Phylogenetic Analysis:

- ✓ *Phylogenetic reconstruction by Automatic Likelihood Model selector (PALM)*

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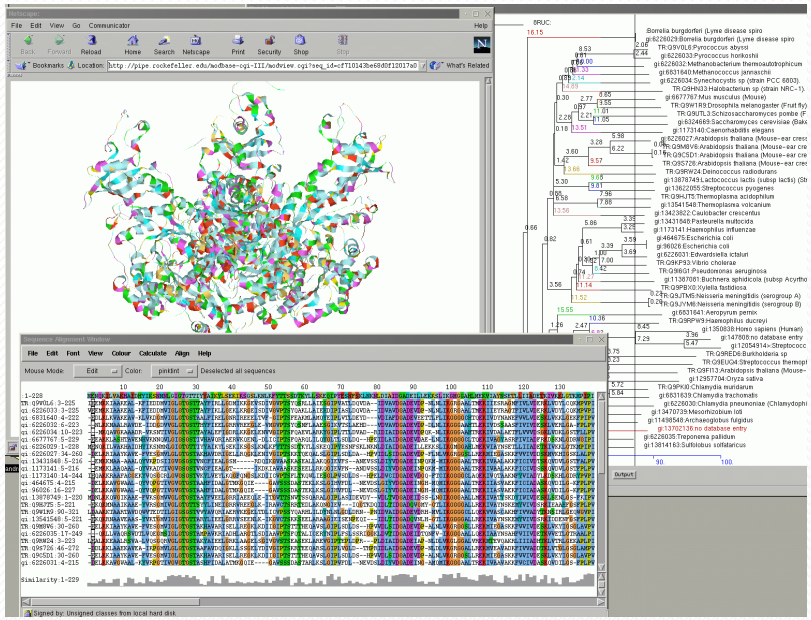
Coding Characters and Defining Homology

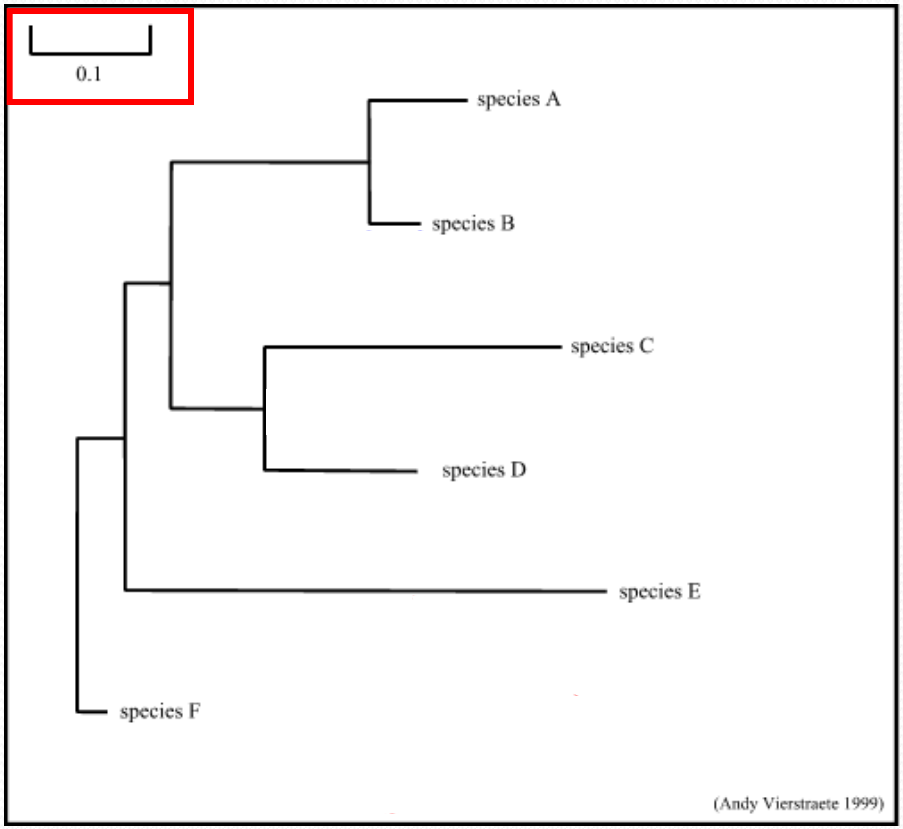
Classical phylogenetic analysis by Morphology



Molecular phylogenetic analysis By Bio-Molecules

Phylogenetic Tree

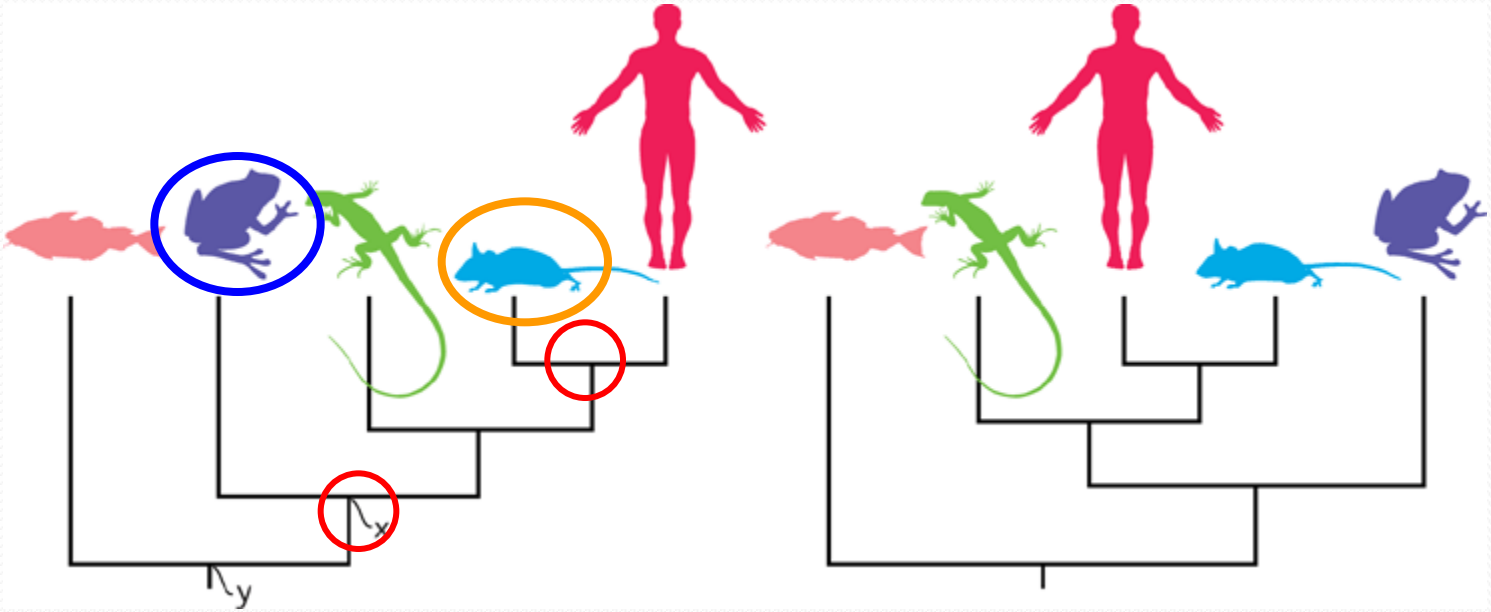
- The tree is composed of nodes connected by branches.



