

PARTIE V : Les logiciels

Programmes

Journées RNG de phylogénie moléculaire et analyse
comparative

Un tour d'horizon de l'offre logicielle en phylogénie

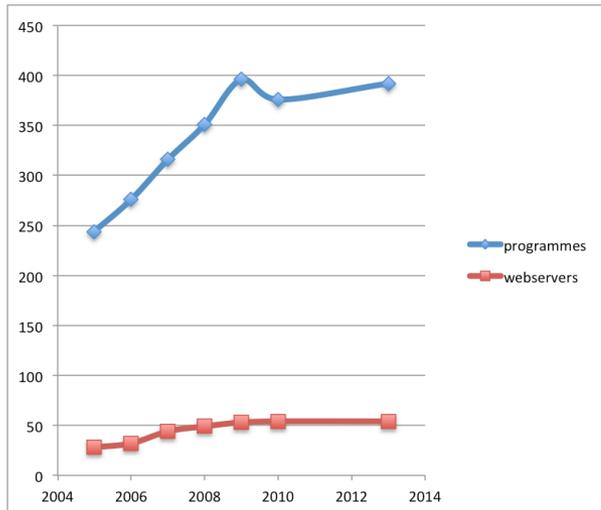
Manolo Gouy

Biométrie et Biologie Evolutive - UMR CNRS 5558

La liste de référence : la page web de Joe Felsenstein

<http://evolution.genetics.washington.edu/phylip/software.html>

En 2014 392 programmes fonctionnant sur toutes les plates-formes et 54 serveurs web d'accès libre



<http://research.amnh.org/users/koloko/softlinks/phylogeny.html>

Maximum likelihood and Bayesian methods

- [PHYLIP](#)
- [PAUP*](#)
- [fastDNAMl](#)
- [MOLPHY](#)
- [PAML](#)
- [Spectrum](#)
- [SplitsTree](#)
- [PLATO](#)
- [TREE-PUZZLE](#)
- [Hadtrees, Prepare and Trees](#)
- [SeqPup](#)
- [Phylo_win](#)
- [PASSML](#)
- [ARB](#)
- [Darwin](#)
- [BAMBE](#)
- [DAMBE](#)
- [Modeltest](#)
- [VeryfastDNAMl](#)
- [PAL](#)
- [dnarates](#)
- [TrExMl](#)
- [HY-PHY](#)
- [Vanilla](#)
- [DT-ModSel](#)
- [Bionumerics](#)
- [fastDNAMlRev](#)
- [RevDNARates](#)
- [rate-evolution](#)
- [MrBayes](#)
- [CONSEL](#)
- [EDIBLE](#)
- [Mesquite](#)
- [PTP](#)
- [Treefinder](#)
- [MetaPIGA](#)
- [RAxML](#)
- [PHASE](#)
- [PHYML](#)
- [BEAST](#)
- [r8s-bootstrap](#)
- [MrBayes tree scanners](#)
- [MrMTgui](#)
- [MrModeltest](#)
- [BootPHYML](#)
- [p4](#)
- [Porn*](#)
- [SIMMAP](#)
- [Spectronet](#)
- [Rhino](#)
- [IM](#)
- [ProtTest](#)
- [ModelGenerator](#)
- [Simplot](#)
- [MDIV](#)
- [MrAIC](#)
- [Modelfit](#)
- [IQPNNI](#)
- [PARAT](#)
- [ALIFRITZ](#)
- [PhyNav](#)
- [DPRML](#)
- [MultiPhyl](#)
- [NimbleTree](#)
- [PaupUp](#)
- [SSA](#)
- [BAli-Phy](#)
- [CoMET](#)
- [BIRCH](#)
- [Mac5](#)
- [BayesPhylogenies](#)
- [Kakusan2](#)
- [GARLI](#)
- [MrBayesPlugin](#)
- [PHYSIG](#)
- [SEMPHY](#)
- [FASTML](#)
- [Rate4Site](#)
- [aLRT](#)
- [McRate](#)
- [PhyloBayes](#)
- [BEST](#)
- [EREM](#)
- [IDEA](#)
- [PROCOV](#)
- [DART](#)
- [PhyloCoCo](#)
- [AMBIORE](#)
- [PRAP](#)
- [SeqState](#)
- [Leaphy](#)
- [NHML](#)
- [SLR](#)
- [rRNA phylogeny](#)
- [Bosque](#)
- [Concatpillar](#)
- [PHYLLAB](#)
- [NEPAL](#)
- [EMBOSS](#)
- [CodeAxe](#)
- [phangorn](#)
- [bms_runner](#)
- [tracer](#)
- [burntrees](#)

PARTIE V : Les logiciels

ALGORITHMES ET SERVICES WEB POUR L'ALIGNEMENT MULTIPLE

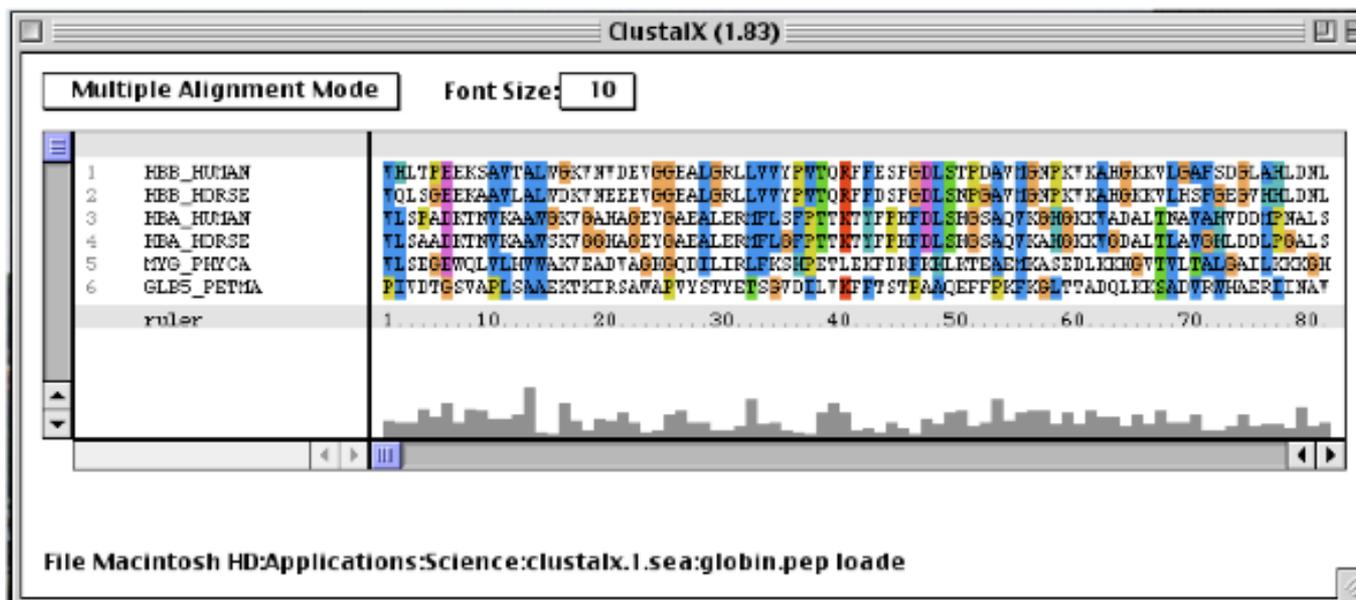
Liste de logiciels d'alignement de séquence :

http://en.wikipedia.org/wiki/List_of_sequence_alignment_software

- 1 Database search only (BLAST, FASTA, HMMER, PSI-BLAST , etc.)
- 2 Pairwise alignment (SSEARCH, SEQALN, MUMmer, etc.)
- 3 Multiple sequence alignment (Clustal , MAFFT, MUSCLE, etc.)
- 4 Genomics analysis (GMAP, BLAT, MAUVE, MGA, etc.)
- 5 Motif finding (MEME, PHI-Blast, ScanProsite, etc.)
- 6 Benchmarking (BAliBASE, etc.)
- 7 Alignment Viewers/Editors
- 8 Short-Read Sequence Alignment (BWA, Shrimp, SOAP, Bowtie, etc.)

CLUSTALW: alignement multiple de séquences nucléotidiques ou protéiques
 CLUSTALX: interface graphique de l'algorithme CLUSTALW.

Des Higgins, Julie Thompson, Toby Gibson. Dublin - Strasbourg - Heidelberg.



Logiciel multiplateformes librement accessible.

Une star de la bioinformatique: 16755 citations de l'article introductif de CLUSTALW; 6137 citations pour CLUSTALX.

ClustalW2

ClustalW2 is a general purpose multiple sequence alignment program for DNA or proteins. It produces biologically meaningful multiple sequence alignments of divergent sequences. It calculates the best match for the selected sequences, and lines them up so that the identities, similarities and differences can be seen. Evolutionary relationships can be seen via viewing Cladograms or Phylograms.

[New users, please read the FAQ.](#)

>> [Download Software](#)



YOUR EMAIL	ALIGNMENT TITLE	RESULTS	ALIGNMENT		
<input type="text"/>	Sequence	interactive	full		
KTUP (WORD SIZE)	WINDOW LENGTH	SCORE TYPE	TOPDIAG	PAIRGAP	
def	def	percent	def	def	
MATRIX	GAP OPEN	NO END GAPS	GAP EXTENSION	GAP DISTANCES	
def	def	yes	def	def	
	ITERATION		NUMITER		
	none		1		
	OUTPUT		PHYLOGENETIC TREE		
OUTPUT FORMAT	OUTPUT ORDER	TREE TYPE	CORRECT DIST.	IGNORE GAPS	CLUSTERING
aln w/numbers	aligned	none	off	off	NJ

<http://www.ebi.ac.uk/Tools/clustalw2/>

Enter or Paste a set of Sequences in any supported format:

Help

Upload a file:

Parcourir...

Run

Reset

Clustal Omega

<http://www.ebi.ac.uk/Tools/msa/clustalo/>

Input form Web services Help & Documentation

[Tools](#) > [Multiple Sequence Alignment](#) > Clustal Omega

Multiple Sequence Alignment

Clustal Omega is a new multiple sequence alignment program that uses seeded guide trees and HMM profile-profile techniques to generate alignments.

STEP 1 - Enter your input sequences

Enter or paste a set of sequences in any supported format:

Or, upload a file:

STEP 2 - Set your parameters

OUTPUT FORMAT

The default settings will fulfill the needs of most users and, for that reason, are not visible.

(Click here, if you want to view or change the default settings.)

STEP 3 - Submit your job

Be notified by email *(Tick this box if you want to be notified by email when the results are available)*

MAFFT version 7

Multiple alignment program for amino acid or nucleotide sequences

Download version

- [Mac OS X](#)
- [Windows](#)
- [Linux](#)
- [Source](#)

Online version

- Alignment**
- [mafft --add](#)
- [Phylogeny](#)
- [Rough tree](#)

[Merits / limitations](#)

[Algorithms](#)

[Tips](#)

[Benchmarks](#)

[Feedback](#)



This service will be unavailable due to maintenance during:
 6:00AM, Nov.23 - 6:00PM, Nov.23 (JST)
 9:00PM, Nov.22 - 9:00AM, Nov.23 (UTC)

All jobs are reset at 4:00AM (JST) every Sunday.

Multiple sequence alignment and NJ / UPGMA phylogeny

New!! (2013/Sep/27)

We made a change in the scoring scheme in version 7.110.
 For problems that require many gaps, alignment quality is (expected to be) improved.
 For conserved dataset, the difference is small.

Scoring scheme:

- New
- Conventional

Input:

Paste protein or DNA sequences in fasta format. [Example](#)

Advanced settings

Strategy (automatic):

- Moderately fast (FFT-NS-2)
- Moderately accurate (FFT-NS-2, FFT-NS-i or L-INS-i; depends on data size)

Strategy (manual):

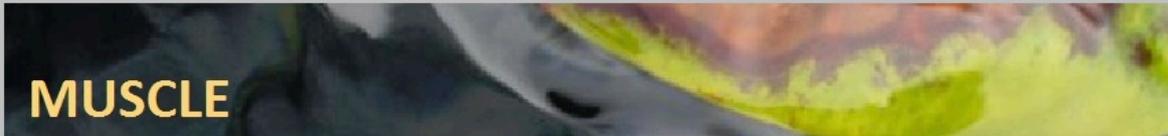
- FFT-NS-1 (Very fast; recommended for >2,000 sequences; progressive method)
- FFT-NS-2 (Fast; progressive method)
- (Medium; iterative refinement method, two cycles only)
- FFT-NS-i (Slow; iterative refinement method)
- L-INS-i (Very slow; recommended for <200 sequences) [Help](#)
- E-INS-i (Very slow; recommended for <200 sequences) [Help](#)
- Q-INS-i (Extremely slow; secondary structure of RNA is considered; recommended for a global alignment of highly diverged RNAs with <200 sequences × <1,000 nucleotides) [Help](#)

Parameters:

Scoring matrix (for amino acid sequences): [Help](#)
 Gap opening penalty: (1.0 - 3.0)
 Offset value: (0.0 - 1.0; functions like gap extension penalty)
 Default offset value has changed (2007/03/03). 0.123 → 0.000

Mafft-homologs (Collects homologs from SwissProt by BLAST and performs profile-based alignments; Protein only): [Help](#)

- On
- Show homologs (if any)
- Number of homologs: (5 - 200)
- Threshold: (1e-5 - 1e-40)



MUSCLE

MUSCLE has been cited by **9,791 papers**
[Google scholar](#)
Last updated 16 Nov 2013

[Downloads](#)

[Documentation](#)

[Support](#)

USEARCH
Ultra-fast sequence analysis

Popular multiple alignment software

MUSCLE is one of the most widely-used methods in biology. On average, MUSCLE is cited by seven new papers every day.

Fast, accurate and easy to use

MUSCLE is one of the best-performing multiple alignment programs according to published benchmark tests, with accuracy and speed that are consistently better than CLUSTALW. MUSCLE can align hundreds of sequences in seconds. Most users learn everything they need to know about MUSCLE in a few minutes—only a handful of command-line options are needed to perform common alignment tasks.

Papers

There are two papers. The first (NAR) introduced the algorithm, and is the primary citation if you use the program. The second (BMC Bioinformatics) gives more technical details, including descriptions of non-default options.

Edgar, R.C. (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput *Nucleic Acids Res.* 32(5):1792-1797 [\[Link to PubMed\]](#).

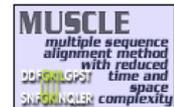
Edgar, R.C. (2004) MUSCLE: a multiple sequence alignment method with reduced time and space complexity *BMC Bioinformatics*, (5) 113 [\[Link to PubMed\]](#).

EBI > Tools > Sequence Analysis

MUSCLE

MUSCLE stands for **M**ultiple **S**equences **C**omparison by **L**og-**E**xpectation. MUSCLE is claimed to achieve both better average accuracy and better speed than [ClustalW2](#) or [T-Coffee](#), depending on the chosen options.

