Help ClustalW

LAUNCH APPLICATION

• INTRODUCTION

Multiple alignments of protein sequences are important tools in studying sequences. The basic information they provide is identification of conserved sequence regions. This is very useful in designing experiments to test and modify the function of specific proteins, in predicting the function and structure of proteins, and in identifying new members of protein families.

Sequences can be aligned across their entire length (global alignment) or only in certain regions (local alignment). This is true for pairwise and multiple alignments. Global alignments need to use gaps (representing insertions/deletions) while local alignments can avoid them, aligning regions between gaps. ClustalW is a fully automatic program for global multiple alignment of DNA and protein sequences. The alignment is progressive and considers the sequence redundancy. Trees can also be calculated from multiple alignments. The program has some adjustable parameters with reasonable defaults.

ClustalW Nucleotide Tutorial
ClustalW Protein Tutorial

For additional help on ClustalW also see:

- **ClustalW FAQ**
- **ClustalW Improving Sensitivity**

• YOUR SEQUENCES

Please make sure that your sequences have different names as the first 30 characters of the name are significant. If clustalw finds two or more sequences with the same name it will fail! View example. Click here for more information on sequence errors.

ClustalW currently supports 7 multiple sequence formats. These are:

- NBRF/PIR
- EMBL / UniProtKB/Swiss-Prot
- Pearson (Fasta)
- GDE
- ALN/ClustalW
- GCG/MSF
- RSF

More on Sequence Formats

Please remove any white space space or empty lines from the beginning of your input.

No bootstrap analysis allowed via the website as it is is too cpu intensive .It is possible to perform bootstrap analysis or to get the Bootstrap values along with the nodes of each branch of the phylogram, to do this you will need to download the software (available

from the clustal page) and run this locally.

- **YOUR EMAIL**

  You must type your email address in this text box if you are running a job via email. It is not necessary to fill in the box if you are running your search interactively.

- **ALIGNMENT TITLE**

  You may type any text you want to help you identify your search results.

- **RESULTS**

  This option lets you choose between email and interactive runs. The email run requires you to type an email address in the email text box, and your results will be delivered when they are ready to your email address, thus avoiding waiting for your results as with an interactive run. For example: joe@somewhere.domain.country.

  The default is interactive.

- **ALIGNMENT**

  You may choose to run a full alignment or using a stringent algorithm for generating the tree guide or a fast algorithm.

- **CPU MODE**

  The multiple CPU option run a special version of clustalw using several linux pc nodes in a parallel fashion to increase the speed of the job without compromising the quality of the results. This option is to be chosen when the user has a large number of sequences (50+ but less than 500) to align. However, care should be taken not to overestimate the quantification of the results. A very large alignment is difficult to read and handle by other software.

- **OUTPUT**

  Here you decide which output format you want your multiple sequence alignment in. The options are ALN, GCG, PHYLIP, PIR and GDE. The output results are stored in a ".aln" file which contains your results in ALN format.

  You can configure your browser to automatically load the results files from clustalw into an suitable application of your choice. Here is a small list of URL's for obtaining such applications for Win95, Macs and UNIX boxes:

  - **belvu - UNIX Multiple sequence alignment viewer -** http://www.cgr.ki.se/cgr/groups/sonnhammer/Belvu.html
  - **njplot - UNIX, Mac & PC - Tree viewer -** http://pbil.univ-lyon1.fr/software/njplot.html
  - GeneDoc - GCG MSF file viewer - **(NB - Use GCG format in the OUTPUT option) -** http://www.psc.edu/biomed/genedoc/
  - **TreeView - Tree viewer for Macs and PC (running Windows)**

http://taxonomy.zoology.gla.ac.uk/rod/treeview.html

- **ClustalX - Graphical Interface X-Windows/Mac/Win9x based version of ClustalW**
  ftp://ftp.ebi.ac.uk/pub/software/dos/clustalx/
  ftp://ftp.ebi.ac.uk/pub/software/mac/clustalx/
  ftp://ftp.ebi.ac.uk/pub/software/unix/clustalx/
- **ClustalW - Command line version**
  ftp://ftp.ebi.ac.uk/pub/software/dos/clustalw/
  ftp://ftp.ebi.ac.uk/pub/software/mac/clustalw/
  ftp://ftp.ebi.ac.uk/pub/software/unix/clustalw/
- **CINEMA -**
  A Colour INteractive Editor for Multiple Alignments
  http://www.bioinf.man.ac.uk/dbbrowser/CINEMA2.1/
- **EMMA-**
  An EMBOSS interface to clustalw.
  http://www.emboss.org/

