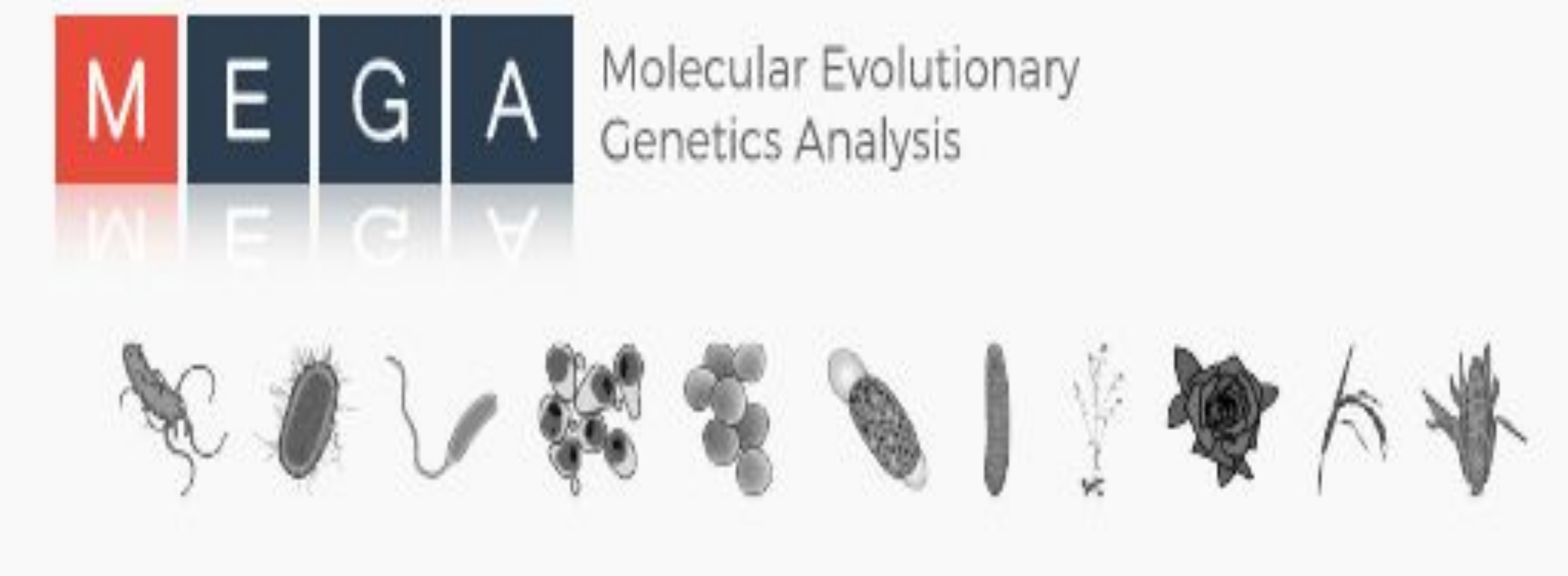
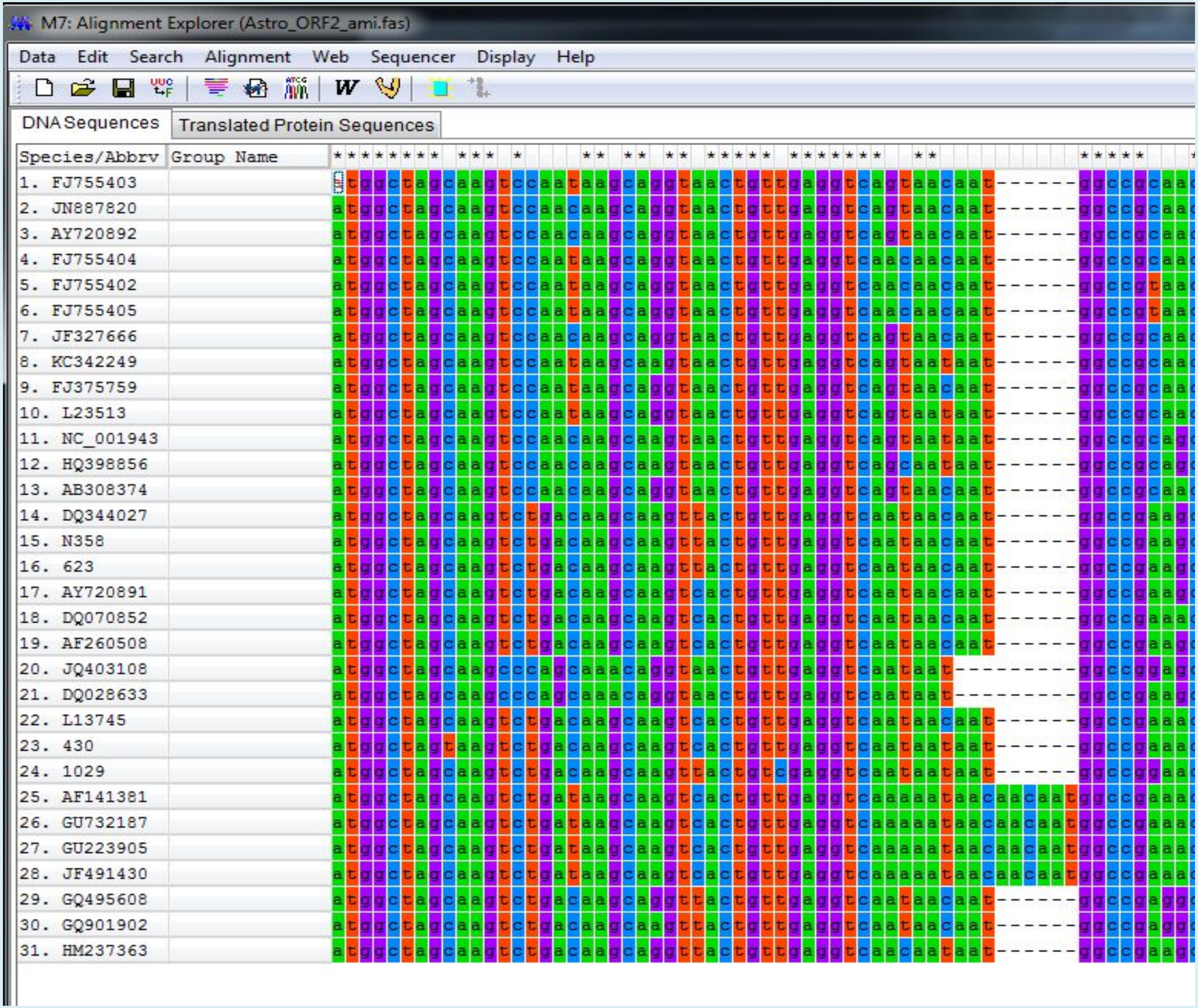
Эволюционные модели и дистанции между последовательностями биополимеров

Молекулярная филогения

Статистические методы оценки деревьев. Анализ молекулярных часов.


MEGA
Molecular Evolutionary
Genetics Analysis



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Species/Abbrv   Group Name   ******** *** *    ** ** ** ***** *******  **          *****   *
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22. L13745                   atggctagcaagtctgacaagcaagtcactgttgaggtcaataacaat------ggccgaaa
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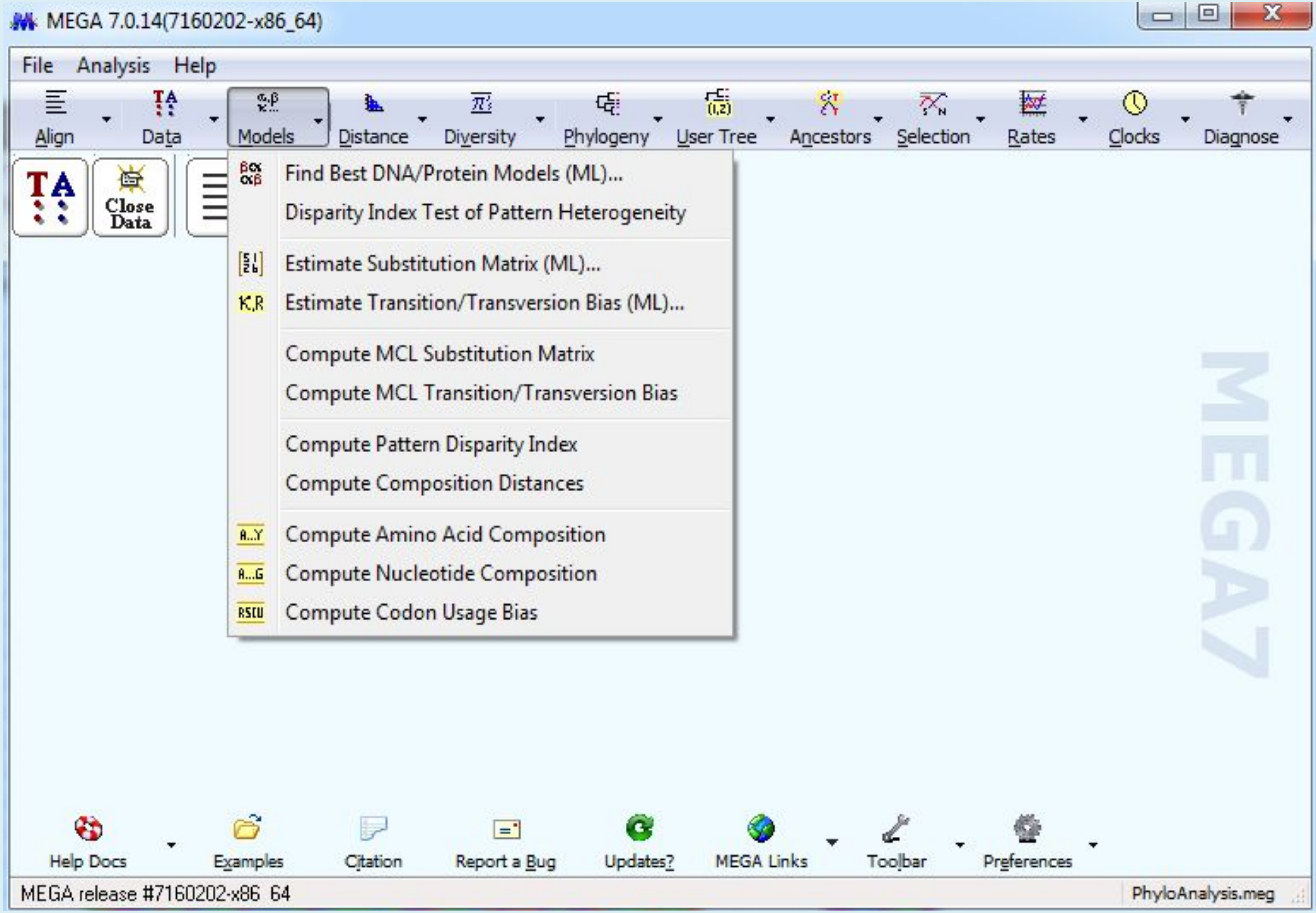
MEGA 7.0.14(7160202-x86_64)
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Help
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Data
Models
Distance
Diversity
Phylogeny
User Tree
Ancestors
Selection
Rates
Clocks
Diagnose
Close Data
Find Best DNA/Protein Models (ML)...
Disparity Index Test of Pattern Heterogeneity
Estimate Substitution Matrix (ML)...
Estimate Transition/Transversion Bias (ML)...
Compute MCL Substitution Matrix
Compute MCL Transition/Transversion Bias
Compute Pattern Disparity Index
Compute Composition Distances
Compute Amino Acid Composition
Compute Nucleotide Composition
Compute Codon Usage Bias
MEGA7
Help Docs
Examples
Citation
Report a Bug
Updates?
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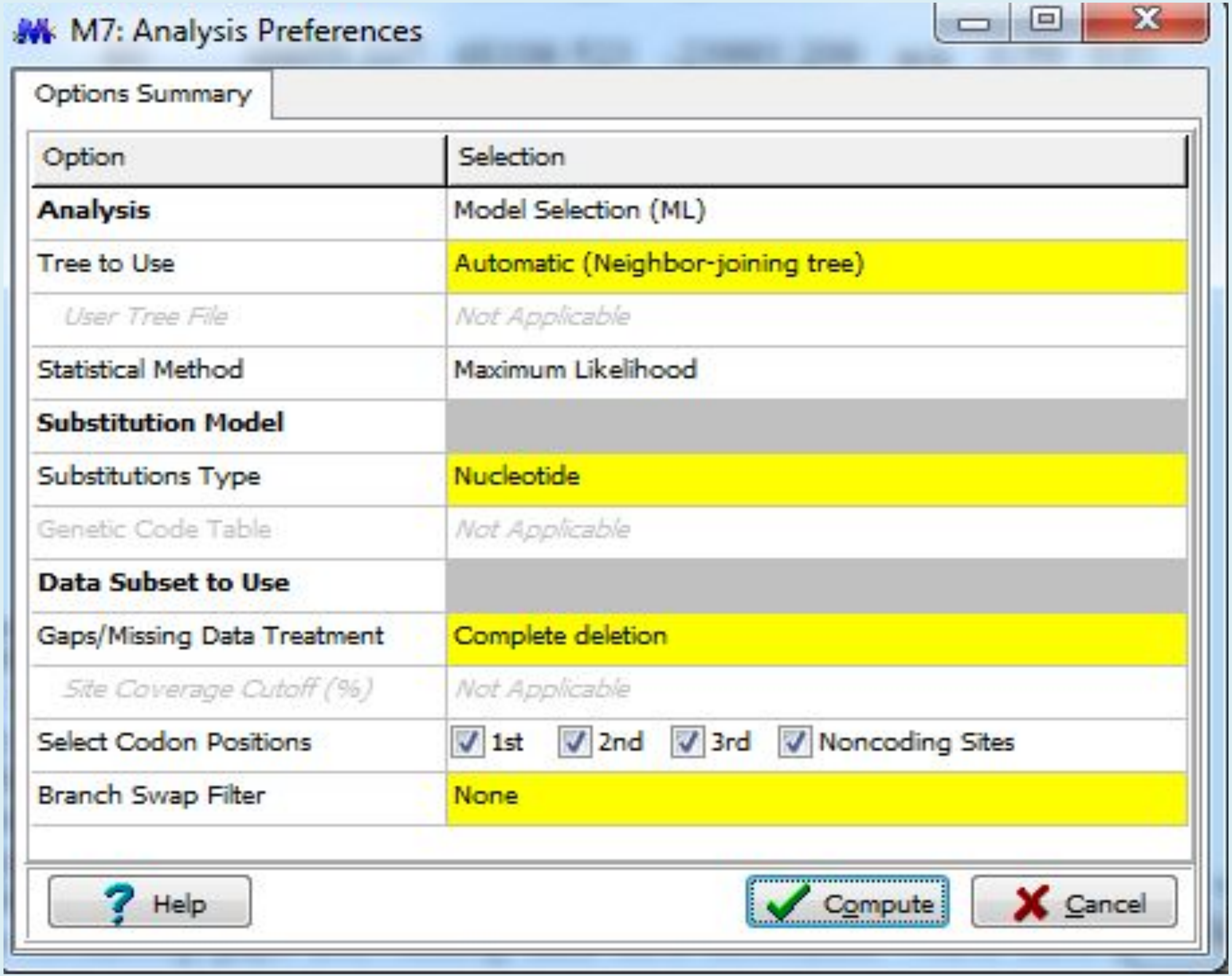

Option	Selection
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Tree to Use	Automatic (Neighbor-joining tree)
User Tree File	*Not Applicable*
Statistical Method	Maximum Likelihood
Substitution Model	
Substitutions Type	Nucleotide
Genetic Code Table	*Not Applicable*
Data Subset to Use	
Gaps/Missing Data Treatment	Complete deletion
Site Coverage Cutoff (%)	*Not Applicable*
Select Codon Positions	☑ 1st ☑ 2nd ☑ 3rd ☑ Noncoding Sites
Branch Swap Filter	None

Для анализа с использованием метода максимального правдоподобия, параметр «branch swap filter» используется для установки строгости оптимизации относительно длины ветви. Более слабый фильтр приведет к более исчерпывающей оптимизации, однако поиск может занять больше времени, но потенциально, большее пространство будет изучено.