- **node :** a node represents a taxonomic unit.
  - Internal nodes
  - External nodes
- **branch (edge):** defines the relationship between the taxa.
- **branch length :** often represents the number of changes that have occurred in that branch.
- **root :** is the common ancestor of all taxa.
- **distance scale :** scale which represents the number of differences between sequences (e.g. 0.1 means 10 % differences between two sequences)

Trees Only Represent The Order Of Branching

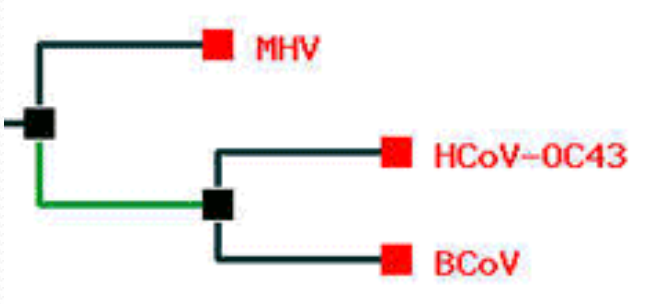
- Same topology in a different style
  - Both trees have identical topologies, with some of the internal nodes rotated.



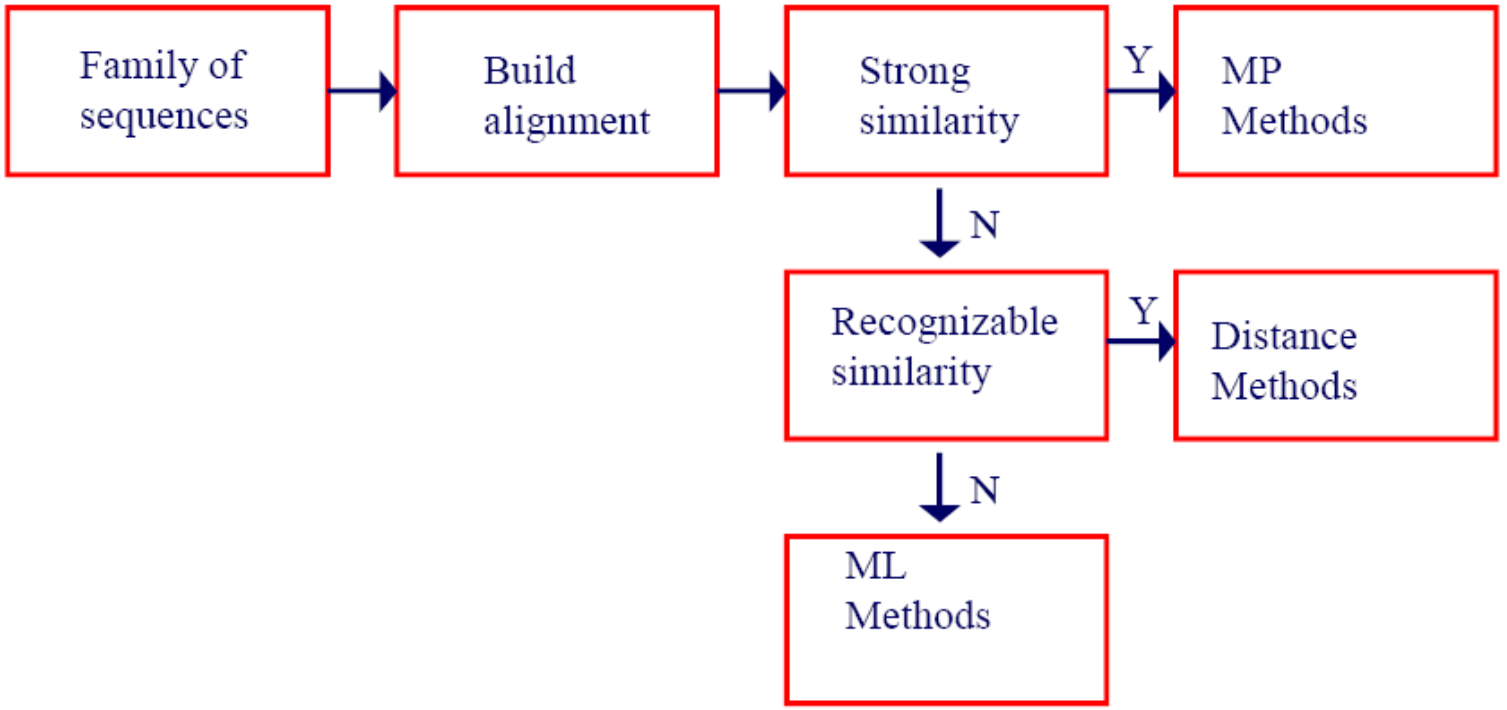
(David A. Baum et al., Science 11 November 2005:Vol. 310. no. 5750, pp. 979 – 980)

The Ways to Construct the tree

- Distance-matrix methods
  - Neighbor-joining
  - Fitch-Margoliash method
  - Using outgroups
- Maximum parsimony
  - Branch and bound
  - Sankoff-Morel-Cedergren algorithm
  - MALIGN and POY
- Maximum likelihood
- Bayesian inference



Flowchart of Analysis



(Mount, *Bioinformatics*)

Distance Method, MP and ML

- Which method should we choose?
- The main disadvantage of distance-matrix methods is their inability to efficiently use information about local high-variation regions that appear across multiple subtrees.
- ML is broadly similar to the maximum-parsimony (MP) method, but maximum likelihood allows additional statistical flexibility by permitting varying rates of evolution across both lineages and sites.
- ML, a better choice?

Maximum Likelihood

- Conditional probability of the data (Aligned sequences) given a hypothesis (a model of substitution with a set of parameter θ, and the tree τ, including topology and branch lengths)

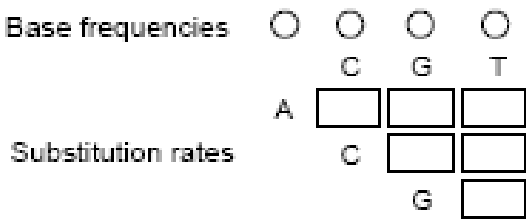
$$L(\tau, \theta) = \text{Prob}(\text{Data} \mid \tau, \theta)$$

Or

Prob(Aligned Sequences| tree, model of evolution)

