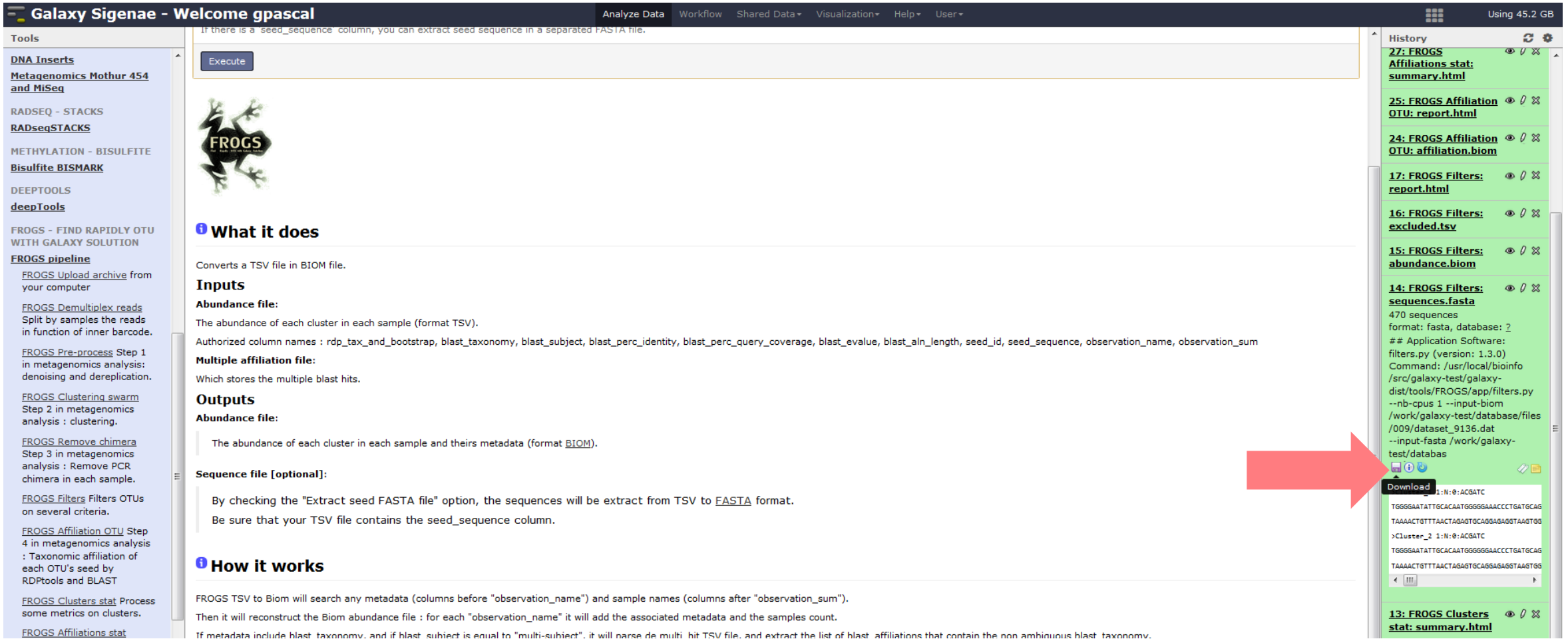
