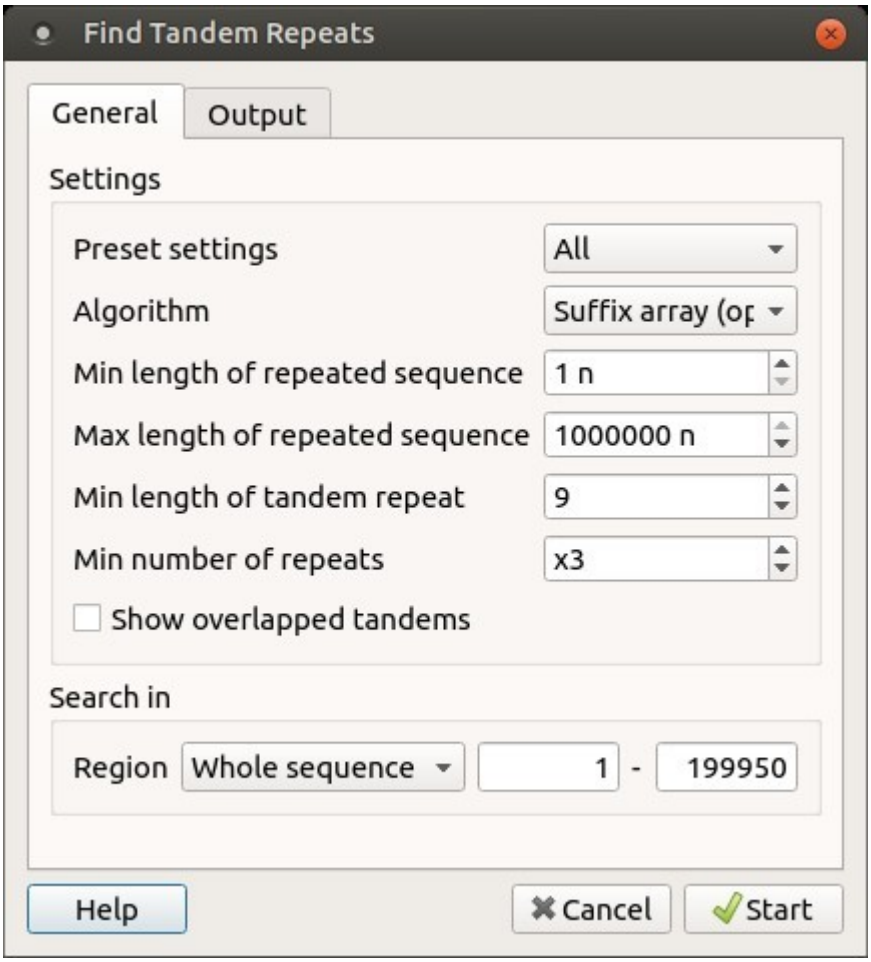
Tandem Repeats Finding

To find tandem repeats, select the *Analyze Find tandem repeats...* context menu item in the *Sequence View* window.

In the opened dialog you can specify the tandem search parameters, the region to search in and the result parameters:



The dialog parameters:

Present Settings — specify the tandem repeats parameters with predefined values by selecting the available preset.

Algorithm — the algorithm parameter allows to select the search algorithm. The default and a fast one is optimized suffix array algorithm.

Min length of repeated sequence - the minimum acceptable repeat length measured in base symbols.

Max length of repeated sequence - the mzximum acceptable repeat length measured in base symbols.

Min length of tandem repeat - the minimum tandem size sets the limit on the minimum acceptable length of the tandem, i.e. the minimum total repeats length of the searched tandem.

Min number of repeats - the minimum number of repeats of a searched tandem.

Show overlapped tandems - check if the plugin should search for the overlapped tandems, otherwise keep unchecked.

Search in - specify the region to search in the whole sequence, a custom region or the region of the current selection (if any).

The output settings can be found in the *Output* tab:

In the *Save annotation(s) to* group, you can set up a file to store annotations. It could be either an existing annotation table object, a new annotation table or auto-annotations table (if it is available).

In the *Annotation parameters* group, you can specify the name of the group and the name of the annotation. If the group name is set to <auto> UGENE will use the group name as the name for the group. You can use the '/' characters in this field as a group name separator to create subgroups. If the annotation name is set to *by type* UGENE will use the annotation type from the *Annotation type:* table as the name for the annotation. Also, you can add a description in the corresponding text field.

- Tandem Repeats Search Result