno
## -q (individual admixture) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run1/genoM_r1.4.Q
## -g (ancestral frequencies) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run1/genoM_r1.4.G
## -i (with masked genotypes) C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/masked/genoM_I.geno
## - diploid
##
## Cross-Entropy (all data): 0.451922
## Cross-Entropy (masked data): 0.587303
## The project is saved into :
## genoM.snmfProject
##
## To load the project, use:
## project = load.snmfProject("genoM.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genoM.snmfProject")
##
## [1] 2016921576
## [1] "*****"
## [1] "* create.dataset *"
## [1] "*****"
## summary of the options:
##
## -n (number of individuals) 50
## -L (number of loci) 400
## -s (seed random init) 2016921576
## -r (percentage of masked data) 0.05
## -x (genotype file in .geno format) C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genoM.geno
## -o (output file in .geno format) C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genoM.snmf/masked/genoM_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen

```

```

oM.snmf/masked/genoM_I.geno:      OK.
##
## [1] "*****"
## [1] "* sNMF K = 4  repetition 2      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/masked/genoM_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run2/genoM_r2.4.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run2/genoM_r2.4.G
##      -i (number max of iterations)    200
##      -a (regularization parameter)    10
##      -s (seed random init)            2016921576
##      -e (tolerance error)              1E-05
##      -p (number of processes)          1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genoM.snmf/masked/genoM
_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 55
##
## Least-square error: 5446.651925
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run2/genoM_r2.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genoM.snmf/K4/run2/genoM_r2.4.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genoM.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run2/genoM_r2.4.Q
##      -g (ancestral frequencies)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run2/genoM_r2.4.G
##      -i (with masked genotypes)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/masked/genoM_I.geno
##      - diploid
##

```

```

## Cross-Entropy (all data):      0.452007
## Cross-Entropy (masked data):  0.574667
## The project is saved into :
##   genoM.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genoM.snmfProject")
##
## To remove the project, use:
##   remove.snmfProject("genoM.snmfProject")
##
## [1] 454649935
## [1] "*****"
## [1] "*"          create.dataset          "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -s (seed random init)           454649935
##      -r (percentage of masked data)  0.05
##      -x (genotype file in .geno format) C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genoM.geno
##      -o (output file in .geno format)  C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genoM.snmf/masked/genoM_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
oM.snmf/masked/genoM_I.geno:      OK.
##
## [1] "*****"
## [1] "* sNMF K = 4  repetition 3      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   4
##      -x (input file)                  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/masked/genoM_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run3/genoM_r3.4.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run3/genoM_r3.4.G
##      -i (number max of iterations)    200
##      -a (regularization parameter)    10
##      -s (seed random init)            454649935
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genoM.snmf/masked/genoM
_I.geno:      OK.
##
##
## Main algorithm:
## [

```

```

## [=====]
## Number of iterations: 70
##
## Least-square error: 5465.808076
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run3/genoM_r3.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genoM.snmf/K4/run3/genoM_r3.4.G:  OK.
##
## [1] "*****"
## [1] "*"      cross-entropy estimation      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   4
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genoM.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run3/genoM_r3.4.Q
##      -g (ancestral frequencies)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run3/genoM_r3.4.G
##      -i (with masked genotypes)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/masked/genoM_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.451796
## Cross-Entropy (masked data):  0.650007
## The project is saved into :
##  genoM.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genoM.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genoM.snmfProject")
##
## [1] 1387684980
## [1] "*****"
## [1] "*"      create.dataset      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -s (seed random init)           1387684980
##      -r (percentage of masked data)  0.05
##      -x (genotype file in .geno format) C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genoM.geno
##      -o (output file in .geno format) C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genoM.snmf/masked/genoM_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
oM.snmf/masked/genoM_I.geno:      OK.
##

```

```

## [1] "*****"
## [1] "* sNMF K = 4  repetition 4      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/masked/genoM_I.geno
##      -q (individual admixture file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run4/genoM_r4.4.Q
##      -g (ancestral frequencies file) C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run4/genoM_r4.4.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           1387684980
##      -e (tolerance error)             1E-05
##      -p (number of processes)        1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genoM.snmf/masked/genoM
_I.geno:      OK.
##
##
## Main algorithm:
##      [                                     ]
##      [=====]
## Number of iterations: 49
##
## Least-square error: 5466.929144
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run4/genoM_r4.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genoM.snmf/K4/run4/genoM_r4.4.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genoM.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run4/genoM_r4.4.Q
##      -g (ancestral frequencies)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run4/genoM_r4.4.G
##      -i (with masked genotypes)     C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/masked/genoM_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.451687
## Cross-Entropy (masked data):  0.592779

```

