Ebbie: automated analysis and storage of small RNA cloning data using a dynamic web server.

(GNU GPL) by H Alexander Ebhardt Tutorial

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Database Management Tool: View All and Lost & Found.	Database Management Tool: View All and Lost & Found.	- Copy/Paste Id of Insert (e.g. from Blastiv search
Review all entries in database review3. Find entries in database review3. Use % as wildcard result).	Review all entries in database review3. Find entries in database review3. Use % as waldcard	result).
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Eound		Found
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group.		group.
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jo Bookmarks Iools Help		Main page of <i>Ebbie</i> .
Ebbie v3.0.8		
Ebbie: automated analysis and storage of	small RNA cloning data using a dynamic web server.	Sequence Analysis:
Before you start:		 Uploading text file containing DNA sequencing data
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Review all entries in database review3 .	Find entries in database review3 . Use % as wildcard	
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Elle Edit View Go Bookmarks Iools Help	Ebbie: analyzing single insert
Ebbie v3.0.8	Automatically deposits insert into MySOL
<i>Ebbic</i> : automated analysis and storage of small RNA cloning data using a dynamic web server.	
no id sequence length sample source group annotation 47 7ms1 txt GTTATATCTGCGTGAGGA 18 Glycine max (soybean genetic map)	 Number (no, automatically)
1 sequences total	 Id (from filename)
New annotation for "7ins1.txt" iroup annotation: 💽 Add a new group to the pull-down menu.	 Insert (nt sequence)
New description/annotation:	 Length (counted insert)
Orientation: N/A	 Sample source (inferred from filename)
Review of BlastN searches (overv: '7ins1.txt') against local databases:	Annotation fields:
No hits found against U. of Oregon Arabidopsis small RNA database.	 Group annotation
BLASTN 2.2.9 [May-01-2004]	• Pull down menu
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search	Add to pull down menu in text field
programs", Nucleic Acids Res. 25:3389-3402.	 Additional comments
(18 letters) Database: mbys.nt	 Orientation (N/A, sense, antisense)
Searching.done	BlastN search results
Score E Sequences producing significant alignments: (bits) Value	 Searches Ebbie associated databases.
YSatWT36 1e-O6	 If negative search result, then only 1 line displayed. Otherwise, whole BlastN search result printed.
Length = 369 Score = 36.2 bits (18), Expect = 1e-06 Identities = 18/18 (100%) Strand = Plus / Plus	Press 'Deposit annotation for ' to update insert annotation and add to BlastN database.

j Ebbie by H Alexander Ebbardt - Mozilla Firefox Fle Edit View Go Bodowska Toola Help	
ind sequence length sample source group annotation 47 7ms1.txt GTTATATCTGCGGTGAGGA 18 Glycine max (soybean genetic map) Y-Sat 1 sequences total 1	 Ebbie: depositing single insert BlastN id and group displayed. MySQL entry displayed. Return to Ebbie's Main Page for more sequence analysis
Return to Ebbie's main page: Ebbie - sequence analysis	anaryoro
Database Management Tool: Annotation Change: Number of insert: Id of insert:	OR: enter number or id of insert for Database Management Tool: Annotation Change
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Ebbie: automated analysis and storage of s	mall RNA cloning data using a dynamic web server.	•	Sequence Analysis:
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Sequence Analysis:			
What text-file containing sequencing data should b next?	e processed		
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Number of insert:	ld of insert:		
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Database Management Tool: View /	All and Lost & Found.		
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Sort list by: length 💌	Find annotation 💌 containing		
Show all entries from database	Lost & Found		
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Ebbie v3.0.8	Program indicates how many primer pairs and how
<i>Ebbie</i> : automated analysis and storage of small RNA cloning data using a dynamic web server.	Flogran indicates now many primer pairs and now
There were 3 primer pairs and 3 inserts deposited into review3.	many inserts were found.
RNA insert 3ins3.tx1 💌	
3 sequences have not been annotated yet. Please select one of the RNA inserts from the above pull down menu.	-• From pull down menu, choose an insert.
Ebbie - sequence analysis	Press: 'Ebbie – sequence analysis submit button to
Ebbie Front Page	start analysis of the insert.

