Biogeographic drivers of evolutionary radiations

Supplementary material

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Figure 5 redrawn with the first 75% of the data discarded as a burn in

Figure 5: Radiation size distributions across repeat simulations for a single immigrating lineage under different rates of internal dispersal (m) and gene flow effect (G). The two rows of panels correspond to different value of gene flow effect (G): 5 and 0.1. The above each panel give the internal dispersal rate (m). Red and blue bars represent fully connected spatial structure and line spatial structure respectively. The habitat network contains 4 patches, each with 1000 individual



Figure 7 redrawn with the first 75% of the data discarded as a burn in

Figure 7: Mean radiation size of the single lineage in the community network, shown on log 10 scale as a function of internal dispersal rate (m). The three columns of panels correspond to three different sizes of community network: 4 patches each with 1000 individuals (a,d), 8 patches each with 500 individuals (b,e), and 8 patches each with 1000 individuals (c,f). The gene flow effect (G) is set as 5 and 0.1 shown as two rows of panels. Blue lines represent results from a line-structured network of local patches, and red lines represent results from a fully-connected structure. The vertical black lines give the predicted value of the critical point m_{crit} for each panel based on the formula $m_{crit} = \frac{1}{G \times J}$ that was described in the methods section.



Figure 8 redrawn with the first 75% of the data discarded as a burn in

Figure 8: Mean radiation size of a single lineage in a community network as a function of internal immigration rate (m) on log 10 based. Results show a broad range of connection networks with different numbers of links in different colours. Panel (a) shows the raw data. Panel (b) shows a scaling collapse based on the same data; here, the horizontal axis shows immigration rate multiplied by number of links in the network. The leftmost part of the graph for relatively low immigration rates thus has a radiation size predicted by immigration rate * number of links rather than depending independently on those two parameters. The figure was produced with gene flow effect (G) equal to 0.1 and community network containing 8 patches each with 1000 individuals.