```

## The project is saved into :
##  genoM.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genoM.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genoM.snmfProject")
##
## [1] 1343355475
## [1] "*****"
## [1] "*"          create.dataset          "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -s (seed random init)              1343355475
##      -r (percentage of masked data)     0.05
##      -x (genotype file in .geno format) C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genoM.geno
##      -o (output file in .geno format)   C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genoM.snmf/masked/genoM_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
oM.snmf/masked/genoM_I.geno:      OK.
##
## [1] "*****"
## [1] "*" sNMF K = 4  repetition 5      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      4
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/masked/genoM_I.geno
##      -q (individual admixture file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run5/genoM_r5.4.Q
##      -g (ancestral frequencies file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run5/genoM_r5.4.G
##      -i (number max of iterations)     200
##      -a (regularization parameter)     10
##      -s (seed random init)              1343355475
##      -e (tolerance error)               1E-05
##      -p (number of processes)          1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genoM.snmf/masked/genoM
_I.geno:      OK.
##
##
## Main algorithm:
## [
## [=====]
## Number of iterations: 85

```

```

##
## Least-square error: 5503.265703
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/
c/genoM.snmf/K4/run5/genoM_r5.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genoM.snmf/K4/run5/genoM_r5.4.G:  OK.
##
## [1] "*****"
## [1] "*"      cross-entropy estimation      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of ancestral pops)   4
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genoM.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run5/genoM_r5.4.Q
##      -g (ancestral frequencies)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run5/genoM_r5.4.G
##      -i (with masked genotypes)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/masked/genoM_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.452355
## Cross-Entropy (masked data):  0.613331
## The project is saved into :
##  genoM.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genoM.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genoM.snmfProject")
##
## [1] 1586640836
## [1] "*****"
## [1] "*"      create.dataset      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -s (seed random init)           1586640836
##      -r (percentage of masked data)  0.05
##      -x (genotype file in .geno format) C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genoM.geno
##      -o (output file in .geno format) C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genoM.snmf/masked/genoM_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
oM.snmf/masked/genoM_I.geno:      OK.
##
## [1] "*****"
## [1] "*" sNMF K = 4  repetition 6      "*"

```



```

## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (input file)                 C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/masked/genoM_I.geno
##      -q (individual admixture file)   C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run6/genoM_r6.4.Q
##      -g (ancestral frequencies file)  C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run6/genoM_r6.4.G
##      -i (number max of iterations)   200
##      -a (regularization parameter)   10
##      -s (seed random init)           1586640836
##      -e (tolerance error)             1E-05
##      -p (number of processes)         1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genoM.snmf/masked/genoM
_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 59
##
## Least-square error: 5472.899392
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run6/genoM_r6.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genoM.snmf/K4/run6/genoM_r6.4.G:  OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genoM.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run6/genoM_r6.4.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run6/genoM_r6.4.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/masked/genoM_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.453102
## Cross-Entropy (masked data):  0.558926
## The project is saved into :
##  genoM.snmfProject

```

```

##
## To load the project, use:
## project = load.snmfProject("genoM.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genoM.snmfProject")
##
## [1] 628146974
## [1] "*****"
## [1] "*"          create.dataset          "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -s (seed random init)              628146974
##      -r (percentage of masked data)      0.05
##      -x (genotype file in .geno format)  C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genoM.geno
##      -o (output file in .geno format)    C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genoM.snmf/masked/genoM_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
oM.snmf/masked/genoM_I.geno:      OK.
##
## [1] "*****"
## [1] "*" sNMF K = 4  repetition 7      "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      4
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/masked/genoM_I.geno
##      -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run7/genoM_r7.4.Q
##      -g (ancestral frequencies file)    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run7/genoM_r7.4.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              628146974
##      -e (tolerance error)                1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genoM.snmf/masked/genoM
_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 74
##
## Least-square error: 5455.788943

```

