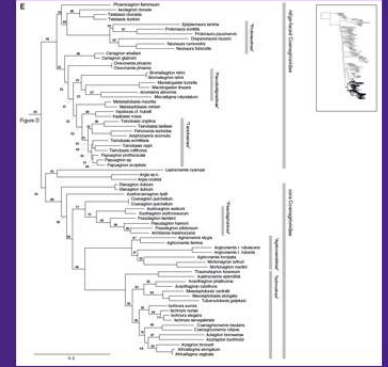
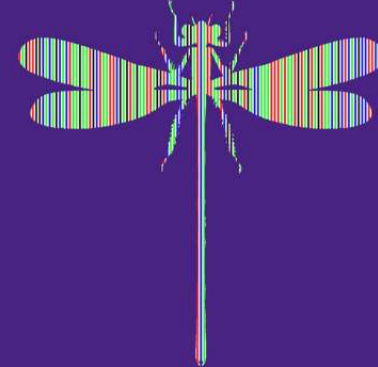


Frank Stokvis  
senior research technician



(student) supervision  
(stacking microscope) photography  
graphic design, ion torrent

16S, 28S, ITS  
±1100 sequences  
MrBayes, RAxML, PAUP\*

TITLE: METH024\_PHYLOGENETIC\_ANALYSES Author: Frank Stokvis  
Version: METH024.01 Authorization Date:

5.2 BAYESIAN INFERENCE

5.2.1 Determining best fit nucleotide substitution model  
The best-fit nucleotide substitution model can be assessed with **MModeltest 2.3**.  
Make a copy of the **MModeltest 2.3** folder for each data partition to prevent the output from being overwritten.  
**PAUP**  
- File/Open/nexus file  
- File/Open/AS Files/MModelblock

**MModeltest 2.3**  
- Run 'run mm.baf'  
- Open 'PAUPBlock.baf' with **WordEdit** (if 'PAUPBlock.baf' has not been generated, run mm.baf in a shorter path or disc e.g. C:\MModeltest)  
- Copy the MrBayes settings from the 'HIERARCHICAL LIKELIHOOD RATIO TESTS (NRTs)'

Letst: nat=6 rates=gamma;  
Postet: statefreq=dirichlet(1,1,1,1);

- Open nexus file with **WordEdit**. Turn off word wrap / View/Word wrap  
- Paste the MrBayes settings at the bottom of the nexus file

5.2.2 Adjusting MrBayes settings  
**WordEdit**  
- Copy the following MrBayes settings

BESTI HRRAYES;  
log start filename=log\_mcmc.tac append;  
Letst: nat=6 rates=gamma;  
Postet: statefreq=dirichlet(1,1,1,1);