 [Download Software](#)



RESULTS	SEARCH TITLE	YOUR EMAIL
<input type="text" value="interactive"/>	<input type="text" value="Sequence"/>	<input type="text"/>
OUTPUT FORMAT	OUTPUT TREE	OUTPUT ORDER
<input type="text" value="FASTA"/>	<input type="text" value="none"/>	<input type="text" value="aligned"/>

Enter or Paste a set of Sequences in any supported format:

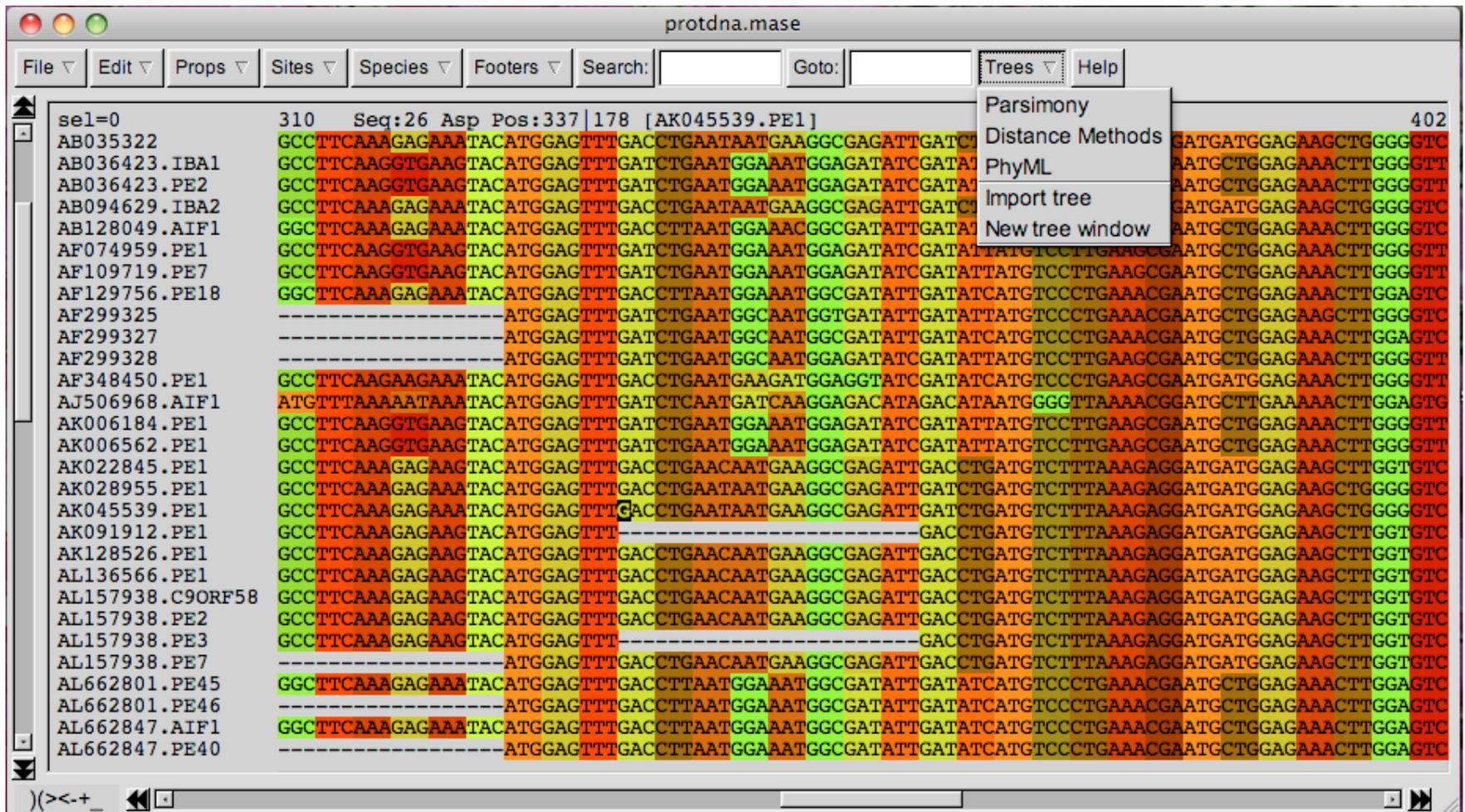
Upload a file:

PARTIE V : Les logiciels

EDITEURS D' ALIGNEMENT MULTIPLE

Pour aujourd' hui : SEAVIEW 4 (4.5.2/ 31 mai 2014)

<http://doua.prabi.fr/software/seaview>



protdna.mase

File Edit Props Sites Species Footers Search: Goto: Trees Help

sel=0 310 Seq:26 Asp Pos:337|178 [AK045539.PE1] 402

AB035322 GCCTTCAAAGAGAAA TACATGGAGTTTGACCTGAATAATGAAGGCGAGATTGATCTGATGATGGAGAAGCTGGGGGTC

AB036423.IBA1 GCCTTCAAGGTGAAGTACATGGAGTTTGATCTGAATGGAAATGGAGATATCGATAAATGCTGGAGAACTTGGGGTT

AB036423.PE2 GCCTTCAAGGTGAAGTACATGGAGTTTGATCTGAATGGAAATGGAGATATCGATAAATGCTGGAGAACTTGGGGTT

AB094629.IBA2 GCCTTCAAAGAGAAA TACATGGAGTTTGACCTGAATAATGAAGGCGAGATTGATCTGATGATGGAGAAGCTGGGGGTC

AB128049.AIF1 GGCTTCAAAGAGAAA TACATGGAGTTTGACCTTAATGGAAACGGCGATATTGATAAATGCTGGAGAACTTGGGGTC

AF074959.PE1 GCCTTCAAGGTGAAGTACATGGAGTTTGATCTGAATGGAAATGGAGATATCGATAATTATGCTTGAAGCGAATGCTGGAGAACTTGGGGTT

AF109719.PE7 GCCTTCAAGGTGAAGTACATGGAGTTTGATCTGAATGGAAATGGAGATATCGATAATTATGCTCCCTGAAGCGAATGCTGGAGAACTTGGGGTT

AF129756.PE18 GGCTTCAAAGAGAAA TACATGGAGTTTGACCTTAATGGAAATGGCGATATTGATATCATGTCCTGAAACGAATGCTGGAGAACTTGGAGTC

AF299325 -----ATGGAGTTTGATCTGAATGGCAATGGTGATATTGATATTATGCTCCCTGAAACGAATGCTGGAGAAGCTTGGGGTC

AF299327 -----ATGGAGTTTGATCTGAATGGCAATGGCGATATTGATATCATGTCCTGAAACGAATGCTGGAGAACTTGGAGTC

AF299328 -----ATGGAGTTTGATCTGAATGGCAATGGAGATATCGATAATTATGCTCCCTGAAGCGAATGCTGGAGAACTTGGGGTT

AF348450.PE1 GCCTTCAAGAAGAAA TACATGGAGTTTGACCTGAATGAAGATGGAGGTATCGATATCATGTCCTGAAACGAATGATGGAGAACTTGGGGTT

AJ506968.AIF1 ATGTTTAAAAAATAAA TACATGGAGTTTGATCTCAATGATCAAGGAGACATAGACATAATGGGGTTAAAACGGATGCTTGAAAACTTGGAGTG

AK006184.PE1 GCCTTCAAGGTGAAGTACATGGAGTTTGATCTGAATGGAAATGGAGATATCGATAATTATGCTCCCTGAAGCGAATGCTGGAGAACTTGGGGTT

AK006562.PE1 GCCTTCAAGGTGAAGTACATGGAGTTTGATCTGAATGGAAATGGAGATATCGATAATTATGCTCCCTGAAGCGAATGCTGGAGAACTTGGGGTT

AK022845.PE1 GCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACCTGATGTCCTTAAAGAGGATGATGGAGAAGCTTGGTGTC

AK028955.PE1 GCCTTCAAAGAGAAA TACATGGAGTTTGACCTGAATAATGAAGGCGAGATTGATCTGATGTCCTTAAAGAGGATGATGGAGAAGCTTGGGGTC

AK045539.PE1 GCCTTCAAAGAGAAA TACATGGAGTTTGACCTGAATAATGAAGGCGAGATTGATCTGATGTCCTTAAAGAGGATGATGGAGAAGCTTGGGGTC

AK091912.PE1 GCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACCTGATGTCCTTAAAGAGGATGATGGAGAAGCTTGGTGTC

AK128526.PE1 GCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACCTGATGTCCTTAAAGAGGATGATGGAGAAGCTTGGTGTC

AL136566.PE1 GCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACCTGATGTCCTTAAAGAGGATGATGGAGAAGCTTGGTGTC

AL157938.C9ORF58 GCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACCTGATGTCCTTAAAGAGGATGATGGAGAAGCTTGGTGTC

AL157938.PE2 GCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACCTGATGTCCTTAAAGAGGATGATGGAGAAGCTTGGTGTC

AL157938.PE3 GCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACCTGATGTCCTTAAAGAGGATGATGGAGAAGCTTGGTGTC

AL157938.PE7 -----ATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACCTGATGTCCTTAAAGAGGATGATGGAGAAGCTTGGTGTC

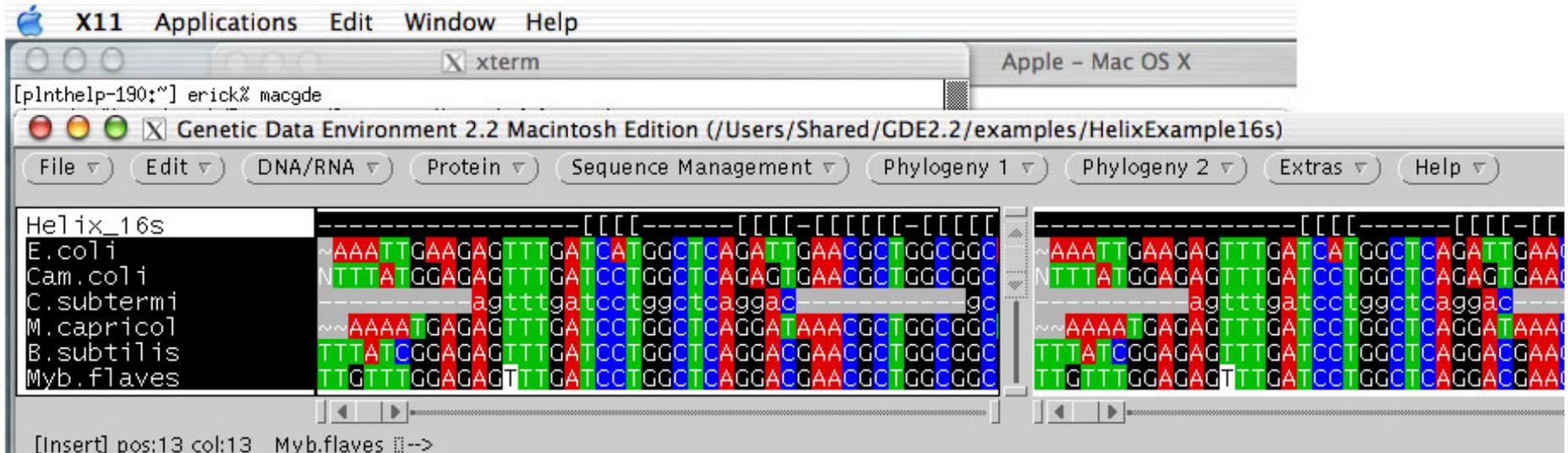
AL662801.PE45 GGCTTCAAAGAGAAA TACATGGAGTTTGACCTTAATGGAAATGGCGATATTGATATCATGTCCTGAAACGAATGCTGGAGAACTTGGAGTC

AL662801.PE46 -----ATGGAGTTTGACCTTAATGGAAATGGCGATATTGATATCATGTCCTGAAACGAATGCTGGAGAACTTGGAGTC

AL662847.AIF1 GGCTTCAAAGAGAAA TACATGGAGTTTGACCTTAATGGAAATGGCGATATTGATATCATGTCCTGAAACGAATGCTGGAGAACTTGGAGTC

AL662847.PE40 -----ATGGAGTTTGACCTTAATGGAAATGGCGATATTGATATCATGTCCTGAAACGAATGCTGGAGAACTTGGAGTC

(><-+ _ << >>)



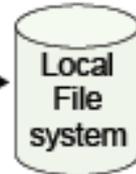
Note: BioEdit is no longer being regularly maintained, and the documentation is out of date and no longer maintained.

Jalview Version 2 - a multiple sequence alignment editor and analysis workbench

The Jalview Desktop



Figures
HTML
EPS
PNG



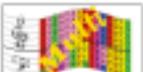
import
from web

Analysis Services

Protein 2ndary structure



Alignment Analysis



Protein Disorder



GLOBPLOT 2

Multiple alignment



Biological Data Services



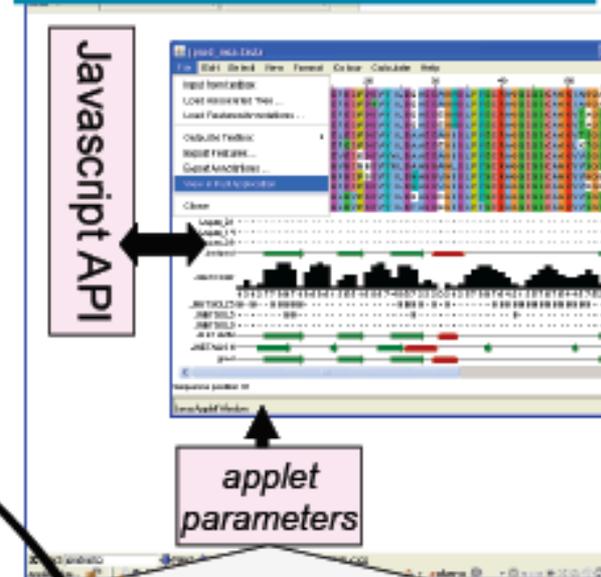
The JalviewLite Applet

Javascript API

applet
parameters

Alignment
And
Annotation

Bioinformatics
Web Server



Welcome to FaBox (1.41) - an online fasta sequence toolbox

[FAQ] 



NEWS:

18.02.2013 Added fasta sequence subtractor
 06.08.2012 Small bug in random sequence generator fixed
 29.08.2011 Update with newick parser
 10.09.2009 FaBox has moved to <http://www.birc.au.dk/software/fabox>
 16.01.2009 Added the fasta2PAML converter
 10.11.2008 FaBox is available for direct download (see Faq)
 07.11.2008 Faq updated: memory problems and downloading FaBox
 04.08.2008 DNA collapser updated, now ignores case differences (ACG = acg)
 31.03.2008 Show variable sites updated to 0- or 1-based sequence position numbering
 25.02.2008 Header extractor updated

Sequence 2 fasta converters (external tools)

[HCV Sequence Conversion Interface - ReadSeq at EBI](#)

Working with fasta headers

Fasta header extractor (and header splitter)	Simple and fast way of extraction the headers from fasta files - and optionally split each header into fields based on a chosen character/word.
Fasta header editor	Simple and fast way of extracting headers, edit them and reapplying them without worrying about the sequence itself.
Fasta header replacer	Some programs do not like the fancy headers in fasta files and you have to live with short, unique names - that are really non-descriptive. Here you can replace headers back and forth by submitting old and new headers - which you'll typically keep in a excel spreadsheet.