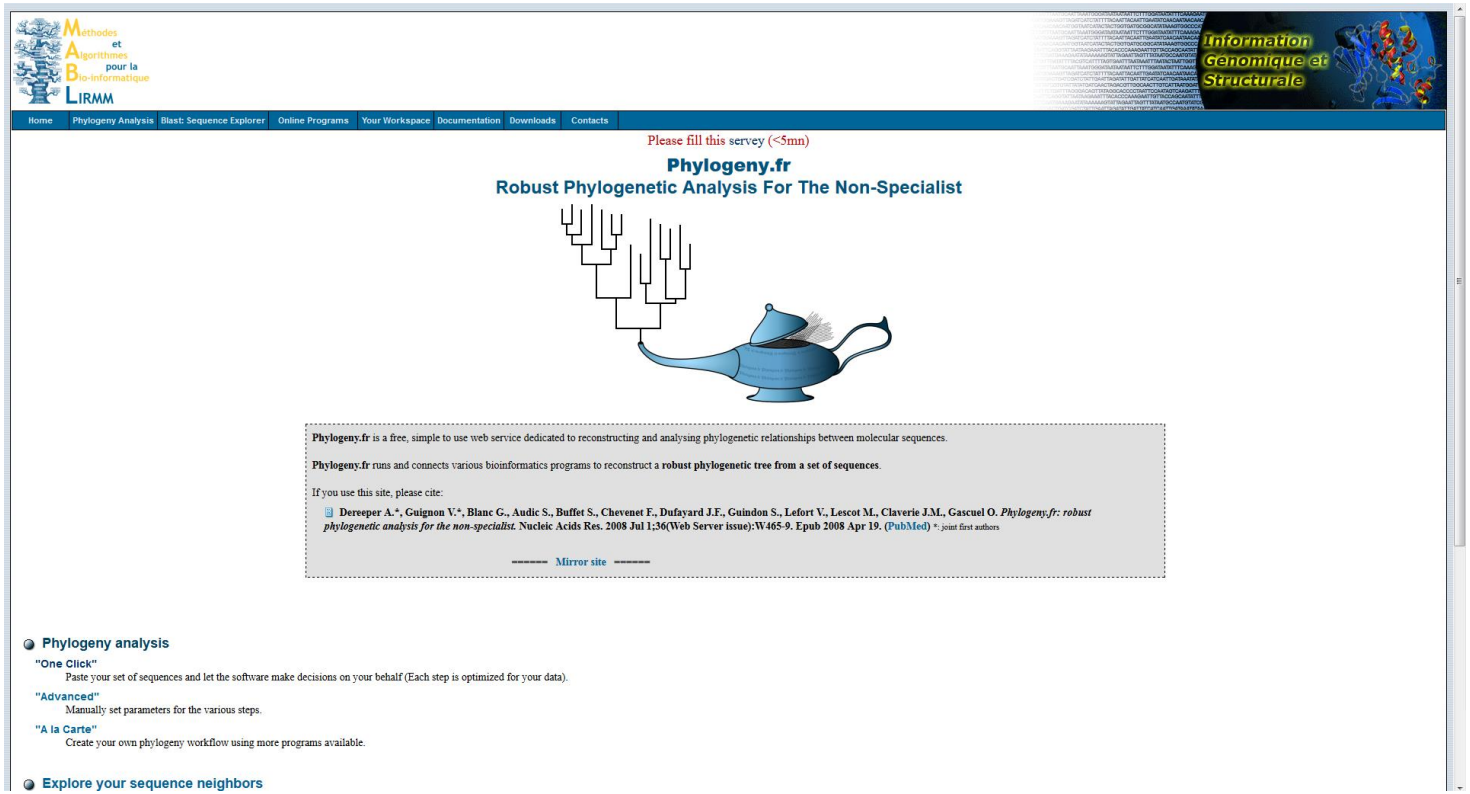
Build a phylogenetics tree

