from Humpries and Parenti (1986)
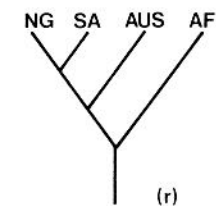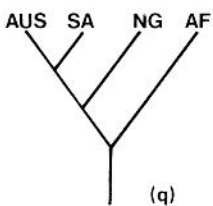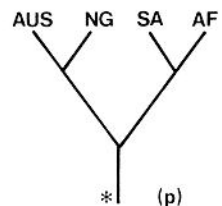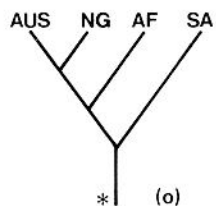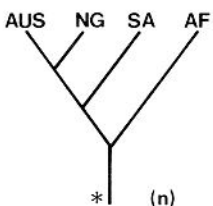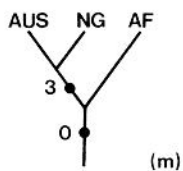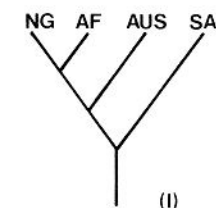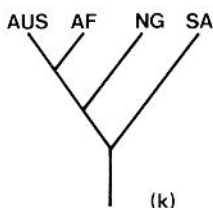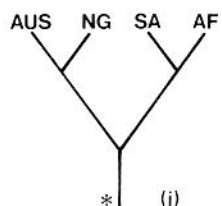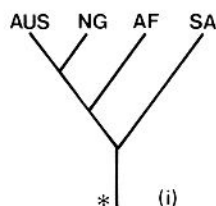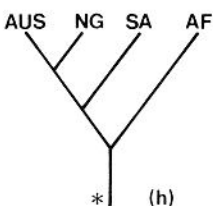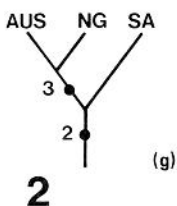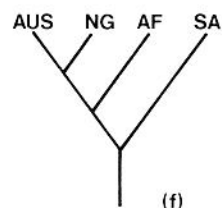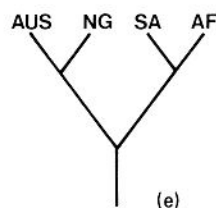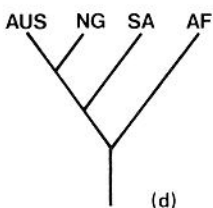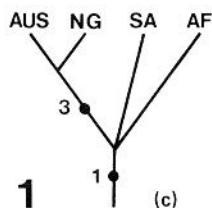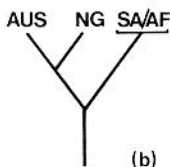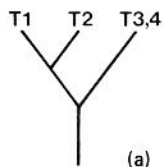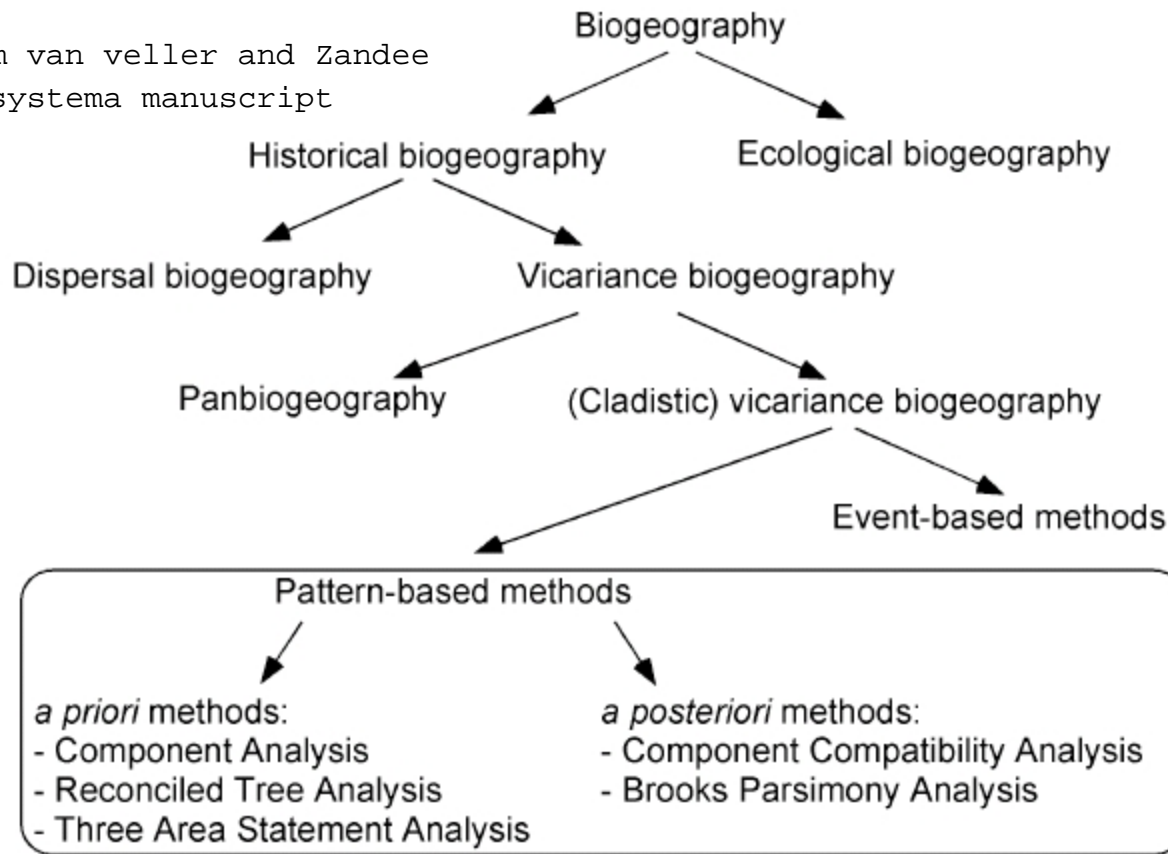
Fig.1. *Hierarchical outline of the scientific discipline of biogeography.*

