

PAUP* 4.0

Phylogenetic Analysis Using Parsimony (and other methods)

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

What is PAUP*?

A multipurpose program for phylogenetic analysis

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

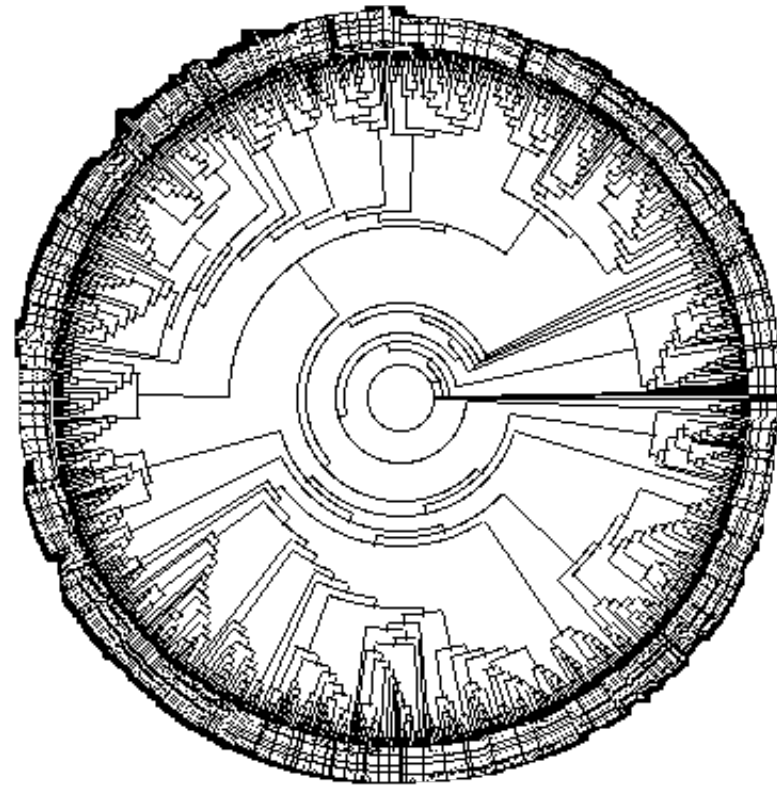
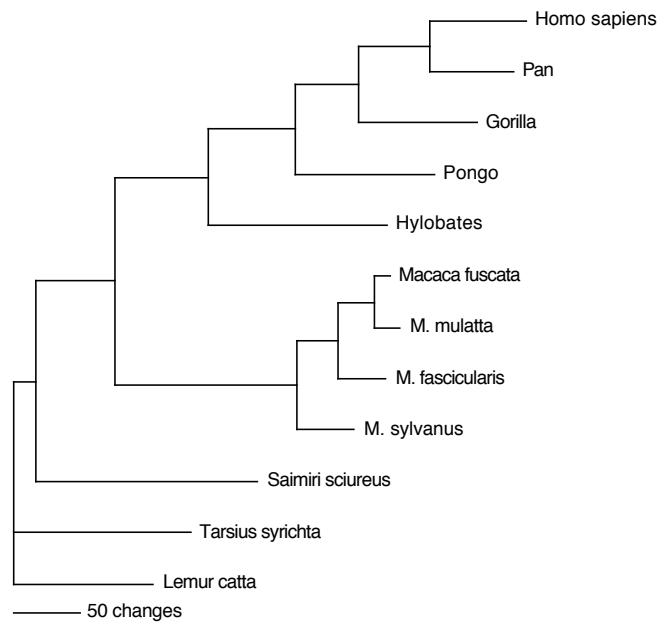
Searching for optimal evolutionary trees:

- 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
- 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

