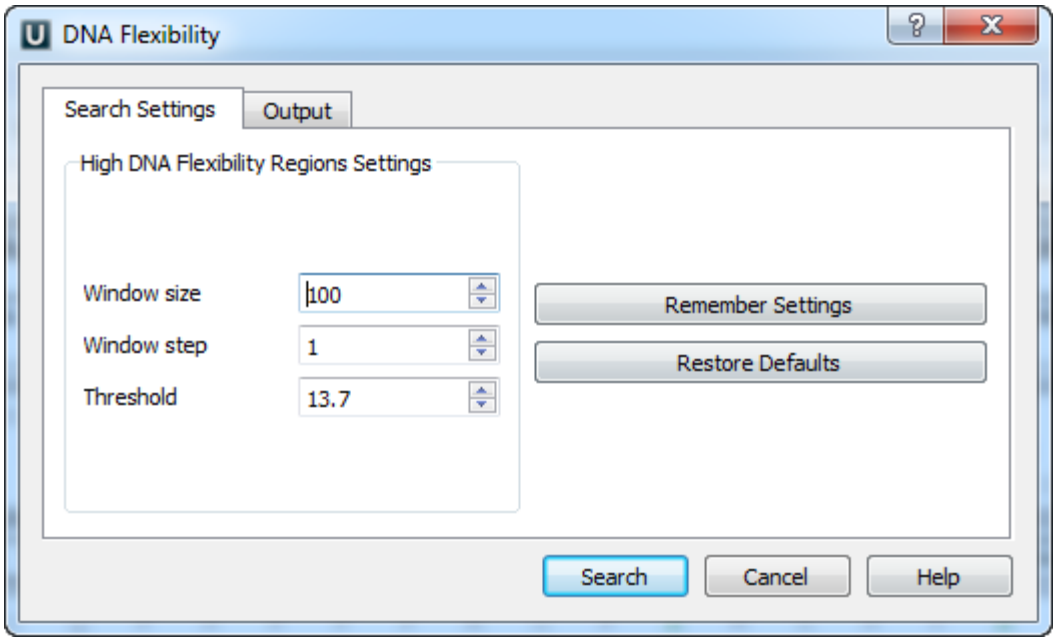
# DNA Flexibility

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:

```
(average window threshold) = (sum of flexibility angles in the window) / (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