



Introduction to **wEMBOS** (EMBOS)

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What is

The logo for the emboss software package. The word "emboss" is written in a bold, blue, sans-serif font with a 3D effect. The letter 'e' is stylized with three red spheres of varying sizes positioned around its top and left sides, resembling a molecular structure or a protein. The entire logo is contained within a white rectangular box with a thin black border.

?

- A free Open Source software analysis package developed for molecular biology
- Programs share a common look and feel
- Incorporates many small and large programs
- Easy to run from the command line
- Retrieval of sequence data from the web
- Easy to call from other programs(e.g. perl)
- Easy to set up behind GUIs and Web interfaces

Scope of applications

- There are many EMBOSS programs (200+)
- Many sequence analysis & display programs
- Protein 3D structure prediction being developed
- Other programs e.g enzyme kinetics

What is wEMBOSS?

- A web interface to the EMBOSS package for sequence analysis
- It's developed by Martin Sarachu (Argentina) and Marc Colet (Belgium)



Features of wEMBOSS:

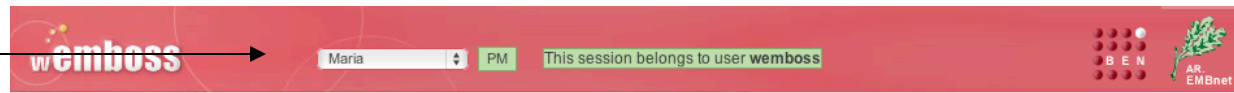
- Each user has a separate and private workspace.
- Organize your work by creating projects and subprojects
- Results saved for easy recover & review
- Inline help
- Keyword search for programs and documentation.



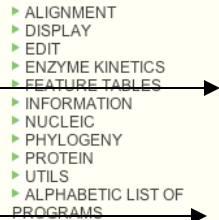
Create a project

- **wEMBOSS** uses the concept of projects
- nucList & protList are automatically created (add names of the sequences you wish to access)

Select project



Create new projects and subprojects



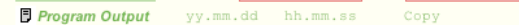
Create new files, view, edit, remove...

Maria project

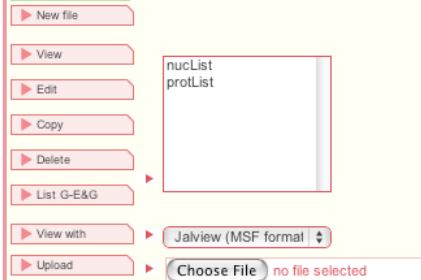
PROJECT MANAGEMENT



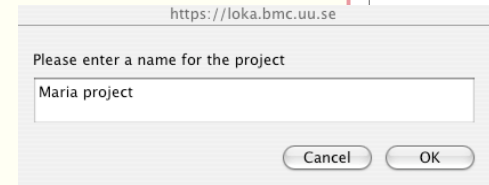
PROJECT RESULTS



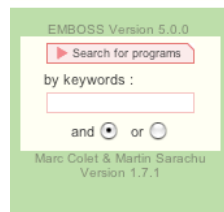
PROJECT FILES



FILE TYPE



Upload files



Project files

- Create a new file and paste the sequence or upload sequence
- Add sequence name to nucList or protList

PROJECT FILES

New file

View

Edit

Copy

Delete

List G-E&G

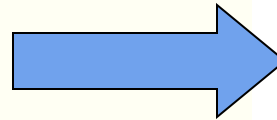
View with: Jalview (MSF format)

Upload: Choose File no file selected

FILE TYPE: *

EDIT FILE add filename to nucList to protList don't add Save as

```
>L07770 L07770.1 Xenopus laevis rhodopsin mRNA, complete cds.
ggtagaacagcttcagttgggatcacaggcttctagggatccttgggcaaaaaaagaac
acagaaggcattctttctatacaagaaggactttatagagctgctaccatgaacggaac
agaaggtccaaaatTTTTATgtcccatgtccaacaaaactggggtggtacgaagcccatt
cgattaccctcagttacttagcagagccatggcaatattcagcactggctgcttacat
gttcctgctcatcctgcttgggttaccaatcaacttcatgacctggtttgttaccatcca
gcacaagaaactcagaacaccctaaactacatcctgctgaacctggtatttgccaatca
cttcatggtcctgtggtgggttcacggtgacaatgtacacctcaatgcaaggctacttcat
ctttggccaaaactggttgctacattgaaggctctttgctacacttgggtggaagtggc
cctctggctcaactggtagtattggccgttgaaagatataatggtggtctgcaagcccatggc
caactccgatccggggagaaccatgctattatgggtgtagcctccacatggatcatggc
tttgtcttggctgctcctcctctctctcctoggatggccagatacatcccagagggaaatgca
atgctcatgccgagtactactacacactgaagcctgaggtcaacaatgaatcctttgt
tatctacatggtcattgtccacttccacttccccgattgtcattctctctgctatgg
tcgctgctctgctgctcactgtcaaagaggtgcagccagcaacaggaatctgtaccacca
```



