NA

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Abstract

This vignette provides an introductory tutorial to the *aflpsim* package [**?**] for the R software [**?**]. This package implements tools to handle, analyse and simulate hybridization using dominant data such as Amplified Fragment Length Polymorphism data (AFLP). *AFLPsim* also implements several genome scan methods. This vignette introduces basic functionalities of the package.

Contents

1 Introduction

This tutorial introduces some basic functionalities of the *AFLPsim* package for R [**?**]. The purpose of this package is to provide tools for handling, analysing and simulating genetic markers data,

Data can be imported from a wide range of formats, including those of popular software (GENETIX, STRUCTURE, Fstat, Genepop), or from simple dataframes of genotypes. Polymorphic sites can be extracted from both nucleotide and amino-acid sequences, with special methods for handling genome-wide SNPs data with maximum efficiency.

In this tutorial, we first introduce the hybrid simulation, and then show how to performe some genome scan methods

2 Getting started

2.1 Installing the package

Before going further, we shall make sure that *adegenet* is well installed on the computer. Current version of the package is 1.3-6. Make sure you have a recent version of R ($\geq$ 2.13.0) by typing:

```
> R.version.string
```

```
[1] "R version 2.15.3 (2013-03-01)"
```

Then, install *adegenet* with dependencies using:

```
> install.packages("adegenet", dep=TRUE)
```

This only installs packages on CRAN. However, some functions in *adegenet* also use *graph*, developed on Bioconductor, an alternative package repository. To install *graph*, type:

```
> source("http://bioconductor.org/biocLite.R")
> biocLite("graph")
```

We can now load the package using:

```
> library(adegenet)
```

You can make sure that the right version of the package is installed using:

```
> packageDescription("aflpsim", fields = "Version")
```

```
[1] NA
```

NA

3 Hybrid simulation

Two functions sare used for simulate hybrids using dominant markers, depending if we have parentals data or we want a simulation from zero: `hybridsim` is used for randomly simulate two populations and hybridize them whereas `hybridize` is used for simulate hybrids from known parental populations. Note that the term 'population', here and later, is employed in a broad sense: it simply refers to any grouping of individuals.

3.1 Complete simulation

These objects can be obtained by reading data files from other software, from a `data.frame` of genotypes, by conversion from a table of allelic frequencies, or even from aligned DNA or proteic sequences (see 'importing data'). Here, we introduce this class using the dataset `nancycats`, which is already stored as a `genind` object:

```
> data(nancycats)
> is.genind(nancycats)


[1] TRUE


> nancycats


   ######################
   ### Genind object ###
   ######################
- genotypes of individuals -

S4 class:  genind
@call: genind(tab = truenames(nancycats)$tab, pop = truenames(nancycats)$pop)

@tab:  237 x 108 matrix of genotypes

@ind.names: vector of  237 individual names
@loc.names: vector of  9 locus names
@loc.nall: number of alleles per locus
@loc.fac: locus factor for the  108 columns of @tab
@all.names: list of  9 components yielding allele names for each locus
@ploidy:  2
@type:  codom

Optionnal contents:
@pop:  factor giving the population of each individual
@pop.names:  factor giving the population of each individual

@other: a list containing: xy
```

A `genind` object is formal S4 object with several slots, accessed using the '`@`' operator (see `class?genind`). Note that the '`$`' is also implemented for adegenet objects, so that slots can be accessed as if they were components of a list.

The structure of `genind` objects is described by:

```
> getClassDef("genind")
```

```
Class "genind" [package "adegenet"]

Slots:

Name:           tab    loc.names      loc.fac     loc.nall    all.names
Class:       matrix    character factorOrNULL     intOrNum   listOrNULL

Name:          call    ind.names          pop    pop.names       ploidy
Class:   callOrNULL    character factorOrNULL   charOrNULL      integer

Name:          type        other
Class:    character   listOrNULL

Extends: "gen", "indInfo"
```

The slightly cryptic output of this function means that `genind` objects possess the following slots:

- `tab`: a matrix of relative allele frequencies (individuals in rows, alleles in columns).
- `loc.names`: a vector of labels for the loci.
- `loc.fac`: a factor indicating which columns in `@tab` correspond to which marker.
- `loc.nall`: the number of alleles in each marker.
- `all.names`: a vector of labels for the alleles.
- `ind.names`: a vector of labels for the individuals.
- `pop`: a factor storing group membership of the individuals.
- `pop.names`: labels used for populations.
- `ploidy`: a single integer indicating the ploidy of the individuals.
- `type`: a character string indicating whether the marker is codominant (`codom`) or presence/absence (`PA`).
- `other`: a list storing optional information.
- `call`: the matched call, i.e. command used to create the object.

Slots can be accessed using '`@`' or '`$`', although in some cases it is more convenient to use accessors (i.e. functions which return specific contents of the object) than accessing the slot directly (see section 'Using accessors').

The main slot in `genind` is the table of allelic frequencies of individuals (in rows) for every alleles in every loci stored in `@tab`. Being frequencies, data sum to one per locus, giving the score of 1 for an homozygote and 0.5 for a diploid heterozygote. The particular case of presence/absence data is described in a dedicated section (see 'Handling presence/absence data'). For instance:

```
> nancycats$tab[10:18,1:10]
```

```
    L1.01 L1.02 L1.03 L1.04 L1.05 L1.06 L1.07 L1.08 L1.09 L1.10
010     0     0     0     0     0   0.0   0.0   0.0   1.0   0.0
011     0     0     0     0     0   0.0   0.0   0.0   0.0   0.5
012     0     0     0     0     0   0.5   0.0   0.5   0.0   0.0
013     0     0     0     0     0   0.5   0.0   0.5   0.0   0.0
014     0     0     0     0     0   0.0   0.0   1.0   0.0   0.0
015     0     0     0     0     0   0.0   0.5   0.0   0.5   0.0
016     0     0     0     0     0   0.5   0.0   0.0   0.5   0.0
017     0     0     0     0     0   0.5   0.0   0.5   0.0   0.0
018     0     0     0     0     0   0.5   0.0   0.0   0.5   0.0
```

Individual '010' is an homozygote for the allele 09 at locus 1, while '018' is an heterozygote with alleles 06 and 09. As user-defined labels are not always valid (for instance, they can be duplicated), generic labels are used for individuals, markers, alleles and eventually population. The true names are stored in the object (components `$[...].names` where `$[...]` can be `ind`, `loc`, `all` or `pop`). For instance :

```
> nancycats$loc.names
```

```
    L1      L2      L3      L4      L5      L6      L7      L8      L9
"fca8" "fca23" "fca43" "fca45" "fca77" "fca78" "fca90" "fca96" "fca37"
```

gives the true marker names, and

```
> nancycats$all.names[[3]]
```

```
   01    02    03    04    05    06    07    08    09    10
"133" "135" "137" "139" "141" "143" "145" "147" "149" "157"
```

gives the allele names for marker 3.

The slot 'ploidy' is an integer giving the level of ploidy of the considered organisms (defaults to 2). This parameter is essential, in particular when switching from individual frequencies (`genind` object) to allele counts per populations (`genpop`).
The slot 'type' describes the type of marker used: codominant (`codom`, e.g. microsatellites) or presence/absence (`PA`, e.g. AFLP). By default, adegenet considers that markers are codominant. Note that actual handling of presence/absence markers has been made available since version 1.2-3. See the dedicated section for more information about presence/absence markers.

Optional content can are also be stored within the object. The slot `@other` is a list that can include any additional information. The optional slot `@pop` (a factor giving a grouping of individuals) is particular in that the behaviour of many functions will check automatically its content and behave accordingly. In fact, each time an argument 'pop' is required by a function, it is first seeked in `@pop`. For instance, using the function `genind2genpop` to convert `nancycats` to a `genpop` object, there is no need to give a 'pop' argument as it exists in the `genind` object:

```
> head(pop(nancycats))
```

```
[1] 1 1 1 1 1 1
Levels: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17

> catpop <- genind2genpop(nancycats)

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

...done.

> catpop

       ######################
       ### Genpop object ###
       ######################
- Alleles counts for populations -

S4 class:  genpop
@call: genind2genpop(x = nancycats)

@tab:  17 x 108 matrix of alleles counts

@pop.names: vector of  17 population names
@loc.names: vector of  9 locus names
@loc.nall: number of alleles per locus
@loc.fac: locus factor for the  108 columns of @tab
@all.names: list of  9 components yielding allele names for each locus
@ploidy:  2
@type:  codom

@other: a list containing: xy
```

Other additional components can be stored (like here, spatial coordinates of populations in $xy) and processed during the conversion if the argument `process.other` is set to `TRUE`. In this case, numeric vectors with a length corresponding to the number of individuals will we averaged per groups; note that any other function than `mean` can be used by providing any function to the argument `other.action`. Matrices with a number of rows corresponding to the number of individuals are processed similarly.

Finally, a `genind` object generally contains its matched call, *i.e.* the instruction that created it. When call is available, it can be used to regenerate an object.

```
> obj <- read.genetix(system.file("files/nancycats.gtx",package="adegenet"))

 Converting data from GENETIX to a genind object...

...done.

> obj$call

read.genetix(file = system.file("files/nancycats.gtx", package = "adegenet"))

> toto <- eval(obj$call)

 Converting data from GENETIX to a genind object...

...done.

> identical(obj,toto)

[1] TRUE
```

3.2 genpop objects

We use the previously built `genpop` object:

```
> catpop


       ######################
       ### Genpop object ###
       ######################
- Alleles counts for populations -

S4 class:  genpop
@call: genind2genpop(x = nancycats)

@tab:  17 x 108 matrix of alleles counts

@pop.names: vector of  17 population names
@loc.names: vector of  9 locus names
@loc.nall: number of alleles per locus
@loc.fac: locus factor for the  108 columns of @tab
@all.names: list of  9 components yielding allele names for each locus
@ploidy:  2
@type:  codom

@other: a list containing: xy


> is.genpop(catpop)


[1] TRUE


> catpop$tab[1:5,1:10]


   L1.01 L1.02 L1.03 L1.04 L1.05 L1.06 L1.07 L1.08 L1.09 L1.10
01     0     0     0     0     0     0     0     2     9     1
02     0     0     0     0     0    10     9     8    14     2
03     0     0     0     4     0     0     0     0     1    10
04     0     0     0     3     0     0     0     1     7    17
05     0     0     0     1     0     0     0     0     7    10
```

The matrix $tab contains alleles counts per population (here, cat colonies). These objects are otherwise very similar to `genind` in their structure, and possess generic names, true names, the matched call and an `@other` slot:

```
> getClassDef("genpop")


Class "genpop" [package "adegenet"]

Slots:

Name:           tab    loc.names      loc.fac     loc.nall    all.names
Class:       matrix    character factorOrNULL     intOrNum   listOrNULL

Name:          call    pop.names       ploidy         type        other
Class:   callOrNULL    character      integer    character   listOrNULL

Extends: "gen", "popInfo"
```

3.3 Using accessors

One advantage of formal (S4) classes is that they allow for interacting simply with possibly complex objects. This is made possible by using accessors, i.e. functions that extract information from an object, rather than accessing the slots directly. Another advantage of this approach is that as long as accessors remain identical on the user's side, the internal structure of an object may change from one release to another without generating errors in old scripts. Although `genind` and `genpop` objects are fairly simple, we recommend using accessors whenever possible to access their content.

Available accessors are:

- `nInd`: returns the number of individuals in the object; only for `genind`.
- `nLoc`: returns the number of loci (SNPs).
- `indNames`†: returns/sets labels for individuals; only for `genind`.
- `locNames`†: returns/sets labels for loci (SNPs).
- `alleles`†: returns/sets alleles.
- `ploidy`†: returns/sets ploidy of the individuals.
- `pop`†: returns/sets a factor grouping individuals; only for `genind`.
- `other`†: returns/sets misc information stored as a list.

where † indicates that a replacement method is available using `<-`; for instance:

```
> head(indNames(nancycats),10)
```

```
   001    002    003    004    005    006    007    008    009    010
"N215" "N216" "N217" "N218" "N219" "N220" "N221" "N222" "N223" "N224"
```

```
> indNames(nancycats) <- paste("cat", 1:nInd(nancycats),sep=".")
> head(indNames(nancycats),10)
```

```
    001      002      003      004      005      006      007      008
 "cat.1"  "cat.2"  "cat.3"  "cat.4"  "cat.5"  "cat.6"  "cat.7"  "cat.8"
    009      010
 "cat.9" "cat.10"
```

Some accessors such as `locNames` may have specific options; for instance:

```
> locNames(nancycats)
```

```
    L1      L2      L3      L4      L5      L6      L7      L8      L9
 "fca8" "fca23" "fca43" "fca45" "fca77" "fca78" "fca90" "fca96" "fca37"
```

returns the names of the loci, while:

```
> temp <- locNames(nancycats, withAlleles=TRUE)
> head(temp, 10)
```

```
 [1] "fca8.117" "fca8.119" "fca8.121" "fca8.123" "fca8.127" "fca8.129"
 [7] "fca8.131" "fca8.133" "fca8.135" "fca8.137"
```

returns the names of the alleles in the form 'loci.allele'.

The slot 'pop' can be retrieved and set using `pop`:

```
> obj <- nancycats[sample(1:50,10)]
> pop(obj)
```

```
 [1] 2 2 1 2 4 2 3 2 2 1
Levels: 2 1 4 3
```

```
> pop(obj) <- rep("newPop",10)
> pop(obj)
```

```
 [1] newPop newPop newPop newPop newPop newPop newPop newPop newPop newPop
Levels: newPop
```

An additional advantage of using accessors is they are most of the time safer to use. For instance, `pop<-` will check the length of the new group membership vector against the data, and complain if there is a mismatch. It also converts the provided replacement to a factor, while the command:

```
> obj@pop <- rep("newPop",10)
```

would generate an error (since replacement is not a factor).