Traits or communities

Clustered
Significant +NTI, +NRI

Random
NTI, NRI Not significant

Over-dispersed
Significant -NTI, -NRI
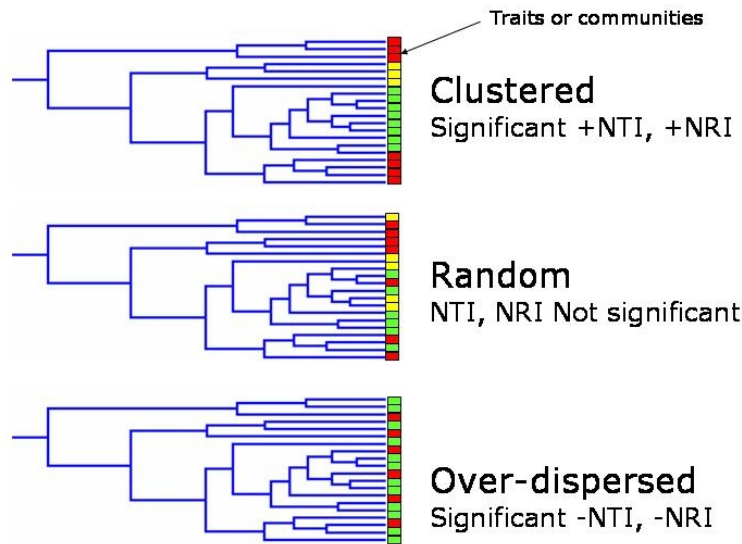
Example of clustering, i.e. significantly high NRI and NTI scores

Phylobetadiversity measures for *Cerabilia* species in New Caledonia showing significant clustering relative to soil type.
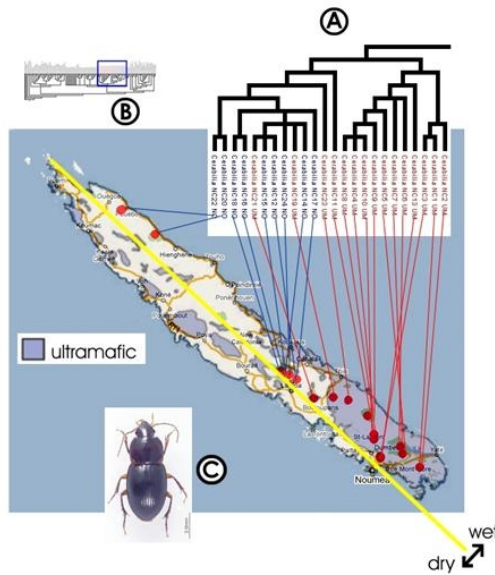
ⒶⒷⒸ

ultramafic

wet
dry

NTI

#NTIComdistNT	new cal	frenpoly	Norf	lorho	taz	AUS
new cal	3.11626	-8.6668	-2.06	-3.9929	-20.0298	-27.978097
frenpoly	-8.6666	4.94483	-0.7060	-0.1368	-15.268	-21.603153
Norf	-2.9865	-0.7061	1.530 9	1.17246	-3.9607	-4.435165
lorho	-3.9929	-0.1368	1.172 62	2.63938	-6.59459	-5.092934
taz	-20.03	-15.268	-3.9607	-6.5946	-2.22963	-26.297978
AUS	-27.979	-21.604	-4.40533	-5.0931	-26.2963	4.295243