PROJECT FILES

New file

View

Edit

Copy

Delete

List G-E&G

View with: Jalview (MSF format)

Upload: Choose File no file selected

FILE TYPE: *

EDIT FILE add filename to nucList to protList don't add Save as

```
#nucleics of Maria
xlhodop
```

Selection of programs/files

- Drop-down menu with all available programs
- Select a program by clicking on its name.
- Choose a sequence to work with from:
 - list selector: to select a sequence from nucList or protList
 - local computer file: to upload a file from your computer
 - EMBOSS database: to access a sequence from a server

The screenshot displays the wemboss web interface. At the top, the user is identified as 'Maria' with a 'PM' status, and a message states 'This session belongs to user wemboss'. The main navigation menu on the left lists various programs under categories like ALIGNMENT, DISPLAY, EDIT, ENZYME KINETICS, FEATURE TABLES, INFORMATION, NUCLEIC, PHYLOGENY, PROTEIN, UTILS, and ALPHABETIC LIST OF PROGRAMS. A sub-menu for 'ALPHABETIC LIST OF PROGRAMS' is expanded, showing a list of programs including abiview, antigenic, backtranambig, backtranseq, banana, biosed, btwisted, cai, chaos, charge, checktrans, chips, cirdna, codcomp, codcopy, coderet, compseq, cons, and cqqplot. The main content area is titled 'wrevseq (Reverse and complement a sequence)'. It includes a 'Run revseq' button, a 'Manual' link, and a 'Hide optional' link. The 'INPUT' section has a dropdown menu for 'Set the parameters for the run (or accept the defaults...)' and three radio button options: 'from the EMBOSS databases or a current project file', 'from the local computer/PC', and 'from the sequence selector (nucList or protList)'. Below these is a text input field for '(nucleic sequence(s) only) select a USA/filename' and two input fields for 'begin ()' and 'end ()'. The 'ADVANCED' section contains two checkboxes: 'Reverse sequence?' and 'Complement sequence?'. The 'OUTPUT' section has a dropdown menu for 'File format for output sequence set' set to 'Pearson fasta' and a 'Run revseq' button. At the bottom, there is a text input field for email notification with the text: 'If you are submitting a long job and would like to be informed by email when it finishes, please enter your email address in the space below:'. A blue arrow points to this input field.

Project results

- Results automatically viewed and saved

Maria project

PROJECT MANAGEMENT

subproject ?

PROJECT RESULTS

Program Output	yy.mm.dd	hh.mm.ss	Copy
revseq	08.04.22	14.30.29	<input type="button" value="Files"/>

PROJECT FILES

error
nucList
protList
x1hodop

no file selected

FILE TYPE

wREVSEQ Output file(s)

