R Notebook

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*.

```r
CH<-read.csv(file="STEP_1/Char_info.csv", header = T, as.is=T, check.names=F)

kable(CH[,c(1:6)], booktabs=TRUE,
      caption = 'Initial characters obtained at Step 1. ')%>%
  kable_styling(full_width = F, font_size=8, latex_options="hold_position") %>%
  column_spec(1, bold = T) %>%
  column_spec(6, width = "10em") %>%
  footnote(c("ID - character ID in this study.",
    "IDR*- character ID in Sharkey et al. (2012)."))
```

Table 1: Initial characters obtained at Step 1.

ID	ID*	CHAR_STATEMENT	STATE_0	STATE_1	DEPENDENCY
C1	3	Notch on medial margin of eye	absent	present	no
C2	23	Position of labrum	anterior	posterior	C2{0,1} < C3{0}
C3	25	Labrum	present	absent	C3{0} > C2{0,1}
C4	353	Forewing costal and radial vein fusion	not_fused	fused_along_their_lengths	no
C5	363	Hind wing subcostal SC vein, absent	no	yes	C5{0,1} <>C6{1,0}
C6	363	Hind wing subcostal SC vein, present	yes	no	C5{0,1} <>C6{1,0}
C7	380	Inner posterior mesotibial spur	simple	modified into a calcar	no
C8	381	Foretibial apical sensillum	present	absent	no
C9	382	Metatibial apical sensillum	present	absent	no

Note:
ID - character ID in this study.
IDR*- character ID in Sharkey et al. (2012).

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).

Step 2. Incorporating anatomical dependencies: constructing amalgamations at the AD level

The pairs of anatomically depenent characters – C_2, C_3 and C_5, C_6 have to be apropriately amalgamated into single characters to adeuqtely model the dependecies. The amalgamation produces the following (see the text in the article):

- $C_3 \oplus C_2 = C_{3,2}\{00, 01, 10, 11\}$. $C_{3,2}$ is coded in the matrix as $C_{3,2}\{0\&1, 0\&1, 2, 3\}$.

- C_5 and C_6 are combinded into $C_{5,6}$. The synchronous dependency between these characters has to be eliminated that gives the character $C_{5,6}$ without changing the state pattern.

The recoding of dependent characters constructs the amalgamated characters at the AD level. If a character does not display any dependencies then we treat it as correctly amalgamated at the AD level by default.

The new matrix and character report of the characters amalgamated at the AD level can be found in `STEP_2/Step2_matrix.nex` and `STEP_2/Char_info_step_2.csv` respectively. Let's have a look into them.

```
AN<-read.csv(file="STEP_3/Char_annotation.csv", header = T, as.is=T, check.names=F)

kable(AN, booktabs=TRUE,
      caption = 'Characters linked with HAO terms (Step 3).')%>%
  kable_styling(full_width = F, font_size=8, latex_options="hold_position")
```

Table 2: Characters linked with HAO terms (Step 3).

ID	CHAR_STATEMENT	HAO_ID	HAO_ID_NAME
C1	Notch on medial margin of eye	HAO:0000234	cranium
C3,2	Labrum + Position of labrum	HAO:0000639	mouthparts
C4	Forewing costal and radial vein fusion	HAO:0000351	fore wing
C5,6	Hind wing subcostal SC vein, present	HAO:0000400	hind wing
C7	Inner posterior mesotibial spur	HAO:0001351	mesotibia
C8	Foretibial apical sensillum	HAO:0000350	fore tibia
C9	Metatibial apical sensillum	HAO:0000631	metatibia

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