To configure your browser you must tell it how to handle the following non-registered MIME types:

- application/x-tree njplot %s (or whatever application you choose to handle the MIME type)
- application/x-align belvu %s (or whatever application you choose to handle the MIME type)

JalView: A new experimental option has been added to the results page which involved using a Java Applet called JalView. This is a fully featured MSA editor which allows you not only to edit the alignment but also, to exchange the alignment formats. Please note that JalView is under development. For documentation please click on the JalView Hyperlink or visit the official website at http://www.jalview.org.

OUTORDER

Decide which order the sequences should be printed in the alignment.

COLOUR

Show Colors

A button labeled 'Show Colors' will be displayed in the Alignment section of results page. If you press this button the alignment will be show in color according to the table below.

NOTE: NOTE: This option only works when you have chosen ALN or GCG as the output format.

AVFPMILW	RED	Small (small+ hydrophobic (incl.aromatic -Y))
DE	BLUE	Acidic
RHK	MAGENTA	Basic
STYHCNGQ	GREEN	Hydroxyl + Amine + Basic - Q
Others	Gray	

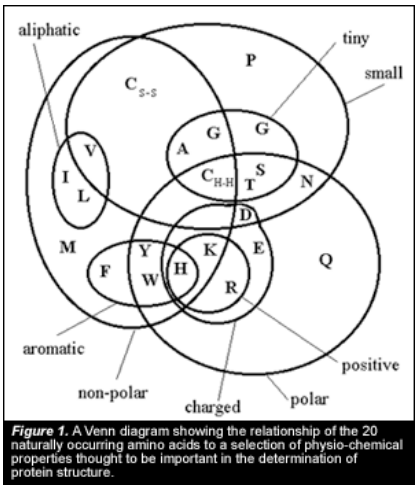


Figure 1. A Venn diagram showing the relationship of the 20 naturally occurring amino acids to a selection of physio-chemical properties thought to be important in the determination of protein structure.

Hide Colors

A button labeled 'Hide Colors' will be displayed in the result page is the 'Show colors' button has been pressed. This option will display the alignment in normal text with no colors.

The default is not to colour the alignments.

CONSENSUS SYMBOLS:

An alignment will display by default the following symbols denoting the degree
of conservation observed in each column:

"*" means that the residues or nucleotides in that column are identical in all
sequences in the alignment.

":" means that conserved substitutions have been observed, according to the
COLOUR table above.

"." means that semi-conserved substitutions are observed.

More on sequence/alignment formats

FAST PAIRWISE ALIGNMENT OPTIONS:

- **KTUP**
  This option allows you to choose which 'word-length' to use when calculating fast pairwise alignments.(note: make sure you have chosen 'fast' in the ALIGNMENT.

- **WINDOW**
  Use this option to set the window length when calculating fast pairwise alignments.(Note: make sure you have chosen 'fast' in the

ALIGNMENT.

- **SCORE**
  This option allows you to decide which score to take into account when calculating a fast pairwise alignment. (Note: make sure you have chosen 'fast' in the ALIGNMENT.

- **TOPDIAG**
  Select here how many top diagonals should be integrated when calculating a fast pairwise alignment.(Note: make sure you have chosen 'fast' in the ALIGNMENT.

- **PAIRGAP**
  Select here to set the gap penalty when generating fast pairwise alignments.

