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)

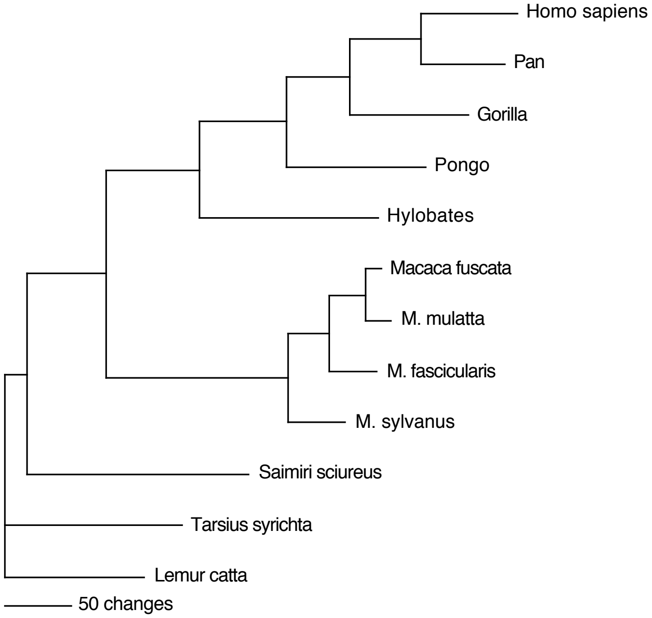
Searching for optimal evolutionary trees:

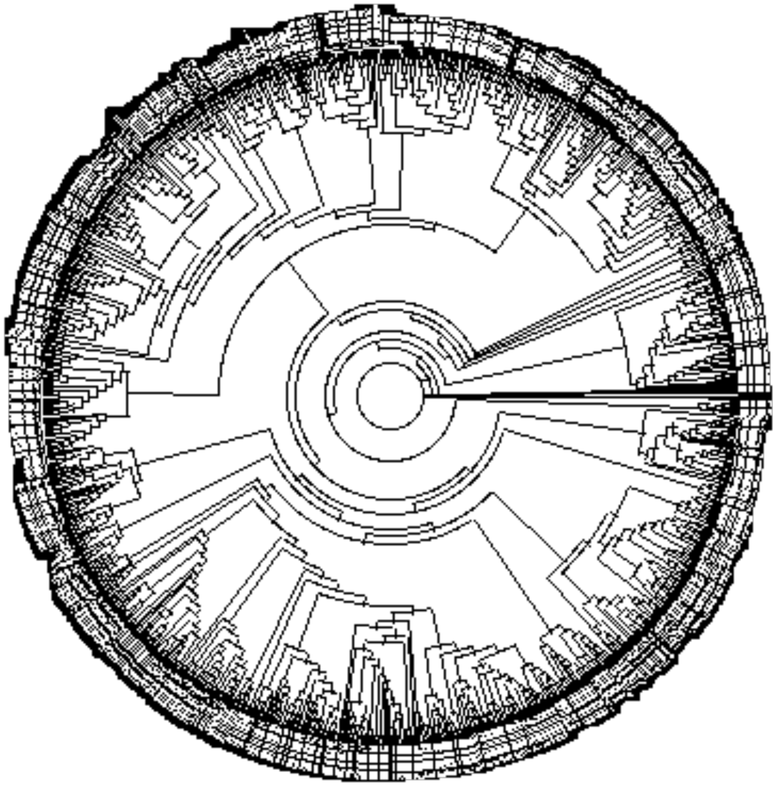
- Parsimony
- Distance
  - Minimum evolution
  - Least-squares
  - Weighted least squares (Fitch-Margoliash)
- Maximum likelihood (under a variety of models)

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/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 substition 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

