



UNIVERSIDAD NACIONAL DE SAN AGUSTÍN

FACULTAD DE INGENIERÍA DE PRODUCCIÓN Y SERVICIOS
CIENCIA DE LA COMPUTACIÓN

Práctica 04: Alineamiento Múltiple

CURSO:

BIOINFORMÁTICA

ALUMNO

KELVIN PAUL PUCHO ZEVALLOS

DOCENTE:

GUADALUPE DEL ROSARIO QUISPE SAJI

8 de Junio del 2022

1. Usando la herramienta MAFT

- Ingresamos a <https://www.uniprot.org/> y en búsqueda avanzada ponemos el gen “gag” de HIV-1.
- Hacemos la búsqueda Avanzada

Searching in UniProtKB [? Help](#)

Term

Protein name [DE] gag

Term

AND Organism [OS] hiv-1

- Seleccionamos 20 genes observados en la db uniprot, y bajamos la secuencia FASTA

Entry	Entry name	Accession	Protein name	Organism	Length
<input checked="" type="checkbox"/>	P03349	GAG_HV1A2	Gag polyprotein	Human immunodeficiency virus type 1 group M subtype B (isolate ARV2/SF2) (HIV-1)	502
<input checked="" type="checkbox"/>	Q75001	GAG_HV1E2	Gag polyprotein	Human immunodeficiency virus type 1 group M subtype C (isolate ETH2220) (HIV-1)	504
<input checked="" type="checkbox"/>	O91079	GAG_HV1YF	Gag polyprotein	Human immunodeficiency virus type 1 group N (isolate YBF30) (HIV-1)	512
<input checked="" type="checkbox"/>	P12495	GAG_HV1Z2	Gag polyprotein	Human immunodeficiency virus type 1 group M subtype D (isolate Z2/CDC-Z34) (HIV-1)	501
<input checked="" type="checkbox"/>	P04591	GAG_HV1H2	Gag polyprotein	Human immunodeficiency virus type 1 group M subtype B (isolate HXB2) (HIV-1)	500
<input checked="" type="checkbox"/>	P05888	GAG_HV1MN	Gag polyprotein	Human immunodeficiency virus type 1 group M subtype B (isolate MN) (HIV-1)	507
<input checked="" type="checkbox"/>	Q9QC00	GAG_HV1K2	Gag polyprotein	Human immunodeficiency virus type 1 group M subtype K (isolate 97ZR-EQTB11) (HIV-1)	495
<input checked="" type="checkbox"/>	O12157	GAG_HV1C2	Gag polyprotein	Human immunodeficiency virus type 1 group M subtype C (isolate 92BR025) (HIV-1)	496
<input checked="" type="checkbox"/>	Q70622	GAG_HV1LW	Gag polyprotein	Human immunodeficiency virus type 1 group M subtype B (isolate LW123) (HIV-1)	500
<input checked="" type="checkbox"/>	Q9IDV8	GAG_HV1YB	Gag polyprotein	Human immunodeficiency virus type 1 group N (isolate YBF106) (HIV-1)	511

- Copiamos las secuencias en formato FASTA hacia la carpeta MAFFT

```
>sp|P03349|GAG_HV1A2 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype B (isolate ARV2/SF2) OX=11685 GN=gag PE=1 SV=3
MGARASVLGGELDKWEKIRLRPGGKKKKYKLKHIWASRELERFAVNPGLLETSEGCRQI
LGQLQPSLQTGEELRSLYNTVATLYCVHQRIEIKDTKEALDKIEEQNKSKKKAQAAA
AAGTGNSSQVSNYPVQNLQGMVHQATSPRTLNAWVKVVEKAFSPEVIMFMSALSEG
ATPQDLNMLNTVGGHQAAMQMLKETINEEAAEDRWHPVHAGPIAPGQMRPRGSDIAG
TTSTLQEQIAGWMTNPPVPGDIYRWIILGLNKIVRMYSPTSILDIRGPKPEFRDYVD
RFYKTLRAEQASQVKNMWTETLLVQNPANPDCKTILKALGPAAATLEEMTACQGVGGPGH
KARVLAEAMSQVNTNPNANIMQGRNFRNQRKTVKFCNGKEGHIACNCRAPRRKGCWRCGR
EGHQMKDCTERQANFLGKIWPSYKGRPGNLFQSRPEPTAPPEESFRFGEEKTTPSQKQEP
IDKELYPLTSLRSLFGNDPSSQ
>sp|Q75001|GAG_HV1E2 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype C (isolate ETH2220) OX=388796 GN=gag PE=3 SV=3
MGARASILRGKLDWEKIRLRPGGKKKKYKLKHIWASRELERFALNPDLDTAGCQKI
IKQLQPALQTGEELKSLFNTVATLYCVHQRIEIKDTKEALDKIEEQNKSKKKAQAGA
ADRGKDSQVSNYPVQNLQGMVHQATSPRTLNAWVKVVEKAFSPEVIMFMSALSEGATPQ
DLNMLNTVGGHQAAMQMLKETINEEAAEDRWHPVHAGPIAPGQMRPRGSDIAGTTST
LQEQIAGWMTNPPVPGDIYRWIILGLNKIVRMYSPTSILDIRGPKPEFRDYVDFFK
TLRAEQATQVKNMWTETLLVQNPANPDCKTILRALPGGASLEEMTACQGVGGPAHKARV
LAEAMSQVNTNPNANIMQGRNFRNQRKTVKFCNGKEGHIACNCRAPRRKGCWRCGR
EGHQMKDCTERQANFLGKIWPSYKGRPGNLFQSRPEPTAPPEESFRFGEEKTTPSQKQEP
IDKELYPLTSLRSLFGNDPSSQ
>sp|O91079|GAG_HV1YF Gag polyprotein OS=Human immunodeficiency virus type 1 group N (isolate YBF30) OX=388818 GN=gag PE=3 SV=3
MGARASVLGGKLDWEKIRLRPGGKKKKYKLKHIWASRELERFALNPDLDTAGCQKI
LNQLEPALQTGEELRSLYNTVATLYCVHQRIEIKDTKEALDKIEEQNKSKKKAQAAA
GAAATDSNISRNYPVQNLQGMVHQATSPRTLNAWVKVVEKAFSPEVIMFMSALSEG
ATPQDLNMLNTVGGHQAAMQMLKETINEEAAEDRWHPVHAGPIAPGQMRPRGSDIAG
TTSTLQEQIAGWMTNPPVPGDIYRWIILGLNKIVRMYSPTSILDIRGPKPEFRDYVD
RFYKTLRAEQASQVKNMWTETLLVQNPANPDCKTILKALGPAAATLEEMTACQGVGGPAH
KARVLAEAMSQVNTNPNANIMQGRNFRNQRKTVKFCNGKEGHIACNCRAPRRKGCWRCGR
EGHQMKDCTERQANFLGKIWPSYKGRPGNLFQSRPEPTAPPEESFRFGEEKTTPSQKQEP
IDKELYPLTSLRSLFGNDPSSQ
>sp|P12495|GAG_HV1Z2 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype D (isolate Z2/CDC-Z34) OX=11683 GN=gag PE=1 SV=3
MGARASVLGGKLDWEKIRLRPGGKKKKYKLKHIWASRELERFALNPDLDTAGCQKI
IGQLQPAITRGEELRSLFNTVATLYCVHQRIEIKDTKEALDKIEEQNKSKKKAQAAA
ADAGNSQVSNYPVQNLQGMVHQATSPRTLNAWVKVVEKAFSPEVIMFMSALSEG
ATPQDLNMLNTVGGHQAAMQMLKETINEEAAEDRWHPVHAGPIAPGQMRPRGSDIAG
TTSTLQEQIAGWMTNPPVPGDIYRWIILGLNKIVRMYSPTSILDIRGPKPEFRDYVD
RFYKTLRAEQASQVKNMWTETLLVQNPANPDCKTILKALGPAAATLEEMTACQGVGGPSH
ARVLAEAMSQVNTNPNANIMQGRNFRNQRKTVKFCNGKEGHIACNCRAPRRKGCWRCGR
EGHQMKDCTERQANFLGKIWPSYKGRPGNLFQSRPEPTAPPEESFRFGEEKTTPSQKQEP
IDKELYPLTSLRSLFGNDPSSQ
>sp|P04591|GAG_HV1H2 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype B (isolate HXB2) OX=11706 GN=gag PE=1 SV=3
MGARASVLGGKLDWEKIRLRPGGKKKKYKLKHIWASRELERFAVNPGLLETSEGCRQI
LGQLQPSLQTGEELRSLYNTVATLYCVHQRIEIKDTKEALDKIEEQNKSKKKAQAAA
DTGHSNQVSNYPVQNLQGMVHQATSPRTLNAWVKVVEKAFSPEVIMFMSALSEGAT
PQDLNMLNTVGGHQAAMQMLKETINEEAAEDRWHPVHAGPIAPGQMRPRGSDIAGTT
```