MULTIPLE SEQUENCE ALIGNMENT OPTIONS:

- **MATRIX**
  This option allows you to choose which matrix series to use when generating the multiple sequence alignment. The program goes through the chosen matrix series, spanning the full range of amino acid distances.
  - *BLOSUM (Henikoff).* These matrices appear to be the best available for carrying out data base similarity searches. The matrix used is Blosum30.
  - *PAM (Dayhoff).* These have been extremely widely used since the late '70s. We use the PAM 350 matrix.
  - *GONNET.* These matrices were derived using almost the same procedure as the Dayhoff one (above) but are much more up to date and are based on a far larger data set. They appear to be more sensitive than the Dayhoff series. We use the GONNET 250 matrix.

    We also supply an identity matrix which gives a score of 10 to two identical amino acids and a score of zero otherwise.

  - Default values are:
    - ***DNA:*** *DNA Identity matrix.*
    - ***Protein:*** *Gonnet 250.*

More on Matrices

- **GAPOPEN**
  You can set here the penalty for opening a gap.

  Default values are:
  - ***DNA:*** *15.0*
  - ***Protein:*** 10.0

- **ENDGAP**
  You can set here the penalty for closing a gap.

  Default value is -1.

- **GAPEXT**
  You can set here the penalty for extending a gap.

  Default values are:
  - ***DNA:*** *6.66*
  - ***Protein:*** 0.2

- **GAPDIST**
  You can set here the gap separation penalty.

  Default value is 4.

More about gaps.

- **EXAMPLE**

e.g. A multiple sequence alignment was done with ClustalW. 5 sequences were input in the fasta format (Download):

```
>FOSB_MOUSE Protein fosB
      MFQAFPGDYD SGSRCSSSPS AESQYLSSVD SFGSPPTAAA SQECAGLGEM PGSFVPTVTA
      ITTSQDLQWL VQPTLISSMA QSQGQPLASQ PPAVDPYDMP GTSYSTPGLS AYSTGGASGS
      GGPSTSTTTS GPVSARPARA RPRRPREETL TPEEEEKRRV RRERNKLAAA KCRNRRRELT
      DRLQAETDQL EEEKAELESE IAELQKEKER LEFVLVAHKP GCKIPYEEGP GPGPLAEVRD
      LPGSTSAKED GFGWLLPPPP PPPLPFQSSR DAPPNLTASL FTHSEVQVLG DPFPVVSPSY
      TSSFVLTCPE VSAFAGAQRT SGSEQPSDPL NSPSLLAL

>FOSB_HUMAN Protein fosB
      MFQAFPGDYD SGSRCSSSPS AESQYLSSVD SFGSPPTAAA SQECAGLGEM PGSFVPTVTA
      ITTSQDLQWL VQPTLISSMA QSQGQPLASQ PPVVDPYDMP GTSYSTPGMS GYSSGGASGS
      GGPSTSGTTS GPGPARPARA RPRRPREETL TPEEEEKRRV RRERNKLAAA KCRNRRRELT
      DRLQAETDQL EEEKAELESE IAELQKEKER LEFVLVAHKP GCKIPYEEGP GPGPLAEVRD
      LPGSAPAKED GFSWLLPPPP PPPLPFQTSQ DAPPNLTASL FTHSEVQVLG DPFPVVNPSY
      TSSFVLTCPE VSAFAGAQRT SGSDQPSDPL NSPSLLAL

>FOS_CHICK Proto-oncogene protein c-fos
      MMYQGFAGEY EAPSSRCSSA SPAGDSLTYY PSPADSFSSM GSPVNSQDFC TDLAVSSANF
      VPTVTAISTS PDLQWLVQPT LISSVAPSQN RGHPYGVPAP APPAAYSRPA VLKAPGGRGQ
      SIGRRGKVEQ LSPEEEEKRR IRRERNKMAA AKCRNRRREL TDTLQAETDQ LEEEKSALQA
      EIANLLKEKE KLEFILAAHR PACKMPEELR FSEELAAATA LDLGAPSPAA AEEAFALPLM
      TEAPPAVPPK EPSGSGLELK AEPFDELLFS AGPREASRSV PDMDLPGASS FYASDWEPLG
      AGSGGELEPL CTPVVTCTPC PSTYTSTFVF TYPEADAFPS CAAAHRKGSS SNEPSSDSLS
      SPTLLAL

>FOS_RAT Proto-oncogene protein c-fos
      MMFSGFNADY EASSSRCSSA SPAGDSLSYY HSPADSFSSM GSPVNTQDFC ADLSVSSANF
      IPTVTAISTS PDLQWLVQPT LVSSVAPSQT RAPHPYGLPT PSTGAYARAG VVKTMSGGRA
      QSIGRRGKVE QLSPEEEEKR RIRRERNKMA AAKCRNRRRE LTDTLQAETD QLEDEKSALQ
      TEIANLLKEK EKLEFILAAH RPACKIPNDL GFPEEMSVTS LDLTGGLPEA TTPESEEAFT
      LPLLNDPEPK PSLEPVKNIS NMELKAEPFD DFLFPASSRP SGSETARSVP DVDLSGSFYA
      ADWEPLHSSS LGMGPMVTEL EPLCTPVVTC TPSCTTYTSS FVFTYPEADS FPSCAAAHRK
      GSSSNEPSSD SLSSPTLLAL

>FOS_MOUSE Proto-oncogene protein c-fos
      MMFSGFNADY EASSSRCSSA SPAGDSLSYY HSPADSFSSM GSPVNTQDFC ADLSVSSANF
      IPTVTAISTS PDLQWLVQPT LVSSVAPSQT RAPHPYGLPT QSAGAYARAG MVKTVSGGRA
      QSIGRRGKVE QLSPEEEEKR RIRRERNKMA AAKCRNRRRE LTDTLQAETD QLEDEKSALQ
      TEIANLLKEK EKLEFILAAH RPACKIPDDL GFPEEMSVAS LDLTGGLPEA STPESEEAFT
      LPLLNDPEPK PSLEPVKSIS NVELKAEPFD DFLFPASSRP SGSETSRSVP DVDLSGSFYA
      ADWEPLHSNS LGMGPMVTEL EPLCTPVVTC TPGCTTYTSS FVFTYPEADS FPSCAAAHRK
      GSSSNEPSSD SLSSPTLLAL
```