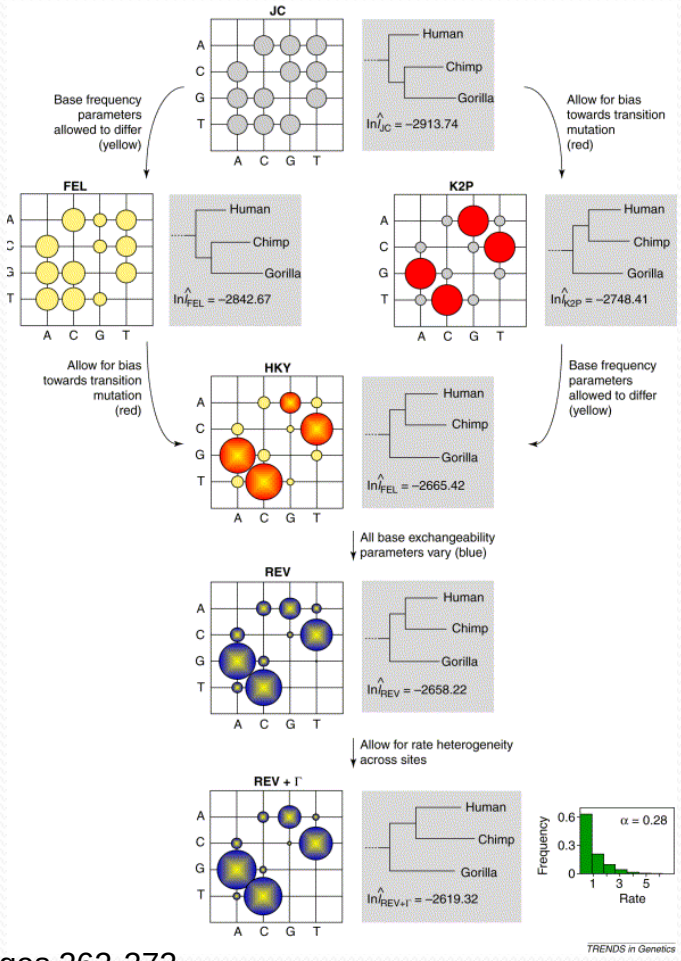
Illustration of DNA substitution Model

$$Q = \begin{pmatrix} -(x_1+x_2+x_3) & x_1 & x_2 & x_3 \\ \frac{\pi_1 x_1}{\pi_2} & -(\frac{\pi_1 x_1}{\pi_2}+x_4+x_5) & x_4 & x_5 \\ \frac{\pi_1 x_2}{\pi_3} & \frac{\pi_2 x_4}{\pi_3} & -(\frac{\pi_1 x_2}{\pi_3}+\frac{\pi_2 x_4}{\pi_3}+x_6) & x_6 \\ \frac{\pi_1 x_3}{\pi_4} & \frac{\pi_2 x_5}{\pi_4} & \frac{\pi_3 x_6}{\pi_4} & -(\frac{\pi_1 x_3}{\pi_4}+\frac{\pi_2 x_5}{\pi_4}+\frac{\pi_3 x_6}{\pi_4}) \end{pmatrix}$$



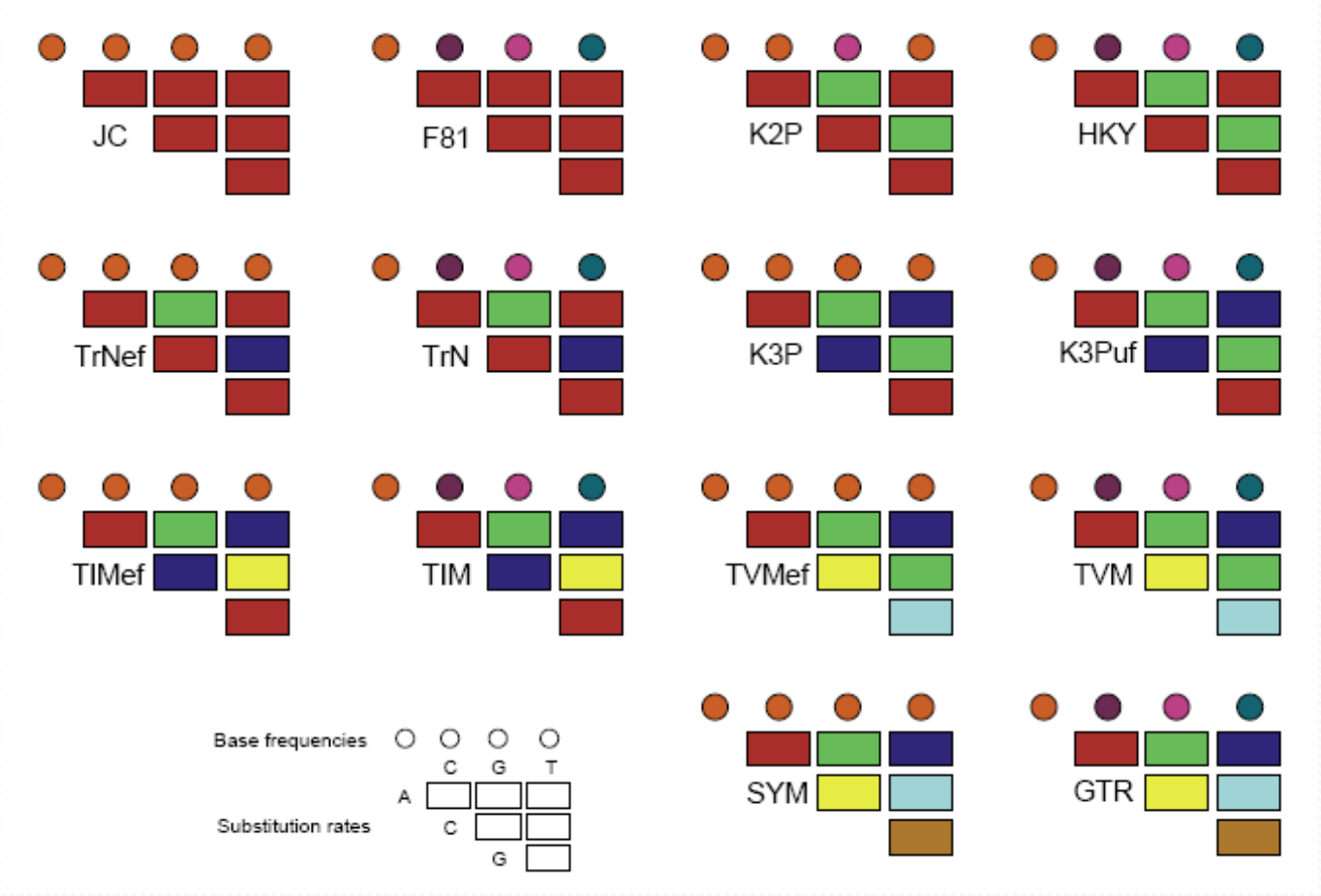
GTR (for four characters, as is often the case in phylogenetics) requires 6 substitution rate parameters (x1~x6), as well as 4 equilibrium base frequency parameters.