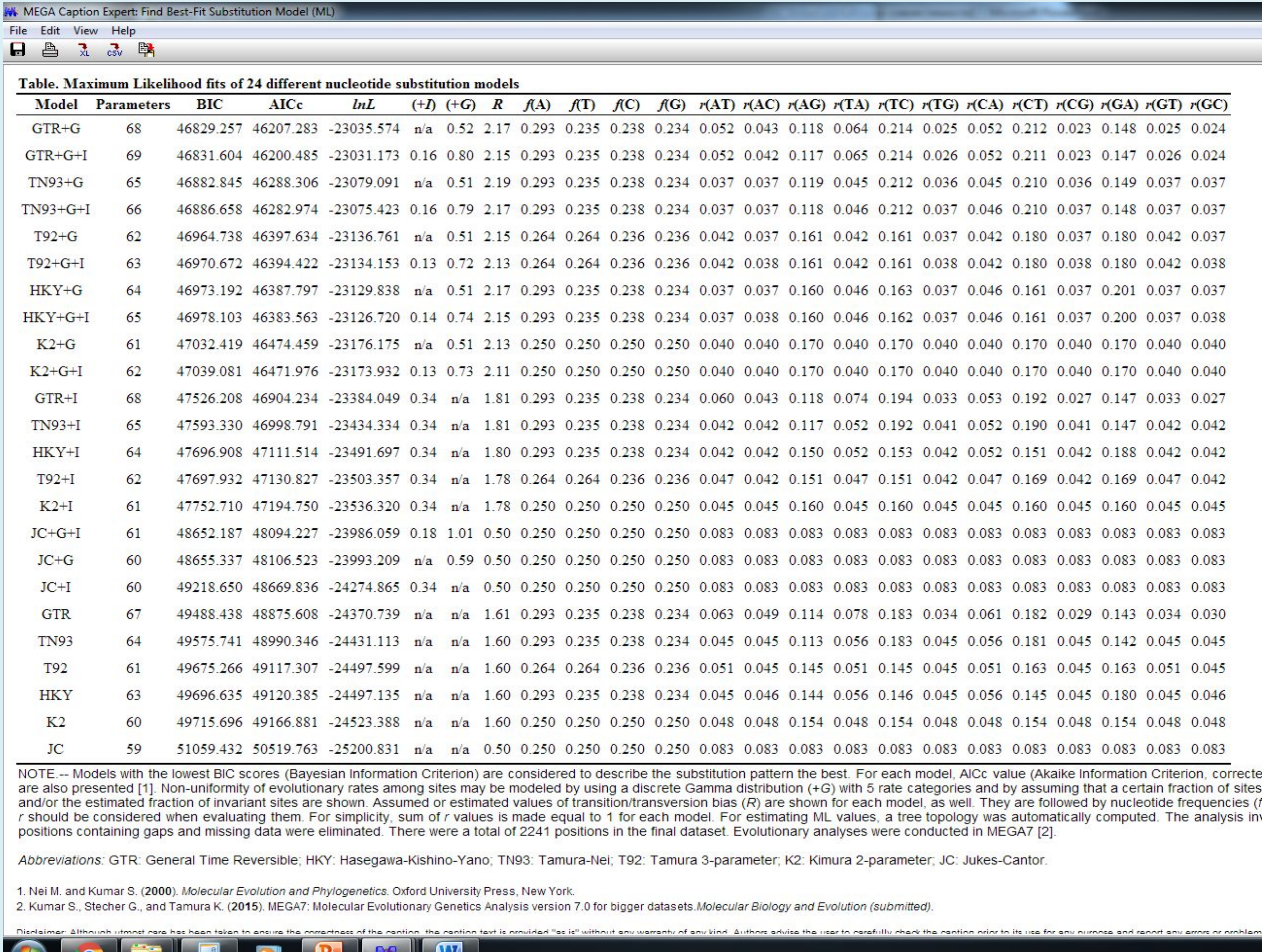

Table. Maximum Likelihood fits of 24 different nucleotide substitution models

Model	Parameters	BIC	AICc	*lnL*	(+*I*)	(+*G*)	*R*	*f*(A)	*f*(T)	*f*(C)	*f*(G)	*r*(AT)	*r*(AC)	*r*(AG)	*r*(TA)	*r*(TC)	*r*(TG)	*r*(CA)	*r*(CT)	*r*(CG)	*r*(GA)	*r*(GT)	*r*(GC)
GTR+G	68	46829.257	46207.283	-23035.574	n/a	0.52	2.17	0.293	0.235	0.238	0.234	0.052	0.043	0.118	0.064	0.214	0.025	0.052	0.212	0.023	0.148	0.025	0.024
GTR+G+I	69	46831.604	46200.485	-23031.173	0.16	0.80	2.15	0.293	0.235	0.238	0.234	0.052	0.042	0.117	0.065	0.214	0.026	0.052	0.211	0.023	0.147	0.026	0.024
TN93+G	65	46882.845	46288.306	-23079.091	n/a	0.51	2.19	0.293	0.235	0.238	0.234	0.037	0.037	0.119	0.045	0.212	0.036	0.045	0.210	0.036	0.149	0.037	0.037
TN93+G+I	66	46886.658	46282.974	-23075.423	0.16	0.79	2.17	0.293	0.235	0.238	0.234	0.037	0.037	0.118	0.046	0.212	0.037	0.046	0.210	0.037	0.148	0.037	0.037
T92+G	62	46964.738	46397.634	-23136.761	n/a	0.51	2.15	0.264	0.264	0.236	0.236	0.042	0.037	0.161	0.042	0.161	0.037	0.042	0.180	0.037	0.180	0.042	0.037
T92+G+I	63	46970.672	46394.422	-23134.153	0.13	0.72	2.13	0.264	0.264	0.236	0.236	0.042	0.038	0.161	0.042	0.161	0.038	0.042	0.180	0.038	0.180	0.042	0.038
HKY+G	64	46973.192	46387.797	-23129.838	n/a	0.51	2.17	0.293	0.235	0.238	0.234	0.037	0.037	0.160	0.046	0.163	0.037	0.046	0.161	0.037	0.201	0.037	0.037
HKY+G+I	65	46978.103	46383.563	-23126.720	0.14	0.74	2.15	0.293	0.235	0.238	0.234	0.037	0.038	0.160	0.046	0.162	0.037	0.046	0.161	0.037	0.200	0.037	0.038
K2+G	61	47032.419	46474.459	-23176.175	n/a	0.51	2.13	0.250	0.250	0.250	0.250	0.040	0.040	0.170	0.040	0.170	0.040	0.040	0.170	0.040	0.170	0.040	0.040
K2+G+I	62	47039.081	46471.976	-23173.932	0.13	0.73	2.11	0.250	0.250	0.250	0.250	0.040	0.040	0.170	0.040	0.170	0.040	0.040	0.170	0.040	0.170	0.040	0.040
GTR+I	68	47526.208	46904.234	-23384.049	0.34	n/a	1.81	0.293	0.235	0.238	0.234	0.060	0.043	0.118	0.074	0.194	0.033	0.053	0.192	0.027	0.147	0.033	0.027
TN93+I	65	47593.330	46998.791	-23434.334	0.34	n/a	1.81	0.293	0.235	0.238	0.234	0.042	0.042	0.117	0.052	0.192	0.041	0.052	0.190	0.041	0.147	0.042	0.042
HKY+I	64	47696.908	47111.514	-23491.697	0.34	n/a	1.80	0.293	0.235	0.238	0.234	0.042	0.042	0.150	0.052	0.153	0.042	0.052	0.151	0.042	0.188	0.042	0.042
T92+I	62	47697.932	47130.827	-23503.357	0.34	n/a	1.78	0.264	0.264	0.236	0.236	0.047	0.042	0.151	0.047	0.151	0.042	0.047	0.169	0.042	0.169	0.047	0.042
K2+I	61	47752.710	47194.750	-23536.320	0.34	n/a	1.78	0.250	0.250	0.250	0.250	0.045	0.045	0.160	0.045	0.160	0.045	0.045	0.160	0.045	0.160	0.045	0.045
JC+G+I	61	48652.187	48094.227	-23986.059	0.18	1.01	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
JC+G	60	48655.337	48106.523	-23993.209	n/a	0.59	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
JC+I	60	49218.650	48669.836	-24274.865	0.34	n/a	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
GTR	67	49488.438	48875.608	-24370.739	n/a	n/a	1.61	0.293	0.235	0.238	0.234	0.063	0.049	0.114	0.078	0.183	0.034	0.061	0.182	0.029	0.143	0.034	0.030
TN93	64	49575.741	48990.346	-24431.113	n/a	n/a	1.60	0.293	0.235	0.238	0.234	0.045	0.045	0.113	0.056	0.183	0.045	0.056	0.181	0.045	0.142	0.045	0.045
T92	61	49675.266	49117.307	-24497.599	n/a	n/a	1.60	0.264	0.264	0.236	0.236	0.051	0.045	0.145	0.051	0.145	0.045	0.051	0.163	0.045	0.163	0.051	0.045
HKY	63	49696.635	49120.385	-24497.135	n/a	n/a	1.60	0.293	0.235	0.238	0.234	0.045	0.046	0.144	0.056	0.146	0.045	0.056	0.145	0.045	0.180	0.045	0.046
K2	60	49715.696	49166.881	-24523.388	n/a	n/a	1.60	0.250	0.250	0.250	0.250	0.048	0.048	0.154	0.048	0.154	0.048	0.048	0.154	0.048	0.154	0.048	0.048
JC	59	51059.432	50519.763	-25200.831	n/a	n/a	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083

NOTE.-- Models with the lowest BIC scores (Bayesian Information Criterion) are considered to describe the substitution pattern the best. For each model, AICc value (Akaike Information Criterion, correcte
are also presented [1]. Non-uniformity of evolutionary rates among sites may be modeled by using a discrete Gamma distribution (+*G*) with 5 rate categories and by assuming that a certain fraction of sites
and/or the estimated fraction of invariant sites are shown. Assumed or estimated values of transition/transversion bias (*R*) are shown for each model, as well. They are followed by nucleotide frequencies (*f*
r should be considered when evaluating them. For simplicity, sum of *r* values is made equal to 1 for each model. For estimating ML values, a tree topology was automatically computed. The analysis inv
positions containing gaps and missing data were eliminated. There were a total of 2241 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [2].

Abbreviations: GTR: General Time Reversible; HKY: Hasegawa-Kishino-Yano; TN93: Tamura-Nei; T92: Tamura 3-parameter; K2: Kimura 2-parameter; JC: Jukes-Cantor.

1. Nei M. and Kumar S. (**2000**). *Molecular Evolution and Phylogenetics.* Oxford University Press, New York.
2. Kumar S., Stecher G., and Tamura K. (**2015**). MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets.*Molecular Biology and Evolution (submitted).*

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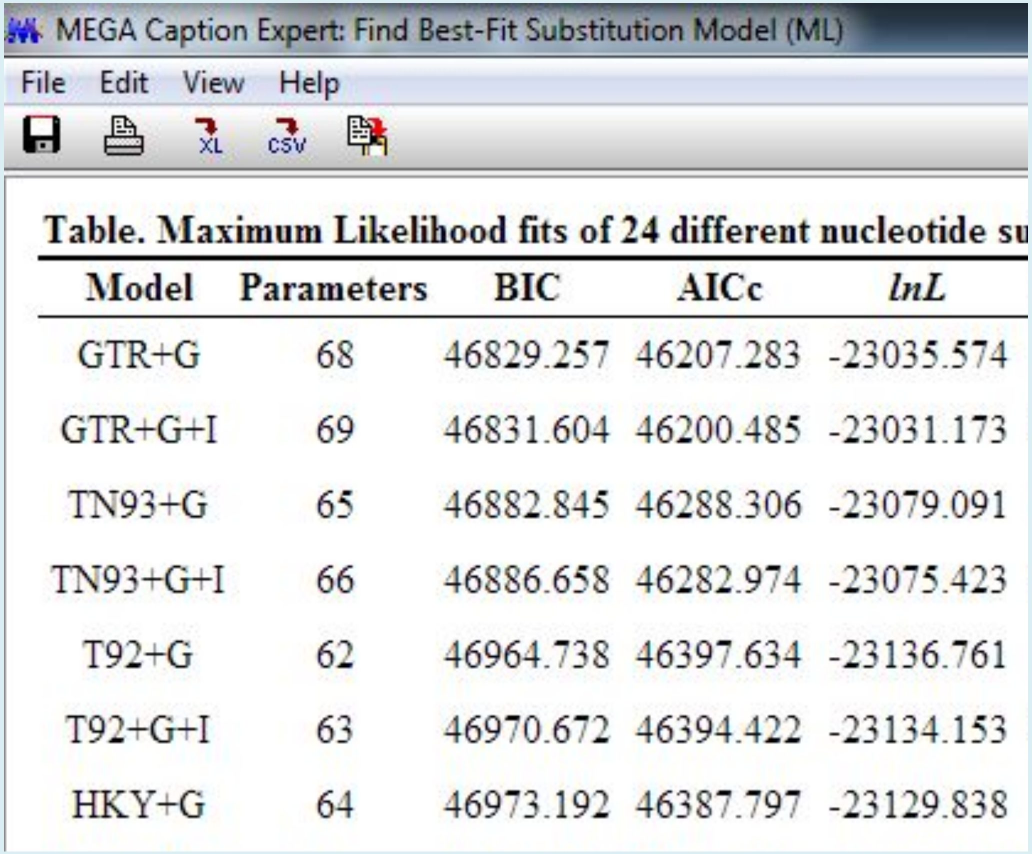

Table. Maximum Likelihood fits of 24 different nucleotide su

Model	Parameters	BIC	AICc	*lnL*
GTR+G	68	46829.257	46207.283	-23035.574
GTR+G+I	69	46831.604	46200.485	-23031.173
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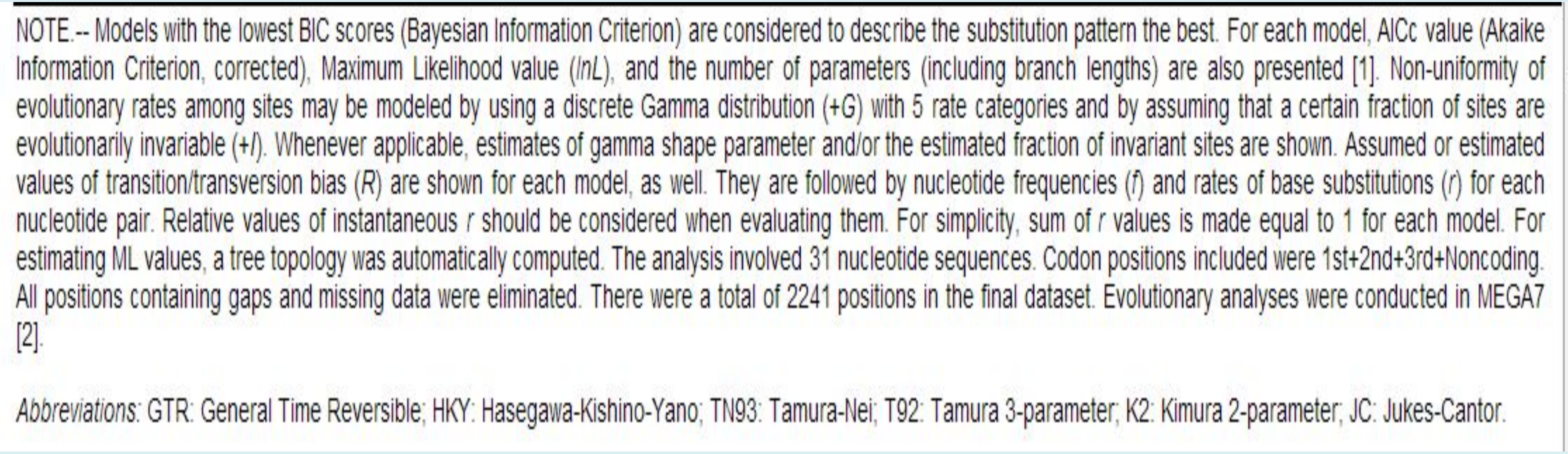
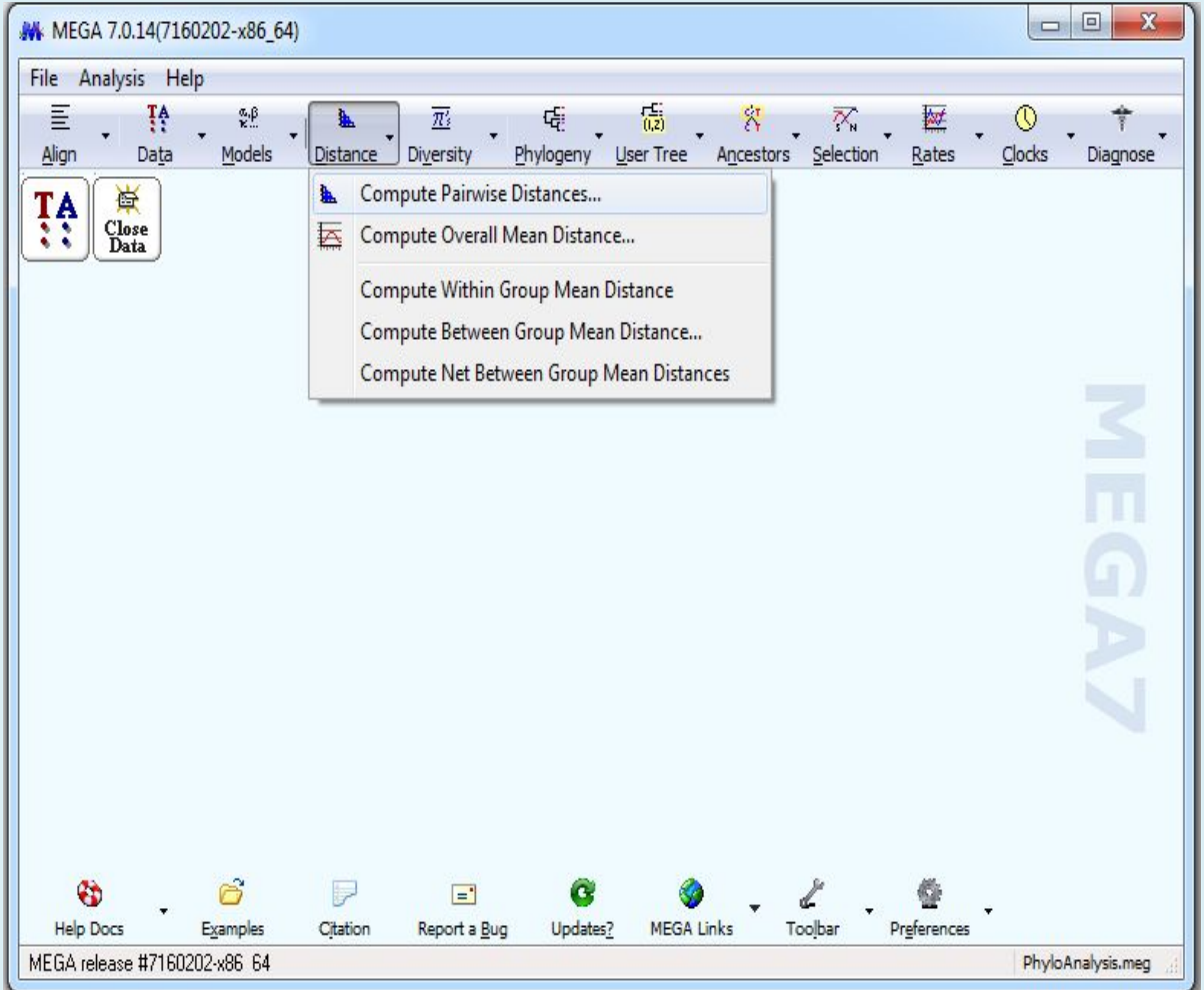


NOTE.-- Models with the lowest BIC scores (Bayesian Information Criterion) are considered to describe the substitution pattern the best. For each model, AICc value (Akaike Information Criterion, corrected), Maximum Likelihood value (*lnL*), and the number of parameters (including branch lengths) are also presented [1]. Non-uniformity of evolutionary rates among sites may be modeled by using a discrete Gamma distribution (+*G*) with 5 rate categories and by assuming that a certain fraction of sites are evolutionarily invariable (+*I*). Whenever applicable, estimates of gamma shape parameter and/or the estimated fraction of invariant sites are shown. Assumed or estimated values of transition/transversion bias (*R*) are shown for each model, as well. They are followed by nucleotide frequencies (*f*) and rates of base substitutions (*r*) for each nucleotide pair. Relative values of instantaneous *r* should be considered when evaluating them. For simplicity, sum of *r* values is made equal to 1 for each model. For estimating ML values, a tree topology was automatically computed. The analysis involved 31 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 2241 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [2].

Abbreviations: GTR: General Time Reversible; HKY: Hasegawa-Kishino-Yano; TN93: Tamura-Nei; T92: Tamura 3-parameter; K2: Kimura 2-parameter; JC: Jukes-Cantor.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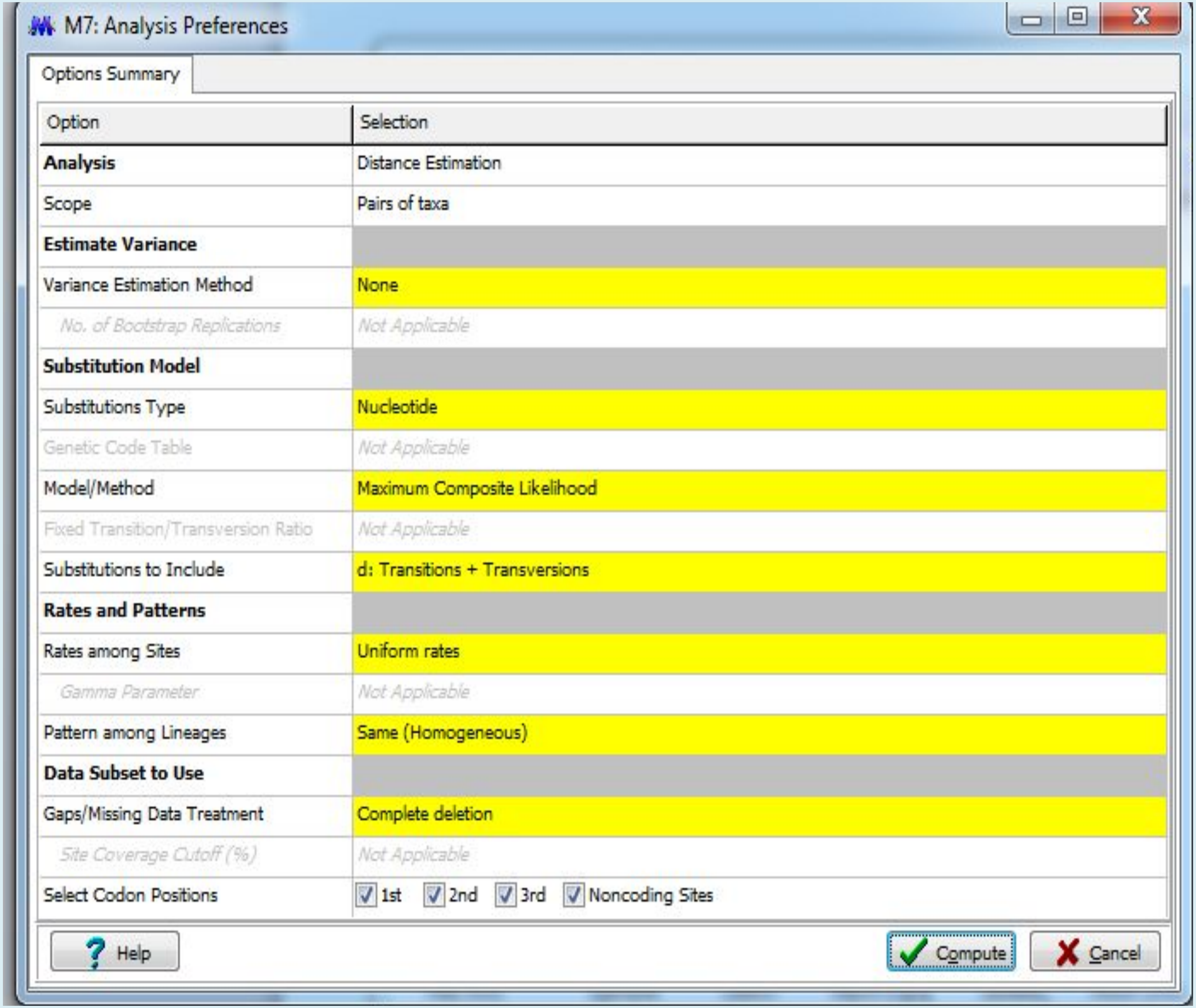

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Model/Method	Maximum Composite Likelihood
Fixed Transition/Transversion Ratio	*Not Applicable*
Substitutions to Include	d: Transitions + Transversions
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Rates among Sites	Uniform rates
Gamma Parameter	*Not Applicable*
Pattern among Lineages	Same (Homogeneous)
Data Subset to Use	
Gaps/Missing Data Treatment	Complete deletion
Site Coverage Cutoff (%)	*Not Applicable*
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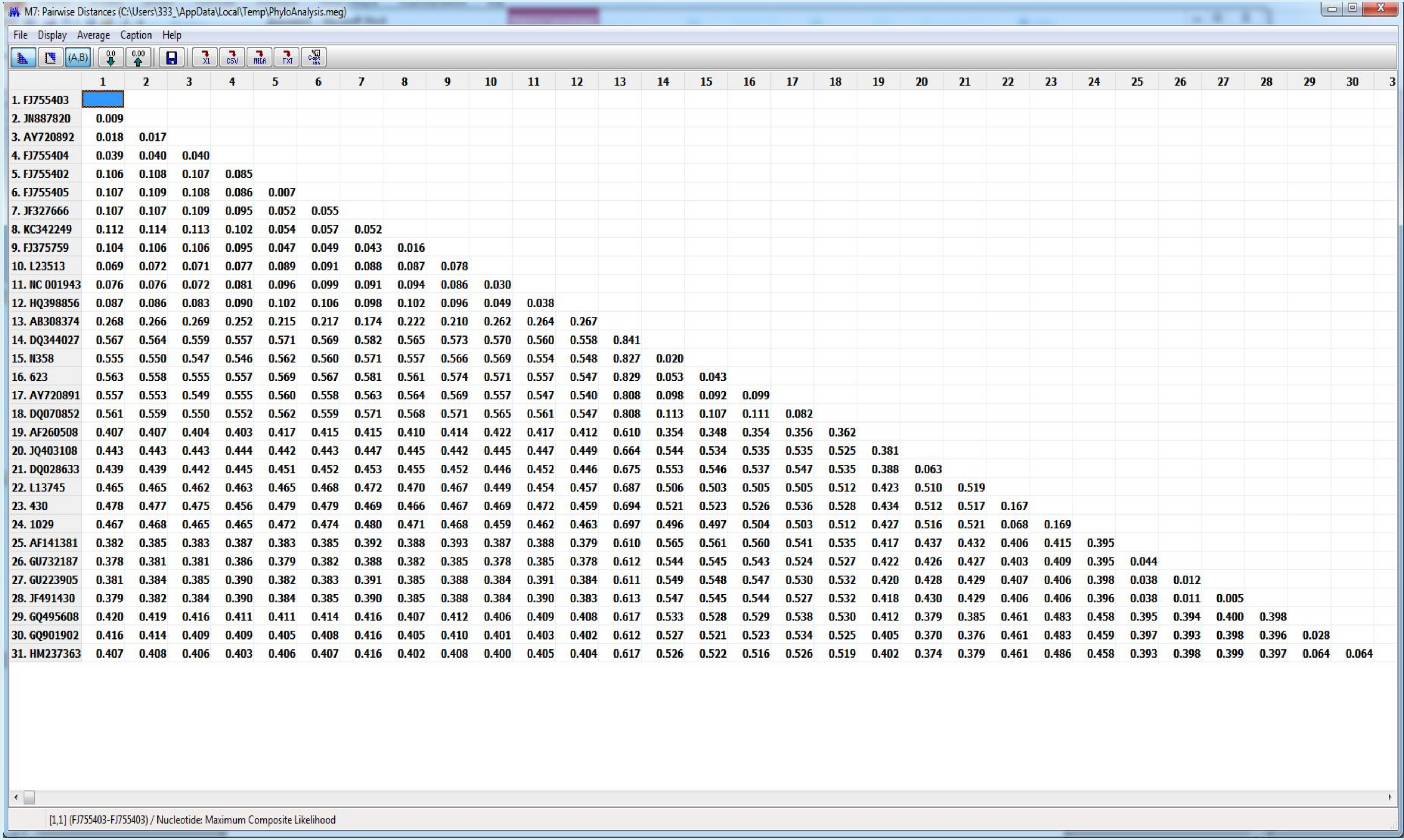