Working with fasta datasets/alignments

Fasta sequence extractor	Simple and fast way of extracting some sequences from a large sequence set, based on a list of headers or fuzzy matching.
Fasta sequence subtractor	Simple and fast way of removing some sequences from a large sequence set, based on a list of headers or fuzzy matching.
Fasta sequence joiner	Simple and fast way of joining a set of fasta sequences into one sequence
Fasta dataset splitter/divider	Simple and fast way of dividing your dataset into two sets by a header keyword. It will split into sets WITH and WITHOUT the given header keyword (like 'females/males', 'population1/population2')
Fasta alignment joiner	Simple and fast way of joining two alignments, sequence by sequence. It will join alignment 1, sequence 1 with alignment 2, sequence 1 and so on.... (see example)
Alignment trimmer	Trims an alignment to the shortest sequence. It simply removes the boundary areas that are full of gaps.
Show variable sites only	Extracts all the variable sites from an alignment

PARTIE V : Les logiciels

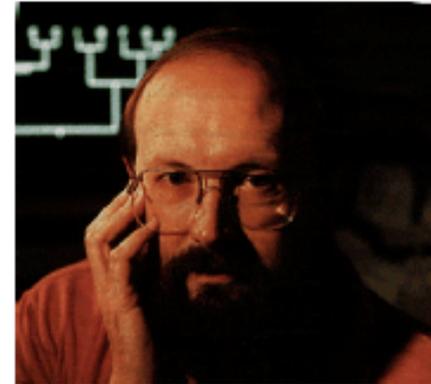
LES LOGICIELS DE RECONSTRUCTION PHYLOGÉNÉTIQUE

PHYLIP : Phylogeny Inference Package

(version 3.695)

<http://evolution.genetics.washington.edu/phylip.html>

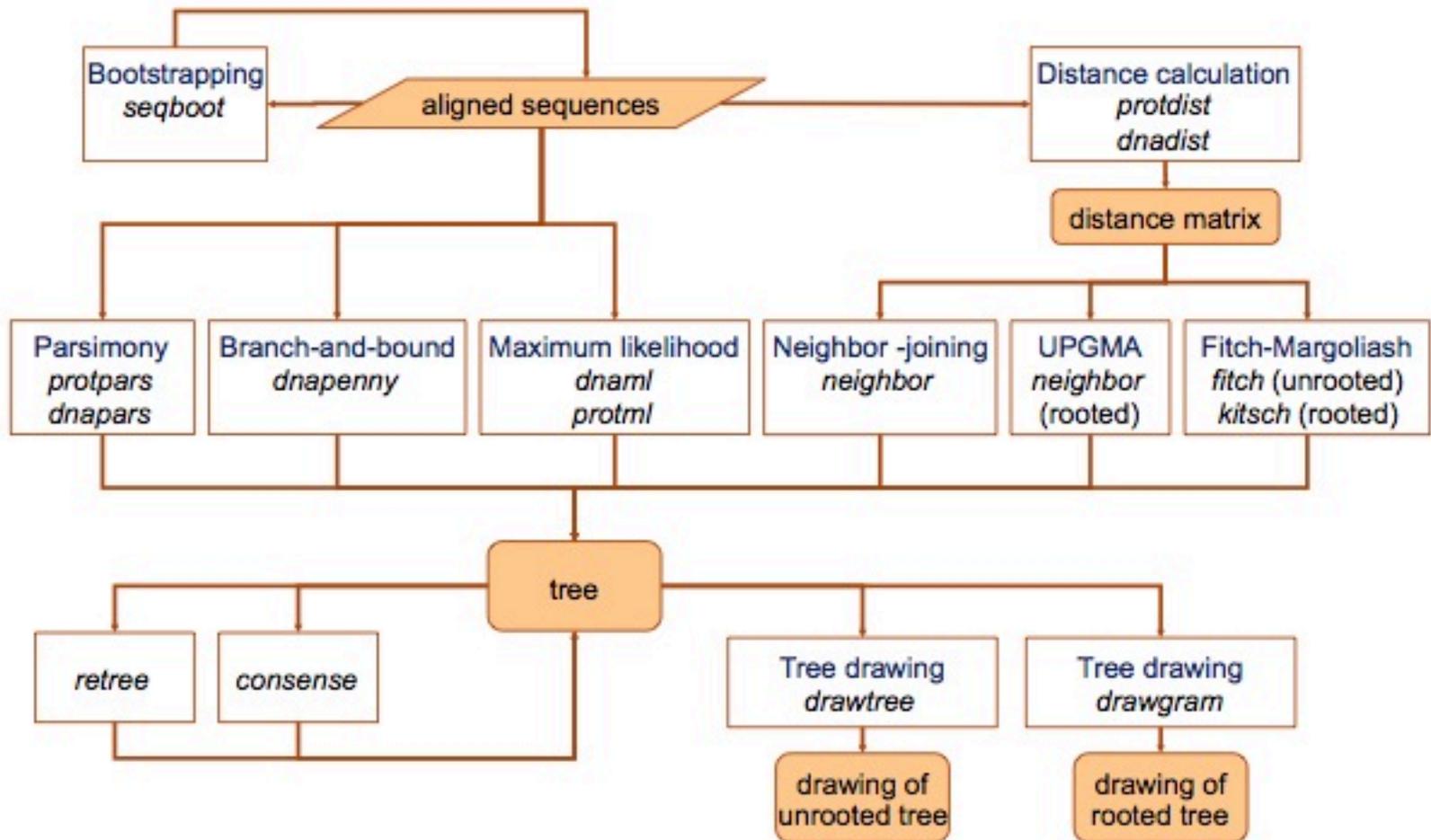
Joe Felsenstein,
University of Washington at Seattle



Logiciel multiplateformes librement accessible, qui rassemble un vaste éventail de méthodes dont le code est public :

- Parcimonie
- Distances
- Maximum de vraisemblance (DNA/RNA et protéines)
- Bootstrap

Utilisation en mode ligne, par succession de commandes, qui nécessite une bonne connaissance de l'outil.



PAUP: Phylogenetic Analysis Using Parsimony

<http://paup.csit.fsu.edu>

4.0b10 (04/03/2002)

David Swofford,
Florida State University



PAUP* Version 4

...tools for inferring and interpreting phylogenetic trees

Analyze

- Molecular sequences
- Morphological data
- Other data types

Using

- Maximum likelihood
- Parsimony
- Distance methods



Logiciel disponible sous MacOS avec interface graphique, et sous Windows et Unix en mode commande. Le détail des algorithmes est parfois difficilement accessible.

Coût des licences individuelles : 85 à 150 \$ selon la version
10 utilisateurs = 500 \$

TnT - 1.0

File Trees Optimize Data Analyze Settings Format Help

Start swapping from 375 trees (score 47.932-53.932)...

Repl. Algor.	Tree	Score	Best Score	Time	Rearrang.	
---	TBR	385 of 386	-----	47.932	0:00:05	356,005

Completed TBR branch-swapping.
 Total rearrangements examined: 356,005.
 Note: some trees of different length may become identical if collapsed.
 Best score (TBR): 47.932-53.932. 386 trees found.
 5.64 secs.

Note: for consensus calculation, trees will be temporarily collapsed (when min. branch length = 0)

Bremer supports (from 386 trees, cut 0)

```

  A
  |
  |-----5.993?-----|
  |                   |
  |                   |-----5.351-----| | | | |
  |                   |                   |
  |                   |                   |-----B-----|
  |                   |                   |                   |
  |                   |                   |                   |-----C-----|
  |                   |                   |                   |
  |                   |                   |                   |-----I-----|
  |                   |                   |                   |
  |                   |                   |                   |-----K-----|
  |                   |                   |                   |
  |                   |                   |                   |-----0.004-----|
  |                   |                   |                   |                   |
  |                   |                   |                   |                   |-----J-----|
  |                   |                   |                   |                   |
  |                   |                   |                   |                   |-----0.004-----|
  |                   |                   |                   |                   |                   |
  |                   |                   |                   |                   |                   |-----H-----|
  |                   |                   |                   |                   |                   |
  |                   |                   |                   |                   |                   |-----3.979-----|
  |                   |                   |                   |                   |                   |
  |                   |                   |                   |                   |                   |-----G-----|
  
```

Enter command:

C:\tnt\now\contin.tnt 386 trees Lines 45-65 of 70 No log file open, no tree file open

Inicio | Microsoft PowerPoint -... | TnT - 1.0 | ES 13:59

PHYML - A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood.

<http://atgc.lirmm.fr/phyml>

Stéphane Guindon, Olivier Gascuel
LIRMM, Montpellier.

Algorithme rapide d'estimation phylogénétique au maximum de vraisemblance.

Catalogue de modèles évolutifs nucléotidiques et protéiques très complet.

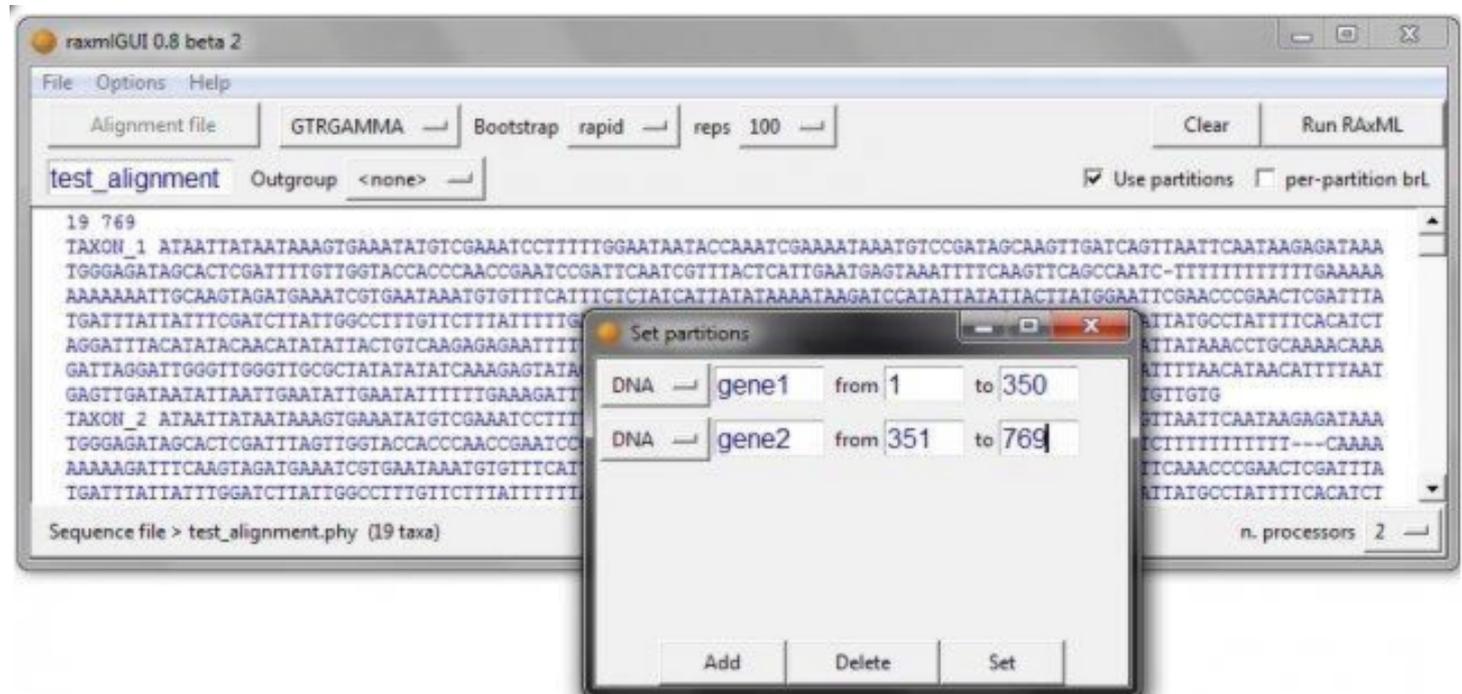
Possibilité de tests de bootstrap.

Logiciel multiplateformes sans interface graphique.

Serveur web pour exécuter PHYML librement accessible.

RAxML (Randomized Axelerated Maximum Likelihood) is a program for sequential and parallel Maximum Likelihood based inference of large phylogenetic trees. It can also be used for post- analyses of sets of phylogenetic trees, analyses of alignments and, evolutionary placement of short reads.

It has originally been derived from fastDNAmI which in turn was derived from Joe Felsenstein’s dnaml which is part of the PHYLIP package.



TREE-PUZZLE: Maximum likelihood analysis for nucleotide, amino acid, and two-state data.

<http://www.tree-puzzle.de/>

Heiko Schmidt, Korbinian Strimmer, Martin Vingron, and Arndt von Haeseler. Jülich, Munich, Düsseldorf



« TREE-PUZZLE reconstructs phylogenetic trees from molecular sequence data by maximum likelihood. It implements a fast tree search algorithm, quartet puzzling, that allows analysis of large data sets and automatically assigns estimations of support to each internal branch. TREEPUZZLE also computes pairwise maximum likelihood distances as well as branch lengths for user specified trees. »

MrBayes: Bayesian Inference of Phylogeny

<http://mrbayes.csit.fsu.edu/index.php>



John Huelsenbeck, Fredrik Ronquist, Bret Larget,
Paul van der Mark.

Logiciel librement accessible.

- A common command-line interface for Macintosh, Windows, and UNIX operating systems
- Ability to analyze nucleotide, amino acid, restriction site, and morphological data
- Mixing of data types, such as molecular and morphological characters, in a single analysis
- An abundance of evolutionary models, including 4 X 4, doublet, and codon models for nucleotide data and many of the standard rate matrices for amino acid data
- Estimation of positively selected sites in a fully hierarchical Bayes framework

PhyloBayes 3.3f and PhyloBayes MPI 1.5a:

PhyloBayes is a Bayesian Monte Carlo Markov Chain (MCMC) sampler for phylogenetic reconstruction using protein alignments. Compared to other phylogenetic MCMC samplers (e.g. [MrBayes](#)), the main distinguishing feature of PhyloBayes is the underlying probabilistic model, [CAT](#).

It is particularly well suited for large multigene alignments, such as those used in phylogenomics.

CONSEL: for assessing the confidence of phylogenetic tree selection

CONSEL est un logiciel qui se compose de petits programmes écrits en langage C.

Il calcule la valeur de probabilité (p-value) pour évaluer la confiance dans le problème de sélection.

Bien que CONSEL soit applicable à tout problème de sélection, il est principalement conçu pour la sélection des arbres phylogénétiques.

CONSEL ne pas estimer l'arbre phylogénétique par lui-même, mais CONSEL lire la sortie des autres paquets phylogénétique, comme molphy, PAML, * PAUP, TREE-PUZZLE, et PhyML.

CONSEL calcule la p-value en utilisant testant plusieurs procédures :
Le bootstrap , le test Kishino-Hasegawa, le test Shimodaira-Hasegawa, et le test pondérée Shimodaira-Hasegawa.

<http://www.is.titech.ac.jp/~shimo/prog/consel/>

PARTIE V : Les logiciels

LES LOGICIELS INTÉGRÉ DE RECONSTRUCTION PHYLOGÉNÉTIQUE

MEGA: Molecular Evolutionary Genetics Analysis

<http://www.megasoftware.net/>

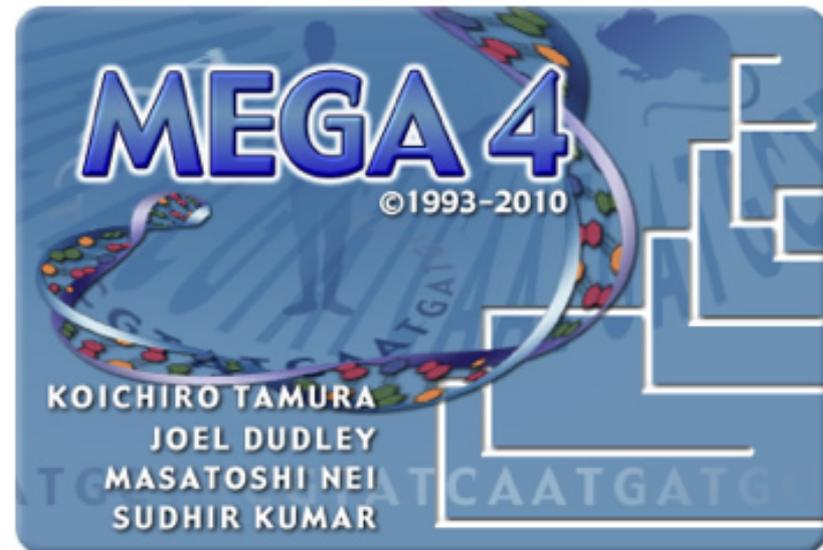
Kumar, Tamura, Nei

Logiciel librement
utilisable pour l'enseignement
et la recherche.