107770.rev [[right click to save locally](#)]

```
>L07770 L07770.1 Xenopus laevis rhodopsin mRNA, complete cds.
acttgc aaagaaat ttttaata caggattt taatgca aggggtct ggctgtct atcctca
ctatat cagacctt gccaaata agcagagg agattgcat gaaatatg ttattata ttacaa
aaataca ttaactt ttcagttg cattgtaa aatgggact ttttggtagtg accatgaataga
agcagcat caat atgtca gaaagacag agataa aataagttgtgc atctctctgggtggg
aggtgccttc agactaatg ttattgtt atgtac agccttgg tgaattcattgaa tccac
ccatttct gctgaa aggateac atcaga atgcaacaa agcttgggcttccc agcagta
atggggtc agctctt acagtg tccaagg ttgggcaga atggggta aatat taaaactgt
ggaattct tgccttgc aacaagt agacagg gcttaagt gatggga attgtgtgaggca
gcgaccct gagacagc cctggg taagctct t atgcagg agacacctgg ctggaagagac
agaaga agcttctgtcttgg aggtggctgc agaggagcc atcttcat caccgaa tggatt
ctttccac agcacagg gttggtgatc aagcagttac ggaactgt tttgtt caagaca atgta
gtgacagg atgtagat agcagagc tcttgg caaagaa agctgggac ggtcatgaa gac
tgggcca aagttag agccttgg tgggtg aagatg tagaatgcca atagggcatagggccac
ccaacag atcagga gaaaaacg accatg ataaca accattct ggtgaccttcttctc agc
cttctgggtggtgac agatctctgtt gctgggctgc agcctctt tggacagtgc agagcag
gcgacctagcaga aagaagatgaca atcagg ggaatggtg aagtgga caatgaacatgta
gataaca aaggatct atgttgacctc aggcctc agtgtgtagtagtctactcc gcatga
gcattgc attccctctgg ggtgatctgg accatcc gaagagaggagg agcagcacaaga
caaaagc atgatcc atgtgaa ggttac acccataaat agcatggttctcccc gaatcggaa
gttggcc atgggcttgc agaccac catatattctt caacggcca aactacc agtgacca
gagggcc acttca ccacca agtgtag caaaga agccttca atgtagca accagtttggcc
aaagatg aagtagcctg cattgaggtg tacattgtc accgtgaa cccacac agggaccat
gaaatgat tggcaaa atacc aggttc agcaggatg tagtttaggggtgttctg agttcttct
gtctggatggt aacaaca aggtcatg aagttgat tggtaaccca agcaggatg agcag
gaacatg taagcagcc agtgctga atattgcc atggctctgcta agtaata actgagggtta
atcgaatgggctctg taccaccc cagtttgttgg acatggggacataaaaaa tttggacc
ttctgttcc gttcatggtagc agctctataaa gtccttctgtg atagaa gaatgctt
ctgtgttctctt tttgccccaa aggatccctaga agcctgtg atccccactgaa gctgtt
tacc
```

Executed EMBOSS command line :

```
revseq -sequence x1hodop -reverse -complement -osformat fasta -auto
wemboss is working at 130.238.34.188 IP address in wEMBOSS Maria project
```

Help within wEMBOSS:

Manual



shuffleseq
sigcleave
silent
sima
sixpack
skipseq
splitter
stretcher
stssearch
supermatcher
syco
tcode
textsearch
tfm
tfscan
tmap
tralign
transeq
trimest
trimseq
twofeat
union
vectorstrip
water
whichdb
wobble
wordcount
wordfinder
wordmatch
wosname
yank

wosname (Finds programs by keywords in their one-line documentation) ▶ Manual
▶ Run wosname ▶ Hide optional

Set the parameters for the run (or accept the defaults...)

INPUT
 Text to search for, or blank to list all programs

ADDITIONAL

- ▶ Use the expanded group names? n y
- ▶ Match all words in the search string? n y
- ▶ Show keywords with program documentation? n y

ADVANCED

- ▶ Search the EMBOSS programs? n y
- ▶ Search the EMBASSY programs? n y

Show programs in one EMBASSY package

- ▶ Put a colon in the group name between two levels? n y
- ▶ Only report those applications that can run in a GUI? n y

OUTPUT

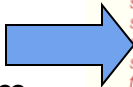
HTMLSECTION

- ▶ Format the output for HTML? n y
- ▶ Output only the group names? n y
- ▶ Output an alphabetic list of programs? n y

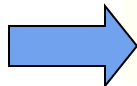
▶ Run wosname

If you are submitting a long job and would like to be informed by email when it finishes, please enter your email address in the space below:

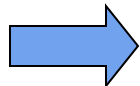
Hold mouse over program



wosname



Search



wEMBOSS program: wosname

- Easy to forget a program name
- To find programs, use **wosname**
- **wosname** finds programs by looking for keywords in the description or the name of the program

wWOSNAME Output file(s)

The screenshot shows the wEMBOSS web interface. At the top, there's a header with the wEMBOSS logo and user information: 'Maria', 'PM', and 'This session belongs to user wemboss'. Below the header, there's a sidebar on the left with a list of programs: shuffleseq, sigcleave, silent, sirna, sixpack, skipseq, splitter, stretcher, stssearch, supermatcher, syco, tcode, textsearch, tm, tscan, tmap, tranalign, transeq, trimest, trimseq, twofeat, union, vectorstrip, water, whichdb, wobble, wordcount, wordfinder, wordmatch, wosname, and yank. The main content area is titled 'wosname (Finds programs by keywords in their one-line documentation)'. It has a 'Manual' link and a 'Run wosname' button. Below this, there's a section 'Set the parameters for the run (or accept the defaults...)' with an 'INPUT' field for 'Text to search for, or blank to list all programs'. There are also 'ADDITIONAL' and 'ADVANCED' sections with various options and radio buttons. At the bottom, there's an 'OUTPUT' section with 'HTMLSECTION' options and a 'Run wosname' button. A blue arrow points from the 'Run wosname' button to the right.

