EMBOSS

European Molecular Biology Open Software Suite

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...qué es EMBOSS?

- Suite de análisis especialmente desarrollada para biología molecular (EMBnet).
- Toolkit para aplicaciones o workflows.
- Código Abierto.
- Provee alrededor de 150 programas.
- Integra otros programas (EMBASSY).
- Soporta todas las plataformas UNIX más comunes.
- EMBOSS para MS/WINDOWS en desarrollo.

...150 programas?

- Alineamiento de Secuencias.
- Búsqueda de secuencias en bases de datos.
- Identificación de motivos en proteínas.
- Identificación de repeticiones.
- Análisis de uso codónico.
- Identificación de patrones.
- Herramientas de presentación.
- Visualización.
- etc....

http://emboss.sourceforge.net/

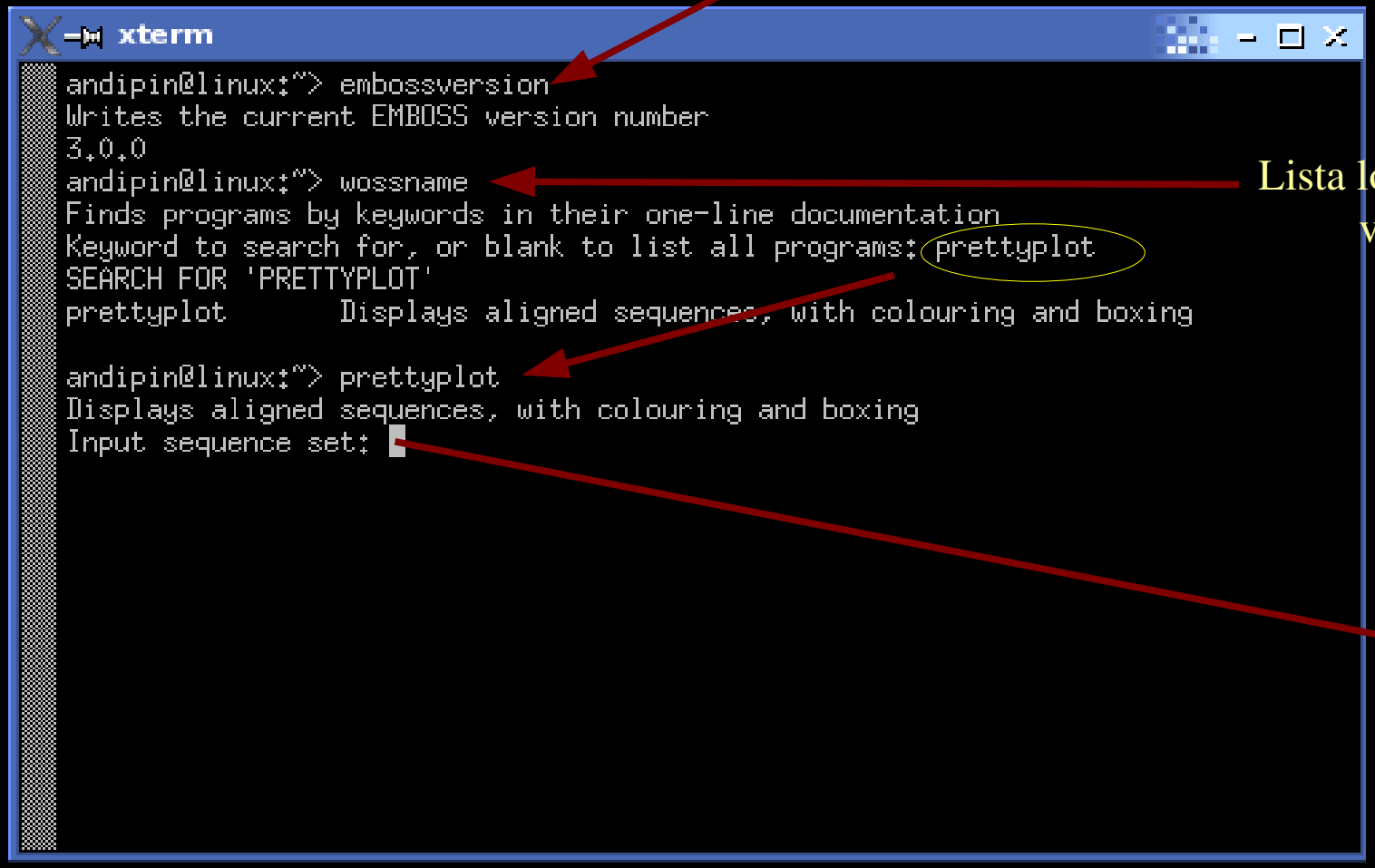
... algo de historia.

