



MEGA

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¿QUÉ ES MEGA?

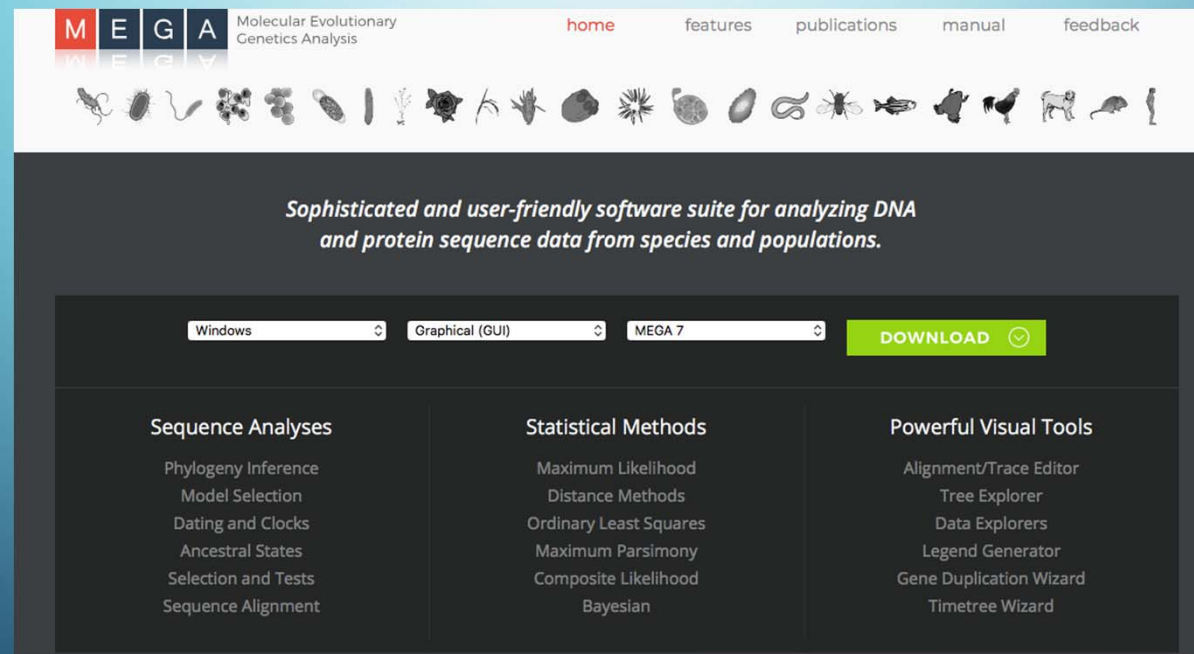
- Mega (Análisis de Genética Molecular) es un software para realizar análisis estadísticos de la evolución molecular y para construir árboles filogenéticos.

CARACTERÍSTICAS DE MEGA

- Alineamiento de secuencias
- Visualización de secuencias
- Métodos de estimación de distancias
- Métodos de creación y visualización de árboles ...

INSTALACIÓN

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



INSTALACIÓN

- Usuarios Windows: Descargar versión 7 para Windows.
- Usuarios Mac:
 - Descargar Wine.
 - Descargar versión 7 para Windows e instalar con Wine.
- Descarga Wine: <http://www.caseitproject.org/download-form/>
> Rellenar formulario y descargar Wine...zip.