Warning	
SEARCH FOR 'PROTEIN'	
antigenic	Finds antigenic sites in proteins
backtranambig	Back translate a protein sequence to ambiguous codons
backtranseq	Back translate a protein sequence
charge	Protein charge plot
checktrans	Reports STOP codons and ORF statistics of a protein
comseq	Count composition of dimer/trimer/etc words in a sequence
digest	Protein proteolytic enzyme or reagent cleavage digest
emowse	Protein identification by mass spectrometry
epestfind	Finds PEST motifs as potential proteolytic cleavage sites
fproml	Protein phylogeny by maximum likelihood
fpromlk	Protein phylogeny by maximum likelihood
fprotdist	Protein distance algorithm
fprotpars	Protein parsimony algorithm
freak	Residue/base frequency table or plot
fuzzpro	Protein pattern search
fuzztran	Protein pattern search after translation
garnier	Predicts protein secondary structure
helixturnhelix	Report nucleic acid binding motifs
hmoment	Hydrophobic moment calculation
iep	Calculates the isoelectric point of a protein
makeprotseq	Creates random protein sequences
msbar	Mutate sequence beyond all recognition
mwcontam	Shows molwts that match across a set of files
mwfilter	Filter noisy molwts from mass spec output
octanol	Displays protein hydropathy
oddbcomp	Find protein sequence regions with a biased composition
patmatdb	Search a protein sequence with a motif
patmatmotifs	Search a PROSITE motif database with a protein sequence
pepcoil	Predicts coiled coil regions
pepinfo	Plots simple amino acid properties in parallel
pepnet	Displays proteins as a helical net
pepstats	Protein statistics
pepwheel	Shows protein sequences as helices
pepwindow	Displays protein hydropathy
pepwindowall	Displays protein hydropathy of a set of sequences
preg	Regular expression search of a protein sequence
profit	Scan a sequence or database with a matrix or profile
prophecy	Creates matrices/profiles from multiple alignments
prophet	Gapped alignment for profiles
pscan	Scans proteins using PRINTS
psiphi	Phi and psi torsion angles from protein coordinates
shuffleseq	Shuffles a set of sequences maintaining composition

wEMBOSS program: seqret

- Reads in a sequence and writes it out
- Reformat sequences
- Get sequences from databases

wSEQRET Output file(s)

wseqret (Reads and writes (returns) sequences)

[▶ Manual](#)
[▶ Hide o](#)

[▶ Run seqret](#)

Set the parameters for the run (or accept the defaults...)

INPUT

[▶ Use feature information?](#)

Sequence(s) from the EMBOSS databases or a current project file
 from the local computer/PC
 from the sequence selector (nuclist or protlist)

filename or USA (dbname:entry) begin (1) end (1684) N rev

ADVANCED

[▶ Read one sequence and stop?](#)