Output was in the format:

The sequences are aligned with each other, with the query sequence at the top and subsequent sequences below. Gaps are represented by the "-" symbol. The running total number of amino acids or nucleotides are shown on the right. The degree of similarity is illustrated underneath the alignments with a series of consensus symbols.

Consensus Symbols

An alignment will display by default the following symbols denoting the degree of conservation observed in each column:

"*" means that the residues or nucleotides in that column are identical in all sequences in the alignment.

":" means that conserved substitutions have been observed, according to the COLOUR table above.

"." means that semi-conserved substitutions are observed.

```
FOS_RAT          MMFSGFNADYEASSSRCSSASPAGDSLSYYHSPADSFSSMGSPVNTQDFCADLSVSSANF 60
FOS_MOUSE        MMFSGFNADYEASSSRCSSASPAGDSLSYYHSPADSFSSMGSPVNTQDFCADLSVSSANF 60
FOS_CHICK        MMYQGFAGEYEAPSSRCSSASPAGDSLTYYPSPADSFSSMGSPVNSQDFCTDLAVSSANF 60
FOSB_MOUSE       -MFQAFPGDYDS-GSRCSS-SPSAESQ--YLSSVDSFGSPPTAAASQE-CAGLGEMPGSF 54
FOSB_HUMAN       -MFQAFPGDYDS-GSRCSS-SPSAESQ--YLSSVDSFGSPPTAAASQE-CAGLGEMPGSF 54
                  *:..* .:*:: .***** **:.:*   * *..***.*  :.. :*: *:.*.  ...*

FOS_RAT          IPTVTAISTSPDLQWLVQPTLVSSVAPSQ-------TRAPHPYGLPTPS-TGAYARAGVV 112
FOS_MOUSE        IPTVTAISTSPDLQWLVQPTLVSSVAPSQ-------TRAPHPYGLPTQS-AGAYARAGMV 112
FOS_CHICK        VPTVTAISTSPDLQWLVQPTLISSVAPSQ-------NRG-HPYGVPAPAPPAAYSRPAVL 112
FOSB_MOUSE       VPTVTAITTSQDLQWLVQPTLISSMAQSQGQPLASQPPAVDPYDMPGTS----YSTPGLS 110
FOSB_HUMAN       VPTVTAITTSQDLQWLVQPTLISSMAQSQGQPLASQPPVVDPYDMPGTS----YSTPGMS 110
                 :******:** **********:**:* **... ::.    .**.:*  :    *: ..:

FOS_RAT          KTMSGGRAQSIG--------------------RRGKVEQLSPEEEEKRRIRRERNKMAAA 152
FOS_MOUSE        KTVSGGRAQSIG--------------------RRGKVEQLSPEEEEKRRIRRERNKMAAA 152
FOS_CHICK        KAP-GGRGQSIG--------------------RRGKVEQLSPEEEEKRRIRRERNKMAAA 151
FOSB_MOUSE       AYSTGGASGSGGPSTSTTTSGPVSARPARARPRRPREETLTPEEEEKRRVRRERNKLAAA 170
FOSB_HUMAN       GYSSGGASGSGGPSTSGTTSGPGPARPARARPRRPREETLTPEEEEKRRVRRERNKLAAA 170
