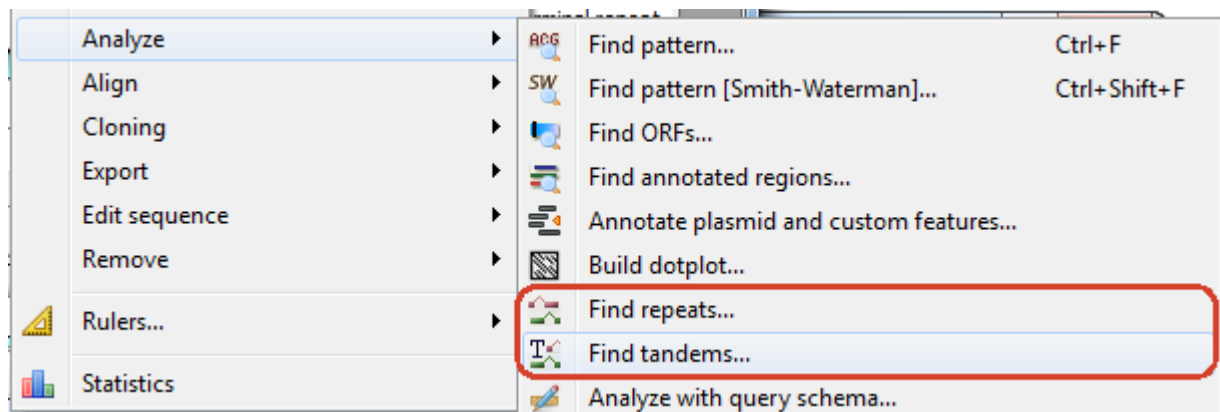


Repeats Finding

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 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:

