Pedigrees and kinship analysis in forensic genetics

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Exercise set III. Kinship analysis with linked markers

The **KLINK** program used in these exercises can be run in two way:

- *Online*: Freely available at https://magnusdv.shinyapps.io/klink. (Not intended for sensitive case data.)
- *From R*: This version runs locally on your computer and does not require internet connection. Once the package is installed, the app opens with a single command:

```r
install.packages("KLINK")
KLINK::launchApp()
```

Linkage Lab is freely available online here: https://magnusdv.shinyapps.io/linkagelab.

Exercise III-1 (Continuation of Familias case)

In this exercise we continue with the half-sibling case created in Familias in Exercise II-2.

a) Open the file you created (perhaps *halfsib_case.fam*) in KLINK.
    i. Verify that the pedigrees and genotypes are correct.
    ii. Where are the two markers located? Are they linked? (Hint: Look at *Linkage map*.)
    iii. What is the centiMorgan distance between the markers?
b) Calculate the LR in KLINK.
    i. Does the *No link* LR agree with the result you obtained with Familias?
    ii. What is the LR accounting for linkage? How much (in %) does it differ from the unlinked LR?
c) Set the mutation model to *Simple*.
    i. What is the mutation rate with this model? (Hint: Look at *Marker data*.)
    ii. How much does the LR change?

Exercise III-2 (Linkage Lab)

In this exercise we use Linkage Lab to investigate the half-sibling case even further.

a) Enter the case data (as described in Exercise II-2) into Linkage Lab. Remember that Linkage Lab expects alleles to be coded as 1,2,3,4 for both markers. For instance, the genotypes `16/17` and `17/17` for vWA should be entered as `1/2` and `2/2`. For the allele frequencies, use the frequencies given in the Exercise II-2 (it does not matter what you use for alleles 3 and 4).
b) Enter the cM distance you found in the previous exercise, in the *Dist (cM)* field. Check that the resulting LR (yellow dot in the graph) agrees with the LR you obtained in KLINK.
c) What would the LR be if the markers were completely linked?
d) Suppose the genotype of the first individual was `16/16` instead of `16/17`. Use Linkage Lab to describe how linkage would affect the LR in this case.

Exercise III-3 (KLINK - larger example)

In this exercise we analyse one of the built-in examples in KLINK. To get started, open the KLINK app (either online or locally in R) and click the green button named “Example 2”.

a) Describe the kinship case. What are the hypotheses?
b) How many markers are used? How many linked pairs are there?
c) Some chromosomes have more than two markers. How does KLINK handle this?
d) Compute the LRs. What is the total LR with and without linkage?
e) Turn off mutation modelling and recalculate the LRs. What happens? Explain why.
f) Re-do the LRs using the original mutation models, and download the results. Examine the different sheets of the Excel document.