This user guide accompanies the "Exon_Detect_GUI" software that accompanies the paper "Filter-Based Methodology for the Location of Hot Spots in Proteins and Exons in DNA" by Ramachandran et al., "IEEE Transactions on Biomedical Engineering", Volume: 59, Issue: 6, June 2012.

General Description

The software implements the filter-based exon location methodology described in the above paper with the aid of a user-friendly graphical user interface (GUI). The GUI, namely, "Exon Detect GUI", can be used to design and apply an invese-Chebyshev filter and an optimized band-pass notch (BPN) filter. Since the characteristic frequency, $2\pi/3$, is fixed for the exon-location procedure, there is no need to tune the BPN filter, as was required for hot-spot location.

Contents

The package consists of an m-file and a fig file namely

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Exon_Detect_GUI.m,  and
Exon_Detect_GUI.fig,
```

this user guide, and an example DNA FASTA file containing sample DNA sequences.

The fig file contains the GUI layout, and the m-file contains the callback functions along with all the other necessary functions.

Note: For the GUIs to work, it is mandatory for a GUI m-file and its matching fig file to have identical names. They should differ only by filename extension.

Minimum Requirements

The software has been written and tested on the Microsoft Windows platform. Versions of Windows above XP are compatible.

At the minimum, the software requires Matlab as well as the Signal Processing and the Optimization toolboxes to execute.

Compatibility

The software would be compatible with any of the versions of Matlab and the toolboxes released since 2009.

Input

All DNA sequences desired to be processed must be stored in a single text file in FASTA format. Please see accompanying test data for exact formatting.

GUI Component Descriptions and Typical Operating Procedure

Most of the components of the "Exon_Detect_GUI" are the same as those of the "HSpot_Detect_GUI". Hence the operating procedures for the two GUIs are also very similar. We highlight only the differences here and, for further details, refer the reader to the detailed user guide accompanying the "HSpot_Detect_GUI".

Data Type: The type of the input sequences is different. The HSpot_Detect_GUI deals with protein sequences while the Exon_Detect_GUI deals with DNA sequences.

Characteristic Frequency: For exon location, this is fixed at $2\pi/3$, whereas, for hot-spot location, this depends on the type of the functional group under consideration.

BPN Filter Tuning: Since we have a fixed characteristic frequency for exon location that can be accurately determined, there is no need for tuning the BPN filter being used.