PAUP* 4.0

Phylogenetic Analysis Using Parsimony (and other methods)

- Version 1.0: ~1983
- Version 3.1: ~1993
- Version 4.0: 1996–?

“Commercial” (Sinauer Associates)
http://paup.sc.fsu.edu
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/algorithimic
  - Neighbor-joining (including BioNJ)
  - UPGMA
Decent graphics
Confidence and hypothesis testing

- Bootstrap
- Jackknife
- Kishino-Hasegawa test
- Shimodaira-Hasegawa test
- Shimodaira approximately unbiased test
- 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** (new)
  • 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 (SSE-2, Altivec)
• 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
PAUP* 4.0 Platforms

Linux/Unix/OS X Terminal
PAUP* 4.0 Platforms

Microsoft Windows (full GUI coming soon)
Helpers/Collaborators

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