OUTPUT

File format for output sequence set

[▶ Run seqret](#)

```
107770.fasta [ right click to save locally ]

>L07770 L07770.1 Xenopus laevis rhodopsin mRNA, complete cds.
ggtagaacagcttcagttgggatcacaggctcttagggatcctttgggcaaaaaaagaaac
acagaaggcattctttctatacaagaaaggactttatagagctgctaccatgaacggaac
agaaggtccaaatttttatgtcccatgtccaacaaaactggggtgtacgaagccatt
cgattaccctcagttacttagcagagccatggcaatattcagcactggctgcttacat
gttctgctcatcctgcttgggttaccatcaactcatgacctgtttgttaccatcca
gcacaagaaactcagaacaccctaaaactacatcctgctgaacctggattttgcaatca
cttcatggctcctgtgtgggttcacggtgacaatgtacacctcaatgcacggctacttcat
ctttggcacaactggttgcacattgaagctctcttgcacactgggtggggaagtggc
cctctggctcactggtagtattggccttgaaagataatggtgctgcaagcccatggc
caactccgattcggggagaaacctgctattatgggtgtagccttcacatggatcattggc
ttgtcttgtgctgctcctcctctctcggatggctccagatacatcccagagggaatgca
atgctcatgaggagtagactactacacactgaagcctgaggtcacaacatgaatcctttgt
tatctacatgttcattgtccacttcaccatccctgattgctacatctctctgctatgg
tcgctgctgctgactgtcaagaggctgcagcccagcaacaggaaatctgctaccacca
gaaggtgagaaaagggtcaccagaatggttgttatcattggctgtttctcctgactgt
ttgggtgccctatgctatgtggcattctacatctcaccaccagggtcctaactttgg
ccagctctcatgacctcccagcttctttgccaagagctctgctatctacaactcctgt
catctacattgtctgaacaaacagttccgtaactgcttgatcaccacctgtgctgtgg
aaagaatccattcgggtgatgaagatggctcctctgcagccacctccaagacagaagctc
ttctgtctctccagccagggtgctcctgcataagagctcaccagggtgctcagggt
ccgctgcctcaacaaattcccatcacttaagcctgtctacttgggtgcgaaggcaagaa
ttccacagtttaataatttaccacctctgcccacacctggacactgtaagagctgacc
ccattactgctgggaaggcccaagcttgggtgcatctgatgtgatccttcagcagaaa
atgggtggattcaatgaattcaccaggctgtacataacaaataacattagctgaaggc
acctcccaccagagaatgcaacacttatttactctgcttcttctgacatattgatgc
tgetctattcattggtcactaacaaaaagccatttacaatgcaactgaaagtaagt
atttttgtaataataaacatatttcatgcaatctcctctgcttattggcaaggtctgat
atagtgaggatagacagccagacccttgcattaaaatcctgtatataaaattctttgg
aagt
```

Executed EMBOSS command line :
seqret -nofeature -sequence embl:L07770 -nofirstonly -osformat fasta -auto
wemboos is working at 130.238.34.188 IP address in wEMBOSS Maria project

If you are submitting a long job and would like to be informed by email when it finishes, please enter your email address in the space below:

wEMBOSS program: showdb

- Displays information of the currently available databases

The screenshot displays the wEMBOSS web interface. At the top, the user is logged in as 'Maria' with 'PM' permissions. The main content area is titled 'wshowdb (Displays information on the currently available databases)'. It features a 'Set the parameters for the run (or accept the defaults...)' section with an 'INPUT' field for a database name and an 'ADDITIONAL' section with several checkboxes for output options. A blue arrow points from the 'ADDITIONAL' section to the output area. The output area shows a 'Warning' message and a table of available databases. Below the table, the executed EMBOSS command line is displayed.

Warning

#	Name	Type	ID	Qry	All	Comment
#	=====	====	==	===	==	=====
1	tpir	P	OK	OK	OK	PIR using NBRF access for 4 files
2	tsw	P	OK	OK	OK	Swissprot native format with EMBL CD-ROM index
3	tswnew	P	OK	OK	OK	Swissnew as 3 files in native format with EMBL CD-ROM in
4	twp	P	OK	OK	OK	EMBL new in native format with EMBL CD-ROM index
5	tembl	N	OK	OK	OK	EMBL in native format with EMBL CD-ROM index
6	tgb	N	OK	-	-	Genbank IDs
7	tgenbank	N	OK	OK	OK	GenBank in native format with EMBL CD-ROM index

Executed EMBOSS command line :
showdb -nohtml -protein -nucleic -nofull -nomethods -nofields -nodefined -norelease -noonly -heading -type -id -query -all -commen
auto
wemboss is working at 130.238.34.188 IP address in wEMBOSS Maria project