Relationships Among Some Standard Models Of Nucleotide Evolution

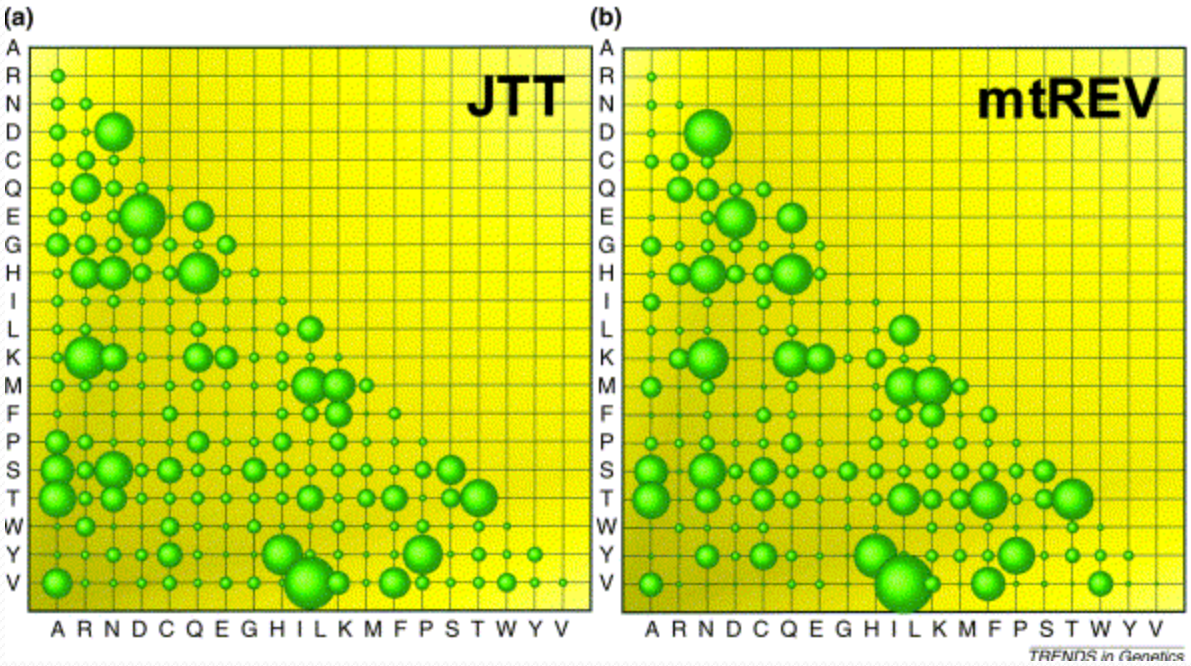


Trends in Genetics
Volume 17, Issue 5, 1 May 2001, Pages 262-272

Illustration of Models for DNA



Models of Amino Acid Replacement



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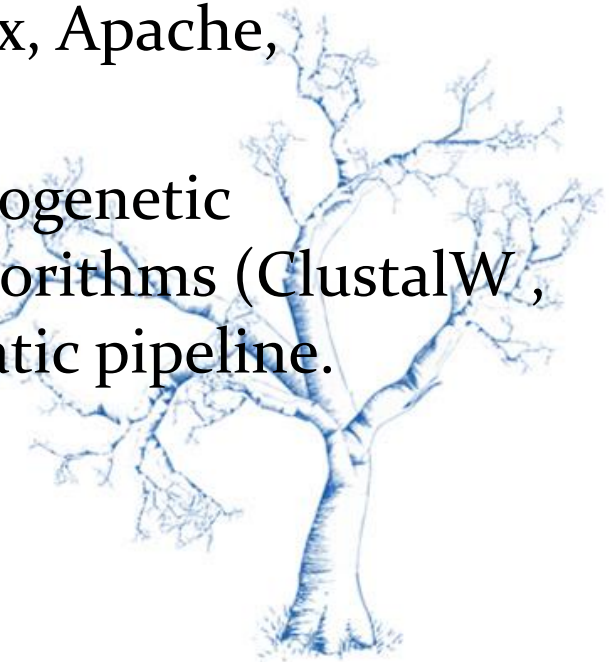
Background for PALM

- Model fitting in phylogenetics has been suggested for many years, yet many authors still arbitrarily choose their models, often using the default models implemented in standard computer programs for phylogenetic estimation.
- Here, we want to show the way that a best-fit model can be readily identified. Consequently, given the relevance of models, model fitting should be routine in any phylogenetic analysis that uses models of evolution.

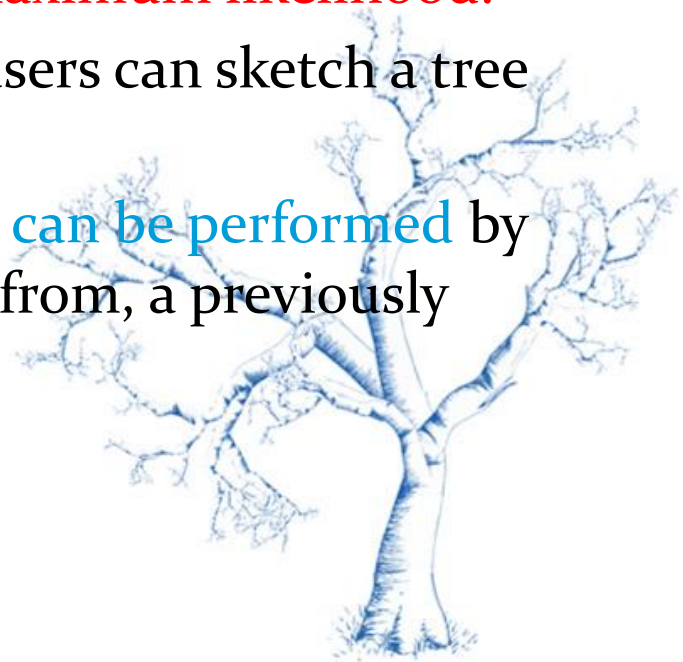
Motivation I

- Provide a seamless way to conduct the complex phylogenetic analysis for Biologists
- An integrated and user-optimized framework for biomolecular phylogenetic analysis
- PALM uses an open-source LAPP (Linux, Apache, PostgreSql, PHP) structure and
- PALM infers genetic distances and phylogenetic relationships using well-established algorithms (ClustalW , PhyML, ProtTest, Modeltest) in automatic pipeline.



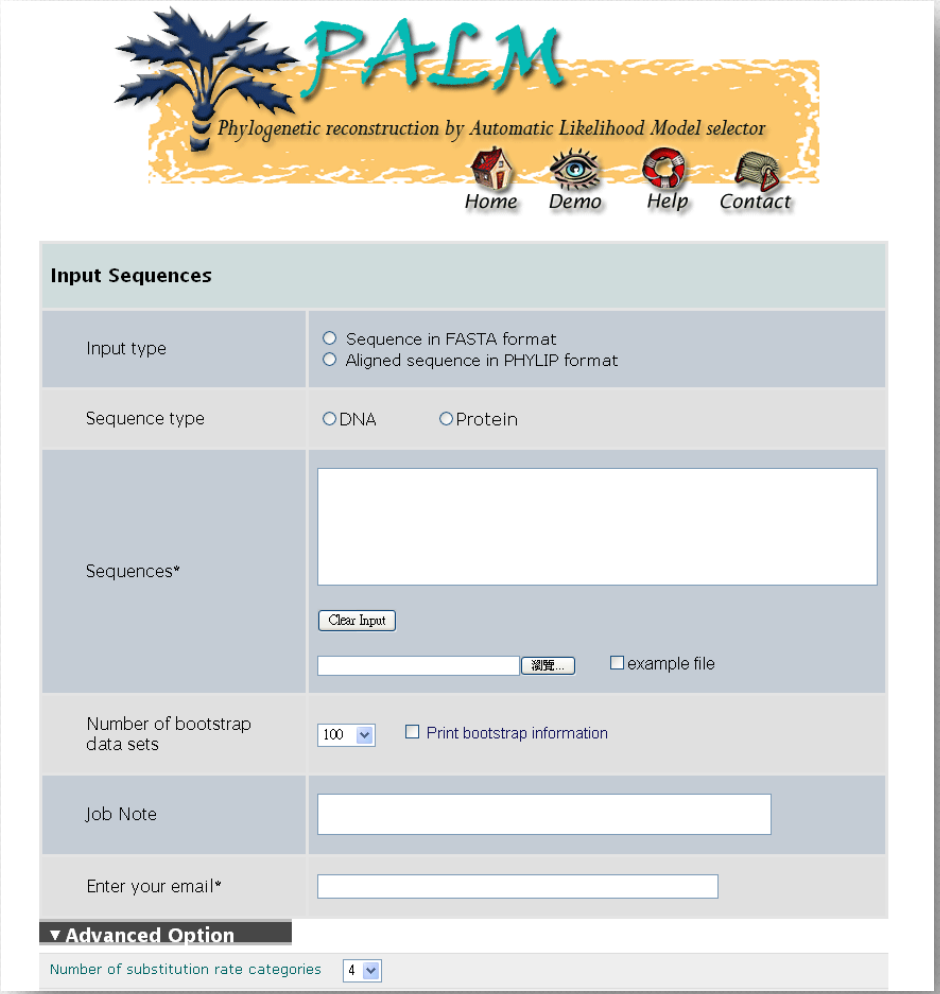
Motivation II

- Model can be selected by following methods including hierarchical likelihood ratio tests (hLRTs), Akaike information criterion (AIC), and Bayesian information criterion (BIC)
- PALM can help user to construct the tree with bootstrap based on best substitution model chosen by maximum likelihood.
- Through a user-friendly web interface, users can sketch a tree effortlessly in multiple steps
- Furthermore, iterative tree construction can be performed by adding sequences to, or removing them from, a previously submitted job