- EGCG (1988) surgió como colaboración entre la EMBnet y otros institutos, utilizaba las librerías de GCG.
- Pensado para el Sanger Center.
- Problemas de licenciamiento: imposible distribuir más licencias académicas.
- Se inicia el desarrollo de EMBOSS.

Cómo luce EMBOSS?

Linea de comandos!

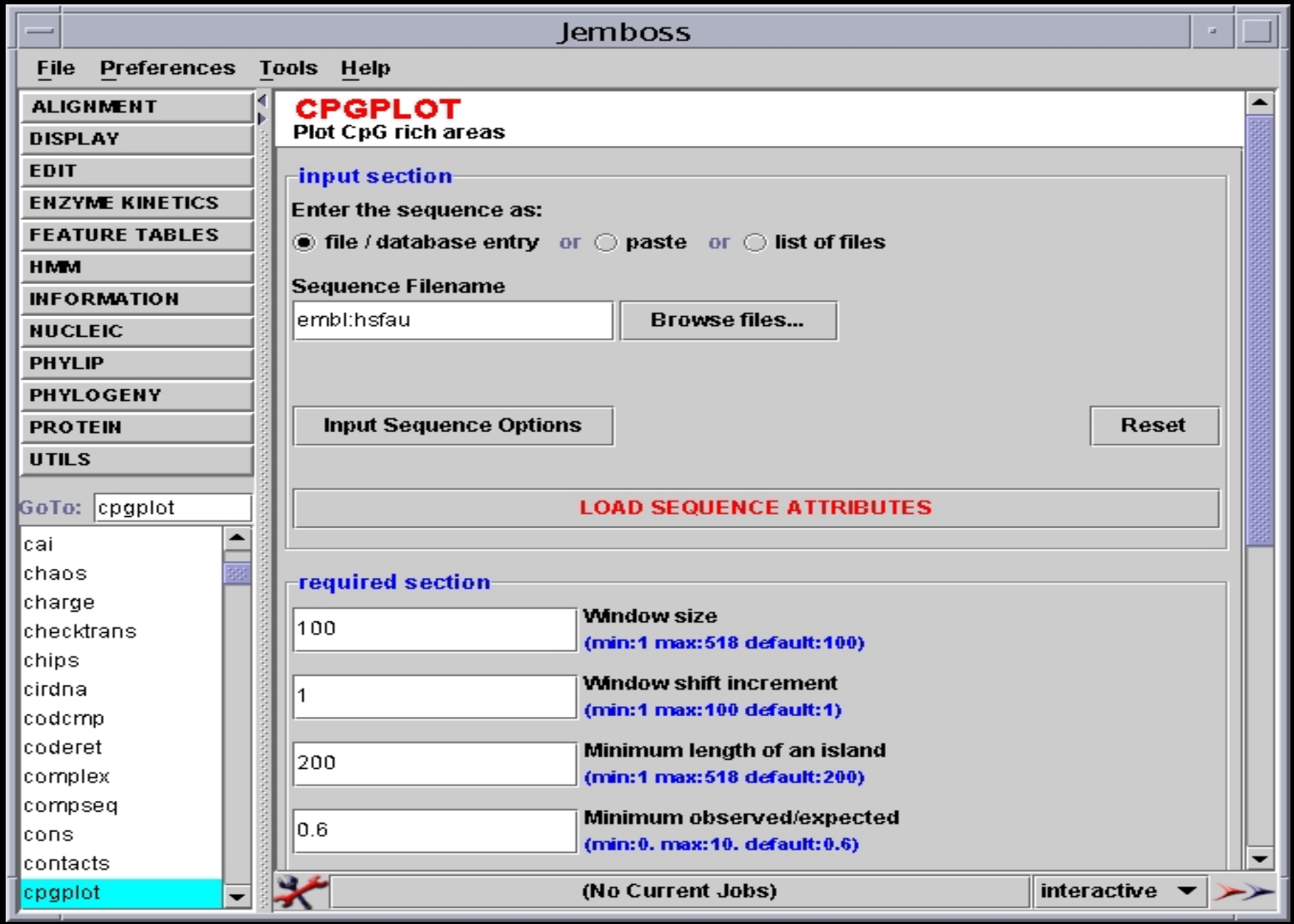
Muestra la versión de EMBOSS instalada

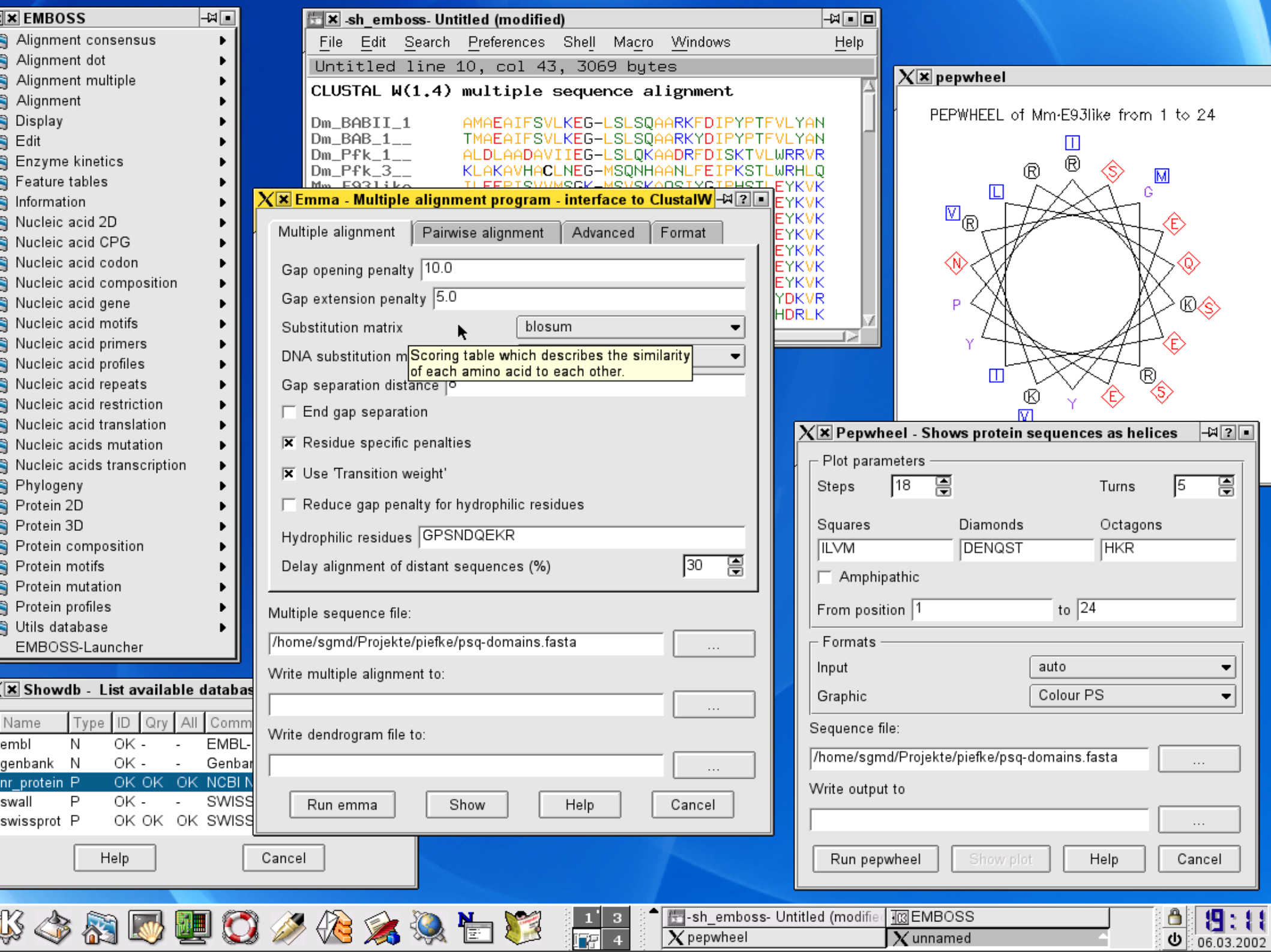


Lista los programas de la actual versión de EMBOSS

Ruta a Archivo

GUIs para EMBOSS




EMBOSS
Alignment consensus
Alignment dot
Alignment multiple
Alignment
Display
Edit
Enzyme kinetics
Feature tables
Information
Nucleic acid 2D
Nucleic acid CPG
Nucleic acid codon
Nucleic acid composition
Nucleic acid gene
Nucleic acid motifs
Nucleic acid primers
Nucleic acid profiles
Nucleic acid repeats
Nucleic acid restriction
Nucleic acid translation
Nucleic acids mutation
Nucleic acids transcription
Phylogeny
Protein 2D
Protein 3D
Protein composition
Protein motifs
Protein mutation
Protein profiles
Utils database
EMBOSS-Launcher
-sh_emboss- Untitled (modified)