M7: Pairwise Distances (C:\Users\333_\AppData\Local\Temp\PhyloAnalysis.meg)

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1. FJ755403																															
2. JN887820	0.009																														
3. AY720892	0.018	0.017																													
4. FJ755404	0.039	0.040	0.040																												
5. FJ755402	0.106	0.108	0.107	0.085																											
6. FJ755405	0.107	0.109	0.108	0.086	0.007																										
7. JF327666	0.107	0.107	0.109	0.095	0.052	0.055																									
8. KC342249	0.112	0.114	0.113	0.102	0.054	0.057	0.052																								
9. FJ375759	0.104	0.106	0.106	0.095	0.047	0.049	0.043	0.016																							
10. L23513	0.069	0.072	0.071	0.077	0.089	0.091	0.088	0.087	0.078																						
11. NC 001943	0.076	0.076	0.072	0.081	0.096	0.099	0.091	0.094	0.086	0.030																					
12. HQ398856	0.087	0.086	0.083	0.090	0.102	0.106	0.098	0.102	0.096	0.049	0.038																				
13. AB308374	0.268	0.266	0.269	0.252	0.215	0.217	0.174	0.222	0.210	0.262	0.264	0.267																			
14. DQ344027	0.567	0.564	0.559	0.557	0.571	0.569	0.582	0.565	0.573	0.570	0.560	0.558	0.841																		
15. N358	0.555	0.550	0.547	0.546	0.562	0.560	0.571	0.557	0.566	0.569	0.554	0.548	0.827	0.020																	
16. 623	0.563	0.558	0.555	0.557	0.569	0.567	0.581	0.561	0.574	0.571	0.557	0.547	0.829	0.053	0.043																
17. AY720891	0.557	0.553	0.549	0.555	0.560	0.558	0.563	0.564	0.569	0.557	0.547	0.540	0.808	0.098	0.092	0.099															
18. DQ070852	0.561	0.559	0.550	0.552	0.562	0.559	0.571	0.568	0.571	0.565	0.561	0.547	0.808	0.113	0.107	0.111	0.082														
19. AF260508	0.407	0.407	0.404	0.403	0.417	0.415	0.415	0.410	0.414	0.422	0.417	0.412	0.610	0.354	0.348	0.354	0.356	0.362													
20. JQ403108	0.443	0.443	0.443	0.444	0.442	0.443	0.447	0.445	0.442	0.445	0.447	0.449	0.664	0.544	0.534	0.535	0.535	0.525	0.381												
21. DQ028633	0.439	0.439	0.442	0.445	0.451	0.452	0.453	0.455	0.452	0.446	0.452	0.446	0.675	0.553	0.546	0.537	0.547	0.535	0.388	0.063											
22. L13745	0.465	0.465	0.462	0.463	0.465	0.468	0.472	0.470	0.467	0.449	0.454	0.457	0.687	0.506	0.503	0.505	0.505	0.512	0.423	0.510	0.519										
23. 430	0.478	0.477	0.475	0.456	0.479	0.479	0.469	0.466	0.467	0.469	0.472	0.459	0.694	0.521	0.523	0.526	0.536	0.528	0.434	0.512	0.517	0.167									
24. 1029	0.467	0.468	0.465	0.465	0.472	0.474	0.480	0.471	0.468	0.459	0.462	0.463	0.697	0.496	0.497	0.504	0.503	0.512	0.427	0.516	0.521	0.068	0.169								
25. AF141381	0.382	0.385	0.383	0.387	0.383	0.385	0.392	0.388	0.393	0.387	0.388	0.379	0.610	0.565	0.561	0.560	0.541	0.535	0.417	0.437	0.432	0.406	0.415	0.395							
26. GU732187	0.378	0.381	0.381	0.386	0.379	0.382	0.388	0.382	0.385	0.378	0.385	0.378	0.612	0.544	0.545	0.543	0.524	0.527	0.422	0.426	0.427	0.403	0.409	0.395	0.044						
27. GU223905	0.381	0.384	0.385	0.390	0.382	0.383	0.391	0.385	0.388	0.384	0.391	0.384	0.611	0.549	0.548	0.547	0.530	0.532	0.420	0.428	0.429	0.407	0.406	0.398	0.038	0.012					
28. JF491430	0.379	0.382	0.384	0.390	0.384	0.385	0.390	0.385	0.388	0.384	0.390	0.383	0.613	0.547	0.545	0.544	0.527	0.532	0.418	0.430	0.429	0.406	0.406	0.396	0.038	0.011	0.005				
29. GQ495608	0.420	0.419	0.416	0.411	0.411	0.414	0.416	0.407	0.412	0.406	0.409	0.408	0.617	0.533	0.528	0.529	0.538	0.530	0.412	0.379	0.385	0.461	0.483	0.458	0.395	0.394	0.400	0.398			
30. GQ901902	0.416	0.414	0.409	0.409	0.405	0.408	0.416	0.405	0.410	0.401	0.403	0.402	0.612	0.527	0.521	0.523	0.534	0.525	0.405	0.370	0.376	0.461	0.483	0.459	0.397	0.393	0.398	0.396	0.028		
31. HM237363	0.407	0.408	0.406	0.403	0.406	0.407	0.416	0.402	0.408	0.400	0.405	0.404	0.617	0.526	0.522	0.516	0.526	0.519	0.402	0.374	0.379	0.461	0.486	0.458	0.393	0.398	0.399	0.397	0.064	0.064	

[1,1] (FJ755403-FJ755403) / Nucleotide: Maximum Composite Likelihood


MEGA 7.0.14(7160202 x86_64)
File
Analysis
Help
Align
Data
Models
Distance
Diversity
Phylogeny
User Tree
Ancestors
Selection
Open A File/Session ... Ctrl+O
Explore Active Data F4
Export Data...
Save Data Session to File...
Select Genetic Code Table...
Select Genes and Domains...
Select Taxa and Groups...
Help Docs
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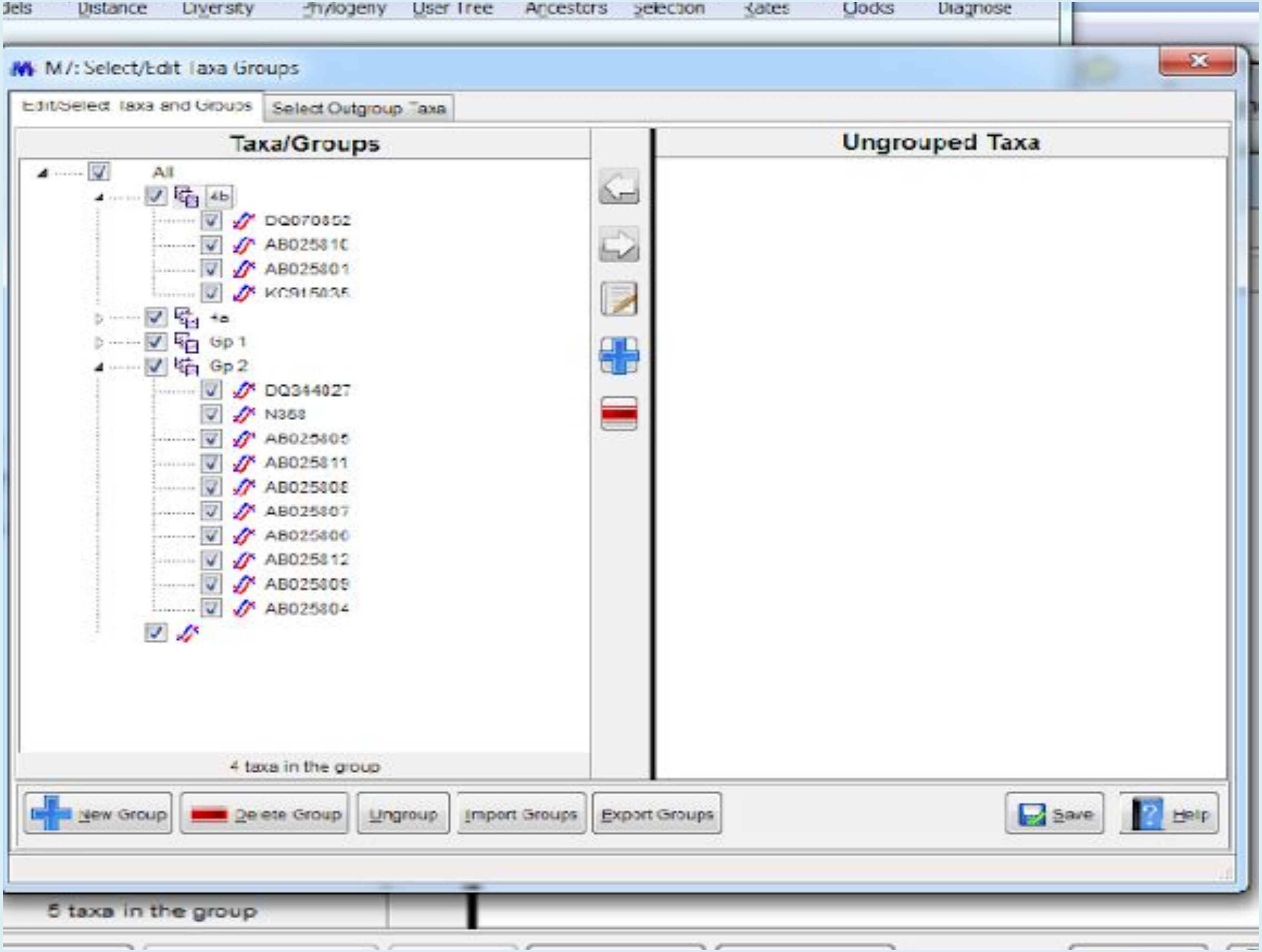
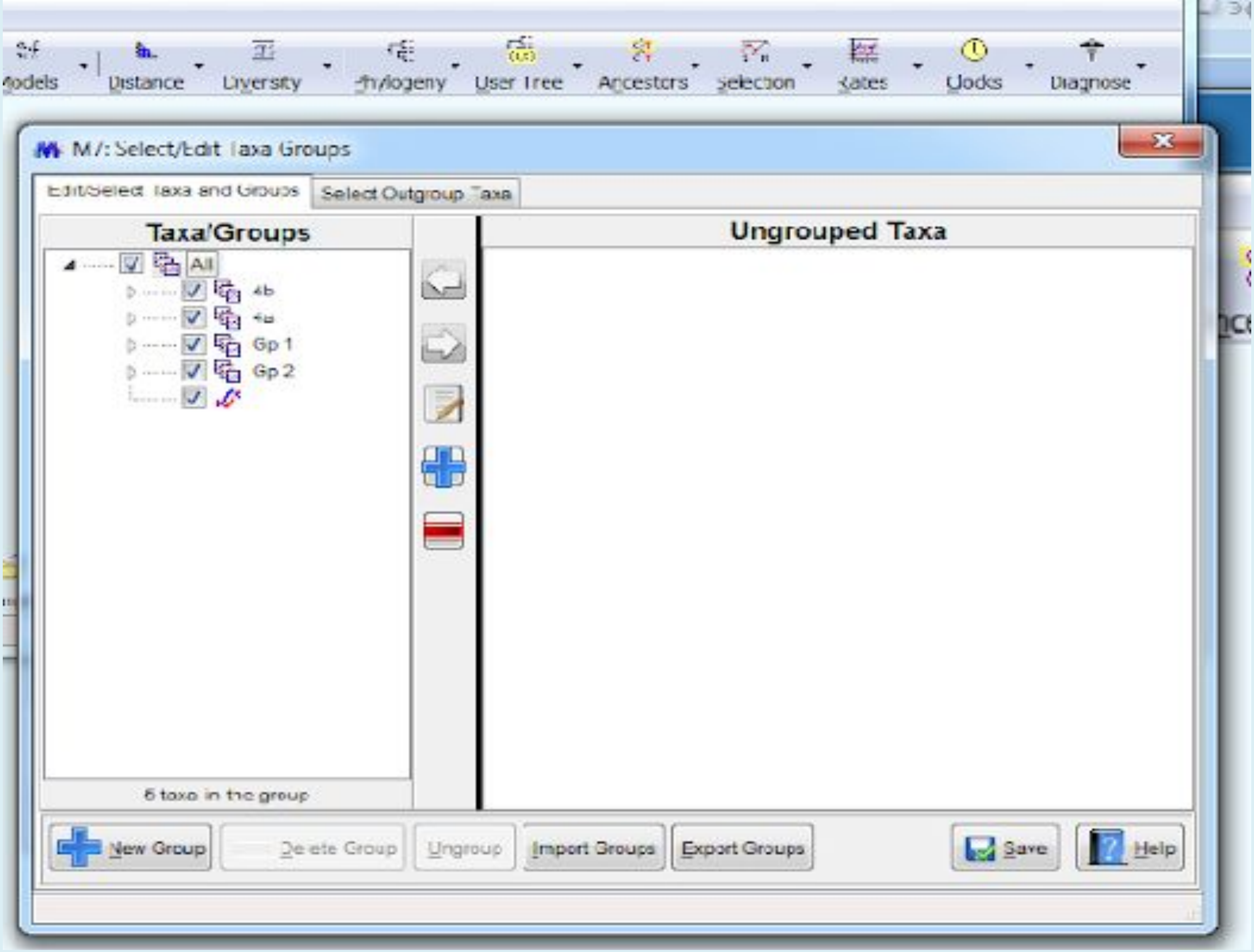
Toolbar



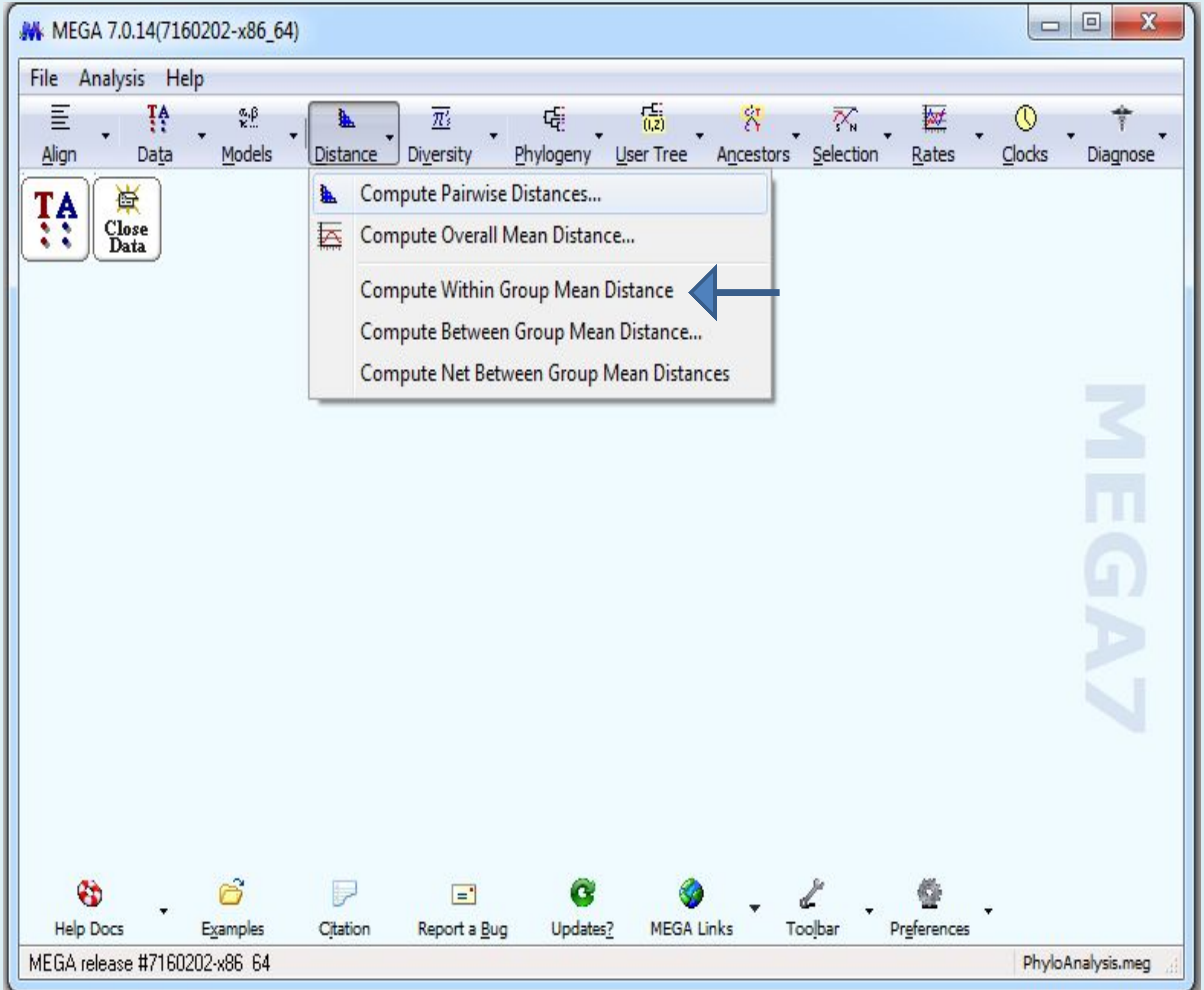
- ☑ All
  - ☑ 4b
    - ☑ DQ070852
    - ☑ AB025810
    - ☑ AB025801
    - ☑ KC915835
  - ☑ 4a
  - ☑ Gp 1
  - ☑ Gp 2
    - ☑ DQ344027
    - ☑ N368
    - ☑ AB025805
    - ☑ AB025811
    - ☑ AB025808
    - ☑ AB025807
    - ☑ AB025806
    - ☑ AB025812
    - ☑ AB025809
    - ☑ AB025804
  - ☑