Component Programs of PALM

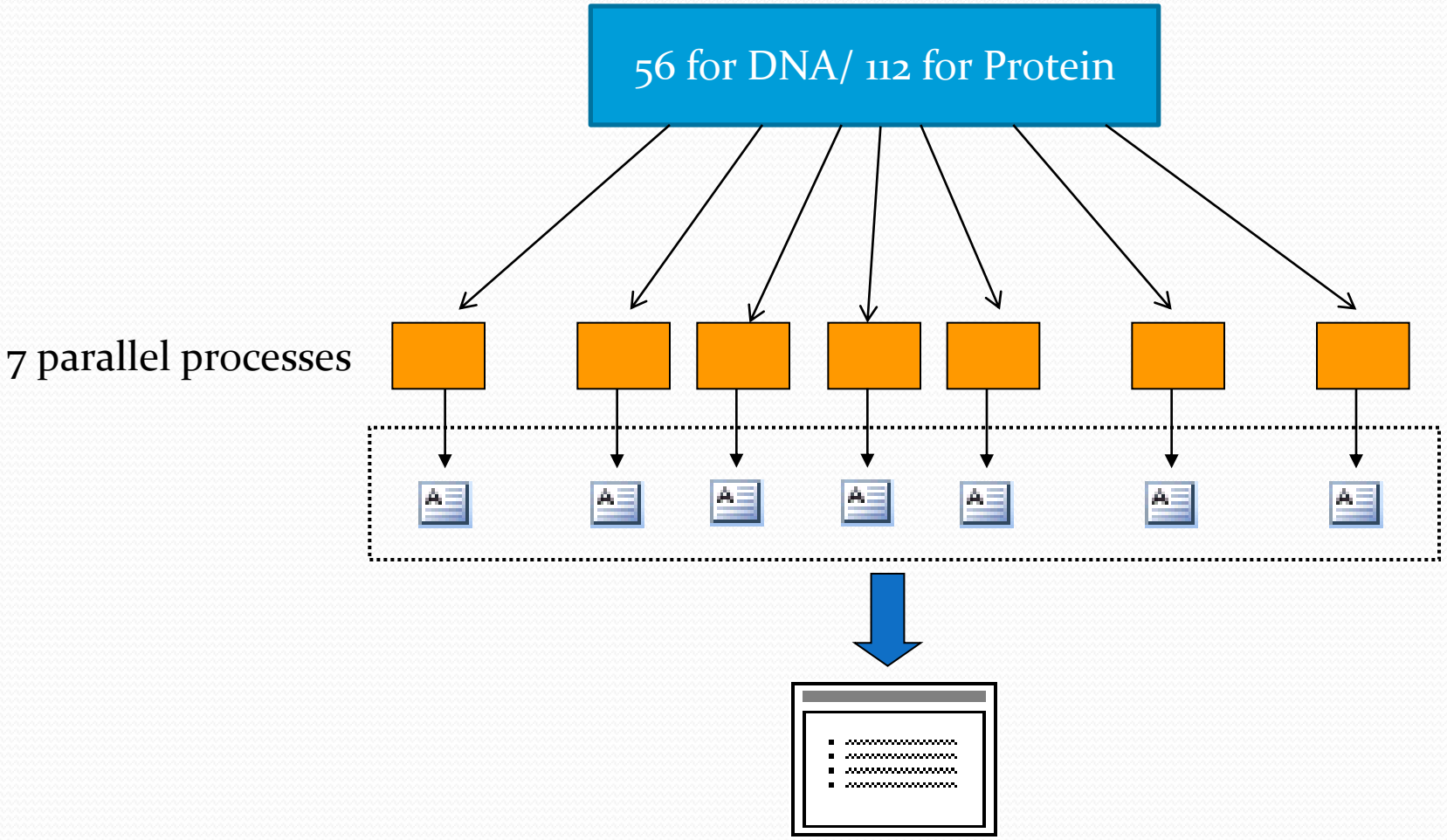
- PhyML 3.0
- ModelTest 3.7
- ProtTest 2.0
- ClustalW 2.0.8
- Seqret (EMBOSS)



Models Used in PALM

- For DNA (56 models)
  - JC69, K80, F81, HKY, TrN, TrNef, K3P, K3Puf, TIM, TIMef, TVM, TVMef, SYM, GTR
  - +I, +G
- For Protein (112 models), **Time consuming**
  - LG, DCMut, JTT, MtREV, MtMam, MtArt, Dayhoff, WAG, RtREV, CpREV, Blosum62, VT, HIVb, HIVw
  - +I, +G, +F

Distribution Computing by PalmMonitor for Each Substitution Model



Decreasing Time by PALMmonitor

- According the algorithm used in PALM, models will take a lot of time to calculate the value of maximum likelihood.
  - JTT, MtREV 1h:22:21
  - MtMam, MtArt 1h:51:25
  - Dayhoff ,WAG 1h:33:51
  - RtREV, CpREV 1h:33:50
  - Blosum62, VT 1h:15:58
  - HIVb, HIVw 1h:35:02
  - LG, DC, Mut 1h:38:36

Over 10 Hours

- All Models by PALMmonitor 1h:11:11

Source: 99 sequences with 247 residues for each

Parallel Computing on Bootstrapping

DNA : DNA_Big_24.phy (24 sequences, average 5000 bps substitution model: HKY85- Default)

Bootstrap	100	1000
Runtime	11h:47m:5s	~120 h
Runtime (5 cores/ 8 cores)	2h:53m:2s	17h:52m:15s

1/6

Protein : Pseq (20 sequences, average 820 a.a., substitution model: LG - Default)

