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Supplementary Text for the Article *Congruence and diversity of butterfly-host plant associations at higher taxonomical levels*

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The Dataset S1 is provided in order to allow users to re-analyse the data using alternative classifications, including the transfer of genera to different subfamilies as the ones considered in the article. Please note that updates to the compilation and data sets will be posted in <http://papilionoidea.myspecies.info>.

All analyses were performed using *R* (R Development Core Team, 2010), but the data can be easily exported for use with other software. Within *R* we used the *ape* package (Paradis *et al.*, 2004):

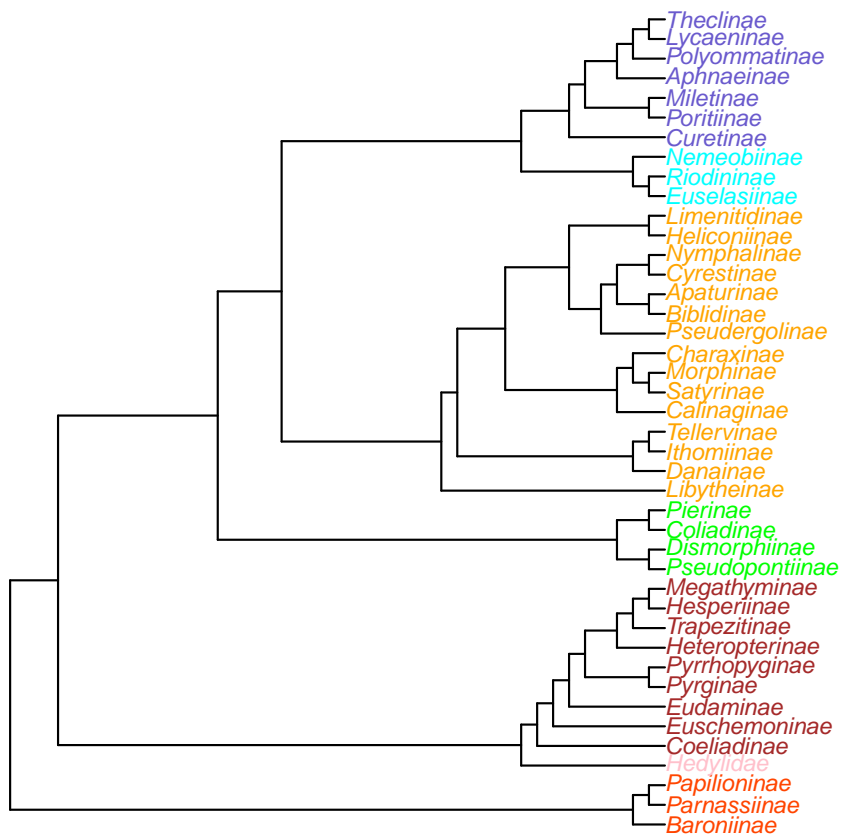
```
> library(ape)
```

Substitute `data.dir` with the working directory in your system, then load the data:

```
> data.dir <- "~/CEBA/Rdata/"  
> load(paste(data.dir, "DatasetS1.rda", sep=""))
```

You can plot the phylograms with the functions in package *ape*:

```
> plot(Alternative1.tree,  
+      tip.color=c(rep("orangered",3), "pink", rep("brown",9),  
+               rep("green",4), rep("orange",15), rep("cyan",3),  
+               rep("slateblue",7)), cex=.7)
```



The object `Summary.table` shows how many species of each genus feed on a particular plant order, and how the genera were assigned to each subfamily in our compilation.

```
> dim(Summary.table)
```

```
[1] 1193 63
```

```
> Summary.table[1:6,1:6]
```

	Genus	Subfamily	Alismatales	Apiales	Aquifoliales	Arecales
76	Apatura	Apaturinae	0	0	0	0
119	Asterocampa	Apaturinae	0	0	0	0

248	Chitoria	Apaturinae	0	0	0	0
333	Dilipa	Apaturinae	0	0	0	0
348	Doxocopa	Apaturinae	0	0	0	0
409	Eulaceura	Apaturinae	0	0	0	0

If necessary, the assignment of genera to subfamily can be changed, or the total number of species feeding in a particular host plant order can be updated. Then the R-function `aggregate` can be used to provided totals for each subfamily:

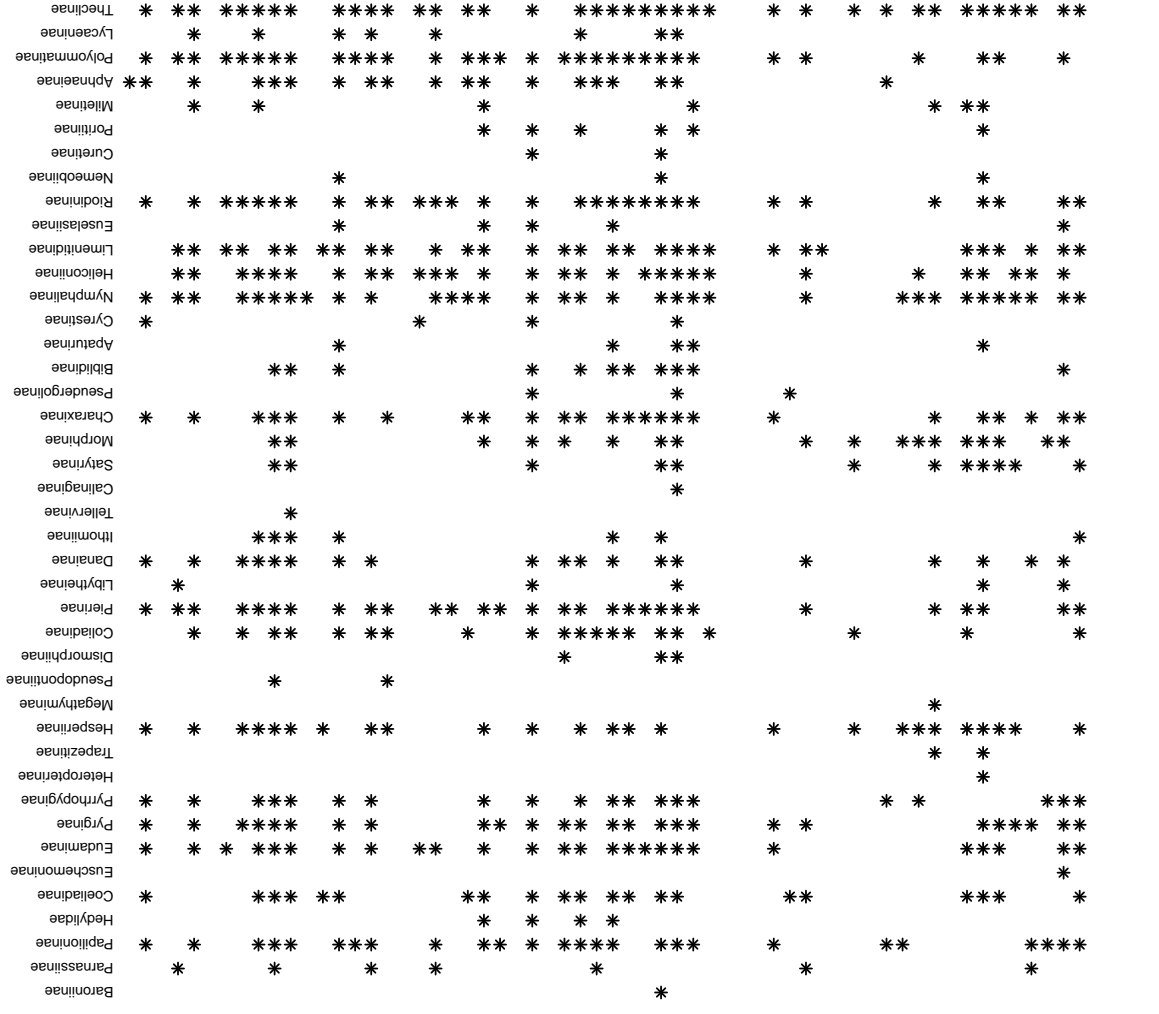
```
> new.C <- aggregate(Summary.table[,-(1:2)],
+                    by=list(Subfamily=Summary.table$Subfamily),
+                    sum)
> new.C[1:6,1:7]
```

	Subfamily	Alismatales	Apiales	Aquifoliales	Arecales	Asparagales	Asterales
1	Apaturinae	0	0	0	0	0	0
2	Aphnaeinae	0	1	0	0	0	14
3	Baroniinae	0	0	0	0	0	0
4	Biblidinae	0	0	0	0	0	0
5	Calinaginae	0	0	0	0	0	0
6	Charaxinae	0	2	0	0	1	1

The resulting matrix is equivalent to the association matrix **C** in the article.

The original matrix used in the analysis are stored in R-objects **Aij**, **Cij**, **Xij** and **Zij**. The following code can be used to make a graphic representation of matrix **A**.

```
> par(mar=c(1,3,4,1))
> layout(matrix(c(1,2,2),ncol=3))
> plot(APGorders.tree)
> par(xpd=F)
> plot(1,1,xlim=c(1,ncol(Aij)),ylim=c(1,nrow(Aij)), type="n",axes=F,xlab="",ylab="")
> par(xpd=NA)
> text((1:ncol(Aij))-0.4,rep(65,ncol(Aij)),colnames(Aij),srt=90,cex=.7,pos=4)
> par(xpd=F)
> for (j in 1:ncol(Aij)) {
+   if (sum(Aij[,j])>0) {
+     x <- rep(j,nrow(Aij))
+     y <- 1:nrow(Aij)
+     z <- Aij[,j]
+     points(x[z>0], y[z>0], pch=8)
+   }
+ }
```



## References

- PARADIS, E., CLAUDE, J. & STRIMMER, K., 2004. *APE: analyses of phylogenetics and evolution in R language*. *Bioinformatics*, 20:289–290.
- R DEVELOPMENT CORE TEAM, 2010. *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria. URL <http://www.R-project.org/>. ISBN 3-900051-07-0.