4 taxa in the group

5 taxa in the group



6 taxa in the group


MEGA 7.0.14(7160202-x86_64)
File
Analysis
Help
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Models
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Rates
Clocks
Diagnose
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Close Data
Compute Pairwise Distances...
Compute Overall Mean Distance...
Compute Within Group Mean Distance
Compute Between Group Mean Distance...
Compute Net Between Group Mean Distances
MEGA7
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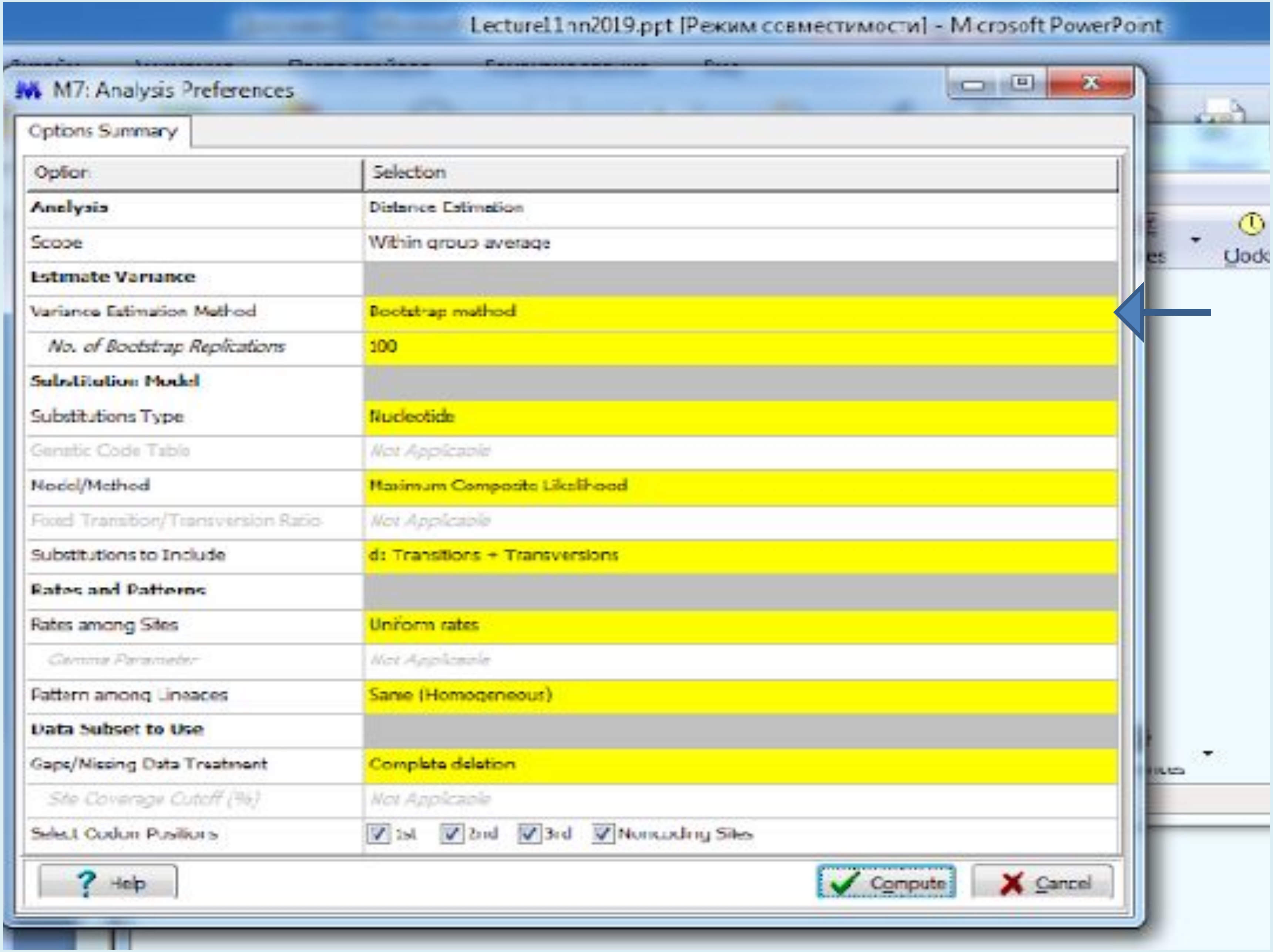
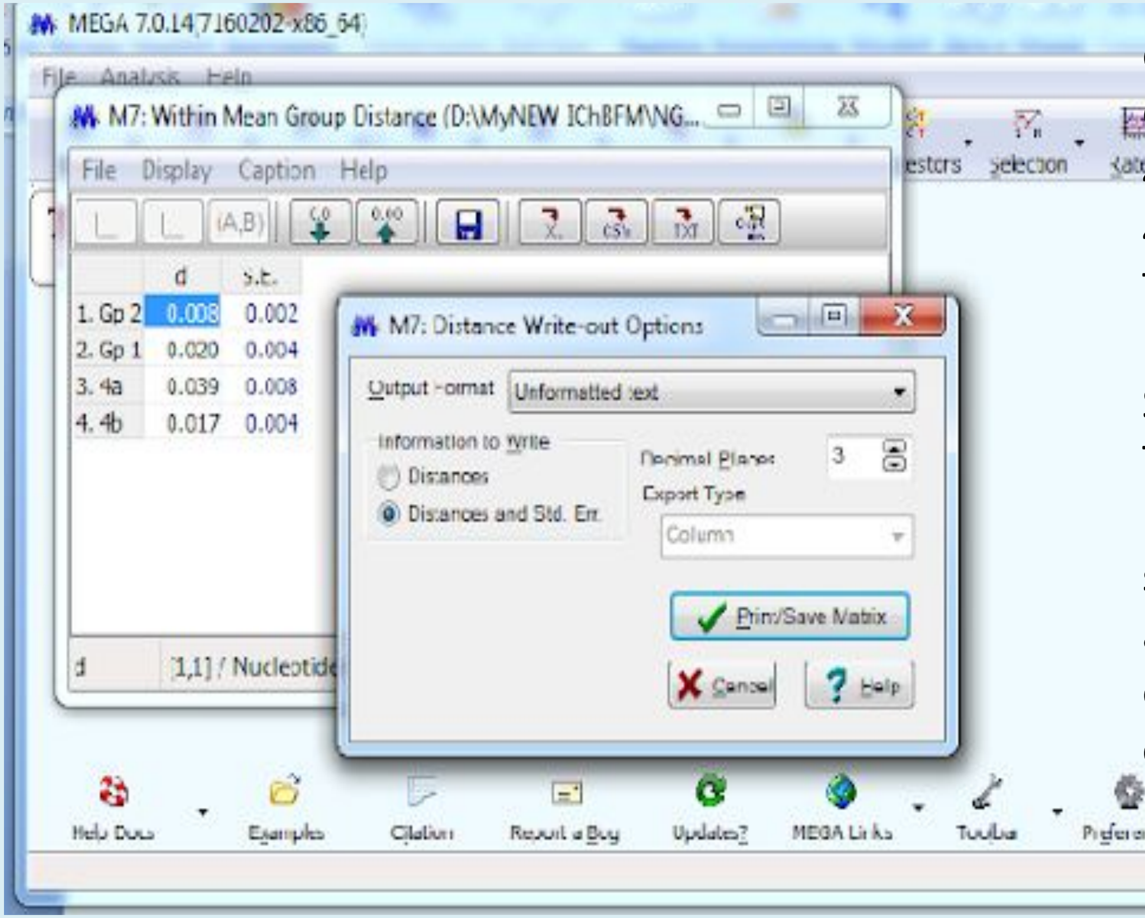
MEGA release #7160202-x86_64
PhyloAnalysis.meg



Option	Selection
Analysis	Distance Estimation
Scope	Within group average
Estimate Variance	
Variance Estimation Method	Bootstrap method
No. of Bootstrap Replications	100
Substitution Model	
Substitutions Type	Nucleotide
Genetic Code Table	*Not Applicable*
Model/Method	Maximum Composite Likelihood
Fixed Transition/Transversion Ratio	*Not Applicable*
Substitutions to Include	d: Transitions + Transversions
Rates and Patterns	
Rates among Sites	Uniform rates
Gamma Parameter	*Not Applicable*
Pattern among Lineages	Same (Homogeneous)
Data Subset to Use	
Gaps/Missing Data Treatment	Complete deletion
Site Coverage Cutoff (%)	*Not Applicable*
Select Codon Positions	☑ 1st ☑ 2nd ☑ 3rd ☑ Noncoding Sites



	d	S.E.
1. Gp 2	0.008	0.002
2. Gp 1	0.020	0.004
3. 4a	0.039	0.008
4. 4b	0.017	0.004

d [1,1] / Nucleotide

Output Format: Unformatted text

Information to Write
○ Distances
● Distances and Std. Err

Decimal Places: 3

Export Type: Column

Gp 2	0.008	0.002
Gp 1	0.020	0.004
4a	0.039	0.008
4b	0.017	0.004

Table. Estimates of Average Evolutionary Divergence over Sequence Pairs within Groups

The number of base substitutions per site from averaging over all sequence pairs within each group are shown. Standard error estimate(s) are shown in the last column. Analyses were conducted using the Maximum Composite Likelihood model [1]. The analysis involved 23 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 2306 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [2].

```
[1] #Gp_2
[2] #Gp_1
[3] #4a
[4] #4b

[           1         2         3         4 ]
[1]              [ 0.008 ][ 0.017 ][ 0.019 ]
[2]     0.042             [ 0.018 ][ 0.020 ]
[3]     0.091     0.099            [ 0.015 ]
[4]     0.104     0.111     0.082
```

Table. Estimates of Evolutionary Divergence over Sequence Pairs between Groups

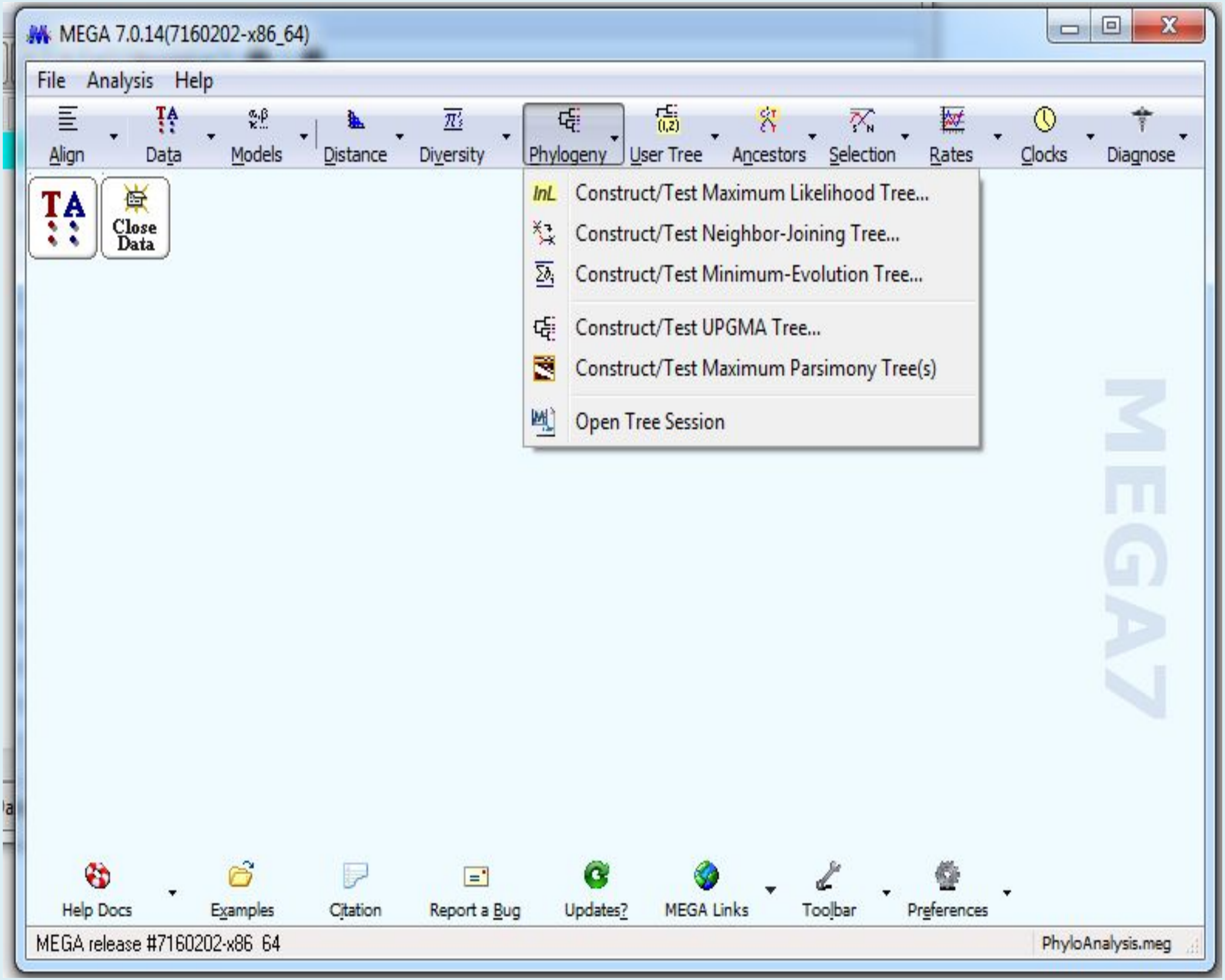
The number of base substitutions per site from averaging over all sequence pairs between groups are shown. Standard error estimate(s) are shown above the diagonal. Analyses were conducted using the Maximum Composite Likelihood model [1]. The analysis involved 23 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 2306 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [2].

Таблица 1. Матрица средних значений генетических расстояний (число нуклеотидных замен на сайт) между генотипами HAstV. В квадратных скобках приведено стандартное отклонение, рассчитанное по 1000 реплик.

	1	2	3	4	5	6	8
[1]							
[2]	0.259 [0.008]						
[3]	0.228 [0.007]	0.241 [0.007]					
[4]	0.236 [0.007]	0.271 [0.007]	0.269 [0.009]				
[5]	0.232 [0.006]	0.276 [0.008]	0.236 [0.008]	0.251 [0.007]			
[6]	0.329 [0.010]	0.335 [0.009]	0.318 [0.010]	0.362 [0.010]	0.309 [0.010]		
[8]	0.201 [0.007]	0.241 [0.008]	0.230 [0.009]	0.164 [0.005]	0.207 [0.006]	0.322 [0.009]	

Таблица 2. Средние значения генетических расстояний (число нуклеотидных замен на сайт) внутри генотипов HAstV. В квадратных скобках приведено стандартное отклонение, рассчитанное по 1000 реплик.

HastV-1	0.085 [0.002]
HastV-2	0.174 [0.004]
HastV-3	0.025 [0.001]
HastV-4	0.085 [0.003]
HastV-5	0.081 [0.004]
HAstV-6	0.055 [0.002]


MEGA 7.0.14(7160202-x86_64)
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Diversity
Phylogeny
User Tree
Ancestors
Selection
Rates
Clocks
Diagnose
TA
Close Data
Construct/Test Maximum Likelihood Tree...
Construct/Test Neighbor-Joining Tree...
Construct/Test Minimum-Evolution Tree...
Construct/Test UPGMA Tree...
Construct/Test Maximum Parsimony Tree(s)
Open Tree Session
MEGA7
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Examples
Citation
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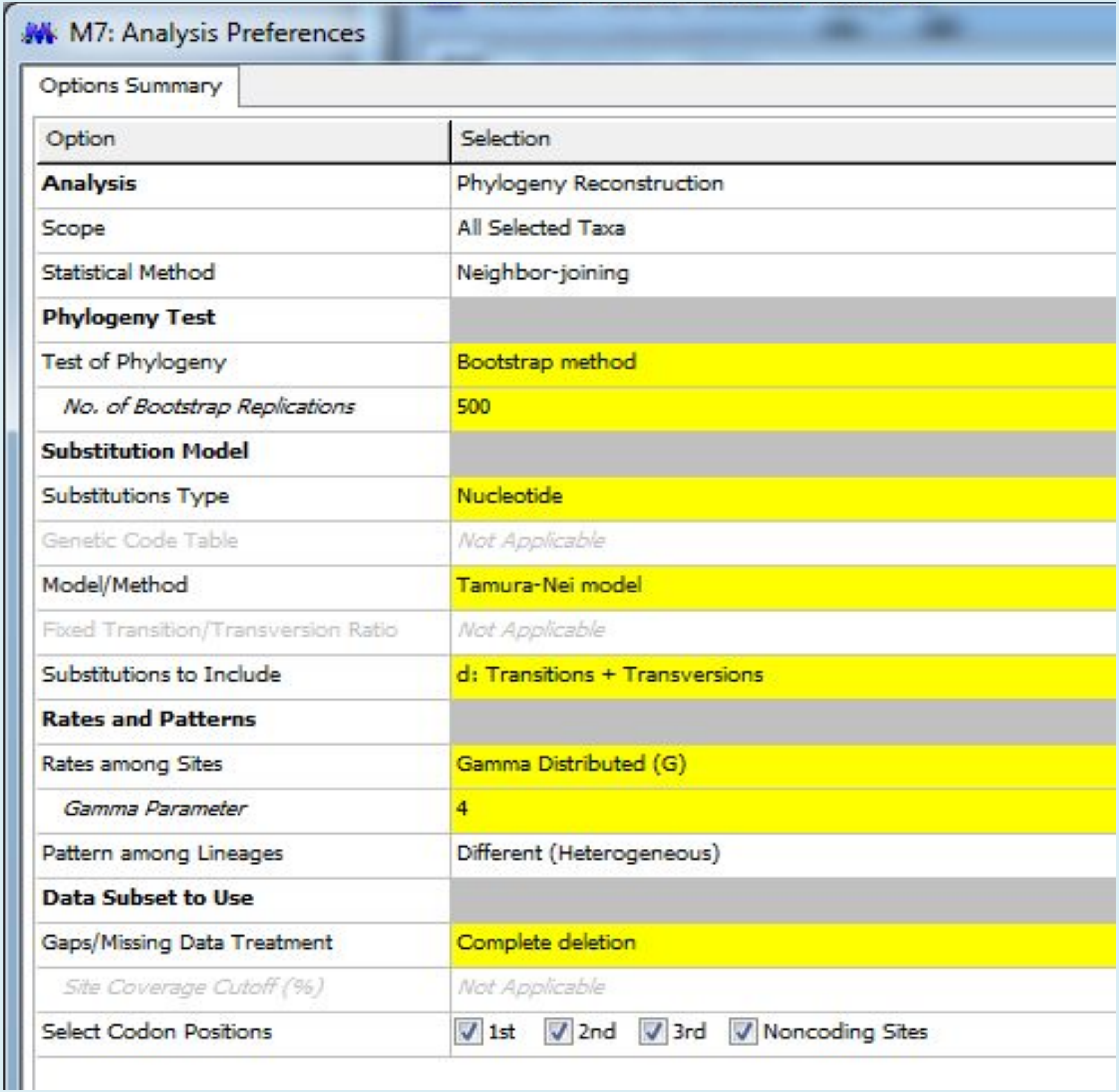
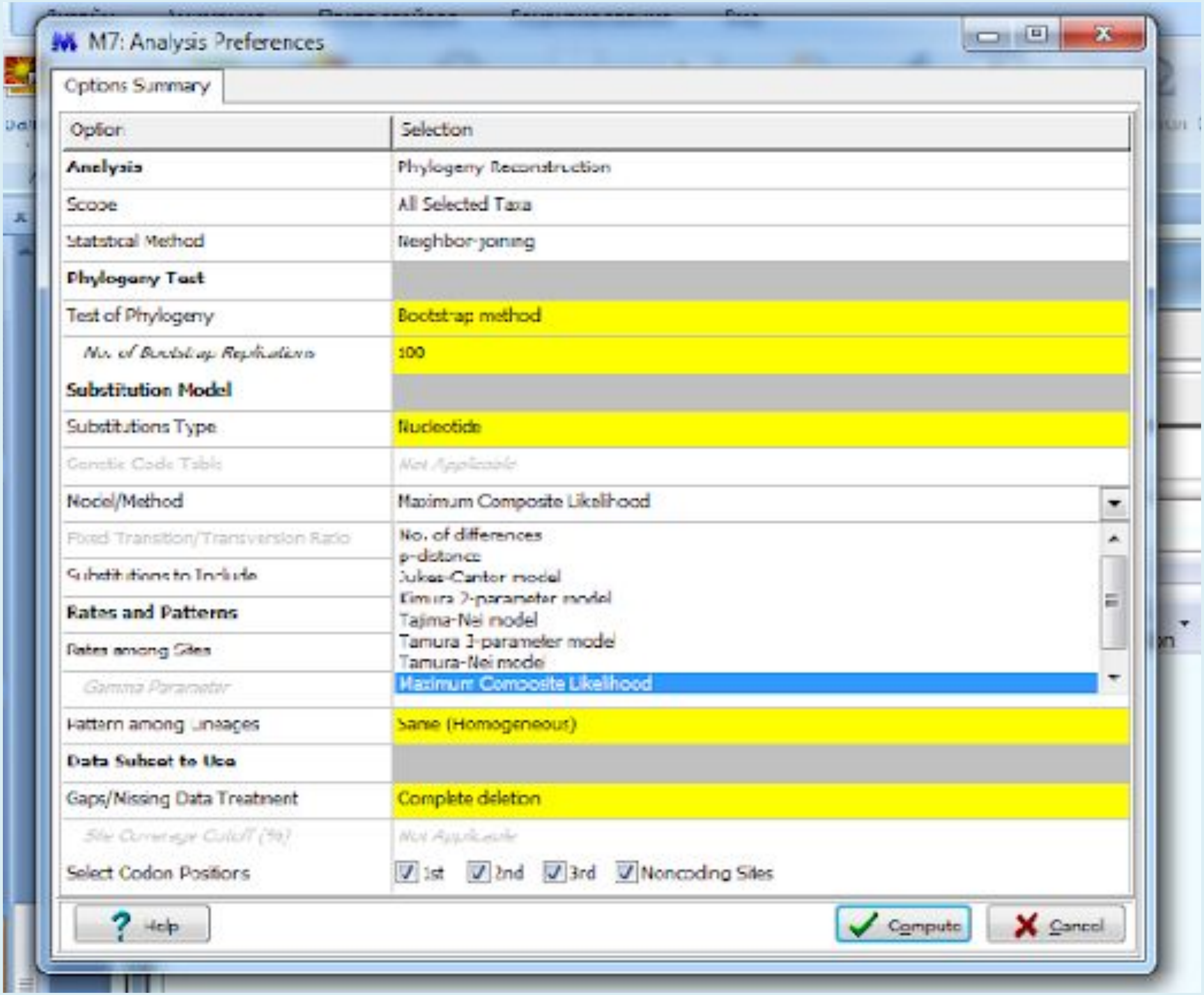
MEGA release #7160202-x86_64
PhyloAnalysis.meg



Option	Selection
Analysis	Phylogeny Reconstruction
Scope	All Selected Taxa
Statistical Method	Neighbor-joining
Phylogeny Test	
Test of Phylogeny	Bootstrap method
No. of Bootstrap Replications	500
Substitution Model	
Substitutions Type	Nucleotide
Genetic Code Table	*Not Applicable*
Model/Method	Tamura-Nei model
Fixed Transition/Transversion Ratio	*Not Applicable*
Substitutions to Include	d: Transitions + Transversions
Rates and Patterns	
Rates among Sites	Gamma Distributed (G)
Gamma Parameter	4
Pattern among Lineages	Different (Heterogeneous)
Data Subset to Use	
Gaps/Missing Data Treatment	Complete deletion
Site Coverage Cutoff (%)	*Not Applicable*
Select Codon Positions	☑ 1st ☑ 2nd ☑ 3rd ☑ Noncoding Sites



Option	Selection
Analysis	Phylogeny Reconstruction
Scope	All Selected Taxa
Statistical Method	Neighbor-joining
Phylogeny Test	
Test of Phylogeny	Bootstrap method
No. of Bootstrap Replications	100
Substitution Model	
Substitutions Type	Nucleotide
Genetic Code Table	*Not Applicable*
Model/Method	Maximum Composite Likelihood
Fixed Transition/Transversion Ratio	No. of differences p-distance
Substitutions to Include	Jukes-Cantor model
Rates and Patterns	Kimura 2-parameter model Tajima-Nei model
Rates among Sites	Tamura 3-parameter model Tamura-Nei model
Gamma Parameter	Maximum Composite Likelihood
Pattern among Lineages	Same (Homogeneous)
Data Subset to Use	
Gaps/Missing Data Treatment	Complete deletion
Site Coverage Cutoff (%)	*Not Applicable*
Select Codon Positions	☑ 1st ☑ 2nd ☑ 3rd ☑ Noncoding Sites

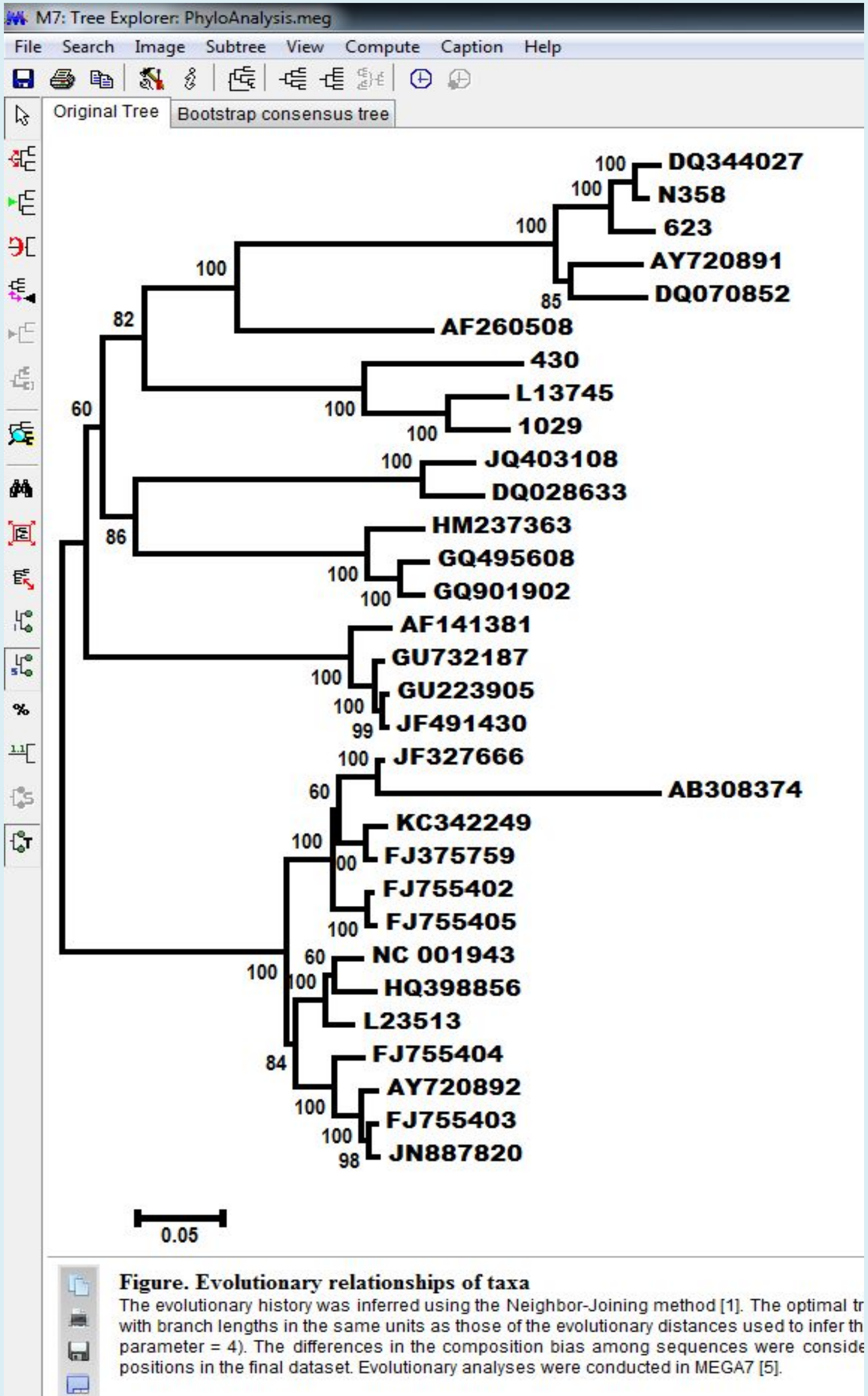


Figure. Evolutionary relationships of taxa
The evolutionary history was inferred using the Neighbor-Joining method [1]. The optimal tr
with branch lengths in the same units as those of the evolutionary distances used to infer th
parameter = 4). The differences in the composition bias among sequences were conside
positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [5].

