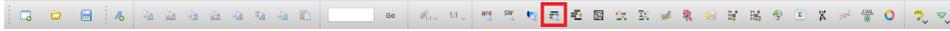


# Find Group of Annotated Regions

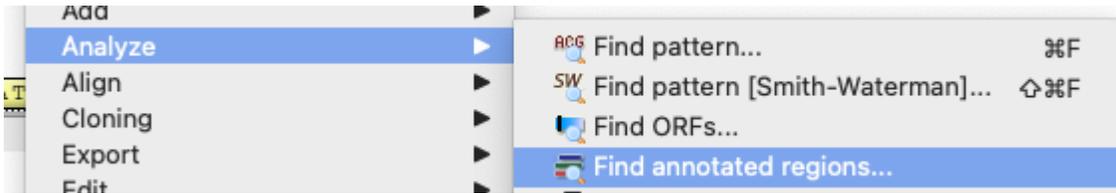
The *Find Group of Annotated Regions* feature provides an algorithm to search for sequence regions that contain a predefined set of annotations.

Open a DNA sequence in the *Sequence View*. There are two ways to open the *Find Repeats* dialog:

1. By clicking on the toolbar button:

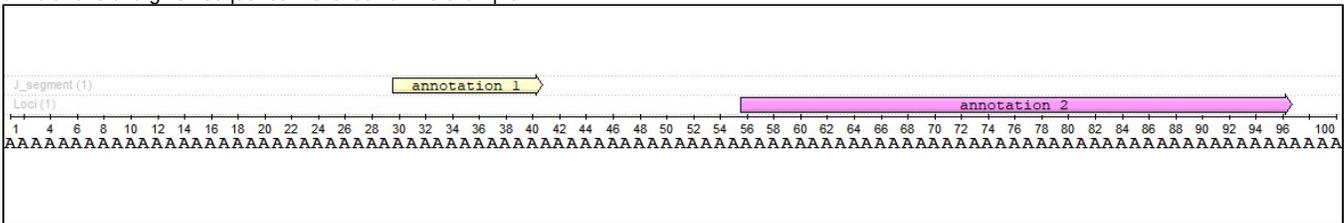


2. By selecting the *Analyze Find annotated regions...* context menu item:



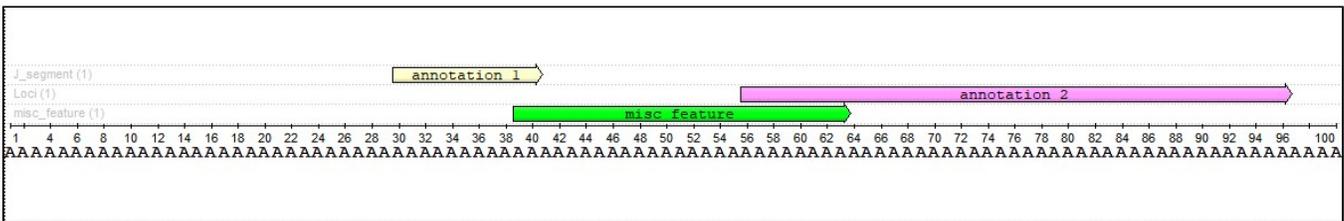
## Algorithm

This tool has been designed to search for annotations that intersect (or completely overlap - it depends on the specified parameters) other, already existing annotations of a given sequence. Let's look at the example:

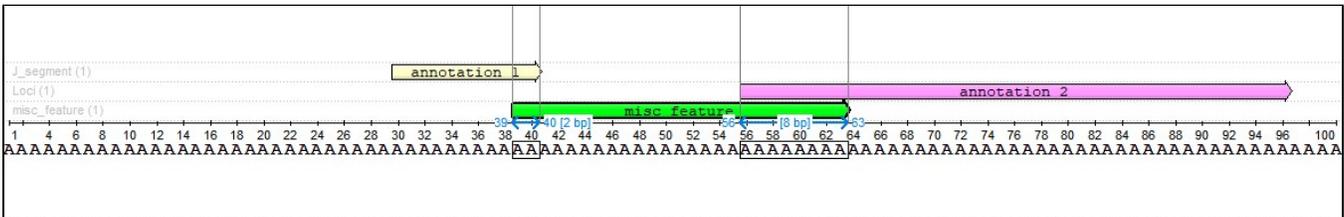


We have a sequence with two annotations. Annotations have different lengths and do not intersect each other. The *annotation 2* length is **four** times the *annotation 1* length (41 vs. 11 bases).

