

Phylogenetics Z620 Homework 4

The data for this homework assignment is available at:

<http://mypage.iu.edu/~ehouswor/Fall2005/BioZ620/BirdData.txt>

The data come from a study of Adenylate Kinase Intron 5 in various birds by Leo Shapiro and John Dumbacher and are available from the journal BioOne, online, at

<http://www.bioone.org/bioone/?request=get-document&issn=0004-8038&volume=118&issue=01&page=0248#i0004-8038-118-01-0248-t02>

I have renamed the species so that the names are 10 characters long. The original names, common names, and coded names are as follows:

Pitohui dichrous A	Hooded Pitohui A	Pitohui1A
Pitohui dichrous B	Hooded Pitohui B	Pitohui1B
Pitohui dichrous C	Hooded Pitohui C	Pitohui1C
Pitohui kirhocephalus A	Variable Pitohui A	Pitohui2A
Pitohui kirhocephalus B	Variable Pitohui B	Pitohui2B
Pitohui kirhocephalus C	Variable Pitohui C	Pitohui3C
Colluricincla megarhyncha A	Rufus or Little Strike Thrush A	Rufus A
Colluricincla megarhyncha B	Rufus or Little Strike Thrush B	Rufus B
Pachycephala pectoralis	Golden Whistler	Whistler1
Pachycephala schlegelii	Regent Whistler	Whistler2
Pachycephala socor	Sclater's Whistler	Whistler3
Rhagologus leucostigma	Mottled Whistler	Whistler4
Cicinnurus magnificus	Magnificent Bird of Paradise	Paradise1
Melampitta gigantea	Greater Melampitta	Paradise2
Paradisaea raggiana	Raggiana Bird of Paradise	Paradise3
Molothrus aeneus	Bronzed Cowbird	Cowbird1
Molothrus ater	Brown-headed Cowbird	Cowbird2

1) Look at the data. Do you think the data meet the assumptions needed for parsimony methods to be valid?

2) Whether valid or not, use parsimony to create a phylogeny for these species. Use the two Cowbirds as an outgroup either by creating new characters with large weights as demonstrated in class or by re-treesing the phylogeny (or as you can in PAUP). Create a nice graphic of the rooted phylogeny with branch lengths. Compare your phylogeny to the phylogeny given in the paper of Shapiro and Dumbacher. What are the similarities and differences? Explain what might cause disagreements between your phylogeny and theirs.

3) How much longer does a branch-and-bound algorithm take for these data than a heuristic search? (When the data follow the assumptions that make parsimony valid, branch-and-bound algorithms have good bounds and are relatively efficient. That would not be the case if the data were more variable.)