Figure. Evolutionary relationships of taxa
The evolutionary history was inferred using the Neighbor-Joining method [1]. The optimal tree with the sum of branch length = 2.17322002 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches [2]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Tamura-Nei method [3] and are in the units of the number of base substitutions per site. The rate variation among sites was modeled with a gamma distribution (shape parameter = 4). The differences in the composition bias among sequences were considered in evolutionary comparisons [4]. The analysis involved 31 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 2241 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [5].

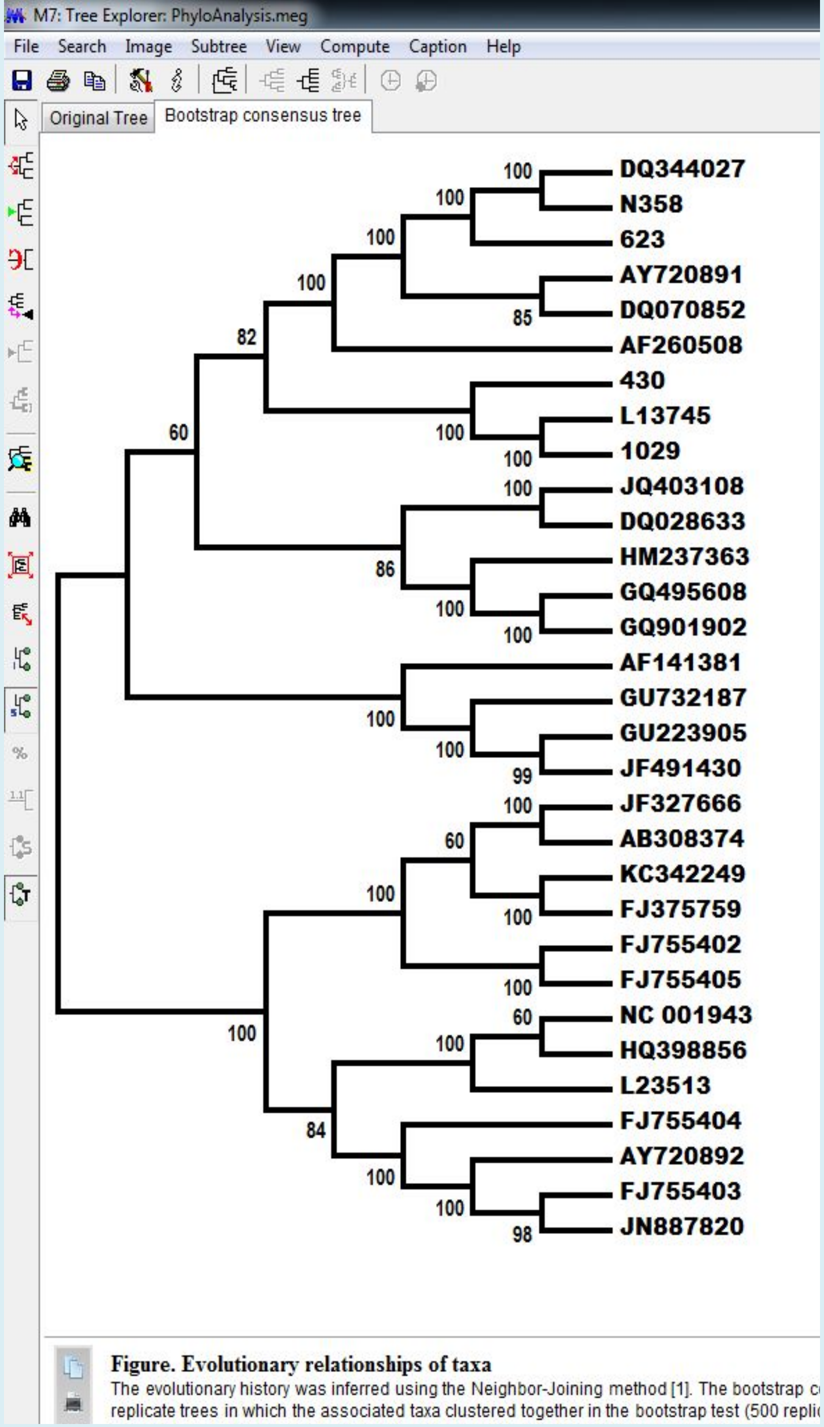
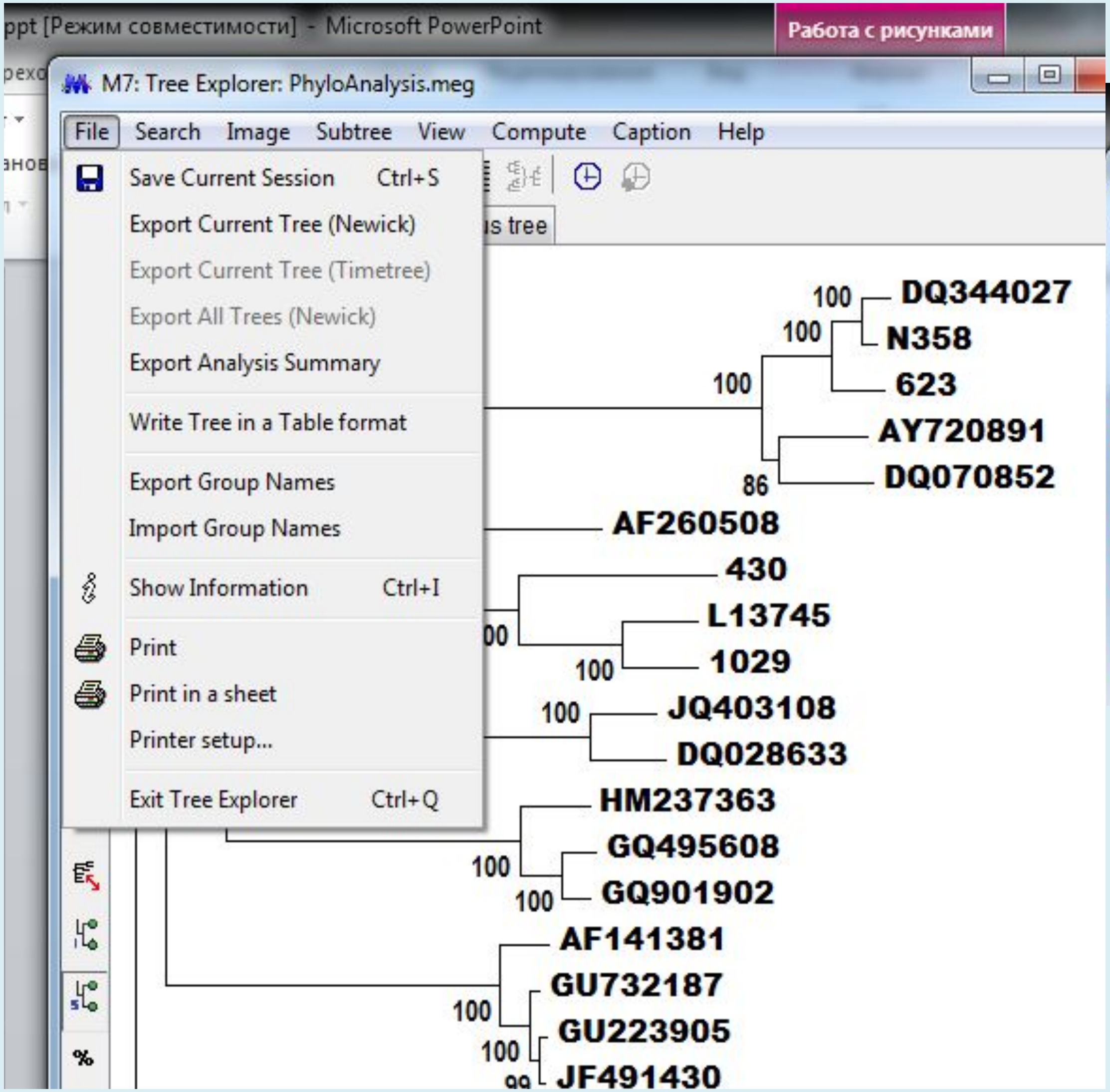


Figure. Evolutionary relationships of taxa

The evolutionary history was inferred using the Neighbor-Joining method [1]. The bootstrap c
replicate trees in which the associated taxa clustered together in the bootstrap test (500 repli


ppt [Режим совместимости] - Microsoft PowerPoint
Работа с рисунками
M7: Tree Explorer: PhyloAnalysis.meg
File
Search
Image
Subtree
View
Compute
Caption
Help
Save Current Session Ctrl+S
Export Current Tree (Newick)
Export Current Tree (Timetree)
Export All Trees (Newick)
Export Analysis Summary
Write Tree in a Table format
Export Group Names
Import Group Names
Show Information Ctrl+I
Print
Print in a sheet
Printer setup...
Exit Tree Explorer Ctrl+Q
DQ344027
N358
623
AY720891
DQ070852
AF260508
430
L13745
1029
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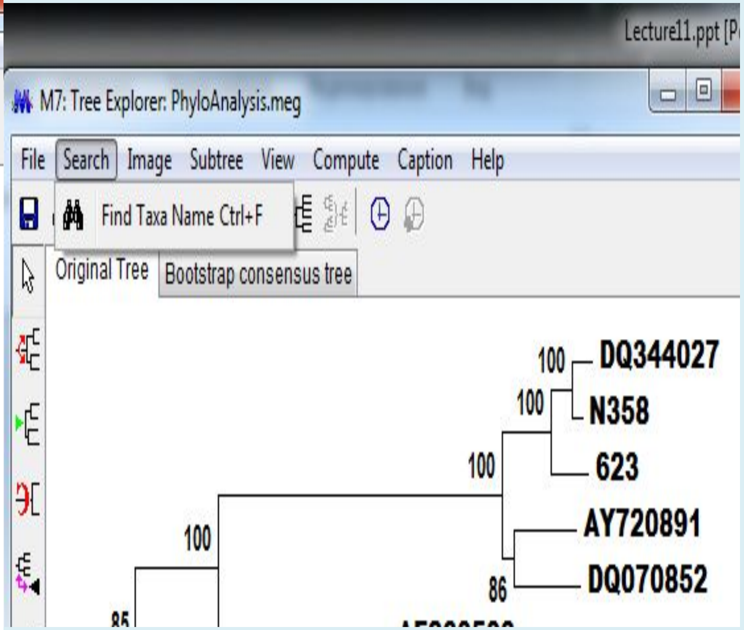
DQ028633
HM237363
GQ495608
GQ901902
AF141381
GU732187
GU223905
JF491430
100
86


Lecture11.ppt
M7: Tree Explorer: PhyloAnalysis.meg
File
Search
Image
Subtree
View
Compute
Caption
Help
Find Taxa Name Ctrl+F
Original Tree
Bootstrap consensus tree
DQ344027
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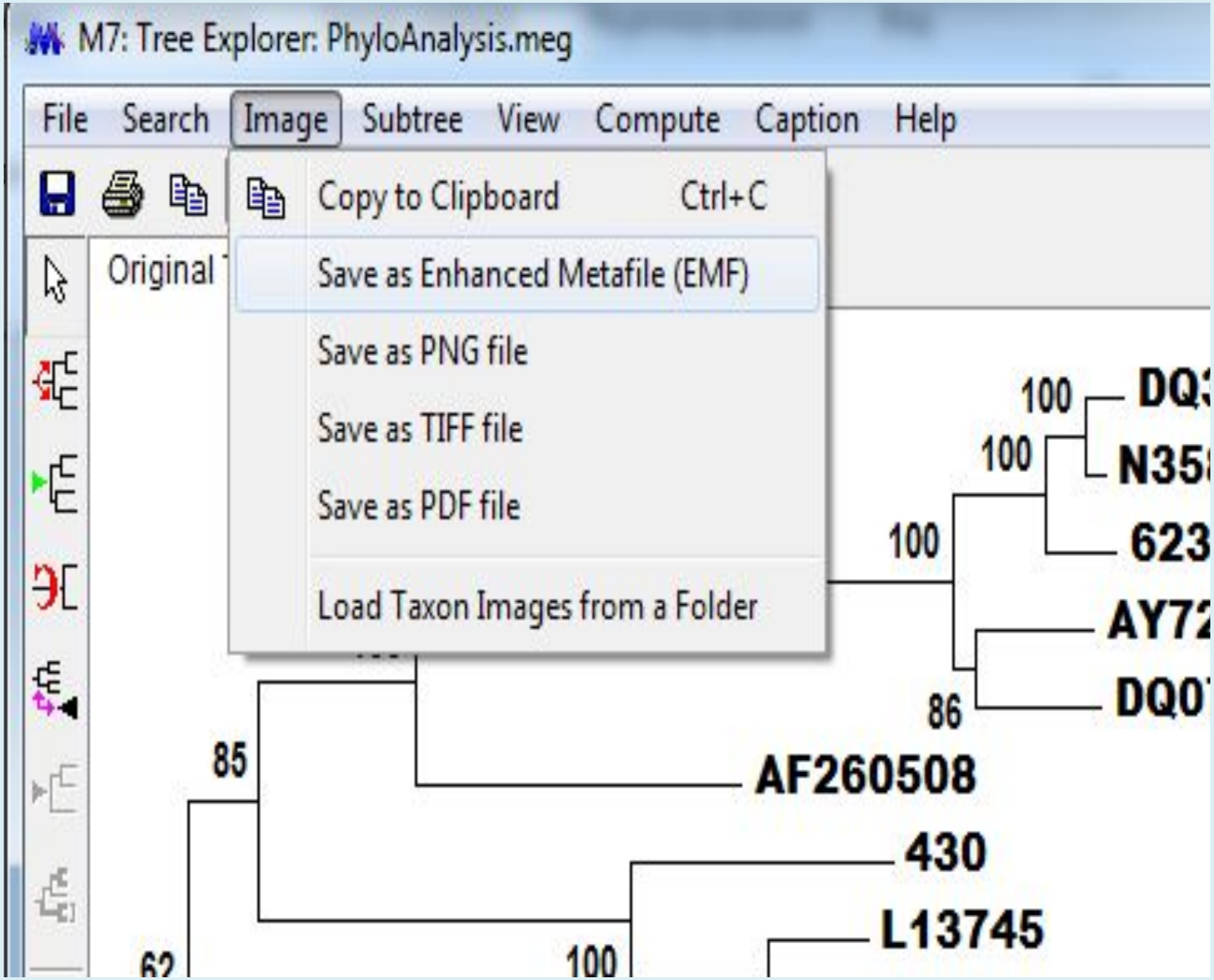
M7: Tree Explorer: PhyloAnalysis.meg
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Save as TIFF file
Save as PDF file
Load Taxon Images from a Folder
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AY72
DQ0
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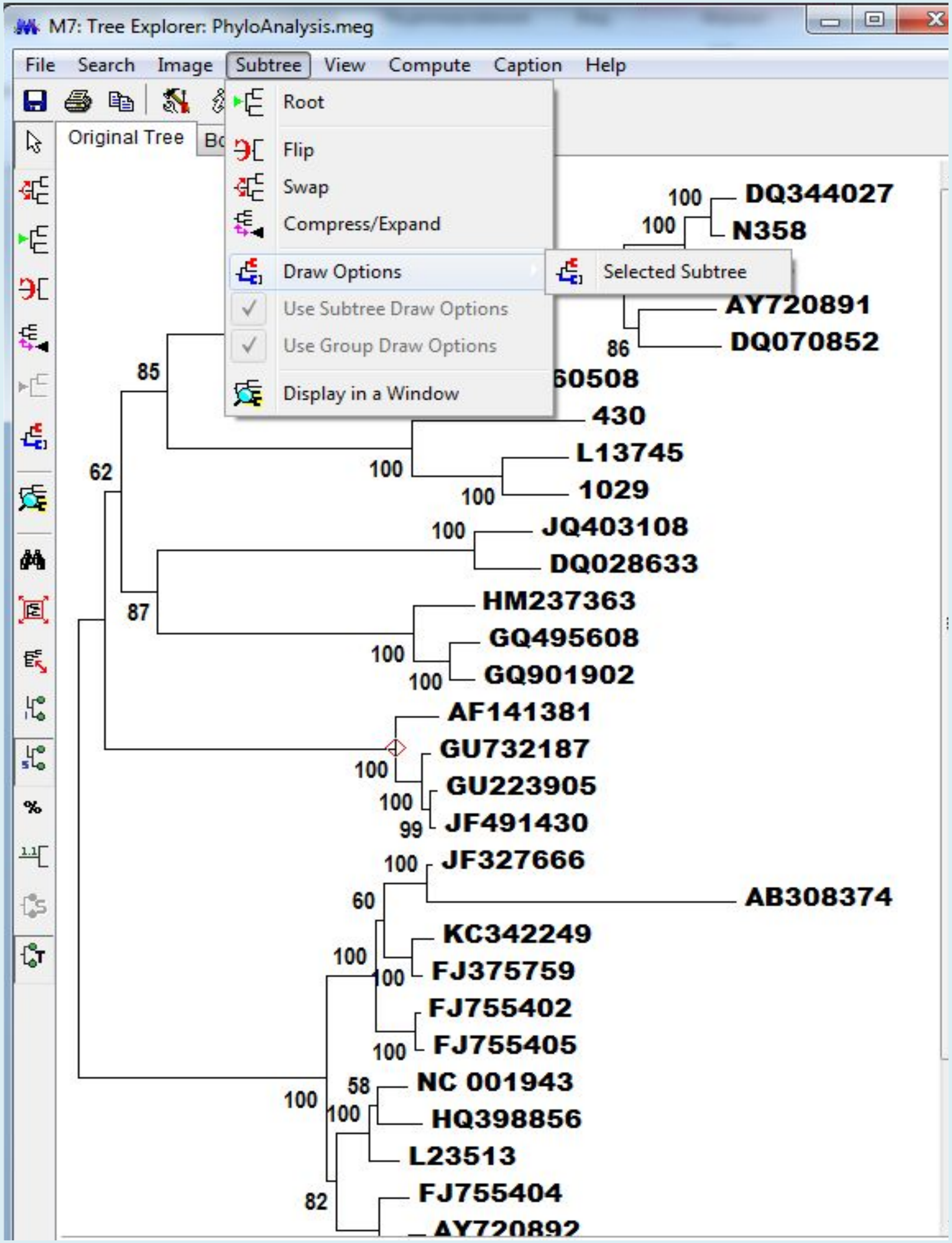
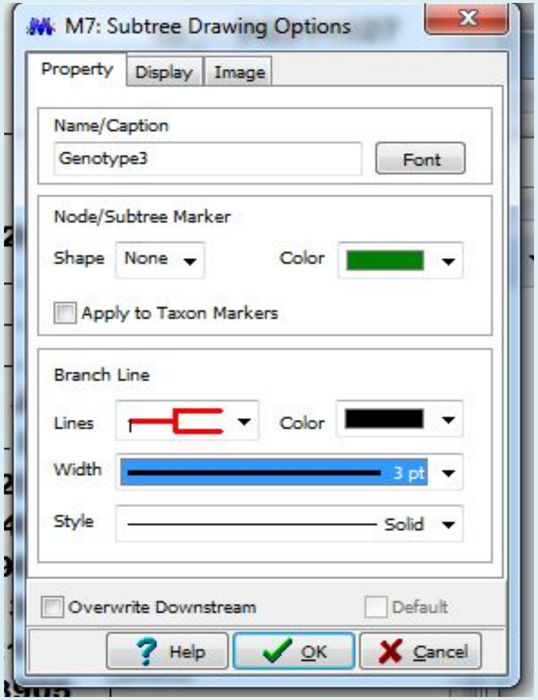
430
L13745