Examples of other wEMBOSS programs

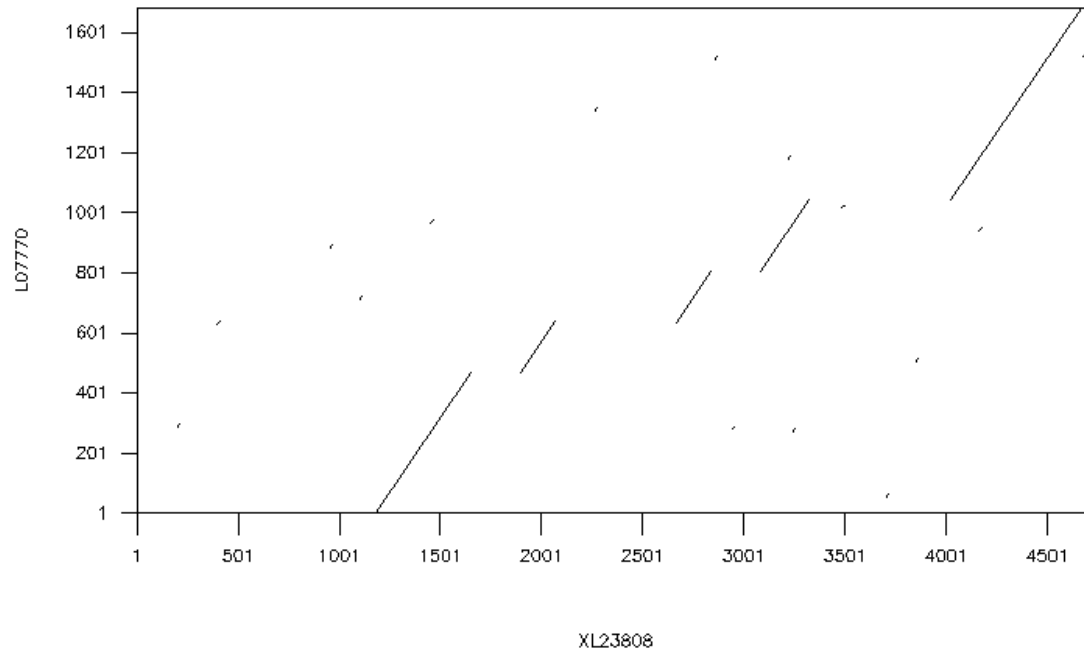
- Pairwise alignment -Dotup
- Global and local alignment – needle, water
- Protein translation – plotorf, getorf, transeq
- Protein fingerprint - pscan
- Primers - eprimer3
- Microsatellites -equicktandem

Pairwise alignment - Dotup

- One sequence is represented on each axis and significant matching regions are distributed along diagonals in the matrix.

Dottup: fasta::xl23808:XL23808[1:4734] vs fasta::xlrhodo...

