Colleen Nooney, Stuart Barber*, Arief Gusnanto, and Walter R. Gilks

Supplementary material for "A statistical method for analysing cospeciation in tritrophic ecology using electrical circuit theory"

1 Type I Error: Additional Plots

The bitrophic empirical cumulative distribution functions for the second parameter combination in section 3.1 of the main paper are displayed in Figure S1. The empirical CDF for our p-values and Hommola *et al.* (2009) lies close to the desired diagonal line.

The tritrophic empirical cumulative distribution functions for the second parameter combination in section 3.1 of the main paper are displayed in Figure S2. The empirical CDF for our p-values lies close to the desired diagonal line for all parameter combinations.

2 Power Simulations: Additional Plots

The rejection rate plots for Simulation Method 3 in section 3.2 of the main paper are displayed in Figure S3. The rejection rates increase as the systems become more cospeciated and the rejection rates are higher for systems with 20 tips compared to systems with 10 tips. Our rejection rates are higher than Hommola *et al.* (2009) in the 10 and 20 tip case.

Colleen Nooney, Stuart Barber*, **Arief Gusnanto, Walter R. Gilks:** Department of Statistics, School of Mathematics, University of Leeds, Leeds LS2 9JT, UK. Email: S.Barber@leeds.ac.uk

Permutation	P_λ	$P_{MW.H}$	$P_{HW.M}$	$P_{HM.W}$
H	0.134	0.908	0.156	0.152
M	0.963	0.054	0.998	0.249
W	0.031	0.082	0.035	0.982
HM	0.957	0.028	0.213	0.132
HW	0.127	0.248	0.010	0.238
MW	0.957	0.062	0.067	0.265
HMW	0.954	0.048	0.012	0.139

Table S1. The *p*-values obtained using the method of Mramba *et al.* (2013) applied to the hostplants (H), leaf-mining moths (M) and parasitoid wasps (W) dataset (Lopez-Vaamonde *et al.*, 2005). Significant *p*-values are highlighted in bold. The rows indicate which phylogenetic trees have been permuted. The columns correspond to the different *p*-values obtained using the method of Mramba *et al.* (2013).

3 Applications: Labelled Phylogenies

The phylogenetic trees for the Lopez-Vaamonde *et al.* (2005) dataset consisiting of hostplants, leaf-mining moths and parasitoid wasps are plotted individually, with edge lengths and species labels, in Figure S4.

4 Applications: Mramba *et al.* (2013) *p*-values

The *p*-values for Mramba *et al.* (2013) method applied to the tritrophic dataset in section 4 of the main paper are given in Table S1. The tritrophic dataset consists of hostplants (H), leaf-mining moths (M) and parasitoid wasps (W) (Lopez-Vaamonde *et al.*, 2005). The rows represent the permutations, and the columns represent the different *p*-values of Mramba *et al.* (2013) method. A simple interpretation guide for the relationship between the possible permutations and the *p*-values is given in Table 1 in the main paper.
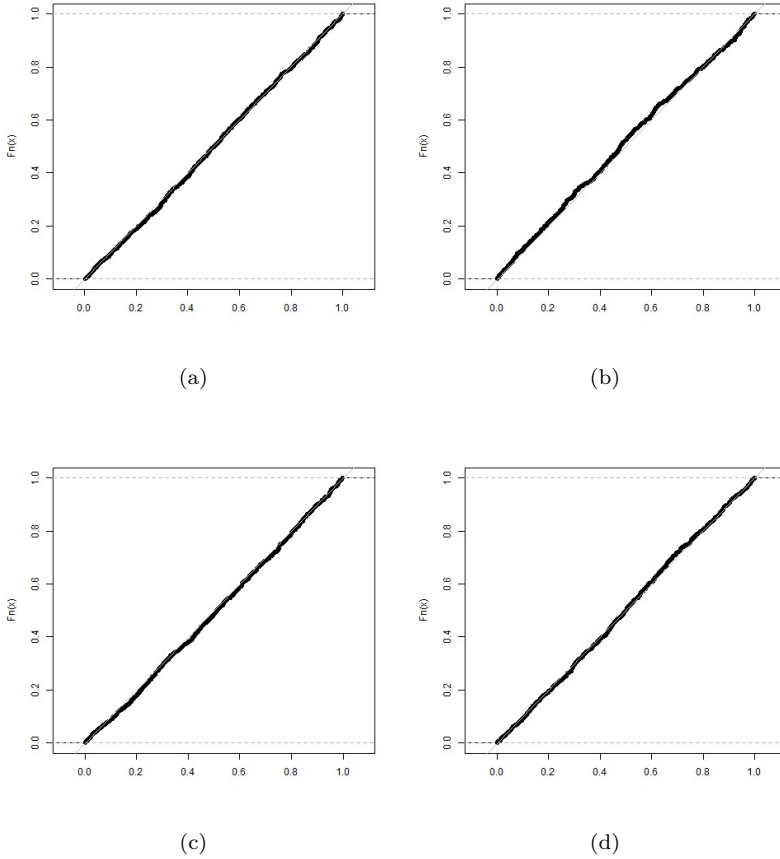
(a)

