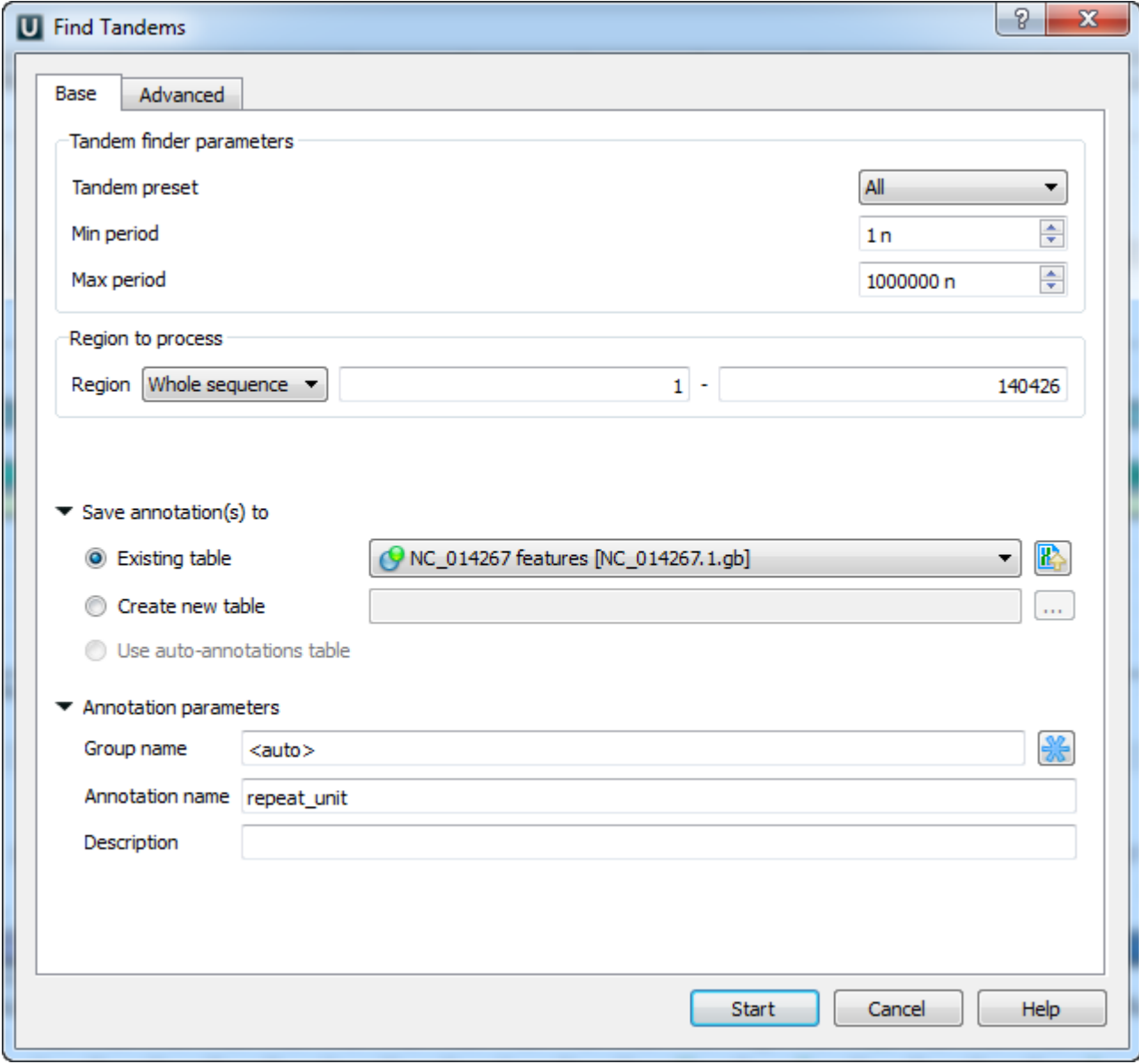


# Tandem Repeats Finding

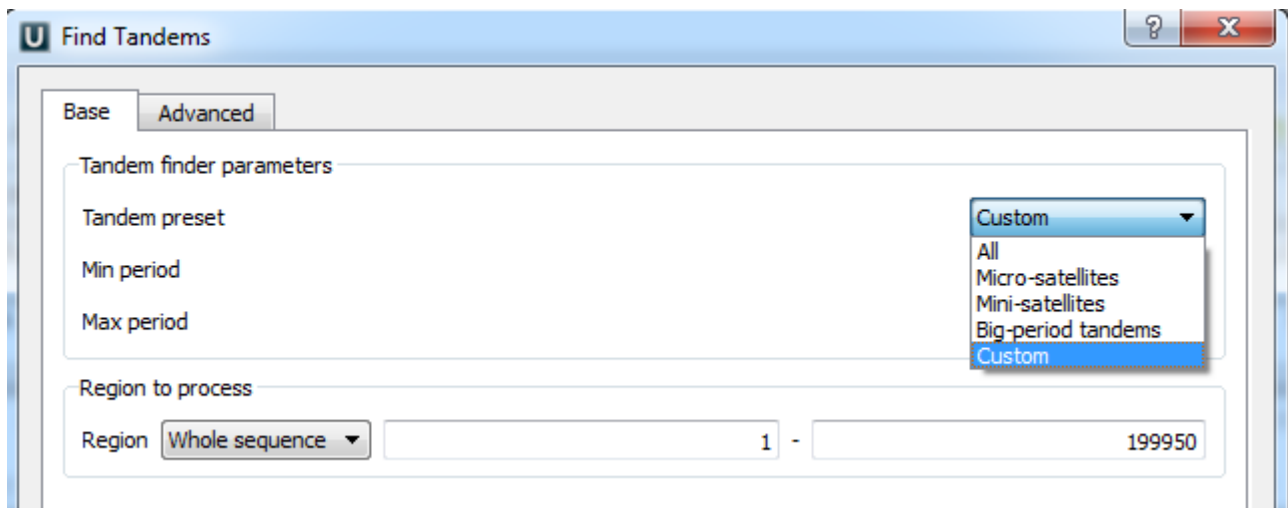
To find tandem repeats, select the *Analyze Find tandems...* context menu item in the *Sequence View* window.

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

The image shows a software dialog box titled "Find Tandems". It has a standard Windows-style title bar with a question mark icon, a close button (X), and a maximize button. The dialog is divided into two tabs: "Base" (selected) and "Advanced". Under the "Base" tab, there are three sections. The first section, "Tandem finder parameters", contains a "Tandem preset" dropdown menu set to "All", and two numeric input fields: "Min period" set to "1 n" and "Max period" set to "1000000 n". The second section, "Region to process", has a "Region" dropdown set to "Whole sequence" and two text input fields for a range, containing "1" and "140426" separated by a hyphen. The third section, "Save annotation(s) to", has three radio buttons: "Existing table" (selected), "Create new table", and "Use auto-annotations table". The "Existing table" option is linked to a dropdown menu showing "NC\_014267 features [NC\_014267.1.gb]". The "Create new table" option is linked