                    :** . * *.::: :::.. .: .: : .** : * *:********:******:***

FOS_RAT          KCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEFILAAHRPACKIPNDLGF 212
FOS_MOUSE        KCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEFILAAHRPACKIPDDLGF 212
FOS_CHICK        KCRNRRRELTDTLQAETDQLEEEKSALQAEIANLLKEKEKLEFILAAHRPACKMPEELRF 211
FOSB_MOUSE       KCRNRRRELTDRLQAETDQLEEEKAELESEIAELQKEKERLEFVLVAHKPGCKIPYEEG- 229
FOSB_HUMAN       KCRNRRRELTDRLQAETDQLEEEKAELESEIAELQKEKERLEFVLVAHKPGCKIPYEEG- 229
                 *********** *********:**: *::***:* ****:***:*.**:*.**:* :

FOS_RAT          PEEMSVTS-LDLTGGLPEATTPESEEAFTLPLLNDPEPK-PSLEPVKNISNMELKAEPFD 270
FOS_MOUSE        PEEMSVAS-LDLTGGLPEASTPESEEAFTLPLLNDPEPK-PSLEPVKSISNVELKAEPFD 270
FOS_CHICK        SEELAAATALDLG----APSPAAAEEAFALPLMTEAPPAVPPKEPSG--SGLELKAEPFD 265
FOSB_MOUSE       PGPGPLAEVRDLPG-----STSAKEDGFGWLLPPPPPPP-----------------LPFQ 267
FOSB_HUMAN       PGPGPLAEVRDLPG-----SAPAKEDGFSWLLPPPPPPP-----------------LPFQ 267
                .   . :   ** .     :..  *:.*   *   . *                    **:

FOS_RAT          DFLFPASSRPSGSETARSVPDVDLSG--SFYAADWEPLHSSSLGMGPMVTELEPLCTPVV 328
FOS_MOUSE        DFLFPASSRPSGSETSRSVPDVDLSG--SFYAADWEPLHSNSLGMGPMVTELEPLCTPVV 328
FOS_CHICK        ELLFSAGPR----EASRSVPDMDLPGASSFYASDWEPLGAGSGG------ELEPLCTPVV 315
FOSB_MOUSE       --------------SSRDAP-PNLTA--SLFTHS----------------EVQVLGDPFP 294
FOSB_HUMAN       --------------TSQDAP-PNLTA--SLFTHS----------------EVQVLGDPFP 294
                             ::::..*  :*..  *::: .                *:: *  *.

FOS_RAT          TCTPSCTTYTSSFVFTYPEADSFPSCAAAHRKGSSSNEPSSDSLSSPTLLAL 380
FOS_MOUSE        TCTPGCTTYTSSFVFTYPEADSFPSCAAAHRKGSSSNEPSSDSLSSPTLLAL 380
FOS_CHICK        TCTPCPSTYTSTFVFTYPEADAFPSCAAAHRKGSSSNEPSSDSLSSPTLLAL 367
FOSB_MOUSE       VVSP---SYTSSFVLTCPEVSAF---AGAQR--TSGSEQPSDPLNSPSLLAL 338
FOSB_HUMAN       VVNP---SYTSSFVLTCPEVSAF---AGAQR--TSGSDQPSDPLNSPSLLAL 338
                 . .*   :***:**:* **..:*   *.*:*  :*..: .**.*.**:****
```

• EDITING AN ALIGNMENT

You can edit the alignment using jalview. Click on the button below to view the above alignment.