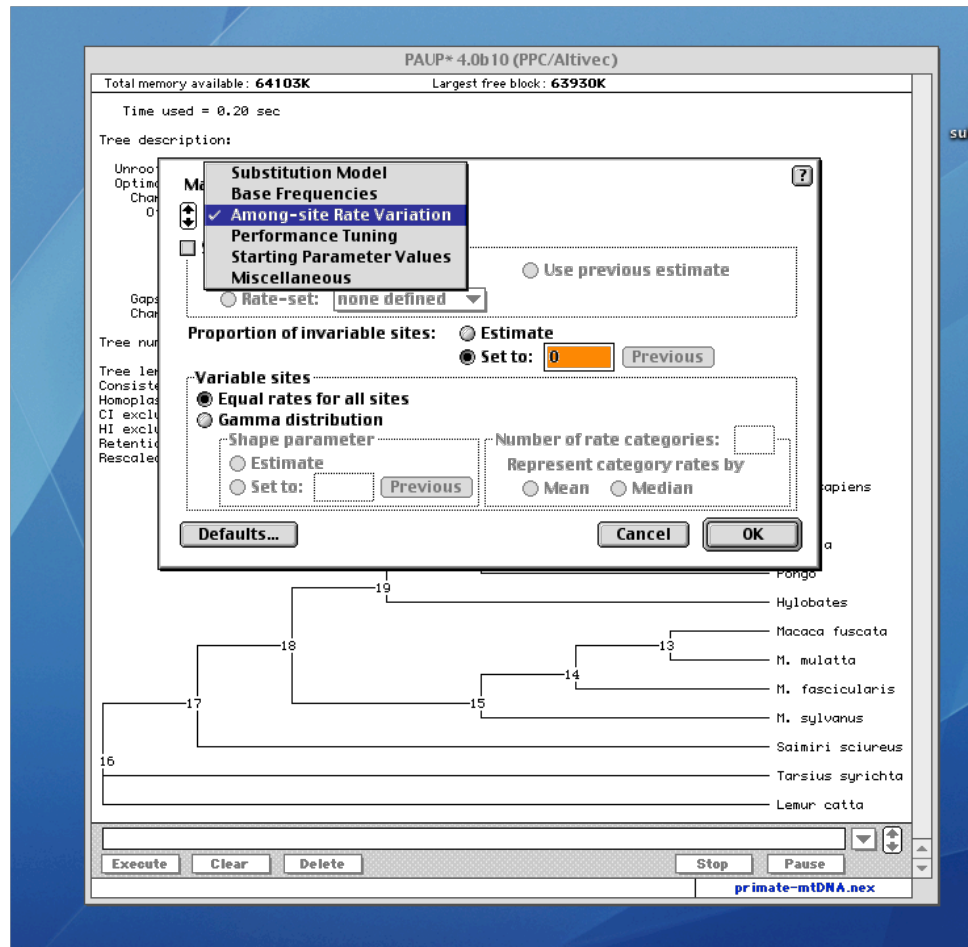
- Summarizing agreement among trees
 - Strict consensus
 - Majority-rule consensus
 - Adams consensus
 - Agreement subtrees
- Filtering/sorting trees
 - By compatibility with consensus
 - By tree score
- Tree output and description
 - Cladograms
 - Phylograms
 - Unrooted trees
- Reconstruction of ancestral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

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")