tmp	1/11/2016 03:40	Carpeta de archivos	
usr	9/1/2018 02:02	Carpeta de archivos	
gag.fasta	8/6/2022 18:03	Archivo FASTA	13 KB
mafft	28/6/2019 22:15	Archivo por lotes ...	1 KB
mafft-signed	21/5/2019 03:43	Script de Windows...	11 KB
testdata	20/11/2015 03:51	Documento de tex...	1 KB

e. Abrimos mafft y escribimos gag.fasta

```
C:\Windows\system32\cmd.exe
Página de códigos activa: 65001

Preparing environment to run MAFFT on Windows.
This may take a while, if real-time scanning by anti-virus software is on.

It may take a while before the calculation starts
if being scanned by anti-virus software.
Also consider using a faster version for Windows 10:
https://mafft.cbrc.jp/alignment/software/wsl.html

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MAFFT v7.490 (2021/Oct/30)

MBE 30:772-780 (2013), NAR 30:3059-3066 (2002)
https://mafft.cbrc.jp/alignment/software/

-----

Input file? (FASTA format; Folder="D:\CURSOS_2022_II\Bioinformatica\clase_5\mafft-win")
@
```

f. Seleccionamos el formato de entrada y escribimos el formato de salida

```
C:\Windows\system32\cmd.exe

Input file? (FASTA format; Folder="D:\CURSOS_2022_II\Bioinformatica\clase_5\mafft-win")
@gag.fasta
OK. infile = gag.fasta

Output file?
@gag.aln
OK. outfile = gag.aln

Output format?
1. Clustal format / Sorted
2. Clustal format / Input order
3. Fasta format / Sorted
4. Fasta format / Input order
5. Phylip format / Sorted
6. Phylip format / Input order
@4
OK. arguments = --inputorder

Strategy?
1. --auto
2. FFT-NS-1 (fast)
3. FFT-NS-2 (default)
4. G-INS-i (accurate)
5. L-INS-i (accurate)
6. E-INS-i (accurate)
@
```

g. En estrategia seleccionamos la opción 5; y agregamos el parámetro -ep

```

Strategy?
 1. --auto
 2. FFT-NS-1 (fast)
 3. FFT-NS-2 (default)
 4. G-INS-i (accurate)
 5. L-INS-i (accurate)
 6. E-INS-i (accurate)
@ 5
OK. arguments = --localpair --maxiterate 16 --inputorder

Additional arguments? (--ep # --op # --kappa # etc)
@ --ep_
OK. arguments = --ep --localpair --maxiterate 16 --inputorder

command=
"/usr/bin/mafft" --ep --localpair --maxiterate 16 --inputorder "gag.fasta" > "gag.aln"
Type Y or just enter to run this command.
@ y