```

## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run7/genoM_r7.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genoM.snmf/K4/run7/genoM_r7.4.G:  OK.
##
## [1] "*****"
## [1] "*      cross-entropy estimation      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genoM.geno
##      -q (individual admixture)       C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run7/genoM_r7.4.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run7/genoM_r7.4.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/masked/genoM_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.45124
## Cross-Entropy (masked data):  0.626201
## The project is saved into :
##  genoM.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genoM.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genoM.snmfProject")
##
## [1] 1412192888
## [1] "*****"
## [1] "*      create.dataset      *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -s (seed random init)          1412192888
##      -r (percentage of masked data)  0.05
##      -x (genotype file in .geno format) C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genoM.geno
##      -o (output file in .geno format) C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genoM.snmf/masked/genoM_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
oM.snmf/masked/genoM_I.geno:      OK.
##
## [1] "*****"
## [1] "* sNMF K = 4 repetition 8      *"
## [1] "*****"
## summary of the options:

```

```

##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      4
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/masked/genoM_I.geno
##      -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run8/genoM_r8.4.Q
##      -g (ancestral frequencies file)     C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run8/genoM_r8.4.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              1412192888
##      -e (tolerance error)                1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genoM.snmf/masked/genoM
_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 80
##
## Least-square error: 5443.576918
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run8/genoM_r8.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genoM.snmf/K4/run8/genoM_r8.4.G:  OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      4
##      -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genoM.geno
##      -q (individual admixture)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run8/genoM_r8.4.Q
##      -g (ancestral frequencies)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run8/genoM_r8.4.G
##      -i (with masked genotypes)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/masked/genoM_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.452404
## Cross-Entropy (masked data):  0.570813
## The project is saved into :
##   genoM.snmfProject
##
## To load the project, use:

```

```

## project = load.snmfProject("genoM.snmfProject")
##
## To remove the project, use:
## remove.snmfProject("genoM.snmfProject")
##
## [1] 1344190298
## [1] "*****"
## [1] "*"          create.dataset          "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -s (seed random init)              1344190298
##      -r (percentage of masked data)      0.05
##      -x (genotype file in .geno format)  C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genoM.geno
##      -o (output file in .geno format)    C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genoM.snmf/masked/genoM_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
oM.snmf/masked/genoM_I.geno:      OK.
##
## [1] "*****"
## [1] "* sNMF K = 4  repetition 9          *"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)          50
##      -L (number of loci)                400
##      -K (number of ancestral pops)      4
##      -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/masked/genoM_I.geno
##      -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run9/genoM_r9.4.Q
##      -g (ancestral frequencies file)    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run9/genoM_r9.4.G
##      -i (number max of iterations)      200
##      -a (regularization parameter)      10
##      -s (seed random init)              1344190298
##      -e (tolerance error)               1E-05
##      -p (number of processes)           1
##      - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genoM.snmf/masked/genoM
_I.geno:      OK.
##
##
## Main algorithm:
## [ ]
## [=====]
## Number of iterations: 60
##
## Least-square error: 5491.667055
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run9/genoM_r9.4.Q:      OK.

```

```

## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genoM.snmf/K4/run9/genoM_r9.4.G: OK.
##
## [1] "*****"
## [1] "*" cross-entropy estimation "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -K (number of ancestral pops)   4
##      -x (genotype file)              C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genoM.geno
##      -q (individual admixture)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run9/genoM_r9.4.Q
##      -g (ancestral frequencies)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run9/genoM_r9.4.G
##      -i (with masked genotypes)      C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/masked/genoM_I.geno
##      - diploid
##
## Cross-Entropy (all data):      0.452224
## Cross-Entropy (masked data):  0.613456
## The project is saved into :
##  genoM.snmfProject
##
## To load the project, use:
##  project = load.snmfProject("genoM.snmfProject")
##
## To remove the project, use:
##  remove.snmfProject("genoM.snmfProject")
##
## [1] 1364489729
## [1] "*****"
## [1] "*" create.dataset "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)            400
##      -s (seed random init)          1364489729
##      -r (percentage of masked data)  0.05
##      -x (genotype file in .geno format) C:\Users\llpo0001\Documents\slubi\3bs\p
op_struc\genoM.geno
##      -o (output file in .geno format) C:/Users/llpo0001/Documents/slubi/3bs/p
op_struc/genoM.snmf/masked/genoM_I.geno
##
## Write genotype file with masked data, C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/gen
oM.snmf/masked/genoM_I.geno: OK.
##
## [1] "*****"
## [1] "*" sNMF K = 4 repetition 10 "*"
## [1] "*****"
## summary of the options:
##
##      -n (number of individuals)      50

```

