

Build a phylogenetics tree

With phylogeny.fr

Save your data from FROGS

Galaxy Siginae - Welcome gspascal

Analyze Data Workflow Shared Data Visualization Help User Using 45.2 GB

If there is a 'seed_sequence' column, you can extract seed sequence in a separated FASTA file.

Execute



What it does

Converts a TSV file in BIOM file.

Inputs

Abundance file:
The abundance of each cluster in each sample (format TSV).
Authorized column names : rdp_tax_and_bootstrap, blast_taxonomy, blast_subject, blast_perc_identity, blast_perc_query_coverage, blast_evalue, blast_aln_length, seed_id, seed_sequence, observation_name, observation_sum

Multiple affiliation file:
Which stores the multiple blast hits.

Outputs

Abundance file:
The abundance of each cluster in each sample and theirs metadata (format [BIOM](#)).

Sequence file [optional]:
By checking the "Extract seed FASTA file" option, the sequences will be extract from TSV to [FASTA](#) format.
Be sure that your TSV file contains the seed_sequence column.

How it works

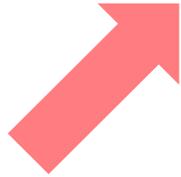
FROGS TSV to Biom will search any metadata (columns before "observation_name") and sample names (columns after "observation_sum").
Then it will reconstruct the Biom abundance file : for each "observation_name" it will add the associated metadata and the samples count.
If metadata include blast_taxonomy, and if blast_subject is equal to "multi-subject", it will parse de multi-hit TSV file, and extract the list of blast affiliations that contain the non-ambiguous blast taxonomy.

History

- 27: FROGS Affiliations stat: summary.html
- 25: FROGS Affiliation OTU: report.html
- 24: FROGS Affiliation OTU: affiliation.biom
- 17: FROGS Filters: report.html
- 16: FROGS Filters: excluded.tsv
- 15: FROGS Filters: abundance.biom
- 14: FROGS Filters: sequences.fasta
470 sequences
format: fasta, database: ?
Application Software:
filters.py (version: 1.3.0)
Command: /usr/local/bioinfo/src/galaxy-test/galaxy-dist/tools/FROGS/app/filters.py --nb-cpus 1 --input-biom /work/galaxy-test/database/files/009/dataset_9136.dat --input-fasta /work/galaxy-test/databas
- 13: FROGS Clusters stat: summary.html



http://phylogeny.lirmm.fr/



The screenshot shows the homepage of the Phylogeny.fr website. At the top left is the LIRMM logo with the text "Methodes et Algorithmes pour la Bio-Informatique". At the top right is a banner for "Information Genomique et Structurale" with a colorful molecular structure. A navigation bar below the logo contains links: Home, Phylogeny Analysis, Blast: Sequence Explorer, Online Programs, Your Workspace, Documentation, Downloads, and Contacts. The main content area features a red text prompt "Please fill this survey (<5mn)", the title "Phylogeny.fr Robust Phylogenetic Analysis For The Non-Specialist", and a blue teapot with a phylogenetic tree growing from its spout. Below this is a dashed box containing text: "Phylogeny.fr is a free, simple to use web service dedicated to reconstructing and analysing phylogenetic relationships between molecular sequences. Phylogeny.fr runs and connects various bioinformatics programs to reconstruct a robust phylogenetic tree from a set of sequences. If you use this site, please cite: Dereeper A., Guignon V., Blanc C., Audic S., Buffet S., Chevenet F., Dufayard J.F., Guindon S., Lefort V., Lescot M., Claverie J.M., Gascuel O. *Phylogeny.fr: robust phylogenetic analysis for the non-specialist*. Nucleic Acids Res. 2008 Jul 1;36(Web Server issue):W465-9. Epub 2008 Apr 19. (PubMed) * joint first authors". A "Mirror site" link is also present. At the bottom left, there are two main sections: "Phylogeny analysis" with sub-options "One Click", "Advanced", and "A la Carte", and "Explore your sequence neighbors".