```

h. La salida se encuentra en el archivo gag.aln representado en 10%

```

Strategy:
  FFT-NS-i (Accurate but slow)
  Iterative refinement method (max. 16 iterations)

If unsure which option to use, try 'mafft --auto input > output'.
For more information, see 'mafft --help', 'mafft --man' and the mafft page.

The default gap scoring scheme has been changed in version 7.110 (2013 Oct).
It tends to insert more gaps into gap-rich regions than previous versions.
To disable this change, add the --leavegappyregion option.

>sp|P03349|GAG_HV1A2 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype B (isolate ARV2/SF2) OX=11685 GN=gag PE=1 SV=3
MGARASVLSGGELDKWEKIRLRPGGKKKYKLKHIVWASRELERFVNPGLLETSEGCROI
LGQLQPSLQTGSSEELRSLYNTVATLYCVHQRIDVKDTKEALEKIEEQNKSK-KKAQQ--
--AAAAAGTGN---SSQVSQINPIVQNLQGQMMHQATSPRTLNAWVKVVEEKAFSPEVIP
MFALSSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAEWDRLHPVHAGPIAPGQMRE
PRGSDIAGTTSTLQEQIGWMTNPPIPVGEIYKRWIILGLNKIVRMYSPTSILDIRQGP
EPFRDYVDRFYKTLRAEQASQDVKNMMTETLLVQANPDPCKTILKALGPAATLEEMTAC
QGVGGPGHKARVLAEAMSQVNTNPA--NIMQQRGNFRNQRKTVCFCNGKEGHIKACNCRAP
RRKGCWKCGEGHQMKDCTE--RQANFLGKIWPSYKGRPGNFIQ-----SRPE
PTAPPEESFRFGEEKTTPTS---QKQEPIDKELY-PLTSLRSLFGNDPSSQ
>sp|Q75001|GAG_HV1ET Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype C (isolate ETH2220) OX=388796 GN=gag PE=3 SV=3
MGARASILRGEKLDWEKIKLRPGGKKHYMLKHLWANRELEKFAINPDLLDTSAGCKQI
IKQLQPALQTGTEELKSLFNTVATLYCVHQKTEIKDTKEALDKIEEQNESQ-QKTOQ--
---AGAADR-----KDSQINPIVQNMQGMHQIPISARTLNAWVKVVEEKAFSPEVIP
MFALTSEGATPQDLNTMLNTVGGHQAAMQMLKDTINEEAAEWDRLHPVHAGPVAPGQMRE
PRGSDIAGTTSTLQEQIWMGTGNNPPVPVGDYKRWIILGLNKIVRMYSPTSILDIRQGP
EPFRDYVDRFYKTLRAEQATQDVKNMMTDTLLVQANPDPCKTILRALGPASLEEMTAC
QGVGGPAHKARVLAEAMSQVNTN---TIMQKSNFKGPKRAIKCFNGKEGHLARNCRAP
RRKGCWKCGEGHQMKDCTE--RQANFLGRLWPSNKGKRGPNFLQSRPEPTAPP-ESLRPE
PTAPPPESFRFEAA--TPS---PKQELKDRE---ALTSLSLFGNDHLLQ
>sp|091079|GAG_HV1YF Gag polyprotein OS=Human immunodeficiency virus type 1 grou--More--(10%)