Name/Caption: Genotype3

Node/Subtree Marker

Shape: None
Color: 🟩

☐ Apply to Taxon Markers

Branch Line

Lines
Color: ■
Width: 3 pt
Style: Solid

☐ Overwrite Downstream
☐ Default

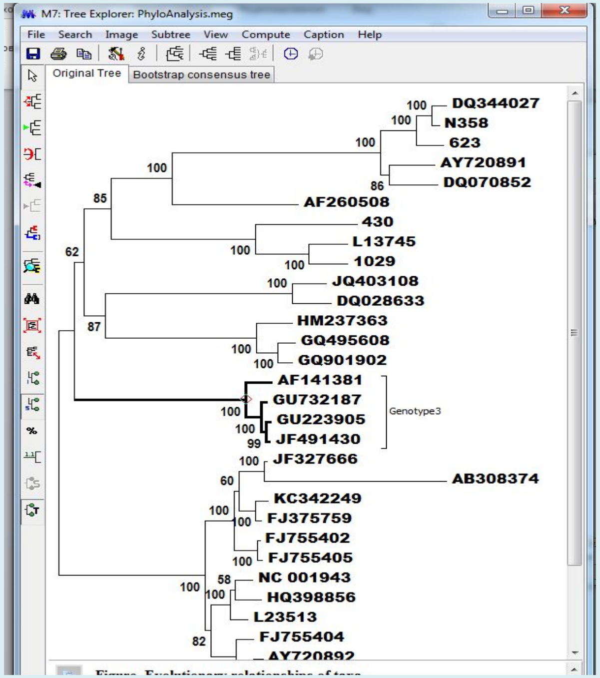
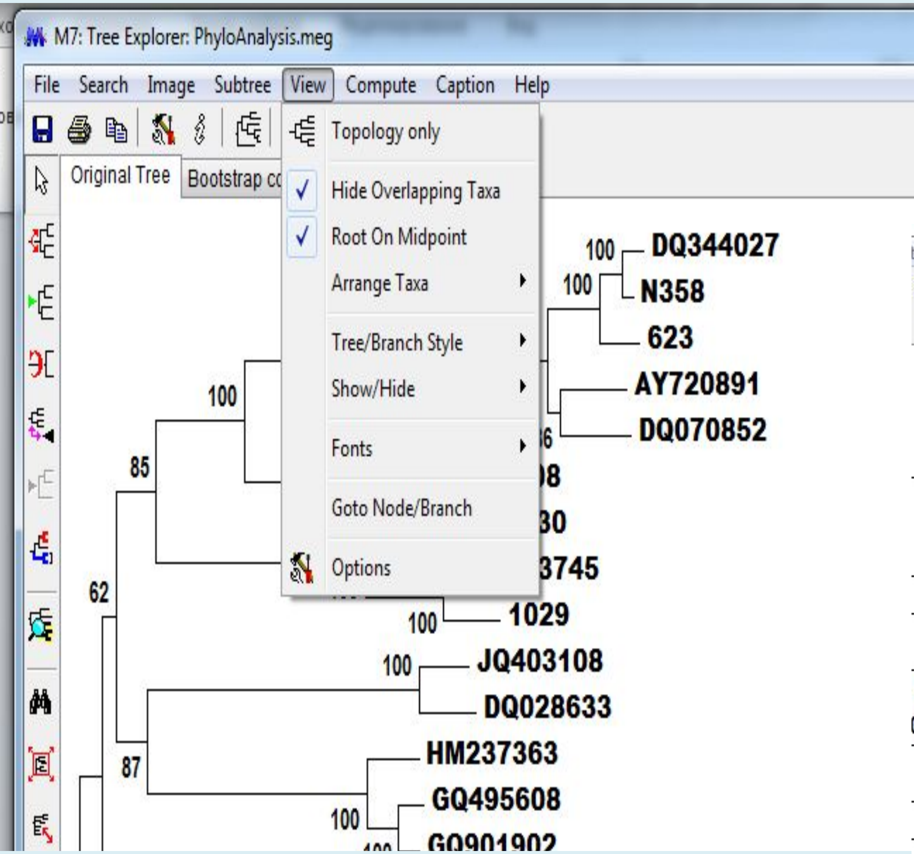
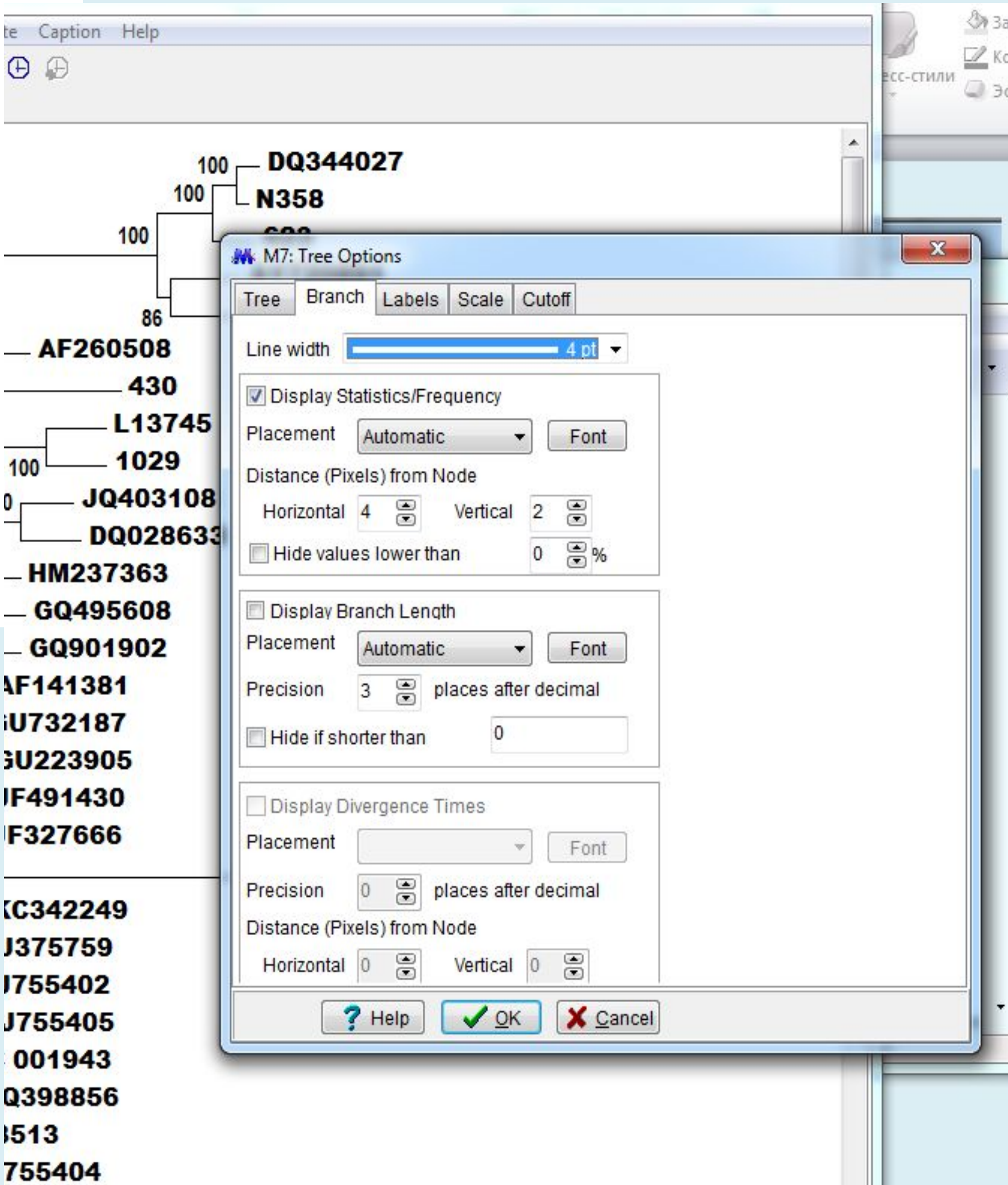


Figure. Evolutionary relationships of taxa





Line width: 4 pt

☑ Display Statistics/Frequency

Placement: Automatic

Distance (Pixels) from Node

Horizontal: 4 Vertical: 2

☐ Hide values lower than 0 %

☐ Display Branch Length

Placement: Automatic

Precision: 3 places after decimal

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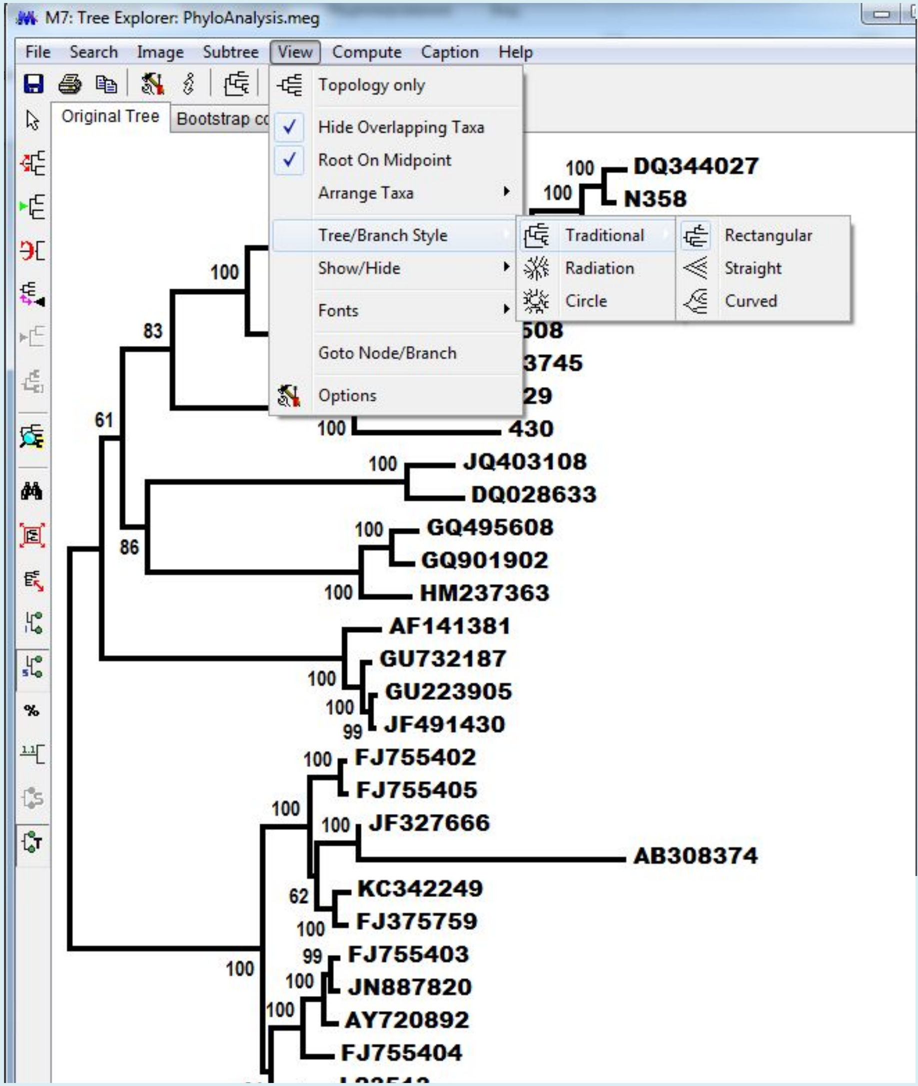
☐ Display Divergence Times

Placement:

Precision: 0 places after decimal

Distance (Pixels) from Node

Horizontal: 0 Vertical: 0


M7: Tree Explorer: PhyloAnalysis.meg
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Topology only
✓ Hide Overlapping Taxa
✓ Root On Midpoint
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Radiation
Circle
Rectangular
Straight
Curved
DQ344027
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DQ028633
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JF491430
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FJ755405
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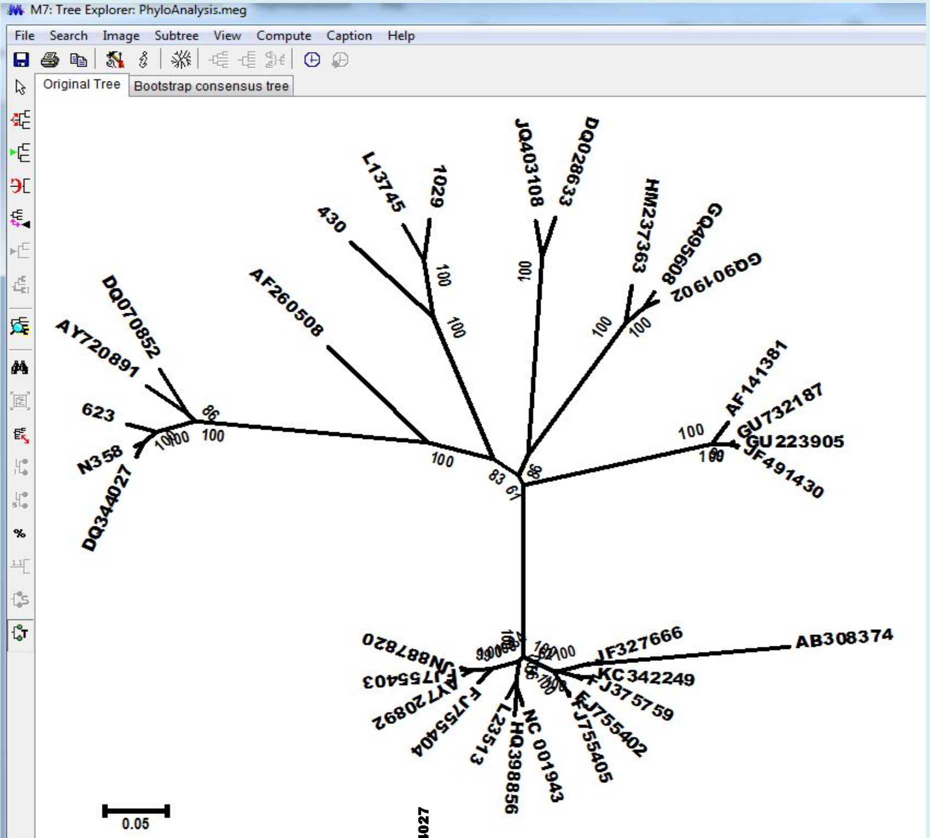
M7: Tree Explorer: PhyloAnalysis.meg
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Help
Original Tree
Bootstrap consensus tree
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1029
JQ403108
DQ028633
HM237363
GQ495608
GQ901902
430
AF260508
DQ070852
AY720891
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N358
DQ344027
AF141381
GU732187
GU223905
JF491430
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AY720892
FJ755404
L23513
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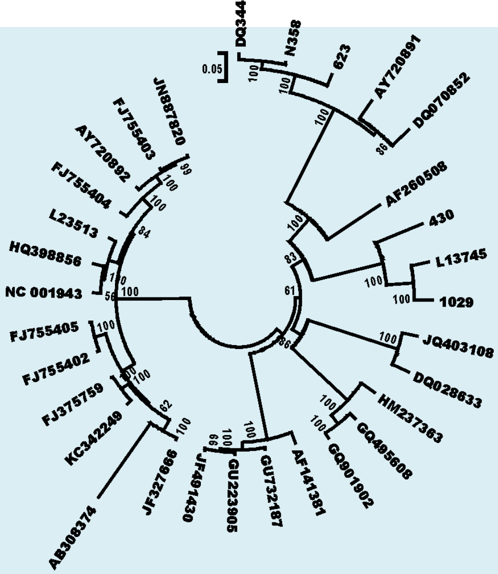
0.05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GQ901902
AF141381
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FJ755402
FJ755405
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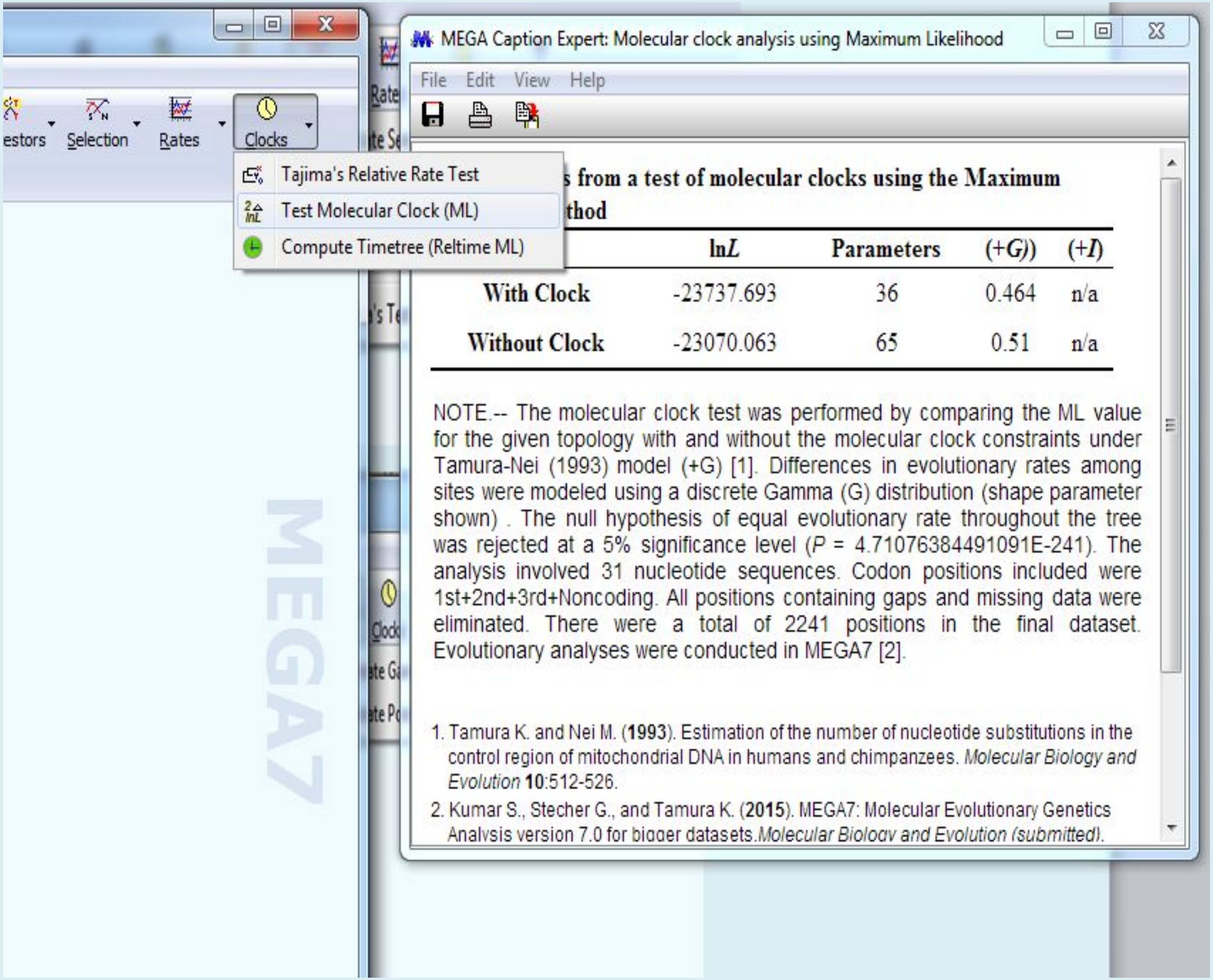
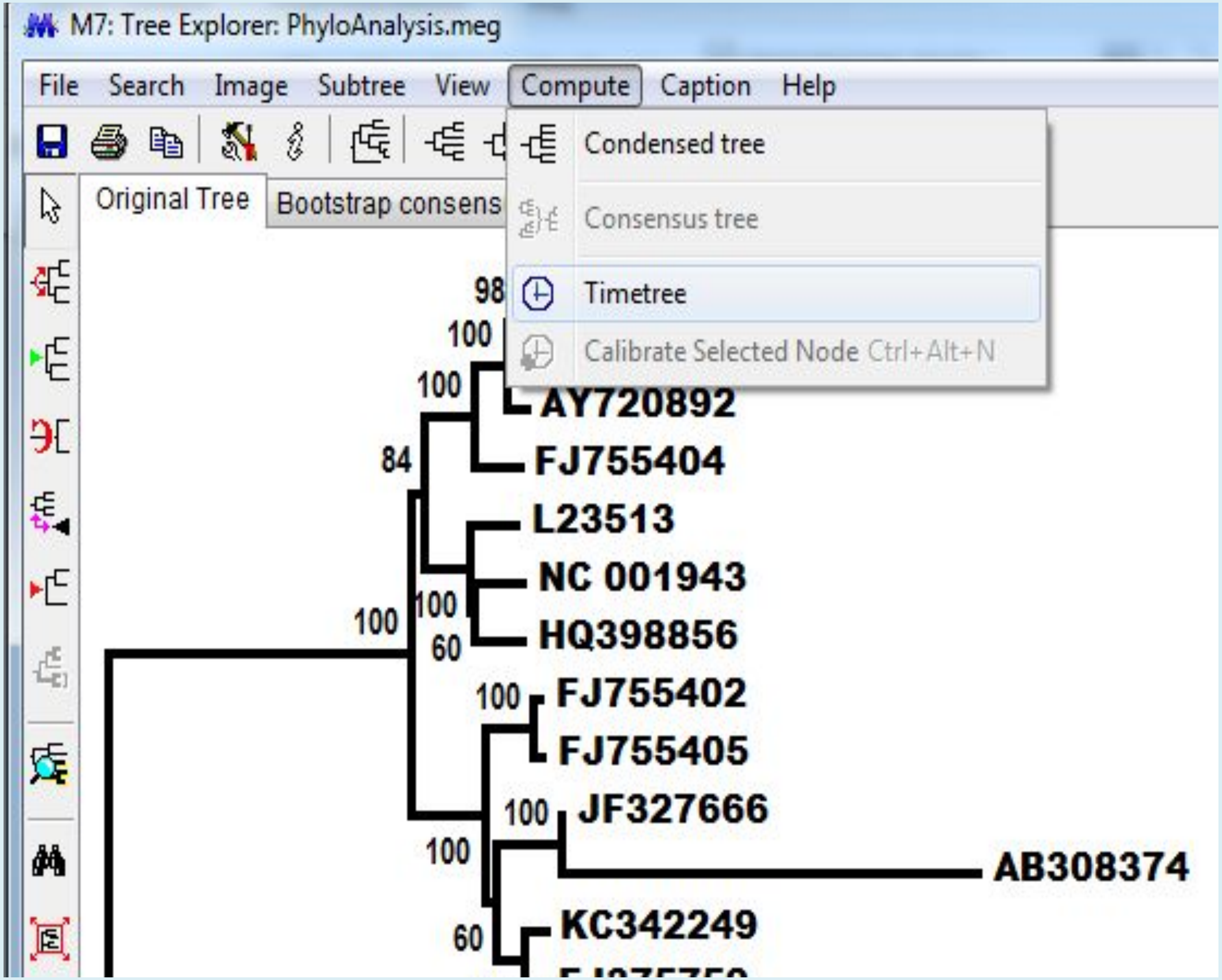


s from a test of molecular clocks using the Maximum thod

	ln*L*	Parameters	(+*G*))	(+*I*)
With Clock	-23737.693	36	0.464	n/a
Without Clock	-23070.063	65	0.51	n/a

NOTE.-- The molecular clock test was performed by comparing the ML value for the given topology with and without the molecular clock constraints under Tamura-Nei (1993) model (+G) [1]. Differences in evolutionary rates among sites were modeled using a discrete Gamma (G) distribution (shape parameter shown) . The null hypothesis of equal evolutionary rate throughout the tree was rejected at a 5% significance level (*P* = 4.71076384491091E-241). The analysis involved 31 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 2241 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [2].