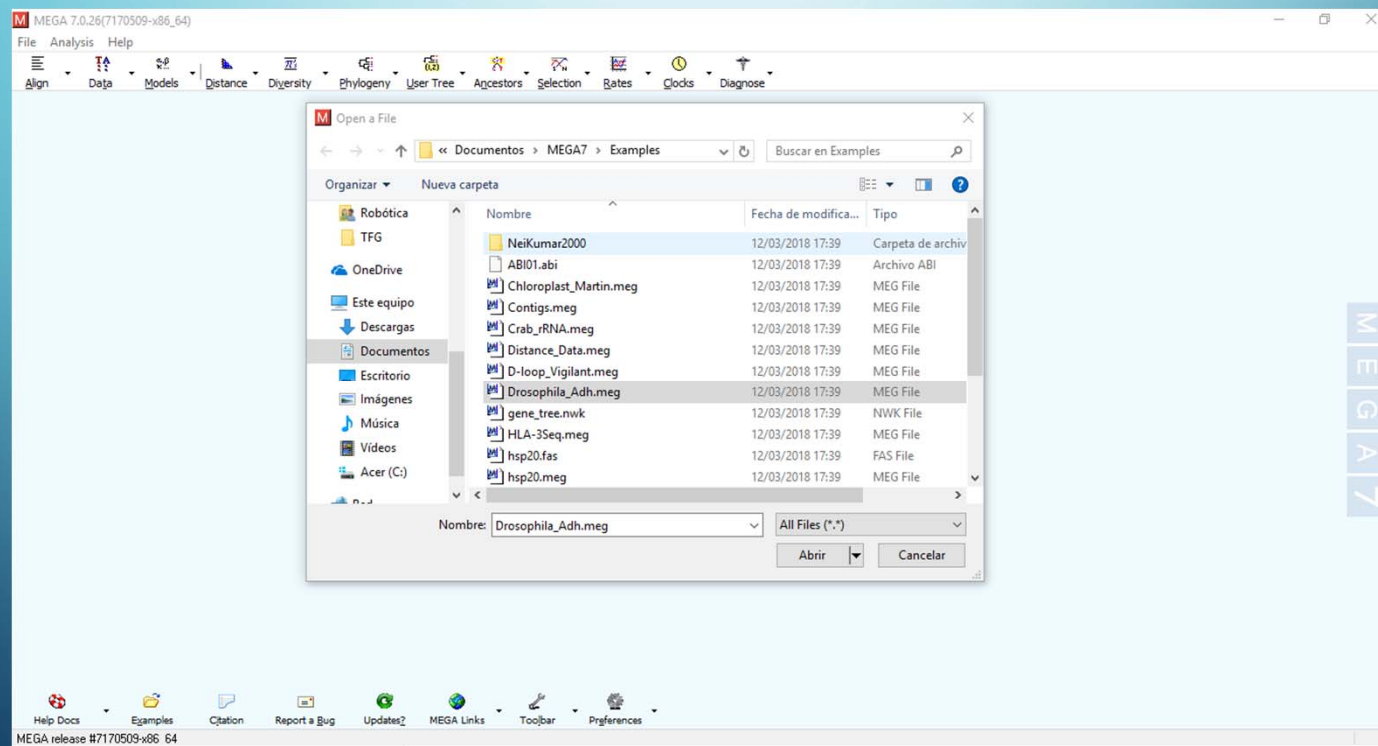
CÁLCULO DE DISTANCIAS POR PARES

- Métodos disponibles:
 - Número de diferencias
 - P- distancia
 - Modelo Jukes-Cantor
 - Kimura (2 y 3 param.)
 - Tajima-Nei
 - Tamura-Nei
 - Máxima verosimilitud

Substitutions type	Nucleotide
Model/Method	✓ No. of differences
Substitutions to Include	p-distance
	Jukes-Cantor model
Rates and Patterns	Kimura 2-parameter model
Rates among Sites	Tajima-Nei model
	Tamura 3-parameter model
<i>Gamma Parameter</i>	Tamura-Nei model
Pattern among Lineages	Maximum Composite Likelihood
Data Subset to Use	LogDet (Tamura-Kumar)
Gaps/Missing Data Treatment	Complete deletion