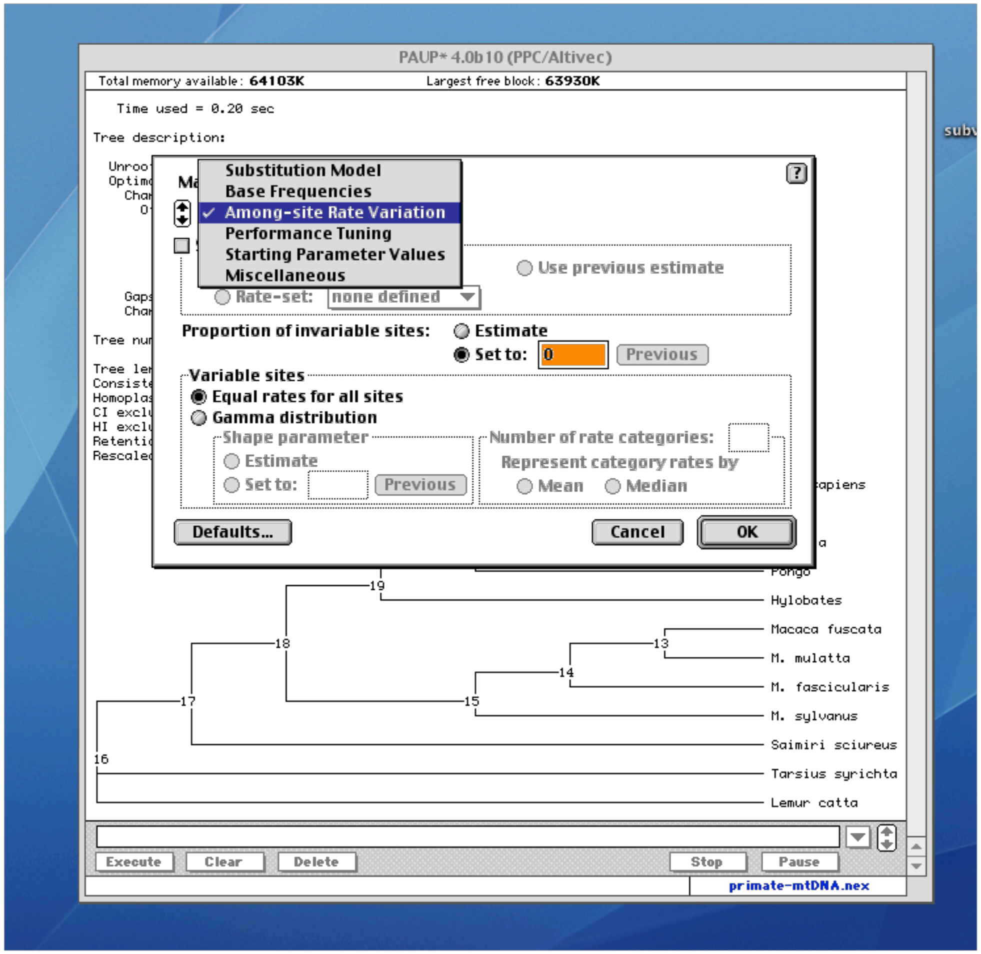
- **Summarizing agreement among trees**
  - Strict consensus
  - Majority-rule consensus
  - Adams consensus
  - Agreement subtrees
- **Filtering/sorting trees**
  - By compatibility with consensus
  - By tree score
- **Tree output and description**
  - Cladograms
  - Phylograms
  - Unrooted trees
-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

Mac Classic



PAUP* 4.0b10 (PPC/Altivec)

Total memory available: **64103K** Largest free block: **63930K**

```
   Time used = 0.20 sec

Tree description:

  Unroo
  Optim
    Char
      O

    Gaps
    Char

Tree nu

Tree le
Consist
Homopla
CI excl
HI excl
Retenti
Rescale
```