1. Tamura K. and Nei M. (**1993**). Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Molecular Biology and Evolution* **10**:512-526.
2. Kumar S., Stecher G., and Tamura K. (**2015**). MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets.*Molecular Biology and Evolution (submitted)*.


M7: Tree Explorer: PhyloAnalysis.meg
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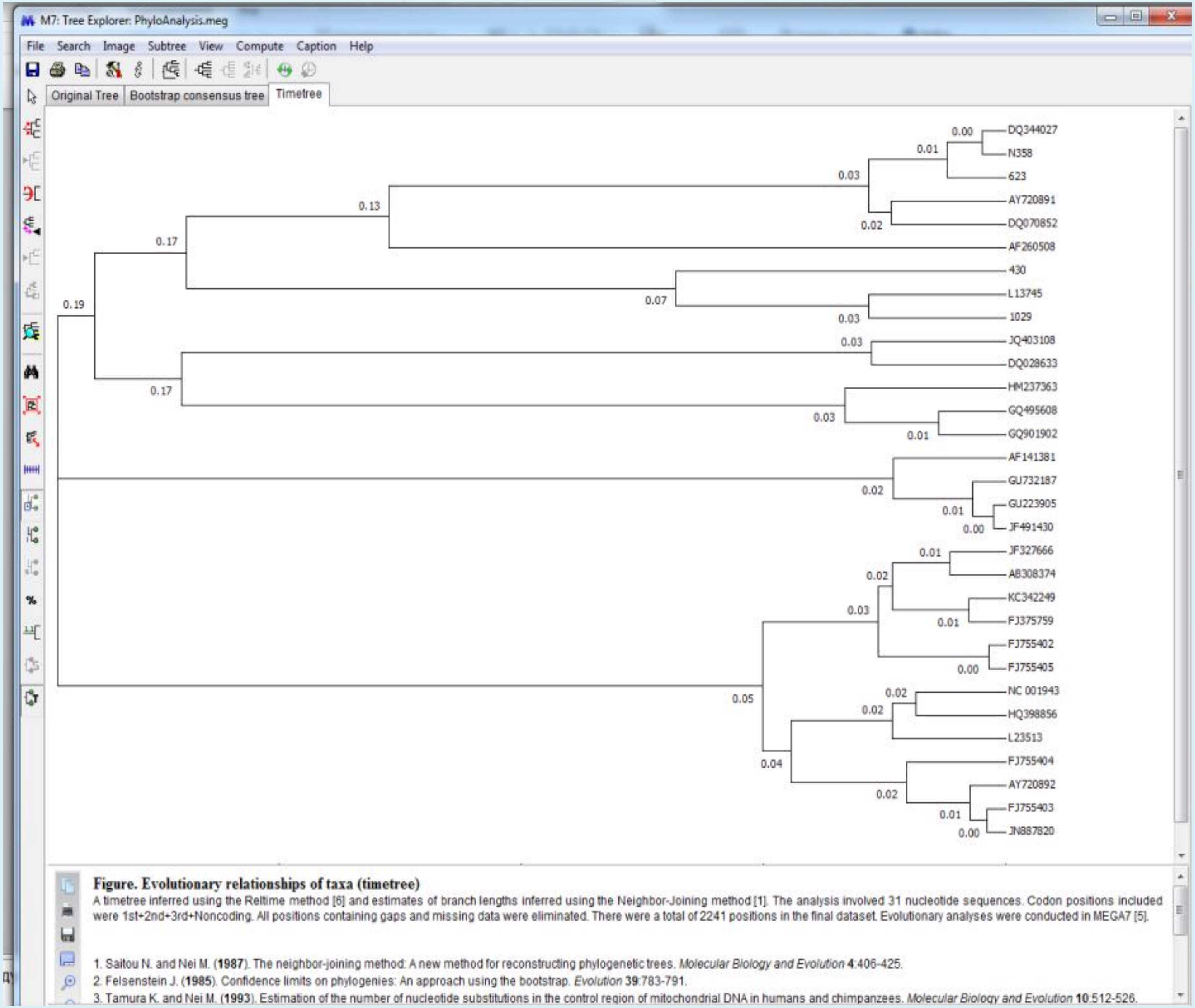
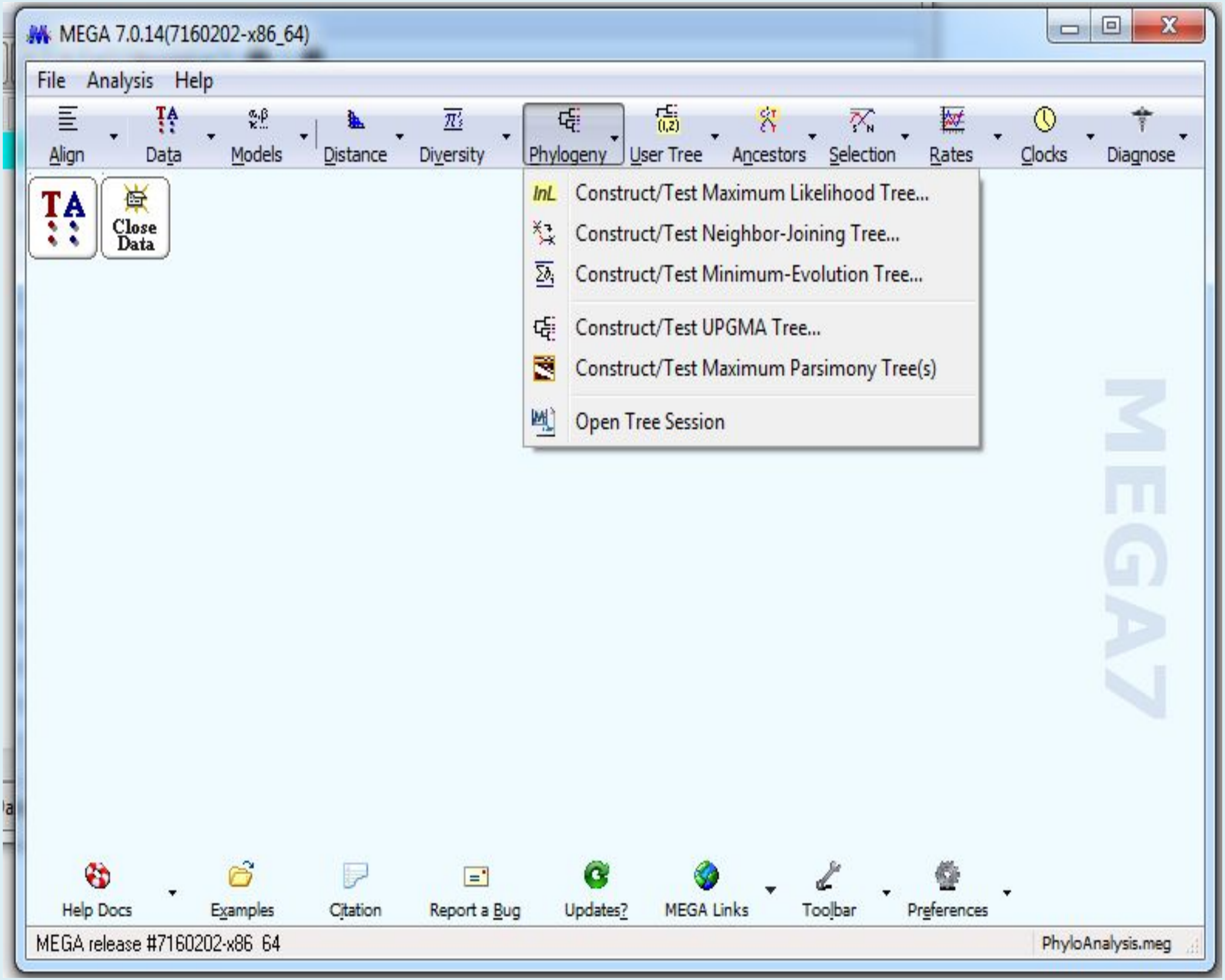


Figure. Evolutionary relationships of taxa (timetree)

A timetree inferred using the Reltime method [6] and estimates of branch lengths inferred using the Neighbor-Joining method [1]. The analysis involved 31 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 2241 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [5].

1. Saitou N. and Nei M. (**1987**). The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* **4**:406-425.
2. Felsenstein J. (**1985**). Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* **39**:783-791.
3. Tamura K. and Nei M. (**1993**). Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Molecular Biology and Evolution* **10**:512-526.


MEGA 7.0.14(7160202-x86_64)
File
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Help
Align
Data
Models
Distance
Diversity
Phylogeny
User Tree
Ancestors
Selection
Rates
Clocks
Diagnose
Close Data
Construct/Test Maximum Likelihood Tree...
Construct/Test Neighbor-Joining Tree...
Construct/Test Minimum-Evolution Tree...
Construct/Test UPGMA Tree...
Construct/Test Maximum Parsimony Tree(s)
Open Tree Session
MEGA7
Help Docs
Examples
Citation
Report a Bug
Updates?
MEGA Links
Toolbar
Preferences
MEGA release #7160202-x86_64
PhyloAnalysis.meg

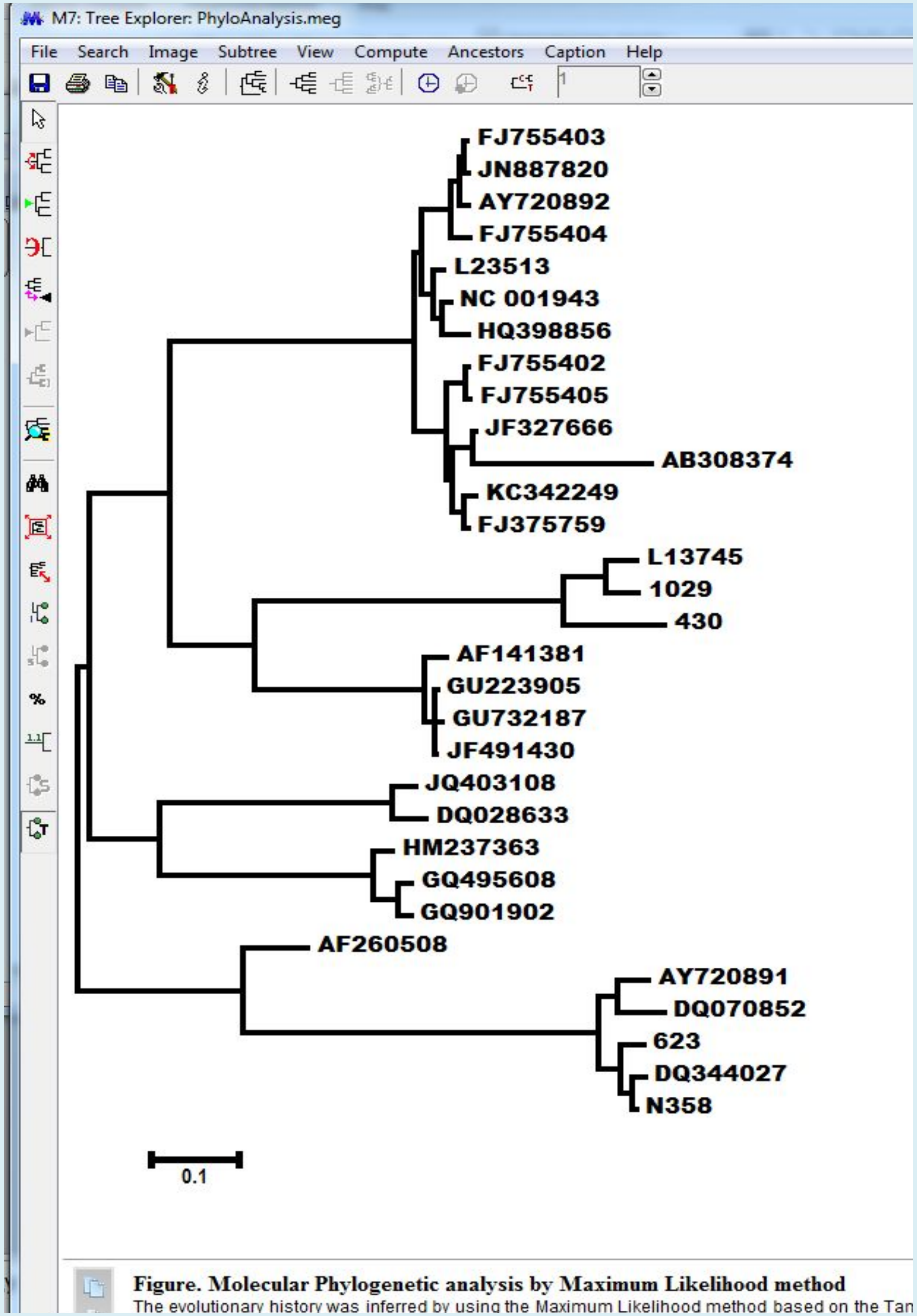


Figure. Molecular Phylogenetic analysis by Maximum Likelihood method

The evolutionary history was inferred by using the Maximum Likelihood method based on the Tan

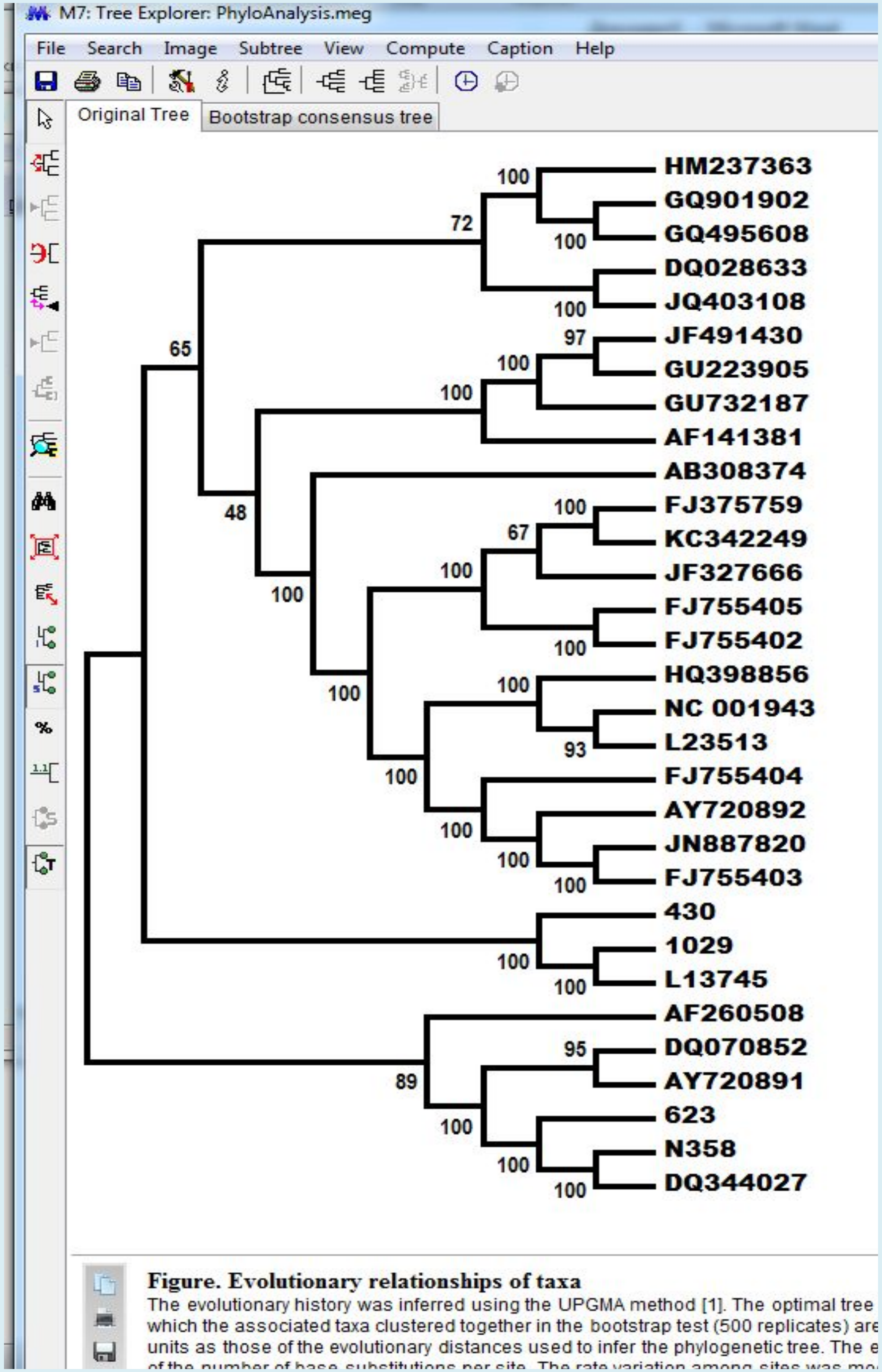
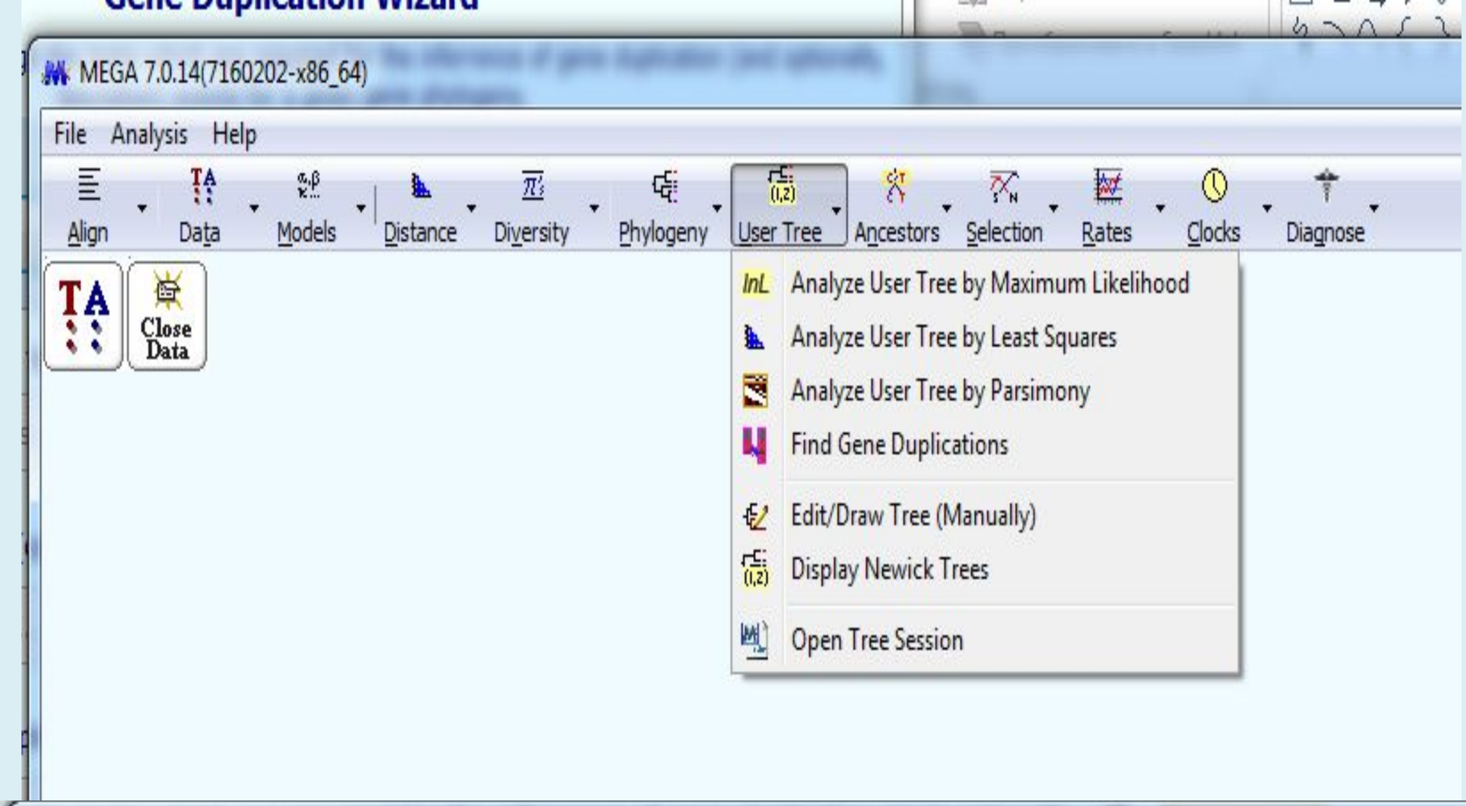