File Edit Search Preferences Shell Macro Windows Help
Untitled line 10, col 43, 3069 bytes
CLUSTAL W(1.4) multiple sequence alignment
Dm_BABII_1 AMAEAIFSVLKEG-LSLSQAARKFDIPYPTFVLYAN
Dm_BAB_1__ TMAEAIFSVLKEG-LSLSQAARKYDIPYPTFVLYAN
Dm_Pfk_1__ ALDLAADAVIIEG-LSLQKAADRFDISKTVLWRRVR
Dm_Pfk_3__ KLAKAVHACLNEG-MSQNHAANLFEIPKSTLWRHLQ
Emma - Multiple alignment program - interface to ClustalW
Multiple alignment
Pairwise alignment
Advanced
Format
Gap opening penalty 10.0
Gap extension penalty 5.0
Substitution matrix blosum
DNA substitution m
Scoring table which describes the similarity of each amino acid to each other.
Gap separation distance 8
End gap separation
Residue specific penalties
Use 'Transition weight'
Reduce gap penalty for hydrophilic residues
Hydrophilic residues GPSNDQEKR
Delay alignment of distant sequences (%) 30
Multiple sequence file:
/home/sgmd/Projekte/piefke/psq-domains.fasta
Write multiple alignment to:
Write dendrogram file to:
Run emma
Show
Help
Cancel
pepwheel
PEPWHEEL of Mm-E93like from 1 to 24
Pepwheel - Shows protein sequences as helices
Plot parameters
Steps 18