```

Alineamiento múltiple en 20%

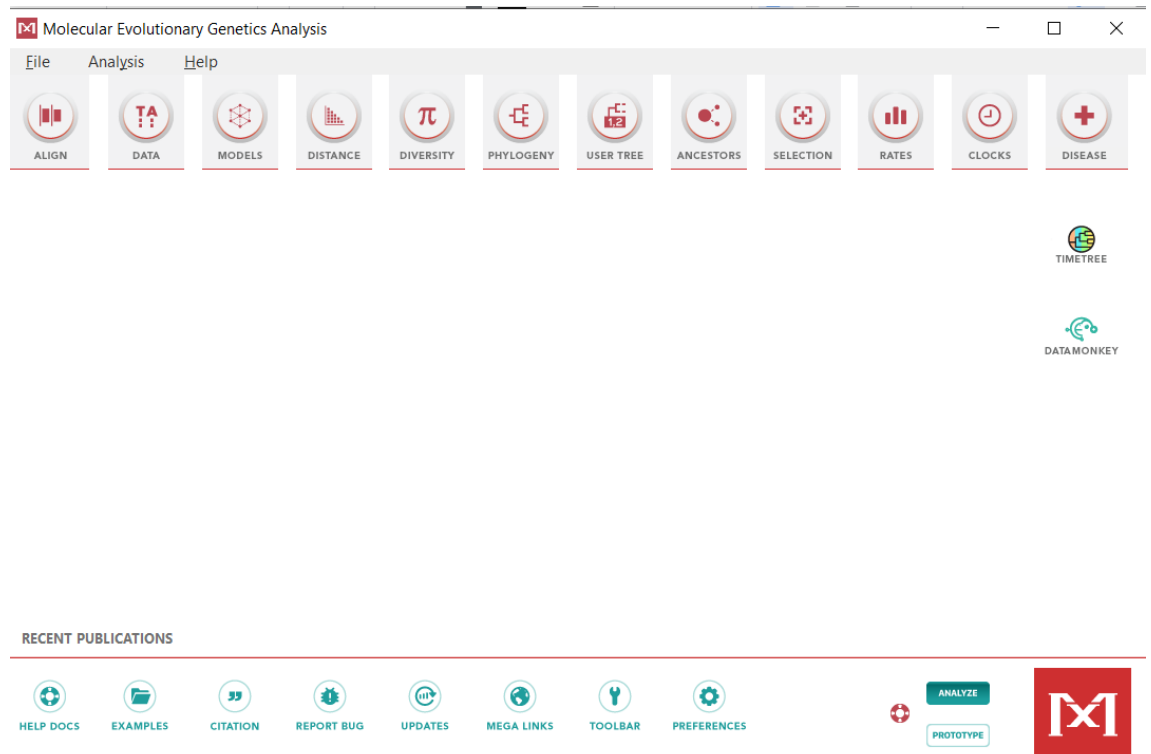
```

>sp|P03349|GAG_HV1A2 Gag polyprotein OS=Human immuredeficiency virus type 1 group M subtype B (isolate ARV2/SF2) OX=11685 GN=gag PE=1 SV=3
MGARASVLSGGELDKWEKIRLRPGGKKKYKLKHIVWASRELERFVNPGLLETSEGCROI
LGQLQPSLQTGSSEELRSLYNTVATLYCVHQRIDVKDTKEALEKIEEQNKSK-KKAQQ--
--AAAAAGTGN---SSQVSQINPIVQNLQGQMMHQATSPRTLNAWVKVVEEKAFSPEVIP
MFALSSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAEWDRLHPVHAGPIAPGQMRE
PRGSDIAGTTSTLQEQIGWMTNPPIPVGEIYKRWIILGLNKIVRMYSPTSILDIRQGP
EPFRDYVDRFYKTLRAEQASQDVKNMMTETLLVQANPDPCKTILKALGPAATLEEMTAC
QGVGGPGHKARVLAEAMSQVNTNPA--NIMQQRGNFRNQRKTVCFCNGKEGHIKACNCRAP
RRKGCWKCGEGHQMKDCTE--RQANFLGKIWPSYKGRPGNFIQ-----SRPE
PTAPPEESFRFGEEKTTPTS---QKQEPIDKELY-PLTSLRSLFGNDPSSQ
>sp|Q75001|GAG_HV1ET Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype C (isolate ETH2220) OX=388796 GN=gag PE=3 SV=3
MGARASILRGEKLDWEKIKLRPGGKKHYMLKHLWANRELEKFAINPDLLDTSAGCKQI
IKQLQPALQTGTEELKSLFNTVATLYCVHQKTEIKDTKEALDKIEEQNESQ-QKTOQ--
---AGAADR-----KDSQINPIVQNMQGMHQIPISARTLNAWVKVVEEKAFSPEVIP
MFALTSEGATPQDLNTMLNTVGGHQAAMQMLKDTINEEAAEWDRLHPVHAGPVAPGQMRE
PRGSDIAGTTSTLQEQIWMGTGNNPPVPVGDYKRWIILGLNKIVRMYSPTSILDIRQGP
EPFRDYVDRFYKTLRAEQATQDVKNMMTDTLLVQANPDPCKTILRALGPASLEEMTAC
QGVGGPAHKARVLAEAMSQVNTN---TIMQKSNFKGPKRAIKCFNGKEGHLARNCRAP
RRKGCWKCGEGHQMKDCTE--RQANFLGRLWPSNKGKRGPNFLQSRPEPTAPP-ESLRPE
PTAPPPESFRFEAA--TPS---PKQELKDRE---ALTSLSLFGNDHLLQ
p N (isolate YB30) OX=388818 GN=gag PE=3 SV=3immunodeficiency virus type 1 grou--More--(10%)
MGARASVLTGGKLDQNEISYLRPGGKKKYRMKHLWASRELERFACNPLNDTADGCAKL
LNQLEPALKTGSSEELRSLYNALAVLYCVHSRIQHINTQEALDKIEKEQEHK-PEPKNPE
AGAAATDS-----NISRNYPVQTAQGMVHQPLTPRTLNAWVKVVEEKAFSPEVIP
MFALSSEGATPQDLNTMLNTVGGHQAAMQMLKEVINEEAAEWDRLHPVHAGPIAPGQMRE
PRGSDIAGTTSTLAEQVAMTANPPVPVGDYKRWIILGLNKIVRMYSPTSILDIRQGP
EPFRDYVDRFYKTLRAEQATQDVKNMMTETLLVQANPDPCKQLKALGPAATLEEMTAC
QGVGGPAHKARVLAEAMSQVNTN---TSVFAQRGNFKGIRKPKTKFCNGKEGHLARNCRAP
RRKGCWKCGEGHQMKDCTE--RQANFLGKIWPSYKGRPGNFIQ-----TTTKE
PTAPPEESFRFGEEKTTPTS---QKQEPIDKELY-PLTSLRSLFGNDPSSQ
>sp|P12495|GAG_HV122 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype D (isolate Z2/CDC-Z34) OX=11683 GN=gag PE=1 SV=3
MGARASVLSGGKLDWEKIKLRPGGKKKYRLKHLWASRELERFANPGLLETSDGCKQI
TGQLQPAIRTGSEELRSLENTVATLYCVHERIEVKDTKEALEKIEEQNKSKNKKAAQ--
---AAADAGN---NSQVSQINPIVQNLQGQMMHQATSPRTLNAWVKVVEEKAFSPEVIP
MFALSSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAEWDRLHPVHAGPIAPGQMRE
PRGSDIAGTTSTLQEQIWMGTGNNPPIPVGEIYKRWIILGLNKIVRMYSPTSILDIRQGP
EPFRDYVDRFYKTLRAEQASQDVKNMMTETLLVQANPDPCKTILKALGPAATLEEMTAC
QGVGGSPHKARVLAEAMSQATNSA-AAVMQQRGNFKGPKRTIKTCFCNGKEGHIKACNCRAP
RRKGCWKCGEGHQLKDCTE--RQANFLGKIWPSHKGKRGPNFIQ-----SRPE
PTAPPAESFRFGEE-ITPS---QKQEQDKELY-PLTSLRSLFGNDPDLLO
>sp|P04591|GAG_HV1H2 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype B (isolate HXB2) OX=11706 GN=gag PE=1 SV=3
--More--(20%)

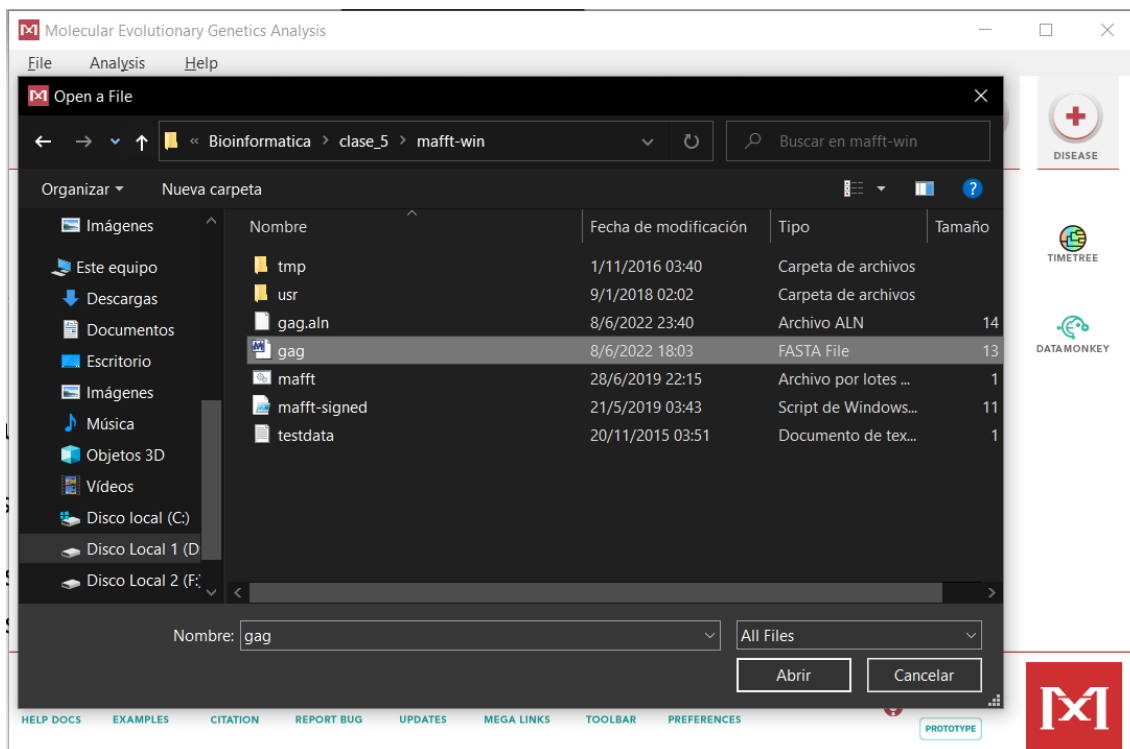
```

