
TED Documentation

Release 0.7.1

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Part I

Introduction

The Time Encoding and Decoding Toolkit (TED) is a library of Python routines, classes, and demo programs that implement time encoding and decoding algorithms. A [MATLAB](#) implementation of the toolbox is also available from the Bionet Group's [code repository page](#).

Additional algorithms for encoding and decoding video signals implemented in Python are available in the Video Time Encoding and Decoding Toolkit.

To get started using the toolbox, go to the [installation](#) page and try running the demos. Check out the [overview](#) page for a high-level introduction to time encoding and decoding concepts.

Part II

Contents

Installation Instructions

1.1 Obtaining the Latest Software

The latest version of the Time Encoding and Decoding Toolkit can be downloaded from the Bionet Group's [code repository page](#).

1.2 Prerequisites

The Python implementation of the Time Encoding and Decoding Toolkit requires that several software packages be present in order to be built and installed (older versions of these packages may work, but have not been tested):

- [Cython](#) 0.11.2 or later.
- [Numpy](#) 1.2.0 or later.
- [Python](#) 2.5 or later.
- [Scipy](#) 0.7.0 or later.

To run the CUDA-dependent implementations, you will also need

- [NVIDIA CUDA Toolkit](#) 3.2 or later.
- [PyCUDA](#) 0.94.2 or later.
- [scikit.cuda](#) 0.04 or later.

To run the demo code and generate plots, the following package is also required:

- [Matplotlib](#) 0.98 or later.

Some of the utility functions may require the following packages:

- [MEncoder](#) 1.0 or later.
- [PyTables](#) 2.1.1 or later.
- [OpenCV](#) 2.1.0 or later.

To build the documentation, the following packages are also required:

- [Docutils](#) 0.5 or later.
- [Jinja2](#) 2.2 or later
- [Pygments](#) 0.8 or later

- [Sphinx 1.0.1](#) or later.
- [Sphinx ReadTheDocs Theme 0.1.6](#) or later.

This software has been tested on Linux; it should also work on other platforms supported by the above packages.

1.3 Building and Installation

To build and install the toolkit, download and unpack the source release and run:

```
python setup.py install
```

from within the main directory in the release. Sample code demonstrating how to use the toolkit is located in the `demos/` subdirectory. If you have [pip](#) installed, you can install the latest package code directly from Github as follows:

```
pip install git+git://github.com/bionet/ted.python.git
```

To rebuild the documentation, run:

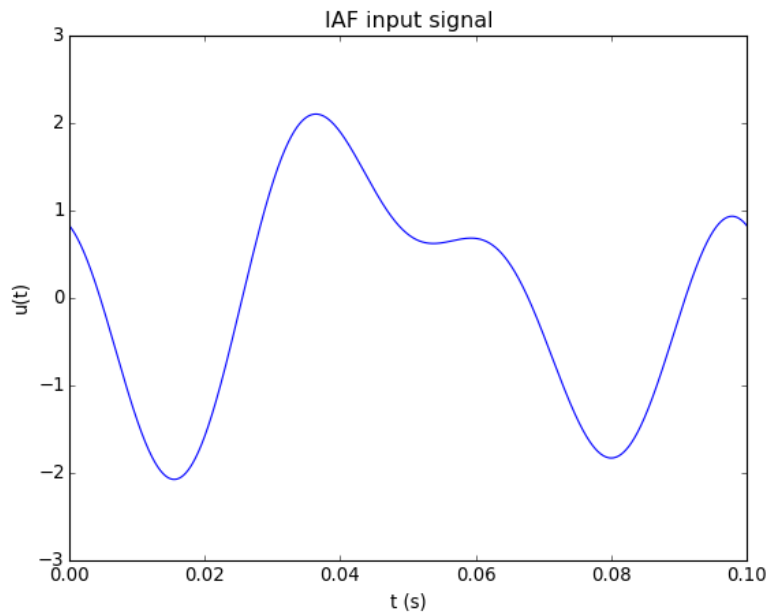
```
make
```

from within the `docs/` subdirectory and follow the directions.

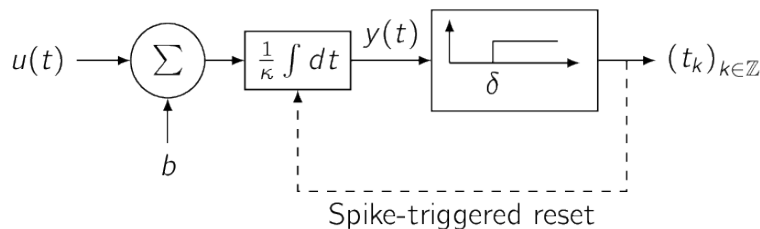
Overview of Time Encoding and Decoding

2.1 What is Time Encoding?

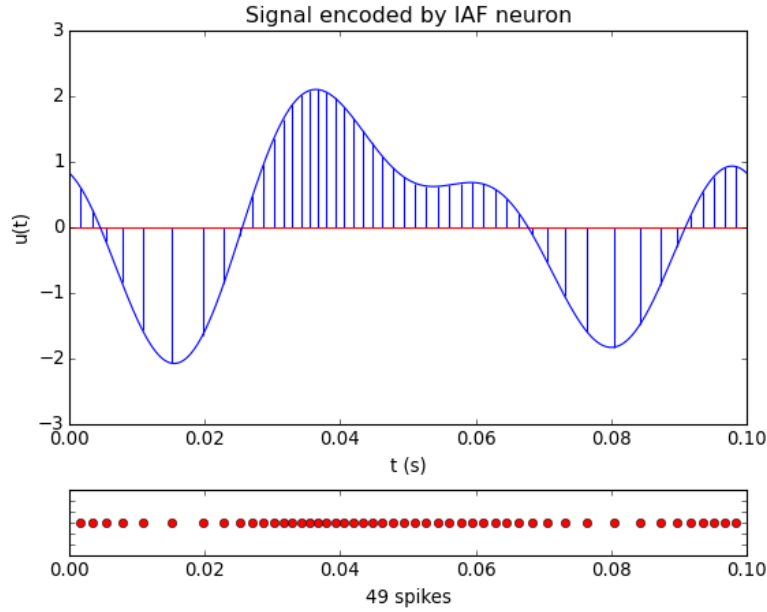
Consider a simple analog signal:



If this signal is bandlimited, then it can be faithfully represented - or *encoded* - by a sequence of uniformly spaced samples - that is, the original analog signal can be *perfectly reconstructed* from the samples. This follows from Shannon's Sampling Theorem. There are both natural and man-made systems, however, that encode analog input information as samples or events that are *non-uniformly* spaced in time. An Integrate-and-Fire neuron, for example, can *time encode* a stimulus signal by transforming it into a sequence of time events or *spikes*: [1]:



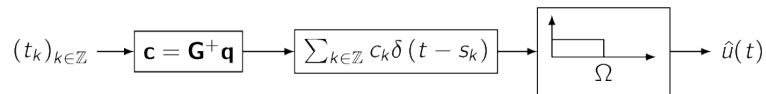
To illustrate the encoding process, the sample signal depicted above (with a bandwidth of 32 Hz and a duration of 100 ms) is encoded below using the Integrate-and-Fire neuron as a series of non-uniformly spaced spikes (represented by the red markers in the plot below):



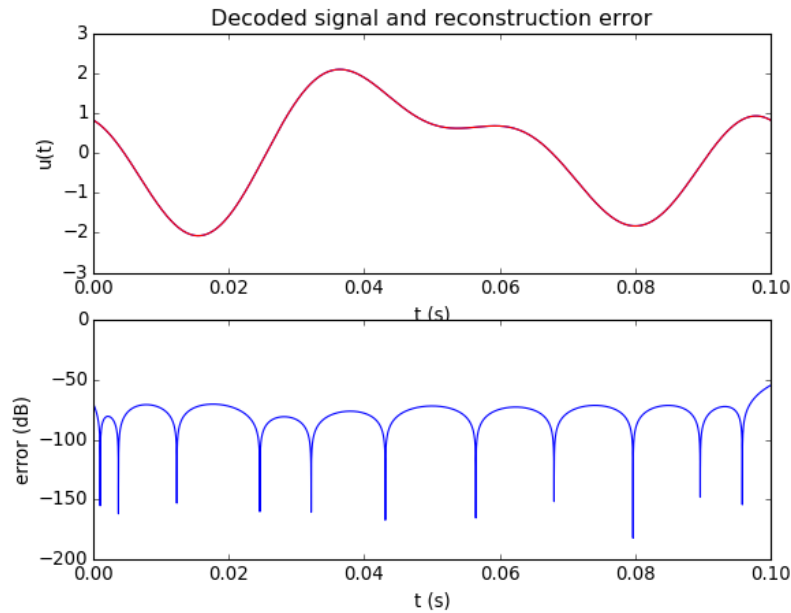
The existence of such systems motivates the question as to whether signals that are encoded in such a manner can be faithfully recovered.

2.2 What is Time Decoding?

Under appropriate conditions [1], a signal that has been time encoded as a sequence of spikes can be faithfully recovered using a *time decoding machine*. The circuit below uses sinc kernels to reconstruct the encoded signal:

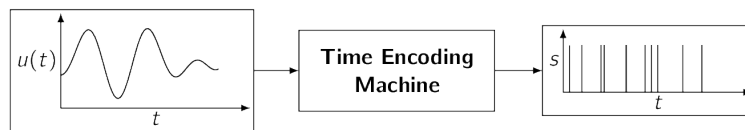


Processing a time encoded signal with the above circuit results in the following reconstruction. Although the actual input signal is discretely represented with traditional computational models, the reconstruction can be made arbitrarily precise for bandlimited stimuli.



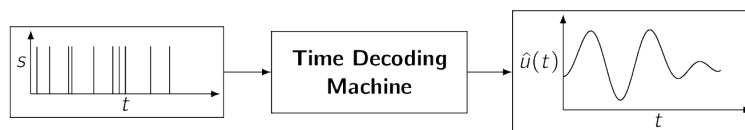
2.3 What are Time Encoding Machines?

A *Time Encoding Machine*, or *TEM* [2], represents analog information in the time domain. TEMs arise in single-input single-output (integrate-and-fire neurons, asynchronous sigma-delta modulators), single-input multi-output (population encoding models), and other classical circuit configurations:



2.4 What are Time Decoding Machines?

A *Time Decoding Machine*, or *TDM* [2], recovers a signal encoded by a Time Encoding Machine according to a fidelity criterion:



2.5 Why Should Neuroscientists Care About Time Encoding?

- Time Encoding Machines are *in silico* models of neural encoding. Under appropriate conditions, these encoders faithfully represent information about stimuli [2].

- The theory underlying time encoding applies to well-understood neuron models such as the (leaky) Integrate-and-Fire neuron [3], the Hodgkin-Huxley neuron, and feedback and feedforward configurations of these models [6].
- The theory of time encoding has been extended to address the representation of scalar-valued stimuli by populations of neurons [7] [8]. In particular, the time encoding and decoding of video signals has been successfully performed using ensembles of neurons [9] [13].

