Genetic Relatedness

Magnus Dehli Vigeland

Exercise set II. Measures of relatedness

Most of these exercises can be solved in either QuickPed, R, or by hand (if you want to show off!)

QuickPed: https://magnusdv.shinyapps.io/quickped/

Exercise II-1

Find the kinship coefficient of the following relationships:

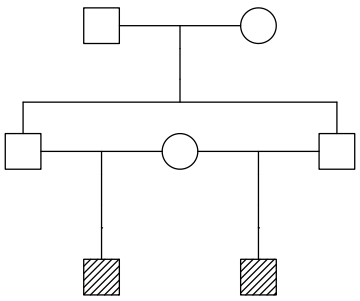
a) Uncle – niece.
b) Half first cousins.

Exercise II-2

a) What is the kinship coefficient between monozygotic twins? (Hint: Use the definition of the kinship coefficient.)
b) Can you think of a relationship with kinship coefficient $\varphi = 1$?

Exercise II-3

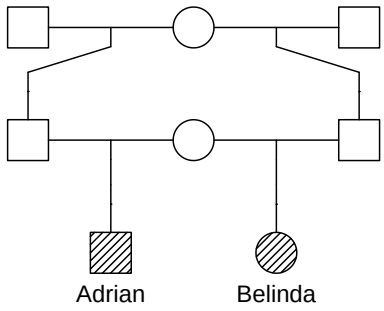
Consider the following pedigree:



a) Describe the relationship between the children. Are they inbred?
b) Show that their IBD coefficients are $\kappa = (\frac{3}{8}, \frac{1}{2}, \frac{1}{8})$.
c) Show the relationship in the IBD triangle.
d) This relationship is sometimes called *3/4-siblings*. Why?

Exercise II-4

Recall the relationship between Adrian and Belinda from the previous exercise set:



a) Compute the kinship coefficient between Adrian and Belinda.
b) Compute their IBD coefficients $(\kappa_0, \kappa_1, \kappa_2)$.
c) Plot the corresponding point in the IBD triangle.
d) (For the mathematically inclined) Explain why Adrian and Belinda may be called *5/8-siblings*.

Exercise II-5 (Realised inbreeding)

In a case of incest a man had a son by his own granddaughter. The purpose of this exercise is to explore the distribution of the realised inbreeding in the offspring.

a) Create and plot the pedigree in R with the following code.

```
x = linearPed(2, sex = 2) |> addSon(parents = c(1, 5))
plot(x)
```

b) What is the inbreeding coefficient of the child?

c) Run the code below to simulate 500 realisations of the recombination in the pedigree. (Note the use of `seed` for reproducibility.)

```
library(ibdsim2)
sims = ibdsim(x, N = 500, seed = 111)
```

d) Plot the autozygous segments of the child in the first simulation.

```
sim1 = sims[[1]]
segs = findPattern(sim1, pattern = list(autozygous = "6"))
karyoHaploid(segs, title = "Autozygous segments")
```

e) For a more detailed picture, plot the full IBD pattern of the first chromosome:

```
haploDraw(x, sim1, chrom = 1)

# Alternative versions using optional parameters
haploDraw(x, sim1, chrom = 1, pos = c(2,4,2,4,4,4))
haploDraw(x, sim1, chrom = 1, pos = c(2,0,0,4,4,4),
          col = c("#FFC1C1", "#B20000", rep("gray90", 4)))
```

f) Use the code below to create a histogram of the realised inbreeding in the 500 simulations. Comment on the result.

```
r = realisedInbreeding(sims, id = 6)
fReal = r$perSimulation$fReal
hist(fReal, main = "Realised inbreeding")
abline(v = 0.125, col = 2, lwd=2)
```

g) Find the standard deviation of the realised inbreeding coefficients.

h) How many autozygous segments will the child typically have? (Hint: `r$perSimulation$nSeg`.)