Please fill this survey (<5mn)

"One Click" Mode Alignment MUSCLE → Curation Gblocks → Phylogeny PhyML

1. Overview 2. Data & Settings

Name of the analysis (optional): A phylogenetic tree from FROGS

Upload your set of sequences in FASTA, EMBL or NEXUS format from a file:

Parcourir... Aucun fichier sélectionné.

Or paste it here (load example of sequences)

Maximum number of sequences is 200 for proteins and 200 for nucleic acids.
Maximum length of sequences is 2000 for proteins and 6000 for nucleic acids.

Names association

Use the Gblocks program to eliminate poorly aligned positions and divergent regions

To receive the results by e-mail, enter your address(es):

Do not attach result files

Submit

Envoi du fichier

grpascal Téléchargements

Rechercher dans : Télécharge...

Nom	Date
Galaxy96-[FROGS_Filters_sequences.fasta].fasta	13/06/201

Aucun aperçu n'est disponible.

Nom du fichier : Galaxy96-[FROGS_Filters_sequences.fasta].fasta

Tous les fichiers (*.*)

Ouvrir Annuler



Please fill this survey (<5mn)



1. Overview 2. Data & Settings

Name of the analysis (optional): A phylogenetic tree from FROGS

Upload your set of sequences in FASTA, EMBL or NEXUS format from

Parcourir... Galaxy96-[FROGS_Filters__sequences.fasta].fasta

Or paste it here (load example of sequences)

Maximum number of sequences is 200 for proteins and 200 for nucleic acids.
Maximum length of sequences is 2000 for proteins and 6000 for nucleic acids.

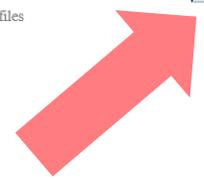
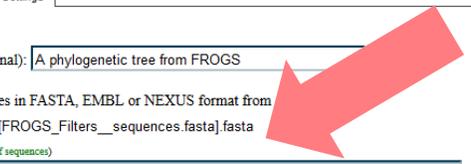
Names association

Use the Gblocks program to eliminate poorly aligned positions and divergent regions

To receive the results by e-mail, enter your address(es):

Do not attach result files

To receive the results by e-mail, enter your address(es): geraldine.pascal@toulouse.inra.fr
 Do not attach result files



Please fill this survey (<5mn)



Tree Rendering results



Preparing TreeDyn input tree! Please wait...

Please cite:

1. Dereeper A., Guignon V., Blanc G., Audic S., Buffet S., Chevenet F., Dufayard J.F., Guindon S., Lefort V., Lescot M., Claverie J.M., Gascuel O. *Phylogeny.fr: robust phylogenetic analysis for the non-specialist*. Nucleic Acids Res. 2008 Jul 1;36(Web Server issue):W465-9. Epub 2008 Apr 19. (PubMed) *: joint first authors
2. Edgar RC. *MUSCLE: multiple sequence alignment with high accuracy and high throughput*. Nucleic Acids Res. 2004, Mar 19;32(5):1792-7. (PubMed)
3. Castresana J. *Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis*. Mol Biol Evol. 2000, Apr;17(4):540-52. (PubMed)
4. Guindon S., Dufayard J.F., Lefort V., Anisimova M., Hordijk W., Gascuel O. *New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0*. Syst Biol. 2010, May;59(3):307-21. (PubMed)
5. Anisimova M., Gascuel O. *Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative*. Syst Biol. 2006, Aug;55(4):539-52. (PubMed)
6. Chevenet F., Brun C., Banuls A.L., Jacq B., Chisten R. *TreeDyn: towards dynamic graphics and annotations for analyses of trees*. BMC Bioinformatics. 2006, Oct 10;7:439. (PubMed)

Your receive an email with the URL

De phylogenyfr-support@lirmm.fr

Sujet **[phylogenyfr-support] Your Phylogeny.fr results: One Click mode (A phylogenetic tree)**

Pour geraldine.pascal@toulouse.inra.fr

This is an automated mail from Phylogeny.fr.

