

RH: Characters correlation

Influence of different modes of morphological character correlation on phylogenetic tree inference

Supplementary material 2 - Simulation parameters

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MORPHOLOGICAL MATRICES SIMULATIONS

“True” Tree simulation - using diversitree R package v 0.9-8 FitzJohn (2012)

- Model
 - Birth-death tree (`diversitree::tree.bd`)
- Parameters
 - Birth (λ) and death (μ) parameters sampled from a uniform distribution (0,1) with $\lambda > \mu$.
 - Stopped when the tree reached 25, 75 or 150 taxa (extinct taxa excluded).

“Normal” matrix simulation - using dispRity R package v 0.4 Guillerme (2016)

- Model
 - Mk or HKY-binary selected randomly (`dispRity::sim.morpho`)
- Parameters
 - States frequency: 0.85 binary characters and 0.15 three states (for Mk only)
 - Transition/transversion ratio (for HKY-binary): 2
 - Character rate (for both models): gamma distribution with a rate $\alpha = 100$ and a shape $\beta = 5$.

- No invariant characters.

“Maximised”, “Minimised” and “Null” matrices

- Maximised
 - Replacing the n characters with a character difference (CD) to all other characters < 0.25 .
- Minimised
 - Replacing the m character with a CD to all other characters > 0.75 .
- Null
 - Randomly replacing $\frac{n+m}{2}$ characters.

TREE INFERENCE PARAMETERS

Maximum parsimony: PAUP version 4.0a151 Swofford (2001)*

- Search settings
 - Max. trees = 500 with auto-increase of 500.
 - Heuristic search with random sequence addition replicated 10 times
- Summary settings

- Summarising up to 1×10^9 trees in a strict majority rule consensus tree (cut off = 50).

Bayesian: MrBayes version 3.2.7 Ronquist et al. (2012)

- Models

- $Mkv + \Gamma_4$

- Priors

- variable rate prior with an exponential shape prior set to 0.5

- MCMC

- Two runs
- Six chains per run
- Generations $< 1 \times 10^9$
- Sample frequency = 200
- ASDS diagnosis frequency = 10000
- ASDS < 0.01
- ESS $\gg 200$

- Summary settings

- Strict majority consensus tree (cut off = 50) with a relative burning of 25%.

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References

FitzJohn, R. G. 2012. Diversitree: comparative phylogenetic analyses of diversification in R. *Methods in Ecology and Evolution* 3:1084–1092.

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Swofford, D. L. 2001. *Paup**: Phylogenetic analysis using parsimony (and other methods) 4.0. b5 .