Species delimitation of Ophiothrix using bPTP 🔗

PLOS One

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ABSTRACT

This test adds Bayesian support (BS) values to the nodes of the input tree and delimit species based on the Phylogenetic Species Concept. Higher BS values indicate all descendants from the node are more likely to be from one species

EXTERNAL LINK

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THIS PROTOCOL ACCOMPANIES THE FOLLOWING PUBLICATION

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PROTOCOL STATUS

Working

Phylogenetic tree

1   The phylogenetic tree generated by the Bayesian Inference was submitted to the Bayesian Poisson Tree Processes - bPTP [56] to test species boundaries.

Analyses

2   The analyses were conducted on the web server (available at http://species.h-its.org/ptp/). The parameters for the run were 500000 MCMC generations, thinning of 100, and Burn-in of 0.25.