We notify you that the computation you submitted is done. You can find all the results at the following web address:

http://phylogeny.lirmm.fr/phylo/cgi/simple_phylogeny.cgi?workflow_id=4675f3b05144ea489e585a886605073b&tab_index=last

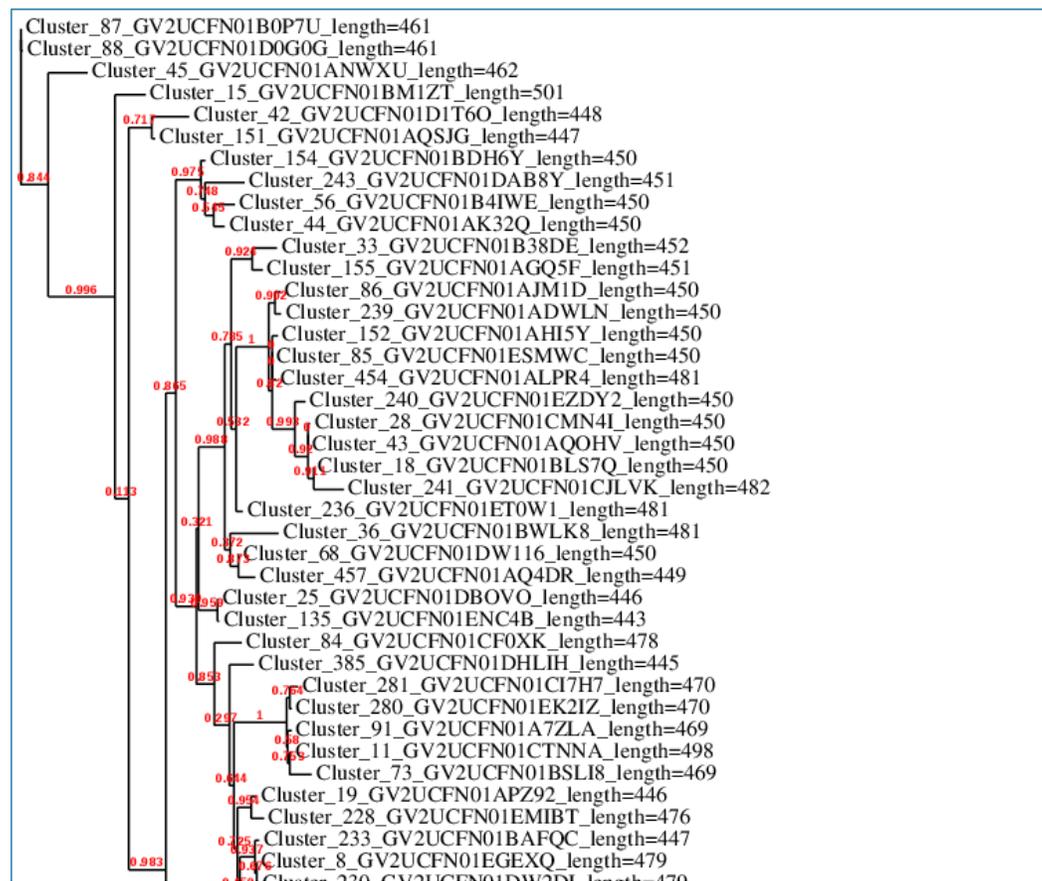
You can reply to this e-mail address and get support in case of trouble.

