

## Accepted Manuscript

Evolutionary Isolation and Phylogenetic Diversity loss under random extinction events

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PII: S0022-5193(17)30506-4  
DOI: [10.1016/j.jtbi.2017.11.005](https://doi.org/10.1016/j.jtbi.2017.11.005)  
Reference: YJTBI 9261



To appear in: *Journal of Theoretical Biology*

Received date: 29 May 2017  
Revised date: 6 November 2017  
Accepted date: 8 November 2017

Please cite this article as: Mike Steel, Vahab Pourfaraj, Abhishek Chaudhary, Arne Mooers, Evolutionary Isolation and Phylogenetic Diversity loss under random extinction events, *Journal of Theoretical Biology* (2017), doi: [10.1016/j.jtbi.2017.11.005](https://doi.org/10.1016/j.jtbi.2017.11.005)

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**Highlights**

- The loss of phylogenetic diversity can be predicted by transforming the loss of summed evolutionary isolation scores.
- We prove that the prediction becomes exact in the large tree limit under neutral models of evolution and extinction.
- Simulations show that the prediction is unbiased and reasonable even for moderate-sized trees.

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