```

##          -L (number of loci)                400
##          -K (number of ancestral pops)       4
##          -x (input file)                    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/masked/genoM_I.geno
##          -q (individual admixture file)      C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run10/genoM_r10.4.Q
##          -g (ancestral frequencies file)    C:/Users/llpo0001/Documents/slubi/3bs/pop_s
truc/genoM.snmf/K4/run10/genoM_r10.4.G
##          -i (number max of iterations)      200
##          -a (regularization parameter)      10
##          -s (seed random init)              1364489729
##          -e (tolerance error)               1E-05
##          -p (number of processes)           1
##          - diploid
##
## Read genotype file C:/Users/llpo0001/Documents/slubi/3bs/pop_struc/genoM.snmf/masked/genoM
_I.geno:      OK.
##
##
## Main algorithm:
## [                                                ]
## [=====]
## Number of iterations: 19
##
## Least-square error: 5464.267372
## Write individual ancestry coefficient file C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run10/genoM_r10.4.Q:      OK.
## Write ancestral allele frequency coefficient file C:/Users/llpo0001/Documents/slubi/3bs/po
p_struc/genoM.snmf/K4/run10/genoM_r10.4.G: OK.
##
## [1] "*****"
## [1] "*"   cross-entropy estimation   "*"
## [1] "*****"
## summary of the options:
##
##          -n (number of individuals)          50
##          -L (number of loci)                400
##          -K (number of ancestral pops)       4
##          -x (genotype file)                  C:\Users\llpo0001\Documents\slubi\3bs\pop_struc
\genoM.geno
##          -q (individual admixture)          C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run10/genoM_r10.4.Q
##          -g (ancestral frequencies)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/K4/run10/genoM_r10.4.G
##          -i (with masked genotypes)        C:/Users/llpo0001/Documents/slubi/3bs/pop_stru
c/genoM.snmf/masked/genoM_I.geno
##          - diploid
##
## Cross-Entropy (all data):      0.452302
## Cross-Entropy (masked data):  0.605012
## The project is saved into :
##   genoM.snmfProject
##
## To load the project, use:
##   project = load.snmfProject("genoM.snmfProject")
##

```

```
## To remove the project, use:  
## remove.snmfProject("genoM.snmfProject")
```

```
# select the run with the lowest cross-entropy value  
best = which.min(cross.entropy(project.missing, K = 4))  
  
# Impute the missing genotypes  
impute(project.missing, "genoM.lfmm",  
        method = 'mode', K = 4, run = best)
```

```
## Missing genotype imputation for K = 4  
## Missing genotype imputation for run = 6  
## Results are written in the file: genoM.lfmm_imputed.lfmm
```

```
# Proportion of correct imputation results  
dat.imp = read.lfmm("genoM.lfmm_imputed.lfmm")  
mean( tutorial.R[dat == 9] == dat.imp[dat == 9] )
```

```
## [1] 0.79
```

```
# main options:  
# K = the number of latent factors  
# Runs with K = 6 using 5 repetitions.  
project = NULL  
project = lfmm("genotypes.lfmm",  
              "gradients.env",  
              K = 6,  
              repetitions = 5,  
              project = "new")
```



```

## The project is saved into :
##   genotypes_gradients.lfmmProject
##
## To load the project, use:
##   project = load.lfmmProject("genotypes_gradients.lfmmProject")
##
## To remove the project, use:
##   remove.lfmmProject("genotypes_gradients.lfmmProject")
##
## [1] "*****"
## [1] "* K = 6  repetition 1  d = 1  *"
## [1] "*****"
## Summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of latent factors)   6
##      -o (output file)                genotypes_gradients.lfmm/K6/run1/genotypes_r1
##      -i (number of iterations)       10000
##      -b (burnin)                     5000
##      -s (seed random init)           1995548244
##      -p (number of processes (CPU))  1
##      -x (genotype file)              genotypes.lfmm
##      -v (variable file)              gradients.env
##      -D (number of covariables)      1
##      -d (the dth covariable)         1
##
## Read variable file:
##   gradients.env      OK.
##
## Read genotype file:
##   genotypes.lfmm     OK.
##
## <<<<
##   Analyse for variable 1
##
##       Start of the Gibbs Sampler algorithm.
##
##   [
##   [=====]
##
##       End of the Gibbs Sampler algorithm.
##
##   ED:20000.37202   DIC: 19991.73639
##
## The statistics for the run are registered in:
##   genotypes_gradients.lfmm/K6/run1/genotypes_r1_s1.6.dic.
##
## The zscores for variable 1 are registered in:
##   genotypes_gradients.lfmm/K6/run1/genotypes_r1_s1.6.zscore.
## The columns are: zscores, -log10(p-values), p-values.
##
## -----
## The execution for variable 1 worked without error.
## >>>>

```