2. Usando la herramienta MEGA.

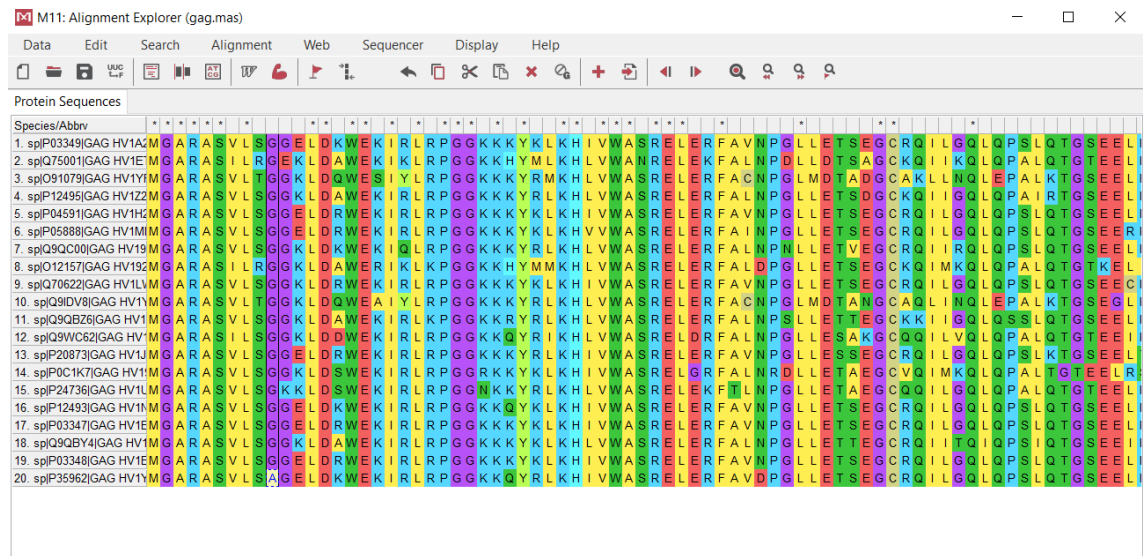
1. Primero descargamos e instalamos MEGA (Molecular Evolutionary Genetics Analysis)