2.6 Why Should Engineers/Computer Scientists Care About Time Encoding?

- Signal representations in the time domain can exploit the increasing time resolution that scaling of integrated circuits technology [2] (Moore's law) continues to offer. Traditional A/D conversion, by contrast, is adversely affected by the power density requirements that call for lower and lower voltages.
- Time encoding theory extends the application domain of well-understood concepts in information theory, communications theory, signal processing and machine learning to asynchronous information representation and computation [6].
- Time encoding theory has been extended to address the faithful representation of real-time (arbitrarily long) signals [10] and non-bandlimited signals [11].

2.7 Further Reading

See the [publications](#) page for the list of articles whose algorithms are implemented in the toolkit. More literature on time encoding and decoding is available on the [Bionet publication server](#).

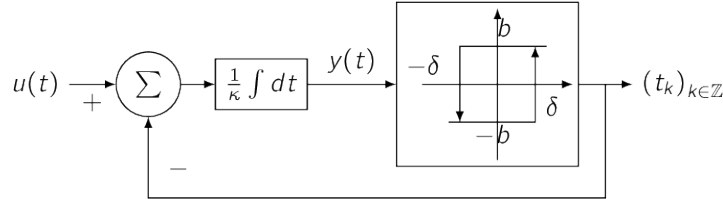
Time Encoding and Decoding Machines

The TED Toolkit provides implementations of a range of time encoding and decoding machines. Brief descriptions of these machines are provided in the following pages, along with links to the relevant articles that describe them in more detail and documentation for the Python functions and classes that implement them.

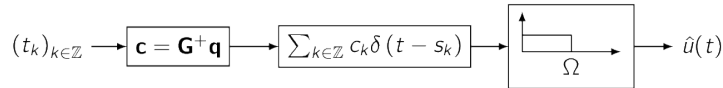
3.1 Asynchronous Sigma-Delta Modulators

3.1.1 Single-Input Single-Output Machines

Time Encoding Machine [2] Encodes a bandlimited signal using an Asynchronous Sigma-Delta Modulator.



Time Decoding Machine [2] Reconstructs a bandlimited signal encoded with an Asynchronous Sigma-Delta Modulator using sinc kernels.



Time Decoding Machine - Fast Approximation Method [4] Reconstructs a bandlimited signal encoded with an Asynchronous Sigma-Delta Modulator using a fast approximation method.

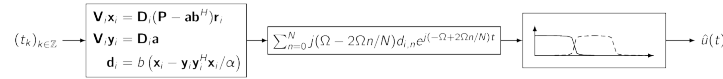
$$(t_k)_{k \in \mathbb{Z}} \longrightarrow \mathbf{d} = \alpha \mathbf{T}^+ \mathbf{SDP}^{-1} \mathbf{q} \longrightarrow \frac{j\Omega}{M} \sum_{n=-M}^M n d_n e^{jn\Omega t/M} \longrightarrow \hat{u}(t)$$

Time Decoding Machine - Real-Time Decoder [10] Decodes a bandlimited, arbitrarily long signal encoded by an Asynchronous Sigma-Delta Modulator by stitching together blocks of data decoded by solving a Vandermonde system using the Björk-Pereyra Algorithm.

$$(t_k)_{k \in \mathbb{Z}} \longrightarrow \mathbf{V}_i \mathbf{d}_i = \mathbf{DP} \mathbf{q}_i \longrightarrow \sum_{n=0}^N j(\Omega - 2\Omega n/N) d_{i,n} e^{j(-\Omega + 2\Omega n/N)t} \longrightarrow \hat{u}(t)$$

Time Decoding Machine - Threshold-Insensitive Real-Time Decoder [10] Decodes a bandlimited, arbitrarily long signal encoded by an Asynchronous Sigma-Delta Modulator by stitching

together blocks of data decoded by solving a Vandermonde system using the Björk-Pereyra Algorithm. This reconstruction method does not require the specification of an integrator threshold.

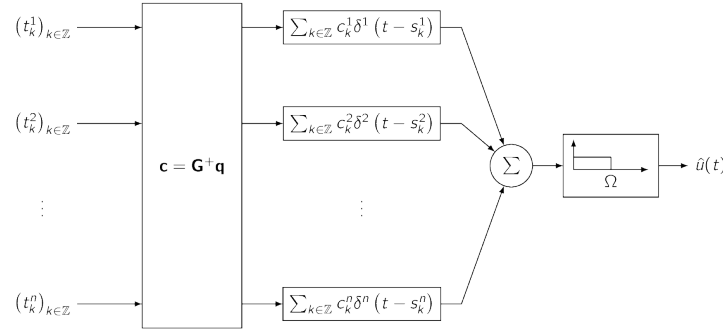


Time Decoding Machine – Threshold-Insensitive Method [2] Reconstructs a bandlimited signal encoded with an Asynchronous Sigma-Delta Modulator using sinc kernels. This reconstruction method does not require the specification of an integrator threshold.

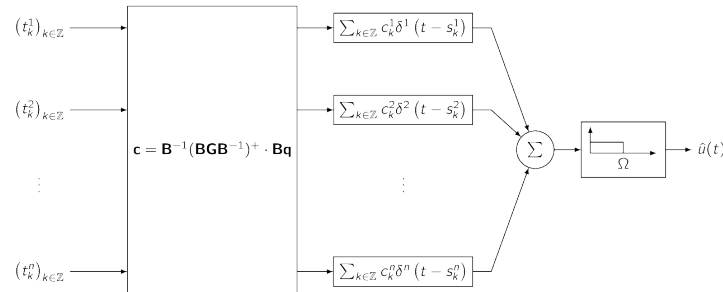


3.1.2 Multi-Input Single-Output Machines

Time Decoding Machine – MISO Decoder [7] Decodes a bandlimited signal encoded by multiple Asynchronous Sigma-Delta Modulators using sinc kernels.



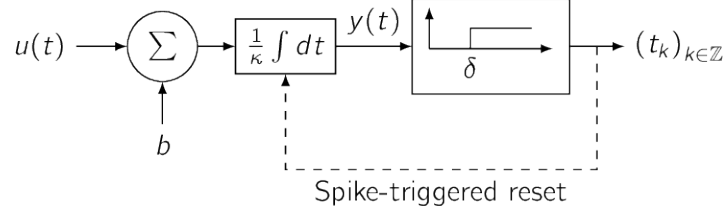
Time Decoding Machine – Threshold-Insensitive MISO Decoder [2] [7] Decodes a bandlimited signal encoded by multiple Asynchronous Sigma-Delta Modulators using sinc kernels. This reconstruction method does not require the specification of an integrator thresholds.



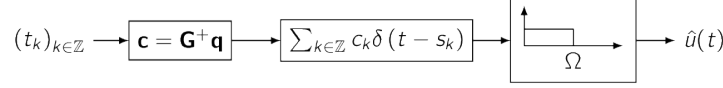
3.2 Integrate-and-Fire Neurons

3.2.1 Single-Input Single-Output Machines

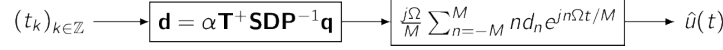
Time Encoding Machine [2] Encodes a bandlimited signal using an Integrate-and-Fire neuron. Leaky and ideal neuron models are supported.



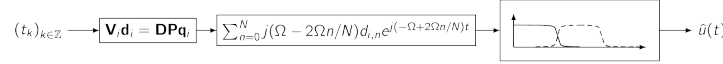
Time Decoding Machine [1] Decodes a bandlimited signal encoded by an Integrate-and-Fire neuron using sinc kernels.



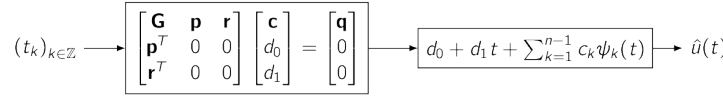
Time Decoding Machine - Fast Approximation Method [4] Decodes a bandlimited signal encoded by an Integrate-and-Fire neuron using a fast approximation method.



Time Decoding Machine - Real-Time Decoder [10] Decodes a bandlimited, arbitrarily long signal encoded by an Integrate-and-Fire neuron by stitching together blocks of data decoded by solving a Vandermonde system using the Björk-Pereyra Algorithm.

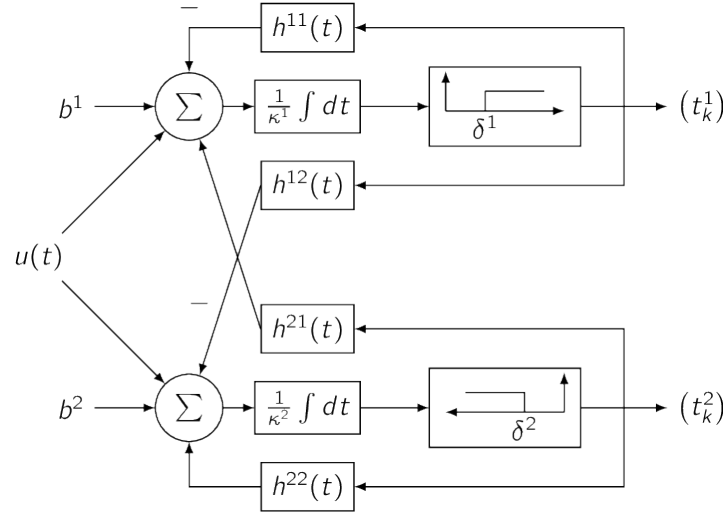


Time Decoding Machine - Spline Interpolation Method [12] Decodes a bandlimited signal encoded by an Integrate-and-Fire neuron using spline interpolation.



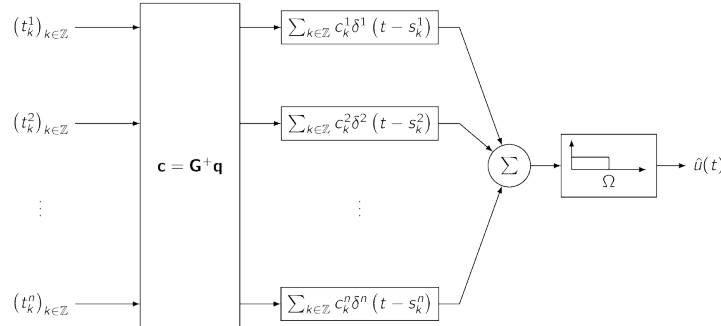
3.2.2 Single-Input Multi-Output Machines

Time Encoding Machine - SIMO Coupled IAF Encoder [12] Encodes a finite energy signal encoded by with multiple coupled ON-OFF Integrate-and-Fire neurons.



3.2.3 Multi-Input Single-Output Machines

Time Decoding Machine – MISO IAF Decoder [7] Decodes a bandlimited signal encoded by multiple Integrate-and-Fire neurons using sinc kernels.