• PHYLOGENETIC TREE

Phylogram is a branching diagram (tree) assumed to be

an estimate of a phylogeny, branch lengths are proportional to the amount of inferred evolutionary change. A Cladogram is a branching diagram (tree) assumed to be an estimate of a phylogeny where the branches are of equal length, thus cladograms show common ancestry, but do not indicate the amount of evolutionary "time" separating taxa. Tree distances can be shown, just click on the diagram to get a menu of options. The ".dnd" file is a file that describes the phylogenetic tree.

These are now in controlled with new buttons in the output file as well as a pop up menu, that is available by right-clicking on the applet. The buttons on the page include "Show as Phylogram Tree", "Show as Cladogram Tree" and "Show Distances".

IMPORTANT!

Please note applets are not printed out with html pages, You will need to:

- Use the "Print Screen" button in the top right corner of your keyboard.
- Open an imaging application like paint or photoshop.
- Go "file>new" from the menu or "control+N" from the keyboard to create a new image.
- Go "edit>paste from the menu or "control+V" from the keyboard to paste your screen capture.
- The use the crop function to trim the image (e.g. "image>crop").
- Then save or print the image.

If you cannot see the tree, your java plug in is probably not working, please reinstall java on your machine or enable it in your internet settings. You can download java from http://java.sun.com/. If you have java running, you can see the version of java you are running in the box below (applet from http://www.javatester.org). You should have at least java version 1.2 to run this applet.

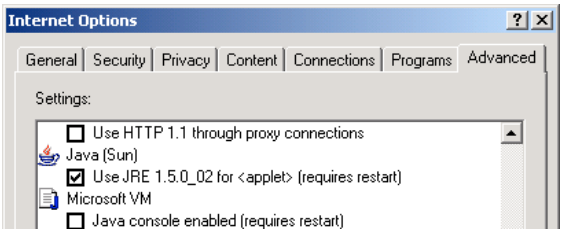
The vendor and version from the JVM:

You should see a pink box above with one line of text that says something like:

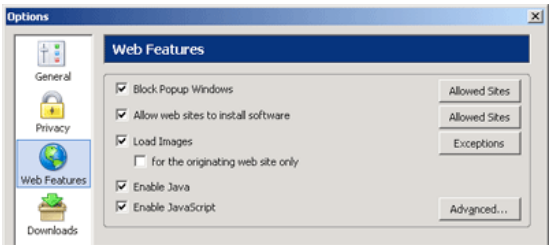
```
Java Version: 1.1.4 from Microsoft Corp.  or
Java Version 1.4.2_05 from Sun Microsystems Inc.  or
Java Version: 1.3.1 from Apple Computer, Inc.  or
Java Version: 1.1.5 from Netscape Communications Corporation
```

For actual results, see expected output.

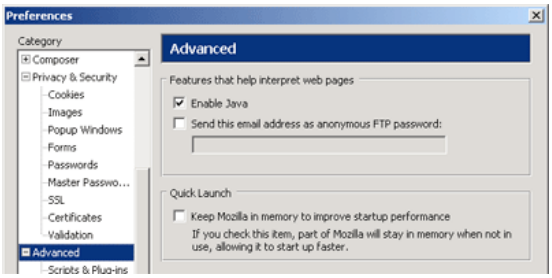
Example of enabling Java in Internet Explorer (Windows)



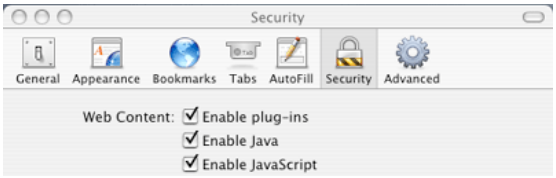
Examples of Enabling Java in Firefox (Windows/Linux)



Example of Enabling java in Mozilla (Windows)



Example of Enabling java in Safari (Mac)



example:

Right-click in the area below for options!