2. Seleccione el archivo Multifasta que desea alinear

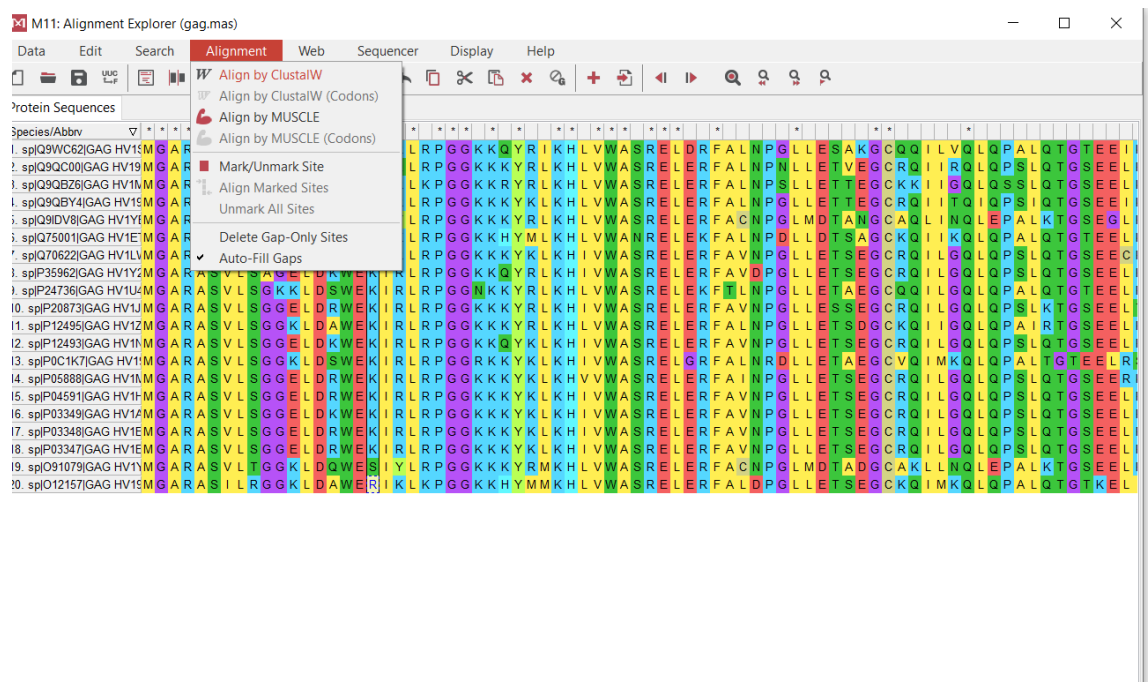


3. Mega abrirá un ventana de Alineamientos de las secuencias de las 20 proteínas



Para realizar la alineación

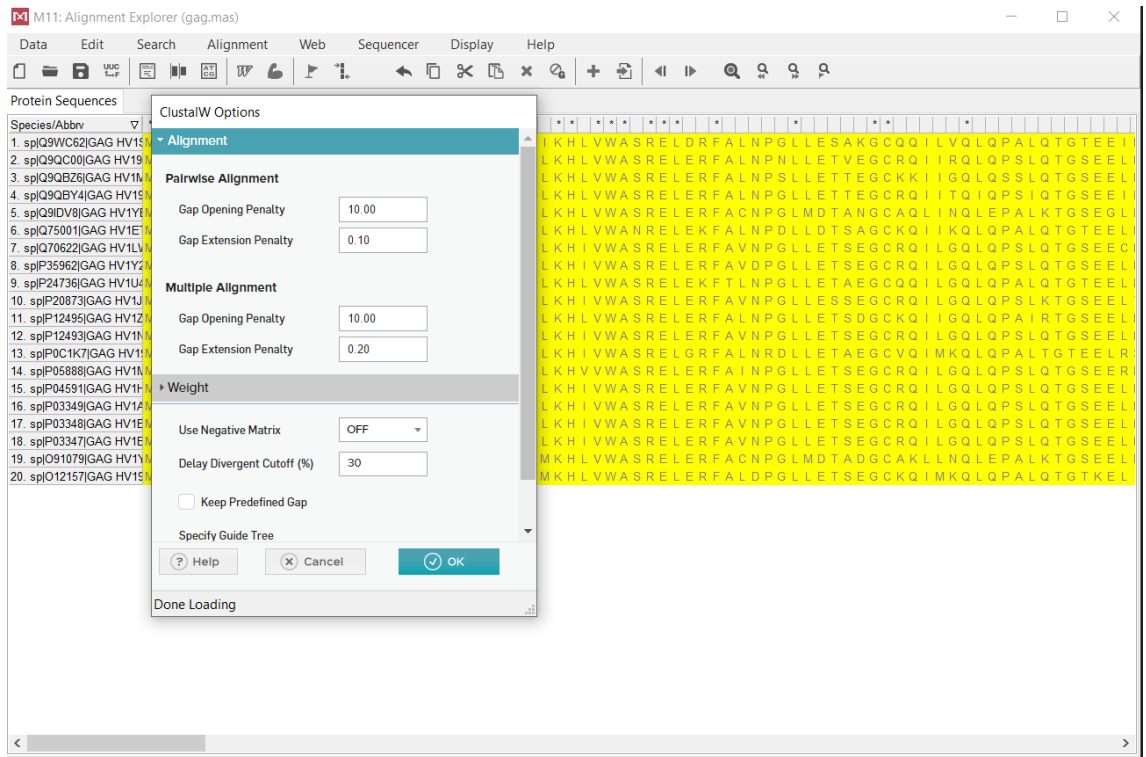
4. Seleccionar secuencias



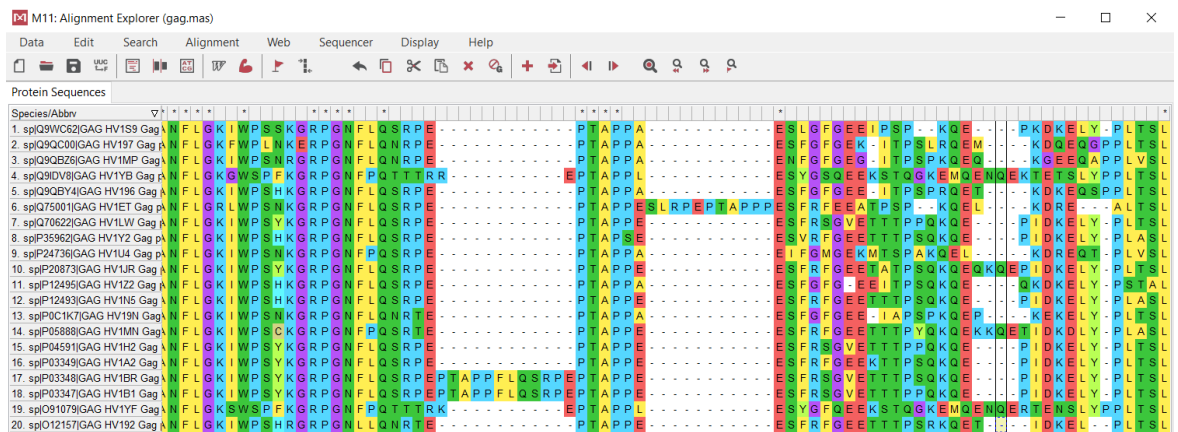
5. Elija el tipo de alineación

a. Alignment, align by CLUSTALW ; ok

Seleccione los parámetros o déjelos por defecto

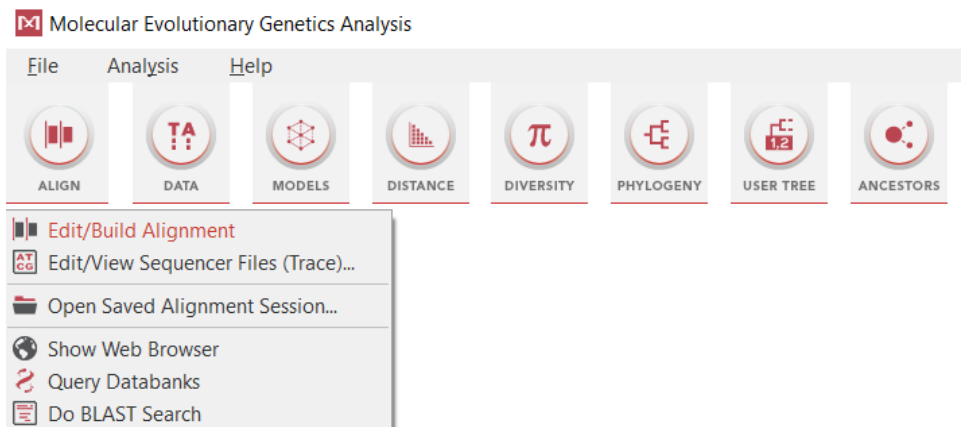


6. Salida POR ALINEAMIENTO CLUSTALW

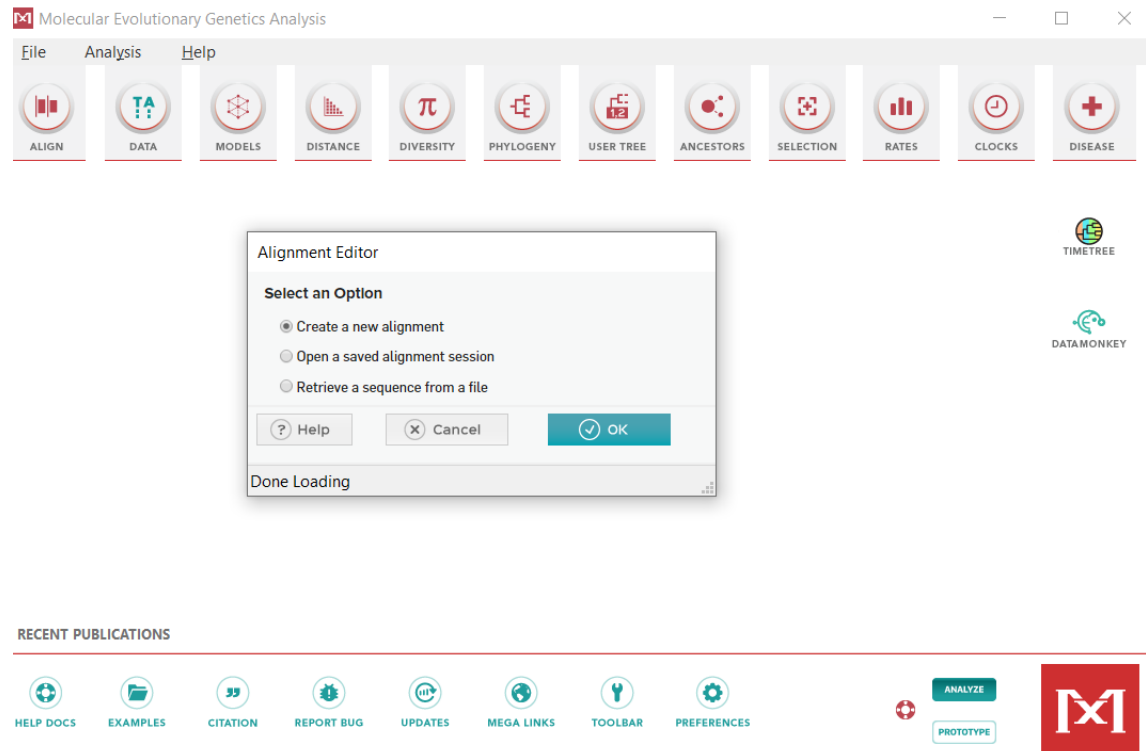


7. Alineación múltiple mediante MUSCLE:
8. Abrimos el programa MEGA
