

# 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)

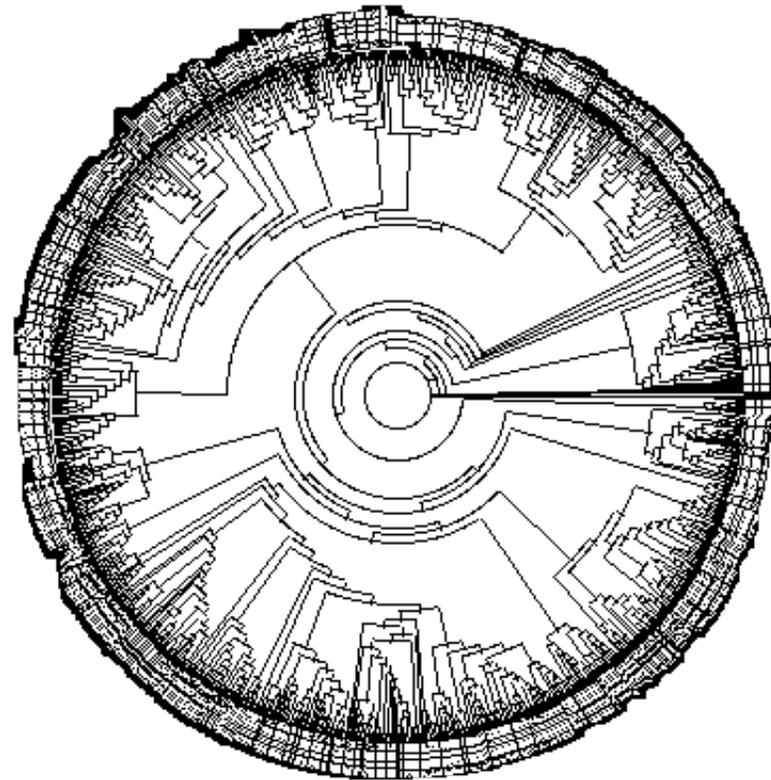
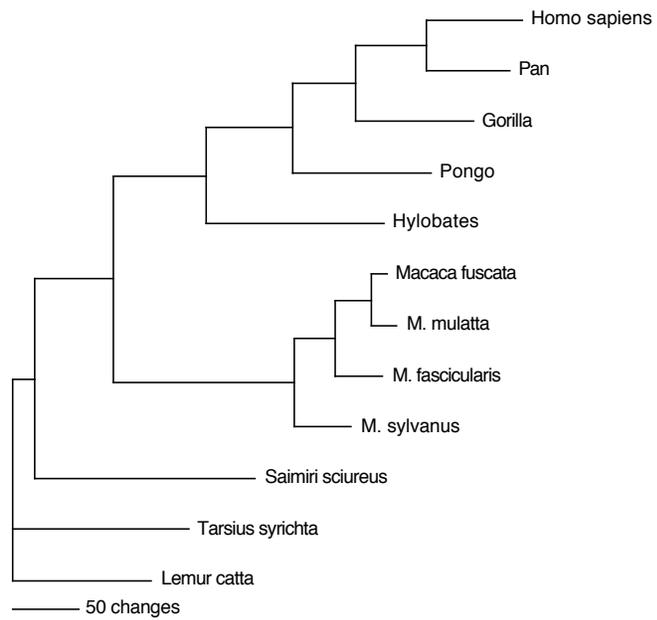
Searching for optimal evolutionary trees:

- 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

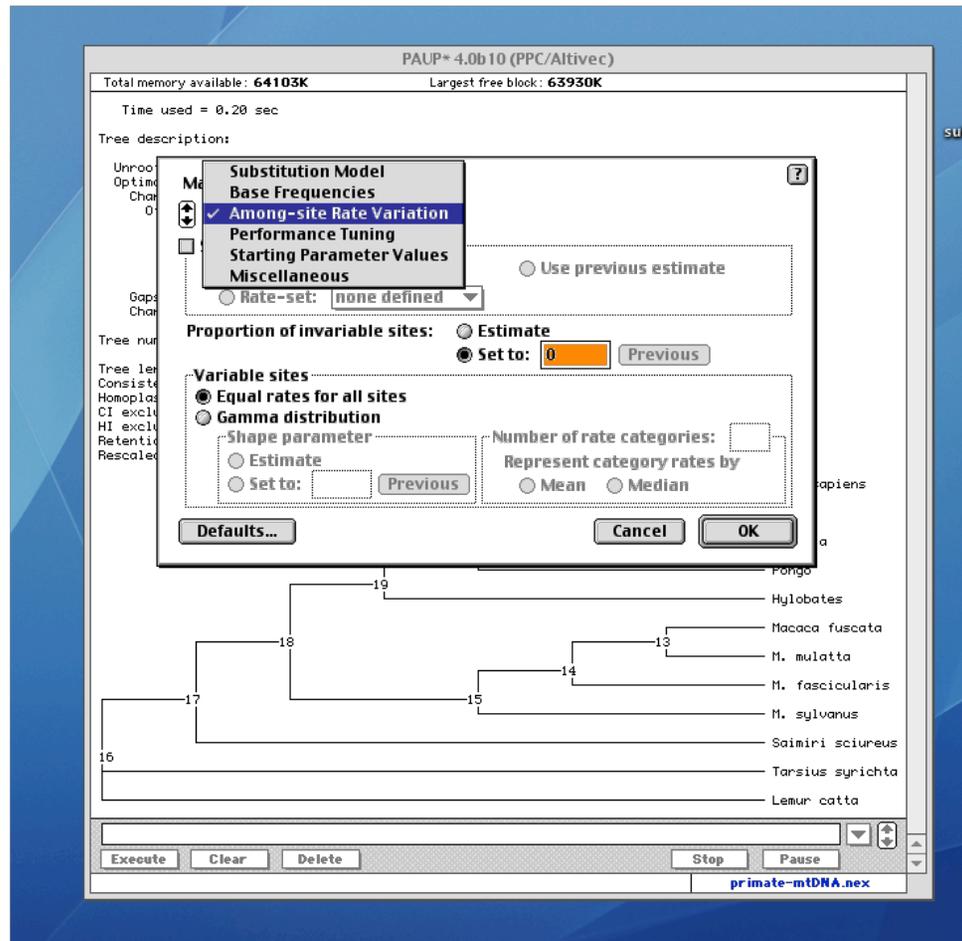
- Summarizing agreement among trees
  - Strict consensus
  - Majority-rule consensus
  - Adams consensus
  - Agreement subtrees
- Filtering/sorting trees
  - By compatibility with consensus
  - By tree score
- Tree output and description
  - Cladograms
  - Phylograms
  - Unrooted trees
- Reconstruction 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")