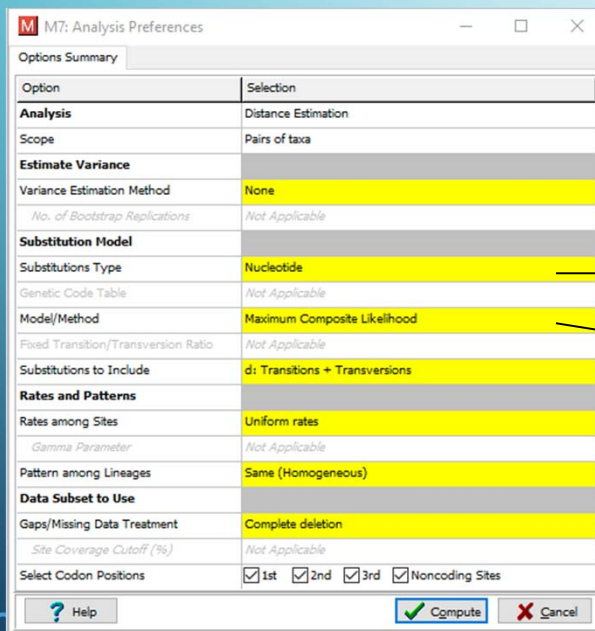
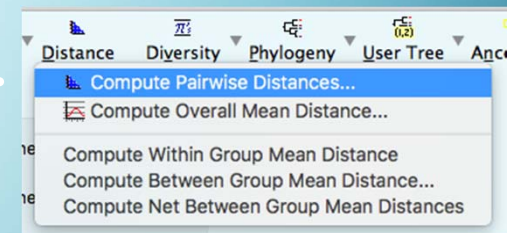
CÁLCULO DE DISTANCIAS POR PARES

- File > Open A File/Session...



CÁLCULO DE DISTANCIAS POR PARES

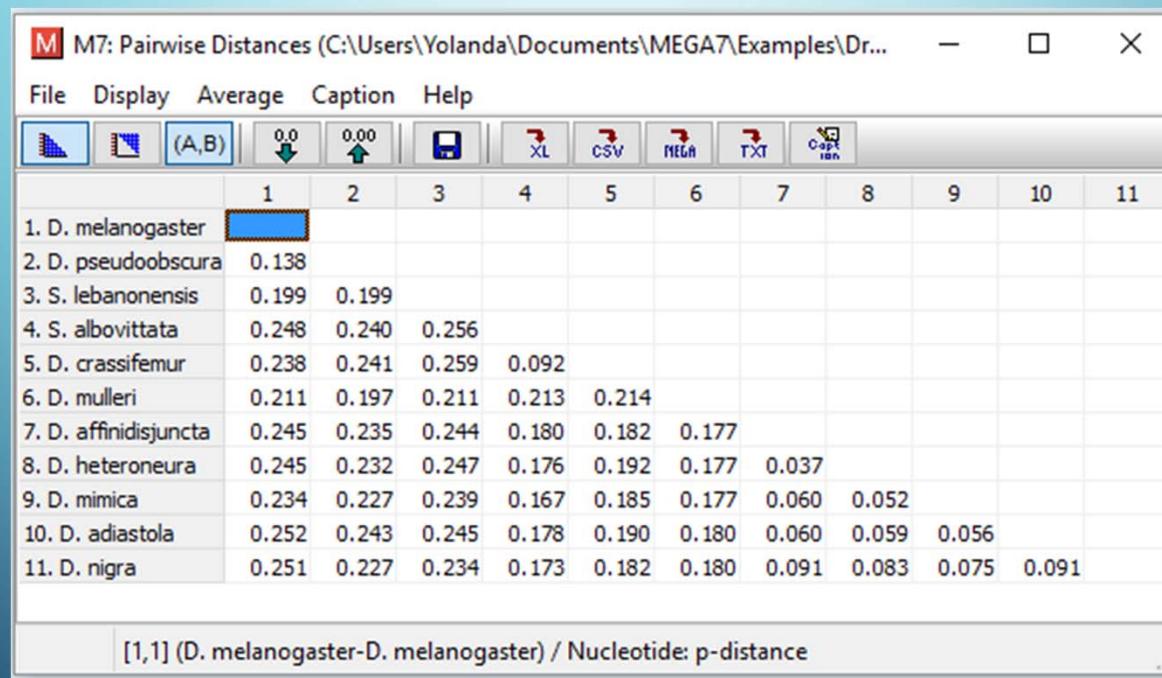
- Distance > Compute Pairwise Distances...
- Selección de opciones:



- Substitutions Type: Nucleotide
- Model/Method: p-distance

CÁLCULO DE DISTANCIAS POR PARES

- Resultado:



The screenshot shows the 'M7: Pairwise Distances' window in MEGA7. The window title is 'M7: Pairwise Distances (C:\Users\Yolanda\Documents\MEGA7\Examples\Dr...'. The menu bar includes 'File', 'Display', 'Average', 'Caption', and 'Help'. The toolbar contains icons for 'A,B', '0.0', '0.00', 'XL', 'CSV', 'MEGA', 'TXT', and 'Caption'. The main area displays a distance matrix for 11 species. The first cell (1,1) is highlighted with a blue box. The status bar at the bottom indicates '[1,1] (D. melanogaster-D. melanogaster) / Nucleotide: p-distance'.

	1	2	3	4	5	6	7	8	9	10	11
1. D. melanogaster											
2. D. pseudoobscura	0.138										
3. S. lebanonensis	0.199	0.199									
4. S. albobittata	0.248	0.240	0.256								
5. D. crassifemur	0.238	0.241	0.259	0.092							
6. D. mulleri	0.211	0.197	0.211	0.213	0.214						
7. D. affinisjuncta	0.245	0.235	0.244	0.180	0.182	0.177					
8. D. heteroneura	0.245	0.232	0.247	0.176	0.192	0.177	0.037				
9. D. mimica	0.234	0.227	0.239	0.167	0.185	0.177	0.060	0.052			
10. D. adistola	0.252	0.243	0.245	0.178	0.190	0.180	0.060	0.059	0.056		
11. D. nigra	0.251	0.227	0.234	0.173	0.182	0.180	0.091	0.083	0.075	0.091	

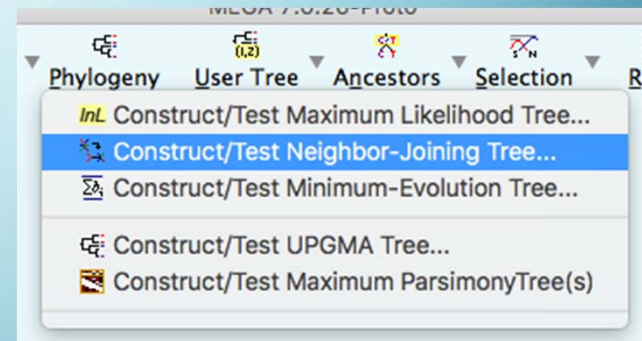
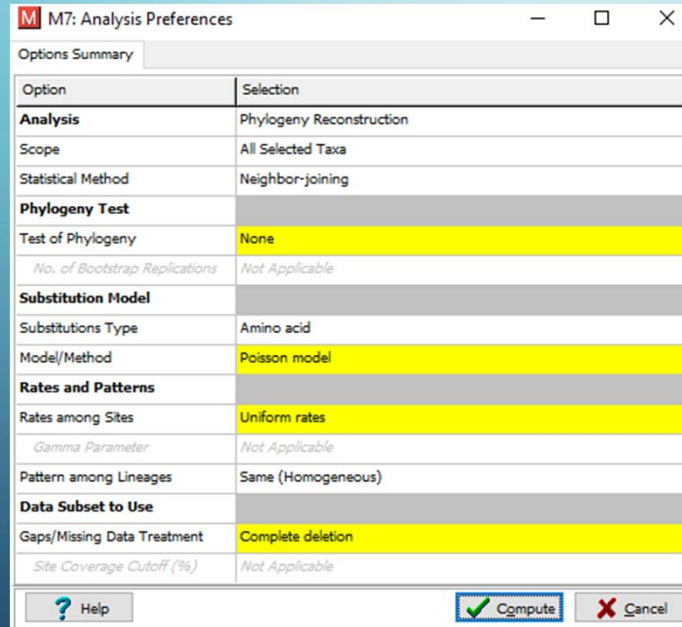
[1,1] (D. melanogaster-D. melanogaster) / Nucleotide: p-distance