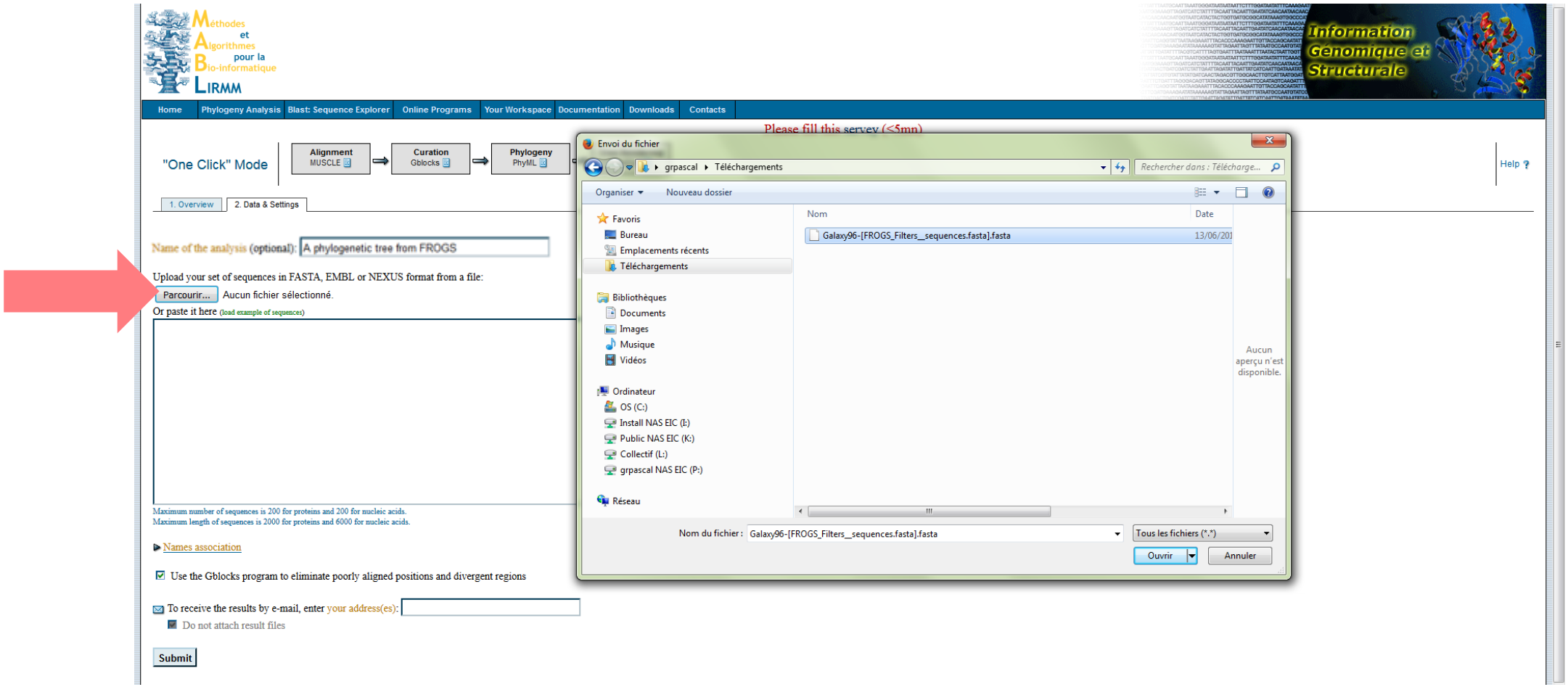
With phylogeny.fr

Save your data from FROGS



http://phylogeny.lirmm.fr/

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Curation Gblocks
Phylogeny PhyML
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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):
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OS (C:)
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Public NAS EIC (K:)
Collectif (L:)
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Réseau
Nom
Date
Galaxy96-[FROGS_Filters__sequences.fasta].fasta
13/06/201
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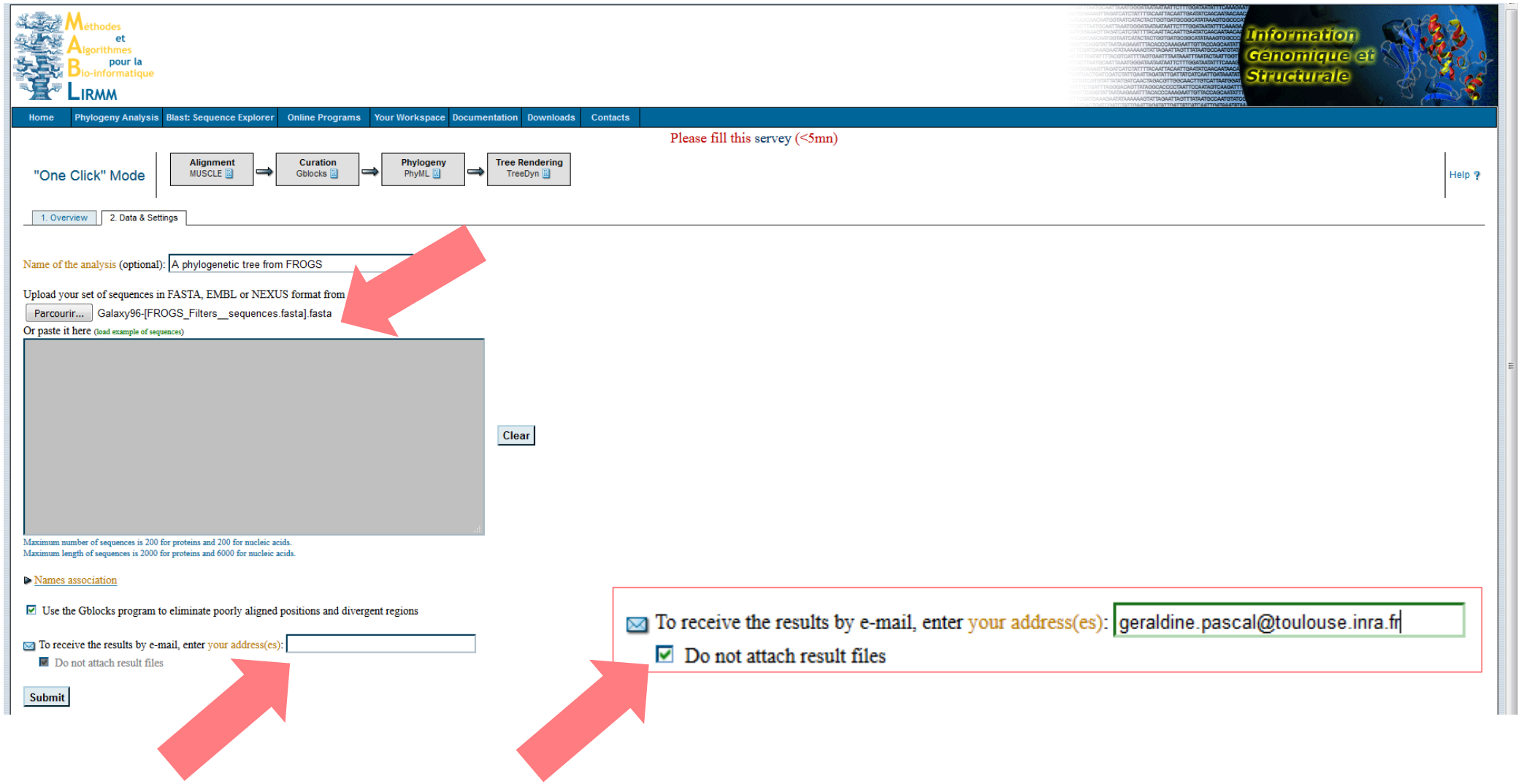
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Clear
Maximum number of sequences is 200 for proteins and 200 for nucleic acids.
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Use the Gblocks program to eliminate poorly aligned positions and divergent regions
To receive the results by e-mail, enter your address(es):
Do not attach result files
Submit
To receive the results by e-mail, enter your address(es): geraldine.pascal@toulouse.inra.fr
Do not attach result files

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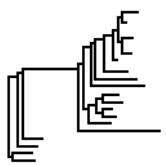
A phylogenetic tree

Alignment MUSCLE → Curation Gblocks → Phylogeny PhyML → Tree Rendering TreeDyn

Help ?