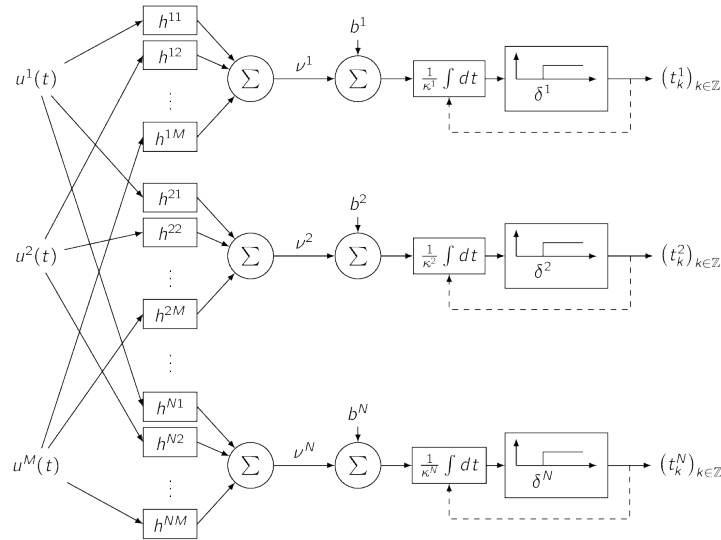


Time Decoding Machine – MISO Coupled IAF Decoder [12] Decodes a finite energy signal encoded by multiple coupled ON-OFF Integrate-and-Fire neurons using spline interpolation.

$$(t_k^j)_{k \in \mathbb{Z}} \longrightarrow \begin{bmatrix} \mathbf{G} & \mathbf{p} & \mathbf{r} \\ \mathbf{p}^T & \mathbf{0} & \mathbf{0} \\ \mathbf{r}^T & \mathbf{0} & \mathbf{0} \end{bmatrix} \begin{bmatrix} \mathbf{c} \\ \mathbf{d}_0 \\ \mathbf{d}_1 \end{bmatrix} = \begin{bmatrix} \mathbf{q} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix} \longrightarrow \mathbf{d}_0 + \mathbf{d}_1 t + \sum_{j=1}^N \sum_{k=1}^{n_j-1} c_k^j \psi_k^j(t) \longrightarrow \hat{\mathbf{u}}(t)$$

3.2.4 Multi-Input Multi-Output Machines

Time Encoding Machine – MIMO Delayed IAF Encoder [12] Encodes several finite energy signals encoded by multiple Integrate-and-Fire neurons with delays.



Time Decoding Machine – MIMO Delayed IAF Decoder [12] Reconstructs several finite energy signals encoded by multiple Integrate-and-Fire neurons with delays using spline interpolation.

$$(t_k^j)_{k \in \mathbb{Z}} \longrightarrow \begin{bmatrix} \mathbf{G} & \mathbf{p} & \mathbf{r} \\ \mathbf{p}^T & \mathbf{0} & \mathbf{0} \\ \mathbf{r}^T & \mathbf{0} & \mathbf{0} \end{bmatrix} \begin{bmatrix} \mathbf{c} \\ \mathbf{d}_0 \\ \mathbf{d}_1 \end{bmatrix} = \begin{bmatrix} \mathbf{q} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix} \longrightarrow \mathbf{d}_0 + \mathbf{d}_1 t + \sum_{j=1}^N \sum_{k=1}^{n_j-1} c_k^j \psi_k^j(t) \longrightarrow \hat{\mathbf{u}}(t)$$

4.1 TED Modules

4.1.1 Asynchronous Sigma-Delta Modulator Routines

Single-Input Single-Output Machines

<code>asdm_decode</code>	ASDM time decoding machine.
<code>asdm_decode_fast</code>	Fast ASDM time decoding machine.
<code>asdm_decode_ins</code>	Threshold-insensitive ASDM time decoding machine.
<code>asdm_encode</code>	ASDM time encoding machine.

`bionet.ted.asdm.asdm_decode`

`bionet.ted.asdm.asdm_decode` (*s*, *dur*, *dt*, *bw*, *b*, *d*, *k*=1.0, *sgn*=-1)

ASDM time decoding machine.

Decode a signal encoded with an Asynchronous Sigma-Delta Modulator.

Parameters **s** : ndarray of floats

Encoded signal. The values represent the time between spikes (in s).

dur : float

Duration of signal (in s).

dt : float

Sampling resolution of original signal; the sampling frequency is 1/dt Hz.

bw : float

Signal bandwidth (in rad/s).

b : float

Encoder bias.

d : float

Encoder threshold.

k : float

Encoder integrator constant.

sgn : {-1, 1}

Sign of first spike.

Returns **u_rec** : ndarray of floats

Recovered signal.

bionet.ted.asdm.asdm_decode_fast

`bionet.ted.asdm.asdm_decode_fast(s, dur, dt, bw, M, b, d, k=1.0, sgn=-1)`

Fast ASDM time decoding machine.

Decode a signal encoded by an Asynchronous Sigma-Delta Modulator using a fast recovery algorithm.

Parameters **s** : numpy array of floats

Encoded signal. The values represent the time between spikes (in s).

dur : float

Duration of signal (in s).

dt : float

Sampling resolution of original signal; the sampling frequency is 1/dt Hz.

bw : float

Signal bandwidth (in rad/s).

M : int

Number of bins used by the fast algorithm.

b : float

Encoder bias.

d : float

Encoder threshold.

k : float

Encoder integrator constant.

sgn : {-1, 1}

Sign of first spike.

Returns **u_rec** : ndarray of floats

Recovered signal.

bionet.ted.asdm.asdm_decode_ins

`bionet.ted.asdm.asdm_decode_ins(s, dur, dt, bw, b, sgn=-1)`

Threshold-insensitive ASDM time decoding machine.

Decode a signal encoded with an Asynchronous Sigma-Delta Modulator using a threshold-insensitive recovery algorithm.

Parameters **s** : ndarray of floats

Encoded signal. The values represent the time between spikes (in s).

dur : float

Duration of signal (in s).

dt : float

Sampling resolution of original signal; the sampling frequency is 1/dt Hz.

bw : float

Signal bandwidth (in rad/s).

b : float

Encoder bias.

sgn : {-1, 1}

Sign of first spike.

Returns **u_rec** : ndarray of floats

Recovered signal.

bionet.ted.asdm.asdm_encode

```
bionet.ted.asdm.asdm_encode(u, dt, b, d, k=1.0, dte=0.0, y=0.0, interval=0.0, sgn=1,  
                             quad_method='trapz', full_output=False)
```

ASDM time encoding machine.

Encode a finite length signal using an Asynchronous Sigma-Delta Modulator.

Parameters **u** : array_like of floats

Signal to encode.

dt : float

Sampling resolution of input signal; the sampling frequency is 1/dt Hz.

b : float

Encoder bias.

d : float

Encoder threshold.

k : float

Encoder integration constant.

dte : float

Sampling resolution assumed by the encoder (s). This may not exceed *dt*.

y : float

Initial value of integrator.

interval : float

Time since last spike (in s).

sgn : {+1, -1}

Sign of integrator.

quad_method : {'rect', 'trapz'}

Quadrature method to use (rectangular or trapezoidal).

full_output : bool

If set, the function returns the encoded data block followed by the given parameters (with updated values for *y*, *interval*, and *sgn*). This is useful when the function is called repeatedly to encode a long signal.

Returns **s** : ndarray of floats

If *full_output* == False, returns the signal encoded as an array of time intervals between spikes.

s, dt, b, d, k, dte, y, interval, sgn, quad_method, full_output : tuple

If *full_output* == True, returns the encoded signal followed by updated encoder parameters.

Notes

When trapezoidal integration is used, the value of the integral will not be computed for the very last entry in *u*.

Multi-Input Single-Output Machines

<code>asdm_decode_pop</code>	Multi-input single-output ASDM time decoding machine.
<code>asdm_decode_pop_ins</code>	Threshold-insensitive multi-input single-output time decoding machine.
<code>asdm_decode_vander</code>	Asynchronous Sigma-Delta Modulator time decoding machine that uses BPA.
<code>asdm_decode_vander_ins</code>	Threshold-insensitive ASDM time decoding machine that uses BPA.

bionet.ted.asdm.asdm_decode_pop

`bionet.ted.asdm.asdm_decode_pop(s_list, dur, dt, bw, b_list, d_list, k_list, sgn_list=[])`

Multi-input single-output ASDM time decoding machine.

Decode a signal encoded by an ensemble of Asynchronous Sigma-Delta Modulators.

Parameters **s_list** : list of ndarrays of floats

Signal encoded by an ensemble of encoders. The values represent the time between spikes (in s). The number of arrays in the list corresponds to the number of encoders in the ensemble.

dur : float

Duration of signal (in s).

dt : float

Sampling resolution of original signal; the sampling frequency is 1/dt Hz.

bw : float

Signal bandwidth (in rad/s).

b_list : list of floats

List of encoder biases.

d_list : list of floats

List of encoder thresholds.

k_list : list of floats

List of encoder integration constants.

sgn_list : list of integers {-1, 1}

List of signs of first spikes in trains.

Returns u_rec : ndarray of floats

Recovered signal.

Notes

The number of spikes contributed by each neuron may differ from the number contributed by other neurons.

`bionet.ted.asdm.asdm_decode_pop_ins`

`bionet.ted.asdm.asdm_decode_pop_ins(s_list, dur, dt, bw, b_list, sgn_list=[])`

Threshold-insensitive multi-input single-output time decoding machine.

Decode a signal encoded by an ensemble of ASDM encoders using a threshold-insensitive recovery algorithm.

Parameters s_list : list of ndarrays of floats

Signal encoded by an ensemble of encoders. The values represent the time between spikes (in s). The number of arrays in the list corresponds to the number of encoders in the ensemble.

dur : float

Duration of signal (in s).

dt : float

Sampling resolution of original signal; the sampling frequency is 1/dt Hz.

bw : float

Signal bandwidth (in rad/s).

b_list : list of floats

List of encoder biases.

Returns u_rec : ndarray of floats

Recovered signal.

Notes

The number of spikes contributed by each neuron may differ from the number contributed by other neurons.

bionet.ted.asdm.asdm_decode_vander

`bionet.ted.asdm.asdm_decode_vander(s, dur, dt, bw, b, d, k, sgn=-1)`

Asynchronous Sigma-Delta Modulator time decoding machine that uses BPA.

Decode a finite length signal encoded with an Asynchronous Sigma-Delta Modulator by efficiently solving a Vandermonde system using the Bjork-Pereyra Algorithm.

Parameters s: array_like of floats

Encoded signal. The values represent the time between spikes (in s).

dur: float

Duration of signal (in s).

dt: float

Sampling resolution of original signal; the sampling frequency is 1/dt Hz.

bw: float

Signal bandwidth (in rad/s).

b: float

Encoder bias.

d: float

Encoder threshold.

k: float

Encoder integration constant.

sgn: {-1, 1}

Sign of first spike.

Returns u_rec : ndarray of floats

Recovered signal.

bionet.ted.asdm.asdm_decode_vander_ins

`bionet.ted.asdm.asdm_decode_vander_ins(s, dur, dt, bw, b, sgn=-1)`

Threshold-insensitive ASDM time decoding machine that uses BPA.

