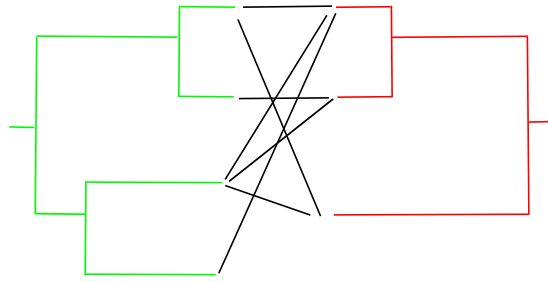


Standardised food web sample from from Madang, collected over 88 plant hosts.

Multigene phylogenies of plant hosts and insect herbivores with associated quantitative interactions.

Host Plants

	A	B	C	D
Herbivores	2	0	8	20
B	0	4	2	0
C	5	0	14	0



Fitting of a linear model to association strengths, with a phylogenetic correlation between interacting species (PBLM).

Quantitative estimates of interaction strength based on PBLM, from sequential removal of interactants.

	A	B	C	D
A	2	0	?	20
B	0	4	?	0
C	5	0	?	0

Mean correlation coefficient between observed and expected values and interaction probabilities.

Binary matrices derived from highest probability model predictions (highest interaction strengths).

	A	B	C	D
A	1	0	1	1
B	0	1	1	0
C	1	0	1	0

Observed

	A	B	C	D
A	0	0	1	0
B	1	1	1	1
C	1	0	1	0

Predicted

Exact hits occur in both observed and expected matrices.

Correlation between observed and predicted binary matrices.

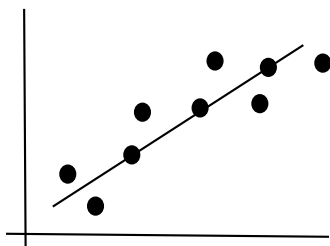


Figure S9.

Null models to test similarity of binary matrices with varying constraints.

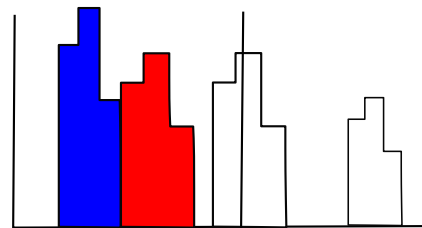
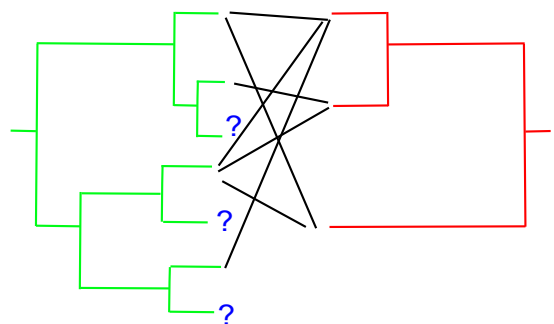


Figure 2.

	A	B	C	D	E	F	G
A	2	0	8	20	?	?	?
B	0	4	2	0	?	?	?
C	5	0	14	0	?	?	?



Covariance matrices, corrected interaction strengths from PBLM and new phylogeny used to predict host use on 34 additional host plants from Wanang, sampled according to abundance.

Input 1

Output 1

Validation

Predictions on expanded hosts