

Project: exclusionPower

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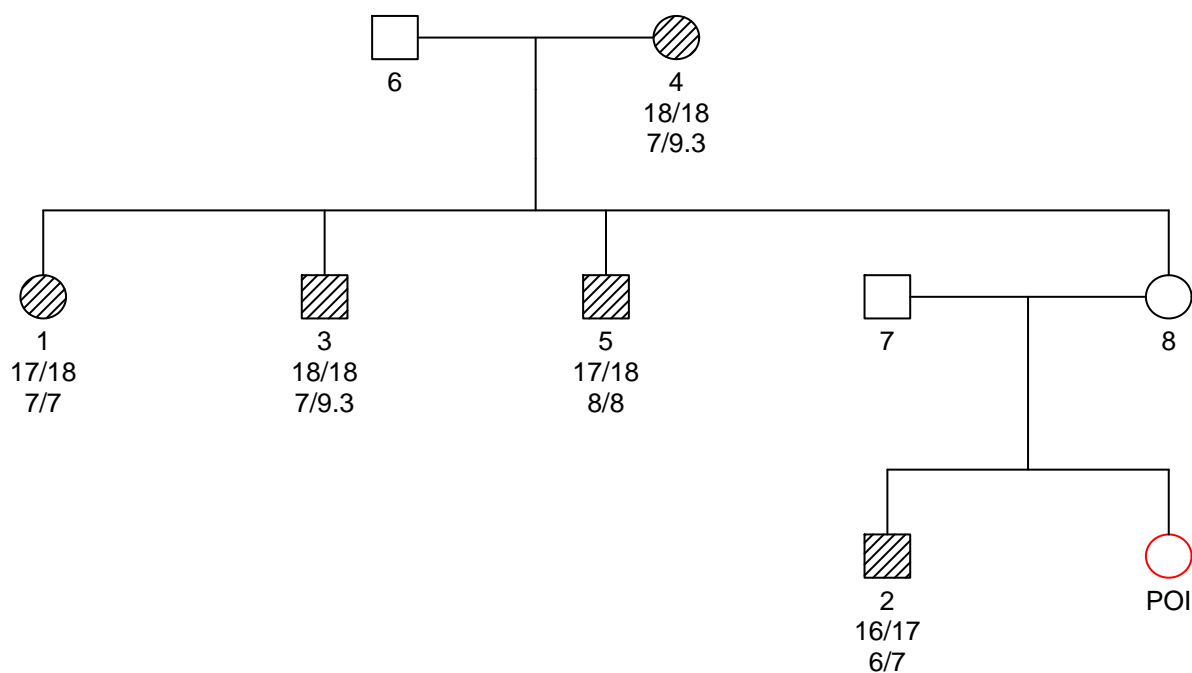
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Missing Grandchild Example

Below is an example based on the Argentina paper, see Figure 6, Kling et al (2017), <https://github.com/thoree/exclusion/blob/master/F21/Kling-missing-PIIS1872497317301758.pdf>. The pedigrees are larger than usual, parents of PO typically not available, and mutations happen. Files are in <https://github.com/thoree/exclusion/tree/master/F21>. The data has been exported from Windows Familias and converted using `forrel::Familias2ped`. Then it was saved using the R function `save`. Below it's loaded (I unsuccessfully tried several ways of direct load from github) and some examples are shown based on the 5 markers published

```
load("exampleA3.RData")
x = exampleA3
library(forrel, quietly = TRUE)
claim = x[[1]][[1]] # remove singleton, just for first plot
knitr::opts_chunk$set(fig.width=12, fig.height=8)
plot(claim, marker = 1:2, cex = 0.8, skip.empty.genotypes = TRUE,
     shaded = 1:5, col = list(red = "POI"),
     title = "Fig 6, H1, Argentina- paper, Kling et al., 2017")
```

Fig 6, H1, Argentina- paper, Kling et al., 2017



Exclusion probability for first marker:

```

claim = x[[1]]
true = x[[2]]
(PE = exclusionPower(claim, true, ids = "POI", markerindex = 1,
                     verbose = FALSE))

```

```
## [1] 0.5213632
```

Let's check the answer with some acrobatics, since `oneMarkerDistribution` does not accept lists:

```

library(pedprobr)
H2 = x[[2]][[1]]
H2 = addChildren(H2, father = 2, mother = "POI", id = "NN",
                 verbose = FALSE)
ptrue = oneMarkerDistribution(H2, ids = "POI", partialmarker = 1,
                             verbose = F)

H1 = x[[1]][[1]]
pclaim = oneMarkerDistribution(H1, ids = "POI", partialmarker = 1,
                              verbose = F)

I1 = (pclaim == 0)
PE.check = sum(I1*ptrue)
c("PE = ", PE, "PE.check =", PE.check)

```

```

## [1] "PE = " "0.521363167706383" "PE.check ="
## [4] "0.521363167706383"

```

A closer look at the second marker: We see that there must be a mutation in 5 and mutations are modelled only for this marker. In this case, theproportional' model with mutation rate 0.005, was specified in Windows Familias. In the ped-suite, we can look at the mutation model (output omitted)

```

library(pedmut)
m = claim$markerdata[[2]]
mutmod(m)

```

Exclusion probability for second marker (problem with `markerindex` see <https://github.com/magnusdv/forrel/issues/23>; skip the rest for now)

```

exclusionPower(claim, true, ids = "POI", markerindex = 2,
               verbose = FALSE)

```

```
## [1] 0.5213632
```

Exclusion probability for markers 1,2,3,4,5

```

nMarkers = 5
PE = rep(NA, nMarkers)
for (i in 1:5)
  PE[i] = exclusionPower(claim, true, ids = "POI", markerindex = i, plot = FALSE,
                        verbose = FALSE)
PE.all = 1 - prod(1-PE)
c("PE = " = PE.all)

```

```

##      PE =
## 0.9748794

```