Decode a finite length signal encoded with an Asynchronous Sigma-Delta Modulator by efficiently solving a threshold-insensitive Vandermonde system using the Bjork-Pereyra Algorithm.

Parameters s: array_like of floats

Encoded signal. The values represent the time between spikes (in s).

dur: float

Duration of signal (in s).

dt: float

Sampling resolution of original signal; the sampling frequency is 1/dt Hz.

bw: float

Signal bandwidth (in rad/s).

b: float

Encoder bias.

sgn: {-1, 1}

Sign of first spike.

Returns **u_rec** : ndarray of floats

Recovered signal.

Supporting Routines

`asdm_recoverable` ASDM time encoding parameter check.

bionet.ted.asdm.asdm_recoverable

`bionet.ted.asdm.asdm_recoverable(u, bw, b, d, k)`

ASDM time encoding parameter check.

Determine whether a signal encoded with an Asynchronous Sigma-Delta Modulator using the specified parameters can be perfectly recovered.

Parameters **u: array_like of floats**

Signal to test.

bw: float

Signal bandwidth (in rad/s).

b: float

Decoder bias.

d: float

Decoder threshold.

k: float

Decoder integration constant.

Returns **rec** : bool

True if the specified signal is recoverable.

Raises **ValueError**

When the signal cannot be perfectly recovered.

Notes

The bound assumed by this check is not as strict as that described in most of Prof. Lazar's papers.

4.1.2 Integrate-and-Fire Neuron Routines (Sinc Kernel)

Single-Input Single-Output Machines

<code>iaf_decode</code>	IAF time decoding machine.
<code>iaf_decode_fast</code>	Fast IAF time decoding machine.
<code>iaf_decode_spline</code>	Spline interpolation IAF time decoding machine.
<code>iaf_decode_vander</code>	IAF time decoding machine that uses BPA.
<code>iaf_encode</code>	IAF time encoding machine.

`bionet.ted.iaf.iaf_decode`

`bionet.ted.iaf.iaf_decode` (*s*, *dur*, *dt*, *bw*, *b*, *d*, *R=inf*, *C=1.0*)

IAF time decoding machine.

Decode a finite length signal encoded with an Integrate-and-Fire neuron.

Parameters *s* : ndarray of floats

Encoded signal. The values represent the time between spikes (in s).

dur : float

Duration of signal (in s).

dt : float

Sampling resolution of original signal; the sampling frequency is 1/dt Hz.

bw : float

Signal bandwidth (in rad/s).

b : float

Encoder bias.

d : float

Encoder threshold.

R : float

Neuron resistance.

C : float

Neuron capacitance.

Returns *u_rec* : ndarray of floats

Recovered signal.

`bionet.ted.iaf.iaf_decode_fast`

`bionet.ted.iaf.iaf_decode_fast` (*s*, *dur*, *dt*, *bw*, *M*, *b*, *d*, *R=inf*, *C=1.0*)

Fast IAF time decoding machine.

Decode a signal encoded with an Integrate-and-Fire neuron using a fast recovery algorithm.

Parameters *s* : array_like of floats

Encoded signal. The values represent the time between spikes (in s).

dur : float

Duration of signal (in s).

dt : float

Sampling resolution of original signal; the sampling frequency is $1/\text{dt}$ Hz.

bw : float

Signal bandwidth (in rad/s).

M : int

Number of bins used by the fast algorithm.

b : float

Encoder bias.

d : float

Encoder threshold.

R : float

Neuron resistance.

C : float

Neuron capacitance.

Returns **u_rec** : ndarray of floats

Recovered signal.

bionet.ted.iaf.iaf_decode_spline

`bionet.ted.iaf.iaf_decode_spline(s, dur, dt, b, d, R=inf, C=1.0)`

Spline interpolation IAF time decoding machine.

Decode a signal encoded with an IAF neuron using spline interpolation.

Parameters **s** : array_like of floats

Encoded signal. The values represent the time between spikes (in s).

dur : float

Duration of signal (in s).

dt : float

Sampling resolution of original signal; the sampling frequency is $1/\text{dt}$ Hz.

b : float

Encoder bias.

d : float

Encoder threshold.

R : float

Neuron resistance.

C : float

Neuron capacitance.

Returns **u_rec** : ndarray of floats

Recovered signal.

`bionet.ted.iaf.iaf_decode_vander`

`bionet.ted.iaf.iaf_decode_vander(s, dur, dt, bw, b, d, R, C)`

IAF time decoding machine that uses BPA.

Decode a finite length signal encoded with an Integrate-and-Fire neuron by efficiently solving a Vandermonde system using the Bjork-Pereyra Algorithm.

Parameters **s**: array_like of floats

Encoded signal. The values represent the time between spikes (in s).

dur: float

Duration of signal (in s).

dt: float

Sampling resolution of original signal; the sampling frequency is 1/dt Hz.

bw: float

Signal bandwidth (in rad/s).

b: float

Encoder bias.

d: float

Encoder threshold.

R: float

Neuron resistance.

C: float

Neuron capacitance.

Returns **u_rec** : ndarray of floats

Recovered signal.

`bionet.ted.iaf.iaf_encode`

`bionet.ted.iaf.iaf_encode(u, dt, b, d, R=inf, C=1.0, dte=0, y=0.0, interval=0.0, quad_method='trapz', full_output=False)`

IAF time encoding machine.

Encode a finite length signal with an Integrate-and-Fire neuron.

Parameters **u** : array_like of floats

Signal to encode.

dt : float

Sampling resolution of input signal; the sampling frequency is 1/dt Hz.

b : float

Encoder bias.

d : float

Encoder threshold.

R : float

Neuron resistance.

C : float

Neuron capacitance.

dte : float

Sampling resolution assumed by the encoder (s). This may not exceed *dt*.

y : float

Initial value of integrator.

interval : float

Time since last spike (in s).

quad_method : {'rect', 'trapz'}

Quadrature method to use (rectangular or trapezoidal) when the neuron is ideal; exponential Euler integration is used when the neuron is leaky.

full_output : bool

If set, the function returns the encoded data block followed by the given parameters (with updated values for *y* and *interval*). This is useful when the function is called repeatedly to encode a long signal.

Returns **s** : ndarray of floats

If *full_output* == False, returns the signal encoded as an array of time intervals between spikes.

[s, dt, b, d, R, C, dte, y, interval, quad_method, full_output] : list

If *full_output* == True, returns the encoded signal followed by updated encoder parameters.

Notes

When trapezoidal integration is used, the value of the integral will not be computed for the very last entry in *u*.

Single-Input Multi-Output Machines

`iaf_encode_coupled` Single-input multi-output coupled IAF time encoding machine.

`bionet.ted.iaf.iaf_encode_coupled`

`bionet.ted.iaf.iaf_encode_coupled(u, dt, b_list, d_list, k_list, h_list, type_list)`

Single-input multi-output coupled IAF time encoding machine.

Encode a signal with an ensemble of coupled ideal ON-OFF Integrate-and-Fire neurons.

Parameters **u** : array_like of floats

Signal to encode.

dt : float

Sampling resolution of input signal; the sampling frequency is 1/dt Hz.

b_list : list of floats

List of encoder biases.

d_list : list of floats

List of encoder thresholds.

k_list : list of floats

List of encoder integration constants.

h_list : M x M array_like of functions

Coupling functions. Function $h_list[i][j]$ describes the coupling from the integrator output of neuron i to the input of neuron j .

type_list : list of integers {-1, 1}

Neuron types. A value of -1 indicates that a neuron is an OFF-type neuron, while a value of 1 indicates that it is an ON-type neuron.

Returns **s_list** : list of ndarrays of floats

Encoded signal.

Multi-Input Single-Output Machines

<code>iaf_decode_coupled</code>	Multi-input single-output coupled IAF time decoding machine.
<code>iaf_decode_pop</code>	Multi-input single-output IAF time decoding machine.
<code>iaf_decode_spline_pop</code>	Multi-input single-output spline interpolation IAF time decoding machine.

`bionet.ted.iaf.iaf_decode_coupled`

`bionet.ted.iaf.iaf_decode_coupled(s_list, dur, dt, b_list, d_list, k_list, h_list)`

Multi-input single-output coupled IAF time decoding machine.

Decode a signal encoded with an ensemble of coupled ON-OFF Integrate-and-Fire neurons.

Parameters **s_list** : list of ndarrays of floats

Signal encoded by an ensemble of coupled encoders. The values represent the time between spikes (in s). The number of arrays in the list corresponds to the number of encoders in the ensemble.

dur : float

Duration of signal (in s).

dt : float

Sampling resolution of original signal; the sampling frequency is 1/dt Hz.

b_list : list of floats

List of encoder biases.

d_list : list of floats

List of encoder thresholds.

k_list : list of floats

List of encoder integration constants.

h_list : M x M array_like of functions

Coupling functions. Function $h_list[i][j]$ describes the coupling from the integrator output of neuron i to the input of neuron j .

Returns **u_rec** : ndarray of floats

Recovered signal.

Notes

The number of spikes contributed by each neuron may differ from the number contributed by other neurons.

bionet.ted.iaf.iaf_decode_pop

`bionet.ted.iaf.iaf_decode_pop(s_list, dur, dt, bw, b_list, d_list, R_list, C_list)`

Multi-input single-output IAF time decoding machine.

Decode a signal encoded with an ensemble of Integrate-and-Fire neurons.

Parameters **s_list** : list of ndarrays of floats

Signal encoded by an ensemble of encoders. The values represent the time between spikes (in s). The number of arrays in the list corresponds to the number of encoders in the ensemble.

dur : float

Duration of signal (in s).

dt : float

Sampling resolution of original signal; the sampling frequency is $1/\text{dt}$ Hz.

bw : float

Signal bandwidth (in rad/s).

b_list : list of floats

List of encoder biases.

d_list : list of floats

List of encoder thresholds.

R_list : list of floats

List of encoder neuron resistances.

C_list : list of floats.

List of encoder neuron capacitances.

Returns **u_rec** : ndarray of floats

Recovered signal.

Notes

The number of spikes contributed by each neuron may differ from the number contributed by other neurons.

`bionet.ted.iaf.iaf_decode_spline_pop`

`bionet.ted.iaf.iaf_decode_spline_pop(s_list, dur, dt, b_list, d_list, R_list, C_list)`

Multi-input single-output spline interpolation IAF time decoding machine.

Decode a signal encoded with an ensemble of Integrate-and-Fire neurons using spline interpolation.

Parameters `s_list`: list of ndarrays of floats

Signal encoded by an ensemble of encoders. The values represent the time between spikes (in s). The number of arrays in the list corresponds to the number of encoders in the ensemble.

`dur`: float

Duration of signal (in s).

`dt`: float

Sampling resolution of original signal; the sampling frequency is 1/dt Hz.

`b_list`: list of floats

List of encoder biases.

`d_list`: list of floats

List of encoder thresholds.

`R_list`: list of floats

List of encoder neuron resistances.

`C_list`: list of floats.

Returns `u_rec` : ndarray of floats

Recovered signal.

Notes

The number of spikes contributed by each neuron may differ from the number contributed by other neurons.