Ecrit pour plateforme Windows.

Principaux algorithmes:

- Alignement par ClustalW
- Calcul de distances nucléotidiques et protéiques avec/sans variation du taux entre sites.
- Calcul de distances synonymes et non synonymes (Ka/Ks)
- Reconstruction d'arbre: NJ, ME, Parcimonie
- Tests statistiques: bootstrap, comparaison de taux entre lignées.



MEGA MOLECULAR EVOLUTIONARY GENETICS ANALYSIS

Authors: Koichiro Tamura, Glen Stecher, Daniel Peterson, and Sudhir Kumar

MEGA 6

Version 6.0.5

Follow @iluvmega

Windows



Download V6.0

Updated: Jan 22 2014
Build: 6140122

Mac OS



Download v5.2

Updated: June 11 2013
Build: 5130611

Computational Core



Download V6.0

Updated: Dec 11 2013
Build: 6131211

Other Versions



Other Versions

Alignments & Data

Data Types

Web Data Acquisition

Manual & Automated Alignments

Major Analyses

Models and Parameters

Infer Phylogenies

Compute Distances

Tests of Selection

Ancestral Sequences

Clocks and Rates

Substitution Models

DNA/RNA

Codon

Protein

Rates & Composition

About MEGA

MEGA is an integrated tool for conducting sequence alignment, inferring phylogenetic trees, estimating divergence times, mining online databases, estimating rates of molecular evolution, inferring ancestral sequences, and testing evolutionary hypotheses. MEGA is used by biologists in a large number of laboratories for reconstructing the evolutionary histories of species and inferring the extent and nature of the selective forces shaping the evolution of genes and species.

- [Download PDF](#)

About MEGA Computational Core (MEGA-CC)

MEGA-CC provides a command line interface to the computational core in MEGA enabling researchers to automate and pipeline analyses via scripts, other applications, or the built-in file iterator system. - [Download PDF](#)

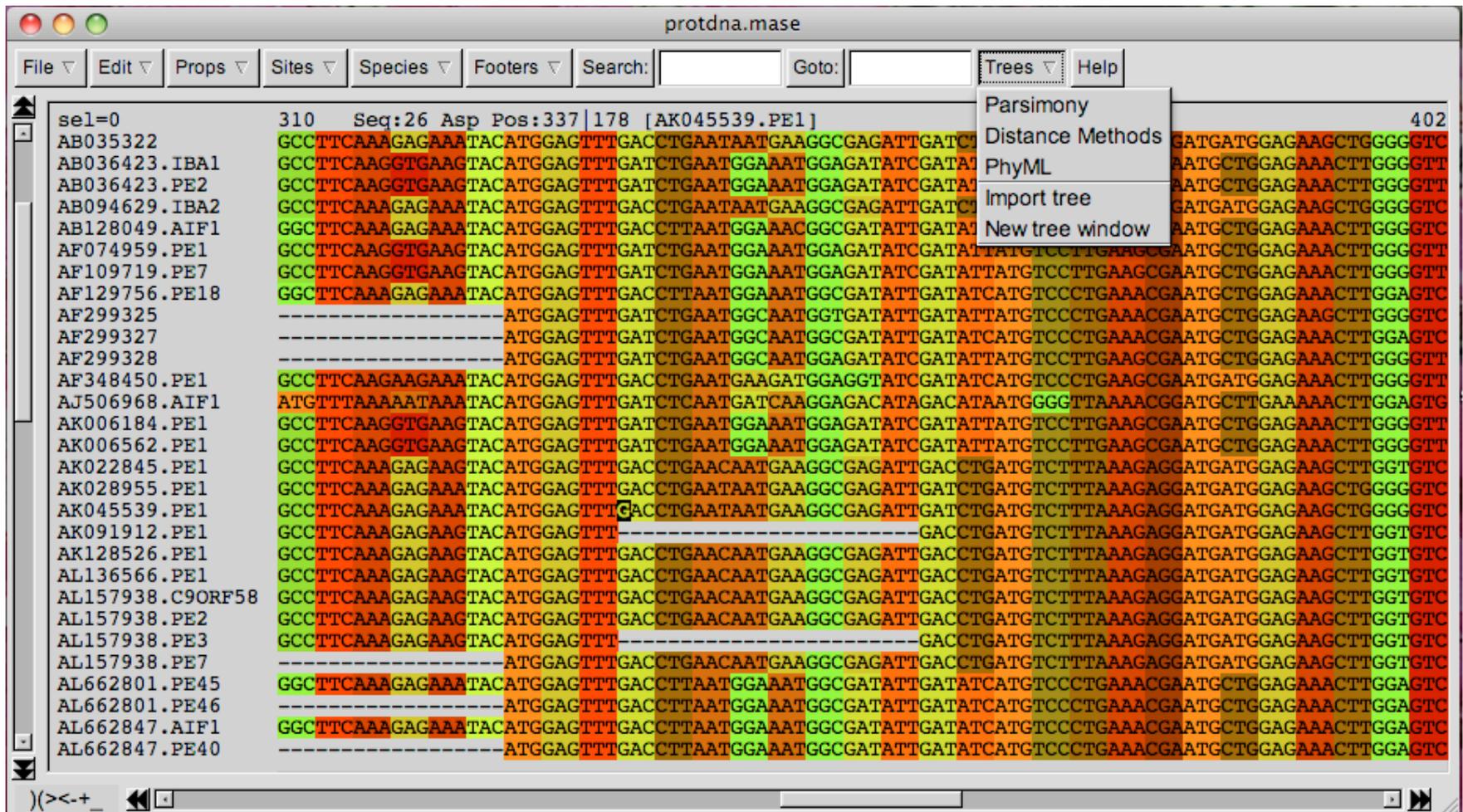
MEGA 6 Toolbar (Mouse-Over to Preview)



follow us on
twitter

Pour aujourd' hui : SEAVIEW 4 (4.5.2/ 31 mai 2014)

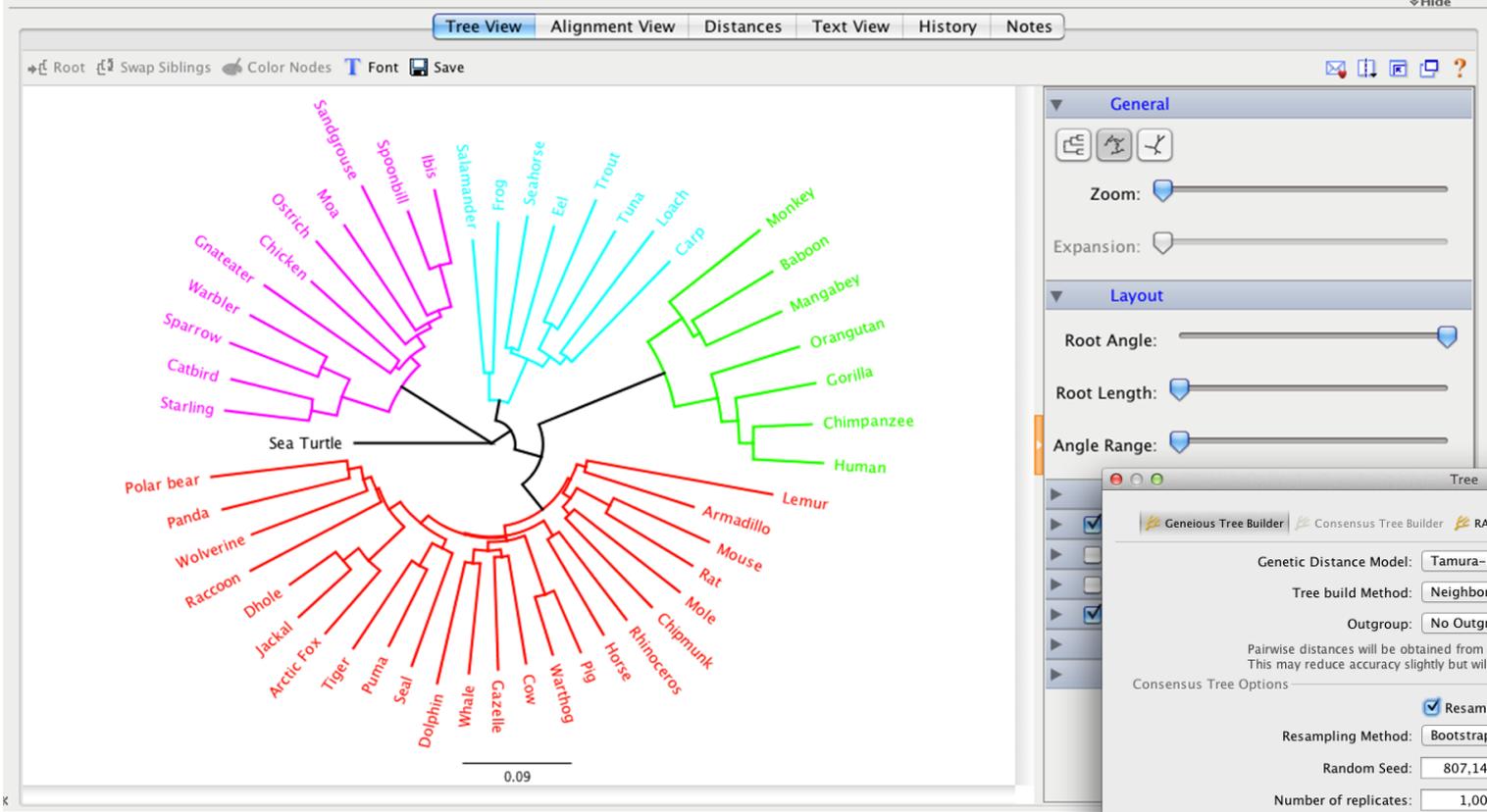
<http://doua.prabi.fr/software/seaview>



The screenshot shows the SEAVIEW 4 software interface. The main window displays a sequence alignment for 'protdna.mase'. The alignment is shown in a grid format with sequence identifiers on the left and sequence data on the right. A 'Trees' menu is open, showing options: Parsimony, Distance Methods, PhyML, Import tree, and New tree window. The sequence data is color-coded by nucleotide type: G (green), C (red), T (blue), and A (yellow). The alignment is currently at position 337 of a 178 bp sequence.

Seq ID	Sequence
sel=0	310 Seq:26 Asp Pos:337 178 [AK045539.PE1]
AB035322	GCC TTC AAG GAG AAA TAC ATG GAG TTT GAC CTG AATA ATG AAG GC GAG ATT GAT C
AB036423.IBA1	GCC TTC AAG GTG AAG TAC ATG GAG TTT GAT CTG AAT GG AAA TGG AG ATAT CG ATA
AB036423.PE2	GCC TTC AAG GTG AAG TAC ATG GAG TTT GAT CTG AAT GG AAA TGG AG ATAT CG ATA
AB094629.IBA2	GCC TTC AAG GAG AAA TAC ATG GAG TTT GAC CTG AATA ATG AAG GC GAG ATT GAT C
AB128049.AIF1	GGC TTC AAG GAG AAA TAC ATG GAG TTT GAC CTTAAT GG AAA C GGC GAT ATT GATA
AF074959.PE1	GCC TTC AAG GTG AAG TAC ATG GAG TTT GAT CTG AAT GG AAA TGG AG ATAT CG ATA
AF109719.PE7	GCC TTC AAG GTG AAG TAC ATG GAG TTT GAT CTG AAT GG AAA TGG AG ATAT CG ATA
AF129756.PE18	GGC TTC AAG GAG AAA TAC ATG GAG TTT GAC CTTAAT GG AAA TGG C GAT ATT GATA
AF299325	-----ATGGAGTTTGATCTGAATGGCAATGGTGATATTGATATTATGTCCTTGAAGCGAATGCTGGAGAACTTGGGGT
AF299327	-----ATGGAGTTTGATCTGAATGGCAATGGCGATATTGATATCATGTCCTTGAACGAATGCTGGAGAACTTGGAGT
AF299328	-----ATGGAGTTTGATCTGAATGGCAATGGAGATATCGATATTATGTCCTTGAAGCGAATGCTGGAGAACTTGGGGT
AF348450.PE1	GCC TTC AAG AAG AAA TAC ATG GAG TTT GAC CTG AAT GA AG ATG GAG GTAT CG ATAT CAT GTC CTT GA AG CGA ATG ATG GAG AA CT TGG GG T
AJ506968.AIF1	ATG TTT AAA AATA AAA TAC ATG GAG TTT GAT CTCAATGATCAAGGAGACATAGACATAATGGGGTTAAAACGGATGCTTGAAAACTTGGAGTG
AK006184.PE1	GCC TTC AAG GTG AAG TAC ATG GAG TTT GAT CTG AAT GG AAA TGG AG ATAT CG ATATTATGTCCTTGAAGCGAATGCTGGAGAACTTGGGGT
AK006562.PE1	GCC TTC AAG GTG AAG TAC ATG GAG TTT GAT CTG AAT GG AAA TGG AG ATAT CG ATATTATGTCCTTGAAGCGAATGCTGGAGAACTTGGGGT
AK022845.PE1	GCC TTC AAG GAG AAG TAC ATG GAG TTT GAC CTG AACAATGAAGGC GAG ATT GAC CTG ATG TC TTT AAA GAG GATGATGGAGAAGCTTGGTGTC
AK028955.PE1	GCC TTC AAG GAG AAA TAC ATG GAG TTT GAC CTG AATA ATG AAG GC GAG ATT GAT CTG ATG TC TTT AAA GAG GATGATGGAGAAGCTTGGGGT
AK045539.PE1	GCC TTC AAG GAG AAA TAC ATG GAG TTT GAC CTG AATA ATG AAG GC GAG ATT GAT CTG ATG TC TTT AAA GAG GATGATGGAGAAGCTTGGGGT
AK091912.PE1	GCC TTC AAG GAG AAG TAC ATG GAG TTT -----GAC CTG ATG TC TTT AAA GAG GATGATGGAGAAGCTTGGTGTC
AK128526.PE1	GCC TTC AAG GAG AAG TAC ATG GAG TTT GAC CTG AACAATGAAGGC GAG ATT GAC CTG ATG TC TTT AAA GAG GATGATGGAGAAGCTTGGTGTC
AL136566.PE1	GCC TTC AAG GAG AAG TAC ATG GAG TTT GAC CTG AACAATGAAGGC GAG ATT GAC CTG ATG TC TTT AAA GAG GATGATGGAGAAGCTTGGTGTC
AL157938.C9ORF58	GCC TTC AAG GAG AAG TAC ATG GAG TTT GAC CTG AACAATGAAGGC GAG ATT GAC CTG ATG TC TTT AAA GAG GATGATGGAGAAGCTTGGTGTC
AL157938.PE2	GCC TTC AAG GAG AAG TAC ATG GAG TTT GAC CTG AACAATGAAGGC GAG ATT GAC CTG ATG TC TTT AAA GAG GATGATGGAGAAGCTTGGTGTC
AL157938.PE3	GCC TTC AAG GAG AAG TAC ATG GAG TTT -----GAC CTG ATG TC TTT AAA GAG GATGATGGAGAAGCTTGGTGTC
AL157938.PE7	-----ATGGAGTTTGACCTGAACAATGAAGGC GAG ATT GAC CTG ATG TC TTT AAA GAG GATGATGGAGAAGCTTGGTGTC
AL662801.PE45	GGC TTC AAG GAG AAA TAC ATG GAG TTT GAC CTTAATGGAAA TGG C GAT ATT GAT ATCATGTCCTTGAACGAATGCTGGAGAACTTGGAGT
AL662801.PE46	-----ATGGAGTTTGACCTTAATGGAAA TGG C GAT ATT GAT ATCATGTCCTTGAACGAATGCTGGAGAACTTGGAGT
AL662847.AIF1	GGC TTC AAG GAG AAA TAC ATG GAG TTT GAC CTTAATGGAAA TGG C GAT ATT GAT ATCATGTCCTTGAACGAATGCTGGAGAACTTGGAGT
AL662847.PE40	-----ATGGAGTTTGACCTTAATGGAAA TGG C GAT ATT GAT ATCATGTCCTTGAACGAATGCTGGAGAACTTGGAGT

Name ▲	Bin	Size	# Sequences	Sequence Length	Description	Max Sequence Length	Min Sequence Length
COXII	-	125 KB	51	705	Neighbor-Joining tree of COXII CDS fr...705	684	-
NADH2	-	5 KB	-	-	Neighbor-Joining tree of NADH2 prot...-	-	-
People	-	7 KB	5	426	Neighbor-Joining tree of sequences f...-	-	-
Three Kingdoms	-	204 KB	43	1,300	Neighbor-Joining tree of Alanyl-tRNA...-	-	-



General

Zoom:

Expansion:

Layout

Root Angle:

Root Length:

Angle Range:

Tree

Geneious Tree Builder Consensus Tree Builder RAxML MrBayes Garli PHYLML FastTree

Genetic Distance Model: Tamura-Nei

Tree build Method: Neighbor-Joining

Outgroup: No Outgroup

Pairwise distances will be obtained from the multiple sequence alignment. This may reduce accuracy slightly but will produce results faster.

