

ISFG summer school - virtual edition 2021

Pedigree analysis in R

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Solutions for exercise set II

We start by loading the **pedsuite**, which automatically includes **pedtools** and **pedprobr**.

```
library(pedsuite)
```

Exercise II-1 (Creating pedigrees)

No answer.

Exercise II-2 (Pedigree shortcuts)

No answer

Exercise II-3 (Marker genotypes and plotting options)

c) The following code recreates the figure:

```
plot(x, m, sep = "", missing = "?", shaded = 3:5, showEmpty = T,  
     deceased = 2, col = list(red = 3:5), labs = NULL)
```

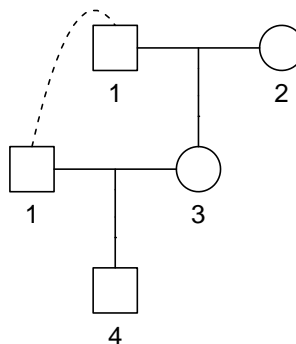
Exercise II-4 (Creating and loading a pedigree file)

No answer

Exercise II-5 (Inbred pedigrees)

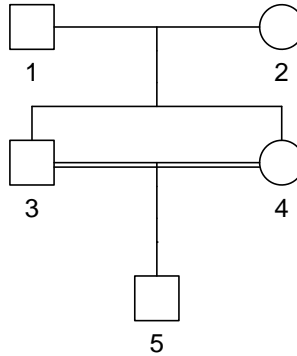
a) Father-daughter incest:

```
x = nuclearPed(1, sex = 2)  
x = addChildren(x, father = 1, mother = 3, nch = 1)  
plot(x, margin = c(1,1,1,1))
```



b) Brother-sister incest:

```
x = nuclearPed(2, sex = 1:2)  
x = addChildren(x, father = 3, mother = 4, nch = 1)  
plot(x, margin = c(1,1,1,1))
```



Exercise II-6 (Pedigree likelihoods)

a) 0.0081

b) 0.0010125, as calculated with the following code:

```
x = nuclearPed(3)
m = marker(x, geno = c(NA, NA, "A/A", "B/B", "A/B"), afreq = c(A = 0.9, B = 0.1))
likelihood(x, m)
```

```
## [1] 0.0010125
```

c) For a), both children's genotypes are forced, so we only have to find the probability of observing A/A and B/B in the parents. With the stated frequencies the standard Hardy-Weinberg proportions give $(0.1)^2 \cdot (0.9)^2 = 0.0081$, confirming the previous result.

In b) both parents must have genotype A/B. Assuming HWE the complete calculation becomes:

$$P(\text{parents}) \cdot P(\text{children} \mid \text{parents}) = (2 \cdot 0.1 \cdot 0.9)^2 \cdot (0.5^2 \cdot 0.5^2 \cdot 0.5) = 0.0010125$$