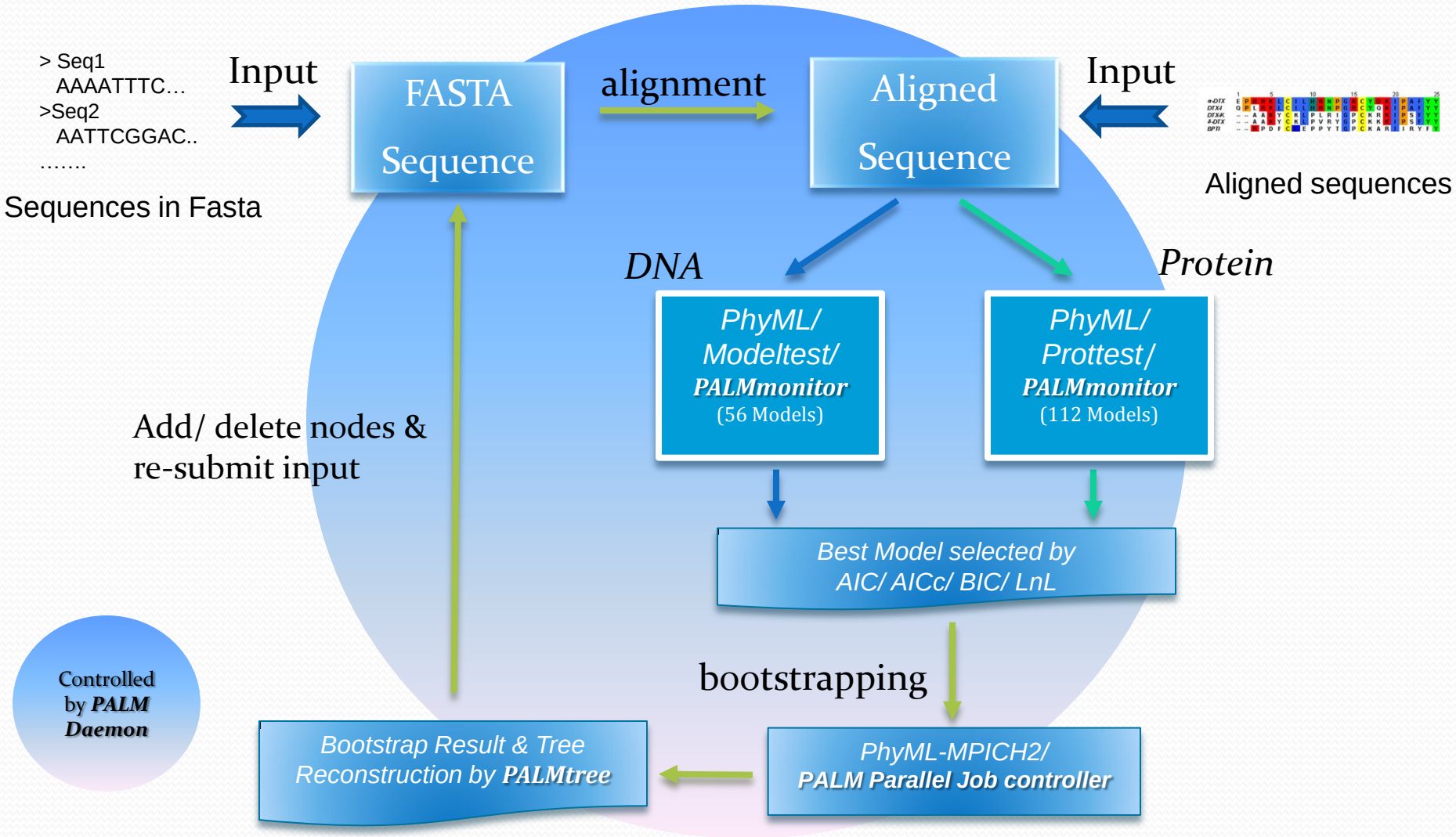
Bootstrap	100	1000
Runtime	17h:31m:33s	~175 h
Runtime (5 cores/ 8 cores)	5h:15m:19s	36h:55m:10s

1/6

Input and Output of PALM

- Input format (Protein and DNA)
  - Fasta format
  - Phylip format: Aligned Sequences
  - User tree (if submitted and valid)
- Output
  - Tree topology by php and GD library
  - Tree file in Newick format
  - Aligned Sequence in phylip format
  - Best model selected by PALM

Flowchart of PALM



Result of PALM

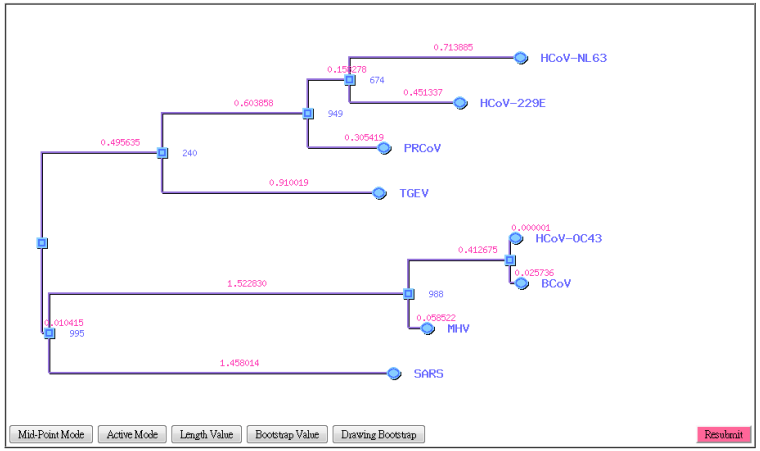
A

PALM
Phylogenetic reconstruction by Automatic Likelihood Model selector
Home Demo Help Contact

PALM Result

Job ID	20080821060606361	**Number of Substitution Rate Category**	4
Job Note	test for speed in protein	**Model Selection Criterion**	LnL
Sequence Type	Protein	**Optimization of Tree Topology**	Yes
Number of Bootstrap	1000	**Optimization of Branch Length**	Yes
Starting Tree	BIONJ		

B



C

Best Model Selected	JTT+I+G+F
Model Selection Criterion	LnL
AIC	2336.50
-lnL	1134.25

D

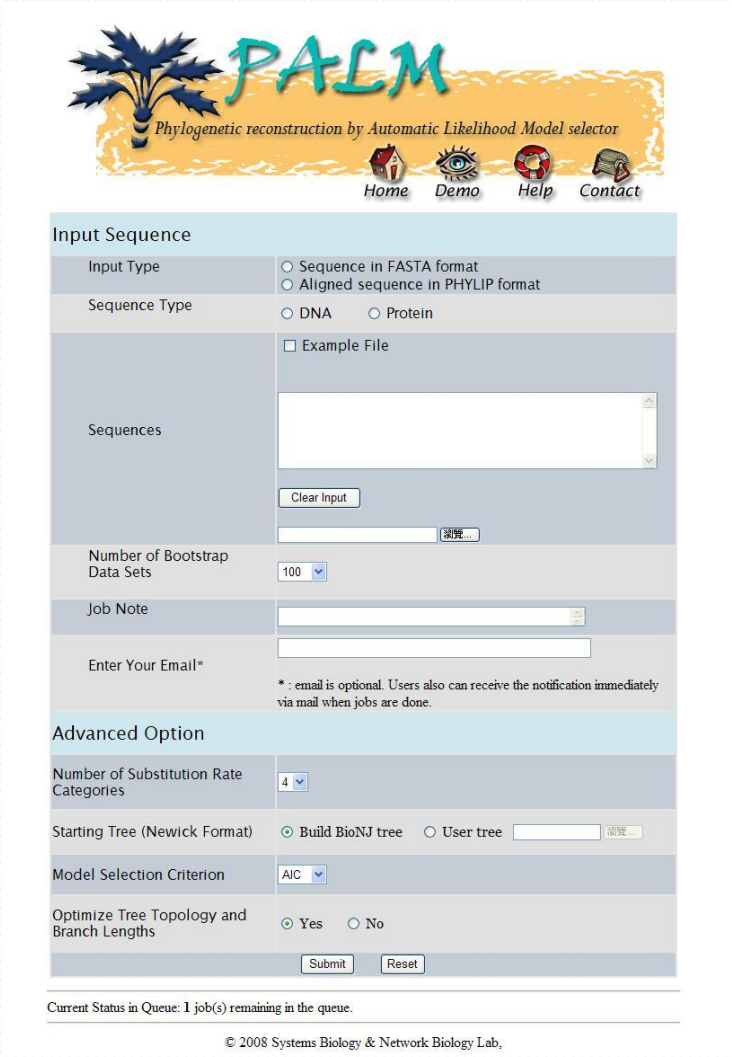
Model	**deltaAIC**	**AIC**	**-lnL***	**AICw**
JTT+I+G+F	2.00	2336.50	-1134.25	0.12
JTT+G+F	0.00	2334.50	-1134.25	0.33
WAG+I+G+F	2.78	2337.28	-1134.64	0.08
WAG+G+F	0.78	2335.28	-1134.64	0.23
WAG+I+F	5.17	2339.67	-1136.83	0.03
WAG+F	3.50	2338.00	-1137.00	0.06