Mon 21 Apr 2008 13:46:34



wEMBOSS program: water

- Does a local alignment of two sequences

```
L07770      88  aggactttatagagctgctaccatgaacggaacagaaggtccaaatTTTT      137
      |||...|||...|||...|||...|||...|||...|||...|||...|||
BMU59922    10  AGGACTTTAAAGAGCCGCCAATATGAACGGAACAGAAGGCCCAAACTTTT      59

L07770     138  atgtccccatgtccaacaaaactgggggtggtacgaagccattcgattac      187
      |..|...|||...|||...|||...|||...|||...|||...|||...|||
BMU59922    60  ACATACCCCATGTCCAACAAGACTGGGGTGGTACGAAGCCATTCGAATAC      109

L07770     188  cctcagtattacttagcagagccatggcaatattcagcactg-gctgctt      236
      |||...|||...|||...|||...|||...|||...|||...|||...|||
BMU59922   110  CCTCAGTATTACCTGGCAGAGCCATGGCAATACTCCGTTTTGTGC-GCAT      158

L07770     237  acatgttcctgctcatcctgcttgggttaccaatcaacttcatgaccttg      286
      |||...|||...|||...|||...|||...|||...|||...|||...|||
BMU59922   159  ACATGTTCTCTGCTCATCTCTTGGGTTCCCAATCAACTTCATGACCTTG      208

L07770     287  tttgttaccatccagcacaagaaactcagaacaccocctaaactacatcct      336
      |..|...|||...|||...|||...|||...|||...|||...|||...|||
BMU59922   209  TACGTCACCATCCAGCACAAGAAGCTCCGGACACCCTTAAACTATATCCT      258

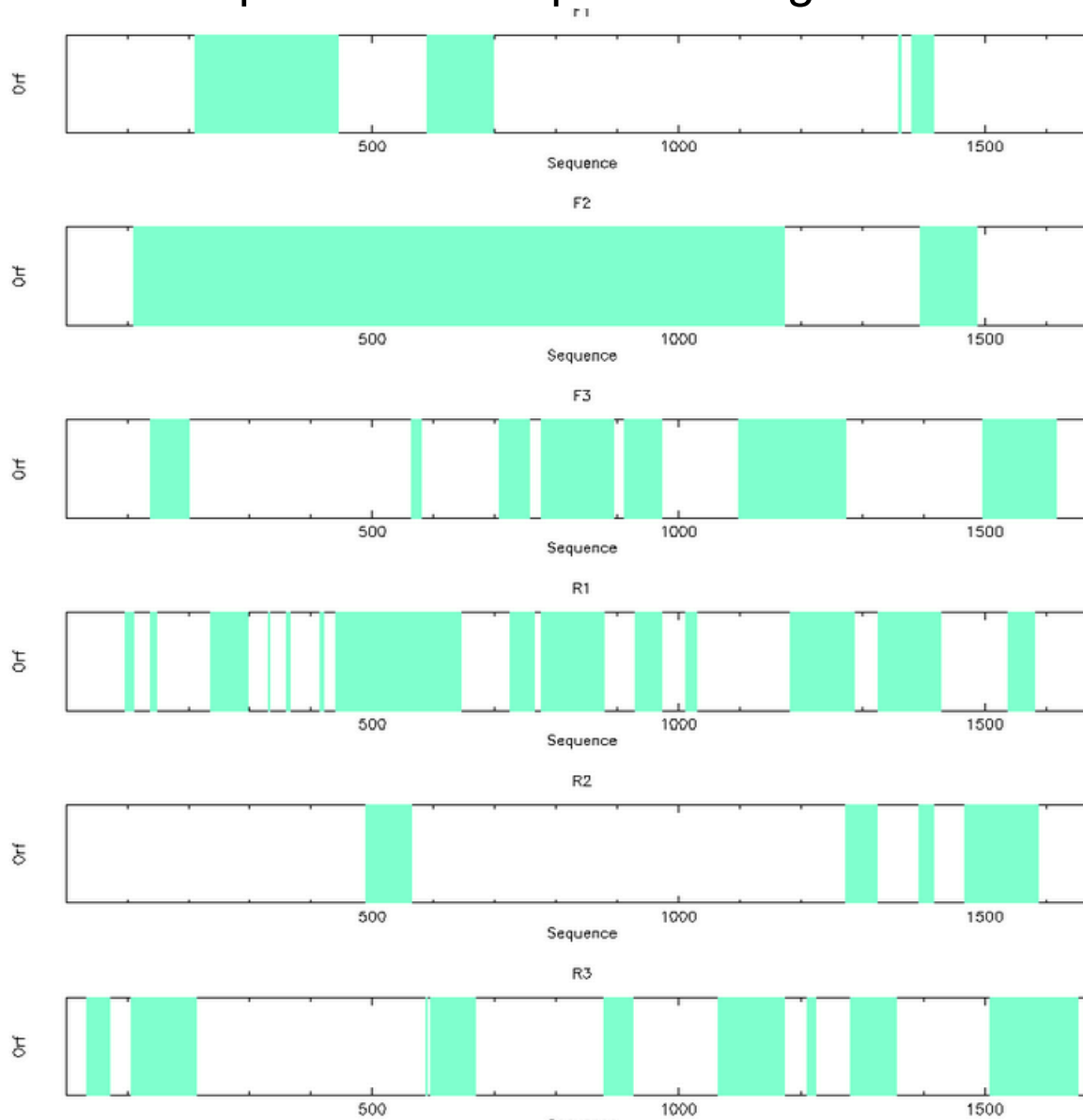
L07770     337  gctgaacctgggtatttgccaatcacttcatggctcctgtgtgggttcacgg      386
      |||...|||...|||...|||...|||...|||...|||...|||...|||
BMU59922   259  GCTGAATTTGGCCCTTGCCAACCACTTCATGGTCCTGTGTGGATTACCG      308

L07770     387  tgacaatgtacacctcaatgcacggctacttcatctttggccaaactgggt      436
      |...|||...|||...|||...|||...|||...|||...|||...|||
BMU59922   309  TCACAATGTACTCCTCAATGAACGGATACTTCGTCTTCGGACAAACCGGT      358

L07770     437  tgctacattgaaggcttctttgctacacttgggtggtgaagtggccctctg      486
      |||...|||...|||...|||...|||...|||...|||...|||...|||
BMU59922   359  TGCTATGTTGAAGGCTTCTTCGCTACCCTTGGTGGTGAAATCGCCCTTTG      408
```


wEMBOSS program: plotorf

- Translates sequences to 6 open reading frames.



Pick primers -eprimer3

wEPRIMER3 (Picks PCR primers and hybridization oligos)

Set the parameters for the run (or accept the defaults...)

