Genetic Relatedness

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Solutions for exercise set II

Note: Solutions in R are given here; most of the exercises can also be solved (usually faster) in QuickPed.

```
library(pedsuite)
```

Exercise II-1

a) $\varphi = \frac{1}{8} = 0.125$.
b) $\varphi = \frac{1}{32} = 0.03125$.

Exercise II-2

a) Outbred monozygotic twins have kinship coefficient $\varphi = 0.5$.
b) A kinship coefficient of $\varphi = 1$ is possible only asymptotically, for example after infinitely many generations of full-sib mating. (The *realised* kinship coefficient may be 1 in a finite pedigree, however.)

Exercise II-3

a) Maternal half siblings, and also first cousins through the fathers. The children are not inbred.

b) Solution in R:

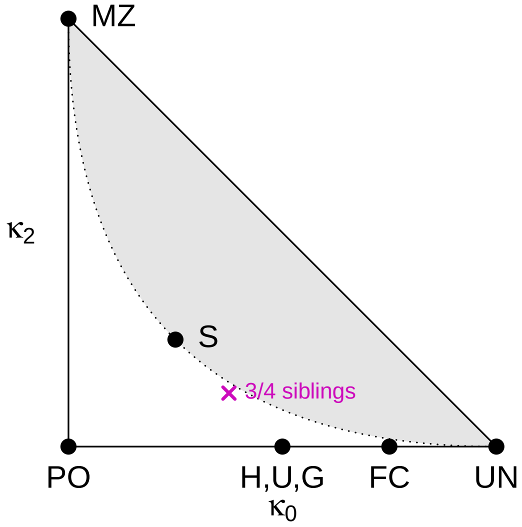
```
x = nuclearPed(2) |> addSon(c(3,5)) |> addSon(c(4,5))
k = kappaIBD(x, 6:7)
k
```

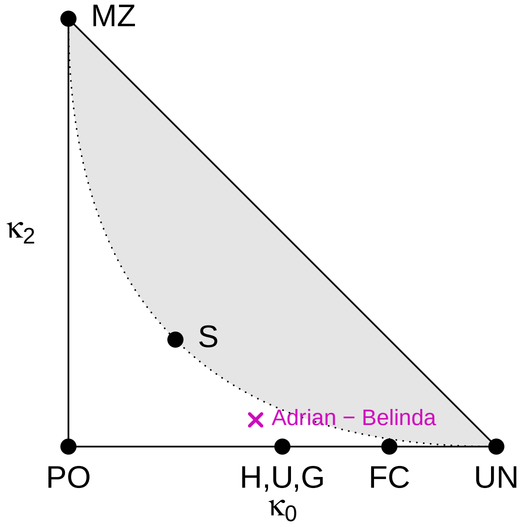
```
## [1] 0.375 0.500 0.125
```

c) The point is shown in the left-most triangle below. R code:

```
showInTriangle(k, label = "3/4 siblings", pos = 4)
```

d) The point is exactly halfway between half and full siblings. And $\frac{3}{4}$ is halfway between $\frac{1}{2}$ and 1.





Exercise II-4

a) The kinship coefficient is $\frac{5}{32} = 0.15625$:

```r
x = halfSibStack(2) |> swapSex(8)
plot(x, hatched = leaves)
kinship(x, 7:8)
```

```
## [1] 0.15625
```

b) $(\frac{7}{16}, \frac{1}{2}, \frac{1}{16}) = (0.4375, 0.5, 0.0625)$, as found by

```r
k = kappaIBD(x, c(7,8))
k
```

```
## [1] 0.4375 0.5000 0.0625
```

c) The point is shown in the right-most triangle above. R code:

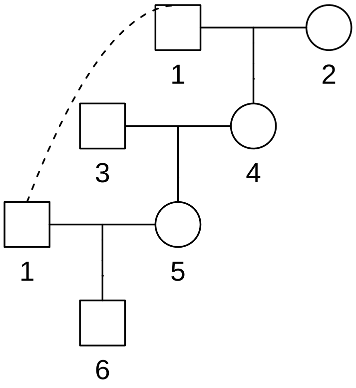
```r
showInTriangle(k, label = "Adrian - Belinda", pos = 4)
```

d) The point can be written as $\frac{3}{4}H + \frac{1}{4}S$, where H and S corresponds to half and full siblings, respectively. Thus, arithmetically speaking, their “fraction of siblingship” is $\frac{3}{4} \cdot \frac{1}{2} + \frac{1}{4} \cdot 1 = \frac{5}{8}$

Exercise II-5 (Realised inbreeding)

a)

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



b)

