

Genetic Relatedness

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Exercise set I. Pedigrees and relationships

A note about QuickPed:

Several of the exercises below can be solved using **QuickPed**, which can be run in two ways:

- Online at <https://magnusdv.shinyapps.io/quickped/>
- From R, without having to worry about network issues or disconnecting due to inactivity

To set up the R alternative, open RStudio and run the following commands to install a few required packages:

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

Then you can run the app:

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

Exercise I-1

Draw pedigrees by hand showing the following relationships.

- a) Grandaunt – grandnephew.
- b) First cousins twice removed.
- c) Half second cousins once removed.

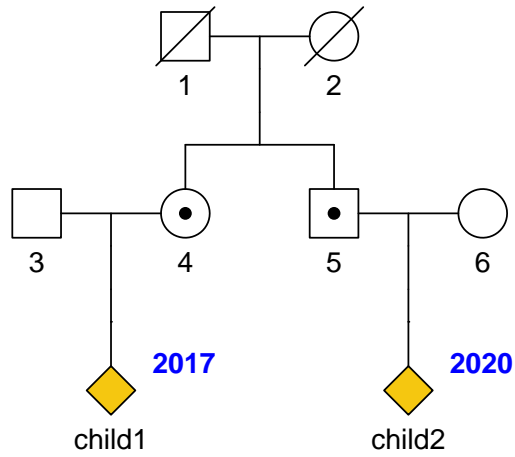
Exercise I-2

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.

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

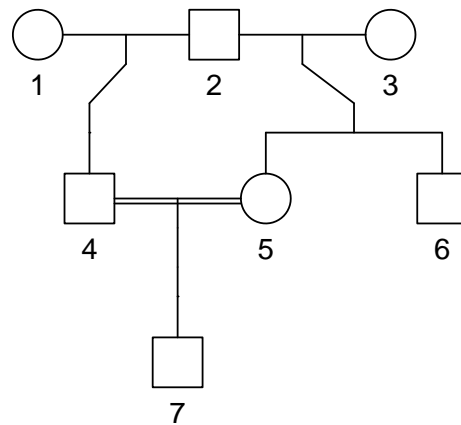
Exercise I-3

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



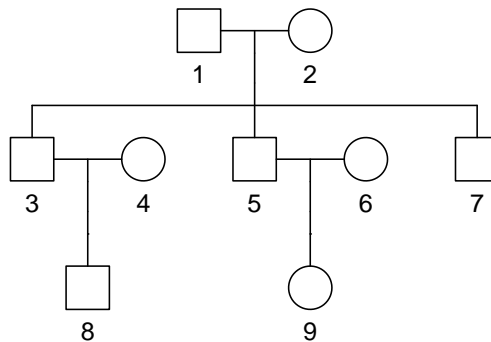
Exercise I-4

- 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?