to an empty text field. The "Use auto-annotations table" option is not linked. Below these is an "Annotation parameters" section with three text input fields: "Group name" (containing "<auto>"), "Annotation name" (containing "repeat\_unit"), and "Description" (empty). At the bottom right of the dialog are three buttons: "Start", "Cancel", and "Help".

The dialog parameters:

*Tandem preset* — specify the tandem repeats parameters with predefined values by selecting the available preset:

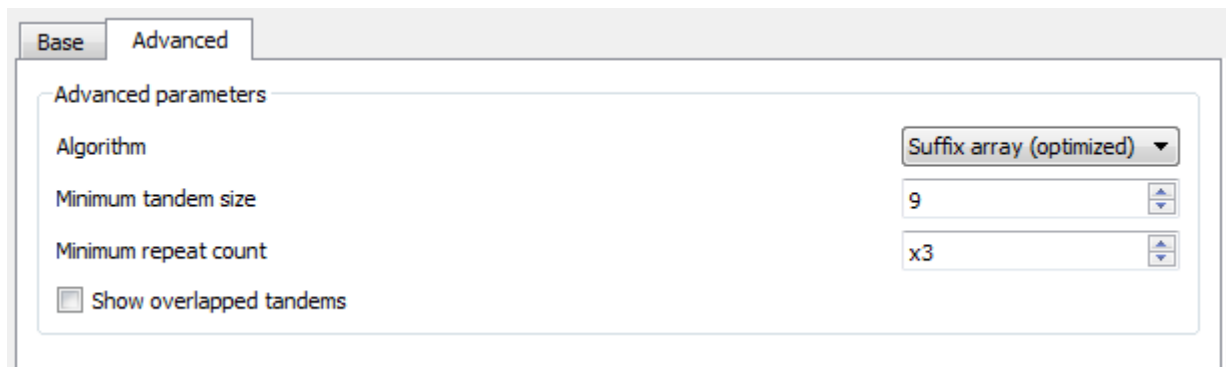


*Min period, Max period* — the minimum and maximum acceptable repeat length measured in base symbols.

*Region to process* — specify the region to search in the whole sequence, a custom region or the region of the current selection (if any).

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.



Additional search options can be found in the *Advanced* tab:

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

*Minimum tandem size* — the minimum tandem size sets the limit on minimum acceptable length of the tandem, i.e. the minimum total repeats length of the searched tandem.

*Minimum repeat count* — 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.

- [Tandem Repeats Search Result](#)