Genetics/MBT 541

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Lecture 2

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Phylogeny methods, part 2
(Searching tree space)
Forming all 4-species trees by adding the next species in all possible places.
A global maximum cannot always be found by going uphill
is rearranged by dissolving the connections to an interior branch:

and reforming them in one of the two possible alternative ways:

Nearest-Neighbor Interchange (NNI) rearrangement of a tree (the triangles are subtrees)
The graph of all 15 bifurcating 5-species unrooted trees, connected by nearest-neighbor interchanges
The same graph with parsimony scores
(try a “greedy” search by NNI’s)
Subtree pruning and regrafting (SPR) rearrangement
Break each branch, separate the subtrees

Connect a branch of one to a branch of another

Here is that result:

Tree bisection and reconnection (TBR) rearrangement
“Greedy” search by addition of species in a fixed order (A, B, C, D, E) in all possible places
“Star decomposition” search for best tree
“Disk covering” – assembly of a tree by overlapping estimated subtrees
A Shortest Hamiltonian Path problem (a) solved by a random path (b), a greedy algorithm (c), and exactly (d) by branch-and-bound.
A search tree of all possible solutions to the SHP problem
Search tree of all 5-species trees using addition of species C, D, E in all possible places
The same search tree with the parsimony score of each tree. Solid lines are traversed by branch-and-bound search.
References


Graham, R. L. and L. R. Foulds. 1982. Unlielihood that minimal phylogenies for a realistic biological study can be constructed in reasonable computational time. *Mathematical Biosciences* 60: 133-142. [...] and again ...