1. Overview | 2. Data & Settings | 3. Alignment | 4. Curation | 5. Phylogeny | 6. Tree Rendering

Tree Rendering results



Waiting for the process is down

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 AL., 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

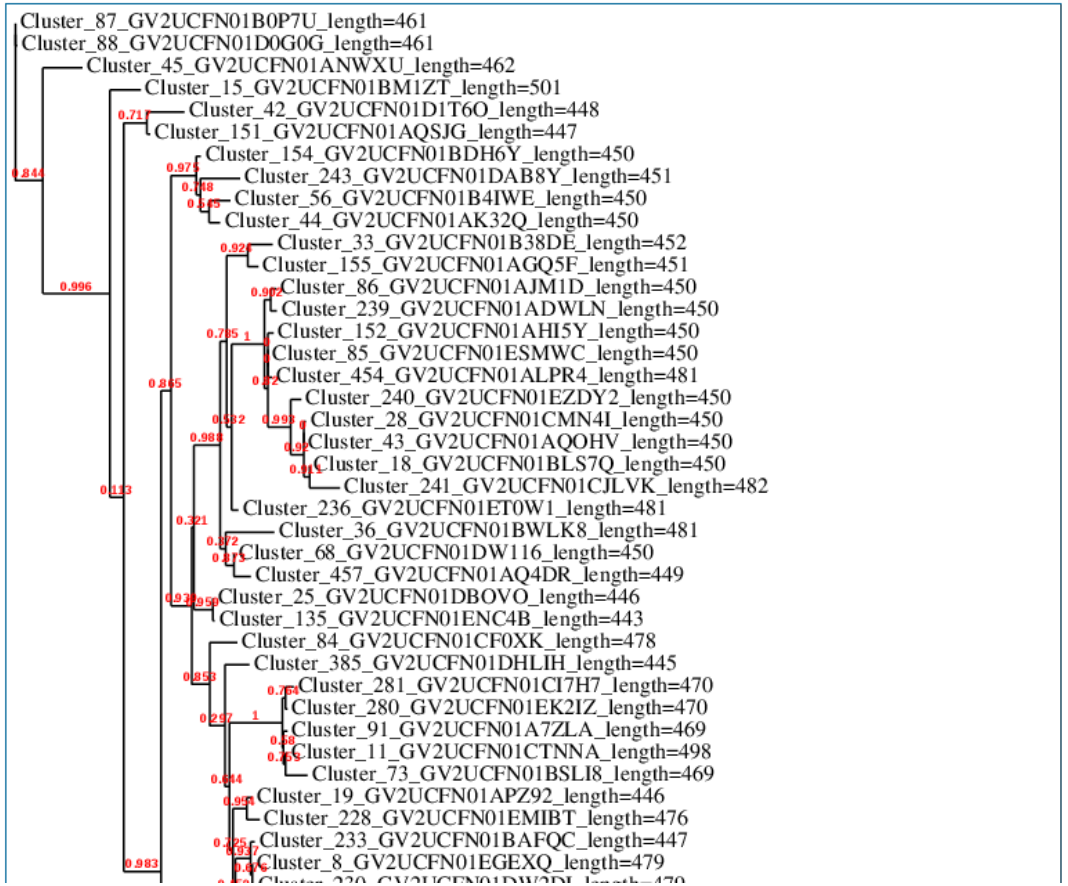


Figure 1: *Phylogenetic tree (the branch length is proportional to the number of substitutions per site).*

Dynamic Tree Edition

Color ☑ leaf ☑ branch using color blue and assign the group name

Reset to original tree | Reroot using **mid-point** rooting | Reroot (**outgroup**)

Flip subtree | **Swap** subtrees | Change **leaf name**

Add **annotations** using color red

Display:

☑ Branch annotation: ◉ Branch support values ○ Branch length values Use color: red

☑ Legend at position 25 , 1750 **Update** Use color: dimgray

☐ Ignore branch length

Leaves font: Times normal 10 **Update**

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.