```

##
## The project is saved into :
##   genotypes_gradients.lfmmProject
##
## To load the project, use:
##   project = load.lfmmProject("genotypes_gradients.lfmmProject")
##
## To remove the project, use:
##   remove.lfmmProject("genotypes_gradients.lfmmProject")
##
## [1] "*****"
## [1] "* K = 6  repetition 2  d = 1  *"
## [1] "*****"
## Summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of latent factors)   6
##      -o (output file)                genotypes_gradients.lfmm/K6/run2/genotypes_r2
##      -i (number of iterations)       10000
##      -b (burnin)                     5000
##      -s (seed random init)           719718538
##      -p (number of processes (CPU))  1
##      -x (genotype file)              genotypes.lfmm
##      -v (variable file)              gradients.env
##      -D (number of covariables)      1
##      -d (the dth covariable)         1
##
## Read variable file:
##   gradients.env      OK.
##
## Read genotype file:
##   genotypes.lfmm     OK.
##
## <<<<
##   Analyse for variable 1
##
##       Start of the Gibbs Sampler algorithm.
##
##   [
##   [=====]
##
##       End of the Gibbs Sampler algorithm.
##
##   ED:20000.30802    DIC: 19934.78652
##
##   The statistics for the run are registered in:
##       genotypes_gradients.lfmm/K6/run2/genotypes_r2_s1.6.dic.
##
##   The zscores for variable 1 are registered in:
##       genotypes_gradients.lfmm/K6/run2/genotypes_r2_s1.6.zscore.
##   The columns are: zscores, -log10(p-values), p-values.
##
##   -----
##   The execution for variable 1 worked without error.
##   >>>>

```

```

##
## The project is saved into :
##   genotypes_gradients.lfmmProject
##
## To load the project, use:
##   project = load.lfmmProject("genotypes_gradients.lfmmProject")
##
## To remove the project, use:
##   remove.lfmmProject("genotypes_gradients.lfmmProject")
##
## [1] "*****"
## [1] "* K = 6  repetition 3  d = 1  *"
## [1] "*****"
## Summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of latent factors)   6
##      -o (output file)                genotypes_gradients.lfmm/K6/run3/genotypes_r3
##      -i (number of iterations)       10000
##      -b (burnin)                     5000
##      -s (seed random init)           70780825
##      -p (number of processes (CPU))  1
##      -x (genotype file)              genotypes.lfmm
##      -v (variable file)              gradients.env
##      -D (number of covariables)      1
##      -d (the dth covariable)         1
##
## Read variable file:
##   gradients.env      OK.
##
## Read genotype file:
##   genotypes.lfmm     OK.
##
## <<<<
##   Analyse for variable 1
##
##       Start of the Gibbs Sampler algorithm.
##
##   [
##   [=====]
##
##       End of the Gibbs Sampler algorithm.
##
##   ED:20000.2911      DIC: 19944.01793
##
##   The statistics for the run are registered in:
##       genotypes_gradients.lfmm/K6/run3/genotypes_r3_s1.6.dic.
##
##   The zscores for variable 1 are registered in:
##       genotypes_gradients.lfmm/K6/run3/genotypes_r3_s1.6.zscore.
##   The columns are: zscores, -log10(p-values), p-values.
##
##   -----
##   The execution for variable 1 worked without error.
##   >>>>

```

```

##
## The project is saved into :
##   genotypes_gradients.lfmmProject
##
## To load the project, use:
##   project = load.lfmmProject("genotypes_gradients.lfmmProject")
##
## To remove the project, use:
##   remove.lfmmProject("genotypes_gradients.lfmmProject")
##
## [1] "*****"
## [1] "* K = 6  repetition 4  d = 1  *"
## [1] "*****"
## Summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of latent factors)   6
##      -o (output file)                genotypes_gradients.lfmm/K6/run4/genotypes_r4
##      -i (number of iterations)       10000
##      -b (burnin)                     5000
##      -s (seed random init)           1921232980
##      -p (number of processes (CPU))  1
##      -x (genotype file)              genotypes.lfmm
##      -v (variable file)              gradients.env
##      -D (number of covariables)      1
##      -d (the dth covariable)         1
##
## Read variable file:
##   gradients.env      OK.
##
## Read genotype file:
##   genotypes.lfmm     OK.
##
## <<<<
##   Analyse for variable 1
##
##       Start of the Gibbs Sampler algorithm.
##
##   [
##   [=====]
##
##       End of the Gibbs Sampler algorithm.
##
##   ED:20000.4082      DIC: 19950.59112
##
##   The statistics for the run are registered in:
##       genotypes_gradients.lfmm/K6/run4/genotypes_r4_s1.6.dic.
##
##   The zscores for variable 1 are registered in:
##       genotypes_gradients.lfmm/K6/run4/genotypes_r4_s1.6.zscore.
##   The columns are: zscores, -log10(p-values), p-values.
##
##   -----
##   The execution for variable 1 worked without error.
##   >>>>

```

```

##
## The project is saved into :
##   genotypes_gradients.lfmmProject
##
## To load the project, use:
##   project = load.lfmmProject("genotypes_gradients.lfmmProject")
##
## To remove the project, use:
##   remove.lfmmProject("genotypes_gradients.lfmmProject")
##
## [1] "*****"
## [1] "* K = 6  repetition 5  d = 1  *"
## [1] "*****"
## Summary of the options:
##
##      -n (number of individuals)      50
##      -L (number of loci)             400
##      -K (number of latent factors)   6
##      -o (output file)                genotypes_gradients.lfmm/K6/run5/genotypes_r5
##      -i (number of iterations)       10000
##      -b (burnin)                     5000
##      -s (seed random init)           2142529601
##      -p (number of processes (CPU))  1
##      -x (genotype file)              genotypes.lfmm
##      -v (variable file)              gradients.env
##      -D (number of covariables)      1
##      -d (the dth covariable)         1
##
## Read variable file:
##   gradients.env      OK.
##
## Read genotype file:
##   genotypes.lfmm     OK.
##
## <<<<
##   Analyse for variable 1
##
##       Start of the Gibbs Sampler algorithm.
##
##   [
##   [=====]
##
##       End of the Gibbs Sampler algorithm.
##
##   ED:20000.31517    DIC: 19996.62196
##
##   The statistics for the run are registered in:
##       genotypes_gradients.lfmm/K6/run5/genotypes_r5_s1.6.dic.
##
##   The zscores for variable 1 are registered in:
##       genotypes_gradients.lfmm/K6/run5/genotypes_r5_s1.6.zscore.
##   The columns are: zscores, -log10(p-values), p-values.
##
##   -----
##   The execution for variable 1 worked without error.
##   >>>>

```

