

Kinship and pedigree analysis: Methods and applications

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Exercise set I. Pedigrees, QuickPed and R

A note about QuickPed:

The QuickPed app is available at <https://magnusdv.shinyapps.io/quickped/>.

It is also possible to run QuickPed from R, enabling to work offline without having to worry about disconnecting due to inactivity, or network issues. To do this, open RStudio and run the following commands to install a few required packages (this is only necessary the first time):

```
packages = c("pedsuite", "shiny", "shinyjs", "shinyBS", "lubridate", "glue", "ggrepel")
for (pkg in packages) {
  if (!requireNamespace(pkg, quietly = T)) install.packages(pkg, dep = T)
}
```

Then you can run the app:

```
shiny::runGitHub("magnusdv/quickped")
```

Exercise I-1

Draw pedigrees by hand showing the following relationships.

- Grandaunt – grandnephew.
- First cousins twice removed.
- Half second cousins once removed.
- Double half first cousins.

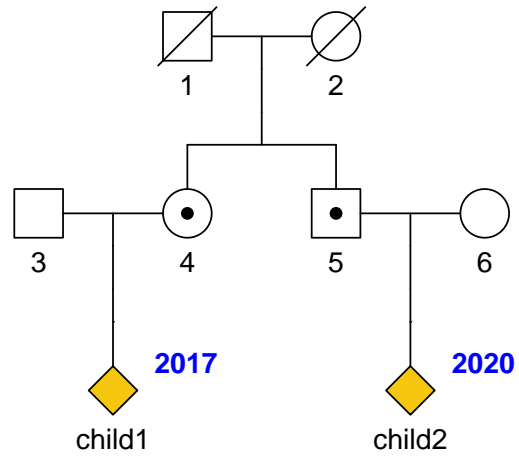
Exercise I-2

You are studying the genealogy of two individuals, Adrian and Belinda. The first piece of information you have is that their fathers are maternal half siblings.

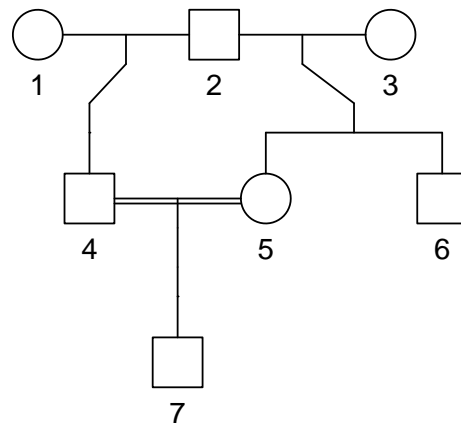
- Draw the pedigree by hand and describe the relationship between Adrian and Belinda.
- It turns out that Adrian and Belinda have the same mother. Draw the pedigree including the new information, and describe the relationship now.
- Draw the final pedigree in QuickPed and use the “Describe relationship” button to verify your answer.
- Is anyone in this pedigree inbred?

Exercise I-3

Recreate the following pedigree plot in QuickPed, as accurately as possible:

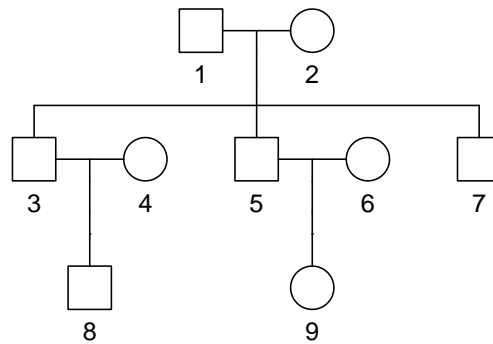
**Exercise I-4**

- Create the pedigree below in QuickPed.
- Describe the relationship between 6 and 7. (Hint: There is a button for that!)
- Click on the “R code” button and verify that the code produces the same pedigree in R.



Exercise I-5

To illustrate a typical workflow for building pedigrees in R, we will create this family:



- a) Use the following code to create the pedigree. Plot the pedigree after each command to track the progress. (With practice you may of course skip the intermediate plots!)

```
x = nuclearPed(nch = 3)
plot(x)
x = addSon(x, 3)      # add a son to individual 3
plot(x)
x = addDaughter(x, 4) # add a daughter to individual 4
plot(x)
x = relabel(x)       # relabel according to plotting order
plot(x)
```

- b) The **pedsuite** works well with *pipe* operator `|>` in R. The pipe makes the result of the previous command become the first argument of the next. For example, the code in a) may be rewritten to this:

```
x = nuclearPed(nch = 3) |>
  addSon(3) |>
  addDaughter(4) |>
  relabel()
```

Verify this by running the code and plot the result.

Exercise I-6 (Bonus exercise if you have time!)

What is the relationship between individuals 7 and 8 in this pedigree?