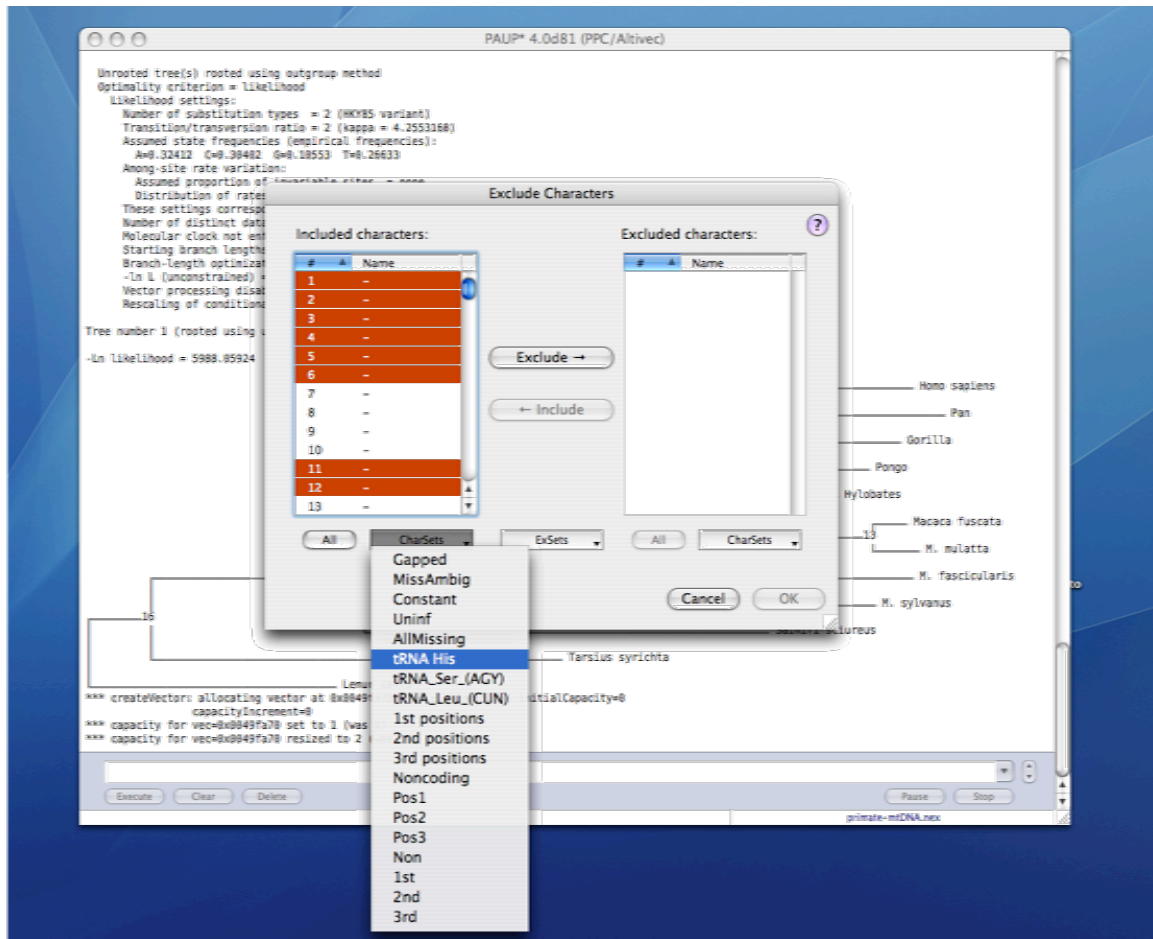
PAUP* 4.0 Platforms

Mac Classic



PAUP* 4.0 Platforms

OS X and Windows (native)



PAUP* 4.0 Platforms

Linux/Unix/OS X Terminal

```
Terminal — tcsh (tty1) — 120x40
154 variable characters are parsimony-uninformative
Number of parsimony-informative characters = 367
Gaps are treated as "missing"
Character-state optimization: Accelerated transformation (ACCTRAN)

Tree number 1 (rooted using user-specified outgroup)

Tree length = 1153
Consistency index (CI) = 0.6496
Homoplasy index (HI) = 0.3504
CI excluding uninformative characters = 0.5844
HI excluding uninformative characters = 0.4156
Retention index (RI) = 0.5960
Rescaled consistency index (RC) = 0.3872

      /----- Homo sapiens
     /----- 22 -----
    /----- Pan
   /----- 21 -----
  /----- Gorilla
 /----- 20 -----
/----- Pongo
|----- 19 -----
|----- Hylobates
|----- 18 -----
|----- 13 -----
|----- Macaca fuscata
|----- 14 -----
|----- M. mulatta
|----- 15 -----
|----- M. fascicularis
|----- 16 -----
|----- M. sylvanus
|----- 17 -----
|----- Saimiri sciureus
|----- 16 -----
|----- Tarsius syrichta
|----- 16 -----
|----- Lemur catta

paup> set criterion=likelihood; lset nst=6[]
```

Helpers/Collaborators



Jim Wilgenbusch (support, documentation, production)



Chuck Bell (coauthor of version 4.0 manual)



John Huelsenbeck



Paul Lewis



David Bryant



Peter Waddell