NRI

#NRIComdist	new cal	frenpoly	Norf	lorho	taz	AUS
new cal	3.106675	-2.431727	1.92267	1.279964	-6.046508	2.0534
frenpoly	-2.429838	16.45987	0.00744	-0.367858	-5.739318	-1.877
Norf	1.922562	0.007246	1.71331	1.855491	-1.729884	1.143
lorho	1.279412	-0.368057	1.85551	0.893695	-3.046583	0.4355
taz	-6.04289	-5.741387	-1.72981	-3.047592	-6.884219	-11.11
AUS	2.184936	1.933563	1.1462	0.43276	-10.831534	6.2984

COMDIST and COMDISTnt commands used with Phylogenetic randomization, 10000 replicates.

Negative values of NRI and NTI indicate high phylogenetic turnover between pairs; positive values indicate that pairs contain more closely related taxa.

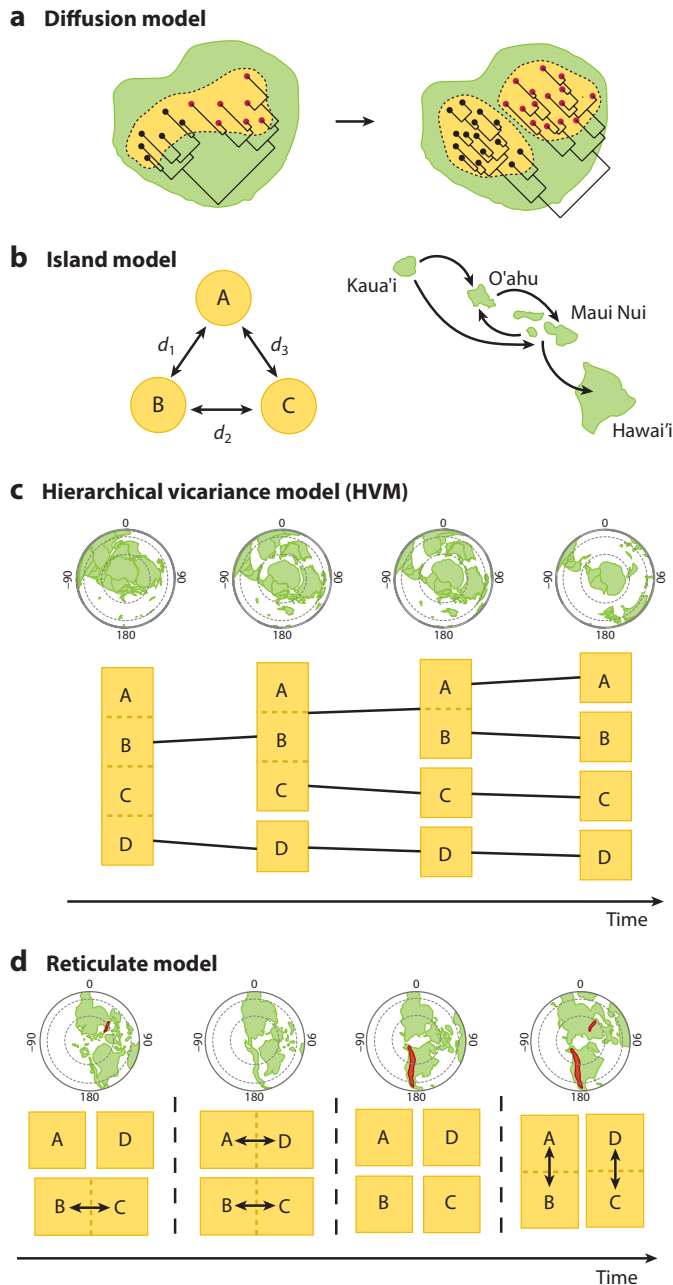Values more than 1.96 are 2SDs past the mean and considered significant.

Figure 1

Model types considered in phylogenetic biogeography. Diffusion models are used primarily for phylogeographic analysis but may also be of interest in classical historical biogeography (*a*). Models that use discrete areas (A–D) fall into the categories of static island models (*b*), hierarchical vicariance models (HVMs) (*c*), and reticulate models (*d*). Static island models may allow variation over time in dispersal rates, d_1 to d_3, but areas are constant. Both HVMs and reticulate models assume different area configurations over time. The empirical examples shown here are the Hawaiian archipelago (island model), Gondwana breakup (HVM), and Northern Hemisphere biogeography (reticulate model).