Consensus Tree Options

Resample tree

Resampling Method: Bootstrap

Random Seed: 807,143

Number of replicates: 1,000

Create Consensus Tree

Sort Topologies

Support Threshold %: 50

Topology Threshold %: 0

Save raw trees

Cancel OK

Data Analysis in Molecular Biology and Evolution

File Edit Alignment Sequences Seq. Analysis Phylogenetics Bioinfo Graphics SeqLab Tools Help

```

-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
          10          20          30          40          50          60
MasturusLanceolatus CGCUGAUUUUUCUCAACCAACCAUAAAAGATTATTCGCCACCCCTTTTTTTTATTTTTAGTTATTTTTGGTTCATTTGAGC
HomoSapiens          CGUUGACUAUUCUCUACAAAACCCACAA
BosTaurus            CGCUGACUAUUCUCAACCAACCAUAAA
BalaenopteraMusculus CGCUGACUAUUCUCAACCAACCCACAA
PongoPygmaeus        CGCUGGCUAUUCUCCACGAAACCCACAA
PanTroglodytes       CGCUGACUAUUCUCUACAAAACCCACAA
GallusGallus          CGAUGAUUAUUUCUCAACCAACCCACAA
AlligatorMississippiensis CGUUGACUCUUCUCUACUAAACCCACAA
** ** * ***** ** ***** **
  
```

C:\Program Files\DAMBE\vertCOI.FAS

Tree Tool

File Edit Tree Help

Options:

- Choose outgroup: MasturusLanceolatus
- Running mode: Search best tree Trees to keep: 1
- Sub. model: GTR
- Clock
- Variable rates over sites Alpha fixed at 0
- Detailed output
- Options related to running speed:
 - Quick Add
 - Randomize input order
 - Rearrange branch
- Resampling
 - Bootstrap
 - Jackknife
- Num. samples: 10

Ready.

Font size Line thickness Vertical spacing Horizontal spacing Draw scale

PARTIE V : Les logiciels

LES SERVICES WEB DE RECONSTRUCTION PHYLOGÉNÉTIQUE

Logiciels pour la biologie

http://bioweb.pasteur.fr/

MacPlus :: Les depe... À la une PC INpact Refurb Store - Mac... Libération.fr > Act... Le blog de la rédac... Facebook | Erwan Co...

Recently Bookmarked passioncycliste.sport... Bio-Rad - Scientists ... http://kobas.cbi.pku... True Single Molecule... Services de séquenç... Discovery could help...

Google Recherche Mes favoris Orthographe Traduire Envoyer à Paramètres

Search NCBI PubMed for



Logiciels pour la biologie



[Documentations](#)

[Banques de données locales](#)

[GenoList](#)

[Logiciels développés à l'Institut Pasteur](#)

[Archive ftp de logiciels](#)

[Logiciels en ligne](#)

- [Recherches dans les banques](#)
- [Conversions de formats de séquences](#)
- [Alignements et comparaisons de séquences](#)
- [Analyses phylogénétiques](#)
- [Recherche de gènes et régions codantes](#)
- [Analyses de séquences de protéines](#)
- [Analyses de séquences d'ADN](#)
- [Analyses d'ARN](#)
- [Recherche et extraction de motifs.HMM](#)
- [Analyses de structure](#)
- [Outils pour les séquences](#)

Le serveur bioweb a évolué. Vous pouvez dès maintenant y accéder via <http://bioweb2.pasteur.fr/>.
Le serveur actuel restera disponible jusque fin février 2008.

Documentations sur les logiciels installés localement

Vous trouverez ici la [liste classée par types](#), ou la [liste alphabétique](#) des logiciels installés sur le serveur Unix (central.pasteur.fr) et accessibles aux utilisateurs locaux. Cette liste vous permet :

- d'accéder à la *documentation* des logiciels
- de savoir comment les utiliser.

La page des [nouveauités](#) vous informe sur les logiciels installés récemment (100 derniers jours).

Logiciels en ligne sur le serveur Web ([carte](#) d'orientation)

- [Recherches dans les banques.](#)
- [Conversions de formats de séquences.](#)
- [Alignements et comparaisons de séquences.](#)
 - [Recherche de séquences similaires dans les banques \(BLAST et FASTA\)](#)
 - [Comparaison et alignement de deux séquences](#)
 - [Alignements multiples](#)
 - [CLUSTALW](#)
 - [autres programmes](#)
- [Analyses de séquences de protéines.](#)
 - [Recherche de motifs](#)
 - [Composants de protéines](#)
 - [Propriétés de protéines](#)
 - [Cinétique Enzymatique](#)
- [Analyses de séquences d'ADN.](#)
 - [Recherche de motifs](#)



- [Operation](#)
- [Topic](#)
- [History installation](#)

Biological software

[Home Page](#) | [Databases](#) | [Softwares developed at Institut Pasteur](#) | [Tools categories](#)

Biological software developed at the Institut Pasteur

- ABCISSE** [\[more\]](#)
ABC systems Information on Sequence Structure and Evolution
- ARIA** [\[more\]](#)
Software for automated NOE assignment and NMR structure calculation
- BISKIT** [\[more\]](#)
Python library for structural bioinformatics research
- BLAST2TAXONOMY** [\[more\]](#)
Blast Taxonomy report
- CONFMAT** [\[more\]](#)
Side chain packing optimization on a given main chain template for protein PDB files
- COSA** [\[more\]](#)
Clustal Output Structural Analysis
- CYTOSCAPE** [\[more\]](#)
Analyzing and Visualizing Networks of Biological Data
- DECORATE** [\[more\]](#)
Side chain packing optimization of a new sequence on a given template main chain
- ENVIRON** [\[more\]](#)
Calculates Energies Associated with Accessible as well as Buried Surface Areas in Proteins
- EXTRACTCDS** [\[more\]](#)
Extract CDS features from a Genbank entry
- FOTOGAL** [\[more\]](#)

Search [more]

Programs

- alignment
- assembly
- database
- display
- genetics
- hmm
- information
- nucleic
- phylogeny
- protein
- sequence
- structure

Workflows

- alignment
- database
- phylogeny
- blast_to_multialign
- hmm_build_search
- mafft-cons-tree
- protein_distance_phylogeny

Tutorials

- data formats
- BMPS_tutorial
- registration
- setpbystep

Welcome to Mobyle, a portal for bioinformatics analyses

Mobyle 1.5 is now available on Mobyle@Pasteur!

- Create your workflows and save them in your Mobyle workspace for fast and easy reuse with BMPS. Please refer to our [BMPS tutorial](#) for more details!
- Rename your jobs and data for easier navigation in your workspace. Just hover the job or bookmark you'd like to bookmark (either on the left menus or in the [data overview](#) or [jobs overview](#) panels), a pencil will appear on the right, enabling you to rename your data and jobs.

Portal news

New services available:

- [blast2](#): The Protein Data Bank is now available via "Protein db" parameter (14/05/2013)
- [T-Coffee](#) is now available, imported from the [mobyte@rpbs portal](#) (14/02/2013)
- [CLUSTAL-OMEGA](#) update to version 1.1.0 which add the support of DNA/RNA. (29/07/2011)
 - [clustalO-multialign](#) aligns a set of protein sequences.
 - [clustalO-sequence](#) adds new sequences to an existing alignment.
 - [clustalO-profile](#) aligns 2 profiles (alignments).
- [stride](#), from the Ressource Parisienne en Bioinformatique Structurale, is a tool for protein secondary structure assignment from atomic coordinates.(20/07/2012)
- [HCA](#), from the Ressource Parisienne en Bioinformatique Structurale, a tool for Hydrophobic Cluster Analysis.(20/07/2012)
- Alignments and Phylogenetic trees can now be edited using [Jalview](#) and [Archaeopteryx](#) and directly bookmarked in your workspace or chained to another program (22/05/2012)
- [transcript_or_bacteria_contig_analysis](#), a workflow developed in the context of the MobyleNet initiative, is dedicated to the detection of CDSs on transcript or bacterial genomic contigs and to the annotation of

Credits

Mobyle is a platform developed jointly by the Institut Pasteur Biology IT Center and the Ressource Parisienne en Bioinformatique Structurale.
More information about this project can be found [here](#).

Tools

PHYLOGENY

MSA

Gblocks, selection of conserved blocks from multiple alignments for their use in phylogenetic analysis

Trimal, tool for the automated removal of spurious sequences or poorly aligned regions from a multiple sequence alignment

M-Coffee, combine several alignment methods into a unique final alignment

Muscle, multiple sequence alignment

Distance

Phylip dnadist and protdist, computes distance matrix from nucleotide sequences

BioNJ, neighbor Joining algorithm improved for molecular sequences

Parsimony

Phylip dnapars and protpars, carries out unrooted parsimony tree on DNA sequences

Maximum likelihood

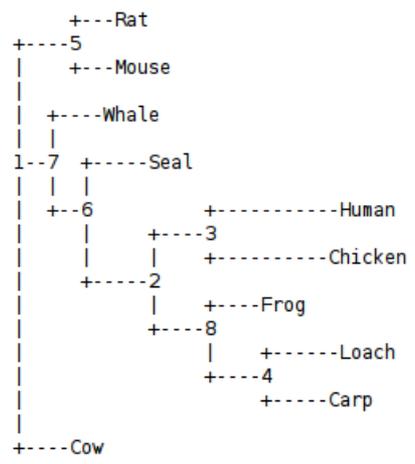
JModelTest2 statistical selection of best-fit models of nucleotide substitution

ProtTest3 statistical selection of best-fit models of amino-acid substitution

PhyML, a ML tree builder

DNA parsimony algorithm, version 3.695

One most parsimonious tree found:



requires a total of 1127.000

between	and	length
1	5	0.076869
5	Rat	0.075323
5	Mouse	0.075359
1	7	0.053114
7	Whale	0.077391
7	6	0.037865
6	Seal	0.090939
6	2	0.093255
2	3	0.081037
3	Human	0.205024
3	Chicken	0.177635
2	8	0.077347
8	Frog	0.089245
8	4	0.083899
4	Loach	0.128652
4	Carp	0.098085
1	Cow	0.077544

History

207: Phylip dnapars and protpars on data 48

206: dnapars protpars Report

205: Phylip dnapars and protpars on data 48

204: dnapars protpars Report

203: Phylip dnapars and protpars on data 48

202: dnapars protpars Report

80 lines
format: **txt**, database: ?

Warning: no access to tty (Bad file descriptor).
Thus no job control in this shell.
[2][H[2][H
DNA parsimony algorithm, version 3.695

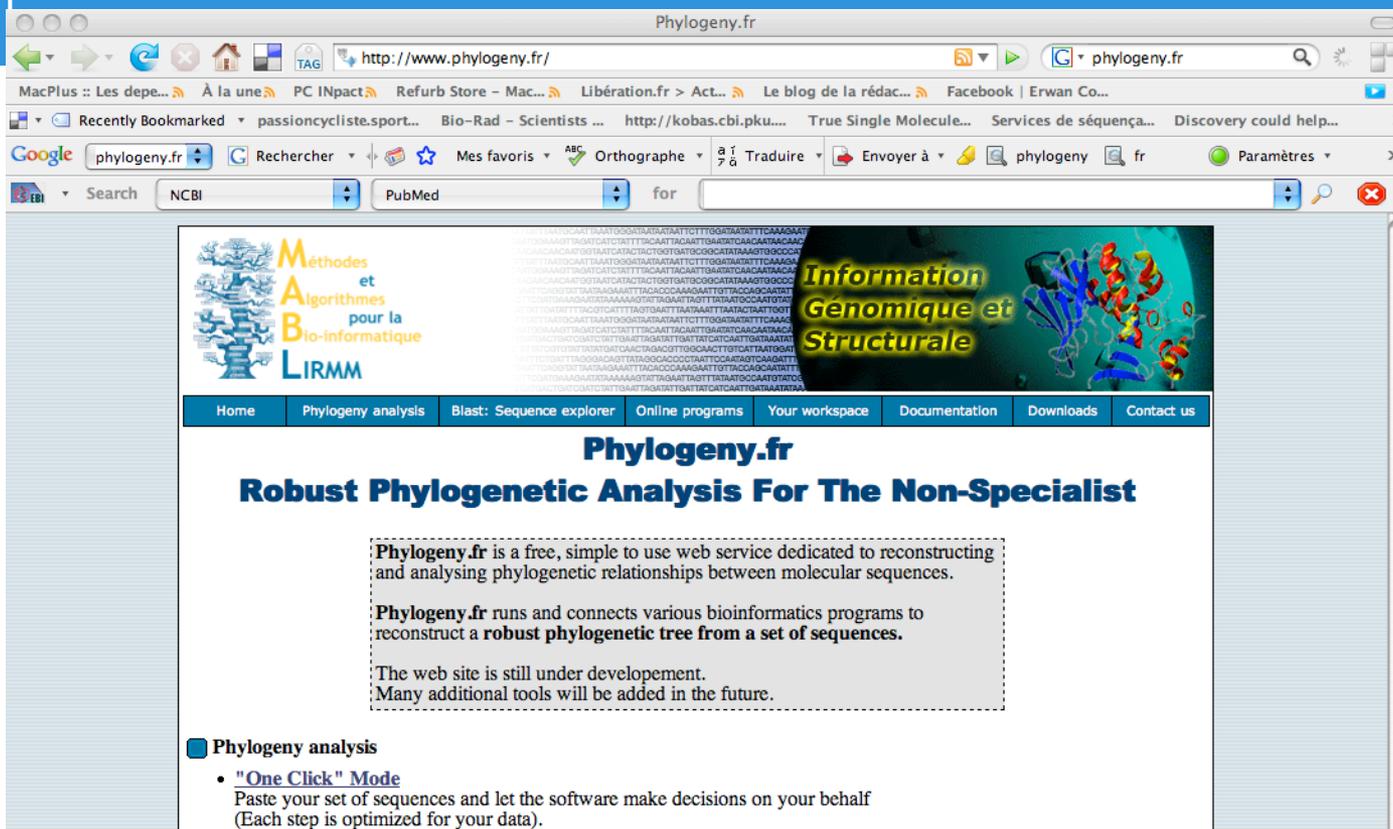
Setting for this run:
U Search for best tree? Yes
S Search option? Mor

DNA parsimony algorithm, version 3.695
2 trees in all found

195: BioNJ Newick Tree

194: BioNJ Newick Tree

193: Distance matrix



Online phylogeny programs

Direct access to the individual tools available on this server.

