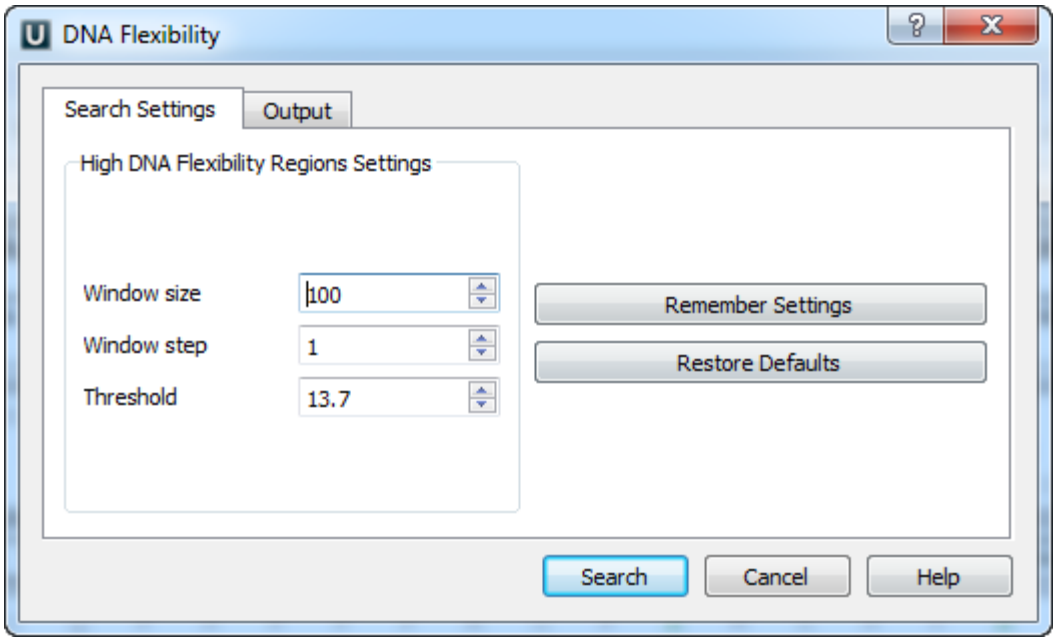
DNA Flexibility

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