Figure. Evolutionary relationships of taxa

The evolutionary history was inferred using the UPGMA method [1]. The optimal tree which the associated taxa clustered together in the bootstrap test (500 replicates) are units as those of the evolutionary distances used to infer the phylogenetic tree. The e of the number of base substitutions per site. The rate variation among sites was mo


Gene Duplication Wizard
MEGA 7.0.14(7160202-x86_64)
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Help
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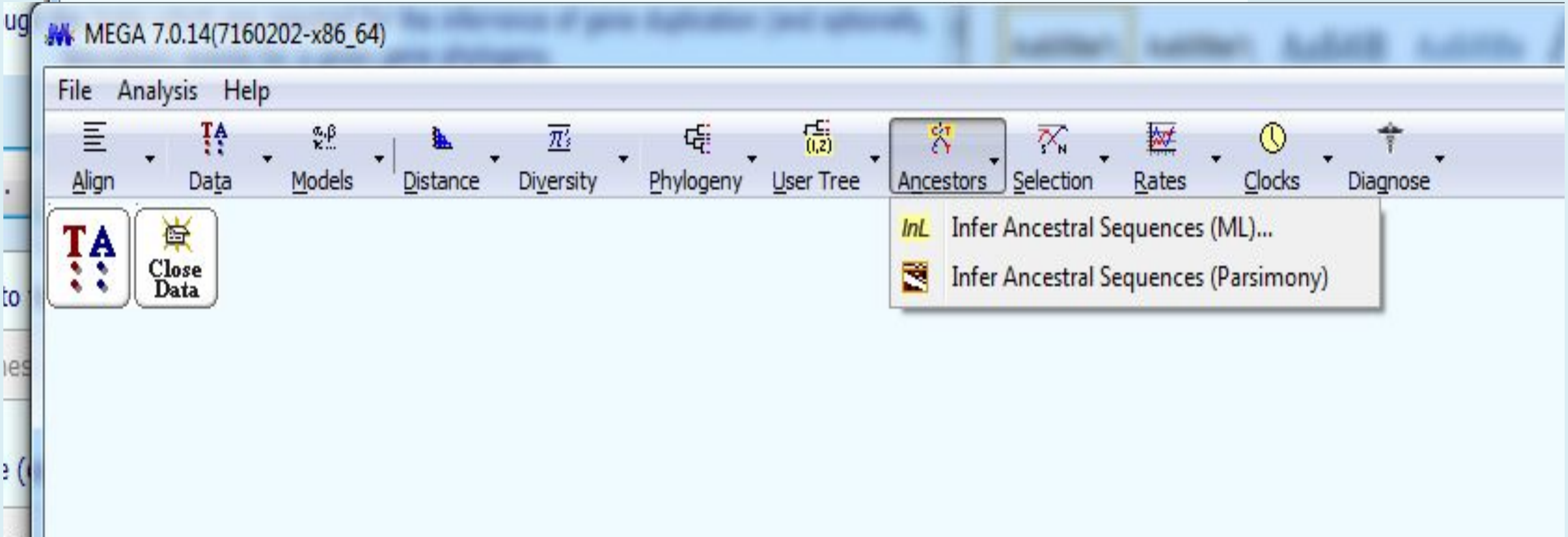
Data
Models
Distance
Diversity
Phylogeny
User Tree
Ancestors
Selection
Rates
Clocks
Diagnose
TA
Close Data
Analyze User Tree by Maximum Likelihood
Analyze User Tree by Least Squares
Analyze User Tree by Parsimony
Find Gene Duplications
Edit/Draw Tree (Manually)
Display Newick Trees
Open Tree Session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Phylogeny
User Tree
Ancestors
Selection
Rates
Clocks
Diagnose
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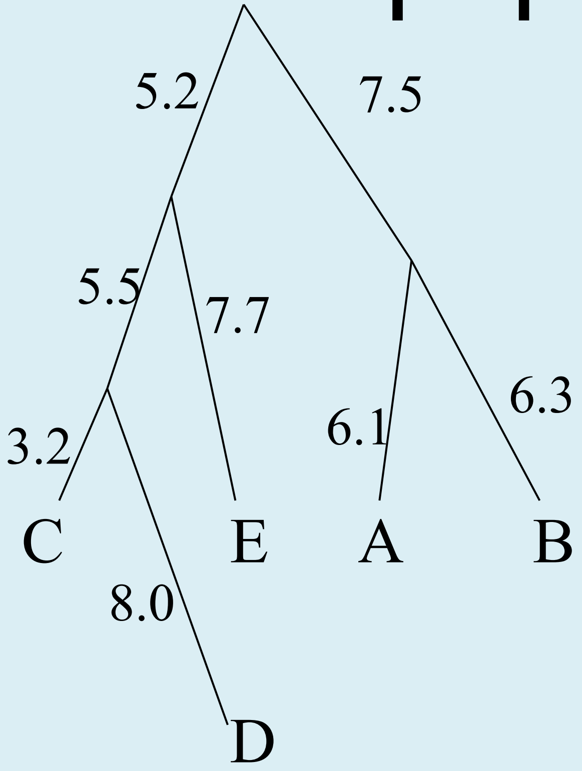
Close Data
Infer Ancestral Sequences (ML)...
Infer Ancestral Sequences (Parsimony)

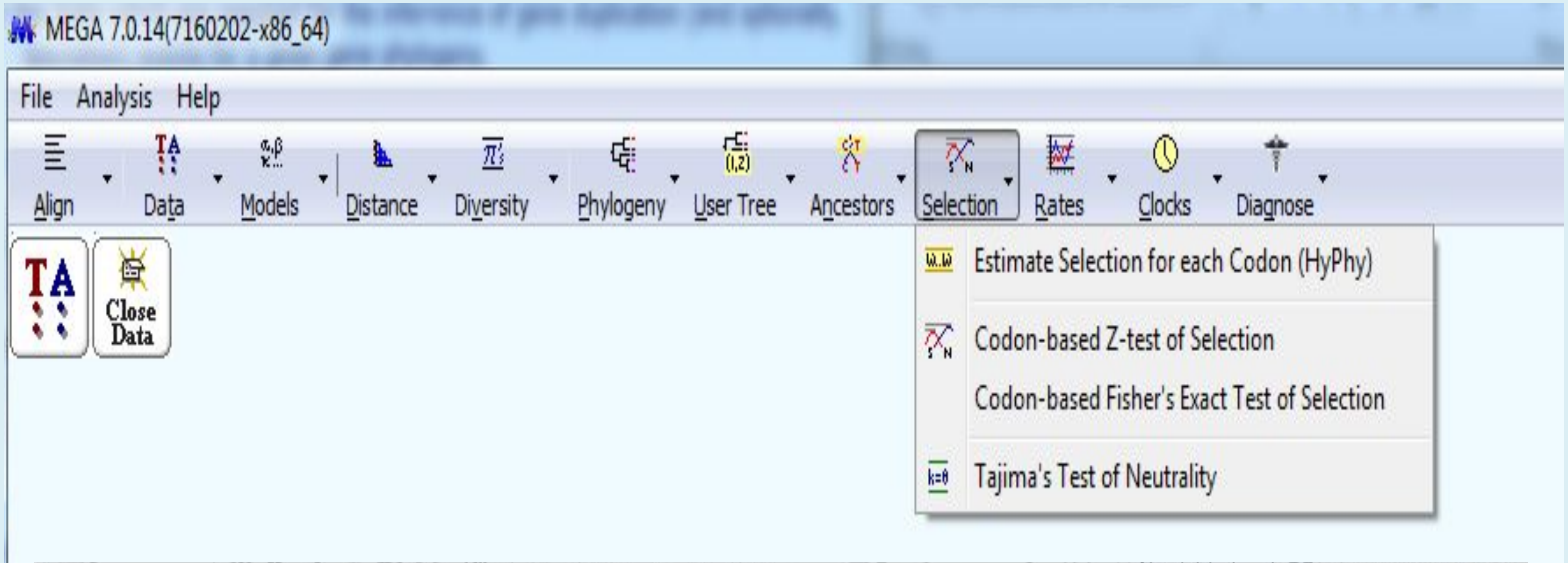
Newick tree format (Скобочная формула)



`(((C,D),E)),(A,B));` только топология

`(((C:3.2,D:8.0):5.5,E:7.7):5.2,(A:6.1,B:6.3):7.5);`

длины ветвей


MEGA 7.0.14(7160202-x86_64)
File Analysis Help
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Models
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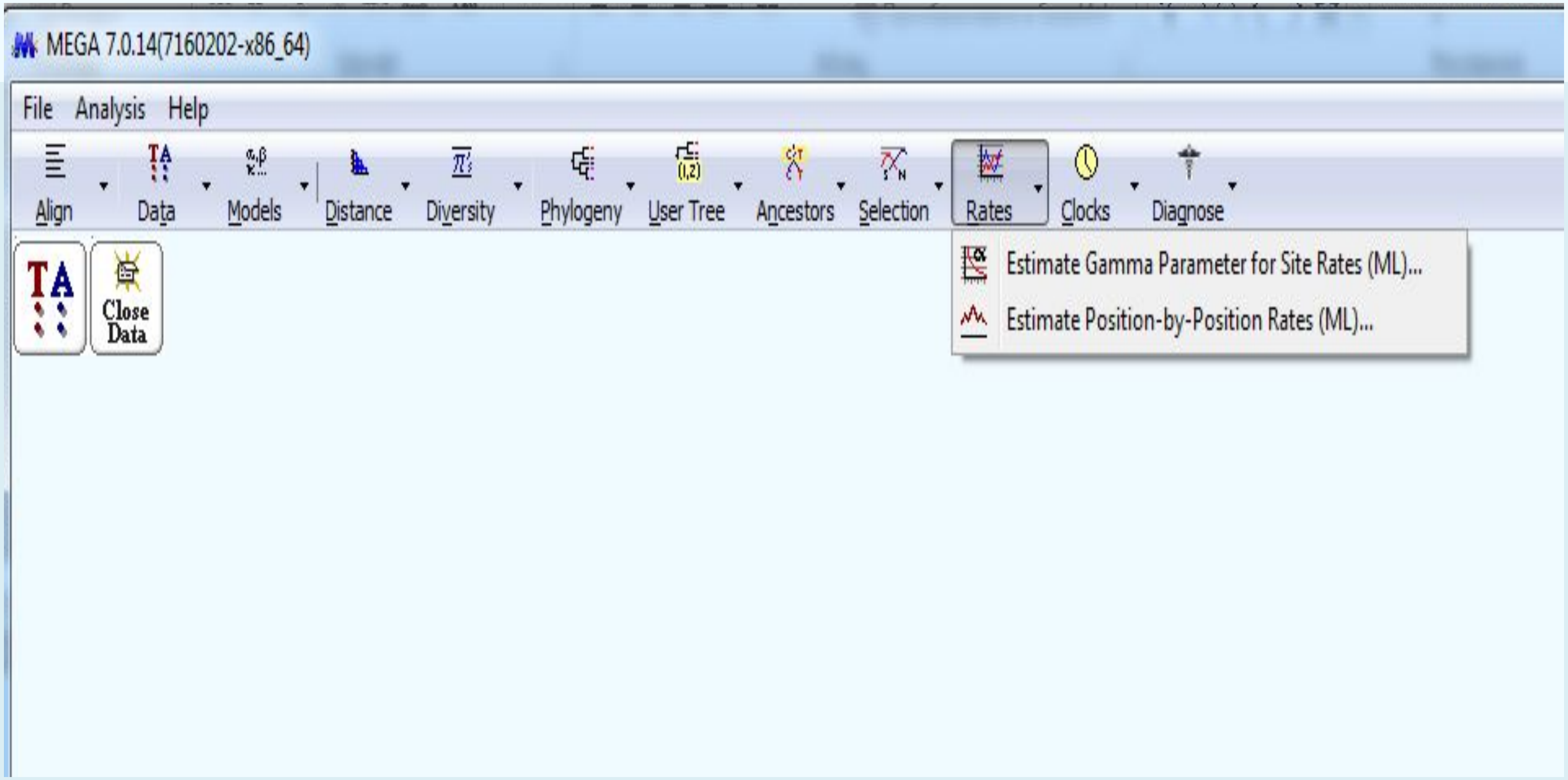
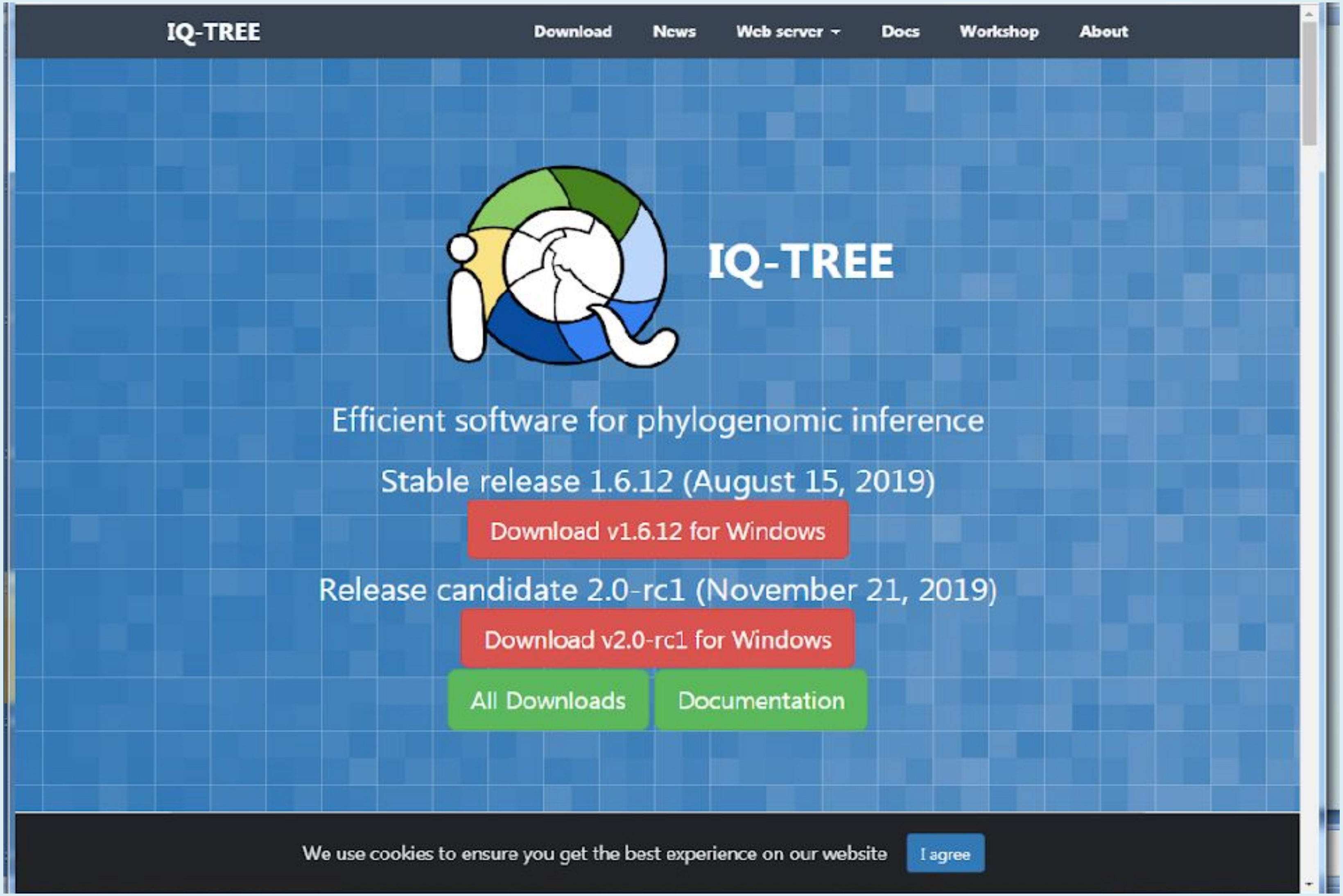
Diversity
Phylogeny
User Tree
Ancestors
Selection
Rates
Clocks
Diagnose
TA
Close Data
Estimate Selection for each Codon (HyPhy)
Codon-based Z-test of Selection
Codon-based Fisher's Exact Test of Selection
Tajima's Test of Neutrality


MEGA 7.0.14(7160202-x86_64)
File Analysis Help
Align
Data
Models
Distance
Diversity
Phylogeny
User Tree
Ancestors
Selection
Rates
Clocks
Diagnose
TA
Close Data
Estimate Gamma Parameter for Site Rates (ML)...
Estimate Position-by-Position Rates (ML)...

http://www.iqtree.org/



Efficient software for phylogenomic inference

Stable release 1.6.12 (August 15, 2019)

Release candidate 2.0-rc1 (November 21, 2019)

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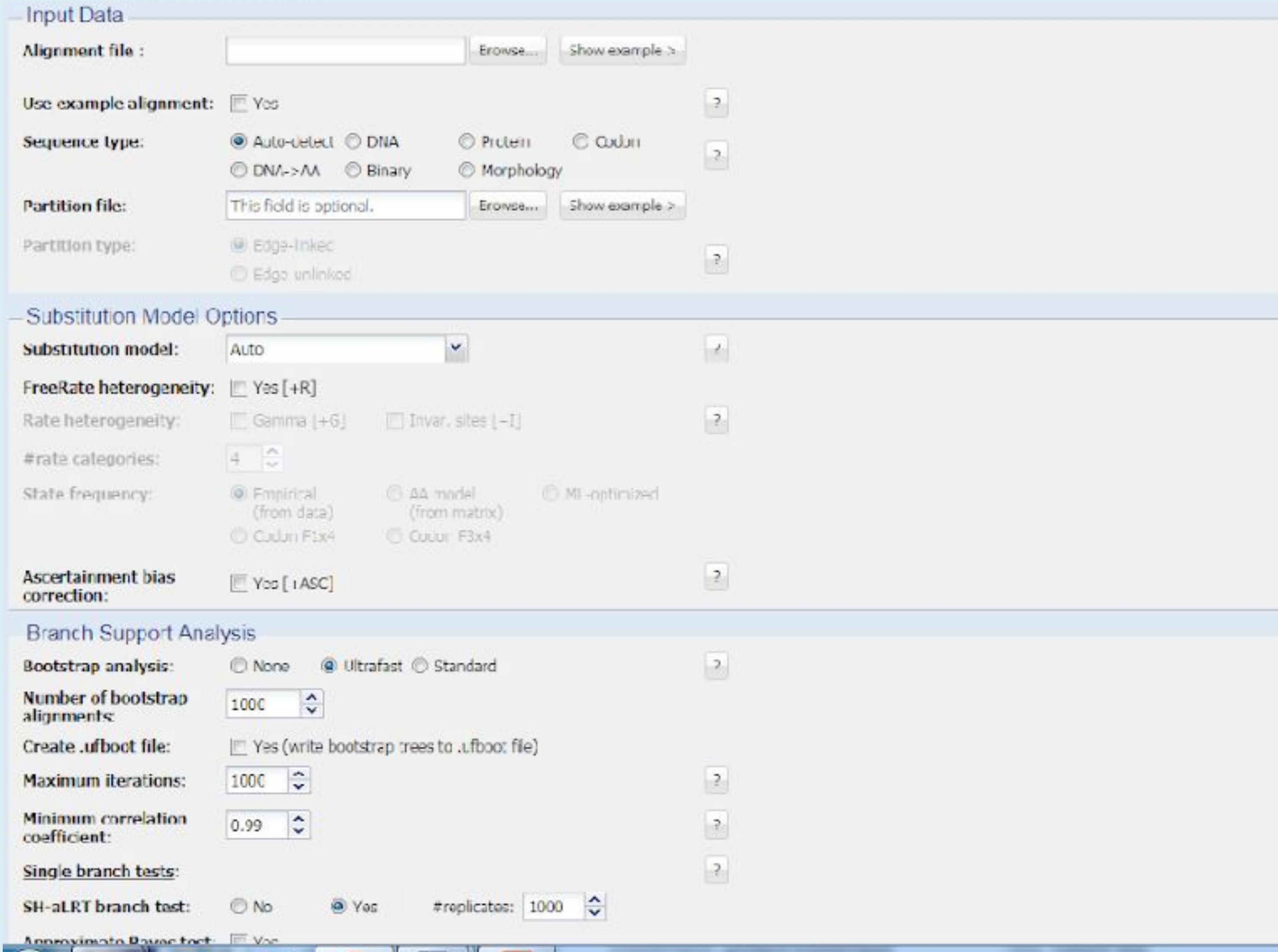

Input Data

Alignment file : [Browse...] [Show example >]

Use example alignment: ☐ Yes

Sequence type: ● Auto-detect ○ DNA ○ Protein ○ Codon ○ DNA->AA ○ Binary ○ Morphology

Partition file: This field is optional. [Browse...] [Show example >]

Partition type: ● Edge-linked ○ Edge-unlinked

Substitution Model Options

Substitution model: Auto

FreeRate heterogeneity: ☐ Yes [+R]

Rate heterogeneity: ☐ Gamma [+G] ☐ Invar. sites [+I]

#rate categories: 4

State frequency: ● Empirical (from data) ○ AA model (from matrix) ○ ML-optimized ○ Codon F1x4 ○ Codon F3x4

Ascertainment bias correction: ☐ Yes [+ASC]

Branch Support Analysis

Bootstrap analysis: ○ None ● Ultrafast ○ Standard

Number of bootstrap alignments: 1000

Create .ufboot file: ☐ Yes (write bootstrap trees to .ufboot file)

Maximum iterations: 1000

Minimum correlation coefficient: 0.99

Single branch tests:

SH-aLRT branch test: ○ No ● Yes #replicates: 1000

Approximate Bayes test: ☐ Yes