(b)

(c)

(d)

Fig. S1. Empirical cumulative distribution functions for our p-values and Hommola *et al.* (2009). Each plot corresponds to simulations with 10 tips on each tree. The first column corresponds to 20 interactions simulated, and the second column corresponds to 25 interactions simulated. The top row contains the p-values for our method, and the bottom row contains the p-values for the method of Hommola *et al.* (2009).
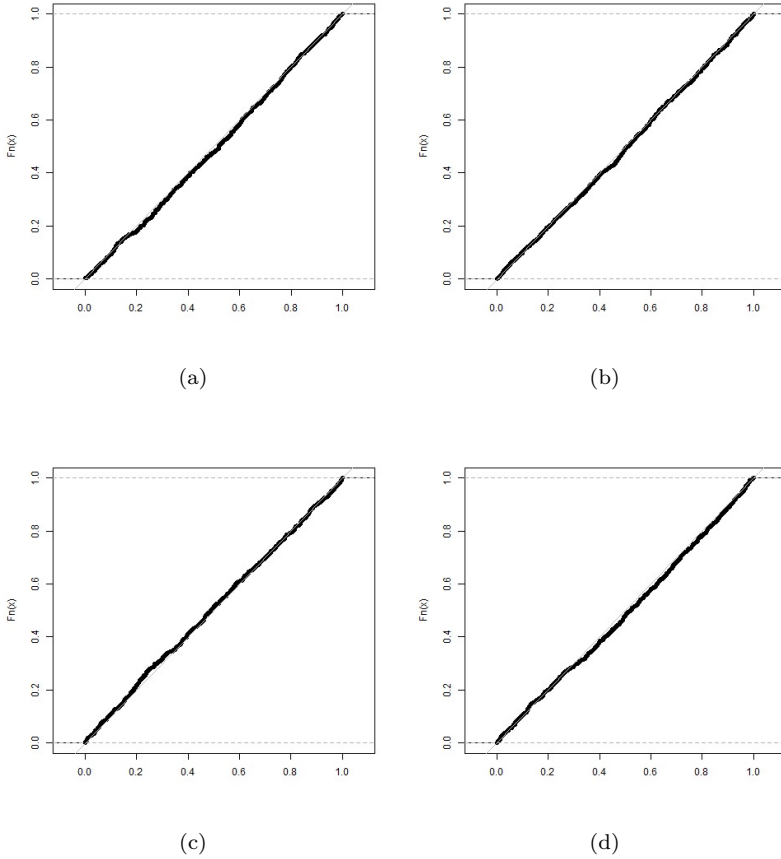
(a)

(b)

(c)

(d)