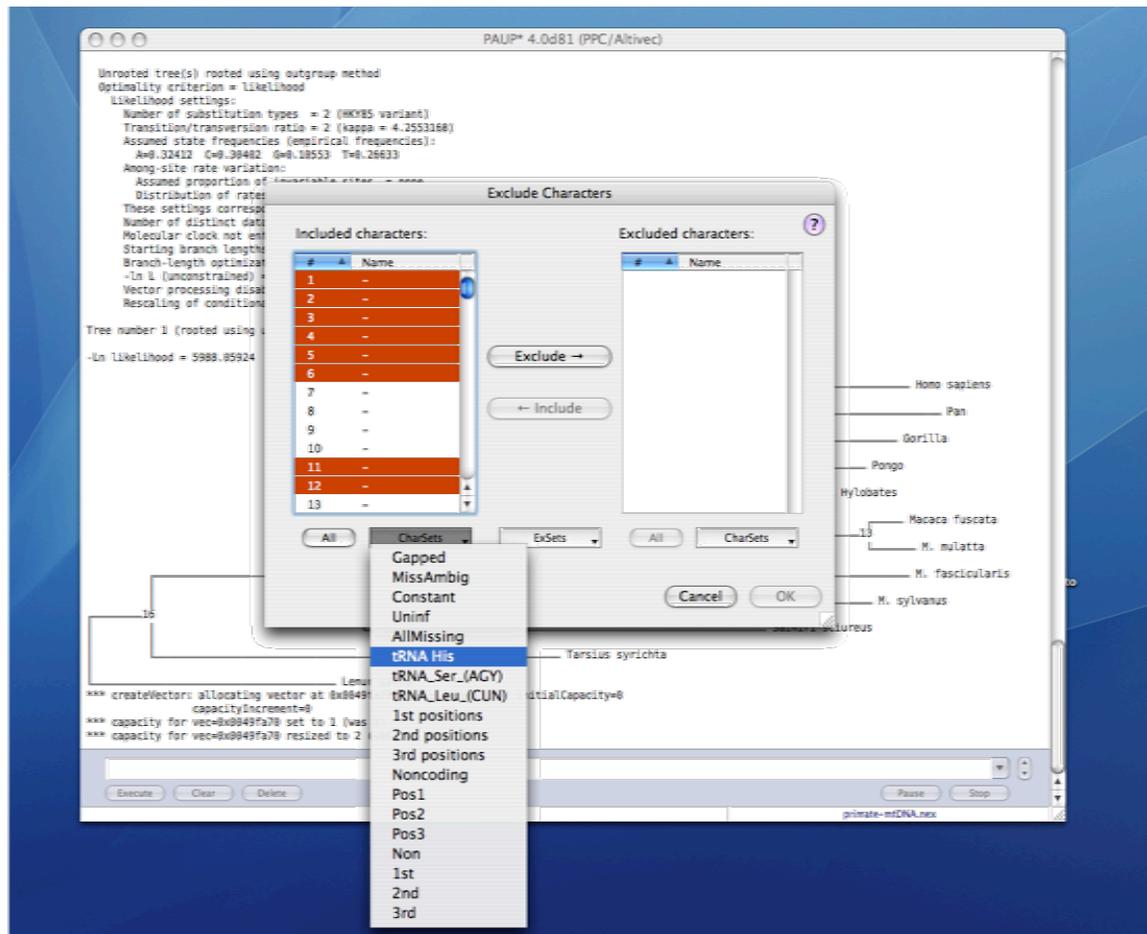
# PAUP\* 4.0 Platforms

## 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