Proportion of invariable sites: ○ Estimate ● Set to: 0

Variable sites

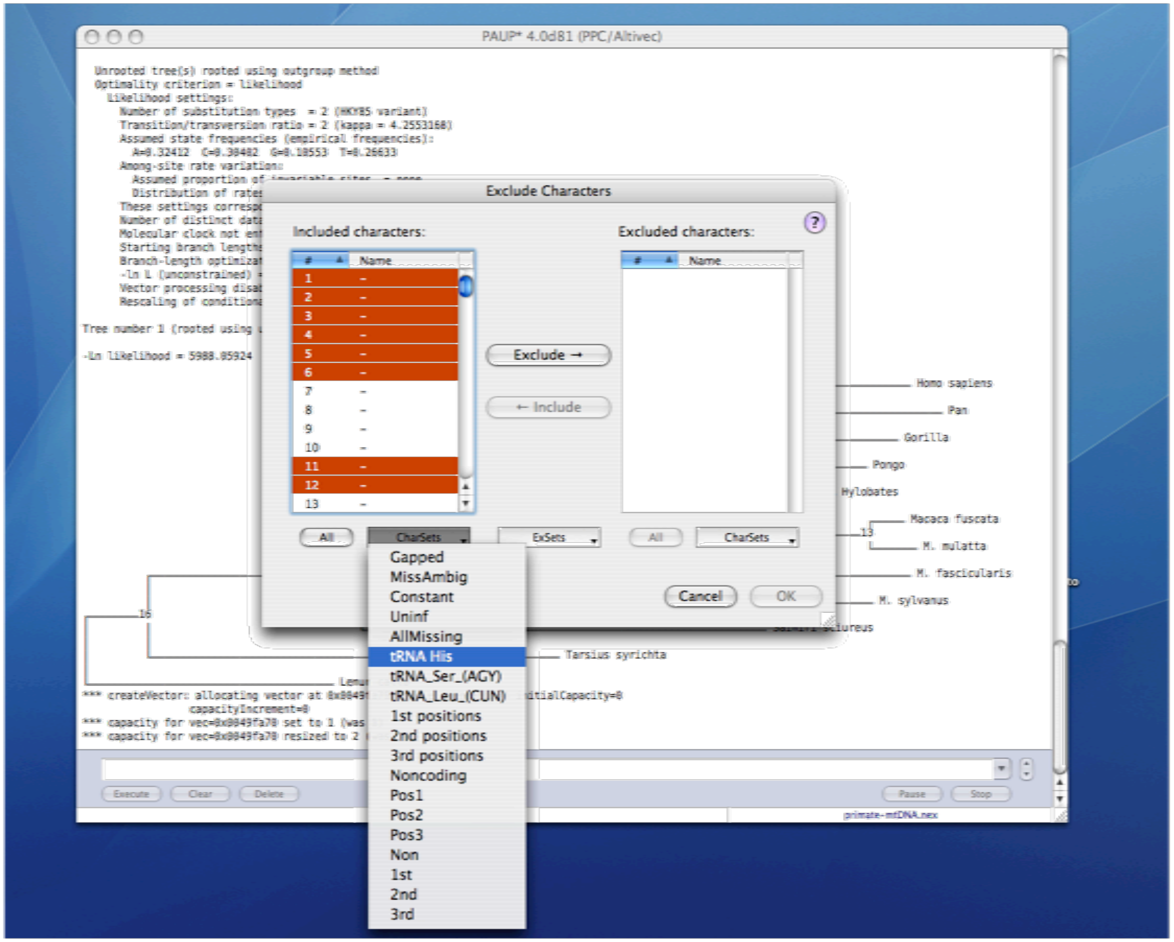
● Equal rates for all sites

○ Gamma distribution

primate-mtDNA.nex

PAUP* 4.0 Platforms

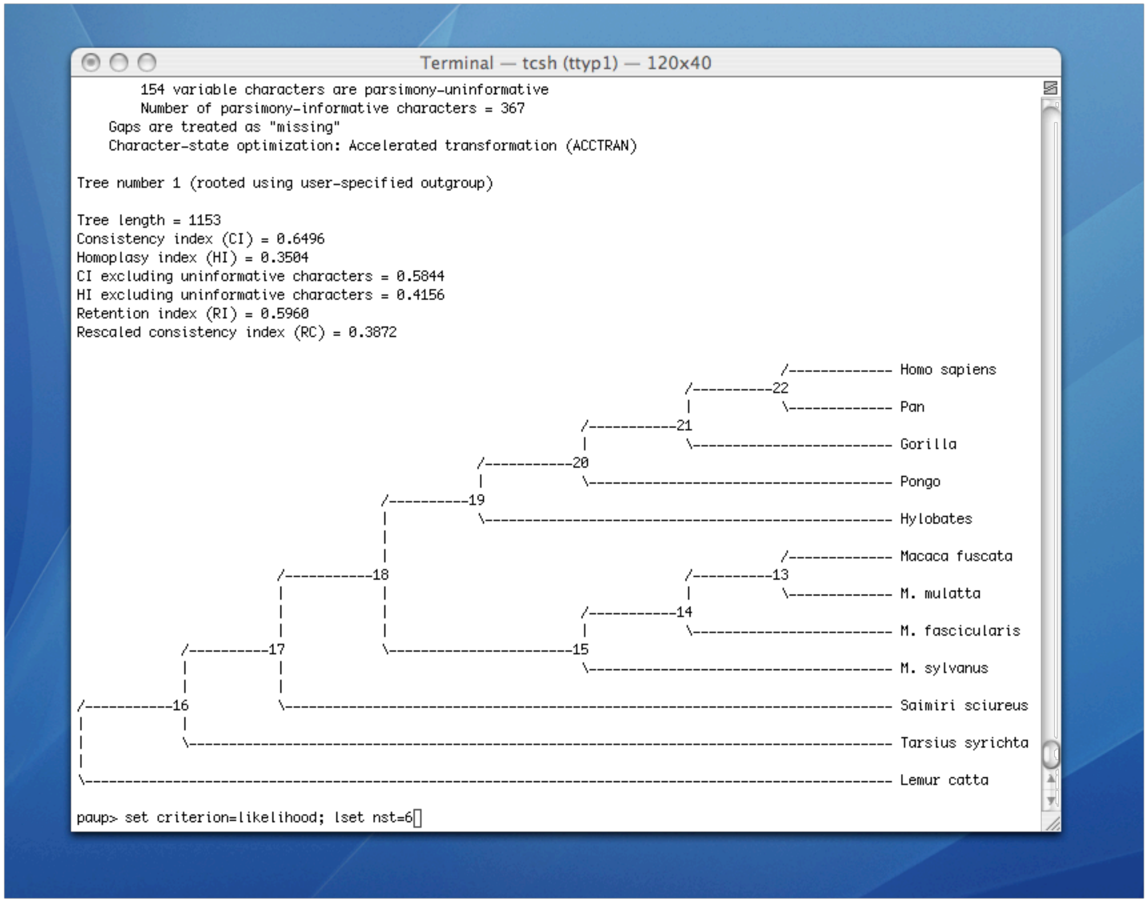
OS X and Windows (native)



```
Unrooted tree(s) rooted using outgroup method
Optimality criterion = likelihood
  Likelihood settings:
    Number of substitution types  = 2 (HKY85 variant)
    Transition/transversion ratio = 2 (kappa = 4.2553168)
    Assumed state frequencies (empirical frequencies):
      A=0.32412  C=0.30482  G=0.10553  T=0.26633
    Among-site rate variation:
      Assumed proportion of invariable sites  = none
      Distribution of rates
    These settings corresp
    Number of distinct data
    Molecular clock not en
    Starting branch length
    Branch-length optimizat
    -ln L (unconstrained) =
    Vector processing disab
    Rescaling of condition

Tree number 1 (rooted using 

-ln likelihood = 5988.05924

*** createVector: allocating vector at 0x0049f                    itialCapacity=0
                     capacityIncrement=0
*** capacity for vec=0x0049fa70 set to 1 (was
*** capacity for vec=0x0049fa70 resized to 2
```

PAUP* 4.0 Platforms

Linux/Unix/OS X Terminal



```
        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
                                      |
                                      |                                                 /------------- Macaca fuscata
                         /-----------18                                     /----------13
                         |            |                                     |           \------------- M. mulatta
                         |            |                        /-----------14
                         |            |                        |            \------------------------- M. fascicularis
             /----------17            \-----------------------15
             |           |                                     \-------------------------------------- M. sylvanus
             |           |
/-----------16           \---------------------------------------------------------------------------- Saimiri sciureus
|            |
|            \---------------------------------------------------------------------------------------- Tarsius syrichta
|
\----------------------------------------------------------------------------------------------------- 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**