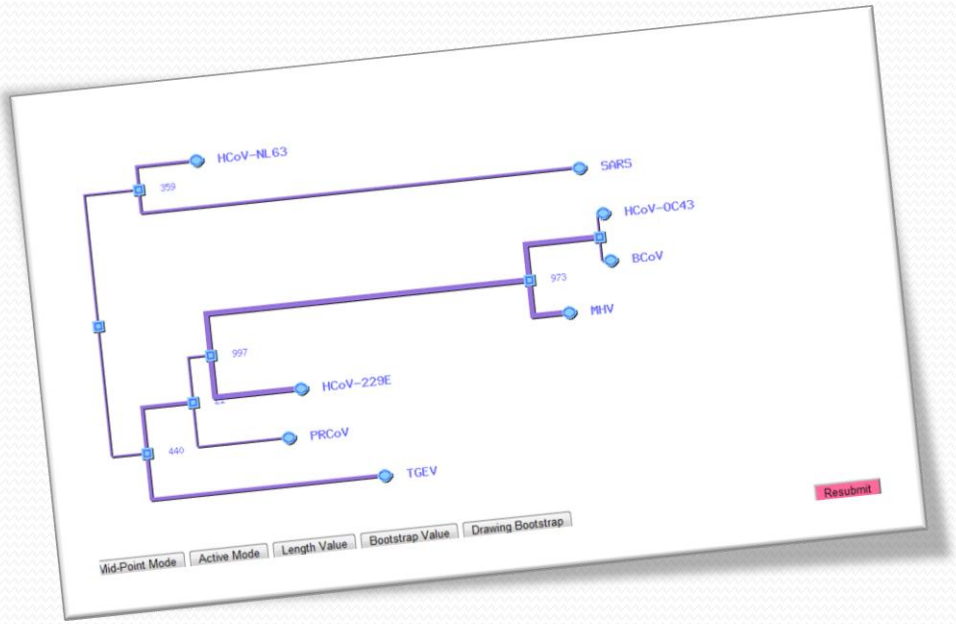
E

Original File	20080821060606361
Phylip File	20080821060606361.phy
Phylogenetic Tree (Newick)	tree20080821060606361.txt
ProtTest Information	ProtTest_20080821060606361.txt
Bootstrap Tree	20080821060606361_phyml_boot_trees.txt
Bootstrap Statistic data	20080821060606361_phyml_boot_stats.txt

The job is computed approximately in 47 minute(s).

