Minfo

A Fourier Information visualization tool and accompanying software

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Introduction

This tool is primarily meant as a quick-and-easy method for estimating the information content in multiple neurons. In the past, the estimation of information in multiple neurons has been limited to a small number of cells. We have recently developed a method in which the information content in many neurons can be estimated. For an in-depth discussion of the method, please consult the following three publications:
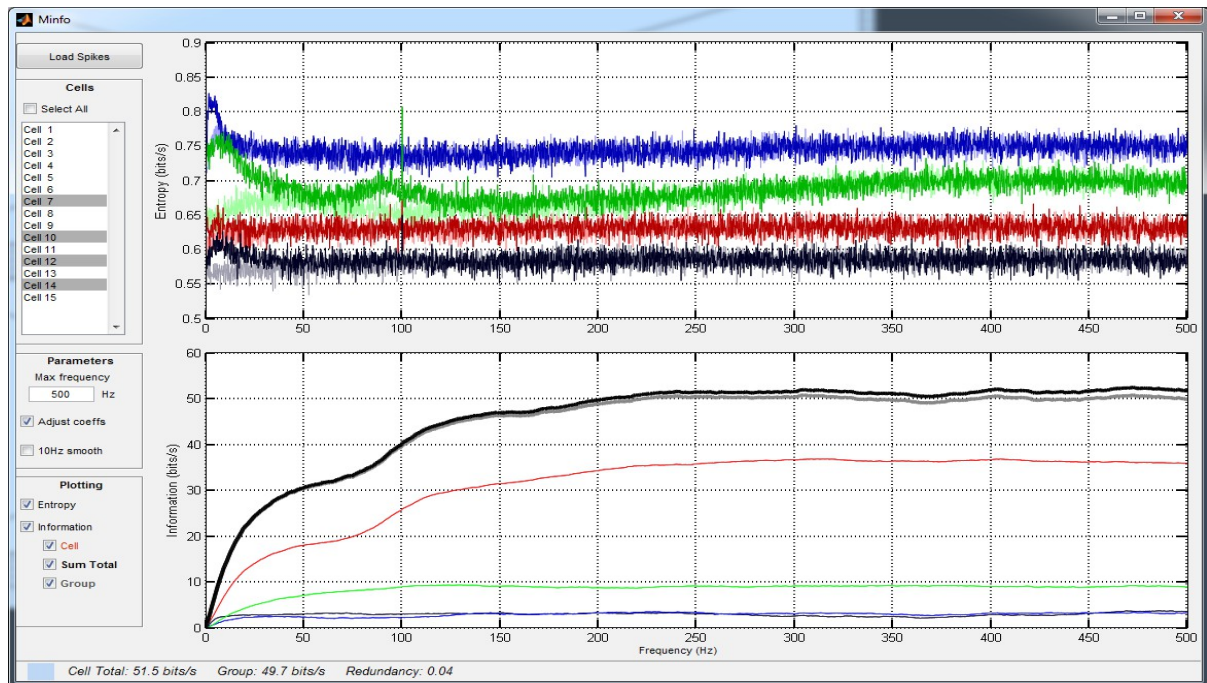
1. Yu Y1, Crumiller M, Knight B, Kaplan E.
   Estimating the amount of information carried by a neuronal population.
   Front Comput Neurosci. 2010 Apr 26;4:10. doi: 10.3389/fncom.2010.00010. ECollection 2010.

2. Crumiller M1, Knight B, Yu Y, Kaplan E.
   Estimating the amount of information conveyed by a population of neurons.
   Front Neurosci. 2011 Jul 15;5:90. doi: 10.3389/fnins.2011.00090. ECollection 2011.

3. Crumiller M, Knight B, Kaplan E (2013).
   The Measurement of Information Transmitted by a Neural Population: Promises and Challenges.
   Entropy. 2013. 15, no. 9: 3507-3527.

This tool is developed using Mathworks Matlab® software. A description of both the tool and the accompanying methods are described in this document, in order to assist in integration with other projects.