Multi-Input Multi-Output Machines

<code>iaf_decode_delay</code>	Multi-input multi-output delayed IAF time decoding machine.
<code>iaf_encode_delay</code>	Multi-input multi-output delayed IAF time encoding machine.
<code>iaf_encode_pop</code>	Multi-input multi-output IAF time encoding machine.

bionet.ted.iaf.iaf_decode_delay

`bionet.ted.iaf.iaf_decode_delay(s_list, T, dt, b_list, d_list, k_list, a_list, w_list)`

Multi-input multi-output delayed IAF time decoding machine.

Decode several signals encoded with an ensemble of ideal Integrate-and-Fire neurons with delays.

Parameters **s_list** : list of ndarrays of floats

Signals encoded by an ensemble of encoders. The values represent the time between spikes (in s). The number of arrays in the list corresponds to the number of encoders in the ensemble.

T : float

Temporal support of signals (in s).

dt : float

Sampling resolution of input signals; the sampling frequency is 1/dt Hz.

b_list : list of floats

List of encoder biases.

d_list : list of floats

List of encoder thresholds.

k_list : list of floats

List of encoder integration constants.

a_list : N x M array_like of floats.

Delays (in s).

w_list : N x M array_like of floats.

Scaling factors.

Returns **u_list** : list of ndarrays of floats

Decoded signals.

Notes

The specified signal length $\max(\text{map}(\text{sum}, s_list))$ must exceed the support T over which the signal is decoded by the length of the longest delay.

bionet.ted.iaf.iaf_encode_delay

`bionet.ted.iaf.iaf_encode_delay(u_list, t_start, dt, b_list, d_list, k_list, a_list, w_list, y_list=None, interval_list=None, full_output=False)`

Multi-input multi-output delayed IAF time encoding machine.

Encode several signals with an ensemble of ideal Integrate-and-Fire neurons with delays.

Parameters **u_list** : list of ndarrays of floats

Signals to encode. Each of the ndarrays must be of the same length.

t_start : float

Time at which to begin encoding (in s).

dt : float

Sampling resolution of input signals; the sampling frequency is 1/dt Hz.

b_list : list of floats

List of encoder biases.

d_list : list of floats

List of encoder thresholds.

k_list : list of floats

List of encoder integration constants.

a_list : N x M array_like of floats.

Neuron delays (in s).

w_list : N x M array_like of floats.

Scaling factors.

y_list : list of floats

Initial values of integrators.

interval_list : list of floats

Times since last spikes (in s).

full_output : bool

If set, the function returns the encoded data block followed by the given parameters (with updated values for *y* and *interval*). This is useful when the function is called repeatedly to encode a long signal.

Returns **s_list** : list of ndarrays of floats

If *full_output* == False, returns the signals encoded as a list of arrays of time intervals between spikes.

[*s_list*, *t_start*, *dt*, *b_list*, *d_list*, *k_list*, *a_list*, *w_list*, *y_list*,

interval_list, **u_list_prev**, **full_output**] : list

If *full_output* == True, returns the encoded signals followed by updated encoder parameters.

Notes

t_start must exceed *max(a)*.

bionet.ted.iaf.iaf_encode_pop

`bionet.ted.iaf.iaf_encode_pop(u_list, dt, b_list, d_list, R_list, C_list, dte=0, y=None, interval=None, quad_method='trapz', full_output=False)`

Multi-input multi-output IAF time encoding machine.

Encode several signals with an ensemble of Integrate-and-Fire neurons.

Parameters **u_list** : list of ndarrays

Signals to encode.

dt : float

Sampling resolution of input signal; the sampling frequency is $1/\text{dt}$ Hz.

b_list : list of floats

List of encoder biases.

d_list : list of floats

List of encoder thresholds.

R_list : list of floats

List of encoder resistances.

C_list : list of floats

List of encoder capacitances.

dte : float

Sampling resolution assumed by the encoders. This may not exceed dt .

y : ndarray of floats

Initial values of integrators.

interval : ndarray of float

Times since last spike (in s).

quad_method : {'rect', 'trapz'}

Quadrature method to use (rectangular or trapezoidal) when the neuron is ideal; exponential Euler integration is used when the neuron is leaky.

full_output : bool

If set, the function returns the encoded data block followed by the given parameters (with updated values for y and *interval*). This is useful when the function is called repeatedly to encode a long signal.

Returns s_list : ndarray of floats

If *full_output* == False, returns the signal encoded as an array of time intervals between spikes.

[s_list, dt, b_list, d_list, R_list, C_list, dte, y, interval,

quad_method, full_output] : list

If *full_output* == True, returns the encoded signal followed by updated encoder parameters.

Notes

When trapezoidal integration is used, the value of the integral will not be computed for the very last entry in the arrays in *u_list*. Using this function to encode multiple signals is faster than repeatedly invoking *iaf_encode()* when the number of signals is sufficiently high.

Supporting Routines

`iaf_recoverable` IAF time encoding parameter check.

`bionet.ted.iaf.iaf_recoverable`

`bionet.ted.iaf.iaf_recoverable(u, bw, b, d, R, C)`

IAF time encoding parameter check.

Determine whether a signal encoded with an Integrate-and-Fire neuron with the specified parameters can be perfectly recovered.

Parameters `u` : array_like of floats

Signal to test.

bw : float

Signal bandwidth (in rad/s).

b : float

Decoder bias.

d : float

Decoder threshold.

R : float

Neuron resistance.

C : float

Neuron capacitance.

Returns `rec` : bool

True if the specified signal is recoverable.

Raises `ValueError`

When the signal cannot be perfectly recovered.

4.1.3 Integrate-and-Fire Neuron Routines (Dirichlet Kernel)

Single-Input Single-Output Machines

`iaf_decode` IAF time decoding machine using trigonometric polynomials.

`bionet.ted.iaf_trig.iaf_decode`

`bionet.ted.iaf_trig.iaf_decode(s, dur, dt, bw, b, d, R=inf, C=1.0, M=5, smoothing=0.0)`

IAF time decoding machine using trigonometric polynomials.

Decode a finite length signal encoded with an Integrate-and-Fire neuron assuming that the encoded signal is representable in terms of trigonometric polynomials.

Parameters `s` : ndarray of floats

Encoded signal. The values represent the time between spikes (in s).

dur : float

Duration of signal (in s).

dt : float

Sampling resolution of original signal; the sampling frequency is $1/\text{dt}$ Hz.

bw : float

Signal bandwidth (in rad/s).

b : float

Encoder bias.

d : float

Encoder threshold.

R : float

Neuron resistance.

C : float

Neuron capacitance.

M : int

$2*M+1$ coefficients are used for reconstructing the signal.

smoothing : float

Smoothing parameter.

Returns **u_rec** : ndarray of floats

Recovered signal.

Multi-Input Single-Output Machines

`iaf_decode_pop` Multi-input single-output IAF time decoding machine.

`bionet.ted.iaf_trig.iaf_decode_pop`

`bionet.ted.iaf_trig.iaf_decode_pop(s_list, dur, dt, bw, b_list, d_list, R_list, C_list, M=5, smoothing=0.0)`

Multi-input single-output IAF time decoding machine.

Decode a signal encoded with an ensemble of Integrate-and-Fire neurons assuming that the encoded signal is representable in terms of trigonometric polynomials.

Parameters **s_list** : list of ndarrays of floats

Signal encoded by an ensemble of encoders. The values represent the time between spikes (in s). The number of arrays in the list corresponds to the number of encoders in the ensemble.

dur : float

Duration of signal (in s).

dt : float

Sampling resolution of original signal; the sampling frequency is $1/dt$ Hz.

bw : float

Signal bandwidth (in rad/s).

b_list : list of floats

List of encoder biases.

d_list : list of floats

List of encoder thresholds.

R_list : list of floats

List of encoder neuron resistances.

C_list : list of floats.

List of encoder neuron capacitances.

M : int

$2*M+1$ coefficients are used for reconstructing the signal.

smoothing : float

Smoothing parameter.

Returns u_rec : ndarray of floats

Recovered signal.

Notes

The number of spikes contributed by each neuron may differ from the number contributed by other neurons.

4.1.4 Integrate-and-Fire Neuron CUDA Routines (Sinc Kernel)

These routines make use of [CUDA](#).

Single-Input Single-Output Machines

```
iaf_decode
iaf_decode_pop
iaf_encode
iaf_encode_pop
```

4.1.5 Integrate-and-Fire Neuron CUDA Routines (Dirichlet Kernel)

These routines make use of [CUDA](#).

Single-Input Single-Output Machines

`iaf_decode`

Multi-Input Single-Output Machines

`iaf_decode_pop`

4.1.6 Real-Time Time Encoder and Decoder Classes

Abstract Classes

<code>SignalProcessor</code>	Abstract signal processor.
<code>RealTimeDecoder</code>	Abstract real-time time decoding machine.
<code>RealTimeEncoder</code>	Abstract real-time time encoding machine.

`bionet.ted.rt.SignalProcessor`

class `bionet.ted.rt.SignalProcessor` (*args)

Abstract signal processor.

This class describes a signal processor that retrieves blocks of signal data from a source, applies some processing algorithm to it, and saves the processed blocks.

Notes

The `process()` method must be extended in functional subclasses of this class in order.

Methods

<code>process(get, put)</code>	Process data obtained from <code>get()</code> and write it using <code>put()</code> .
--------------------------------	---

`__init__` (*args)

Initialize a signal processor with the specified parameters.

Methods

<code>__init__</code> (*args)	Initialize a signal processor with the specified parameters.
<code>process</code> (get, put)	Process data obtained in blocks from the function <code>get()</code> and write them out using the function <code>put()</code> .

`bionet.ted.rt.RealTimeDecoder`

class `bionet.ted.rt.RealTimeDecoder` (dt, bw, N, M, K)

Abstract real-time time decoding machine.

This class implements a real-time time decoding machine. It must be subclassed to use a specific decoding algorithm.

Parameters `dt` : float

Sampling resolution of input signal; the sampling frequency is $1/dt$ Hz.

bw : float

Signal bandwidth (in rad/s).

N : int

Number of spikes to process in each block less 1.

M : int

Number of spikes between the starting time of each successive block.

K : int

Number of spikes in the overlap between successive blocks.

Methods

<code>decode(data, ...)</code>	Decode a block of data using the additional parameters.
<code>process(get, put)</code>	Process data obtained from <i>get()</i> and write it using <i>put()</i> .

`__init__(dt, bw, N, M, K)`

Methods

<code>__init__(dt, bw, N, M, K)</code>	
<code>decode(*args)</code>	Decode a block of data.
<code>process(get, put)</code>	Decode data returned in blocks by function <i>get()</i> and write it to some destination using the function <i>put()</i> .
<code>window(t, ll, lr, rl, rr)</code>	Return a window defined over the vector of times <i>t</i> that forms a partition of unity over all time.

bionet.ted.rt.RealTimeEncoder

class `bionet.ted.rt.RealTimeEncoder(*args)`

Abstract real-time time encoding machine.

This class implements a real-time time encoding machine. It must be subclassed to use a specific encoding algorithm.

