

Pedigree analysis in R

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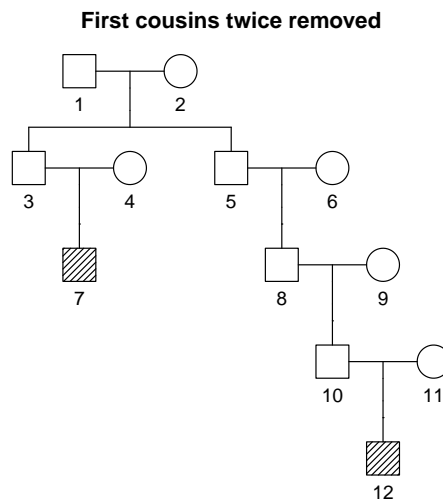
Solutions for exercise set I

Exercise I-1

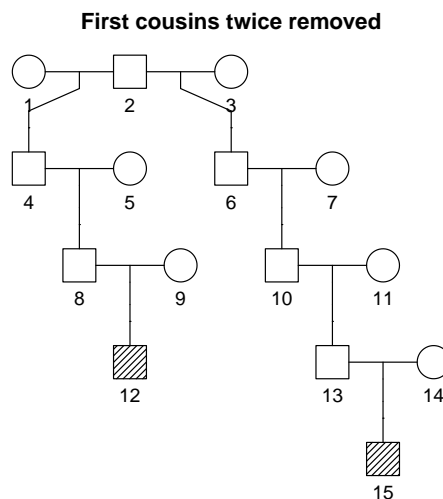
R code for producing the pedigrees is given below.

```
library(pedtools)
```

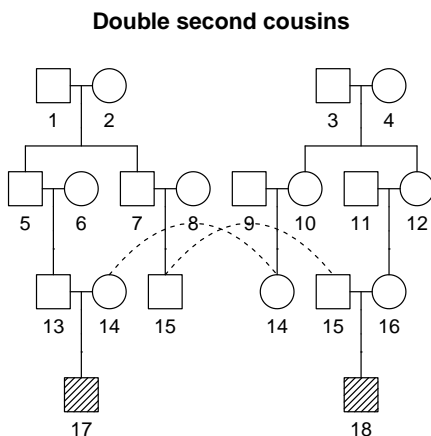
```
a) x1 = cousinPed(1, removal = 2)
   plot(x1, hatched = leaves, title = "First cousins twice removed")
```



```
b) x2 = halfCousinPed(2, removal = 1)
   plot(x2, hatched = leaves, title = "Half second cousins once removed")
```



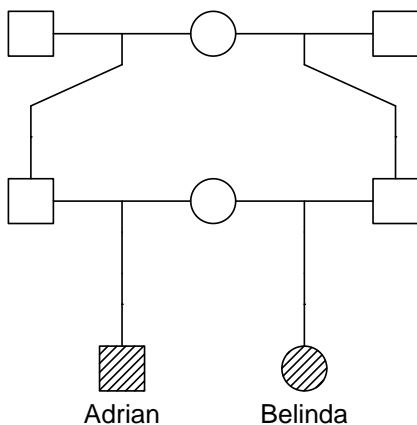
```
c) x3 = doubleCousins(degree1 = 2, degree2 = 2)
plot(x3, hatched = leaves, title = "Double second cousins")
```



Exercise I-2

- Adrian and Belinda are half first cousins.
- With the new information, Adrian and Belinda are simultaneous (maternal) half siblings and first half cousins. The pedigree can be produced as follows:

```
x = halfSibStack(2)
x = swapSex(x, 8)
plot(x, hatched = leaves, labs = c(Adrian = 7, Belinda = 8), margin = c(1,1,1,1))
```



Exercise I-3

- The marker is an autosomal STR marker. Reasons: allele labels; more than two alleles.
- Five alleles (13, 14, 15, 21 and 2) are observed. The alleles names indicate the number of repeats.
- Both 4 and 5 has genotype 13/14 (because of their parents).
- Individual 3 has genotype 21/22 (because his children must have gotten 13 from their mother).
- The possible genotypes are 13/13, 13/14, 13/15 and 14/15, each with probability $\frac{1}{4}$.

Exercise I-4

a) `2 - 4 / 2 + 3 ^ 2`

```
## [1] 9
```

b) `1:4 + 1 + c(0, 0, 0, 10)`

```
## [1] 2 3 4 15
```

c) `sqrt(c(1,4,9,16))`

```
## [1] 1 2 3 4
```

```
10^(1:3)
```

```
## [1] 10 100 1000
```

```
log10(1000)
```

```
## [1] 3
```

```
exp(1)
```

```
## [1] 2.718282
```

d) `x = 0`
`y = 1:5`
`z = seq(from = 6, to = 10)`
`c(x, y, z)`

```
## [1] 0 1 2 3 4 5 6 7 8 9 10
```

e) `y = list(a = 1:3, b = "foo")`
`y$a = c(y$a, 4:6)`
`y$b = c(y$b, "bar")`
`y$c = c(T, F)`
`y`

```
## $a
```

```
## [1] 1 2 3 4 5 6
```

```
##
```

```
## $b
```

```
## [1] "foo" "bar"
```

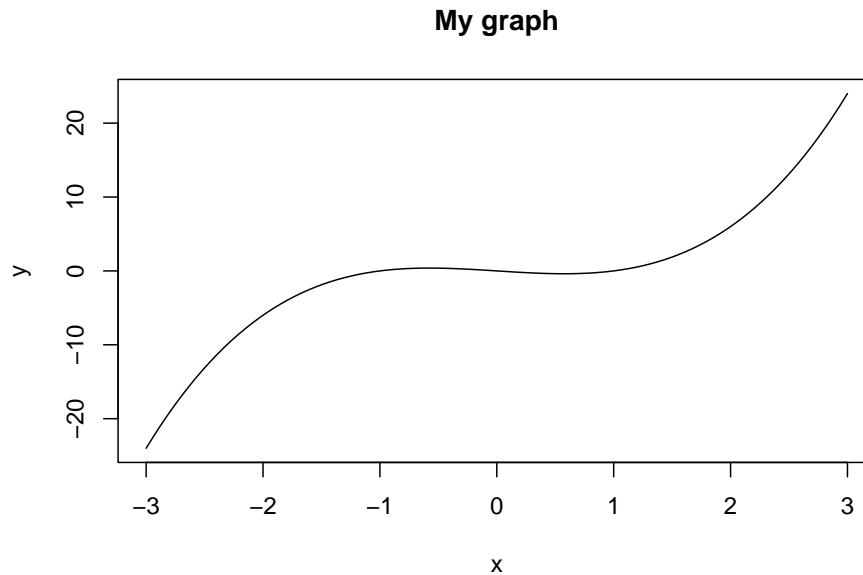
```
##
```

```
## $c
```

```
## [1] TRUE FALSE
```

Exercise I-5

```
x = seq(-3, 3, length = 100)
y = x^3 - x
plot(x, y, type = "l", main = "My graph")
```



Exercise I-6

(No answer)

Exercise I-7

- a) B (forced inheritance from the mother).
- b) A/B (deduced from her children 5 and 6).
- c) A/B. (She got B from her father, but has given an A to her son individual 10). She inherited A from her mother.
- d) Neither genotype is possible to determine from the data.
- e) 10 and 11 are maternal half siblings. 5 is the (maternal) uncle of 11. 4 and 9 are unrelated.