9. En la barra de menú, hacemos clic en:

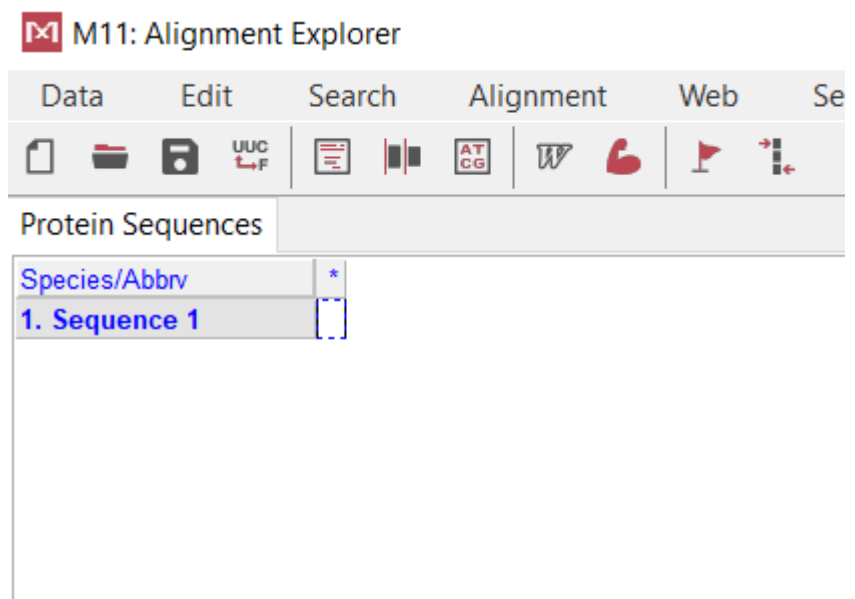
Alinear Editar/Construir Alineación;



10. Seleccionamos: Crear una nueva alineación (pulse en OK) y Proteína (ya que vamos a tratar con secuencias de proteínas)

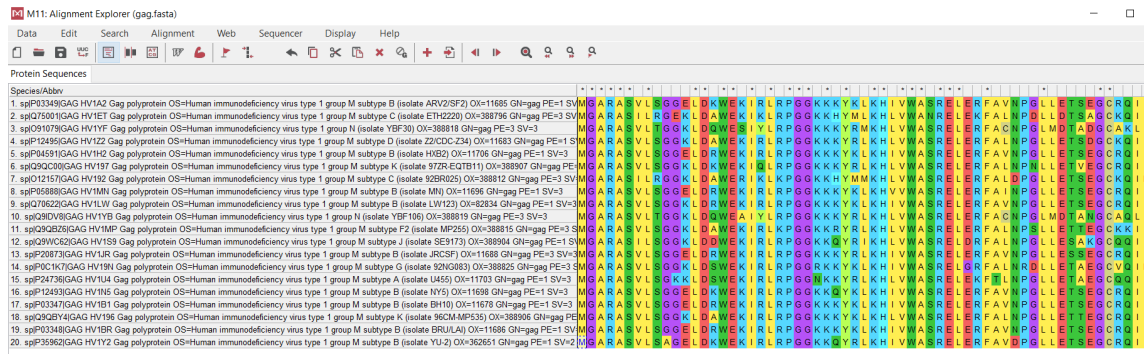


11. Tras abrir la ventana "Alignment Explorer", importe el archivo multi-FASTA (G1.fasta).

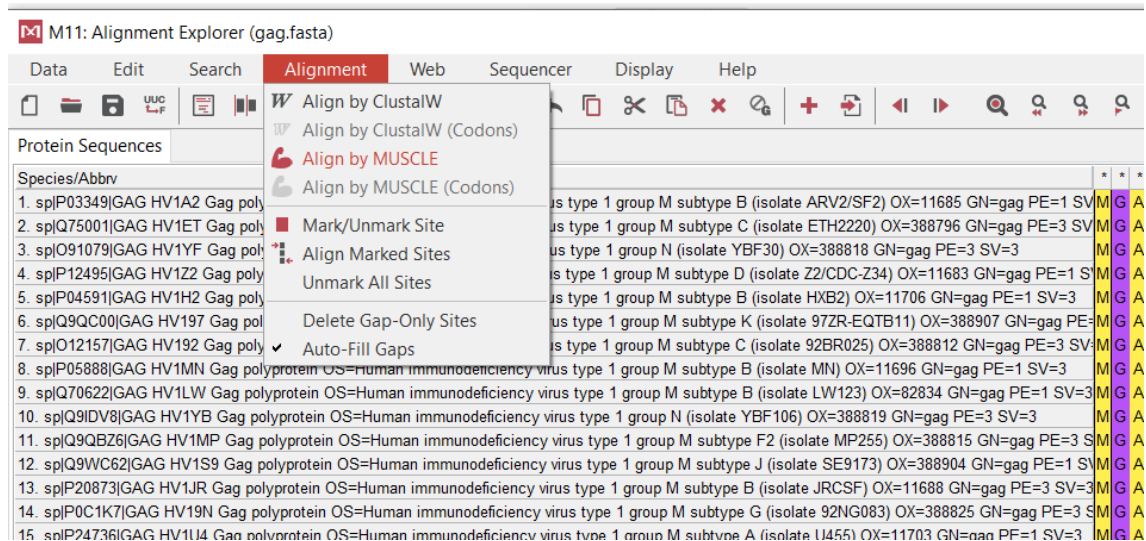


12. Para ello, copie y pegue las secuencias en formato FASTA en el programa o, en el menú, vaya a Editar

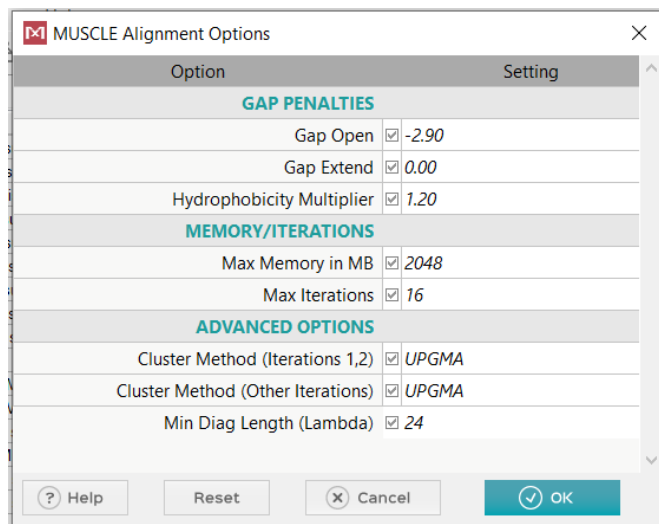
Insertar secuencia desde archivo y seleccionar el archivo multi-FASTA;



