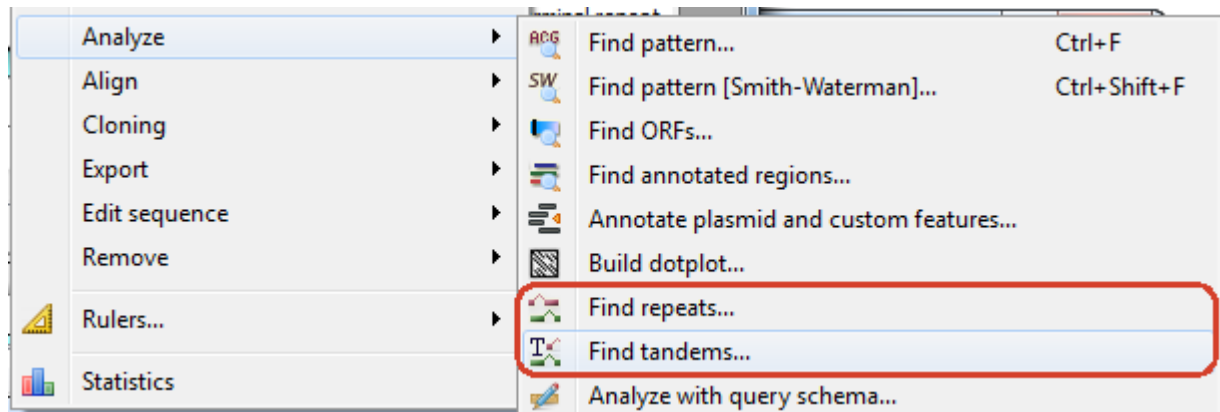


Repeats Finding

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

BaseAdvanced

Repeat finder parameters

Window size

100bp1k

Minimum identity 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:

Find Repeats

Base

Advanced

Advanced parameters

☐ Custom algorithm

Auto

☐ Search only for repeats that lie inside of an annotated region

...

☐ Search only for repeats that have an annotated region inside

...

☐ Filter repeats that have an annotated region inside

...

Nested repeats filter algorithm

☐ Search for inverted repeats

☐ Exclude tandems areas

Disjoint repeats

Estimated repeats count: 0

Help

Cancel

Start

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