Turns 5
Squares
Diamonds
Octagons
ILVM
DENQST
HKR
Amphipathic
From position 1
to 24
Formats
Input auto
Graphic Colour PS
Sequence file:
/home/sgmd/Projekte/piefke/psq-domains.fasta
Write output to
Run pepwheel
Show plot
Help
Cancel
Showdb - List available databas
Name Type ID Qry All Comm
embl N OK - - EMBL-
genbank N OK - - Genbar
nr_protein P OK OK OK NCBI N
swall P OK - - SWISS
swissprot P OK OK OK SWISS
Help
Cancel
-sh_emboss- Untitled (modifie
EMBOSS
pepwheel
unnamed
06.03.2002

EMBOSS

megamerger
meme
merger
msbar
mwcontam
mwfilter
needle
newcpgreport
newcpgseek
newseq
noreturn
notseq
nthseq
octanol
oddcomp
palindrome
pasteseq
patmatdb
patmatmotifs
pepcoil
pepinfo
pepnet
pepstats
pepwheel
pepwindow
pepwindowall
plotcon
plotorf
polydot
preg
prettyplot
prettyseq
primersearch
profit
prophecy
prophet
pscan

PEPWHEEL

(Shows protein sequences as helices)

Help ?

Fields with a coloured background are optional and can safely be ignored...

[Hide optional fields]

1. SET THE PARAMETERS FOR THE RUN (OR ACCEPT THE DEFAULTS...)

input section

Select an input sequence.

Use one of the following three fields: *(file must contain a protein sequence)*

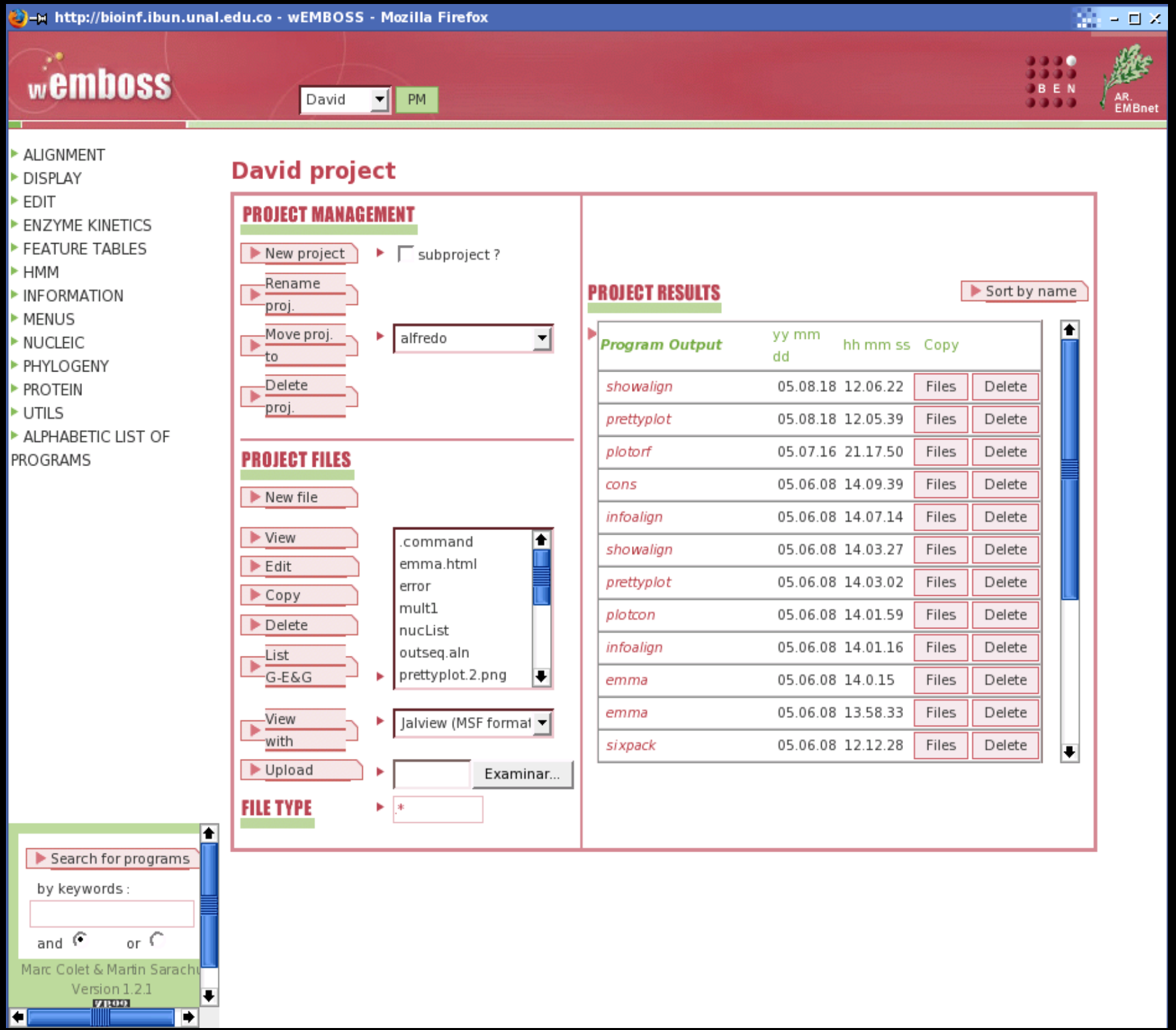
1. To access a sequence from a database, enter the USA path here: *(dbname:entry)*
2. Or, upload a sequence file from your local computer here: Examinar...
3. Or enter the sequence data manually here:

output section

Plot the wheel? Yes

Number of steps (integer) 18

Number of turns (integer) 5


http://bioinf.ibun.unal.edu.co - wEMBOSS - Mozilla Firefox
wemboss
David
PM
BEN
AR. EMBnet
ALIGNMENT
DISPLAY
EDIT
ENZYME KINETICS
FEATURE TABLES
HMM
INFORMATION
MENUS
NUCLEIC
PHYLOGENY
PROTEIN
UTILS
ALPHABETIC LIST OF PROGRAMS
David project
PROJECT MANAGEMENT
New project
subproject ?
Rename proj.
Move proj. to
alfredo
Delete proj.
PROJECT FILES
New file
View
Edit
Copy
Delete
List G-E&G
.command
emma.html
error
mult1
nucList
outseq.aln
prettyplot.2.png
View with
Jalview (MSF format
Upload
Examinar...
FILE TYPE
*
PROJECT RESULTS
Sort by name
Program Output
yy mm dd
hh mm ss
Copy
showalign 05.08.18 12.06.22 Files Delete
prettyplot 05.08.18 12.05.39 Files Delete
plotorf 05.07.16 21.17.50 Files Delete
cons 05.06.08 14.09.39 Files Delete
infoalign 05.06.08 14.07.14 Files Delete
showalign 05.06.08 14.03.27 Files Delete
prettyplot 05.06.08 14.03.02 Files Delete
plotcon 05.06.08 14.01.59 Files Delete
infoalign 05.06.08 14.01.16 Files Delete
emma 05.06.08 14.0.15 Files Delete
emma 05.06.08 13.58.33 Files Delete
sixpack 05.06.08 12.12.28 Files Delete
Search for programs
by keywords :
and
or
Marc Colet & Martin Sarachu
Version 1.2.1

Workflows con EMBOSS