Notes

The *encode()* method must be extended to contain a time encoding algorithm implementation in functional subclasses of this class.

Methods

<code>encode(data, ...)</code>	Encode a block of data using the additional parameters.
<code>process(get, put)</code>	Process data obtained from <i>get()</i> and write it using <i>put()</i> .

`__init__(*args)`
Initialize a real-time time encoder.

Methods

<code>__init__(*args)</code>	Initialize a real-time time encoder.
<code>encode(*args)</code>	Encode a block of data.
<code>process(get, put)</code>	Encode data returned in blocks by function <i>get()</i> and write it to some destination using the function <i>put()</i> .

Asynchronous Sigma-Delta Modulator Classes

<code>ASDMRealTimeDecoder</code>	Real-time ASDM time decoding machine.
<code>ASDMRealTimeDecoderIns</code>	Real-time threshold-insensitive ASDM time decoding machine.
<code>ASDMRealTimeEncoder</code>	Real-time ASDM time encoding machine.

`bionet.ted.rt.ASDMRealTimeDecoder`

class `bionet.ted.rt.ASDMRealTimeDecoder` (*dt, bw, b, d, k, N, M, K*)
Real-time ASDM time decoding machine.

This class implements a real-time time decoding machine that decodes data encoded using an Asynchronous Sigma-Delta Modulator.

Parameters **dt** : float

Sampling resolution of input signal; the sampling frequency is 1/dt Hz.

bw : float

Signal bandwidth (in rad/s).

b : float

Encoder bias.

d : float

Decoder threshold.

k : float

Decoder integration constant.

N : int

Number of spikes to process in each block less 1.

M : int

Number of spikes between the starting time of each successive block.

K : int

Number of spikes in the overlap between successive blocks.

Methods

<code>decode(data, ...)</code>	Decode a block of data using the additional parameters.
<code>process(get, put)</code>	Process data obtained from <i>get()</i> and write it using <i>put()</i> .

`__init__` (*dt, bw, b, d, k, N, M, K*)

Methods

<code>__init__(dt, bw, b, d, k, N, M, K)</code>	
<code>decode(data)</code>	Decode a block of data that was encoded with an ASDM encoder.
<code>process(get, put)</code>	Decode data returned in blocks by function <i>get()</i> and write it to some destination using <i>put()</i> .
<code>window(t, ll, lr, rl, rr)</code>	Return a window defined over the vector of times <i>t</i> that forms a partition of unity over all times.

bionet.ted.rt.ASDMRealTimeDecoderIns

class `bionet.ted.rt.ASDMRealTimeDecoderIns` (*dt, bw, b, N, M, K*)

Real-time threshold-insensitive ASDM time decoding machine.

This class implements a threshold-insensitive real-time time decoding machine that decodes data encoded using an Asynchronous Sigma-Delta Modulator.

Parameters *dt* : float

Sampling resolution of input signal; the sampling frequency is $1/dt$ Hz.

bw : float

Signal bandwidth (in rad/s).

b : float

Encoder bias.

N : int

Number of spikes to process in each block less 1.

M : int

Number of spikes between the starting time of each successive block.

K : int

Number of spikes in the overlap between successive blocks.

Methods

<code>decode(data, ...)</code>	Decode a block of data using the additional parameters.
<code>process(get, put)</code>	Process data obtained from <i>get()</i> and write it using <i>put()</i> .

`__init__(dt, bw, b, N, M, K)`

Methods

<code>__init__(dt, bw, b, N, M, K)</code>	
<code>decode(data)</code>	Decode a block of data that was encoded with an ASDM encoder.
<code>process(get, put)</code>	Decode data returned in blocks by function <i>get()</i> and write it to some destination using the <i>put()</i> function.
<code>window(t, ll, lr, rl, rr)</code>	Return a window defined over the vector of times <i>t</i> that forms a partition of unity over all times.

bionet.ted.rt.ASDMRealTimeEncoder

class `bionet.ted.rt.ASDMRealTimeEncoder` (*dt, b, d, k=1.0, dte=0.0, quad_method='trapz'*)
Real-time ASDM time encoding machine.

This class implements a real-time time encoding machine that uses an Asynchronous Sigma-Delta Modulator to encode data.

Parameters *dt* : float

Sampling resolution of input signal; the sampling frequency is $1/dt$ Hz.

b : float

Encoder bias.

d : float

Encoder threshold.

k : float

Encoder integration constant.

dte : float

Sampling resolution assumed by the encoder. This may not exceed *dt*.

quad_method : {'rect', 'trapz'}

Quadrature method to use (rectangular or trapezoidal).

Methods

<code>encode(data, ...)</code>	Encode a block of data using the additional parameters.
<code>process(get, put)</code>	Process data obtained from <i>get()</i> and write it using <i>put()</i> .

`__init__` (*dt, b, d, k=1.0, dte=0.0, quad_method='trapz'*)

Methods

<code>__init__</code> (<i>dt, b, d[, k, dte, quad_method]</i>)	
<code>encode(data)</code>	Encode a block of data with an ASDM encoder.
<code>process(get, put)</code>	Encode data returned in blocks by function <i>get()</i> and write it to some destination.

Integrate-and-Fire Neuron Classes and Routines

<code>IAFRealTimeDecoder</code>	Real-time IAF neuron time decoding machine.
<code>IAFRealTimeEncoder</code>	Real-time IAF neuron time encoding machine.
<code>iaf_decode_delay</code>	Real-time multi-input multi-output delayed IAF time decoding machine.
<code>iaf_encode_delay</code>	Real-time multi-input multi-output delayed IAF time encoding machine.

bionet.ted.rt.IAFRealTimeDecoder

class `bionet.ted.rt.IAFRealTimeDecoder` (*dt, bw, b, d, R, C, N, M, K*)
Real-time IAF neuron time decoding machine.

This class implements a real-time time decoding machine that decodes data encoded using an Integrate-and-Fire neuron.

Parameters **dt** : float

Sampling resolution of input signal; the sampling frequency is $1/dt$ Hz.

bw : float

Signal bandwidth (in rad/s).

b : float

Encoder bias.

d : float

Decoder threshold.

R : float

Neuron resistance.

C : float

Neuron capacitance.

N : int

Number of spikes to process in each block less 1.

M : int

Number of spikes between the starting time of each successive block.

K : int

Number of spikes in the overlap between successive blocks.

Methods

<code>decode(data, ...)</code>	Decode a block of data using the additional parameters.
<code>process(get, put)</code>	Process data obtained from <i>get()</i> and write it using <i>put()</i> .
<code>__init__(dt, bw, b, d, R, C, N, M, K)</code>	

Methods

<code>__init__(dt, bw, b, d, R, C, N, M, K)</code>	
<code>decode(data)</code>	Decode a block of data that was encoded with an IAF neuron.
<code>process(get, put)</code>	Decode data returned in blocks by function <i>get()</i> and write it to some destination.
<code>window(t, ll, lr, rl, rr)</code>	Return a window defined over the vector of times <i>t</i> that forms a partition of unity.

bionet.ted.rt.IAFRealTimeEncoder

```
class bionet.ted.rt.IAFRealTimeEncoder (dt, b, d, R=inf, C=1.0, dte=0.0,
                                         quad_method='trapz')
```

Real-time IAF neuron time encoding machine.

This class implements a real-time time encoding machine that uses an Integrate-and-Fire neuron to encode data.

Parameters **dt** : float

Sampling resolution of input signal; the sampling frequency is $1/dt$ Hz.

b : float

Encoder bias.

d : float

Encoder threshold.

R : float

Neuron resistance.

C : float

Neuron capacitance.

dte : float

Sampling resolution assumed by the encoder. This may not exceed dt .

quad_method : {'rect', 'trapz'}

Quadrature method to use (rectangular or trapezoidal).

Methods

encode(data, ...)	Encode a block of data using the additional parameters.
process(get, put)	Process data obtained from <i>get()</i> and write it using <i>put()</i> .

`__init__(dt, b, d, R=inf, C=1.0, dte=0.0, quad_method='trapz')`

Methods

<code>__init__(dt, b, d[, R, C, dte, quad_method])</code>	
<code>encode(data)</code>	Encode a block of data with an IAF neuron.
<code>process(get, put)</code>	Encode data returned in blocks by function <i>get()</i> and write it to some dest

bionet.ted.rt.iaf_decode_delay

`bionet.ted.rt.iaf_decode_delay(s_list, T_block, T_overlap, dt, b_list, d_list, k_list, a_list, w_list)`

Real-time multi-input multi-output delayed IAF time decoding machine.

Decode several signals encoded with an ensemble of ideal Integrate-and-Fire neurons with delays.

Parameters **s** : list of ndarrays of floats

Signals encoded by an ensemble of encoders. The values represent the time between spikes (in s). The number of arrays in the list corresponds to the number of encoders in the ensemble.

T_block : float

Length of block to decode during each iteration (in s).

T_overlap : float

Length of overlap between successive blocks (in s).

dt : float

Sampling resolution of input signals; the sampling frequency is $1/\text{dt}$ Hz.

b_list : list

List of encoder biases. Must be of length N .

d_list : list

List of encoder thresholds. Must be of length N .

k_list : list

List of encoder integration constants. Must be of length N .

a_list : array_like

Array of neuron delays (in s). Must be of shape (N, M) .

w_list : array_like

Array of scaling factors. Must be of shape (N, M) .

Returns **u_list** : list

Decoded signals.

`bionet.ted.rt.iaf_encode_delay`

`bionet.ted.rt.iaf_encode_delay(u_list, T_block, t_begin, dt, b_list, d_list, k_list, a_list, w_list)`

Real-time multi-input multi-output delayed IAF time encoding machine.

Encode several with an ensemble of ideal Integrate-and-Fire neurons with delays.

Parameters **u_list** : list

Signals to encode. Must contain M arrays of equal length.

T_block : float

Length of block to encode (in s) during each iteration.

t_begin : float

Time at which to begin encoding (in s).

dt : float

Sampling resolution of input signals; the sampling frequency is $1/\text{dt}$ Hz.

b_list : list

List of encoder biases. Must be of length M .

d_list : list

List of encoder thresholds. Must be of length M .

k_list : list

List of encoder integration constants. Must be of length M .

a_list : array_like

Array of neuron delays (in s). Must have shape (N, M) .

w_list : array_like

Array of scaling factors. Must have shape (N, M) .

Returns s_list : list

List of arrays of interspike intervals.

4.1.7 Routines for Solving Vandermonde Systems

<code>bpa</code>	Solve a Vandermonde system using BPA.
------------------	---------------------------------------

bionet.ted.bpa.bpa

`bionet.ted.bpa.bpa(V, b)`

Solve a Vandermonde system using BPA.

Solve a Vandermonde linear system using the Bjork-Pereyra algorithm.

Parameters V : ndarray of floats, shape (M, M)

A Vandermonde matrix.

b : ndarray of floats, shape $(M,)$

The system solved by this routine is $\text{dot}(V, d) == b$.

Returns d : ndarray of floats, shape $(M,)$

System solution.

See also:

`numpy.linalg.solve`

Notes

The matrix is assumed to be oriented such that its second column contains the arguments that would need to be passed to the `vander()` function in order to construct the matrix.

4.2 Utility Modules

4.2.1 Animation Routines

<code>animate</code>	Animate sequence of frames.
<code>animate2</code>	Animate two sequence of frames simultaneously.
<code>animate_compare</code>	Animate two sequence of frames and their difference simultaneously.
<code>frame_compare</code>	Compare corresponding frames in two video sequences.

bionet.utils.animate.animate

`bionet.utils.animate.animate(data, step=1, delay=0)`

Animate sequence of frames.

Animate a sequence of $N_y \times N_x$ bitmap frames stored in a $M \times N_y \times N_x$ data array.

Parameters `data` : numpy.ndarray

Sequence of M 2D bitmaps stored as an array with shape (M, N_y, N_x) .

step : int

Skip *step* frames between each displayed frames.

delay : float

Wait *delay* seconds between each frame refresh.

`bionet.utils.animate.animate2`

`bionet.utils.animate.animate2(data_1, data_2, step=1, delay=0)`

Animate two sequence of frames simultaneously.

Animate two sequences of $N_y \times N_x$ bitmap frames stored in two $M \times N_y \times N_x$ data arrays.

Parameters `data_1` : numpy.ndarray

Sequence of M 2D bitmaps stored as an array with shape (M, N_y, N_x) .

data_2 : numpy.ndarray

Sequence of M 2D bitmaps stored as an array with shape (M, N_y, N_x) .

step : int

Skip *step* frames between each displayed frames.

delay : float

Wait *delay* seconds between each frame refresh.

`bionet.utils.animate.animate_compare`

`bionet.utils.animate.animate_compare(data_1, data_2, step=1, delay=0)`

Animate two sequence of frames and their difference simultaneously.

Animate two sequences of $N_y \times N_x$ bitmap frames stored in two $M \times N_y \times N_x$ data arrays simultaneously with their difference.

Parameters `data_1` : numpy.ndarray

Sequence of M 2D bitmaps stored as an array with shape (M, N_y, N_x) .

data_2 : numpy.ndarray

Sequence of M 2D bitmaps stored as an array with shape (M, N_y, N_x) .

step : int

Skip *step* frames between each displayed frames.

delay : float

Wait *delay* seconds between each frame refresh.

bionet.utils.animate.frame_compare

`bionet.utils.animate.frame_compare(data_1, data_2, i=0)`

Compare corresponding frames in two video sequences.

Simultaneously display two corresponding frames from two video sequences of identical length.

Parameters `data_1` : `numpy.ndarray`

Sequence of M 2D bitmaps stored as an array with shape (M, Ny, Nx) .

`data_2` : `numpy.ndarray`

Sequence of M 2D bitmaps stored as an array with shape (M, Ny, Nx) .

`i` : `int`

Index of frame to display.

4.2.2 Band-Limited Function Routines

<code>gen_band_limited</code>	Generate a uniformly sampled, band-limited signal.
-------------------------------	--

bionet.utils.band_limited.gen_band_limited

`bionet.utils.band_limited.gen_band_limited(dur, dt, fmax, np=None, nc=3)`

Generate a uniformly sampled, band-limited signal.

Parameters `dur` : `float`

Duration of signal (s).

`dt` : `float`

Sampling resolution; the sampling frequency is $1/dt$ Hz.

`fmax` : `float`

Maximum frequency (Hz).

`np` : `float`

Noise power. If `np != None`, Gaussian white noise is added to the generated signal before the latter is filtered.

`nc` : `int`

Number of discrete frequency components in generated signal.

Returns `u` : `ndarray` of floats

Generated signal.

4.2.3 Miscellaneous Routines and Classes

<code>chunks</code>	Chunk generator.
<code>func_timer</code>	Time the execution of a function.
<code>SerialBuffer</code>	Serial buffer class.

bionet.utils.misc.chunks

`bionet.utils.misc.chunks(seq, n)`
 Chunk generator.

Return a generator whose *next()* method returns length *n* subsequences of the given sequence. If *len(seq) % n != 0*, the last subsequence returned will contain fewer than *n* entries.

Parameters *seq* : iterable
 Sequence to split into chunks.
 n : int
 Chunk size.

Returns *g* : generator
 Generator that will return length *n* chunks of *seq*.

bionet.utils.misc.func_timer

`bionet.utils.misc.func_timer(f)`
 Time the execution of a function.

Parameters *f* : function
 Function to time.

bionet.utils.misc.SerialBuffer

class `bionet.utils.misc.SerialBuffer(get, n=1)`
 Serial buffer class.

This class implements a buffer that automatically replenishes its contents from a specified serial data source when it contains too little data to honor a read request.

Parameters *get* : function
 Data retrieval function. Must return an empty sequence or None when it can no longer retrieve any data.
 n : int
 Number of initial entries to load into buffer.

Methods

<code>clear()</code>	Empty buffer.
<code>read(n=1)</code>	Read <i>n</i> elements from buffer.
<code>replenish(n=1)</code>	Replenish buffer to contain at least <i>n</i> elements.

`__init__(get, n=1)`

Methods

<code>__init__(get[, n])</code>	
<code>clear()</code>	Remove all elements from the buffer.
<code>read([n])</code>	Read a block of data (default length = 1).
<code>replenish([n])</code>	Attempt to replenish the buffer such that it contains at least n entries (but do not throw any exceptions).

4.2.4 Extra Numpy Routines

<code>crand</code>	Complex random values in a given shape.
<code>hilb</code>	Construct a Hilbert matrix.
<code>iceil</code>	Return the ceiling of the input, element-wise.
<code>ifloor</code>	Return the floor of the input, element-wise.
<code>iround</code>	Round an array to the nearest integer.
<code>mdot</code>	Dot product of several arrays.
<code>mpower</code>	Matrix power function.
<code>rank</code>	Compute matrix rank.

bionet.utils.numpy_extras.crand

`bionet.utils.numpy_extras.crand(*args)`
Complex random values in a given shape.

Create an array of the given shape whose entries are complex numbers with real and imaginary parts sampled from a uniform distribution over $[0, 1)$.

Parameters `d0, d1, ..., dn` : int

Shape of the output.

Returns `out` : `numpy.ndarray`

Complex random variables.

bionet.utils.numpy_extras.hilb

`bionet.utils.numpy_extras.hilb(n)`
Construct a Hilbert matrix.

Parameters `n` : int

Number of rows and columns in matrix.

Returns `h` : `numpy.ndarray`

Generated Hilbert matrix of shape (n, n) .

bionet.utils.numpy_extras.iceil

`bionet.utils.numpy_extras.iceil(x)`

Return the ceiling of the input, element-wise.

The ceil of the scalar x is the smallest integer i , such that $i \geq x$. It is often denoted as :math:\lceil x

ceil'.

Parameters x : array_like

Input data.

Returns y : {numpy.ndarray, scalar}

The ceiling of each element in x , with *int* dtype.

bionet.utils.numpy_extras.ifloor

bionet.utils.numpy_extras.ifloor(x)

Return the floor of the input, element-wise.

The floor of the scalar x is the largest integer i , such that $i \leq x$. It is often denoted as :math:\lfloor x

floor'.

Parameters x : array_like

Input data.

Returns y : {numpy.ndarray, scalar}

The floor of each element in x , with *int* dtype.

bionet.utils.numpy_extras.iround

bionet.utils.numpy_extras.iround(x)

Round an array to the nearest integer.

Parameters x : array_like

Input data.

Returns y : {numpy.ndarray, scalar}

The rounded elements in x , with *int* dtype.

bionet.utils.numpy_extras.mdot

bionet.utils.numpy_extras.mdot(*args)

Dot product of several arrays.

Compute the dot product of several arrays in the order they are listed.

bionet.utils.numpy_extras.mpower

bionet.utils.numpy_extras.mpower(x, y)

Matrix power function.

Compute x raised to the power y where x is a square matrix and y is a scalar.

Notes

The matrix `x` must be non-defective.

`bionet.utils.numpy_extras.rank`

`bionet.utils.numpy_extras.rank(x, *args)`

Compute matrix rank.

Estimate the number of linearly independent rows or columns of the matrix `x`.

Parameters `x` : array_like, shape (M, N)

Matrix to analyze.

tol : float

Tolerance; the default is $\max(\text{svd}(x)[1]) * \max(\text{shape}(x)) * 1e-13$

Returns `r` : int

Estimated rank of matrix.

4.2.5 Plotting Utilities

<code>contour</code>	Create a 3D contour plot.
<code>contourf</code>	Create a 3D contourf plot.
<code>plot_compare</code>	Compare two signals and plot the difference between them.
<code>plot_encoded</code>	Plot a time-encoded signal.
<code>plot_fourier</code>	Plot the Discrete Fourier Transform of a signal.
<code>plot_raster</code>	Plot several time sequences as a raster.
<code>plot_signal</code>	Plot a signal.
<code>surf</code>	Create a surface plot.
<code>wireframe</code>	Plot a 3D wireframe.

`bionet.utils.plotting.contour`

`bionet.utils.plotting.contour(X, Y, Z, *args)`

Create a 3D contour plot.

Argument	Description
<code>X, Y, Z</code>	Data values as <code>numpy.array</code> s
<code>extend3d</code>	Whether to extend contour in 3D (default: False)
<code>stride</code>	Stride (step size) for extending contour
<code>zdir</code>	The direction to use: x, y or z (default)
<code>offset</code>	If specified plot a projection of the contour lines on this position in plane normal to <code>zdir</code>

The positional and other keyword arguments are passed on to `contour()`

Returns a `contour`

bionet.utils.plotting.contourf

`bionet.utils.plotting.contourf(X, Y, Z, *args)`

Create a 3D contourf plot.

Argument	Description
<i>X, Y, Z</i>	Data values as numpy.arrays
<i>zdir</i>	The direction to use: x, y or z (default)
<i>offset</i>	If specified plot a projection of the filled contour on this position in plane normal to zdir

The positional and keyword arguments are passed on to `contourf()`

Returns a `contourf`

Changed in version 1.1.0: The *zdir* and *offset* kwargs were added.

bionet.utils.plotting.plot_compare

`bionet.utils.plotting.plot_compare(t, u, v, fig_title="", file_name="")`

Compare two signals and plot the difference between them.

Parameters *t* : ndarray of floats

Times (s) at which the signal is defined.

u, v : ndarrays of floats

Signal samples.

fig_title : string

Plot title.

file_name : string

File in which to save the plot.

bionet.utils.plotting.plot_encoded

`bionet.utils.plotting.plot_encoded(t, u, s, fig_title="", file_name="")`

Plot a time-encoded signal.

Parameters *t* : ndarray of floats

Times (in s) at which the original signal was sampled.

u : ndarray of floats

Signal samples.

s : ndarray of floats

Intervals between encoded signal spikes.

fig_title : string

Plot title.

file_name : string

File in which to save the plot.

Notes

The spike times (i.e., the cumulative sum of the interspike intervals) must all occur within the interval $t_{-min}(t)$.