MÉTODOS DE CONSTRUCCIÓN DE ÁRBOLES

- Máxima verosimilitud
- Neighbor-Joining (NJ)
- Método de evolución mínima
- Unweighted Pair-Group Method (UPGMA)
- Máxima parsimonia (MP)

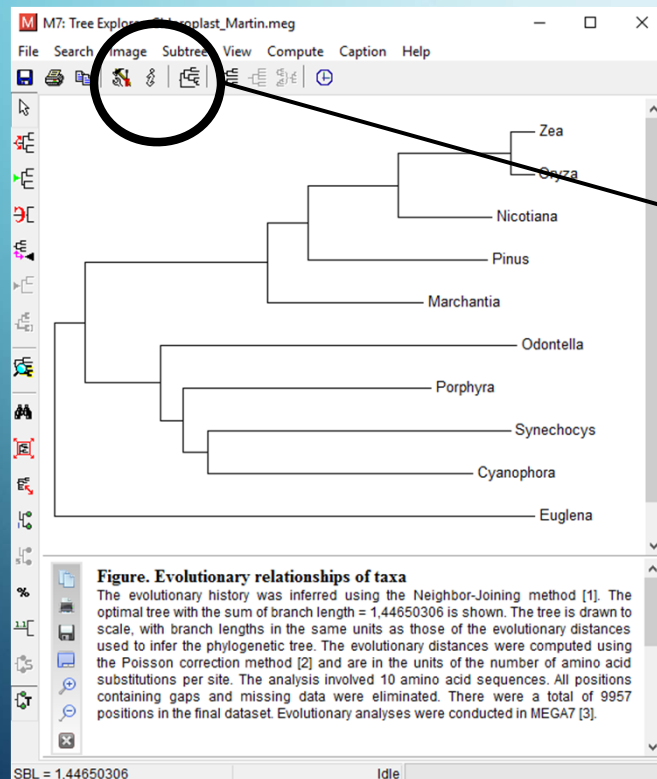
NEIGHBOR-JOINING (NJ)

- Phylogeny > Construct Neighbor-Joining Tree...
- Opciones:



NEIGHBOR-JOINING (NJ)

- Resultado:



The screenshot shows the 'M7: Information' window with the 'Tree' tab selected. It displays the following information:

Type	Value
Type	Unrooted
SBL	1,446,503,06

NEIGHBOR-JOINING (NJ)

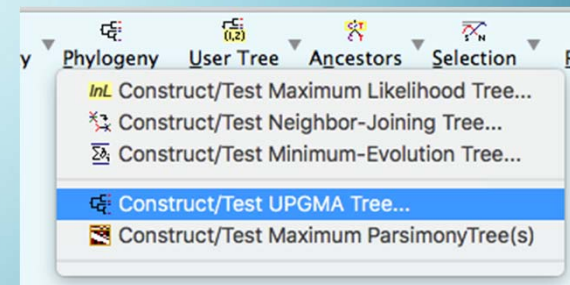
- File > Export Current Tree (Newick) > Export

UPGMA

- Phylogeny > Construct UPGMA Tree...
- Opciones:

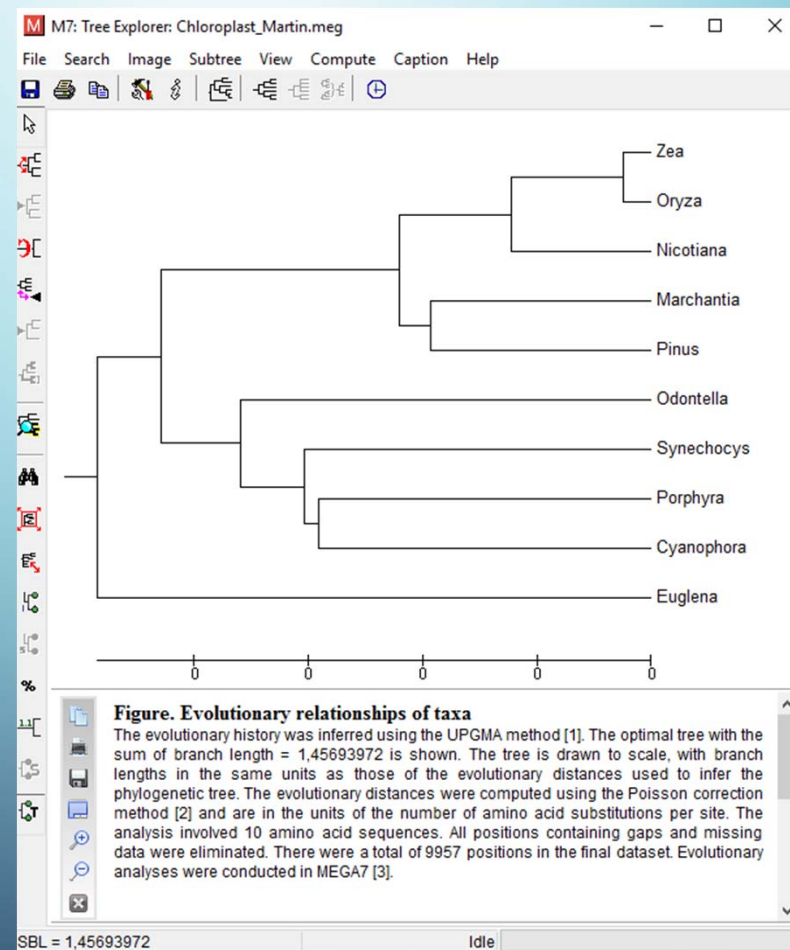
Option	Selection
Analysis	Phylogeny Reconstruction
Scope	All Selected Taxa
Statistical Method	UPGMA
Phylogeny Test	
Test of Phylogeny	None
<i>No. of Bootstrap Replications</i>	<i>Not Applicable</i>
Substitution Model	
Substitutions Type	Amino acid
Model/Method	Poisson model
Rates and Patterns	
Rates among Sites	Uniform rates
<i>Gamma Parameter</i>	<i>Not Applicable</i>
Pattern among Lineages	Same (Homogeneous)
Data Subset to Use	
Gaps/Missing Data Treatment	Complete deletion
<i>Site Coverage Cutoff (%)</i>	<i>Not Applicable</i>

? Help Compute Cancel



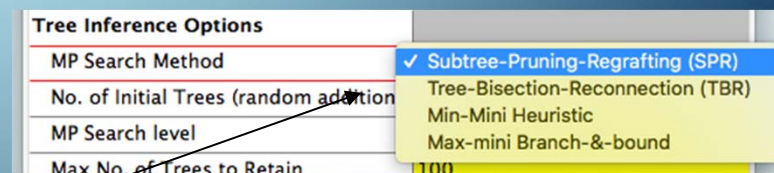
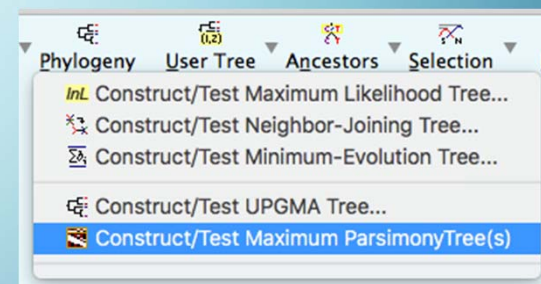
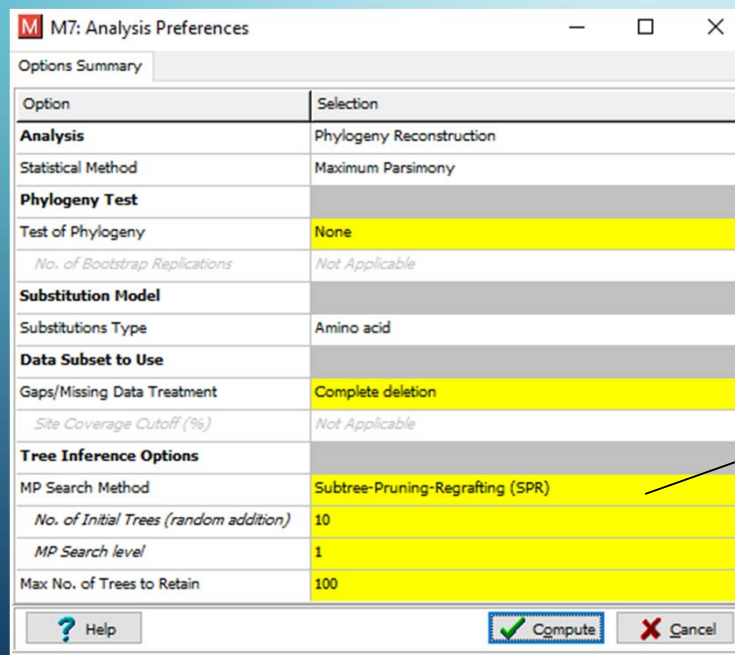
UPGMA

