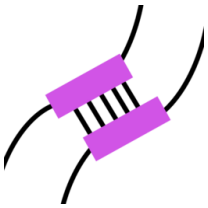
Using the Sticky Finder Application (03/10/2025)

To make our complementary sequence finder ("Sticky Finder") more accessible to users without a coding background, we provide **Sticky Finder.exe**, which can be used without installing Python or downloading additional scripts.

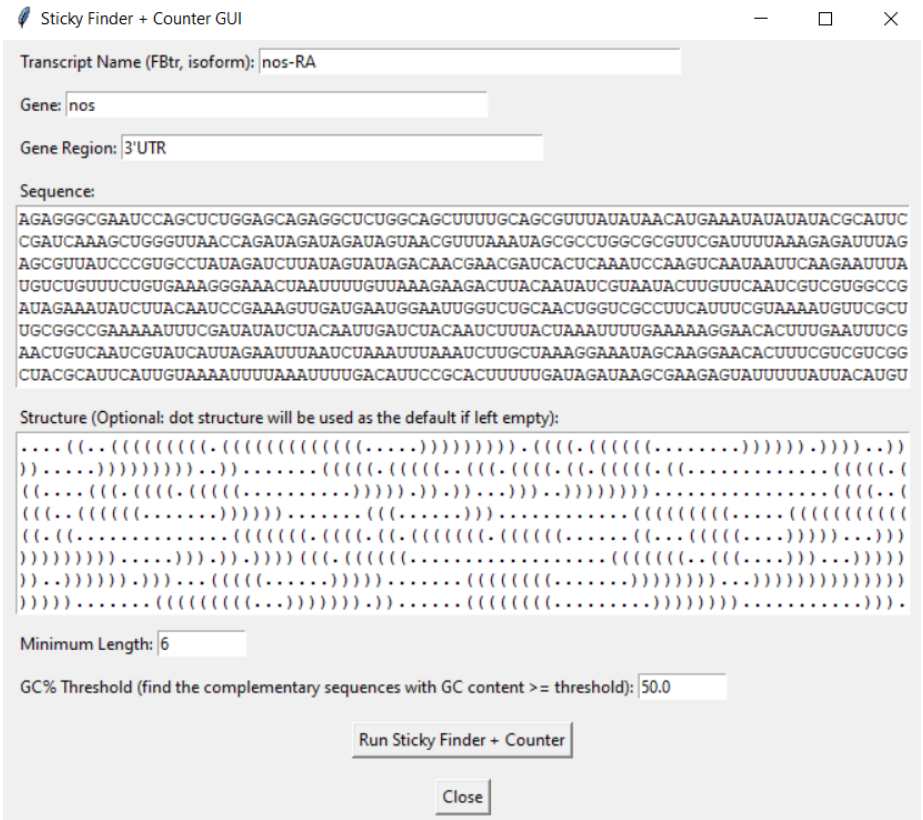
This application features a graphical user interface (GUI) developed by Siran Tian using Tkinter, based on the scripts **"sticky_finder_v3.py"** and **"sticky_finder_v3_counter.py"** from https://github.com/AnneyYeZiqing/sticky_finder. The original scripts were written by Ziqing Ye and later modified by Siran Tian in the Trcek Lab at Johns Hopkins University**.**

Application Icon:



How to Use Sticky Finder

1. **Launching the Application:** Once installed, double-click on the application icon.
2. **User Interface:** A window will appear, displaying the main interface of Sticky Finder:



3. Search the complementary sequences:

To identify complementary sequences, fill in the following required and optional fields:

Input Parameters

a. Transcript name (required): The isoform of the RNA sequence. You can enter the same name as your gene name. The default is "nos-RA."

b. Gene (required): The name of the gene of interest. The default is "nos."

c. Gene region (required): The region of the gene from which the sequence is taken. This can be any defined region, such as 5'UTR, CDS, 3'UTR, or full length. The default is "3' UTR of nos."

d. Sequence (required): The primary RNA sequence. Both "T" and "U" are accepted as input. The default sequence corresponds to the "nos 3'UTR".

e. Structure (optional): The predicted dot-bracket structure from RNA structure prediction tools such as RNAfold. If left blank, a dot-structure of the same length as your RNA will be used. The default structure is the structure of nos 3'UTR predicted by the RNAfold.

f. Minimum length (required): The minimum length of the complementary sequences.

- For palindromes and sense/antisense sequences, this refers to the entire sequence length.
- For inverted repeats, it refers to half the sequence length.
- The default is 6 nucleotides.

g. GC% threshold (required): The threshold (%) for GC content. The program will generate a file containing complementary sequences with GC content equal to or above the threshold. The default is 50%.

h. Click "Run Sticky Finder + Counter" to start the analysis.

i. The program will generate three output files based on the selected parameters. Using the default settings, the following files will be created:

1. nos_palindromes+IRs_min=6nt – Contains palindromes and inverted repeats with a minimum length of 6 nucleotides. The file includes specific sequences, locations, and structural information in an Excel sheet.
2. nos_sense-antisense_min=6nt – Contains sense and antisense sequences with a minimum length of 6 nucleotides. The file includes specific sequences, locations, and structural information in an Excel sheet.
3. nos_CSs-by-GC_min=6_gc_threshold=50.0_S1 – Contains all complementary sequences of at least 6 nucleotides with a GC content of ≥ 50%.

Important Notes

- Sticky Finder currently considers only Watson-Crick base pairing (G-C, A-U, or A-T) and does not account for G-U wobble base pair.
- The identified sticky sequences are complementary within the same sequence rather than two different sequences.
- Future updates will enhance the application's functionality and applicability.