Multiple Alignment:

MUSCLE
T-Coffee / 3D-Coffee
ClustalW
ProbCons

Phylogeny:

PhyML
TNT
BioNJ
MrBayes

Tree viewers:

TreeDyn
Drawgram
Drawtree
ATV

Utilities:

Gblocks
Jalview
Readseq
Format converter



anonymous working on project default 0 Kb of 1.00 Gb (0.00%) no active jobs   logout

Alignment Tools

- ClustalW (v. 2.0.10)
- Muscle (v. 3.7)
- Lagan (v. 2.0)
- MLAGAN (v. 2.0)

To report an error, please contact us at: phylemon@cipf.es

Jobs that are running more than 24 hours, will be killed

New features in Phylemon 2.0 :

- Web Design: It was completely re-designed.
- Tools: Many tools have been upgraded.
- Help: A complete wiki-help is available.
- Performance improvements: Many libraries have been upgraded and several analysis.
- Bandwidth usage: Server communication was improved. The bandwidth reduced.
- Bug fixes: Several small bugs have been detected and fixed.

Phylogeny Tools

- Phylip (v. 3.68)
- Phyml Best AIC Tree (v. 1.02b)
- PhyML (v. 3.00)
- TreePuzzle (v. 5.2)
- MrBayes (v. 3.2.0)

Evolutionary Test Tools

- Model Selection
- Relative Rates Tests
- Adaptation Tests

use of new web technologies and standards supported browsers
Internet Explorer 8. Explorer 6 and 7 are no longer supported.

for molecular evolution, phylogenetics, phylogenomics and
increasing demand of molecular sequence analyses for experts and

similar web resources:

analyses, format conversions, files storage and edition of



CIPRES

Cyberinfrastructure for
Phylogenetic Research

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[News](#)

Publications

- Nearly 200 Publications enabled by the CIPRES Science Gateway
- View the CIPRES Science Gateway GCE10 paper [PDF]

Usage Statistics

- Current Usage Statistics

User Demographics

- Who's using the Gateway?

Survey Results

- Aug 10, 2010 Survey Summary

The CIPRES Science Gateway V. 3.1

The CIPRES Science Gateway V. 3.1 is a public resource for inference of large phylogenetic trees. It is designed to provide all researchers with access to large computational resources of the NSF TeraGrid through a simple browser interface. The CIPRES Science Gateway provides new hybrid parallel versions of RAxML (7.2.7) and MrBayes (3.1.2), as well as parallel GARLI (1.0) code to insure the fastest possible run times for submitted jobs. Through a collaboration with Alexandros Stamatakis and Wayne Pfeiffer, we now offer the fastest hybrid versions of RAxML [pdf] and MrBayes [pdf] currently available.

[▶ Use the CIPRES Science Gateway](#)

High Performance Parallel Codes for Large Tree Inference on TeraGrid:

[RAxML \(7.2.7\)](#); [MrBayes \(3.1.2\)](#); [GARLI \(1.0\)](#)

High Performance Parallel Codes for Sequence Alignment on TeraGrid:

[MAFFT \(6.822\)](#)

Serial Codes for Tree Inference:

[PAUP*](#) (Parsimony); [Poy](#) (Simultaneous Sequence Alignment and Tree Inference).

Serial Codes for Sequence Alignment:

[ClustalW](#), [Contraalign](#), [FSA](#), [MUSCLE](#), [PROBCONS](#), [PROBALIGN](#).

Learn more about: [Requirements](#); [Limitations](#); [Architecture](#); [Known Issues](#)

CIPRES Portal V 1.15 and CIPRES Portal V 2.2 have now ceased operations.

South of France bioinformatics platform

Home

Organization

Citations & Statistics

Partners

Online programs

FastME

Downloads

Online execution

Papers & contacts

User guide

Binaries

Databases

Datasets

NGS

Fast and accurate phylogeny reconstruction algorithms based on the minimum-evolution principle.

Desper R., Gascuel O. Journal of Computational Biology. 2002 9(5):687-705.

Please cite [THESE](#) papers if you use FastME.

Server load: 45%



FastME online execution

Input Data

Input data (distance matrix, Phylip format)

Choisissez un fichier

Aucun fichier choisi

File

Example file

Number of data sets

1

Tree Building

Use starting topology(s)

Choisissez un fichier

Aucun fichier choisi

yes

no

Algorithm

balanced_GME ↕

Tree Refinement

Tree refinement with NNI

balanced NNI

OLS NNI

Tree refinement with SPR

balanced SPR

Tree refinement with TBR

balanced TBR

Branch length estimation

Select the branch lengths type to assign to the topology

balanced

OLS

none

Name of your analysis

Your email



Montpellier bioinformatics platform

- Home
- Organization
- Citations & Statistics
- Partners
- Online programs
- PhyML
 - Benchmarks
 - Datasets
 - Downloads
 - FAQ
 - News
 - Online execution
 - Papers & contacts
 - PhyML versions
 - User guide
- Binaries
- Databases
- Datasets

PhyML 3.0: new algorithms, methods and utilities

Please cite:
"A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood."
 Guindon S., Gascuel O.
 Systematic Biology, 52(5):696-704, 2003.

Server load: 22%

PhyML online execution

Input Data

Sequences (PHYLIP format) File Example file

Data Type DNA Amino-Acids

Sequence file interleaved sequential

Number of data sets

Substitution Model

Substitution model

Equilibrium frequencies optimized empirical

Transition / transversion ratio (DNA models) fixed estimated

Proportion of invariable sites fixed estimated

Number of substitution rate categories

Gamma shape parameter fixed estimated

Tree Searching

Starting tree(s) File BIONJ

Type of tree improvement

Number of random starting tree yes no

http://
molevol.cmima.csic.es/
castresana/
Gblocks_server.html

Trimal server = Phylemon2

Castresana Lab

Animal Phylogeny and Systematics Programme

Institut de
Biologia Evolutiva
(CSIC-UPF)

Gblocks Server

Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis

About the Gblocks Server

Version 0.91b, January 2002

Copyright © Jose Castresana

 **Gblocks** eliminates poorly aligned positions and divergent regions of a DNA or protein alignment so that it becomes more suitable for phylogenetic analysis. This server implements the most important features of the Gblocks program to make its use as simple as possible without losing the functionality that it is necessary in most of the cases. Other options can be changed in the stand-alone program. You can see here an [example output file](#) showing the blocks selected from a protein alignment. Further information can be found in the [online documentation](#). Please see the [Gblocks](#) page for citations.

Gblocks Server

Paste an alignment in NBRF/PIR or FASTA format:

Or upload an alignment file:

Type of sequence:

DNA || Protein || Codons

Options for a less stringent selection:

Allow smaller final blocks

Allow gap positions within the final blocks

Allow less strict flanking positions

Options for a more stringent selection:

Do not allow many contiguous nonconserved positions

http://genome.cs.iastate.edu/supertree/userdata_analysis/userdata_analysis.html



Construct supertree using MRF

Select the Browse button to choose a tree file to upload. When you press the **Build supertree** button, this script computes the **MRF Supertree**.

Note: Since this problem is NP-hard, it may take very long time to get the result if your input data has a large number of taxa.

The output is in NEXUS tree format. You can also view the tree using Christian Zmasek's [ATV applet](#).

Enter the tree file to process (NEXUS format): aucun fichier sél.

Algorithm:

- Branch and Bound (find the global optimal result, used for *the number of taxa less than 20*)
- Heuristic Search (current version limits *the number of taxa less than or equal to 64*)

[MRF](#)

[MRP](#)

[MinCutSupertree](#)

[Other](#)

[Online Help](#)

PARTIE V : Les logiciels

**OUTILS SPÉCIFIQUES À UNE FAMILLE DE
GENES. EX : RRNA**

ARB: A software environment for maintaining databases of molecular sequences, and for analyzing the sequence data, with emphasis on phylogeny reconstruction.

<http://www.arb-home.de/>

Technical University of Munich



Principaux modules d'ARB:

<http://www.arb-silva.de/>

ARB_DB: A central database of aligned homologous sequences taken from public databases or supplied by the user.

ARB_NT: Phylogenetic trees derived from the data or imported from other sources. Different tree topologies, complete trees, and subtrees can be stored and used for walking through the database. Trees can be used to define subsets of data.

ARB_ALIGN: This tool searches for the most similar sequences in the database and inserts the new sequence into an existing alignment.

ARB_PHYL: tools and integrated foreign software (PHYLIP, DE SOETE, fastDNAmI) allow calculation of similarity/distance matrices, conservation profiles, selection masks and phylogenetic tree reconstruction.

arb-6.0-rc3 (most recent release candidate) : Last Update : 2014-May-29

FORMATION 12/2014

SILVA

Welcome to the SILVA rRNA database project

A comprehensive on-line resource for quality checked and aligned ribosomal RNA sequence data.

SILVA provides comprehensive, quality checked and regularly updated datasets of aligned small (16S/18S, SSU) and large subunit (23S/28S, LSU) ribosomal RNA (rRNA) sequences for all three domains of life (*Bacteria*, *Archaea* and *Eukarya*).

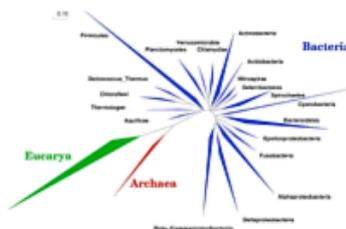
SILVA are the official databases of the software package ARB.

For more background information → [Click here](#)

ARB

The software package ARB represents a graphically-oriented, fully-integrated package of cooperating software tools for handling and analysis of sequence information.

The ARB project has been started more than 15 years ago by Wolfgang Ludwig at the Technical University in Munich, Germany, see www.arb-home.de.



The MEGX.net data portal

Visit our partner site www.megx.net, the data portal for Marine Ecological Genomics, to get a feeling how your research can be improved using integrated databases.



News

12.05.2014

Thank You for 2000 Citations



The SILVA team says THANK YOU for citing us over 2000 times. We are honoured by your trust and motivated to make SILVA the best resource for rRNAs ever.

01.05.2014

Sneak preview on SILVA release 119

First statistics about SILVA release 119.

26.04.2014

Preparation of SILVA release 119 has started

SILVA 119 will come as a full release. Preparation has started and we expect the release to be finished in June 2014.

11.04.2014

ARB 6 release candidate available

Get it now, put it through its paces and tell us what you think!

[go to Archive ->](#)

SILVA 115 - full release

	SSU Parc	SSU Ref	SSU Ref NR	LSU Parc	LSU Ref
Minimal length	300	1200/900	1200/900	300	1900
Quality filtering	basic	strong	strong	basic	strong
Guide Tree	no	no	yes	no	yes
Release date	23.08.13	23.08.13	23.08.13	23.08.13	23.08.13
Aligned rRNA sequences	3,808,884	1,426,414	479,726	361,874	39,412



ANNOUNCEMENTS

RDP News

05/23/2014 Informatics Professional job opening at RDP
Work with a team developing important bioinformatics resources.

05/16/2014 Tree Builder Java applet fix in the works
Some problems displaying and interacting with Tree Builder results have been addressed

05/16/2014 RDP staff at ASM, Boston
Poster at 10:45 Sun. morning; ASMCUE workshop info online

05/14/2014 The RDP Paired-end Reads Assembler
The RDP Paired-end Reads Assembler is available for download at RDP Resources page

05/14/2014 Fungal ITS training set
The Fungal ITS training set available for download on RDP Resources page

05/07/2014 FrameBot speed improved
The speed of the FrameBot increased by one to two orders of magnitude

03/26/2014 Informatics Professional job opening at RDP
Work with a team developing important bioinformatics resources.

03/19/2014 All services should be back online!
Sorry for the interruption.

03/19/2014 RDP Site Issues
Some services temporarily unavailable.

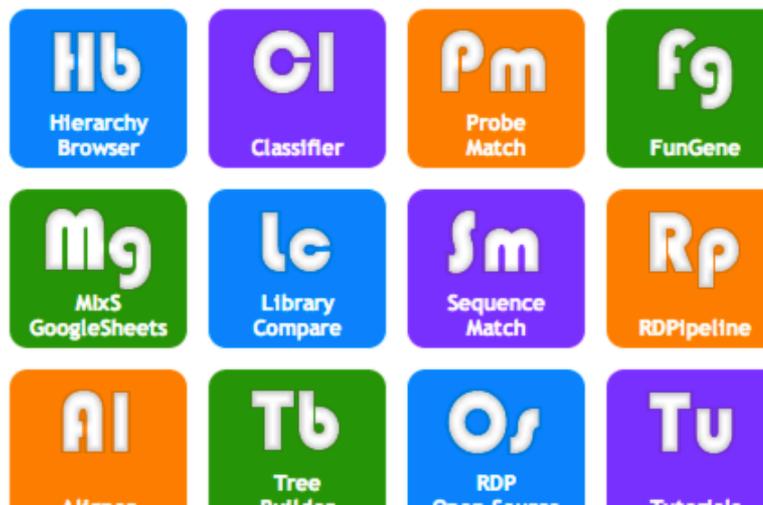
RDP Release 11, Update 2 :: March 7, 2014

2,929,433 16S rRNAs :: 95,365 Fungal 28S rRNAs
Find out what's new in RDP Release 11.2 [here](#).

Cite RDP's latest tool articles.

RDP provides quality-controlled, aligned and annotated Bacterial and Archaeal 16S rRNA sequences, and Fungal 28S rRNA sequences, and a suite of analysis tools to the scientific community. New to RDP release 11:

- RDP tools have been updated to work with the new fungal 28S rRNA sequence collection.
- A new Fungal 28S Aligner and updated Bacterial and Archaeal 16S Aligner. We optimized the parameters for these secondary-structure based Infernal aligners to provide improved handling for partial sequences.
- Updated RDPipeline offers extended processing and analysis tools to process high-throughput sequencing data, including single-strand and paired-end reads.
- Most of the RDP tools are now available as open source packages for users to incorporate in their local workflow.



green genes

16S rRNA gene database and workbench compatible with ARB
greengenes.lbl.gov



Browse



Export



Slice



Consensus



Compare



Search



Probes



Align



Trim



Download



More Tools

Functions

Home
 Browse
 Export
 Slice
 Consensus
 Compare
 Search
 Probe
 Align
 Trim
 Download
 Curate
 More Tools...

About

Citation
 Tutorial
 FAQ
 Objectives
 Methods
 Contact

My Interest List

0 sequences

greengenes: 16S rDNA data and tools

The greengenes web application provides access to the current and comprehensive 16S rRNA gene sequence alignment for browsing, blasting, probing, and downloading. The data and tools presented by greengenes can assist the researcher in choosing phylogenetically specific probes, interpreting microarray results, and aligning/annotating novel sequences. If you are an **ARB** user, you can use greengenes to keep your own local database current.