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	BlastN analysis of insert
<i>Ebbie</i> : automated analysis and storage of small RNA cloning data using a dynamic web server.	
no id sequence length sample source group annotation	Crown expectations added (V/ Cat' to task means
	Group annotation: added Y-Sat to text menu.
1 sequences total	
New annotation for '3ins3.txt1'	
Group annotation. Add a new group to the pull-down menu. Y-Sat	
New description/annotation:	
·	
	1
Orientation sense 🔽	
N/A	
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Review of BlastN searches (query: '3ins3.txtl') against local databases:	
No. Mar found a sector of H. of Ourseau Analytic size and D DM (A details are	
140 htts 10und against U. of Oregon Arabidopsis small KIVA dalabase.	
BLASTN 2.2.9 [May-01-2004]	
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Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,	
Gapped BLAST and FSI-BLAST; a new generation of protein database search	
programs", Nucleic Acids Res. 25:3389-3402.	
00arte 31ns3 tvt1	
(22 letters)	
Datandase: muys.nt 4 sequences: 8991 total letters	
• • • • • • • • • • • • • • • • • • • •	
Searching.done	
Score F	
Sequences producing significant alignments: Obits Value	
YSatWI <u>44</u> 7e-09	
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Score = 44.1 bits (22), Expect = 7e-09	1
Augustites - 22/22 (1004) Strand = Plus / Plus	
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n For Tou To Equation Too Tob	<i>EDDIE:</i> Multiple inserts.
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	 MvSQL entry of previous insert depicted.
<i>Lbbie</i> : automated analysis and storage of small KIVA cloning data using a dynamic web server.	
olastupdate: 3ins3.txt1 Y-Sat	Choose next insert from null down menu (number of
no id sequence length sample source group annotation	
44 3ins3.txt1 GITAGGTGGTATCGTGGATGAC 22 Lycopersicon esculentum Y-Sat	inserts remaining is shown below)
semiences total	
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PNA insert: 3ins3.txd2 💌	
2 sequences have not been annotated yet.	
Please select one of the RNA inserts from the above pull down menu.	
Ebbie - sequence analysis	
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Ebbie: automated analysis and storage of small RNA cloning data using a dynamic web server.	• Y-Sat appears in alphabetical order (not case
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New annotation for 'Sins3.txt3'	
Group prostation and did a wave array to the will desay we wave	
New description/a IRNA smRNA mental second s	
Orientation N/A	
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Review of BlastN searches (query: '3ins3.txt3') against local databases:	
No hits found against U. of Oregon Arabidopsis small RNA database.	
No hits found against Cucumber Mosaic Virus / Y-Satellite database.	
No hits found against Previously cloned small RNAs (review I) database.	
No hits found against Previously cloned small RNAs (review 2) database.	
No hits found against Previously cloned small RNAs (review3) database.	

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Database Management Tool: Annotation Change.	Change group annotation.			
no id sequence length sample source group annotation 44 3ms3 txt1 GTTAGGTGGTATCGTGGATGAC 22 Lycopersicon esculentum Y-Sat	Update additional annotation			
1 sequences total				
New annotation for '3ins3.txt1'	Submit updated information.			
Group annotation: Y-Sat 💌 Add a new group to the pull-down menu:				
New description/annotation: smRNA from Y-Sat				
Change annotation of '3ins3.tx1'.				

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Your current cloning primers for database review3 are recorded as: Your 5' cloning primer is: 5'-ATCGTAGGCACCTAAA.3' antisense: 5'-TTTCAGGTGCCTACGAT.3' Your 3' cloning primer is: 5'-GAAGAGCCTACGACGA-3' antisense: 5'-TCGTCGTAGGCTCTTC-3'		
If you want to change the current recorded primers, please do so here:		
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Database Management Tool: Annotation Change.		
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