Fig. S2. Empirical cumulative distribution functions for our tritrophic p-values. Each plot corresponds to simulations with 10 tips on Trees X and Y, and 15 tips on Tree Z. Each plot represents a different number of interactions simulated. From top left to bottom right, 10, 15, 20 and 25 interactions.
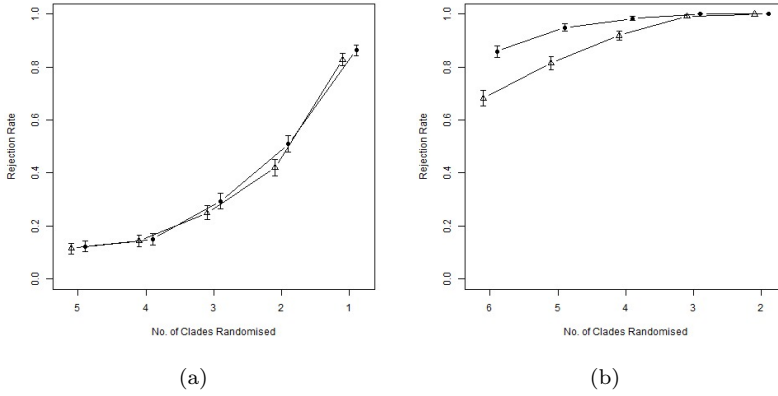
(a)   (b)

Fig. S3. Rejection rates for the p-values generated using our method and the method of Hommola *et al.* (2009) at the $\alpha = 0.05$ significance level, under Simulation Method 3. Black dots are the rates obtained using our method and triangles are the rates calculated for Hommola *et al.* (2009) p-values. The plot on the left corresponds to 10 tip trees and the plot on the right coresponds to 20 tips trees.

(a) Hostplant

(b) Leaf-mining moth
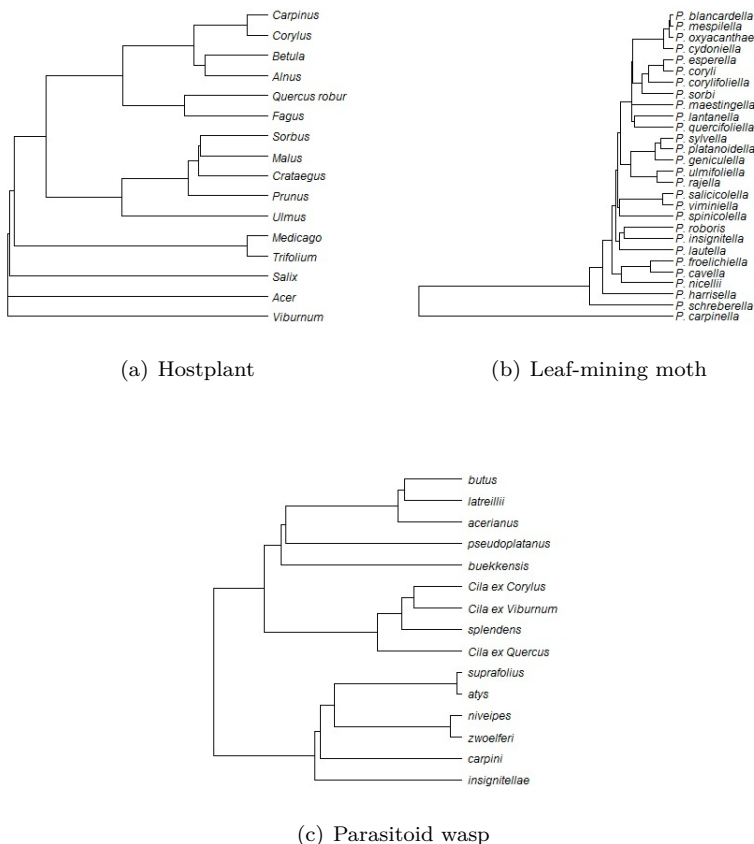

(c) Parasitoid wasp

Fig. S4. Individual phylogenetic trees for the hostplant, leaf-mining moth and parasitoid wasp tritrophic dataset (Lopez-Vaamonde *et al.*, 2005). Each phylogenetic tree is plotted using edge lengths. Leaf node species labels are also displayed.

References

Hommola, K., Smith, J. E., Qiu, Y., and Gilks, W. R. 2009. A permutation test of host–parasite cospeciation. *Molecular Biology and Evolution*, 26(7): 1457–1468.

Lopez-Vaamonde, C., Godfray, H., West, S., Hansson, C., and Cook, J. 2005. The evolution of host use and unusual reproductive strategies in achrysocharoides parasitoid wasps. *Journal of Evolutionary Biology*, 18(4): 1029–1041.

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