News:

- Graduate and postdoctoral fellowships in plant-microbe interactions at the University of Alaska with Lee Taylor are available, [read more](#).
- Have you registered for the [International Workshop on Ribosomal RNA Technology](#) in Bremen, Germany (April 7-9, 2008)? Topics include: Databases, Phylogeny, Computational Tools, PhyloChips, and Ecology. Hope to meet you there.
- We have a postdoctoral position available for a bioinformaticist to design a microarray for detection and antibiotic resistance profiling of select bacterial pathogens. [Read more ...](#)
- Thank you to all the Molecular Microbial Ecologists who joined us in discussing methods to analyze data and draw meaningful conclusions. The [special session](#) at the [AGU Fall Meeting in San Francisco](#) (December 10 - 14, 2007) helped us carve out future work to improve the analysis pipelines!
- Summer 2007 Greengenes Tutorial: The annual live tutorial for 16S rRNA gene library analysis took place on July 31st at Lawrence Berkeley Lab. Please contact [Jonathan Davies](#) if you have any follow-up questions.
- Spring PhyloChip Data Analysis PowWow (April 25th, UC Berkeley) Notes: Ideas were exchanged on how to explore data generated by the G2 PhyloChip. The hot topic was how to integrate PhyloChip output with a second matrix containing treatment categories, environmental observations or patient history, as examples. Also, [Jacques Ravel](#) provided an alpha version of new software his TIGR team is developing for projecting multi-array experiments onto a phylogenetic tree. Attendees included researchers from LBL, UCB, JGI, LLNL, and Affymetrix. Contact [Kristen DeAngelis](#) if you would like to be a part of the next PowWow.
- Are you the world expert on the taxonomy of a particular phylogenetic lineage? Have you checked this database and nobody has got it right? [Tell us!](#) - we will fix it.
- We have supplemented the greengenes (Hugenholtz) taxonomy using a new automated curation tool, GRUNT (GRouping, Ungrouping, Naming Tool) developed by Daniel Dalevi. It removes most of the grunt work involved in group naming curation. Feedback welcome via [this link](#).
- We thank Jakob Fredslund for developing a tool, [Gexcellent](#), to convert XML trees to Newick format!
- We thank [J.P. Euzéby](#) and Hans Trüper for expert [etymological advice](#).



V5^{le} BIBI

Bio Informatic Bacteria Identification

^{le}BIBI V5 is the latest version of ^{lc}BIBI, the software environment for sequence based phylogenetic identification of prokaryots (*Bacteria* and *Archaea*). First version initially written by [Devulder et AL. 2003](#). The main developer is Jean-Pierre Flandrois (database construction and general scripts) with help of Manolo Gouy for tree visualisation programs.

For any question : jean-pierre.flandrois@univ-lyon1.fr OR (see below) on Twitter [Follow @bioinfobact](#)

Enter the QUERY sequences

[SEQs ONLY in FASTA FORMAT!](#)

>this_is_the_FASTA_FORMAT
ATCGATGCATGCATGC-ETC.

BIBI's parameters

[Sequences Databases](#) (Currently compiled 10/Feb/2014 at 16:46)

procaryota_SSU-rDNA-16S_TSstringent

Nb seqs to align : 20 Seq_Id : Query

Alignment : Fastest Phylogeny : Not exclude positions with gaps

Run BIBI now and WAIT (the page will be empty for a while)

RESET

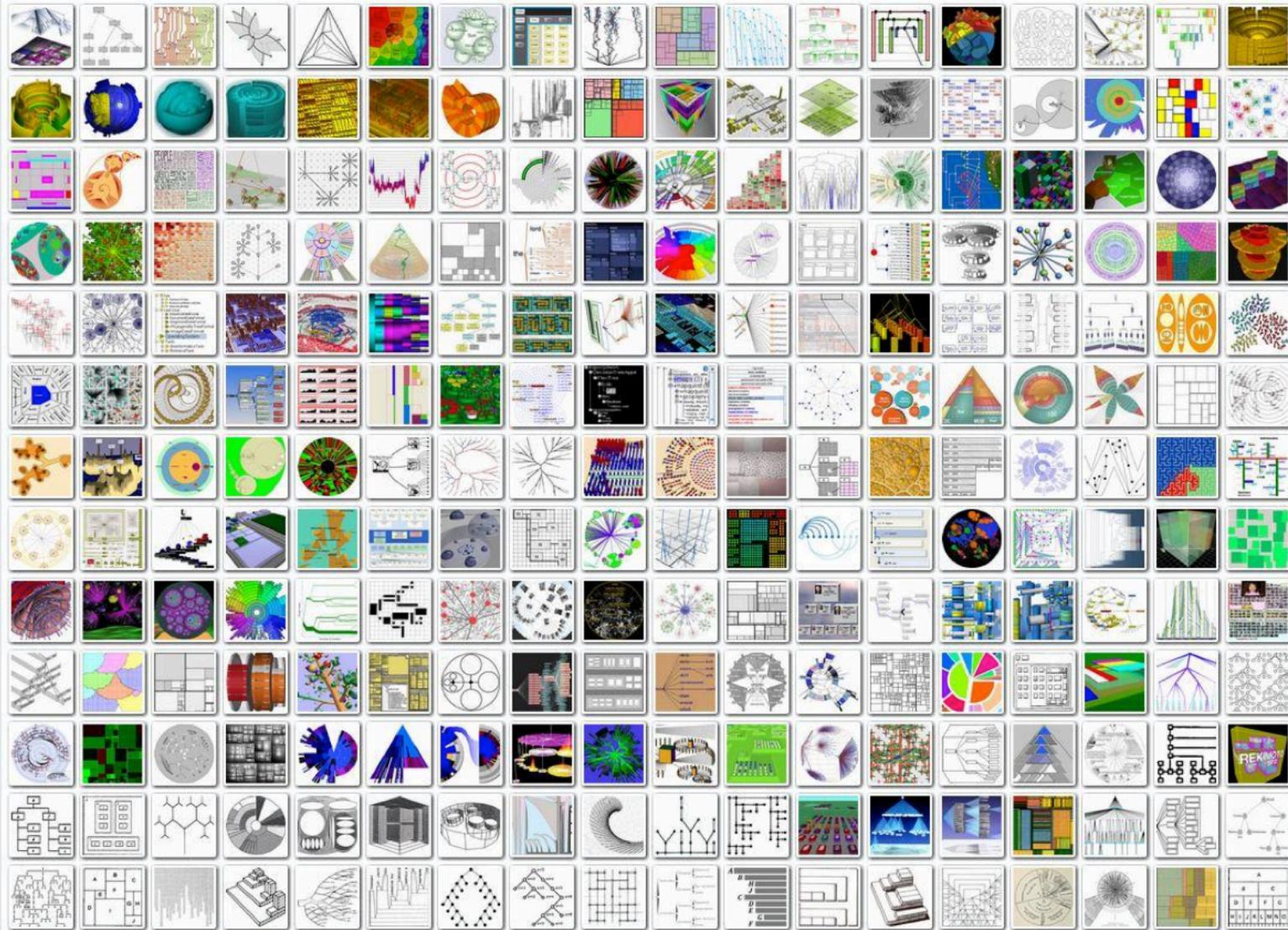
Tests sequences

Tests sequences

Actinobacteria_Groel2-HSP65 Get test sequences

PARTIE V : Les logiciels

LOGICIELS DE REPRÉSENTATION D' ARBRES PHYLOGÉNÉTIQUES



<http://treevis.net>

<http://evolution.genetics.washington.edu/>

http://bioinfo.unice.fr/biodiv/Tree_editors.html



TreeView

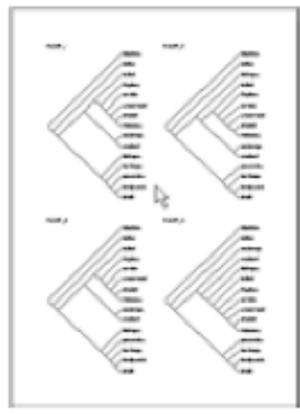
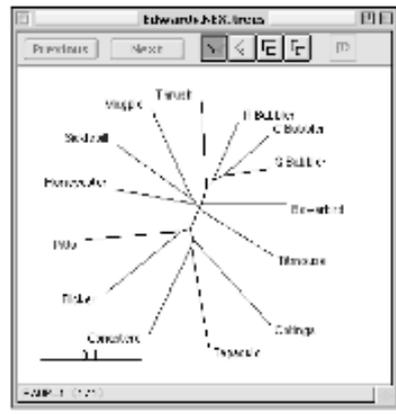
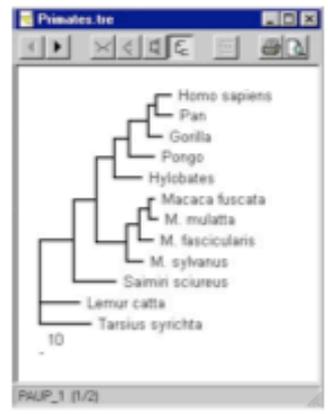
Tree drawing software for Apple Macintosh and Windows

Rod Page,
Glasgow University

NEW! (and now [Linux and Unix](#))

<http://taxonomy.zoology.gla.ac.uk/rod/treeview.html>

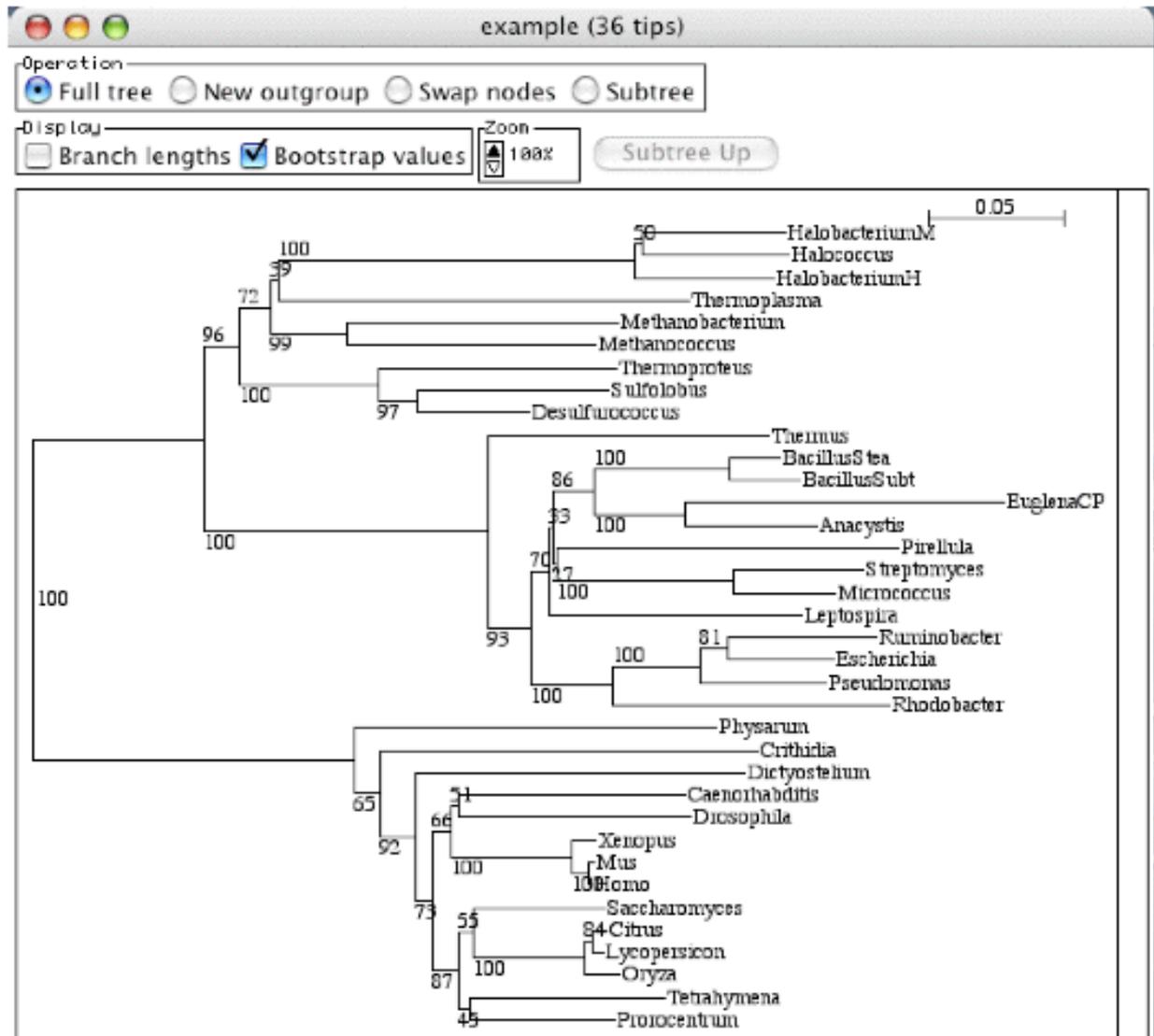
Macintosh and Windows platforms. Reads various tree file formats (NEXUS, PHYLIP, Hennig86, NONA, MEGA, ClustalW/X). Supports PICT on MacOS, Windows metafile on Windows for copying pictures into other applications. Prints multiple trees per page, and one tree over more than one page.



Logiciel libre
multiplateformes.

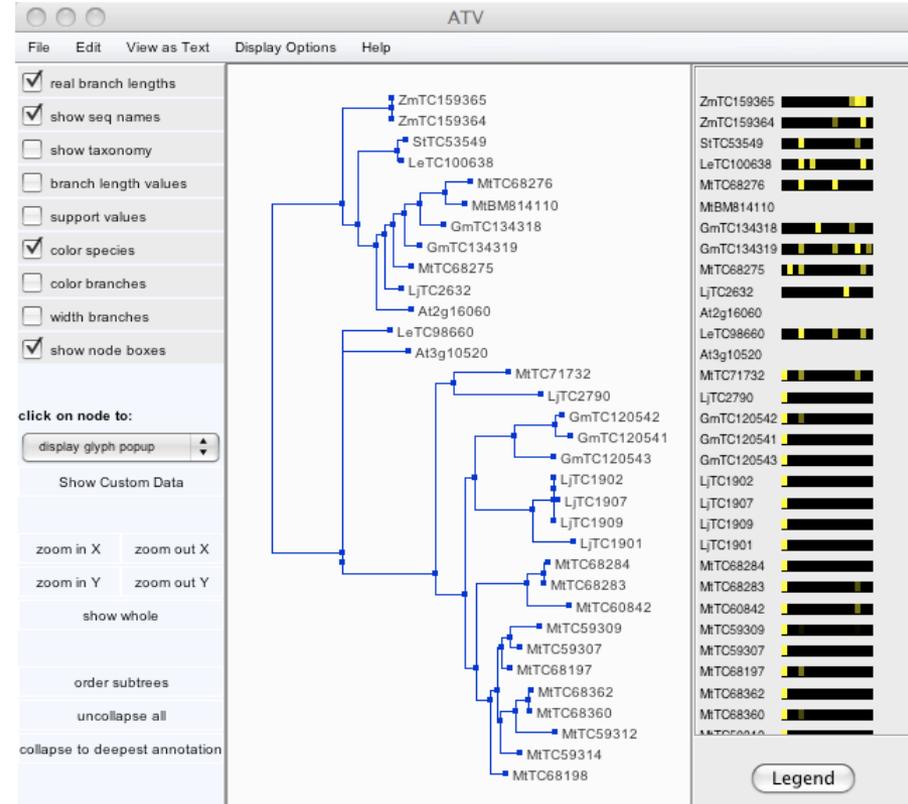
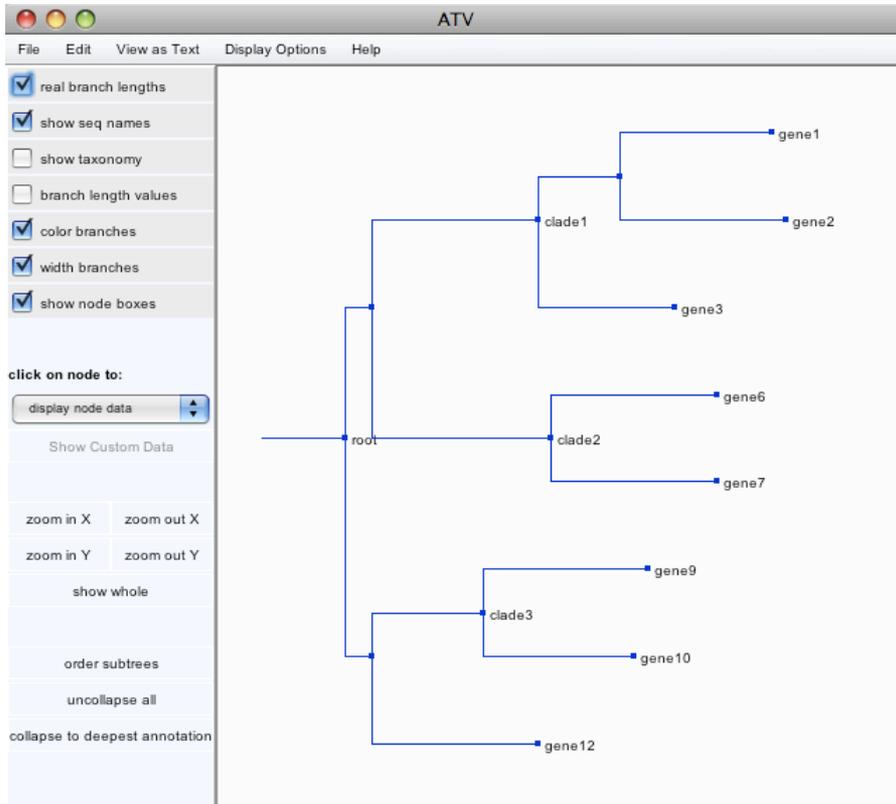
Fonctions:

- enracinement,
- copier/coller,
- multifurcations,
- zoom,
- recherche cible,
- impression sur plusieurs pages.