4 Importing/exporting data

4.1 Importing data from GENETIX, STRUCTURE, FSTAT, Genepop

Data can be read from the software GENETIX (extension .gtx), STRUCTURE (.str or .stru), FSTAT (.dat) and Genepop (.gen) files, using the corresponding `read` function: `read.genetix`, `read.structure`, `read.fstat`, and `read.genepop`. These functions take as main argument the path (as a string of characters) to an input file, and produce a `genind` object. Alternatively, one can use the function `import2genind` which detects a file format from its extension and uses the appropriate routine. For instance:

```
> obj1 <- read.genetix(system.file("files/nancycats.gtx",package="adegenet"))

 Converting data from GENETIX to a genind object...
...done.

> obj2 <- import2genind(system.file("files/nancycats.gtx", package="adegenet"))

 Converting data from GENETIX to a genind object...
...done.

> all.equal(obj1,obj2)

[1] "Attributes: < Component 2: target, current do not match when deparsed >"

>
```

The only difference between `obj1` and `obj2` is their call (which is normal as they were obtained from different command lines).

4.2 Importing data from other software

Raw genetic markers data are often stored as tables with individuals in row and markers in column, where each entry is a character string coding the alleles possessed at one locus. Such data are easily imported into R as a `data.frame`, using for instance `read.table` for text files or `read.csv` for comma-separated text files. Then, the obtained `data.frame` can be converted into a `genind` object using `df2genind`.

There are only a few pre-requisite the data should meet for this conversion to be possible. The easiest and clearest way of coding data is using a separator between alleles. For instance, "80/78", "80|78", or "80,78" are different ways of coding a genotype at a microsatellite locus with alleles '80' and 78". Note that for haploid data, no separator shall be used. The only contraint when using

a separator is that the same separator is used in all the dataset. There are no contraints as to i) the type of separator used or ii) the ploidy of the data. These parameters can be set in `df2genind` through arguments `sep` and `ploidy`, respectively.

Alternatively, no separator may be used provided a fixed number of characters is used to code each allele. For instance, in a diploid organism, "0101" is an homozygote 1/1 while "1209" is a heterozygote 12/09 in a two-character per allele coding scheme. In a tetraploid system with one character per allele, "1209" will be understood as 1/2/0/9.

Here, we provide an example using randomly generated tetraploid data and no separator.

```
> temp <- lapply(1:30, function(i) sample(1:9, 4, replace=TRUE))
> temp <- sapply(temp, paste, collapse="")
> temp <- matrix(temp, nrow=10, dimnames=list(paste("ind",1:10), paste("loc",1:3)))
> temp


       loc 1  loc 2  loc 3
ind 1  "8716" "8993" "4698"
ind 2  "8943" "6442" "8857"
ind 3  "7714" "8445" "7826"
ind 4  "4799" "6435" "8331"
ind 5  "5221" "6767" "4246"
ind 6  "4579" "1135" "6815"
ind 7  "4519" "7765" "7338"
ind 8  "1693" "5137" "5669"
ind 9  "7622" "7133" "4472"
ind 10 "4891" "7869" "9779"


> obj <- df2genind(temp, ploidy=4, sep="")
> obj


   ####################
   ### Genind object ###
   ####################
- genotypes of individuals -

S4 class:  genind
@call: df2genind(X = temp, sep = "", ploidy = 4)

@tab:  10 x 27 matrix of genotypes

@ind.names: vector of  10 individual names
@loc.names: vector of  3 locus names
@loc.nall: number of alleles per locus
@loc.fac: locus factor for the  27 columns of @tab
@all.names: list of  3 components yielding allele names for each locus
@ploidy:  4
@type:  codom

Optionnal contents:
@pop:  - empty -
@pop.names:  - empty -

@other: - empty -
```

`obj` is a `genind` containing the same information, but recoded as a matrix of allele frequencies (`$tab` slot). We can check that the conversion was exact by converting back the object into a table of character strings (function `genind2df`):

```
> genind2df(obj, sep="|")
```

```
         loc 1   loc 2   loc 3
ind 1  1|6|7|8 3|8|9|9 4|6|8|9
ind 2  3|4|8|9 2|4|4|6 5|7|8|8
ind 3  1|4|7|7 4|4|5|8 2|6|7|8
ind 4  4|7|9|9 3|4|5|6 1|3|3|8
ind 5  1|2|2|5 6|6|7|7 2|4|4|6
ind 6  4|5|7|9 1|1|3|5 1|5|6|8
ind 7  1|4|5|9 5|6|7|7 3|3|7|8
ind 8  1|3|6|9 1|3|5|7 5|6|6|9
ind 9  2|2|6|7 1|3|3|7 2|4|4|7
ind 10 1|4|8|9 6|7|8|9 7|7|9|9
```

4.3 Handling presence/absence data

adegenet was primarly designed to handle codominant, multiallelic markers like microsatellites. However, dominant markers like AFLP can be used as well. In such a case, only presence/absence of alleles can be deduced accurately from the genotypes. This has several consequences, like the unability to compute allele frequencies. Hence, some functionalities in *adegenet* won't be available for dominant markers.

From version 1.2-3 of *adegenet*, the distinction between both types of markers is made by the slot `@type` of genind or genpop objects, which equals `codom` for codominant markers, and `PA` for presence/absence data. In the latter case, the 'tab' slot of a genind object no longer contains allele frequencies, but only presence/absence of alleles in a genotype. Similarly, the `tab` slot of a genpop object not longer contains counts of alleles in the populations; instead, it contains the number of genotypes in each population possessing at least one copy of the concerned alleles. Moreover, in the case of presence/absence, the slots 'loc.nall', 'loc.fac', and 'all.names' become useless, and are thus all set to NULL.

Objects of type 'PA' are otherwise handled like usual (type 'codom') objects. Operations that are not available for PA type will issue an appropriate error message.

Here is an example using a toy dataset 'AFLP.txt' that can be downloaded from the adegenet website, section 'Documentation':

```
> dat <- read.table(system.file("files/AFLP.txt",package="adegenet"), header=TRUE)
> dat
```

```
     loc1 loc2 loc3 loc4
indA    1    0    1    1
indB    0    1    1    1
indC    1    1    0    1
indD    0   NA    1   NA
indE    1    1    0    0
indF    1    0    1    1
indG    0    1    1    0
```

The function `df2genind` is used to obtain a genind object:

```
> obj <- genind(dat, ploidy=1, type="PA")
> obj
```

```
   ######################
   ### Genind object ###
   ######################
- genotypes of individuals -

S4 class:  genind
@call: genind(tab = dat, ploidy = 1, type = "PA")

@tab:  7 x 4 matrix of genotypes

@ind.names: vector of  7 individual names
@loc.names: vector of  4 locus names
@loc.nall: NULL
@loc.fac: NULL
@all.names: NULL
@ploidy:  1
@type:  PA

Optionnal contents:
@pop:  - empty -
@pop.names:  - empty -

@other: - empty -


> truenames(obj)


     loc1 loc2 loc3 loc4
indA    1    0    1    1
indB    0    1    1    1
indC    1    1    0    1
indD    0   NA    1   NA
indE    1    1    0    0
indF    1    0    1    1
indG    0    1    1    0
```

One can see that for instance, the summary of this object is more simple (no numbers of alleles per locus, no heterozygosity):

```
> pop(obj) <- rep(c('a','b'),4:3)
> summary(obj)


 # Total number of genotypes:  7

 # Population sample sizes:
a b
4 3

 # Percentage of missing data:
[1] 7.142857
```

But we can still perform basic manipulation, like converting our object into a genpop:

```
> obj2 <- genind2genpop(obj)


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

...done.


> obj2
```

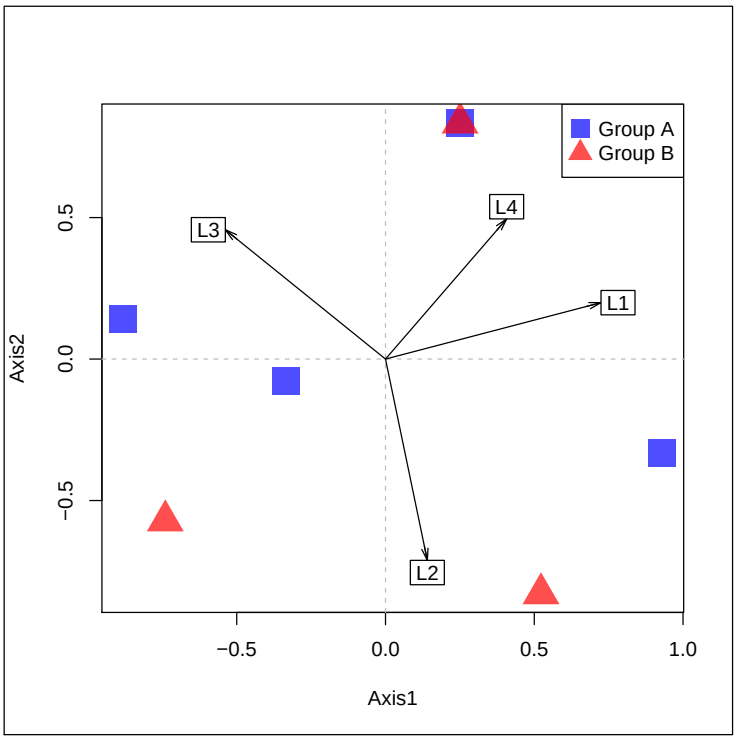
```
       ######################
       ### Genpop object ###
       ######################
- Alleles counts for populations -

S4 class:  genpop
@call: genind2genpop(x = obj)

@tab:  2 x 4 matrix of alleles counts

@pop.names: vector of  2 population names
@loc.names: vector of  4 locus names
@loc.nall: NULL
@loc.fac: NULL
@all.names: NULL
@ploidy:  1
@type:  PA

@other: - empty -


> truenames(obj2)


  loc1 loc2 loc3 loc4
a    2    2    3    3
b    2    2    2    1
```

To continue with the toy example, we can proceed to a simple PCA. NAs are first replaced:

```
> objNoNa <- na.replace(obj,met=0)


 Replaced 2 missing values


> objNoNa@tab


  L1 L2 L3 L4
1  1  0  1  1
2  0  1  1  1
3  1  1  0  1
4  0  0  1  0
5  1  1  0  0
6  1  0  1  1
7  0  1  1  0
```

Now the PCA is performed and plotted:

```
> library(ade4)
> pca1 <- dudi.pca(objNoNa,scannf=FALSE,scale=FALSE)
> temp <- as.integer(pop(objNoNa))
> myCol <- transp(c("blue","red"),.7)[temp]
> myPch <- c(15,17)[temp]
> plot(pca1$li, col=myCol, cex=3, pch=myPch)
> abline(h=0,v=0,col="grey",lty=2)
> s.arrow(pca1$c1, add.plot=TRUE)
> legend("topright", pch=c(15,17), col=transp(c("blue","red"),.7), leg=c("Group A","Group B"), pt.cex=2)
```



More generally, multivariate analyses from ade4, sPCA (`spca`), DAPC (`dapc`), the global and local tests (`global.rtest`, `local.rtest`), or the Monmonier's algorithm (`monmonier`) will work just fine with presence/absence data. However, it is clear that the usual Euclidean distance (used in PCA and sPCA), as well as many other distances, is not as accurate to measure genetic dissimilarity using presence/absence data as it is when using allele frequencies. The reason for this is that in presence/absence data, a part of the information is simply hidden. For instance, two individuals possessing the same allele will be considered at the same distance, whether they possess one or more copies of the allele. This might be especially problematic in organisms having a high degree of ploidy.

4.4 SNPs data

In *adegenet*, SNP data can be handled in two different ways. For relatively small datasets (up to a few thousand SNPs) SNPs can be handled as usual codominant markers such as microsatellites using `genind` objects. In the case of genome-wide SNP data (from hundreds of thousands to millions of SNPs), `genind` objects are no longer efficient representation of the data. In this case, we use `genlight` objects to store and handle information with maximum efficiency and minimum memory requirements. See the vignette *adegenet-genomics* for more information. Below, we introduce only the case of SNPs handled using `genind` objects.

The most convenient way to convert SNPs into a `genind` is using `df2genind`, which is described in the previous section. Let `dat` be an input matrix, as can be read into R using `read.table` or `read.csv`, with genotypes in row and SNP loci in columns.

```
> dat <- matrix(sample(c("a","t","g","c"), 15, replace=TRUE),nrow=3)
> rownames(dat) <- paste("genot.", 1:3)
> colnames(dat) <- 1:5
> dat
```

```
         1   2   3   4   5
genot. 1 "t" "t" "g" "t" "c"
genot. 2 "a" "g" "g" "c" "c"
genot. 3 "t" "g" "c" "c" "t"
```

```
> obj <- df2genind(dat, ploidy=1)
> truenames(obj)
```

```
         1.a 1.t 2.g 2.t 3.c 3.g 4.c 4.t 5.c 5.t
genot. 1   0   1   0   1   0   1   0   1   1   0
genot. 2   1   0   1   0   0   1   1   0   1   0
genot. 3   0   1   1   0   1   0   1   0   0   1
```

`obj` is a `genind` containing the SNPs information, which can be used for further analysis in adegenet.

4.5 Extracting polymorphism from DNA sequences

This section only covers the cases of relatively small datasets which can be handled efficiently using `genind` objects. For bigger (near full-genomes) datasets, SNPs can be extracted from *fasta* files into a `genlight` object using `fasta2genlight`. See the vignette *adegenet-genomics* for more information.

