PARAMO pipeline

Phylogenetic Ancestral Reconstruction of Anatomy by Mapping Ontologies

STEP 1. Initial character matrix

This is an R Markdown Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Cmd+Shift+Enter*.

```
MT<-read.csv("matrix_PARAMO.csv", header = T, row.names=1, as.is=T, check.names=F)
```

```
apply(MT, 2, unique)
```

```
## $`CHAR:3`
## [1] "0" "1" "?" "-"
##
## $`CHAR:23`
## [1] "1" "?" "-" "0"
##
## $`CHAR:25`
## [1] "0" "?" "1"
##
## $`CHAR:353`
## [1] "0" "1" "?" "-"
##
## $`CHAR:363`
## [1] "1" "?" "0"
##
## $`CHAR:380`
## [1] "0" "?" "1" "-"
##
## $`CHAR:381`
## [1] "0" "-" "1" "?"
##
## $`CHAR:382`
## [1] "1" "-" "?" "0"
```

Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Cmd+Option+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Cmd+Shift+K* to preview the HTML file).

The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.