IMPORTANT:
To use this option you will need to input a sequence alignment. Please make sure this alignment is in PIR or PHYLIP format. ALN and GCG MSF files are not supported so you will have to convert your MSF files to PIR format with, for example, GCG's ToPir:

```
topir pileup.msf{*} -outf=pileup.pir
```

Please refer to the GCG documentation to find out how to use this program correctly. You may then use this file as input (cut and paste or upload) to this service.

The method used is the NJ (Neighbour Joining) method of Saitou and Nei. First you calculate distances (percent divergence) between all pairs of sequence from a multiple alignment; second you apply the NJ method to the distance matrix.

This option allows you to choose the following output formats for the tree:

- Neighbour
- Phylip
- Distance

In order to view these trees you must have a program capable of displaying the data. Please refer to this pages section on OUTPUT for more information.

- **Kimura Correction of distances**
  This options allows you to set on distances correction (correction for multiple substitutions). This is because, as sequences diverge, more than one substitution will happen at many sites. However, you only see one difference when you look at the present day sequences. Therefore, this option has the effect of stretching branch lengths in trees (especially long branches). The corrections used here (for DNA or proteins) are both due to Motoo Kimura.

- **Ignore Gaps in alignment**
  With this option, any alignment positions where ANY of the sequences have a gap will be ignored. This means that 'like' will be compared to 'like' in all distances. It also, automatically throws away the most ambiguous parts of the alignment, which are concentrated around gaps (usually). The disadvantage is that you may throw away much of the data if there are many gaps.

UPLOAD A FILE

You may upload a file from your computer which containing a valid **set** of sequences in any format (GCG, FASTA, EMBL, GenBank, PIR, NBRF, Phylip or UniProtKB/Swiss-Prot) using this option. Please note that this option only works with Netscape Browsers or Internet Explorer version 5 or later. Some word processors may yield unpredictable results as hidden/control characters may be present in the files. It is best to save files with the Unix format option to avoid hidden windows characters. Some examples of common sequence formats may be seen here.

SCORES TABLE

Scores Table is a new view to ClustalW output. Users can sort the scores by Alignment Score, Sequence Number, Sequence Name and Sequence Length.

REFERENCES

Higgins D., Thompson J., Gibson T. Thompson J. D., Higgins D. G., Gibson T. J.(1994).
CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting,position-specific gap penalties and weight matrix choice.
Nucleic Acids Res. 22:4673-4680. VIEW

ClustalW WWW Service at the European Bioinformatics Institute
http://www.ebi.ac.uk/clustalw
Rodrigo Lopez, Services Program

Andrew Lloyd
The Clustal W WW server at the EBI
embnet.news volume 4.2 1997
http://www.ebi.ac.uk/embnet.news/vol4_3/clustalw1.html

The program in use in this service can be obtained freely from:
http://www.sgi.com/chembio/resources/clustalw/parallel_clustalw.html

Parry-Smith, D.J., Payne, A.WR, Michie, A.D. and Attwood, T. K. (1997)
CINEMA - A novel Colour INteractive Editor for Multiple Alignments.
Gene, 211(2), GC45-56. VIEW
http://www.bioinf.man.ac.uk/dbbrowser/CINEMA2.1/

Attwood, T. K., Payne, A. W.R., Michie, A.D. and Parry-Smith, D.J. (1997)
A Colour INteractive Editor for Multiple Alignments - CINEMA, EMBnet.news, 3 (3).

Jalview - a java multiple alignment editor

http://www.jalview.org

pfaat (Protein Family Alignment Annotation Tool)
http://pfaat.sourceforge.net/

- **OTHER SERVICES:**

This services is also available as an application from the EBI's srs server: http://srs.ebi.ac.uk/

N.B. DbClustal can be launched from Wu-Blast2 and NCBI-Blast2 you can choose some of the sequences from your score list and align them with your query sequence. You may also then paste your .aln files back into ClustalW (bootstrapping) in order to colour your alignments, view the phylogenetic trees or launch jalview.