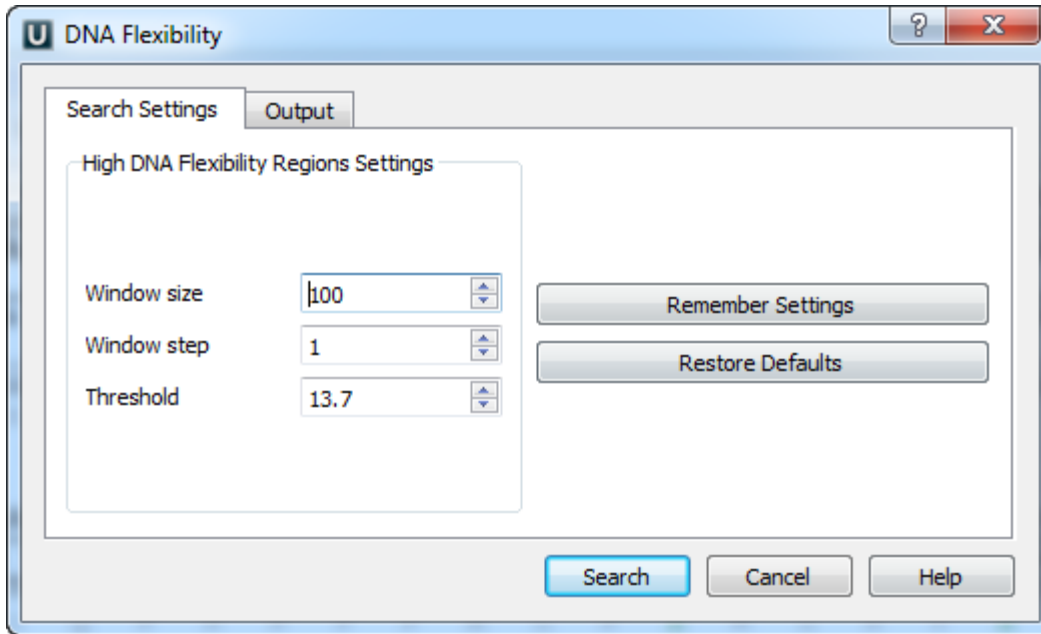


DNA Flexibility

To search for regions of high DNA helix flexibility in a DNA sequence, open the sequence in the *Sequence View* and select the *Analyze Find high DNA flexibility regions* item in the context menu. Note that only standard DNA alphabet is supported, i.e. the sequence should consist of characters A, C, G, T and N.

The following dialog appears:



The calculation is made for overlapping windows along a given sequence. If there are two or more consecutive windows with an average flexibility threshold (in each window) greater than the specified *Threshold* parameter, such area is marked by an *annotation*.

The average threshold in a window is calculated by the following formula:

$$(\text{average window threshold}) = (\text{sum of flexibility angles in the window}) / (\text{the window size} - 1)$$

The following flexibility angles are used during the calculation:

| Dinucleotide | Angle | Dinucleotide | Angle |
|--------------|-------|--------------|-------|
| AA | 7.6 | CA | 14.6 |
| AC | 10.9 | CC | 7.2 |
| AG | 8.8 | CG | 11.1 |
| AT | 12.5 | CT | 8.8 |
| GA | 8.2 | TA | 25 |
| GC | 8.9 | TC | 8.2 |
| GG | 7.2 | TG | 14.6 |
| GT | 10.9 | TT | 7.6 |

A minimum value is used when N characters is present in a dinucleotide:

- **CN, NC, GN, NG, NN: 7.2**
- **AN, NA, TN, NT : 7.6**

- [Configuring Dialog Settings](#)
- [Result Annotations](#)