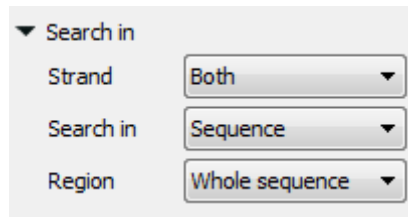


Search in



The image shows a search configuration panel with a grey background. At the top left, there is a dropdown menu labeled 'Search in' with a downward arrow. Below it are three rows, each with a label on the left and a dropdown menu on the right. The first row has the label 'Strand' and a dropdown menu showing 'Both'. The second row has the label 'Search in' and a dropdown menu showing 'Sequence'. The third row has the label 'Region' and a dropdown menu showing 'Whole sequence'.

In this group you can specify where to search for a pattern: in what region and in which strand (for nucleotide sequences). Also for nucleotide sequences it is possible to search for a pattern on the sequence translations.

Strand — for nucleotide sequences only. Specifies on which strand to search for a pattern: *Direct*, *Reverse-complementary* or *Both* strands.

Search in — for nucleotide sequences you can select the *Translation* value for this option. In this case the input pattern will be searched in the amino acid translations.

Region — specifies the sequence range where to search for a pattern. You can search in the whole sequence, specify a custom region or search in the selected region.