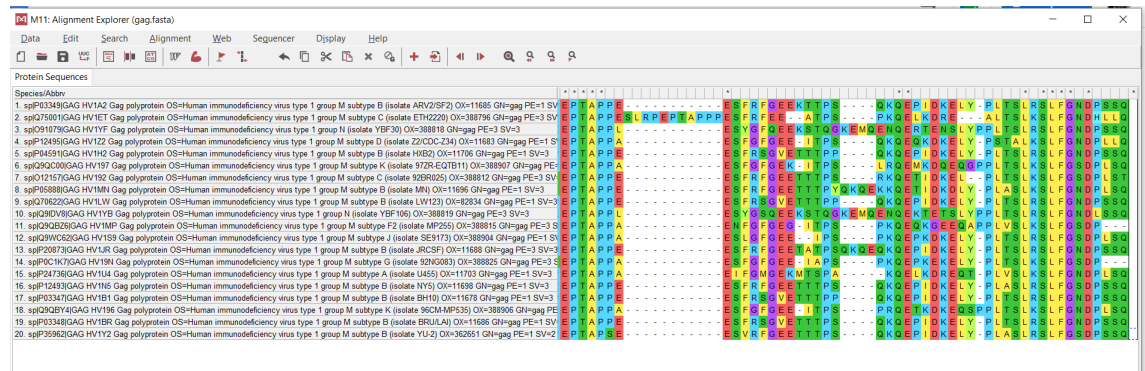
13. En el menú, Alineación ; Alinear por MUSCLE;



14. Deje los parámetros por defecto y pida al programa que se alinee;



15. Salida POR ALINEAMIENTO MUSCLE



16. Obtener la distancia entre las secuencias:
17. Vuelve a la ventana principal de MEGA;
18. En la barra de menú, haga clic en:

Distancia Calcular la distancia entre pares



19. Dejar en los siguientes parámetros:
 - a. Método de estimación de la varianza: Ninguno
 - b. Modelo/método: distancia p
 - c. Tasas entre centros: Tasas uniformes
 - d. Tratamiento de las lagunas/los datos que faltan: supresión por parejas

M11: Analysis Preferences

Distance Estimation

Option	Setting
ANALYSIS	
Scope	→ <i>Pairs of taxa</i>
ESTIMATE VARIANCE	
Variance Estimation Method	→ <i>None</i>
No. of Bootstrap Replications	→ <i>Not Applicable</i>
SUBSTITUTION MODEL	
Substitutions Type	→ <i>Amino acid</i>
Model/Method	→ <i>p-distance</i>
RATES AND PATTERNS	
Rates among Sites	→ <i>Uniform Rates</i>
Gamma Parameter	→ <i>Not Applicable</i>
Pattern among Lineages	→ <i>Same (Homogeneous)</i>
DATA SUBSET TO USE	
Gaps/Missing Data Treatment	→ <i>Pairwise deletion</i>
Site Coverage Cutoff (%)	→ <i>Not Applicable</i>

20. Calcula el resultado;

M11: Pairwise Distances (gagMUSCLE.meg)

	1	2	3	4	5	6
1. sp P03349 GAG HV1A2 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype B (isolate ARV2/SF2) OX=11685 GN=gag PE=1 SV=3						
2. sp Q75001 GAG HV1ET Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype C (isolate ETH2220) OX=388796 GN=gag PE=3 SV=3	0.17444					
3. sp O91079 GAG HV1YF Gag polyprotein OS=Human immunodeficiency virus type 1 group N (isolate YBF30) OX=388818 GN=gag PE=3 SV=3	0.25697	0.26379				
4. sp P12495 GAG HV1Z2 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype D (isolate Z2/CDC-234) OX=11683 GN=gag PE=1 SV=3	0.10020	0.19954	0.24800			
5. sp P04591 GAG HV1H2 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype B (isolate HX82) OX=11706 GN=gag PE=1 SV=3	0.04000	0.16667	0.25400	0.11022		
6. sp P05888 GAG HV1MN Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype B (isolate MN) OX=11696 GN=gag PE=1 SV=3	0.06400	0.17073	0.26786	0.11022	0.05600	
7. sp Q9QC00 GAG HV197 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype K (isolate 97ZR-EQTB11) OX=388907 GN=gag PE=3 SV=2	0.15182	0.16701	0.25455	0.13360	0.14777	
8. sp O12157 GAG HV192 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype C (isolate 92BR025) OX=388812 GN=gag PE=3 SV=3	0.15726	0.10549	0.27823	0.15992	0.16364	
9. sp Q70622 GAG HV1LW Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype B (isolate LW123) OX=82834 GN=gag PE=1 SV=3	0.04200	0.16870	0.25000	0.10822	0.01000	
10. sp Q9IDV8 GAG HV1YB Gag polyprotein OS=Human immunodeficiency virus type 1 group N (isolate YBF106) OX=388819 GN=gag PE=3 SV=3	0.26200	0.27291	0.07662	0.24346	0.26305	
11. sp Q9QB26 GAG HV1MP Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype F2 (isolate MP255) OX=388815 GN=gag PE=3 SV=2	0.16293	0.16189	0.26829	0.14684	0.15886	
12. sp Q9WC62 GAG HV1S9 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype J (isolate SE9173) OX=388904 GN=gag PE=1 SV=3	0.13682	0.16701	0.26962	0.15091	0.14085	
13. sp P20873 GAG HV1JR Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype B (isolate JRC5F) OX=11688 GN=gag PE=3 SV=3	0.04600	0.16463	0.25198	0.10020	0.04400	
14. sp P0C1K7 GAG HV19N Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype G (isolate 92NG083) OX=388825 GN=gag PE=3 SV=2	0.16370	0.17009	0.26831	0.14919	0.16768	
15. sp P24736 GAG HV1U4 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype A (isolate U455) OX=11703 GN=gag PE=1 SV=3	0.14199	0.15746	0.24549	0.15244	0.14807	

[1,1] (sp|P03349|GAG HV1A2 Gag polyprotein OS=Human immunodeficiency virus type 1 group M subtype B (isolate ARV2/SF2) OX=11685 GN=gag PE=1 SV=3-sp|P03349|GAG HV1A2 Gag polyprotein OS=Human immunodeficiency virus type 1 g

21. Guarde la tabla de distancias en formato CSV en su carpeta (Archivo Exportar/Imprimir distancias),