- Resultado:



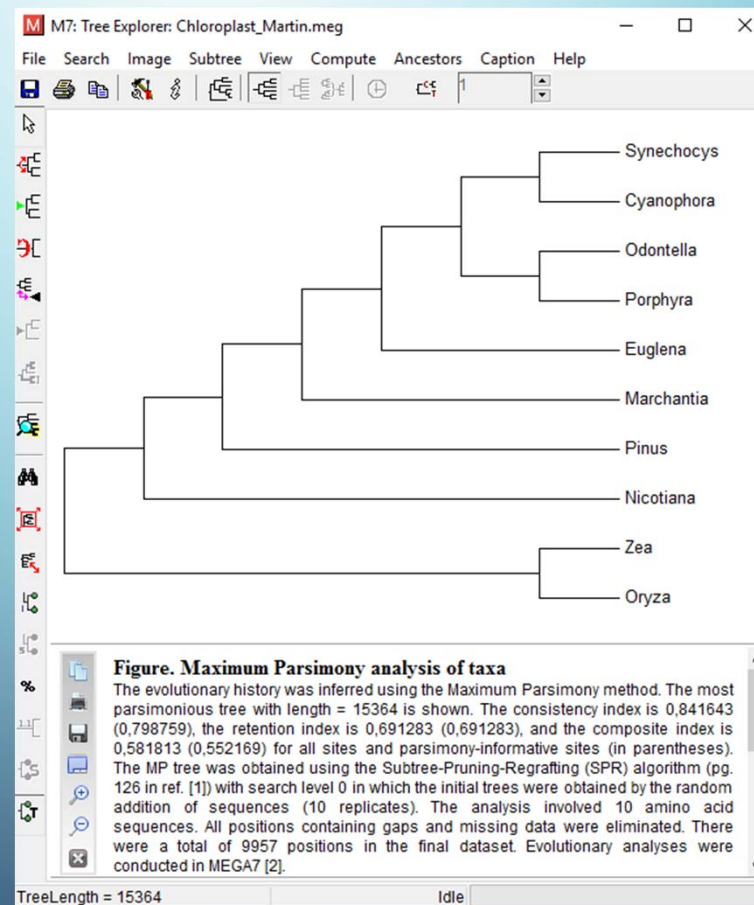
MÁXIMA PERSIMONIA (MP)

- Phylogeny > Construct Maximum Parsimony Tree...
- Opciones:



MÁXIMA PERSIMONIA (MP)

- Resultado:



REFERENCIAS

- [https://en.wikipedia.org/wiki/MEGA, Molecular Evolutionary Genetics Analysis](https://en.wikipedia.org/wiki/MEGA,_Molecular_Evolutionary_Genetics_Analysis)
- [https://www.megasoftware.net/web_help_7/helpfile.htm#hc first time user.htm](https://www.megasoftware.net/web_help_7/helpfile.htm#hc_first_time_user.htm)
- <https://www.megasoftware.net/examples>