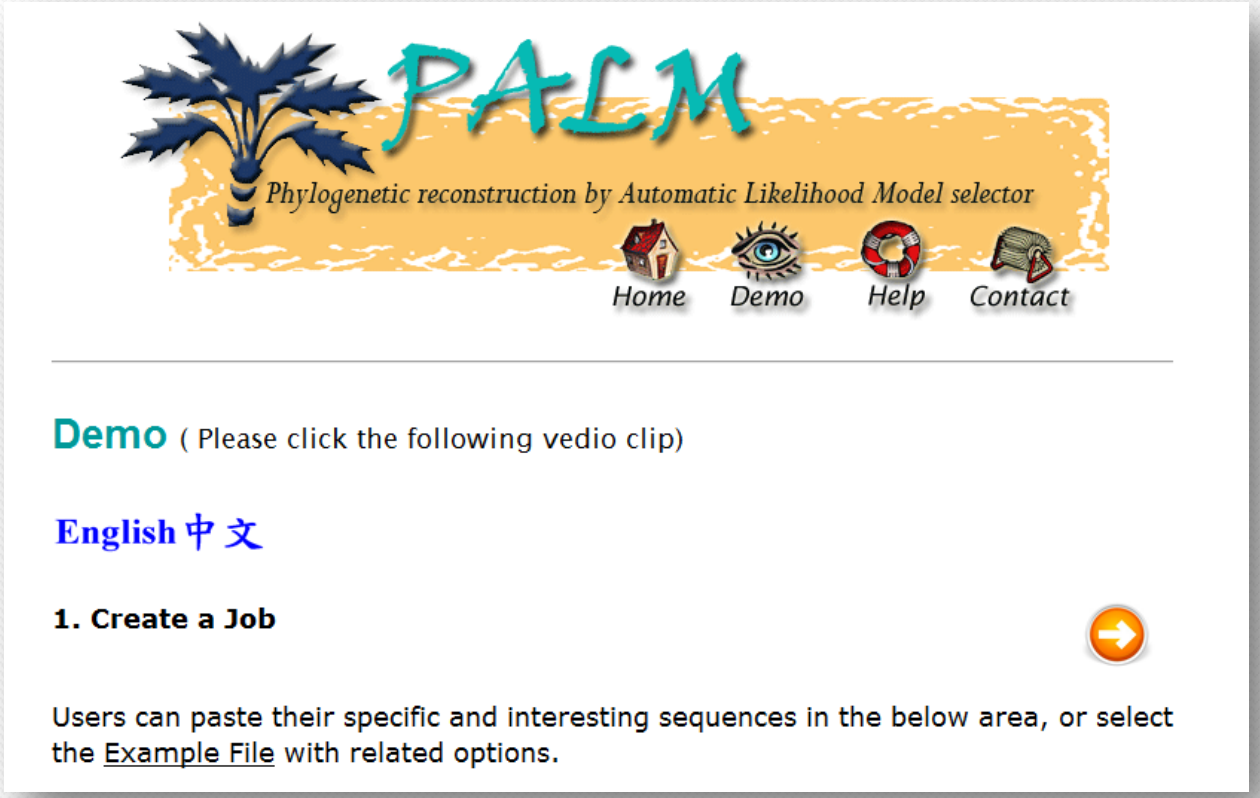
Demonstration of PALM





Access : http://palm.iis.sinica.edu.tw

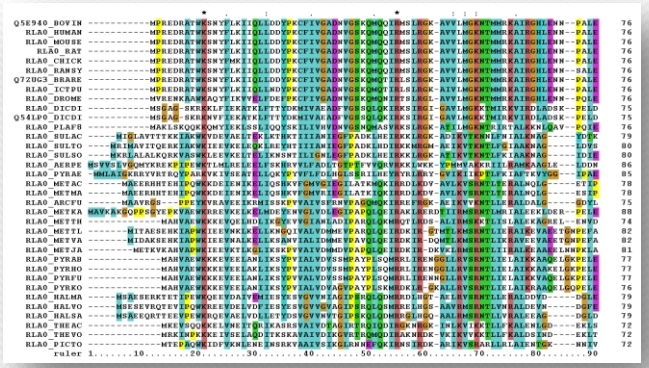
Demo Flash of PALM

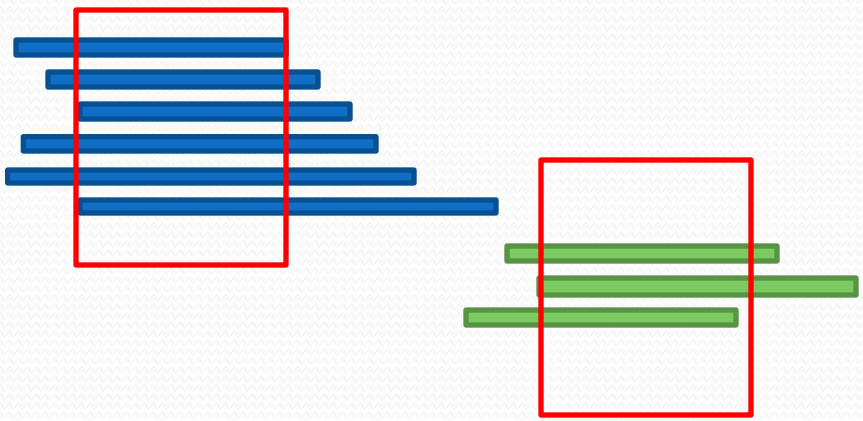


http://palm.iis.sinica.edu.tw/demo.html

Some Suggestions

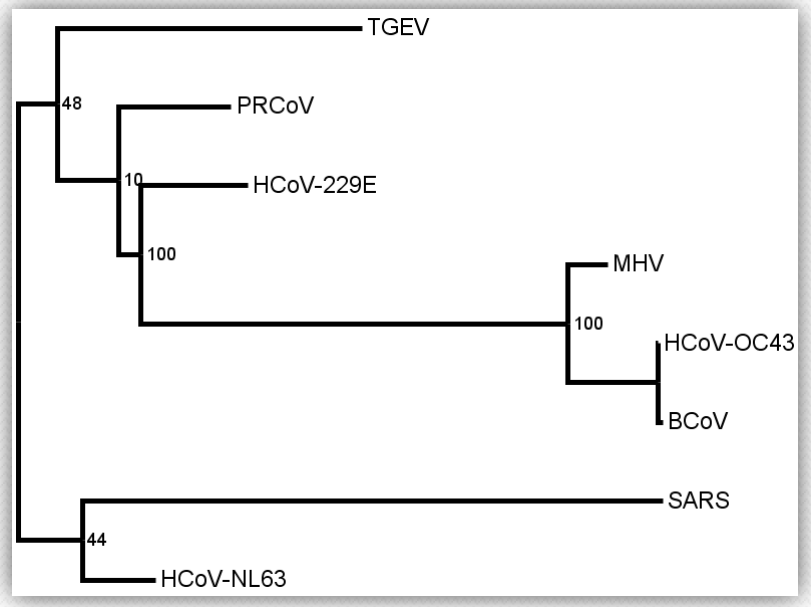
- Please be careful to choose the sequences
- Only well aligned sequences lead to meaningful phylogenetic result.
- RNA editing may introduce bias during analysis. Avoid those regions that may have such conditions.





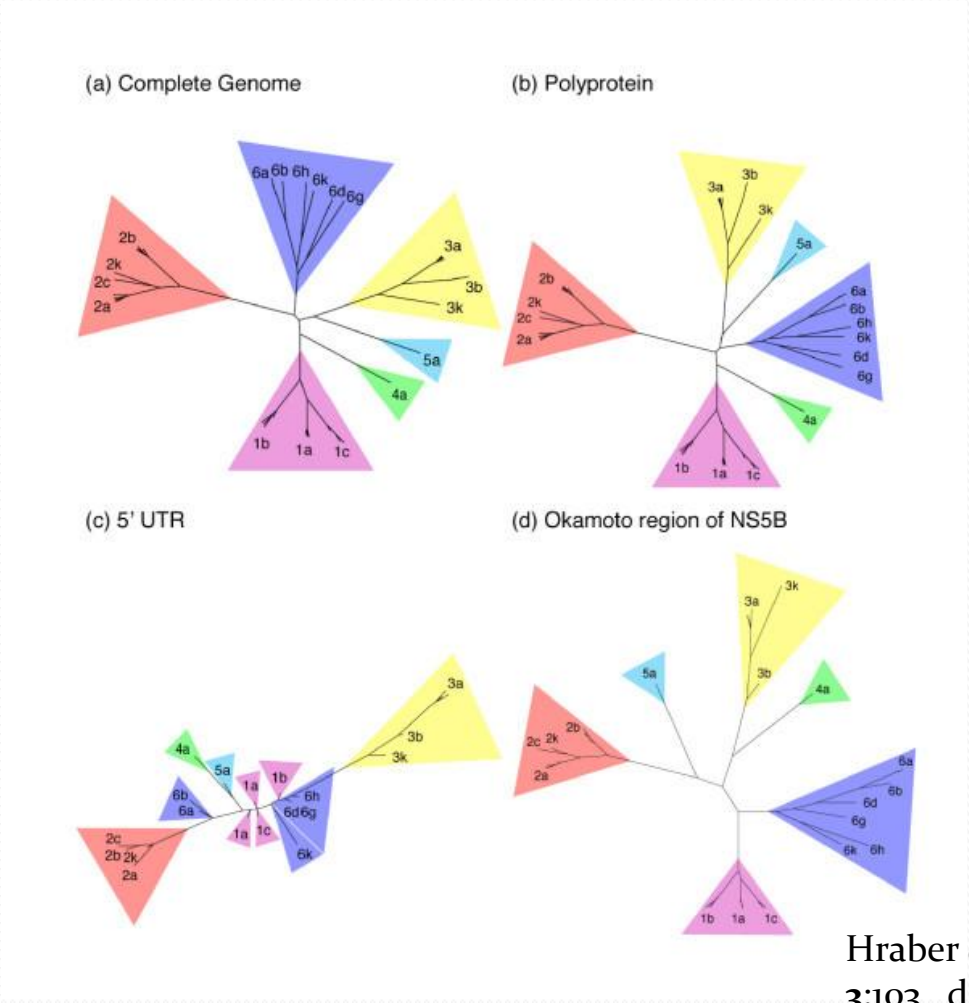
Bootstrap (BS) Analysis

- Bootstrap analysis is the most often used method for statistical evaluation of phylogenies.
- In general:
  - **BS >95%: Often close to 100% confidence in that branch**
  - **BS>75%: Often close to 95% confidence in that branch**
  - BS<75% : Maybe a correct clade due to the original bias cannot be corrected by the re-sampling process.



Input Sequences Make the Tree Different

HIV



Hraber *et al. Virology Journal* 2006 **3**:103 doi:10.1186/1743-422X-3-103

Future Plans for PALM

- Integrate more substitution models into PALM
- Improve and optimize the performance of whole pipeline
- MrBayes will be implemented into this system for Bayesian inference.
- Parallel computing for large scale, ie. 16S RNA tree (near 2000-4000 sequences) reconstruction in metagenomics for revealing microbial community

Acknowledgement

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