Thanks for using Phylogeny.fr

Phylogeny.fr Staff



Tree Rendering results



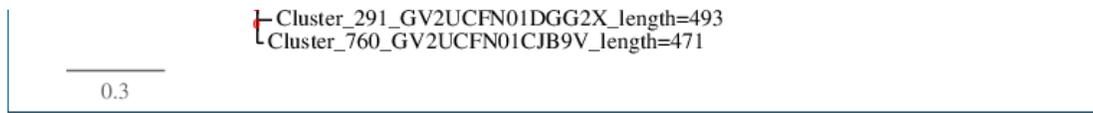


Figure 1: Phylogenetic tree (the branch length is proportional to the number of substitutions per site).

Dynamic Tree Edition

Color leaf using color
 branch and assign the group name

Display:

Branch annotation: Branch support values Branch length values Use color:
 Legend at position Use color:

Ignore branch length

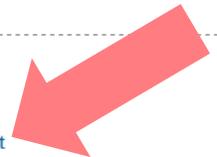
Leaves font:

Tree conformation: Rectangular Radial

Image size: Small Medium Large Extra large

Input:

Tree in Newick format



Tree in Newick format necessary for statistics with Phyloseq

Outputs:

- TreeDyn Graphic File (automatically recognized by TreeDyn if installed)
- Image in Postscript format
- Image in PDF format
- Image in PNG format (bitmap)
- Image in SVG format (vector)
- Rooted tree in Newick format
- Taxon names association table
- Download taxon names association table

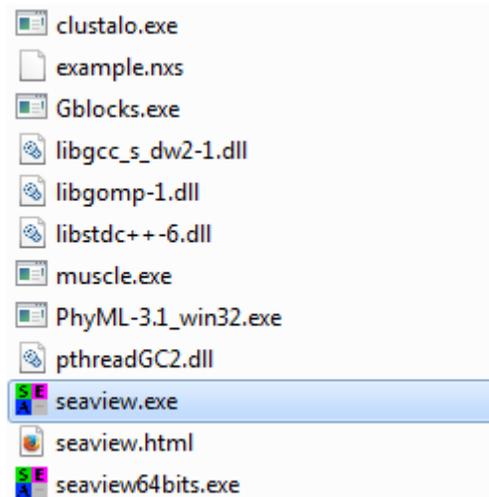
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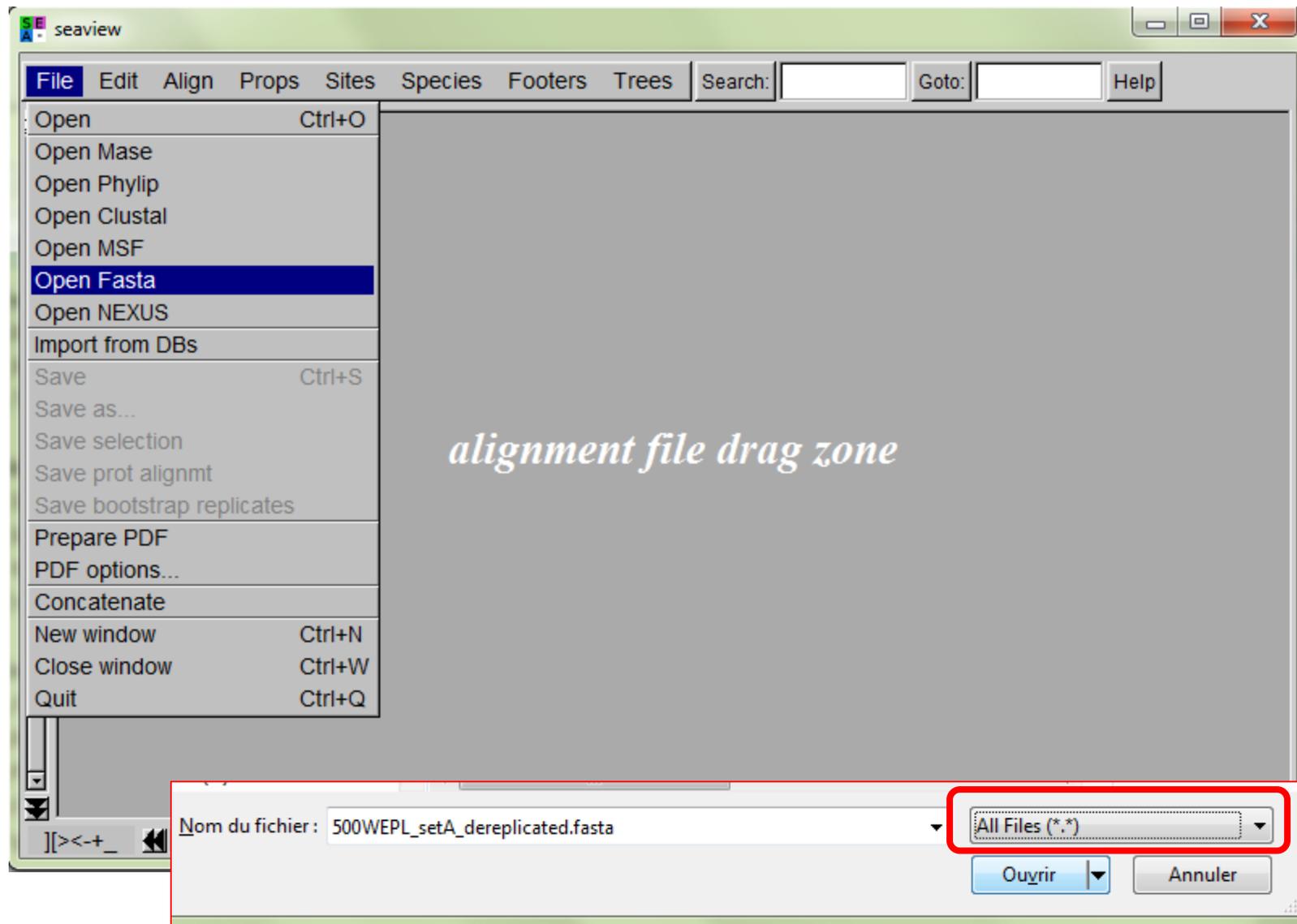
Copy (ctrl+C) the tree in Newick format and save it in a file to use this file in phyloseq.