DNA sequences can be read into R using the *ape* package [**?**], and imported into *adegenet* using `DNAbin2genind`. There are several ways *ape* can be used to read in DNA sequences. The easiest one is reading data from a usual format such as FASTA or Clustal using `read.dna`. Other options include reading data directly from GenBank using `read.GenBank`, or from other public databases using the *seqinr* package and transforming the `alignment` object into a `DNAbin` using `as.DNAbin`. Here, we illustrate this approach by re-using the example of `read.GenBank`. A connection to the internet is required, as sequences are read directly from a distant database.

```
> library(ape)
> ref <- c("U15717", "U15718", "U15719", "U15720",
+          "U15721", "U15722", "U15723", "U15724")
> myDNA <- read.GenBank(ref)
> myDNA
```

```
8 DNA sequences in binary format stored in a list.

All sequences of same length: 1045

Labels: U15717 U15718 U15719 U15720 U15721 U15722 ...

Base composition:
    a     c     g     t
0.267 0.351 0.134 0.247
```

```
> class(myDNA)
```

```
[1] "DNAbin"
```

In *adegenet*, only polymorphic loci are conserved; importing data from a DNA sequence to *adegenet* therefore consists in extracting SNPs from the aligned sequences. This conversion is achieved by `DNAbin2genind`. This function allows one to specify a threshold for polymorphism; for instance, one could retain only SNPs for which the second largest allele frequency is greater than 1% (using the `polyThres` argument). This is achieved using:

```
> obj <- DNAbin2genind(myDNA, polyThres=0.01)
> obj
```

```
   ####################
   ### Genind object ###
   ####################
- genotypes of individuals -

S4 class:  genind
@call: DNAbin2genind(x = myDNA, polyThres = 0.01)

@tab:  8 x 318 matrix of genotypes

@ind.names: vector of  8 individual names
@loc.names: vector of  155 locus names
@loc.nall: number of alleles per locus
@loc.fac: locus factor for the  318 columns of @tab
@all.names: list of  155 components yielding allele names for each locus
@ploidy:  1
@type:  codom

Optionnal contents:
@pop:  - empty -
@pop.names:  - empty -

@other: - empty -
```

Here, out of the 1,045 nucleotides of the sequences, 318 SNPs where extracted and stored as a `genind` object. Positions of the SNPs are stored as names of the loci:

```
> head(locNames(obj))
```

```
L001 L002 L003 L004 L005 L006
"11" "13" "26" "31" "34" "39"
```

4.6 Extracting polymorphism from proteic sequences

Alignments of proteic sequences can be exploited in *adegenet* in the same way as DNA sequences (see section above). Alignments are scanned for polymorphic sites, and only those are retained to form a `genind` object. Loci correspond to the position of the residue in the alignment, and alleles correspond to the different amino-acids (AA). Aligned proteic sequences are stored as objects of class `alignment` in the *seqinr* package [**?**]. See `?as.alignment` for a description of this class. The function extracting polymorphic sites from `alignment` objects is `alignment2genind`.

Its use is fairly simple. It is here illustrated using a small dataset of aligned proteic sequences:

The six aligned protein sequences (`mase.res`) have been scanned for polymorphic sites, and these have been extracted to form the `genind` object `x`. Note that several settings such as the characters corresponding to missing values (i.e., gaps) and the polymorphism threshold for a site to be retained can be specified through the function's arguments (see `?alignment2genind`).

The names of the loci directly provides the indices of polymorphic sites:

Now that polymorphic sites have been converted into a `genind` object, simple distances can be computed between the sequences. Note that *adegenet* does not implement specific distances for protein sequences, we only use the simple Euclidean distance. Fancier protein distances are implemented in R; see for instance `dist.alignment` in the *seqinr* package, and `dist.ml` in the *phangorn* package.

Here is an example for `genpop` using a dataset from *ade4*:

```
> library(ade4)
> data(microsatt)
> microsatt$tab[10:15,12:15]


           INRA32.168 INRA32.170 INRA32.174 INRA32.176
Mtbeliard           0          0          0          1
NDama               0          0          0         12
Normand             1          0          0          2
Parthenais          8          5          0          3
Somba               0          0          0         20
Vosgienne           2          0          0          0
```

`microsatt$tab` contains alleles counts per populations, and can therefore be used to make a `genpop` object. Moreover, column names are set as required, and row names are unique. It is therefore safe to convert these data into a `genpop` using the constructor:

```
> toto <- genpop(microsatt$tab)
> toto


       ######################
       ### Genpop object ###
       ######################
- Alleles counts for populations -

S4 class:  genpop
@call: genpop(tab = microsatt$tab)

@tab:  18 x 112 matrix of alleles counts

@pop.names: vector of  18 population names
@loc.names: vector of  9 locus names
@loc.nall: number of alleles per locus
@loc.fac: locus factor for the  112 columns of @tab
@all.names: list of  9 components yielding allele names for each locus
@ploidy:  2
@type:  codom

@other: - empty -


> summary(toto)
```

```
 # Number of populations:  18

 # Number of alleles per locus:
L1 L2 L3 L4 L5 L6 L7 L8 L9
 8 15 11 10 17 10 14 15 12

 # Number of alleles per population:
01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18
39 69 51 59 52 41 34 48 46 47 43 56 57 52 49 64 56 67

 # Percentage of missing data:
[1] 0
```

4.7 Exporting data

Genotypes in `genind` format can be exported to the R packages *genetics* (using `genind2genotype`) and *hierfstat* (using `genind2hierfstat`). The package *genetics* is now deprecated, but the implemented class `genotype` is still used in various packages. The package *hierfstat* does not define a class, but requires data to be formated in a particular way. It has been removed from CRAN as of R version 2.13.0 for maintainance issues, but is supposed to be back eventually.

Here are examples of how to use these functions:

```
> obj <- genind2genotype(nancycats)
> class(obj)


[1] "data.frame"


> obj[1:4,1:5]


         fca8   fca23   fca43   fca45   fca77
cat.1    <NA> 136/146 139/139 120/116 156/156
cat.2    <NA> 146/146 139/145 126/120 156/156
cat.3 135/143 136/146 141/141 116/116 156/152
cat.4 135/133 138/138 139/141 126/116 150/150


> class(obj$fca8)


[1] "genotype" "factor"


> obj <- genind2hierfstat(nancycats)
> class(obj)


[1] "data.frame"


> obj[1:4,1:5]


      pop fca8 fca23 fca43 fca45
cat.1   1   NA   409   404   103
cat.2   1   NA   909   407   305
cat.3   1  913   409   505   101
cat.4   1  809   505   405   105
```

A more generic way to export data is to produce a `data.frame` of genotypes coded by character strings. This is done by `genind2df`:

```
> obj <- genind2df(nancycats)
> obj[1:5,1:5]
```

```
      pop   fca8  fca23  fca43  fca45
cat.1   1   <NA> 136146 139139 116120
cat.2   1   <NA> 146146 139145 120126
cat.3   1 135143 136146 141141 116116
cat.4   1 133135 138138 139141 116126
cat.5   1 133135 140146 141145 126126
```

However, some software will require alleles to be separated. The argument `sep` allows one to specify any separator. For instance:

```
> genind2df(nancycats,sep="|")[1:5,1:5]
```

```
      pop    fca8   fca23   fca43   fca45
cat.1   1    <NA> 136|146 139|139 116|120
cat.2   1    <NA> 146|146 139|145 120|126
cat.3   1 135|143 136|146 141|141 116|116
cat.4   1 133|135 138|138 139|141 116|126
cat.5   1 133|135 140|146 141|145 126|126
```

Note that tabulations can be obtained as follows using '\t' character.

5 Basics of data analysis

5.1 Manipulating the data

Data manipulation is meant to be particularly flexible in *adegenet*. First, as `genind` and `genpop` objects are basically formed by a data matrix (the `@tab` slot), it is natural to subset these objects like it is done with a matrix. The [operator does this, forming a new object with the retained genotypes/populations and alleles:

```
> data(microbov)
> toto <- genind2genpop(microbov)


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

...done.


> toto


       ######################
       ### Genpop object ###
       ######################
- Alleles counts for populations -

S4 class:  genpop
@call: genind2genpop(x = microbov)

@tab:  15 x 373 matrix of alleles counts

@pop.names: vector of  15 population names
@loc.names: vector of  30 locus names
@loc.nall: number of alleles per locus
@loc.fac: locus factor for the  373 columns of @tab
@all.names: list of  30 components yielding allele names for each locus
@ploidy:  2
@type:  codom

@other: a list containing: coun  breed  spe


> toto@pop.names


              01              02              03              04
        "Borgou"          "Zebu"     "Lagunaire"         "NDama"
              05              06              07              08
         "Somba"        "Aubrac"      "Bazadais" "BlondeAquitaine"
              09              10              11              12
   "BretPieNoire"     "Charolais"        "Gascon"      "Limousin"
              13              14              15
    "MaineAnjou"   "Montbeliard"        "Salers"


> titi <- toto[1:3,]
> titi@pop.names


         1          2          3
   "Borgou"    "Zebu" "Lagunaire"
```

The object `toto` has been subsetted, keeping only the first three populations. Of course, any subsetting available for a matrix can be used with `genind` and `genpop` objects. In addition, we can subset loci directly using the generic marker names:

```
> tata <- titi[,loc="L03"]
> tata


       ######################
       ### Genpop object ###
       ######################
- Alleles counts for populations -

S4 class:  genpop
@call: .local(x = x, i = i, j = j, loc = "L03", drop = drop)

@tab:  3 x 12 matrix of alleles counts

@pop.names: vector of  3 population names
@loc.names: vector of  1 locus names
@loc.nall: number of alleles per locus
@loc.fac: locus factor for the  12 columns of @tab
@all.names: list of  1 components yielding allele names for each locus
@ploidy:  2
@type:  codom

@other: a list containing: coun  breed  spe
```

Now, `tata` only contains the 12 alleles of the third marker of `titi`.

To simplify the task of separating data by marker, the function `seploc` can be used. It returns a list of objects (optionnaly, of data matrices), each corresponding to a marker:

```
> data(nancycats)
> sepCats <- seploc(nancycats)
> class(sepCats)


[1] "list"


> names(sepCats)


[1] "fca8"  "fca23" "fca43" "fca45" "fca77" "fca78" "fca90" "fca96" "fca37"


> sepCats$fca45


   ######################
   ### Genind object ###
   ######################
- genotypes of individuals -

S4 class:  genind
@call: .local(x = x)

@tab:  237 x 9 matrix of genotypes

@ind.names: vector of  237 individual names
@loc.names: vector of  1 locus names
@loc.nall: number of alleles per locus
@loc.fac: locus factor for the  9 columns of @tab
@all.names: list of  1 components yielding allele names for each locus
@ploidy:  2
@type:  codom

Optionnal contents:
@pop:  factor giving the population of each individual
@pop.names:  factor giving the population of each individual

@other: a list containing: xy
```

The object `sepCats$fca45` only contains data of the marker fca45.

Following the same idea, `seppop` allows one to separate genotypes in a `genind` object by population. For instance, we can separate genotype of cattles in the dataset `microbov` by breed:

```
> data(microbov)
> obj <- seppop(microbov)
> class(obj)


[1] "list"


> names(obj)


 [1] "Borgou"          "Zebu"            "Lagunaire"       "NDama"
 [5] "Somba"           "Aubrac"          "Bazadais"        "BlondeAquitaine"
 [9] "BretPieNoire"    "Charolais"       "Gascon"          "Limousin"
[13] "MaineAnjou"      "Montbeliard"     "Salers"


> obj$Borgou


   ######################
   ### Genind object ###
   ######################
- genotypes of individuals -

S4 class:  genind
@call: .local(x = x, i = i, j = j, treatOther = ..1, quiet = ..2, drop = drop)

@tab:  50 x 373 matrix of genotypes

@ind.names: vector of  50 individual names
@loc.names: vector of  30 locus names
@loc.nall: number of alleles per locus
@loc.fac: locus factor for the  373 columns of @tab
@all.names: list of  30 components yielding allele names for each locus
@ploidy:  2
@type:  codom

Optionnal contents:
@pop:  factor giving the population of each individual
@pop.names:  factor giving the population of each individual

@other: a list containing: coun  breed  spe
```

The returned object `obj` is a list of `genind` objects each containing genotypes of a given breed.

A last, rather vicious trick is to separate data by population and by marker. This is easy using `lapply`; one can first separate population then markers, or the contrary. Here, we separate markers inside each breed in `obj`:

```
> obj <- lapply(obj,seploc)
> names(obj)


 [1] "Borgou"          "Zebu"            "Lagunaire"       "NDama"
 [5] "Somba"           "Aubrac"          "Bazadais"        "BlondeAquitaine"
 [9] "BretPieNoire"    "Charolais"       "Gascon"          "Limousin"
[13] "MaineAnjou"      "Montbeliard"     "Salers"
```

```
> class(obj$Borgou)


[1] "list"


> names(obj$Borgou)


 [1] "INRA63"  "INRA5"   "ETH225"  "ILSTS5"  "HEL5"    "HEL1"    "INRA35"
 [8] "ETH152"  "INRA23"  "ETH10"   "HEL9"    "CSSM66"  "INRA32"  "ETH3"
[15] "BM2113"  "BM1824"  "HEL13"   "INRA37"  "BM1818"  "ILSTS6"  "MM12"
[22] "CSRM60"  "ETH185"  "HAUT24"  "HAUT27"  "TGLA227" "TGLA126" "TGLA122"
[29] "TGLA53"  "SPS115"


> obj$Borgou$INRA63


   ######################
   ### Genind object ###
   ######################
- genotypes of individuals -

S4 class:  genind
@call: .local(x = x)

@tab:  50 x 9 matrix of genotypes

@ind.names: vector of  50 individual names
@loc.names: vector of  1 locus names
@loc.nall: number of alleles per locus
@loc.fac: locus factor for the  9 columns of @tab
@all.names: list of  1 components yielding allele names for each locus
@ploidy:  2
@type:  codom

Optionnal contents:
@pop:  factor giving the population of each individual
@pop.names:  factor giving the population of each individual

@other: a list containing: coun  breed  spe
```

For instance, `obj$Borgou$INRA63` contains genotypes of the breed Borgou for the marker INRA63.

Lastly, one may want to pool genotypes in different datasets, but having the same markers, into a single dataset. This is more than just merging the `@tab` components of all datasets, because alleles can differ (they almost always do) and markers are not necessarily sorted the same way. The function `repool` is designed to avoid these problems. It can merge any `genind` provided as arguments as soon as the same markers are used. For instance, it can be used after a `seppop` to retain only some populations:

```
> obj <- seppop(microbov)
> names(obj)


 [1] "Borgou"          "Zebu"            "Lagunaire"       "NDama"
 [5] "Somba"           "Aubrac"          "Bazadais"        "BlondeAquitaine"
 [9] "BretPieNoire"    "Charolais"       "Gascon"          "Limousin"
[13] "MaineAnjou"      "Montbeliard"     "Salers"
```

```
> newObj <- repool(obj$Borgou, obj$Charolais)
> newObj


   ######################
   ### Genind object ###
   ######################
- genotypes of individuals -

S4 class:  genind
@call: repool(obj$Borgou, obj$Charolais)

@tab:  105 x 295 matrix of genotypes

@ind.names: vector of  105 individual names
@loc.names: vector of  30 locus names
@loc.nall: number of alleles per locus
@loc.fac: locus factor for the  295 columns of @tab
@all.names: list of  30 components yielding allele names for each locus
@ploidy:  2
@type:  codom

Optionnal contents:
@pop:  factor giving the population of each individual
@pop.names:  factor giving the population of each individual

@other: - empty -


> newObj$pop.names

        P1          P2
   "Borgou" "Charolais"
```

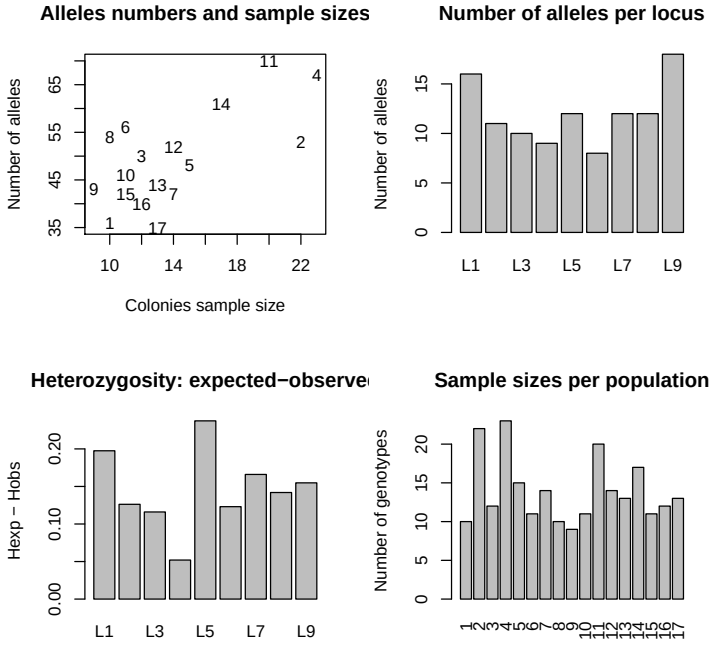
Done !

5.2 Using summaries

Both `genind` and `genpop` objects have a summary providing basic information about data. Informations are both printed and invisibly returned as a list.

```
> toto <- summary(nancycats)


 # Total number of genotypes:  237

 # Population sample sizes:
 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17
10 22 12 23 15 11 14 10  9 11 20 14 13 17 11 12 13

 # Number of alleles per locus:
L1 L2 L3 L4 L5 L6 L7 L8 L9
16 11 10  9 12  8 12 12 18

 # Number of alleles per population:
01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17
36 53 50 67 48 56 42 54 43 46 70 52 44 61 42 40 35

 # Percentage of missing data:
[1] 2.344116

 # Observed heterozygosity:
       L1        L2        L3        L4        L5        L6        L7        L8
0.6682028 0.6666667 0.6793249 0.7083333 0.6329114 0.5654008 0.6497890 0.6184211
       L9
0.4514768

 # Expected heterozygosity:
       L1        L2        L3        L4        L5        L6        L7        L8
0.8657224 0.7928751 0.7953319 0.7603095 0.8702576 0.6884669 0.8157881 0.7603493
       L9
0.6062686
```

```
> names(toto)

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

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



Is mean observed H significantly lower than mean expected H ?

```
> bartlett.test(list(toto$Hexp,toto$Hobs))

        Bartlett test of homogeneity of variances

data:  list(toto$Hexp, toto$Hobs)
Bartlett's K-squared = 0.047, df = 1, p-value = 0.8284

> t.test(toto$Hexp,toto$Hobs,pair=T,var.equal=TRUE,alter="greater")

        Paired t-test

data:  toto$Hexp and toto$Hobs
t = 8.3294, df = 8, p-value = 1.631e-05
alternative hypothesis: true difference in means is greater than 0
95 percent confidence interval:
 0.1134779       Inf
sample estimates:
mean of the differences
              0.1460936
```

Yes, it is.

5.3 Testing for Hardy-Weinberg equilibrium

The Hardy-Weinberg equilibrium test is implemented for `genind` objects. The function to use is `HWE.test.genind`, and requires the package *genetics*. Here we first produce a matrix of p-values (`res="matrix"`) using parametric test. Monte Carlo procedure are more reliable but also more computer-intensive (use `permut=TRUE`).

```
> toto <- HWE.test.genind(nancycats,res="matrix")
> dim(toto)
```

```
[1] 17  9
```

One test is performed per locus and population, *i.e.* 153 tests in this case. Thus, the first question is: which tests are highly significant?

```
> colnames(toto)
```

```
[1] "fca8"  "fca23" "fca43" "fca45" "fca77" "fca78" "fca90" "fca96" "fca37"
```

```
> idx <- which(toto<0.0001,TRUE)
> idx
```

```
    row col
P14  14   2
P02   2   7
P02   2   8
P05   5   9
```

Here, only 4 tests indicate departure from HW. Rows give populations, columns give markers. Now complete tests are returned, but the significant ones are already known.

```
> toto <- HWE.test.genind(nancycats,res="full")
> mapply(function(i,j) toto[[i]][[j]], idx[,2], idx[,1], SIMPLIFY=FALSE)
```

```
$P14

        Pearson's Chi-squared test

data:  tab
X-squared = 49.7996, df = 15, p-value = 1.298e-05


$P02

        Pearson's Chi-squared test

data:  tab
X-squared = 56.7523, df = 15, p-value = 9.04e-07


$P02

        Pearson's Chi-squared test

data:  tab
```

```
X-squared = 92.0716, df = 15, p-value = 4.067e-13


$P05

        Pearson's Chi-squared test

data:  tab
X-squared = 30.0206, df = 6, p-value = 3.896e-05
```

5.4 Measuring and testing population structure (a.k.a F statistics)

Population structure is traditionally measured and tested using F statistics, in particular Fst. Since version 2.13.0 of R, the package *hierfstat*, which implemented most F statistics and related tests, has been removed from CRAN for maintenance issues. As a consequence, *adegenet* has lost a few functionalities, namely general F statistics (function `fstat`) and a test of overall population structure (`gstat.randtest`).

However, it is still possible to compute pairwise Fst using *adegenet*. Pairwise Fst is frequently used as a measure of distance between populations. The function `pairwise.fst` computes Nei's estimator [**?**] of pairwise Fst, defined as:

$$Fst(A,B) = \frac{H_t - (n_A H_s(A) + n_B H_s(B))/(n_A + n_B)}{Ht}$$

where A and B refer to the two populations of sample size n_A and n_B and respective expected heterozygosity $H_s(A)$ and $H_s(B)$, and H_t is the expected heterozygosity in the whole dataset. For a given locus, expected heterozygosity is computed as $1 - \sum p_i^2$, where p_i is the frequency of the ith allele, and the $\sum$ represents summation over all alleles. For multilocus data, the heterozygosity is simply averaged over all loci. These computations are achieved for all pairs of populations by the function `pairwise.fst`; we illustrate this on a subset of individuals of `nancycats` (computations for the whole dataset would take a few tens of seconds):

```
> data(nancycats)
> matFst <- pairwise.fst(nancycats[1:50, treatOther=FALSE])
> matFst


          1         2         3
2 0.08018500
3 0.07140847 0.08200880
4 0.08163151 0.06512457 0.04131227
```

The resulting matrix is Euclidean when there are no missing values:

```
> is.euclid(matFst)


[1] TRUE
```

It can therefore be used in a Principal Coordinate Analysis (which requires Euclideanity), used to build trees, etc.

5.5 Estimating inbreeding

Inbreeding refers to an excess of homozygosity in a given individual due to the mating of genetically related parents. This excess of homozygosity is due to the fact that there are non-negligible chances of inheriting two identical alleles from a recent common ancestor. Inbreeding can be associated to a loss of fitness leading to "*inbreeding depression*". Typically, loss of fitness is caused by recessive deleterious alleles which have usually low frequency in the population, but for which inbred individuals are more likely to be homozygotes.

The inbreeding coefficient F is defined as the probability that at a given locus, two identical alleles have been inherited from a common ancestor. In the absence of inbreeding, the probability of being homozygote at one loci is (for diploid individuals) simply $\sum_i p_i^2$ where i indexes the alleles and p_i is the frequency of allele i. This can be generalized incorporating F as:

$$p(\text{homozygote}) = F + (1 - F) \sum_i p_i^2$$

and even more generally, for any ploidy π:

$$p(\text{homozygote}) = F + (1 - F) \sum_i p_i^\pi$$

This therefore allows for computing the likelihood of a given state (homozygote/heterozygote) in a given genotype (log-likelihood are summed across loci for more than one marker).

This estimation is achieved by `inbreeding`. Depending on the value of the argument `res.type`, the function returns a sample from the likelihood function (`res.type='sample'`) or the likelihood function itself, as a R function (`res.type='function'`). While likelihood functions are quickly obtained and easy to display graphically, sampling from the distributions is more computer intensive but useful to derive summary statistics of the distributions. Here, we illustrate `inbreeding` using the `microbov` dataset, which contains cattle breeds genotypes for 30 microsatellites; to focus on breed Salers only, we use `seppop`:

```
> data(microbov)
> sal <- seppop(microbov)$Salers
> sal


   ######################
   ### Genind object ###
   ######################
- genotypes of individuals -

S4 class:  genind
@call: .local(x = x, i = i, j = j, treatOther = ..1, quiet = ..2, drop = drop)

@tab:  50 x 373 matrix of genotypes

@ind.names: vector of  50 individual names
@loc.names: vector of  30 locus names
@loc.nall: number of alleles per locus
```

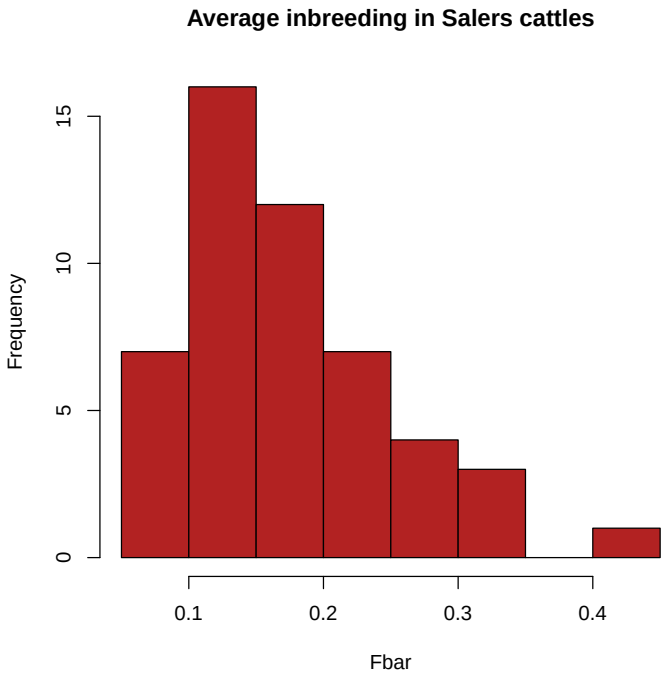
```
@loc.fac: locus factor for the  373 columns of @tab
@all.names: list of  30 components yielding allele names for each locus
@ploidy:  2
@type:  codom

Optionnal contents:
@pop:  factor giving the population of each individual
@pop.names:  factor giving the population of each individual

@other: a list containing: coun  breed  spe
```

We first compute the mean inbreeding for each individual, and plot the resulting distribution:

```
> temp <- inbreeding(sal, N=100)
> class(temp)


[1] "list"


> head(names(temp))


[1] "FRBTSAL9087" "FRBTSAL9088" "FRBTSAL9089" "FRBTSAL9090" "FRBTSAL9091"
[6] "FRBTSAL9093"


> head(temp[[1]],20)


 [1] 0.039678134 0.141240944 0.070507608 0.234807712 0.156165261 0.024079789
 [7] 0.225947433 0.292017608 0.112180178 0.073623489 0.003804735 0.061665423
[13] 0.280750497 0.111344944 0.195517196 0.180942706 0.027672535 0.150688659
[19] 0.129528576 0.344924239
```

`temp` is a list of values sampled from the likelihood distribution of each individual; means values are obtained for all individuals using `sapply`:

```
> Fbar <- sapply(temp, mean)


> hist(Fbar, col="firebrick", main="Average inbreeding in Salers cattles")
```

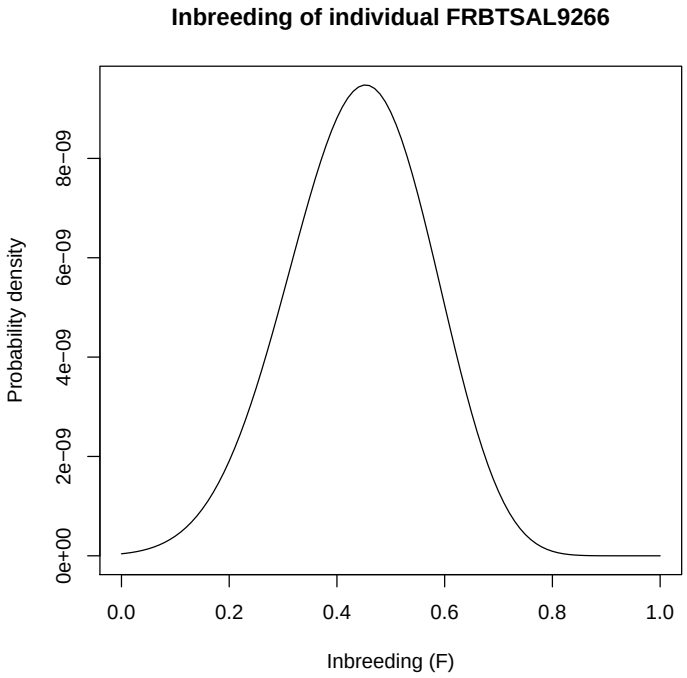


We can see that some individuals (actually, a single one) have higher inbreeding (>0.4). We can recompute inbreeding for this individual, asking for the likelihood function to be returned:

```
> which(Fbar>0.4)

FRBTSAL9266
         37


> F <- inbreeding(sal, res.type="function")[which(Fbar>0.4)]
> F

$FRBTSAL9266
function (F)
{
    args <- lapply(as.list(match.call())[-1L], eval, parent.frame())
    names <- if (is.null(names(args)))
        character(length(args))
    else names(args)
    dovec <- names %in% vectorize.args
    do.call("mapply", c(FUN = FUN, args[dovec], MoreArgs = list(args[!dovec]),
        SIMPLIFY = SIMPLIFY, USE.NAMES = USE.NAMES))
}
<environment: 0xa5d4008>
```

The output object `F` can seem a bit cryptic: it is an function embedded within a hidden environment. This does not matter, however, since it is easily represented:

```
> plot(F$FRBTSAL9266, main=paste("Inbreeding of individual",names(F)), xlab="Inbreeding (F)", ylab="Probability d
```



Indeed, this individual shows subsequent inbreeding, with about 50% chances of being homozygote through inheritance from a common ancestor of its parents.

6 Multivariate analysis

6.1 General overview

Multivariate analysis consists in summarising a strongly multivariate information into a few synthetic variables. In genetics, such approaches are useful to get a simplified picture of the genetic diversity obersved amongst individuals or populations. A review of multivariate analysis in population genetics can be found in [**?**]. Here, we aim at providing an overview of some applications using methods implemented in *ade4* and *adegenet*.

Useful functions include:

- `scaleGen` (*adegenet*): centre/scale allele frequencies and replaces missing data; useful, among other things, before running a principal component analysis (PCA).
- `dudi.pca` (*ade4*): implements PCA; can be used on transformed allele frequencies of individuals or populations.
- `dudi.ca` (*ade4*): implements Correspondance Analysis (CA); can be used on raw allele counts of populations (`@tab` slot in `genpop` objects).
- `dist.genpop` (*adegenet*): implements 5 pairwise genetic distances between populations
- `pairwise.fst` (*adegenet*): implements pairwise F_{ST}, which is also a Euclidean distance between populations.
- `dist` (*stats*): computes pairwise distances between multivariate observations; can be used on raw or transformed allele frequencies.
- `dudi.pco` (*ade4*): implements Principal Coordinates Analysis (PCoA); this methods finds synthetic variables which summarize a Euclidean distance matrix as best as possible; can be used on outputs of `dist`, `dist.genpop`, and `pairwise.fst`.
- `is.euclid` (*ade4*): tests whether a distance matrix is Euclidean, which is a pre-requisite of PCoA.
- `cailliez` (*ade4*): renders a non-Euclidean distance matrix Euclidean by adding a constant to all entries.
- `dapc` (*adegenet*): implements the Discriminant Analysis of Principal Components (DAPC [**?**]), a powerful method for the analysis of population genetic structures; see dedicated vignette (*adegenet-dapc*).
- `sPCA` (*adegenet*): implements the spatial Principal Component Analysis (sPCA [**?**]), a method for the analysis of spatial genetic structures; see dedicated vignette (*adegenet-dapc*).

- `glPca` (*adegenet*): implements PCA for genome-wide SNP data stored as `genlight` objects; see dedicated vignette (*adegenet-genomics*).

Besides the procedures themselves, graphic functions are also often of the utmost importance; these include:

- `scatter` (*ade4,adegenet*): generic function to display multivariate analyses; in practice, the most useful application for genetic data is the one implemented in `adegenet` for DAPC results.
- `s.label` (*ade4*): function used for basic display of principal components.
- `loadingplot` (*adegenet*): function used to display the loadings (i.e., contribution to a given structure) of alleles for a given principal component; annotates and returns the most contributing alleles.
- `s.class` (*ade4*): displays two quantitative variables with known groups of observations, using inertia ellipses for the groups; useful to represent principal components when groups are known.
- `s.chull` (*ade4*): same as `s.class`, except convex polygons are used rather than ellipses.
- `s.value` (*ade4*): graphical display of a quantitative variable distributed over a two-dimensional space; useful to map principal components or allele frequencies over a geographic area.
- `colorplot` (*adegenet*): graphical display of 1 to 3 quantitative variables distributed over a two-dimensional space; useful for combined representations of principal components over a geographic area. Can also be used to produce color versions of traditional scatterplots.
- `transp` (*adegenet*): auxiliary function making colors transparent.
- `num2col` (*adegenet*): auxiliary function transforming a quantitative variable into colors using a given palette.
- `assignplot` (*adegenet*): specific plot of group membership probabilities for DAPC; see dedicated vignette (*adegenet-dapc*).
- `compoplot` (*adegenet*): specific 'STRUCTURE-like' plot of group membership probabilities for DAPC; see dedicated vignette (*adegenet-dapc*).
- `add.scatter` (*ade4*): add inset plots to an existing figure.
- `add.scatter.eig` (*ade4*): specific application of `add.scatter` to add barplots of eigenvalues to an existing figure.

In the sections below, we briefly illustrate how these tools can be combined to extract information from genetic data.

6.2 Performing a Principal Component Analysis on `genind` objects

The tables contained in `genind` objects can be submitted to a Principal Component Analysis (PCA) to seek a summary of the genetic diversity among the sampled individuals. Such analysis is straightforward using *adegenet* to prepare data and *ade4* for the analysis *per se*. One has first to replace missing data (NAs) and transform the allele frequencies in an appropriate way. These operations are achieved by `scaleGen`. NAs are replaced by the mean allele frequency; different scaling options are available (argument `method`), but in general centring is sufficient since allele frequencies have inherently comparable variances.

```
> data(microbov)
> sum(is.na(microbov$tab))
```

```
[1] 6325
```

There are 6325 missing data. They will all be replaced by `scaleGen`:

```
> X <- scaleGen(microbov, missing="mean")
> class(X)
```

```
[1] "matrix"
```

```
> dim(X)
```

```
[1] 704 373
```

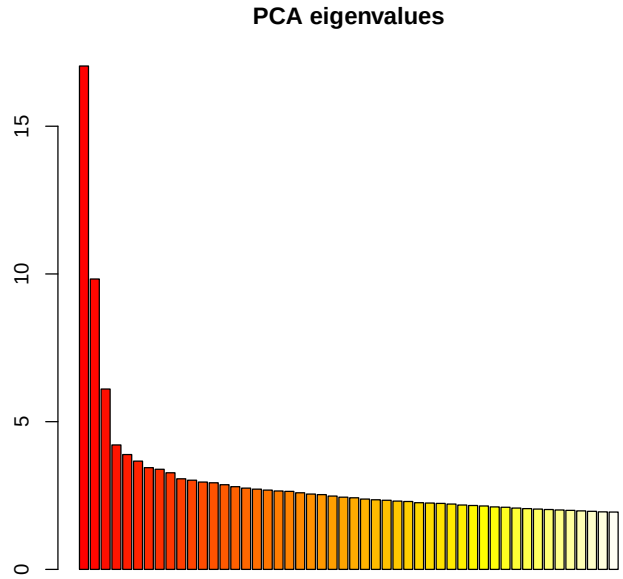
```
> X[1:5,1:5]
```

```
             INRA63.167  INRA63.171 INRA63.173 INRA63.175 INRA63.177
AFBIBOR9503 -0.03801312 -0.05379728  -0.101009  -1.061893 -0.8769237
AFBIBOR9504 -0.03801312 -0.05379728  -0.101009  -1.061893 -0.8769237
AFBIBOR9505 -0.03801312 -0.05379728  -0.101009  -1.061893  0.5498659
AFBIBOR9506 -0.03801312 -0.05379728  -0.101009  -1.061893 -0.8769237
AFBIBOR9507 -0.03801312 -0.05379728  -0.101009  -1.061893  0.5498659
```

Note that alternatively, we could have used `na.replace` to replace missing data, and then left the centring/scaling to `dudi.pca`.

The analysis can now be performed. We disable the scaling in `dudi.pca`, which would erase the scaling choice made earlier in `scaleGen`. Note: in practice, retained axes can be chosen interactively by removing the arguments `scannf=FALSE,nf=3`.

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




```
> pca1

Duality diagramm
class: pca dudi
$call: dudi.pca(df = X, center = FALSE, scale = FALSE, scannf = FALSE,
    nf = 3)

$nf: 3 axis-components saved
$rank: 343
eigen values: 17.04 9.829 6.105 4.212 3.887 ...
  vector length mode    content
1 $cw    373    numeric column weights
2 $lw    704    numeric row weights
3 $eig   343    numeric eigen values

  data.frame nrow ncol content
1 $tab       704  373  modified array
2 $li        704  3    row coordinates
3 $l1        704  3    row normed scores
4 $co        373  3    column coordinates
5 $c1        373  3    column normed scores
other elements: cent norm
```

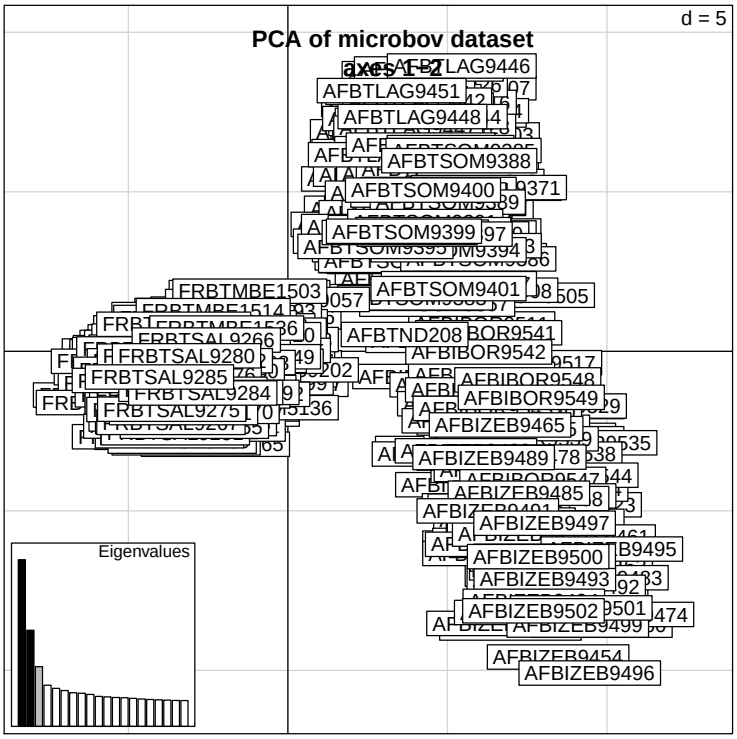
The output object `pca1` is a list containing various information; of particular interest are:

- `$eig`: the eigenvalues of the analysis, indicating the amount of variance represented by each principal component (PC).
- `$li`: the principal components of the analysis; these are the synthetic variables summarizing the genetic diversity, usually visualized using scatterplots.

- `$c1`: the allele loadings, used to compute linear combinations forming the PCs; squared, they represent the contribution to each PCs.

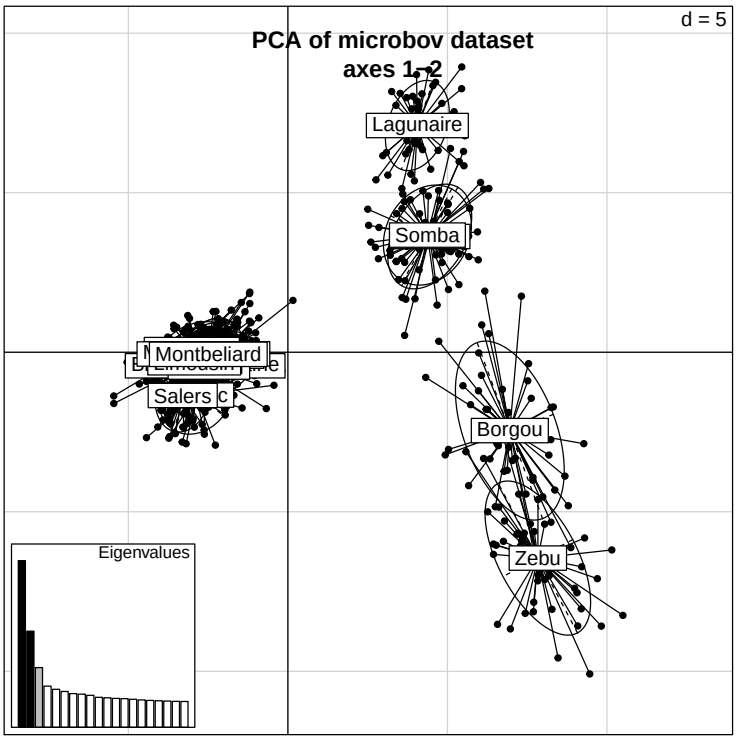
The basic scatterplot for this analysis can be obtained by:

```
> s.label(pca1$li)
> title("PCA of microbov dataset\naxes 1-2")
> add.scatter.eig(pca1$eig[1:20], 3,1,2)
```



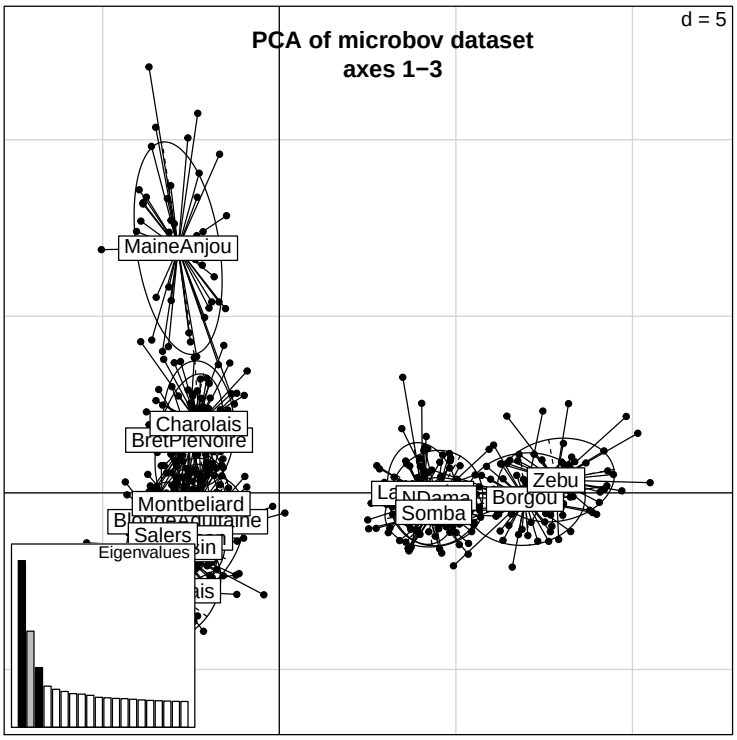
However, this figure can largely be improved. First, we can use `s.class` to represent both the genotypes and inertia ellipses for populations.

```
> s.class(pca1$li, pop(microbov))
> title("PCA of microbov dataset\naxes 1-2")
> add.scatter.eig(pca1$eig[1:20], 3,1,2)
```



This plane shows that the main structuring is between African an French breeds, the second structure reflecting genetic diversity among African breeds. The third axis reflects the diversity among French breeds:

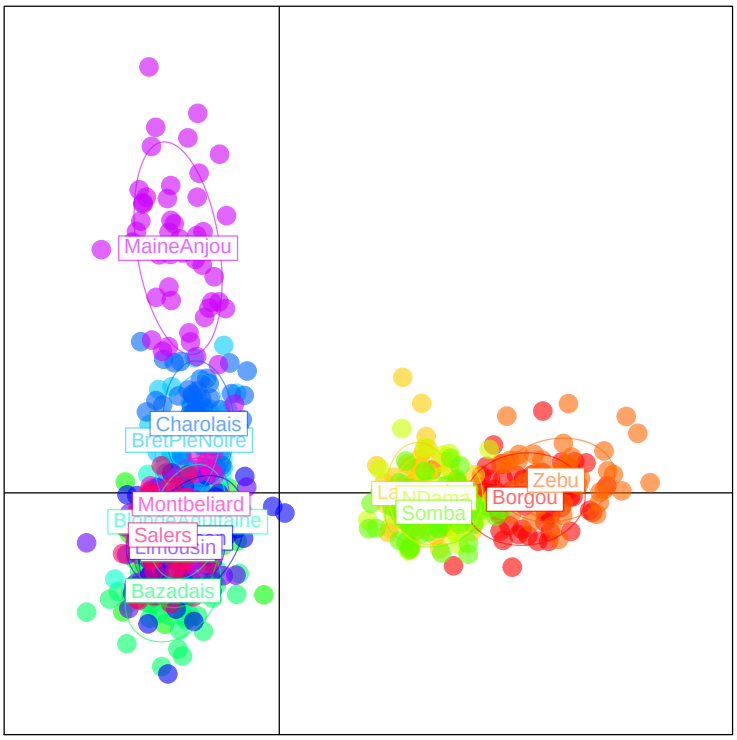
```
> s.class(pca1$li,pop(microbov),xax=1,yax=3,sub="PCA 1-3",csub=2)
> title("PCA of microbov dataset\naxes 1-3")
> add.scatter.eig(pca1$eig[1:20],nf=3,xax=1,yax=3)
```



Overall, all breeds seem well differentiated.

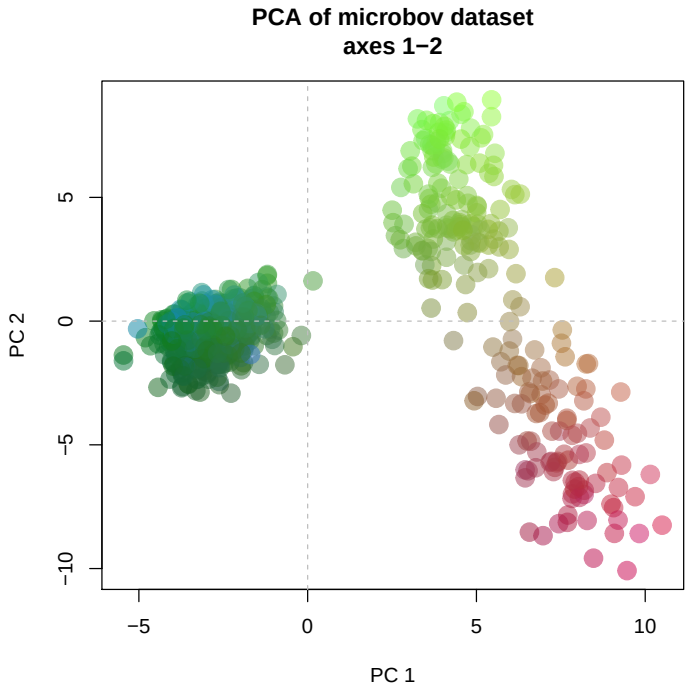
However, we can yet improve these scatterplots, which are fortunately easy to customize. For instance, we can remove the grid, choose different colors for the groups, use larger dots and transparency to better assess the density of points, and remove internal segments of the ellipses:

```
> col <- rainbow(length(levels(pop(microbov))))
> s.class(pca1$li, pop(microbov),xax=1,yax=3, col=transp(col,.6), axesell=FALSE, cstar=0, cpoint=3, grid=FALSE)
```



Let us now assume that we ignore the group memberships. We can still use color in an informative way. For instance, we can recode the principal components represented in the scatterplot on the RGB scale:

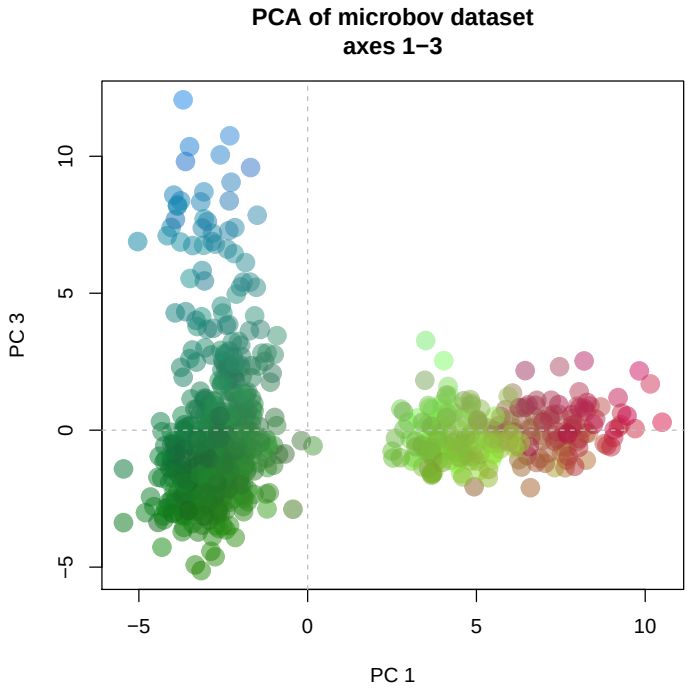
```
> colorplot(pca1$li, pca1$li, transp=TRUE, cex=3, xlab="PC 1", ylab="PC 2")
> title("PCA of microbov dataset\naxes 1-2")
> abline(v=0,h=0,col="grey", lty=2)
```



Colors are based on the first three PCs of the PCA, recoded respectively on the red, green, and blue channel. In this figure, the genetic diversity is represented in two complementary ways: by the distances (further away = more genetically different), and by the colors (more different colors = more genetically different).

We can represent the diversity on the third axis similarly:

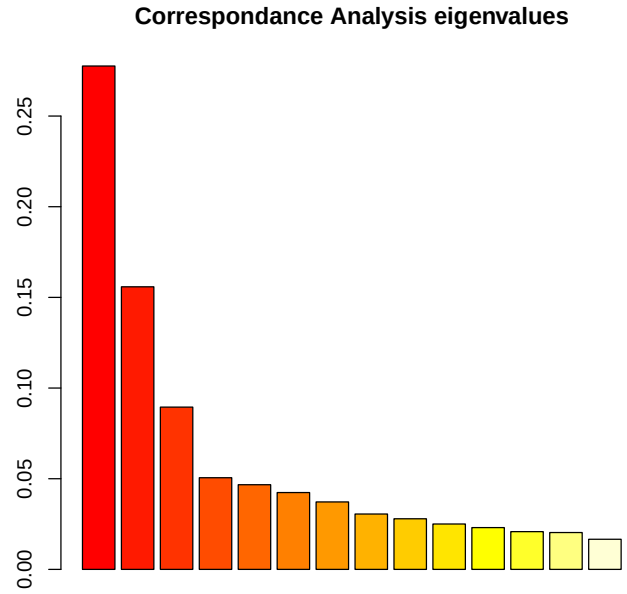
```
> colorplot(pca1$li[c(1,3)], pca1$li, transp=TRUE, cex=3, xlab="PC 1", ylab="PC 3")
> title("PCA of microbov dataset\naxes 1-3")
> abline(v=0,h=0,col="grey", lty=2)
```



6.3 Performing a Correspondance Analysis on genpop objects

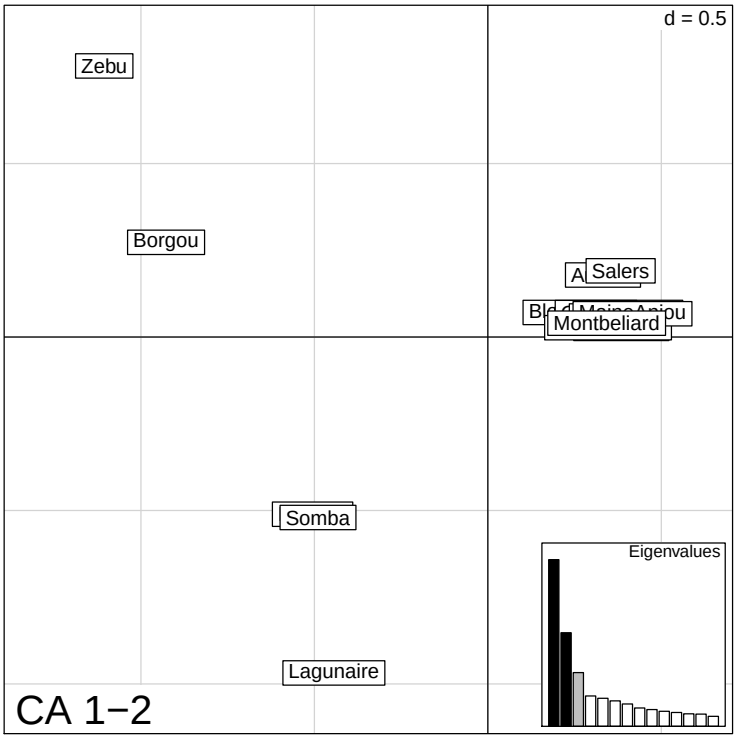
Being contingency tables, the `@tab` slot in `genpop` objects can be submitted to a Correspondance Analysis (CA) to seek a typology of populations. The approach is very similar to the previous one for PCA. Missing data are first replaced during convertion from `genind`, but one could create a `genpop` with NAs and then use `na.replace` to get rid of missing observations.

```
> data(microbov)
> obj <- genind2genpop(microbov,missing="chi2")


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

 Replaced 0 missing values

...done.


> ca1 <- dudi.coa(as.data.frame(obj$tab),scannf=FALSE,nf=3)
> barplot(ca1$eig,main="Correspondance Analysis eigenvalues", col=heat.colors(length(ca1$eig)))
```

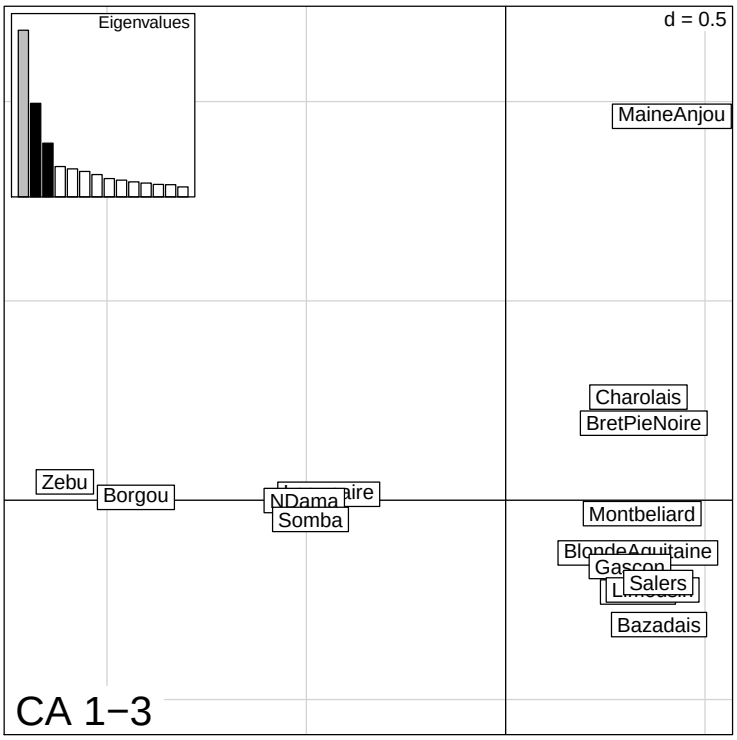


Now we display the resulting typology using a basic scatterplot:

```
> s.label(ca1$li,lab=obj$pop.names,sub="CA 1-2",csub=2)
> add.scatter.eig(ca1$eig,nf=3,xax=1,yax=2,posi="bottomright")
```




```
> s.label(ca1$li,xax=1,yax=3,lab=obj$pop.names,sub="CA 1-3",csub=2)
> add.scatter.eig(ca1$eig,nf=3,xax=2,yax=3,posi="topleft")
```



As in the PCA above, axes are to be interpreted separately in terms of continental differentiation, and between-breeds diversity. Importantly, as in any analysis carried out at a population level, all information about the diversity within populations is lost in this analysis. See the vignette on DAPC for an individual-based approach which is nontheless optimal in terms of group separation (*adegenet-dapc*).

7 Spatial analysis

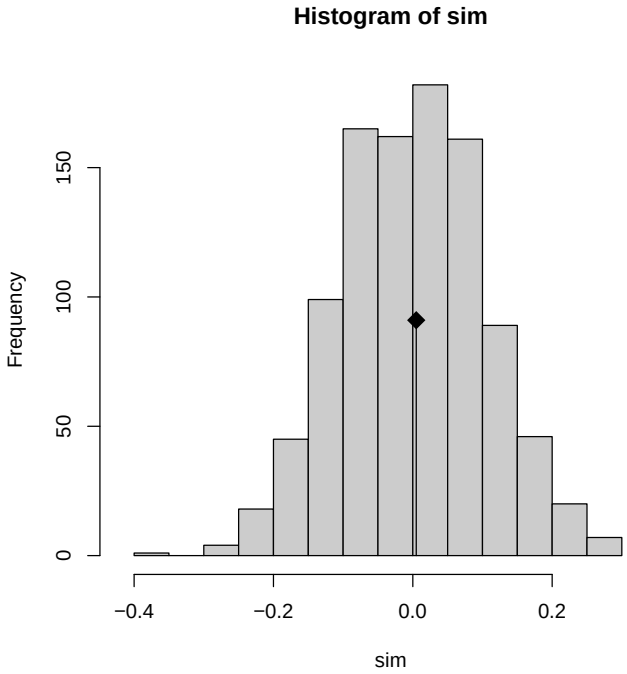
The R software probably offers the largest collection of spatial methods among statistical software. Here, we briefly illustrate two methods commonly used in population genetics. Spatial multivariate analysis is covered in a dedicated vignette; see *adegenet-spca* for more information.

7.1 Isolation by distance

7.1.1 Testing isolation by distance

Isolation by distance (IBD) is tested using Mantel test between a matrix of genetic distances and a matrix of geographic distances. It can be tested using individuals as well as populations. This example uses cat colonies from the city of Nancy. We test the correlation between Edwards' distances and Euclidean geographic distances between colonies.

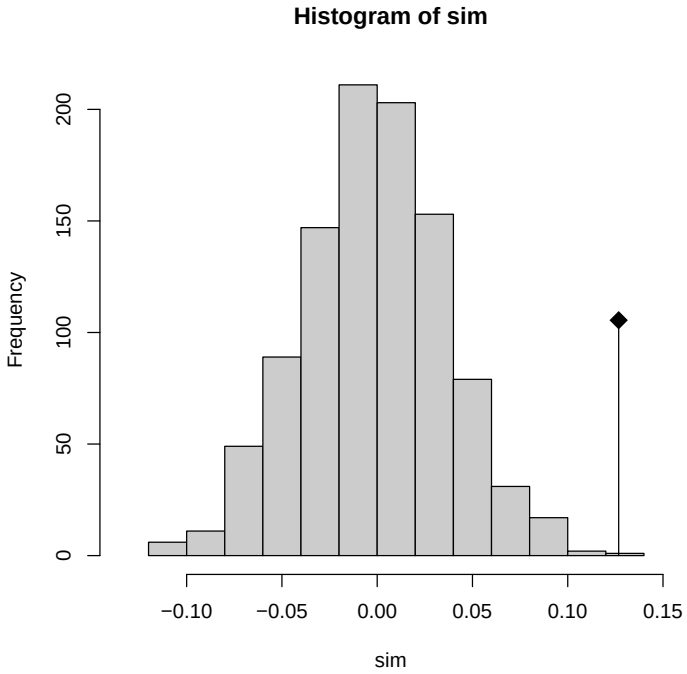
```
> data(nancycats)
> toto <- genind2genpop(nancycats,miss="0")


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

 Replaced 9 missing values

...done.


> Dgen <- dist.genpop(toto,method=2)
> Dgeo <- dist(nancycats$other$xy)
> ibd <- mantel.randtest(Dgen,Dgeo)
> ibd


Monte-Carlo test
Call: mantel.randtest(m1 = Dgen, m2 = Dgeo)

Observation: 0.00492068

Based on 999 replicates
Simulated p-value: 0.486
Alternative hypothesis: greater

      Std.Obs   Expectation      Variance
 0.0499864919 -0.0002404791  0.0106607863


> plot(ibd)
```



The original value of the correlation between the distance matrices is represented by the dot, while histograms represent permuted values (i.e., under the absence of spatial structure). Significant spatial structure would therefore result in the original value being out of the reference distribution. Here, isolation by distance is clearly not significant.

Let us provide another example using a dataset of individuals simulated under an IBD model:

```
> data(spcaIllus)
> x <- spcaIllus$dat2B
> Dgen <- dist(x$tab)
> Dgeo <- dist(other(x)$xy)
> ibd <- mantel.randtest(Dgen,Dgeo)
> ibd


Monte-Carlo test
Call: mantel.randtest(m1 = Dgen, m2 = Dgeo)

Observation: 0.1267341

Based on 999 replicates
Simulated p-value: 0.001
Alternative hypothesis: greater

     Std.Obs  Expectation     Variance
 3.390270211 -0.001255724  0.001425221


> plot(ibd)
```

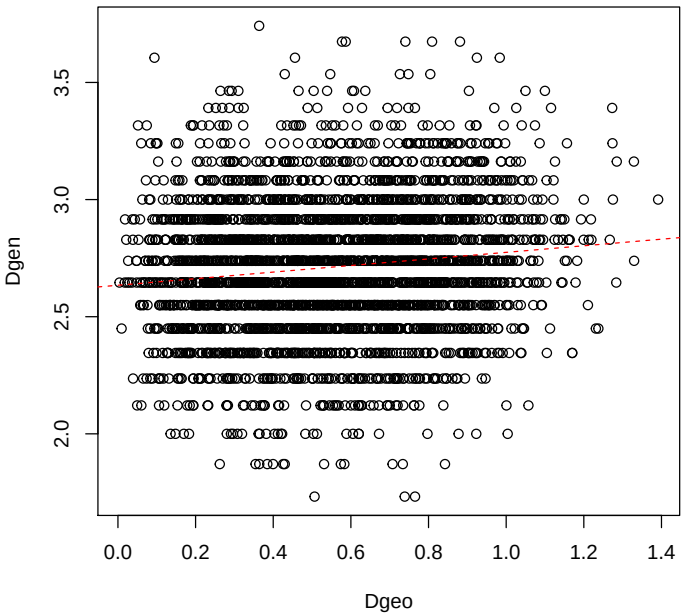


This time there is a clear isolation by distance pattern.

7.1.2 Cline or distant patches?

The correlation between genetic and geographic distances can occur under a range of different biological scenarios. Classical IBD would result in continuous clines of genetic differentiation and cause such correlation. However, distant and differentiated populations would also result in such a pattern. These are slightly different processes and we would like to be able to disentangle them. A very simple first approach is simply plotting both distances:

```
> plot(Dgeo, Dgen)
> abline(lm(Dgen~Dgeo), col="red",lty=2)
```



Most of the time, simple scatterplots fail to provide a good picture of the data as the density of points in the scatterplot is badly displayed. Colors can be used to provide better (and prettier) plots. Local density is measured using a 2-dimensional kernel density estimation (`kde2d`), and the results are displayed using `image`; `colorRampPalette` is used to generate a customized color palette:

```
> dens <- kde2d(Dgeo,Dgen, n=300, lims=c(-.1, 1.5,-.5,4))
> myPal <- colorRampPalette(c("white","blue","gold", "orange", "red"))
> plot(Dgeo, Dgen, pch=20,cex=.5)
> image(dens, col=transp(myPal(300),.7), add=TRUE)
> abline(lm(Dgen~Dgeo))
> title("Isolation by distance plot")
```

The scatterplot clearly shows one single consistent cloud of point, without discontinuities which would have indicated patches. This is reassuring, since the data were actually simulated under an IBD (continuous) model.

7.2 Using Monmonier's algorithm to define genetic boundaries

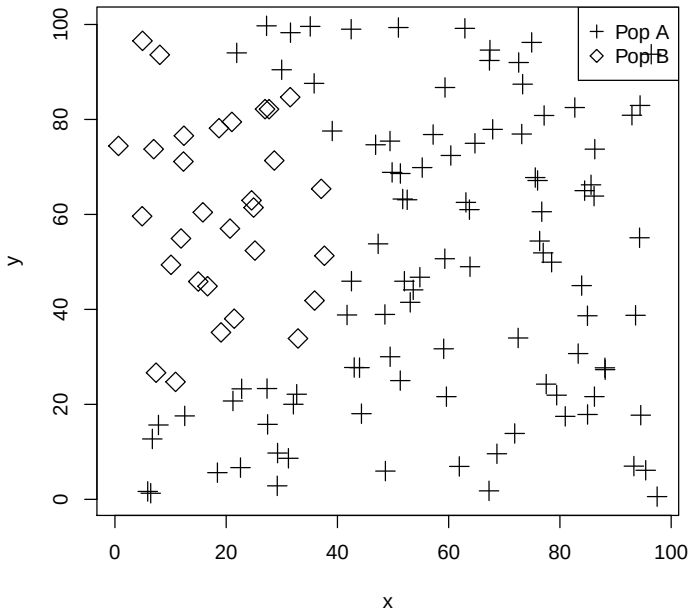
Monmonier's algorithm [**?**] was originally designed to find boundaries of maximum differences between contiguous polygons of a tesselation. As such, the method was basically used in geographical analysis. More recently, [**?**]

suggested that this algorithm could be employed to detect genetic boundaries among georeferecend genotypes (or populations). This algorithm is implemented using a more general approach than the initial one in *adegenet*.

Instead of using Voronoi tesselation as in the original version, the functions `monmonier` and `optimize.monmonier` can handle various neighbouring graphs such as Delaunay triangulation, Gabriel's graph, Relative Neighbours graph, etc. These graphs define spatial connectivity among locations (of genotypes or populations), with couple of locations being neighbours (if connected) or not. Another information is given by a set of markers which define genetic distances among these 'points'. The aim of Monmonier's algorithm is to find the path through the strongest genetic distances between neighbours. A more complete description of the principle of this algorithm will be found in the documentation of `monmonier`. Indeed, the very purpose of this tutorial is simply to show how it can be used on genetic data.

Let's take the example from the function's manpage and detail it. The dataset used is `sim2pop`.

```
> data(sim2pop)
> sim2pop


   ######################
   ### Genind object ###
   ######################
- genotypes of individuals -

S4 class:  genind
@call: old2new(object = sim2pop)

@tab:  130 x 241 matrix of genotypes

@ind.names: vector of  130 individual names
@loc.names: vector of  20 locus names
@loc.nall: number of alleles per locus
@loc.fac: locus factor for the  241 columns of @tab
@all.names: list of  20 components yielding allele names for each locus
@ploidy:  2
@type:  codom

Optionnal contents:
@pop:  factor giving the population of each individual
@pop.names:  factor giving the population of each individual

@other: a list containing: xy


> summary(sim2pop$pop)


P01 P02
100  30


> temp <- sim2pop$pop
> levels(temp) <- c(3,5)
> temp <- as.numeric(as.character(temp))
> plot(sim2pop$other$xy,pch=temp,cex=1.5,xlab='x',ylab='y')
> legend("topright",leg=c("Pop A", "Pop B"),pch=c(3,5))
```



There are two sampled populations in this dataset, with inequal sample sizes (100 and 30). Twenty microsatellite-like loci are available for all genotypes (no missing data). `monmonier` requires several arguments to be specified:

```
> args(monmonier)
```

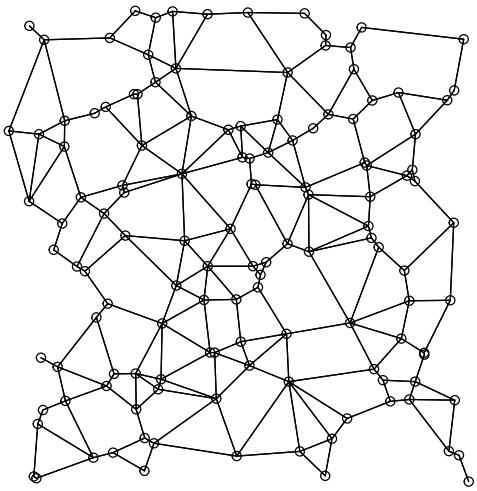
```
function (xy, dist, cn, threshold = NULL, bd.length = NULL, nrun = 1,
    skip.local.diff = rep(0, nrun), scanthres = is.null(threshold),
    allowLoop = TRUE)
NULL
```

The first argument (`xy`) is a matrix of geographic coordinates, already stored in `sim2pop`. Next argument is an object of class `dist`, which is the matrix of pairwise genetic distances. For now, we will use the classical Euclidean distance between allelic profiles of the individuals. This is obtained by:

```
> D <- dist(sim2pop$tab)
```

The next argument (`cn`) is a connection network. Routines for building such networks are scattered over several packages, but all made available through the function `chooseCN`. Here, we disable the interactivity of the function (`ask=FALSE`) and select the second type of graph which is the graph of Gabriel (`type=2`).

```
> gab <- chooseCN(sim2pop$other$xy,ask=FALSE,type=2)
```



The obtained network is automatically plotted by the function. It seems we are now ready to proceed to the algorithm.

```
> mon1 <- monmonier(sim2pop$other$xy,D,gab)
```

monthres1.png

This plot shows all local differences sorted in decreasing order. The idea behind this is that a significant boundary would cause local differences to decrease abruptly after the boundary. This should be used to choose the *threshold*

difference for the algorithm to stop extending the boundary. Here, there is no indication af an actual boundary.

Why do the algorithm fail to find a boundary? Either because there is no genetic differentiation to be found, or because the signal differentiating both populations is too weak to overcome the random noise in genetic distances. What is the F_{st} between the two samples?

```
> pairwise.fst(sim2pop)


           1
2 0.02343044
```

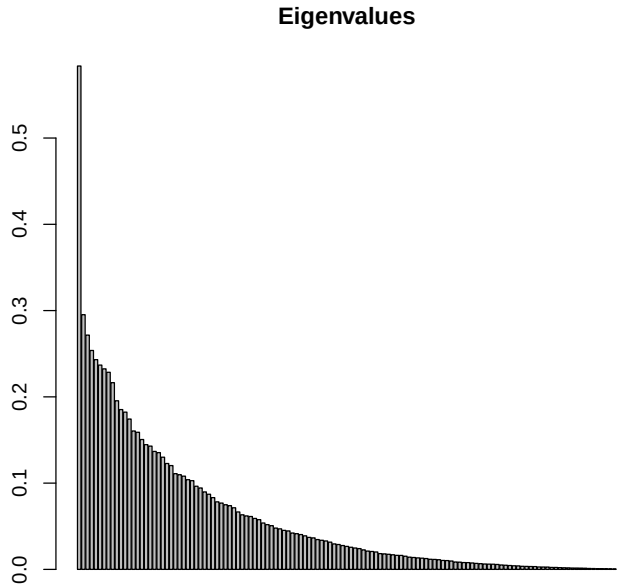
This value would be considered as very weak differentiation ($F_{ST} = 0.023$). Is it significant? We can easily ellaborate a permutation test of this F_{ST} value; to save computational time, we use only a small number of replicates to generate F_{ST} values in absence of population structure:

```
> replicate(10, pairwise.fst(sim2pop, pop=sample(pop(sim2pop))))


 [1] 0.003415881 0.003854108 0.003596763 0.002876525 0.003622251 0.003674871
 [7] 0.003217733 0.004649165 0.002878169 0.003510433
```

F_{ST} values in absence of population structure would be one order of magnitude lower (more replicate would give a very low p-value — just replace `10` by `200` in the above command). In fact, the two samples are indeed genetically differentiated.

Can Monmonier's algorithm find a boundary between the two populations? Yes, if we get rid of the random noise. This can be achieved using a simple ordination method such as Principal Coordinates Analysis.

```
> library(ade4)
> pco1 <- dudi.pco(D,scannf=FALSE,nf=1)
> barplot(pco1$eig,main="Eigenvalues")
```



We retain only the first eigenvalue. The corresponding coordinates are used to redefine the genetic distances among genotypes. The algorithm is then re-run.

```
> D <- dist(pco1$li)
```

```
> mon1 <- monmonier(sim2pop$other$xy,D,gab)
```

```
############################################################
# List of paths of maximum differences between neighbours #
#           Using a Monmonier based algorithm              #
############################################################

$call:monmonier(xy = sim2pop$other$xy, dist = D, cn = gab, scanthres = FALSE)

      # Object content #
Class:  monmonier
$nrun (number of successive runs):  1
$run1: run of the algorithm
$threshold (minimum difference between neighbours):  0.8154
$xy: spatial coordinates
$cn: connection network

      # Runs content #
# Run 1
# First direction
Class:  list
$path:
               x        y
Point_1 14.98299 93.81162

$values:
 2.281778
# Second direction
Class:  list
$path:
               x        y
Point_1 14.98299 93.81162
Point_2 30.74508 87.57724
Point_3 33.66093 86.14115
...

$values:
 2.281778 1.617905 1.95322 ...
```

This may take some time... but never more than five minutes on an 'ordinary' personnal computer. The object `mon1` contains the whole information about the boundaries found. As several boundaries can be seeked at the same time (argument `nrun`), you have to specify about which run and which direction you want to get informations (values of differences or path coordinates). For instance:

```
> names(mon1)

[1] "run1"      "nrun"      "threshold" "xy"        "cn"        "call"

> names(mon1$run1)

[1] "dir1" "dir2"

> mon1$run1$dir1

$path
               x        y
Point_1 14.98299 93.81162

$values
[1] 2.281778
```

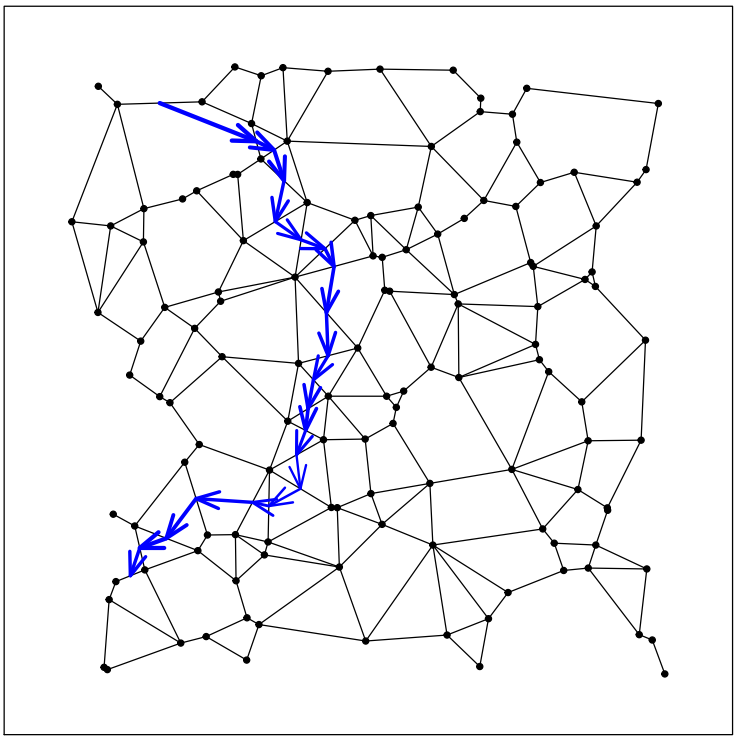
It can also be useful to identify which points are crossed by the barrier; this can be done using `coords.monmonier`:

```
> coords.monmonier(mon1)


$run1
$run1$dir1
           x.hw     y.hw first second
Point_1 14.98299 93.81162    11    125

$run1$dir2
            x.hw     y.hw first second
Point_1  14.98299 93.81162    11    125
Point_2  30.74508 87.57724    44    128
Point_3  33.66093 86.14115    20    128
Point_4  35.28914 81.12578    68    128
Point_5  33.85756 74.45492    68    117
Point_6  38.07622 71.47532    68    122
Point_7  41.97494 70.02783    35    122
Point_8  43.45812 67.12026    69    122
Point_9  42.20206 59.59613    22    122
Point_10 42.48613 52.55145    22    124
Point_11 40.08702 48.61795    13    124
Point_12 39.20791 43.89978    13    127
Point_13 38.81236 40.34516    62    127
Point_14 37.32112 36.35265    62    130
Point_15 37.96426 30.82105    94    130
Point_16 32.79703 28.00517    16    130
Point_17 30.12832 28.60376    85    130
Point_18 20.92496 29.21211    63    119
Point_19 16.05811 22.72600    61    126
Point_20 11.72524 21.15519    89    126
Point_21 10.18696 16.61536    74     89
```

The returned dataframe contains, in this order, the x and y coordinates of the points of the barrier, and the identifiers of the two 'parent' points, that is, the points whose barycenter is the point of the barrier.

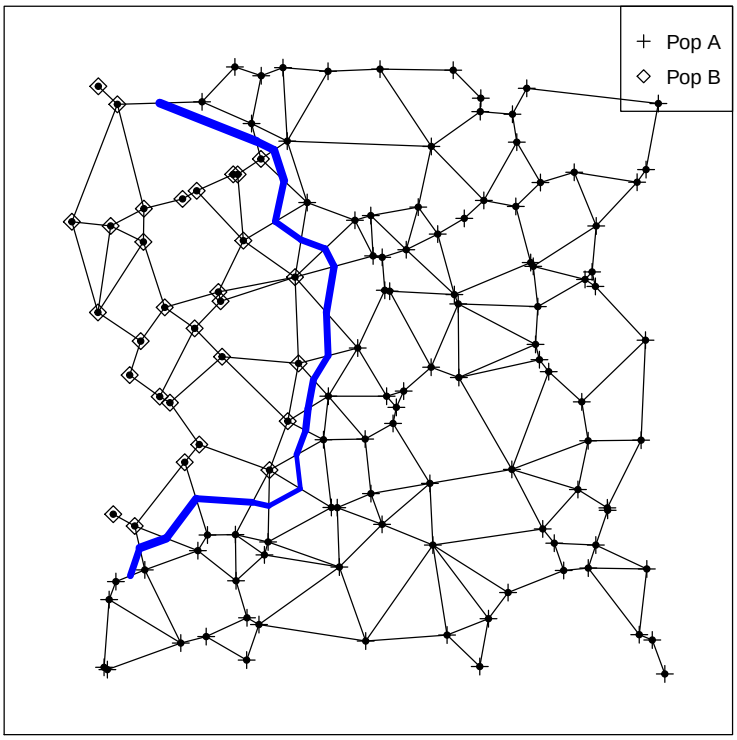
Finally, you can plot very simply the obtained boundary using the method `plot`:

```
> plot(mon1)
```



see arguments in `?plot.monmonier` to customize this representation. Last, we can compare the infered boundary with the actual distribution of populations:

```
> plot(mon1,add.arrows=FALSE,bwd=8)
> temp <- sim2pop$pop
> levels(temp) <- c(3,5)
> temp <- as.numeric(as.character(temp))
> points(sim2pop$other$xy,pch=temp,cex=1.3)
> legend("topright",leg=c("Pop A", "Pop B"),pch=c(3,5))
```



Not too bad...

8 Simulating hybridization

The function `hybridize` allows to simulate hybridization between individuals from two distinct genetic pools, or more broadly between two `genind` objects. Here, we use the example from the manpage of the function, to go a little further. Please have a look at the documentation, especially at the different possible outputs (outputs for the software STRUCTURE is notably available).

```
> temp <- seppop(microbov)
> names(temp)
```

```
 [1] "Borgou"          "Zebu"            "Lagunaire"       "NDama"
 [5] "Somba"           "Aubrac"          "Bazadais"        "BlondeAquitaine"
 [9] "BretPieNoire"    "Charolais"       "Gascon"          "Limousin"
[13] "MaineAnjou"      "Montbeliard"     "Salers"
```

```
> salers <- temp$Salers
> zebu <- temp$Zebu
> zebler <- hybridize(salers, zebu, n=40, pop="zebler")
```

A first generation (F1) of hybrids 'zebler' is obtained. Is it possible to perform a backcross, say, with 'salers' population? Yes, here it is:

```
> F2 <- hybridize(salers, zebler, n=40)
> F3 <- hybridize(salers, F2, n=40)
> F4 <- hybridize(salers, F3, n=40)
```

Finally, note that despite this example shows hybridization between diploid organisms, `hybridize` is not retrained to this case. In fact, organisms with any even level of ploidy can be used, in which case half of the genes is taken from each reference population. Ultimately, more complex mating schemes could be implemented... suggestion or (better) contributions are welcome!

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