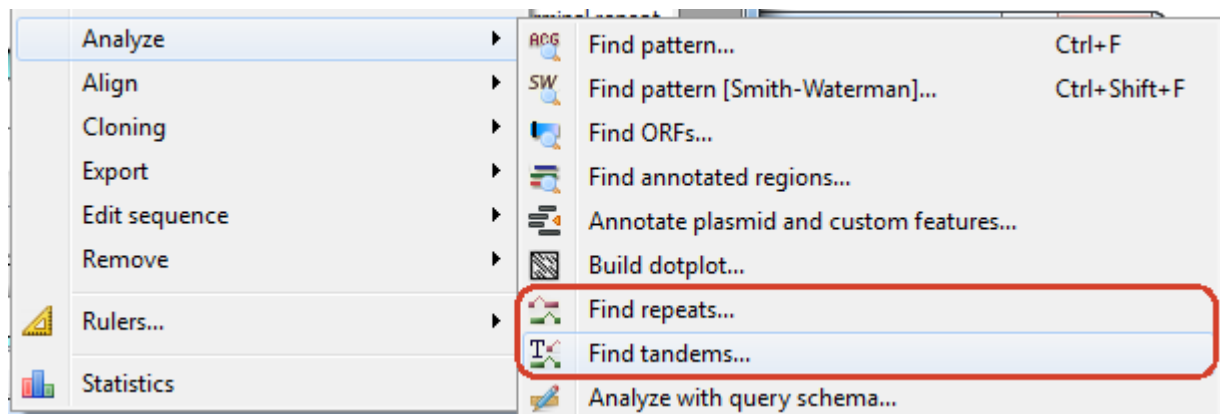


Repeats Finding

Usage example:

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



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

Find Repeats

Base **Advanced**

Repeat finder parameters

Window size 100bp 1k

Minimum indentity per window 100% 100

Minimum distance between repeats 0bp

Maximum distance between repeats 5000bp

Region to process

Region Whole sequence 1 - 199950

▼ Save annotation(s) to

Existing table

Create new table /home/yalgaer/MyDocument.gb

Use auto-annotations table

▼ Annotation parameters

Group name <auto>

Annotation name repeat_unit

Description

Estimated repeats count: 0

Help Cancel Start

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

The *Advanced* tab provides additional repeats finding options:



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

