BPTP SPECIES DELIMITATION

bPTP web server (/ptp/)

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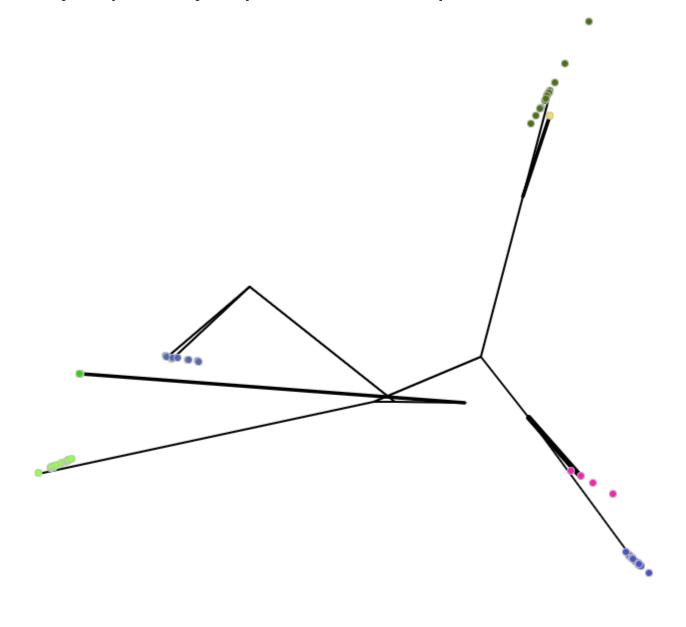
Help (/help/)

About PTP and bPTP (http://cme.h-its.org/exelixis/web/software/PTP/index.html)

PTP paper (http://bioinformatics.oxfordjournals.org/content/29/22/2869)

Download PTP and bPTP (https://github.com/zhangjiajie/SpeciesCounting)

PhyloMap-PTP: PhyloMap visualization of PTP species delimitation result



Save Screen

Clear Screen

Usage: Move mouse cursor on the data point to show the taxa name; Click the left mouse button to show all taxa name belong to this species; Click the right mouse button to fix the taxa name on screen; Press C to clear all taxa names on screen; Press S to save the screen.

Variance explained by first axis: 43.01 % Variance explained by second axis: 19.99 %

What is PhyloMap-PTP and how to interpret the results

Principal Coordinates Analysis (PCoA) has been widely used in species delimitation exercises. Google "pcoa species delimitation" in google scholar, there will be many examples. PhyloMap-PTP is a visualization tool that combines PCoA, PTP and species tree mapping. The original PhyloMap paper can be find here: "J. Zhang, A. M. Mamlouk, T. Martinetz, S. Chang, J. Wang, and R. Hilgenfeld. PhyloMap: an algorithm for visualizing relationships of large sequence data sets and its application to the influenza A virus genome. BMC bioinformatics, 12:248, Jan. 2011." (http://www.biomedcentral.com/1471-2105/12/248) PhyloMap-PTP replaces the "Neural-Gas" clustering in the original PhyloMap with PTP results. It also available as a standalone version here (https://github.com/zhangjiajie/SpeciesCounting).

Each circle in the plot represents a taxa, different species are colored differently. The species tree was mapped onto the plot, one random taxa was chosen from each species as a representative for that species (the leaf node of the mapped species tree.) In the species tree, thicker line means the branch length in the original species tree is longer than the branch in the PhyloMap plot. The horizontal axis is the first axis, and the vertial axis is the second axis. Each axis explains certain amount of variance of the data set. Sometimes, the first axis only separate outgroup taxa from other neighboring taxa, this suggests it might be better to remove the outgroups and rerun the analysis. Note that, neighboring taxa in the PCoA might not really close to each other. Their true distances should be measured alone the branches connecting them.

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Contact through google-group (https://groups.google.com/forum/?hl=en#!forum/ptp-species-delimitation)