INPUT

The sequence from which to choose primers. The sequence must be presented 5' to 3'

from the EMBOSS databases or a current project file
 from the local computer/PC
 from the sequence selector (nuclist or protList)

(nucleic sequence(s) only)
 select a USA/filename
 xlrhodop ... begin (1) [] end (1684) [] N rev

Pick PCR primer(s)? n y

Pick hybridization probe? n y

Primer3 mispriming library file (optional)
 from project(s) data
 from local data

ADDITIONAL

PROGRAMSECTION

5 min: 0 Number of results to return

SEQOPTSECTION

Included region(s)
 Target region(s)
 Excluded region(s)
 Forward input primer sequence to check
 Reverse input primer sequence to check

PRIMERSECTION

0 min: 0 GC clamp

wEPRIMER3 Output file(s)

l07770.eprimer3 [[right click to save locally](#)]

EPRIMER3 RESULTS FOR L07770

#		Start	Len	Tm	GC%	Sequence
1	PRODUCT SIZE: 199					
	FORWARD PRIMER	425	20	60.00	50.00	GGCCAAACTGGTTGCTACAT
	REVERSE PRIMER	604	20	60.14	60.00	GAGGAGGAGCAGCACAAAGAC
2	PRODUCT SIZE: 200					
	FORWARD PRIMER	425	20	60.00	50.00	GGCCAAACTGGTTGCTACAT
	REVERSE PRIMER	605	20	60.28	55.00	AGAGGAGGAGCAGCACAAAGA
3	PRODUCT SIZE: 201					
	FORWARD PRIMER	425	20	60.00	50.00	GGCCAAACTGGTTGCTACAT
	REVERSE PRIMER	606	20	60.28	60.00	GAGAGGAGGAGCAGCACAAAG
4	PRODUCT SIZE: 202					
	FORWARD PRIMER	425	20	60.00	50.00	GGCCAAACTGGTTGCTACAT
	REVERSE PRIMER	607	20	60.28	55.00	AGAGAGGAGGAGCAGCACAA
5	PRODUCT SIZE: 203					
	FORWARD PRIMER	425	20	60.00	50.00	GGCCAAACTGGTTGCTACAT
	REVERSE PRIMER	608	20	60.28	55.00	AAGAGAGGAGGAGCAGCACAA



Executed EMBOSS command line :

```
eprimer3 -sequence xlrhodop -primer -task 1 -nohybridprobe -numreturn 5 -gcclamp 0 -osize 20 -minsize 18 -maxsize 27 -otm 60.0 -mintm 57.0 -maxtm 63.0 -maxdiffm 100.0 -ogcpercent 50.0 -mingc 20.0 -maxgc 80.0 -saltconc 50.0 -dnaconc 50.0 -maxpolyx 5 -productsize 200 -productsizerange 100-300 -productotm 0.0 -productmintm -100000.0 -productmaxtm 100000.0 -noexplanflag -nofileflag -firstbasindex 1 -nopickanyway -maxmispriming 12.00 -pairmaxmispriming 24.00 -nummsaccepted 0 -selfany 8.00 -selfend 3.00 -maxendstability 9.0 -auto
```

wembooss is working at 130.238.34.188 IP address in wEMBOSS Mariawembooss project

Find microsatellites - equicktandem

wemboss Mariawemboss PM This session belongs to user wemboss AR. EMBnet

wequicktandem (Finds tandem repeats) Manual Run equicktandem Hide optional

Set the parameters for the run (or accept the defaults...)

INPUT

Sequence(s) from the EMBOS databases or a current project file
 from the local computer/PC
 from the sequence selector (nuclist or protlist)

(nucleic sequence(s) only)
select a USA/filename
 begin end N rev

REQUIRED

Maximum repeat size
 Threshold score

OUTPUT

Report format Run equicktandem

If you are submitting a long job and would like to be informed by email when it please enter your email address in the space below:

wEQUICKTANDEM Output file(s)

37.oldqtan [[right click to save locally](#)]

24	763	828	4	16
40	2293	2338	4	11

37.qtan [[right click to save locally](#)]

```
#####  
# Program: equicktandem  
# Rndate: Tue 22 Apr 2008 18:40:51  
# Commandline: equicktandem  
# -sequence ctla4  
# -sbegin 1  
# -send 6163  
# -maxrepeat 600  
# -threshold 20  
# -rformat table  
# -auto  
# Report_format: table  
# Report_file: .equicktandem.08.04.22:18.40.51/37.qtan  
#####  
#-----  
#  
# Sequence: 37      from: 1   to: 6163  
# HitCount: 2  
#  
# Threshold: 20  
# Maxrepeat: 600  
#-----  
#  
#-----  
# Start  End  Score  Size  Count  
# 763   828   24     4     16  
# 2293  2338  40     4     11  
#-----  
#-----
```

Executed EMBOS command line :
equicktandem -sequence ctla4 -sbegin 1 -send 6163 -maxrepeat 600 -threshold 20 -rformat table -auto
wemboss is working at 130.238.34.188 IP address in wEMBOSS Mariawemboss project

Start working on the tutorial

