PAUP* 4.0

Phylogenetic Analysis Using Parsimony (*and other methods)

- PAUP Version 1.0: ~1983
- PAUP Version 3.1: ~1993
- Currently on PAUP* version 4.0 (alpha)
  which is still changing quickly
What is PAUP*?

A multipurpose program for phylogenetic analysis

- Simple, intuitive interface
- Wide variety of analyses available in a single program (facilitates exploration)

Searching for optimal evolutionary trees:

- Parsimony
- Distance
  - Minimum evolution
  - Least-squares
  - Weighted least squares (Fitch-Margoliash)
- Maximum likelihood (under a variety of models)
Tree-search algorithms

- Exact
  - Branch and bound
  - Exhaustive search
- Heuristic (local search)
  - Nearest-neighbor interchange (NNI)
  - Subtree pruning-regrafting (SPR)
  - Tree bisection-reconnection (TBR)
  - Edge contract-refine (2-ECR)
  - Star decomposition
  - Quartet puzzling
- Clustering/algorithmic
  - Neighbor-joining (including BioNJ)
  - UPGMA
Decent graphics
Confidence and hypothesis testing

- Bootstrap
- Jackknife
- Kishino-Hasegawa test
- Shimodaira-Hasegawa test
- Shimodaira approximately unbiased test (soon)
- Nonparametric Templeton and winning-sites tests
- Permutation tests
- Partition homogeneity (ILD) test
Models

• **DNA substitution models** (both for distance and ML)
  - Jukes-Cantor
  - Kimura 2-parameter and 3ST
  - HKY85 and Felsenstein84
  - General time reversible (including any arbitrary submodel)

• **Amino acid models**
  - PAM
  - JTT
  - mtREV
  - WAG
  - Any user-specified rate matrix
  - GTR

• **Among-site rate variation**
  - Gamma-distributed
  - Proportion of invariable sites
  - Gamma + $P_{inv}$
  - Site-specific
Other analyses and functions

- Summarizing agreement among trees
  - Strict consensus
  - Majority-rule consensus
  - Adams consensus
  - Agreement subtrees
- Filtering/sorting trees
  - By compatibility with consensus
  - By tree score
- Tree output and description
  - Cladograms
  - Phylograms
  - Unrooted trees
- Reconstruction of ancestral character states
  - Parsimony
  - ML
- Tree-to-tree distances (RF, agreement metric, “ABC”)
- Import/export of foreign formats (PHYLIP, Mega, NBRF, Hennig/Nona/TNT)
Some new features

- Amino acid models
- Vectorized parsimony and likelihood calculations (Altivec, SSE)
- Multithreaded (pthreads, OpenMP) for multiprocessor and multicore machines
- Supertrees (MRP, strict consensus merger, others?)
- Soon?
  - Simple checkpointing
  - Parallel tree evaluation (MPI and PVM)
  - Improved tree-search heuristics (e.g., “ratchet”)
PAUP* 4.0 Platforms

OS X and Windows (native)
PAUP* 4.0 Platforms

Linux/Unix/OS X Terminal
Helpers/Collaborators

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