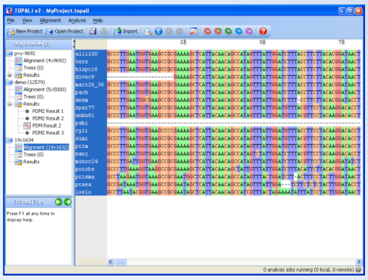
WHAT'S *NEW* IN TOPALi v2

http://www.bioss.ac.uk/knowledge/topali

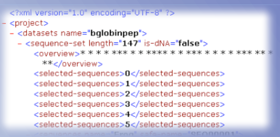
New and improved graphical user interface

TOPALi v2 sports an entirely new graphical user interface that has been redesigned from scratch to improve upon the original TOPALi's interface. On Windows, the interface blends in with Office using the Office Look and Feel, while on Unix or Linux the popular JGoodies "Looks" is used.



XML Based Project Structure

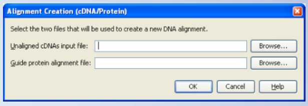
TOPALi now uses a XML based structure for its project files (which are stored compressed), allowing for better compatibility with other programs that want to share its data.



```
  <?xml version="1.0" encoding="UTF-8" ?>
- <project>
 - <datasets name="bglobinpep">
  - <sequence-set length="147" is-dNA="false">
      <overview>* * * * *** * * **** * * *** * * * * *** ** *
       **</overview>
      <selected-sequences>0</selected-sequences>
      <selected-sequences>1</selected-sequences>
      <selected-sequences>2</selected-sequences>
      <selected-sequences>3</selected-sequences>
      <selected-sequences>4</selected-sequences>
      <selected-sequences>5</selected-sequences>
```

Combine cDNA and Guide Protein

Protein multiple alignment algorithms produce better results than do DNA multiple alignment algorithms. TOPALi now allows you to create a DNA alignment by using the data from cDNA and a guide protein alignment when importing a new dataset.



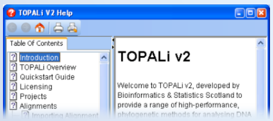
Select the two files that will be used to create a new DNA alignment.

Unaligned cDNAs input file:

Guide protein alignment file:

Integrated JavaHelp User Manual

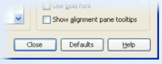
The user manual for TOPALi v2 is now integrated into the application in JavaHelp format, allowing you to easily move between help sections or to print areas of interest.



TOPALi v2

Welcome to TOPALi v2, developed by Bioinformatics & Statistics Scotland to provide a range of high-performance, phylogenetic methods for analysing DNA

All TOPALi dialogs now have access to the help system directly from the dialog, which will jump you straight to the relevant section of help for that dialog.



☐ Use bold font

☐ Show alignment pane tooltips

Alignment Overviews

Using the Alignment Overview feature you can view the entire alignment in a floating window while still working with a close-up area in detail. Scrolling around the overview automatically moves the main display too.

Dim Unselected Sequences

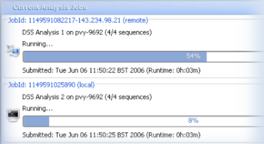
By ticking the option in the Display Settings, you can have TOPALi dim sequences that are not currently selected, making it easier to focus on those that are.

Run Jobs Remotely and in Parallel

TOPALi now runs its main analysis jobs on remote HPC clusters, which frees up your PC for other tasks while you wait on results. You can submit more than one job at a time too, and they'll queue up for running later if no slots are currently available on the cluster.

JobId: 1134134227736.143.234.98.21 (remote)
HMM Analysis 2 on pvy-9692 (4/4 sequences)
Running...
Submitted: Fri Dec 09 13:16:46 GMT 2005 (Runtime: 0h:02m)

JobId: 1134134234561.143.234.98.21 (remote)
DSS Analysis 1 on pvy-9692 (4/4 sequences)
Running...



JobId: 1149591082217-143.234.98.21 (remote)
DSS Analysis 1 on pvy-9692 (4/4 sequences)
Running...
Submitted: Tue Jun 06 11:50:22 BST 2006 (Runtime: 0h:03m)

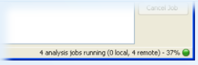
JobId: 1149591025890 (local)
DSS Analysis 2 on pvy-9692 (4/4 sequences)
Running...
Submitted: Tue Jun 06 11:50:25 BST 2006 (Runtime: 0h:03m)

Many of these tasks are designed to run in parallel – both on clusters and on desktop PCs with more than one processor. This obviously has a dramatic effect in reducing the time taken to complete a job.

Support for Drag n Drop

On supported systems, you can use standard drag and drop operations to load alignments or TOPALi projects into the application. TOPALi supports dragging and dropping of more than one alignment at a time too.

Monitor Analysis Jobs

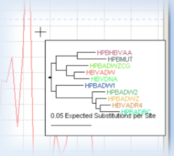


4 analysis jobs running (0 local, 4 remote) - 37%

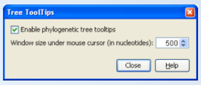
As your analysis jobs run (either locally or remotely) their status is continually tracked by TOPALi and displayed in the status bar. A coloured icon represents overall job status - green for OK, blue for communication errors, and red for critical job errors!

Floating Tree Tooltips

By using floating tree tooltips, you can instantly view a phylogenetic tree of the area currently under the mouse cursor.



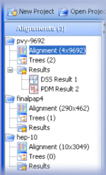
The feature can be enabled on a per-graph basis.



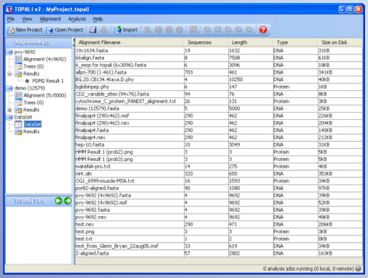
☑ Enable phylogenetic tree tooltips

Window size under mouse cursor (in nucleotides): 500

Work with Multiple, Multiple Alignments



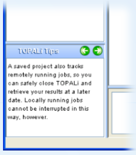
A TOPALi project can now import and deal with as many DNA/Protein alignments as your PC has memory for. Each alignment in listed in a new "tree" view down the left-hand side of the screen, along with all the analysis results that relate to that dataset.



You can also import hundreds of multiple alignments at once into a single dataset entity. Future plans will allow comparison of loci in terms of rate heterogeneity and tree topology.

TOPALi Tips

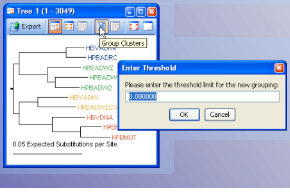
Each area of the TOPALi interface now comes with tips to help you work more effectively with it, requiring less visits to the help system to learn how to use the program.



A saved project also tracks remotely running jobs, so you can safely close TOPALi and retrieve your results at a later date. Locally running jobs cannot be interrupted in this way, however.

Create Groups From Trees and Extract Representatives

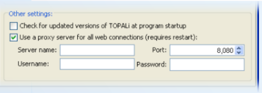
You can use tree similarities to group clusters of sequences that are close to one another in a phylogenetic tree (similar sequences are coloured the same). A representative sequence from each group can then be selected in the original dataset.



Please enter the threshold limit for the new grouping: 0.080000

Support for Authenticating Proxy Servers

If you are behind a proxy server that controls your access to the internet, TOPALi can be set to send all its internet requests through this machine. Support for proxies that require authentication (including NTLM) is included.



Other settings:

☐ Check for updated versions of TOPALi at program startup

☑ Use a proxy server for all web connections (requires restart):

Server name:

Port: 8,080

Username:

Password:

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