Kinship and pedigree analysis: Methods and applications

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Solutions for exercise set III. Kinship testing

Some answers are given in the exercise. Here we add some comments and remaining answers.

The **pedsuite** R packages are used in several solutions:

```r
library(pedsuite)
```

Exercise III-1

a) The marker is an autosomal STR marker. Reasons: allele labels; more than two alleles.
b) Five alleles (13, 14, 15, 21 and 22) are observed. The alleles names indicate the number of repeats.
c) Both 4 and 5 have genotype 13/14 (because of their parents).
d) Individual 3 has genotype 21/22 (because his children must have gotten 13 from their mother).
e) The possible genotypes are 13/13, 13/14, 13/15 and 14/15, each with probability $\frac{1}{4}$.

Exercise III-2

a) The natural hypotheses are:

   - H1: The alleged father (AF) is the biological father.
   - H2: The alleged father and the child are unrelated.

   The corresponding pedigrees can be created in R as follows:

```r
H1 = nuclearPed(fa = "AF", mo = "MO", child = "CH")
H2 = singletons(c("AF", "CH"))
```

b) Possible plot command:

```r
plotPedList(list(H1, H2), hatched = c("AF", "CH"))
```

c) We follow the approach given in the lecture:

```r
# Attach marker data to H1
H1 = addMarker(H1, AF = "a/b", CH = "a/c",
               afreq = c(a = 0.01, b = 0.30, c = 0.69))

# Compute LR
kinshipLR(H1, H2, source = 1)
```

```
## H1:H2 H2:H2
##    25     1
```

d) We find LR $= \frac{2p_a p_b \frac{1}{2} p_c}{2p_a p_b 2p_a p_c} = \frac{1}{4p_a} = 25$.

Exercise III-3

a) See exercise.

b) See exercise. Summary:

```
## List of 2 singletons.
## Labels: S1 (male), S2 (male).
## 15 attached markers.
```

c) We find the LRs as follows:

```
kinshipLR(H1, H2, H3, H4, source = 4)
```

```
##    H1:H4    H2:H4    H3:H4    H4:H4
## 569.3989 805.1175 805.1175   1.0000
```

Comment: The argument `source = 4` secures that marker data from H4 are transferred to the other pedigrees. However, it was not actually needed in this case, since, as stated in the documentation: "*If exactly one of the pedigrees have attached markers, these are transferred to the others.*" In our case this would apply since only H4 contains data.

d) This is not a coincidence. Since the relationships half siblings (H2) and uncle-nephew (H3) have identical IBD coefficients, $(\kappa_0, \kappa_1, \kappa_2) = (0.5, 0.5, 0)$, they are indistinguishable with unlinked markers.

e) We add the new pedigree and find the LRs:

```
H5 = relabel(cousinPed(1), old = 7:8, new = ids)
lr = kinshipLR(H1, H2, H3, H4, H5, source = 4, ref = 4)
lr
```

```
##    H1:H4    H2:H4    H3:H4    H4:H4    H5:H4
## 569.3989 805.1175 805.1175   1.0000 110.0958
```