Build a phylogenetics tree

With seaview (for big number of sequences)

- Download seaview: <http://doua.prabi.fr/software/seaview>
- Install seaview
- Double click on executable





Galaxy23-[FROGS_Filters_sequences.fasta].fasta

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

sel=0 1 Seq:1 Pos:1|1 [Cluster 1] 94

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[><-+_] [Navigation icons]

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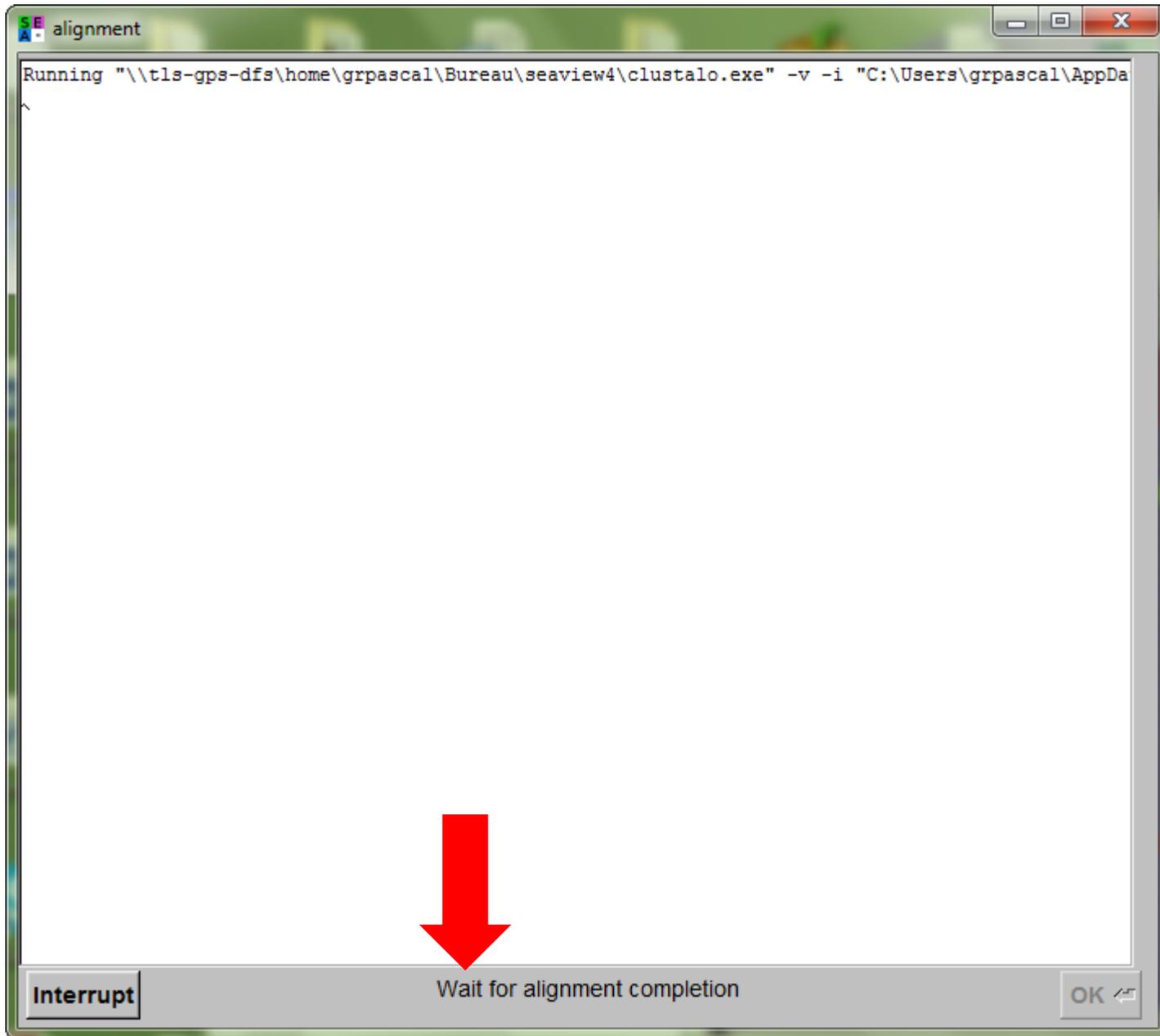
File Edit **Align** Props Sites Species Footers Trees Search: Goto: Help

sel=0 **Align all** os:1|1 [10 72862;size=1] 88

- Align selected sequences
- Align selected sites
- Profile alignment
- De-align selection
- Alignment options

