Repeats Finding

Usage example:

Open a DNA sequence in the Sequence View and select the Analyze Find repeats... context menu item:

	Analyze	► Acc	Find pattern	Ctrl+F
	Align	► SW	Find pattern [Smith-Waterman]	Ctrl+Shift+F
	Cloning	۲ 🖳	Find ORFs	
	Export	۲ 🔫	Find annotated regions	/
	Edit sequence	▶ =	Annotate plasmid and custom features	
4	Remove	۲ (S	Build dotplot	
	Rulers	F 🖾	Find repeats	
		T	Find tandems	
	Statistics	-	Analyze with query schema	

The dialog will appear that allows specifying repeat parameters and the annotations table document to save the results into:

U Find Repeats						
Base Advanced						
Repeat finder parameters						
Window size	47bp 🌩 🚺					
Minimum indentity per window	100% 🚔 🛛 100					
Minimum distance between repeats	0bp 🚖					
Maximum distance between repeats	5000bp 束					
Region to process Region Whole sequence 1 -	4733					
▼ Save annotation(s) to						
CVU55762 features [CVU55762.gb]	-					
Create new table						
 Annotation parameters 						
Group name <auto></auto>	*					
Annotation name repeat_unit	ate,					
Estimated repeats count: 0						
Start	Cancel Help					

The dialogues status line displays approximate repeats number that will be found with the current settings.

The Advanced tab provides additional repeats finding options:

U Find Repeats					
Base Advanced					
Advanced parameters					
Custom algorithm	Diagonals 🔻				
Search only for repeats that lie inside of an annotated region	ate				
Search only for repeats that have an annotated region inside	ate				
Filter repeats that have an annotated region inside	atc				
Nested repeats filter algorithm	Disjoint repeats 🔻				
Search for inverted repeats					
Exclude tandems areas					
Estimated repeats count: 0					
	Start Cancel Help				

The found repeats are saved and displayed as annotations to the DNA sequence:

human_T1 (UCSC April 2002 chr7:115977	709-1 🚫 🖄 🥍 🔝 💽 TE TE Tr. 🖿 🔍 🔍 🔺						
1 200k 40k 60k	80k 100k 120k 140k 160k 180k 199 950 🗵						
repeat_unit (4)	peat unit repeat unit ^						
19 852 19880 19.9k 19920	19940 19960 19980 20k 20020 20 047						
19912							
ST. ST. ST. S	LFFSLFLSLSL						
LSPSLSI	L C F S L S F S L S L S						
FSLPLSL	SVFLSLSLSLSL						
TCTCTCTCCCCTCTCTCTCTC	rctgttttttctctctctttctctctctctctctct						
19 903 19910 19915 19920	19925 19930 19935 19940 19945 19950 19957						
AGAGAGAGGGAGAGAGAGAG	AGACAAAAAGAGAGAGAGAAAAGAGAGAGAGAGAGAGA						
<u>א 3 א 3</u> 9 3 א ק ק ק ק ק ק	<u> </u>						
ERGRERI	E T K R E R E R E R E R						
•	= 4						
Name	Value						
Annotations [MyDocument 1.gb]	*						
Prince at one (0, 4)							
repeat_unit	join(1991219956,1999020034)						
repeat_unit	join(6372763804,6575465831)						
repeat_unit	join(185499185538,189058189097)						
repeat_unit	join(190533190577,190640190684)						
•	4						