Using this function, we can find an annotation that intersects both source annotations and captures their shares depending on their lengths. For example, let's find an intersection 25 bases long. We will have the following annotation:

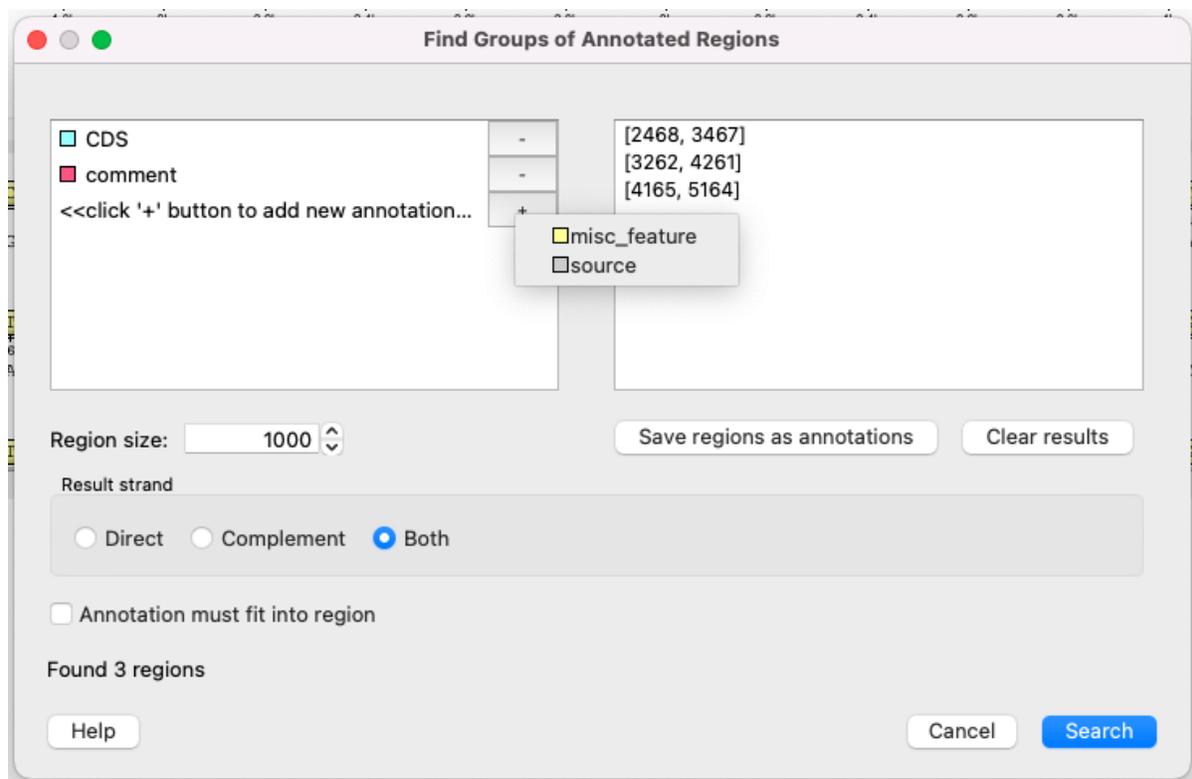


As we can see, the intersection with the first annotation is **two** characters long, and the intersection with the second annotation is **eight** characters long. This result was chosen because the second annotation is **four** times the length of the first annotation.



**NOTE:** A good candidate for this feature could be any file in [Genbank](#) format with a rich set of annotations. [FASTA](#) is not the best option, because this format does not store annotations.

## Parameters



The following parameters are available:

- *Left window* - annotations to search intersection regions for.
- *Right window* - the list of possible intersection regions.
- *Region size* - the length of the new intersection region.
- *Result strand* - select the DNA strand whose annotations will be considered in the search. If, for example, the "Complement" strand is selected, but all chosen annotations are on the direct strand, than nothing will be found.
- *Annotation must fit into region* - all annotations, chosen at the *left window*, must fit completely to the result annotation (completely - not just in a few characters).
- *Save regions as annotations* - store results to annotations.
- *Clear results* - clear the result table.