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8 19616 GCAA GGG GAAAG CCT GACCG CAG AAC ACCG G G GGA GA GAAGT CT AGGAA G AAAG C CTTT GTAA
6 1070; s GCAA GGG GAAAG CCT GACCG CAG AAC ACCG G G GGA GA GAAGT CT AGGAA G AAAG C CTTT GTAA
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8 21030; size=1 TGGGAA ATT GCA AAT GGA GGA AACT C GAT GCAG CCA GCCGG G GT GAAGAAGG CCT TGGGG TG AAAG C CTTT CCGGAGG
8 88738; size=1 TGGGAA ATT GCA AAT GGA GGA AACT C GAT GCAG CCA GCCGG G GT GAAGAAGG CCT TGGGG TG AAAG C CTTT CCGGAGG
8 85282; size=1 TGGGAA ATT GCA AAT GGA GGA AACT C GAT GCAG CCA GCCGG G GT GAAGAAGG CCT TGGGG TG AAAG C CTTT CCGGAGG
8 94568; size=1 TGGGAA ATT GCA AAT GGA GGA AACT C GAT GCAG CCA GCCGG G GT GAAGAAGG CCT TGGGG TG AAAG C CTTT CCGGAGG
8 8968; size=1 TGGGAA ATT GCA AAT GGA GGA AACT C GAT GCAG CCA GCCGG G GT GAAGAAGG CCT TGGGG TG AAAG C CTTT CCGGAGG
8 48491; size=1 TGGGAA ATT GCA AAT GGA GGA AACT C GAT GCAG CCA GCCGG G GT GAAG AGG CCT TGGGG TG AAAG C CTTT CCGGAGG
8 56936; size=1 TGGGAA ATT GCA AAT GGA GGA AACT C GAT GCAG CCA GCCGG G GT GAAGAAGG CCT TGGGG TG AAAG C CTTT CCGGAGG
4 84266; size=1 TGGGAA ATT GGG CAA GGG GAAAG CCT GACCG CAG AAC ACCG G G GGA GA GAAGT CT AGGAA G AAAG C CTTT GTAA
1 83167; size=1 TGGGAA ATT GGG CAA GGA CGAAG CT GACCCAG CCA GCCGG G G GAGGA GAAGG CCT CAGCG TG AAAG C CTTT GATA
8 38364; size=1 TGGGAA ATT GGG CAA GGA CGAAG CT GACCCAG CCA GCCGG G G GAGGA GAAGG CCT CAGCG TG AAAG C CTTT GATA
8 11082; size=1 TGGGAA ATT GGG CAA GGA CGAAG CT GACCCAG CCA GCCGG G G GAGGA GAAGG CCT CAGCG TG AAAG C CTTT GATA
6 22167; size=1 TGGGAA ATT GGG CAA GGA GGA AACT C GACCCAG CCA GCCGG G G GAGGA GAAGG CCT CAGCG TG AAAG C CTTT GATA
8 95060; size=1 TGGGAA ATT GGG CAA GGA GGA AACT C GACCCAG CCA GCCGG G G GAGGA GAAGG CCT CAGCG TG AAAG C CTTT GATA
8 91623; size=1 TGGGAA ATT GGG CAA GGA GGA AACT C GACCCAG CCA GCCGG G G GAGGA GAAGG CCT CAGCG TG AAAG C CTTT GATA
8 77097; size=1 TGGGAA ATT GGG CAA GGA GGA AACT C GACCCAG CCA GCCGG G G GAGGA GAAGG CCT CAGCG TG AAAG C CTTT GATA
8 17847; size=1 TGGGAA ATT GGG CAA GGA GGA AACT C GACCCAG CCA GCCGG G G GAGGA GAAGG CCT CAGCG TG AAAG C CTTT GATA