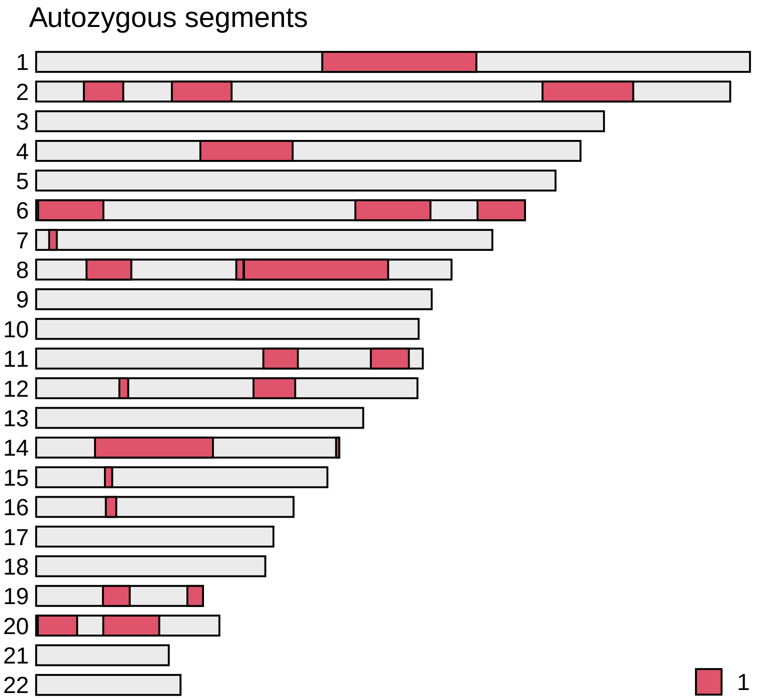
```r
inbreeding(x, 6)
```

```
## [1] 0.125
```

c) (Answer given in the exercise.)

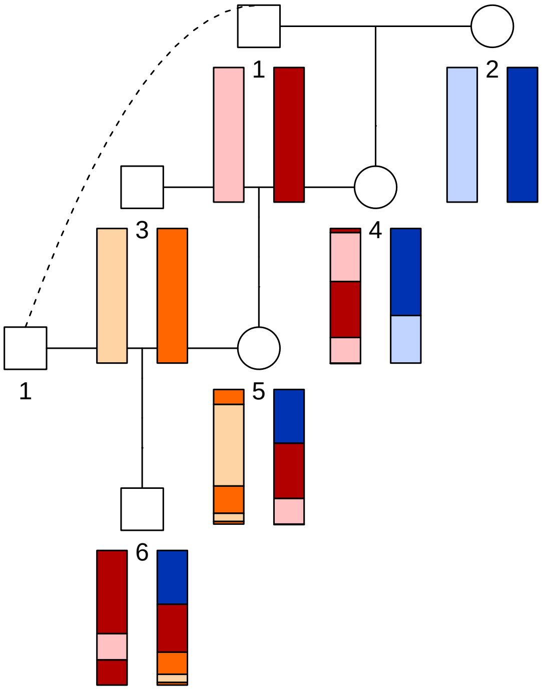
d)

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



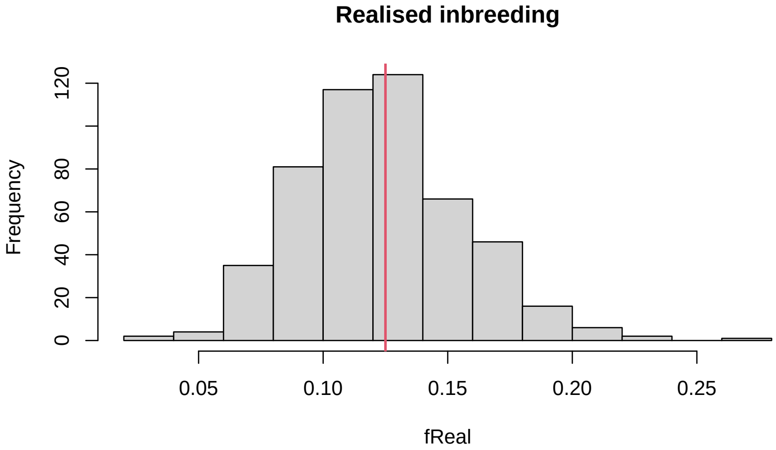
e)

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



f) The histogram shows that there is substantial natural variation around the expected value $f = 1/8$.

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



g)

```
sd(fReal)
```

```
## [1] 0.03283838
```

h) The number of segments in each simulation is contained in the `nSeg` column of `r$perSimulation`. A summary of these numbers show that the numbers range from 8 to 32, with an average of 20 segments:

```
summary(r$perSimulation$nSeg)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##    8.00   17.00   20.00   19.72   23.00   32.00 
```