```
##
## The project is saved into :
##   genotypes_gradients.lfmmProject
##
## To load the project, use:
##   project = load.lfmmProject("genotypes_gradients.lfmmProject")
##
## To remove the project, use:
##   remove.lfmmProject("genotypes_gradients.lfmmProject")
```

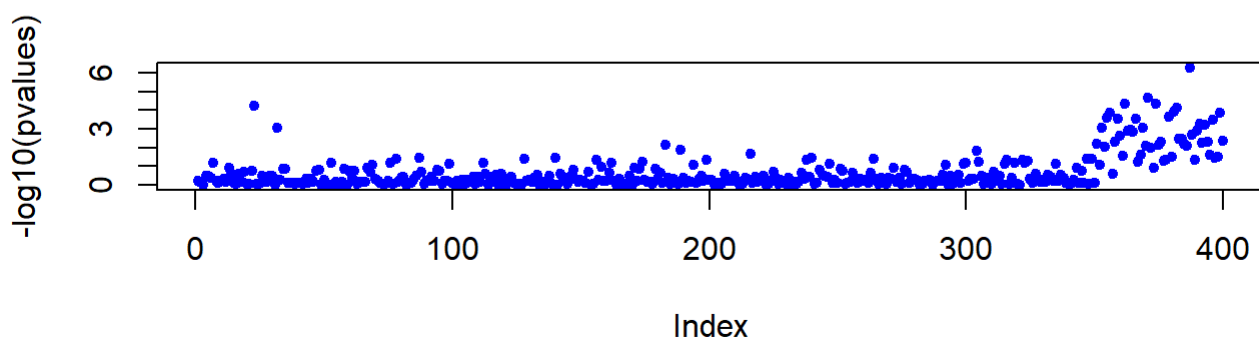
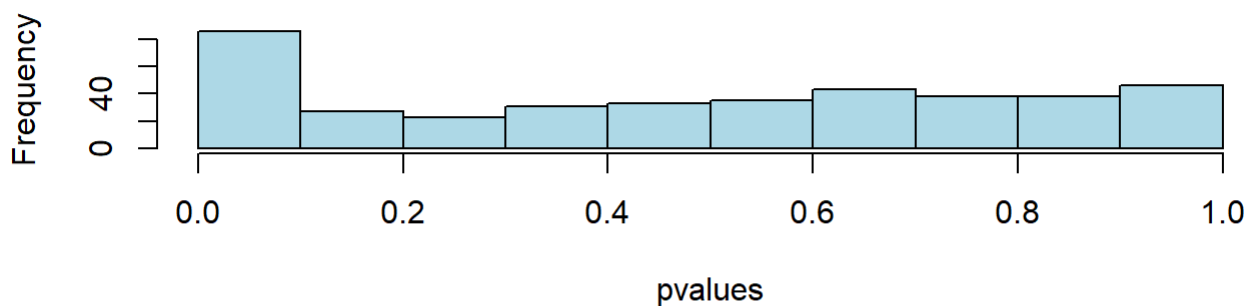
lfmm uses a very naive imputation method which has low power when genotypes are missing: See `impute()` for a better imputation method.

Note that lfmm has an improved estimation algorithm implemented in lfmm2, which should be the preferred option.

```
p = lfmm.pvalues(project, K = 6)
pvalues = p$pvalues
```

```
# GEA significance test
par(mfrow = c(2,1))
hist(pvalues, col = "lightblue")
plot(-log10(pvalues), pch = 19, col = "blue", cex = .7)
```

Histogram of pvalues



```

for (alpha in c(.05,.1,.15,.2)) {
  # expected FDR
  print(paste("Expected FDR:", alpha))
  L = length(pvalues)

  # return a list of candidates with expected FDR alpha.
  # Benjamini-Hochberg's algorithm:
  w = which(sort(pvalues) < alpha * (1:L) / L)
  candidates = order(pvalues)[w]

  # estimated FDR and True Positive Rate
  Lc = length(candidates)
  estimated.FDR = sum(candidates <= 350)/Lc
  print(paste("Observed FDR:",
              round(estimated.FDR, digits = 2)))
  estimated.TPR = sum(candidates > 350)/50
  print(paste("Estimated TPR:",
              round(estimated.TPR, digits = 2)))
}

```

```

## [1] "Expected FDR: 0.05"
## [1] "Observed FDR: 0.08"
## [1] "Estimated TPR: 0.46"
## [1] "Expected FDR: 0.1"
## [1] "Observed FDR: 0.08"
## [1] "Estimated TPR: 0.72"
## [1] "Expected FDR: 0.15"
## [1] "Observed FDR: 0.12"
## [1] "Estimated TPR: 0.74"
## [1] "Expected FDR: 0.2"
## [1] "Observed FDR: 0.12"
## [1] "Estimated TPR: 0.74"

```

```

# Load simulated data
data("offset_example")
# 200 diploid individuals genotyped at 510 SNP
Y <- offset_example$geno
# 4 environmental variables
X <- offset_example$env

mod.lfmm2 <- lfmm2(input = Y, env = X, K = 2)

```

GEA: Genome-Environment Associations

```

# GEA significance test
# showing the K = 2 estimated factors
plot(mod.lfmm2@U, col = "grey", pch = 19,
     xlab = "Factor 1",
     ylab = "Factor 2")

```