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```
SE alignment
Running "\\tls-gps-dfs\home\grpascal\Bureau\seaview4\clustalo.exe" -v -i "C:\Users\grpascal\AppData
Using 4 threads
Read 96 sequences (type: DNA) from C:\Users\grpascal\AppData\Local\Temp\seaview_tmp5.pir
Using 43 seeds (chosen with constant stride from length sorted seqs) for mBed (from a total of 96
Calculating pairwise ktuple-distances...
Ktuple-distance calculation progress done. CPU time: 0.82u 00:00:00.81 Elapsed: 00:00:01
mBed created 1 cluster/s (with a minimum of 1 and a soft maximum of 100 sequences each)
Distance calculation within sub-clusters done. CPU time: 0.73u 00:00:00.73 Elapsed: 00:00:00
Guide-tree computation (mBed) done.
Progressive alignment progress done. CPU time: 4.82u 00:00:04.81 Elapsed: 00:00:05
Alignment written to C:\Users\grpascal\AppData\Local\Temp\seaview_tmp5.out
WARNING: DNA alignment is still experimental.
```

Cancel Copy all OK ↵

Galaxy23-[FROGS_Filters_sequences.fasta](1).fasta

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

sel=0 1 Seq:1 Pos:1|1 [Cluster 1] Parsimony 94

Cluster_1 YGGGGAAATTTGGACAAATGGGGGAAACCGGATG GAGGACGGCCCTCGGGTGTAAAACCGCTTTAAATGGGAG

Cluster_2 YAGGGAAATTTGGACAAATGGGGGAAACCGGATG GAAGAAAGCAATTCGGTGTAAAACCACTGTCAAGGGAA

Cluster_3 YAGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAAGAAGGCTTCGGTGTAAAACCACTGTCAAGGGAA

Cluster_4 YGGGGAAATTTGGACAAATGGGGGAAACCGGATG GAAGAAGGCTTTGGTGTAAAACCACTTAAGCAGGAA

Cluster_5 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAAGAAGCTTCGGGATGTAAAACCTCGAAGCAACGAA

Cluster_6 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAAGGCCCTAGGGTGTAAAACACTTCAACGGGAA

Cluster_7 YAGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAAGGCCCTAGGGTGTAAAACCGCTTTGCGGGGGAA

Cluster_8 YAGGGAAATTTGGACAAATGGGGGAAACCGGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_9 YAGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_11 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_12 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_13 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_14 YAGGGAAATTTGGACAAATGGGGGAAACCGGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_15 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_16 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_17 YGGGGAAATTTGGACAAATGGGGGAAACCGGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_18 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_19 YGGGGAAATTTGGACAAATGGGGGAAACCGGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_20 YAGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_21 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_22 YAGGGAAATTTGGACAAATGGGGGAAACCGGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_23 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_24 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_25 YAGGGAAATTTGGACAAATGGGGGAAACCGGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_26 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_27 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_28 YGGGGAAATTTGGACAAATGGGGGAAACCGGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_29 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_30 YGGGGAAATTTGGACAAATGGGGGAAACCGGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_31 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_32 YGGGGAAATTTGGACAAATGGGGGAAACCGGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_33 YGGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_34 YGGGGAAATTTGGACAAATGGGGGAAACCGGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

Cluster_35 YAGGGAAATTTGGACAAATGGGGGAAAGCCGATG GAGGAGGGACGGCCGGGAGGAGGAGGAGGCCCTCGGGTGTAAAACCTCGTGGGGGGAA

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PhyML options

Model: **GTR**

Branch Support

aLRT (SH-like) None

Bootstrap with replicates

Show bootstrap trees

Nucleotide equilibrium frequencies

Empirical Optimized

Ts/Tv ratio

Optimized Fixed

Invariable sites

None Optimized Fixed

Across site rate variation

None # of rate categories

Optimized Fixed

Tree searching operations

NNI SPR Best of NNI & SPR

Starting tree

BioNJ Optimize tree topology

User given:

Add: random starts

Quiet



```
tree-building
. Number of data sets: 1
. Nb of bootstrapped data sets: 0
. Compute approximate likelihood ratio test: yes (SH-like branch supports)
. Model name: GTR
. Proportion of invariable sites: 0.000000
. Number of subst. rate categs: ^ 4
. Gamma distribution parameter: estimated
. 'Middle' of each rate class: mean
. Nucleotide equilibrium frequencies: empirical
. Optimise tree topology: yes
. Tree topology search: NNIs
. Starting tree: BioNJ
. Add random input tree: no
. Optimise branch lengths: yes
. Optimise substitution model parameters: yes
. Run ID: none
. Random seed: 1476347211
. Subtree patterns aliasing: no
. Version: 20120412

oooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooo

. 352 patterns found (out of a total of 435 sites).
. 96 sites without polymorphism (22.07%).
. Computing pairwise distances...
. Building BioNJ tree...
. This analysis requires at least 16 of memory space.
. Refining the input tree...
```



Interrupt Wait for tree-building completion OK ↵

File Edit Font Br lengths Br support squared Trim rule:
 Full Swap Re-root Select Subtree Subtree Up Zoom 1.0 Help