Data Format

Data should be stored in a .mat file, and must contain the following variables:

Variable Name	Dimensionality/Data type	Description
spikes	MxT cell matrix • M – number of neurons • T – number of total trials	Spike trains are stored in cell matrixes, which allow for variable-length data. Each row stores the spikes for a unique cell, and each column stores the spikes for each trial. Each cell element is a vector of spike times.
trial_length	1x1 scalar	The length, in seconds, of each trial. This argument is optional; if not provided, the trial length is automatically set to the latest spike in the entire spike train set.
REPEATS	1xT logical vector	This vector indicates which of the T trials are the 'Repeat' trials.
UNIQUES	1xT logical vector	This vecotr indicates which of the T trials are the 'Unique' trials.

Using the Tool

1. Launch the tool from the command line:

   ```
   >> Minfo
   ```

2. Select "Load Spikes" from the top left corner and select the appropriate .MAT file containing data as described above.

3. The Fourier coefficients up to the default maximum frequency (100 Hz) will be automatically calculated, and the resulting information displayed.

4. Cells can be selected via ctrl+clicking on individual neurons. Information is recalculated each time a new cell is selected (the recalculation time is negligible), and the plots are updated.

5. Coefficient Parameters:

   - **Max frequency** – The maximum frequency calculated and displayed. High-frequencies may require more computation time. Note that coefficients are always retained in memory, and recalculation of the coefficients only occurrs when the frequency is extended beyond the maximum that has been used during the current session.
   - **Adjust coefficients** – This feature applies a small statistical correction that compensates for fluctuation in firing rate between trials. Use this is your information curves do not level off.
   - **5 Hz smooth** – Smooths the information and entropy curves with a moving average using a flat window of 5 Hz.

6. Plotting Parameters:

   - **Entropy** – Display frequency versus entropy plots. Each cell is color-coded, with unique entropy plotted slightly darker and repeat entropy plotted slightly lighter than the corresponding information curve below. When this is unchecked, the Information plot takes up the entire display area.
   - **Information** – Display frequency versus information plots. Individual cell information traces are plotted in different colors. The sum total of the individual cell traces is displayed in bold black, and the group information (the non-redundant information conveyed by the group of selected cells) is displayed in bold gray. When Information is unchecked, the Entropy plot takes up the entire display area.

Using the command line

The accompanying .m files can be used independently in the estimation of information of a set of spike trains. In general, the following sequence of commands is used to calculate entropy and/or information rates: We shall assume that a set of spike trains is already stored in the cell array named spikes, with the trial_length, REPEAT, and UNIQUE indices as described above.

```matlab
% generate Fourier coefficients up to 100 Hz
>> [coeffs,frequencies] = spiketime2fourier(spikes,100,trial_length);

% determine number of spikes in each trial
>> spike_count  = cellfun(@length,spikes);

% adjust the Fourier coefficients
>> [coeffs, deleted] = adjust_coeffs(coeffs,spike_count);

% update our REPEAT and UNIQUE indices, since some trials may have been deleted
>> REPEATS(deleted)=[];
>> UNIQUES(deleted)=[];

% Calculate the repeat and unique entropy rates
>> [repeat_cell_entropy, repeat_group_entropy] = ...
    entropy_coeffs(coeffs(:,REPEATS,:),trial_length);
>> [unique_cell_entropy,unique_group_entropy] = ...
    entropy_coeffs(coeffs(:,UNIQUES,:),trial_length);

% Calculate the information and redundancy rates
>> [cell_info, group_info, redundancy] = ...
    information_coeffs(coeffs(:,REPEATS,:),coeffS(:,UNIQUES,:),trial_length);
```

How to Cite

If you have used the Fourier Information Method for scientific publication, please cite the following:

- Yu Y1, Crumiller M, Knight B, Kaplan E. Estimating the amount of information carried by a neuronal population. *Front Comput Neurosci*. 2010 Apr 26;4:10.

- Crumiller M1, Knight B, Yu Y, Kaplan E. Estimating the amount of information conveyed by a population of neurons. *Front Neurosci*. 2011 Jul 15;5:90.

Contact

All software is maintained by Marshall Crumiller. You can best reach me at mcrumiller@rockefeller.edu.