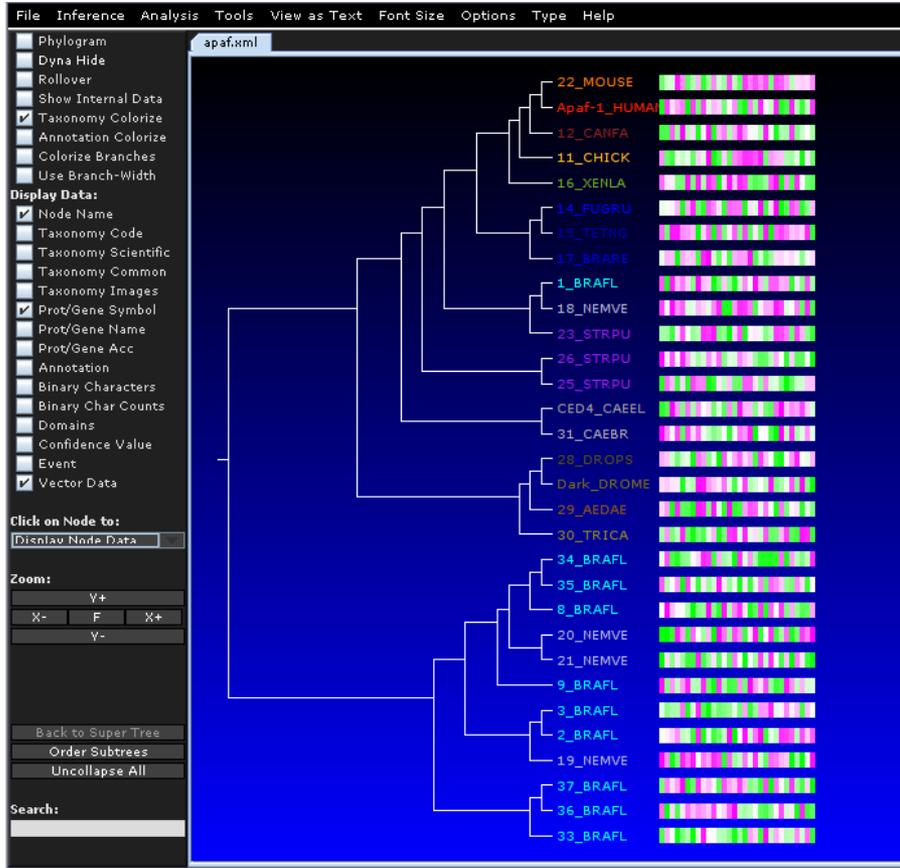


ATV | A Tree Viewer | Archaeopteryx

ATV is a Java tool for the visualization of annotated phylogenetic trees. It can be used both as an applet and as a standalone application.

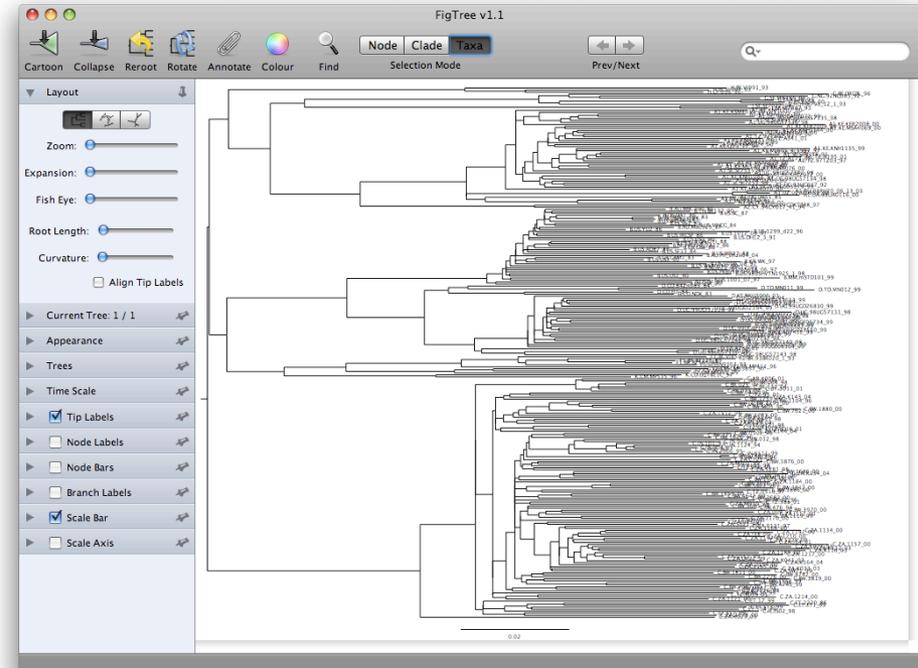


Archaeopteryx



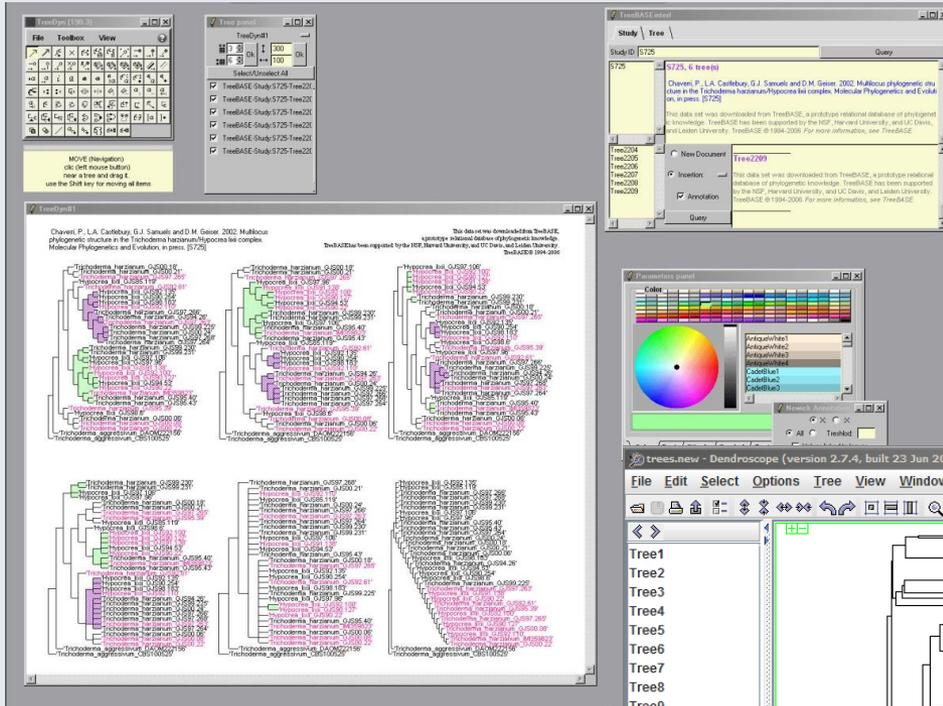
<https://sites.google.com/site/cmzmasek/home/software/archaeopteryx>

FigTree



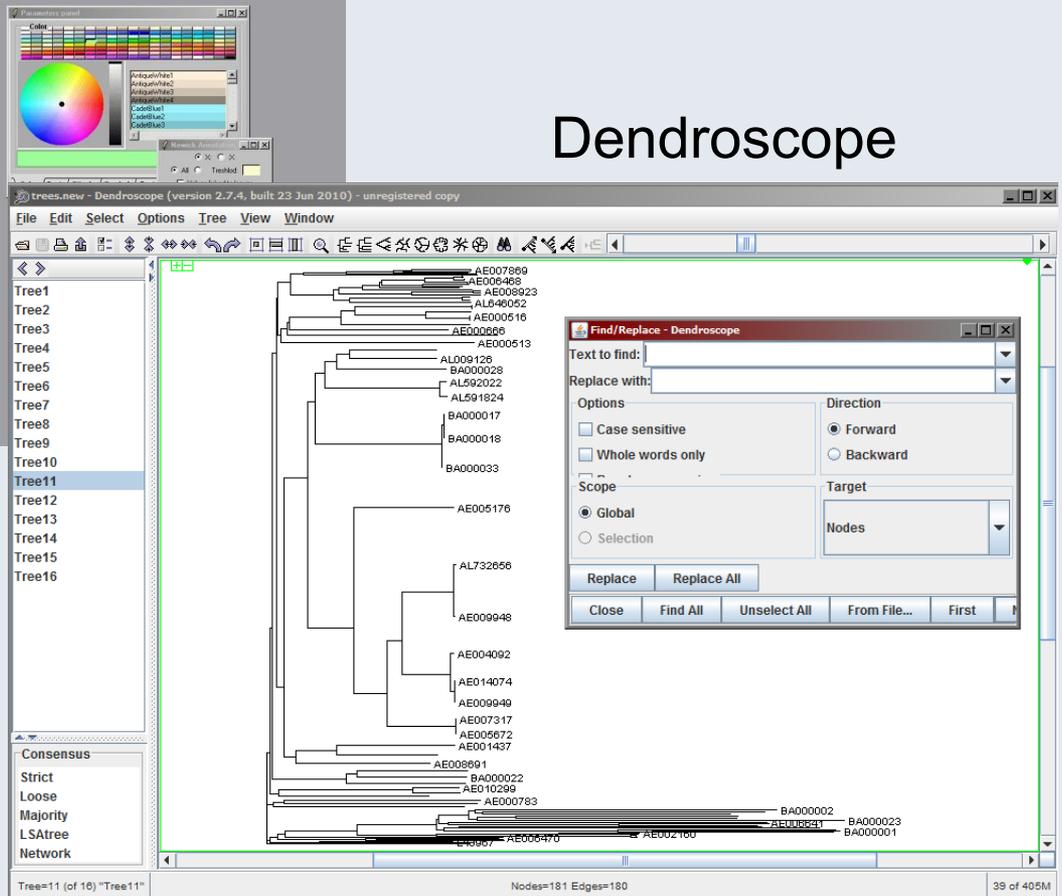
<http://tree.bio.ed.ac.uk/software/figtree/>

TreeDyn/ScriptTree



<http://www.treedyn.org>
<http://lamarck.lirmm.fr/scriptree/>

Dendroscope



<http://ab.inf.uni-tuebingen.de/software/dendroscope/>

Phylodendron  Phylogenetic tree printer

Tree styles

<input type="radio"/>  tree diag	<input checked="" type="radio"/>  cladogram	<input type="radio"/>  phenogram	<input type="radio"/>  eurogram	<input type="radio"/>  curvogram	<input type="radio"/>  swoopogram
---	--	---	--	---	--

Tree data (newick / nh format)

Upload tree file: aucun fichier sél. or paste data or URL in box below

Title:

See sample [data 1](#) and [data 2](#)

Extra options

Output

Format: width: height: (pixels)

For image maps, make hyperlinks to labels

Base URL for labels (URL's in node comments will be hyperlinked)

Font style size

Tree growth

horizontal
 vertical
 regular

use node lengths
 fixed size

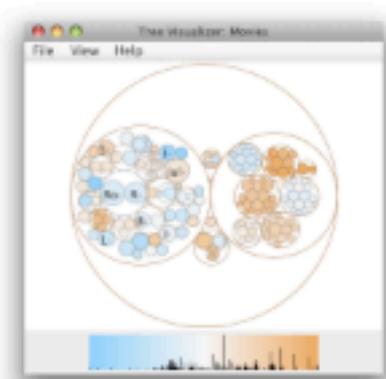
Node position

intermediate
 centered
 V shaped

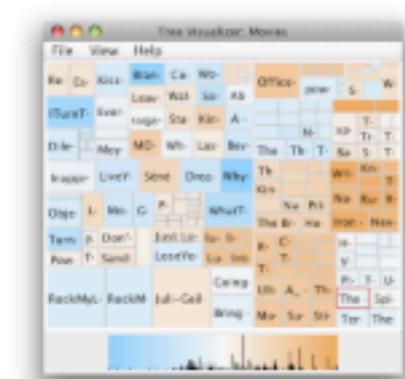
weighted
 inner

Visualization of large tree structures: TreeViz

Circular Treemap:



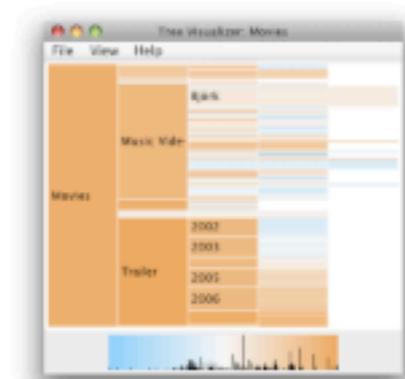
Rectangular Treemap:



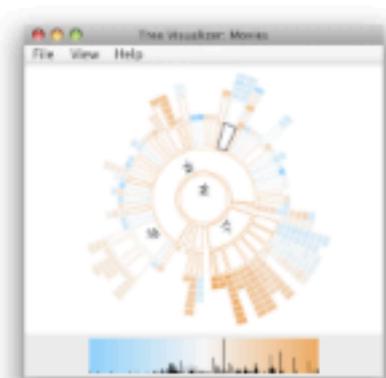
Sunburst Tree:



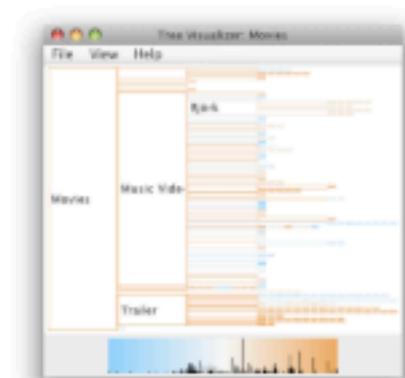
Icicle Tree:



Sunray Tree:



Iceray Tree:



Hyperbolic Tree:

