# Kinship and pedigree analysis: Methods and applications

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## Exercise set III. Kinship testing

Before you start, run the following commands to download some of the datasets used in this course.

```
url = "https://magnusdv.github.io/pedinr/datasets/data.zip"
download.file(url, destfile = "data.zip")
unzip("data.zip")
```

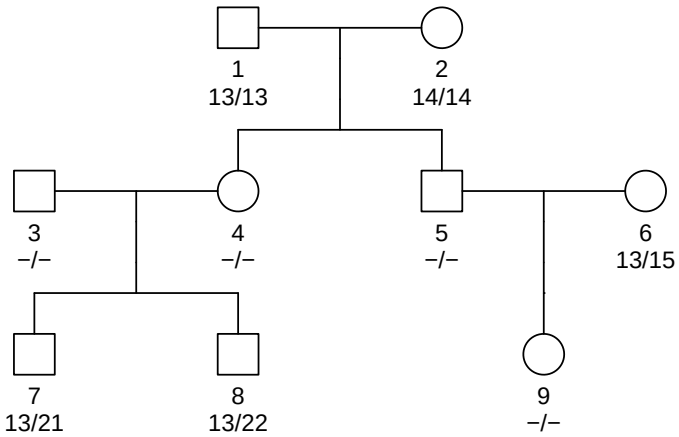
*Note*: The files are put in a subfolder `data` in the current working directory. You can identify this by with the command `getwd()`.

You should also load the **pedsuite** packages:

```
library(pedsuite)
```

### Exercise III-1

Consider the following pedigree, in which some members have been typed with a single DNA marker.




a) What kind of marker is this: SNP or STR? Autosomal or X-linked? How do you know?
b) How many different alleles are observed in the family. What do the allele labels (e.g. `13`) mean?
c) What are the genotypes of individuals 4 and 5?
d) Can you determine the genotype of individual 3?
e) What are the possible genotypes for individual 9, and how likely is each of them?

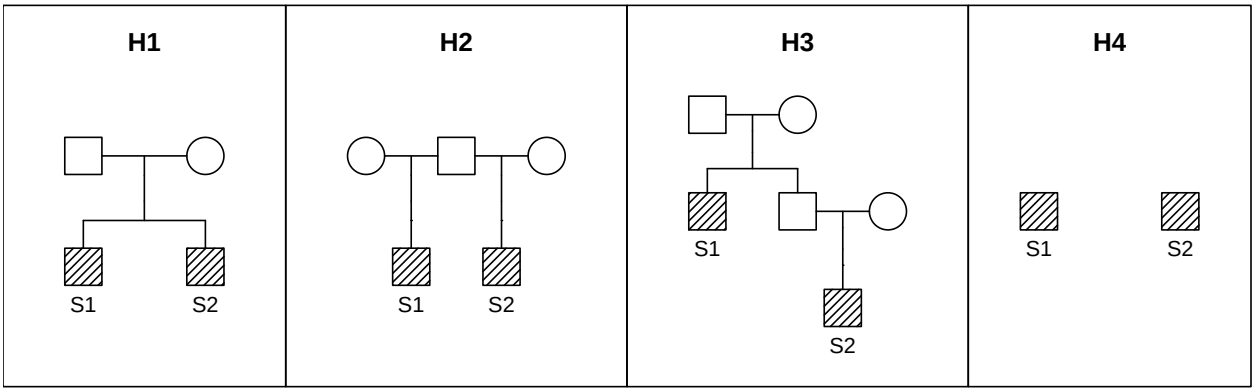
### Exercise III-2

In a paternity case, the alleged father has genotype a/b for a certain marker, while the child, has genotype a/c. The mother is not genotyped.

a) Formulate the natural hypotheses H1 and H2, and create the corresponding pedigree objects in R.
b) Use `plotPedList()` to plot H1 and H2.
c) Use `kinshipLR()` to compute the LR if the allele frequencies are $p_a = 0.01$, $p_b = 0.3$ and $p_c = 0.69$.
d) (Optional) Find a general formula for LR expressed by the allele frequency $p_a$.

### Exercise III-3

In this exercise we will analyse the relationship between two males, S1 and S2, who are genotyped with 15 STR markers. The hypothesised pedigrees are shown below.




a) Define the first three pedigrees by running:

```
ids = c("S1", "S2")
H1 = nuclearPed(children = ids)
H2 = relabel(halfSibPed(), old = 4:5, new = ids)
H3 = relabel(avuncularPed(), old = c(3,6), new = ids)
```

b) Load the marker data and check that the result contains S1 and S2 as singletons.

```
H4 = readPed("../data/kinship-riddle.ped")
H4 = setFreqDatabase(H4, database = NorwegianFrequencies)
summary(H4)
```

c) Find the LRs using H4 as the reference by running

```
lr = kinshipLR(H1, H2, H3, H4, verbose = TRUE, ref = 4)
```

d) Notice that H2 and H3 give identical LRs. Do you think this is a coincidence? Explain!

e) Include a hypothesis specifying that S1 and S2 are first cousins, and find the LR against H4. *Hint*:

```
H5 = relabel(cousinPed(1), old = 7:8, new = ids)
```