`bionet.utils.plotting.plot_fourier`

```
bionet.utils.plotting.plot_fourier(u, fs, fmin=0.0, fmax=None, style='line')
```

Plot the Discrete Fourier Transform of a signal.

Parameters **u** : ndarray of floats

Sampled signal.

fs : float

Sampling rate (Hz).

fmin : float

Minimum frequency to display (Hz).

fmax : float:

Maximum frequency to display (Hz).

style : {'line', 'semilogy', 'stem'}

Set plot style.

Notes

This function may take a long time to run if the frequency range is very large.

`bionet.utils.plotting.plot_raster`

```
bionet.utils.plotting.plot_raster(ts_list, plot_stems=True, plot_axes=True, marker='.',  
                                  markersize=5, fig_title="", file_name="")
```

Plot several time sequences as a raster.

Parameters **ts_list** : list of ndarrays

Time sequences to plot.

plot_stems : bool

Show stems for all events.

plot_axes : bool

Show horizontal axes for all sequences.

marker : char

Marker symbol.

markersize : int

Marker symbol size.

fig_title : string

Plot title.

file_name : string

File in which to save the plot.

bionet.utils.plotting.plot_signal

`bionet.utils.plotting.plot_signal(t, u, fig_title="", file_name="")`

Plot a signal.

Parameters **t** : ndarray of floats

Times (in s) at which the signal is defined.

u : ndarray of floats

Signal samples.

fig_title : string

Plot title.

file_name : string

File in which to save the plot.

bionet.utils.plotting.surf

`bionet.utils.plotting.surf(X, Y, Z, *args)`

Create a surface plot.

By default it will be colored in shades of a solid color, but it also supports color mapping by supplying the *cmap* argument.

Argument	Description
<i>X, Y, Z</i>	Data values as 2D arrays
<i>rstride</i>	Array row stride (step size)
<i>cstride</i>	Array column stride (step size)
<i>color</i>	Color of the surface patches
<i>cmap</i>	A colormap for the surface patches.
<i>facecolors</i>	Face colors for the individual patches
<i>norm</i>	An instance of Normalize to map values to colors
<i>vmin</i>	Minimum value to map
<i>vmax</i>	Maximum value to map
<i>shade</i>	Whether to shade the facecolors

Other arguments are passed on to `Poly3DCollection`

bionet.utils.plotting.wireframe

`bionet.utils.plotting.wireframe(X, Y, Z, *args)`

Plot a 3D wireframe.

Argument	Description
<i>X, Y, Z</i>	Data values as 2D arrays
<i>rstride</i>	Array row stride (step size)
<i>cstride</i>	Array column stride (step size)

Keyword arguments are passed on to `LineCollection`.

Returns a `Line3DCollection`

4.2.6 Extra Pylab Routines

<code>eps</code>	Compute the spacing of floating point numbers.
<code>minmax</code>	Return the range of the given array.
<code>realmax</code>	Return the largest positive floating point number representable with the specified precision on this computer.
<code>realmin</code>	Return the smallest positive floating point number representable with the specified precision on this computer.

`bionet.utils.pylab_extras.eps`

`bionet.utils.pylab_extras.eps(x)`
Compute the spacing of floating point numbers.

`bionet.utils.pylab_extras.minmax`

`bionet.utils.pylab_extras.minmax(x)`
Return the range of the given array. If the array has 2 dimensions, return an array containing the minima and maxima of each of the rows.

`bionet.utils.pylab_extras.realmax`

`bionet.utils.pylab_extras.realmax(t=<type 'numpy.float64'>)`
Return the largest positive floating point number representable with the specified precision on this computer. Double precision is assumed if no floating point type is specified.

`bionet.utils.pylab_extras.realmin`

`bionet.utils.pylab_extras.realmin(t=<type 'numpy.float64'>)`
Return the smallest positive floating point number representable with the specified precision on this computer. Double precision is assumed if no floating point type is specified.

4.2.7 Extra Scipy Routines

<code>ci(z)</code>	Cosine integral of a complex value.
<code>chi(z)</code>	Hyperbolic cosine integral of a complex value.
<code>ei(z)</code>	Exponential integral of a complex value.
<code>si(z)</code>	Sine integral of a complex value.
<code>shi(z)</code>	Hyperbolic sine integral of a complex value.

`bionet.utils.scipy_extras.ci`

`bionet.utils.scipy_extras.ci(z)`
Cosine integral of a complex value.

bionet.utils.scipy_extras.chi

`bionet.utils.scipy_extras.chi` (*z*)
Hyperbolic cosine integral of a complex value.

bionet.utils.scipy_extras.ei

`bionet.utils.scipy_extras.ei` (*z*)
Exponential integral of a complex value.

bionet.utils.scipy_extras.si

`bionet.utils.scipy_extras.si` (*z*)
Sine integral of a complex value.

bionet.utils.scipy_extras.shi

`bionet.utils.scipy_extras.shi` (*z*)
Hyperbolic sine integral of a complex value.

4.2.8 Extra Signal Processing Routines

Error Analysis Routines

<code>db</code>	Convert the specified power value to decibels assuming a reference value of 1.
<code>rms</code>	Compute the root mean squared value of the specified array <i>x</i> .
<code>snr</code>	Compute the signal-to-noise ratio (in dB) of a signal given its reconstruction.

bionet.utils.signal_extras.db

`bionet.utils.signal_extras.db` (*x*)
Convert the specified power value to decibels assuming a reference value of 1.

bionet.utils.signal_extras.rms

`bionet.utils.signal_extras.rms` (*x*)
Compute the root mean squared value of the specified array *x*.

bionet.utils.signal_extras.snr

`bionet.utils.signal_extras.snr` (*u*, *u_rec*, *k_min*=0, *k_max*=None)
Compute the signal-to-noise ratio (in dB) of a signal given its reconstruction.

Parameters *u* : numpy array of floats

Original signal.

u_rec : numpy array of floats

Reconstructed signal.

k_min : int

Lower index into the signal over which to compute the SNR.

k_max : int

Upper index into the signal over which to compute the SNR.

Filtering Routines

<code>downsample</code>	Downsample a vector <code>x</code> by returning every <code>n</code> th entry.
<code>fftfilt</code>	Filter the signal <code>x</code> with the FIR filter described by the coefficients in <code>b</code> using the overlap-add method.
<code>remezord</code>	Calculate the parameters required by the Remez exchange algorithm to construct a finite impulse response (FIR) filter that approximately meets the specified design.
<code>upsample</code>	Upsample a vector <code>x</code> by inserting <code>n-1</code> zeros between every entry.

`bionet.utils.signal_extras.downsample`

`bionet.utils.signal_extras.downsample(x, n, offset=0)`

Downsample a vector `x` by returning every `n`th entry. An optional offset may be specified.

`bionet.utils.signal_extras.fftfilt`

`bionet.utils.signal_extras.fftfilt(b, x, *n)`

Filter the signal `x` with the FIR filter described by the coefficients in `b` using the overlap-add method. If the FFT length `n` is not specified, it and the overlap-add block length are selected so as to minimize the computational cost of the filtering operation.

`bionet.utils.signal_extras.remezord`

`bionet.utils.signal_extras.remezord(freqs, amps, rips, Hz=1, alg='ichige')`

Calculate the parameters required by the Remez exchange algorithm to construct a finite impulse response (FIR) filter that approximately meets the specified design.

Parameters `freqs` : array_like of floats

A monotonic sequence of band edges specified in Hertz. All elements must be non-negative and less than 1/2 the sampling frequency as given by the `Hz` parameter.

amps : array_like of floats

A sequence containing the amplitudes of the signal to be filtered over the various bands.

rips : array_like of floats

A sequence specifying the maximum ripples of each band.

alg : {'herrmann', 'kaiser', 'ichige'}

Filter length approximation algorithm.

Returns `numtaps` : int

Desired number of filter taps.

bands : ndarray of floats

A monotonic sequence containing the band edges.

amps : ndarray of floats

Desired gain for each band region.

weights : ndarray of floats

Filter design weights.

See also:

`scipy.signal.remez`

bionet.utils.signal_extras.upsample

`bionet.utils.signal_extras.upsample(x, n, offset=0)`

Upsample a vector `x` by inserting `n-1` zeros between every entry. An optional offset may be specified.

Miscellaneous Routines

<code>nextpow2</code>	Return the first integer <code>N</code> such that $2^{**N} \geq \text{abs}(x)$
<code>oddceil</code>	Return the smallest odd integer no less than <code>x</code> .
<code>odddround</code>	Return the nearest odd integer from <code>x</code> .

bionet.utils.signal_extras.nextpow2

`bionet.utils.signal_extras.nextpow2(x)`

Return the first integer `N` such that $2^{**N} \geq \text{abs}(x)$

bionet.utils.signal_extras.oddceil

`bionet.utils.signal_extras.oddceil(x)`

Return the smallest odd integer no less than `x`.

bionet.utils.signal_extras.odddround

`bionet.utils.signal_extras.odddround(x)`

Return the nearest odd integer from `x`.

4.2.9 Trigonometric Polynomial Routines

<code>em</code>	Trigonometric polynomial basis function.
<code>gen_dirichlet_coeffs</code>	Generate random Dirichlet coefficients for a real signal.
<code>gen_trig_poly</code>	Construct a trigonometric polynomial with specified Dirichlet coefficients.
<code>gen_trig_poly_2d</code>	Construct a 2D trigonometric polynomial.
<code>get_dirichlet_coeffs</code>	Compute the Dirichlet coefficients of a trigonometric polynomial.
<code>scale_down_coeffs</code>	Scale down Dirichlet coefficients.

bionet.utils.trig_poly.em

`bionet.utils.trig_poly.em(m, t, Omega, M)`

Trigonometric polynomial basis function.

Parameters `m` : int

Order of basis function.

`t` : numpy.ndarray

Times over which to compute the function.

Omega : float

Bandwidth (in rad/s).

M : int

Trigonometric polynomial order.

Returns `u` : numpy.ndarray

Basis function $\exp(1j*m*Omega*t/M)/\sqrt{T}$, where $T == 2*pi*M/Omega$.

bionet.utils.trig_poly.gen_dirichlet_coeffs

`bionet.utils.trig_poly.gen_dirichlet_coeffs(M)`

Generate random Dirichlet coefficients for a real signal.

Parameters `M` : int

Trigonometric polynomial order.

Returns `am` : numpy.ndarray

Array of Dirichlet coefficients with shape $(2*M+1)$. The coefficients are ordered such that `am[0]` contains the coefficient for $m == -M$.

bionet.utils.trig_poly.gen_trig_poly

`bionet.utils.trig_poly.gen_trig_poly(T, dt, am, method='fft', scale_down=False)`

Construct a trigonometric polynomial with specified Dirichlet coefficients.

Parameters `T` : float

Period (i.e., duration) of the trigonometric polynomial.

`dt` : float

Time resolution.

`am` : int or numpy.ndarray

Trigonometric polynomial order or array of Dirichlet coefficients. If the latter, the length of the array must be odd.

method : {'fft', 'inner'}

Method to use when computing coefficients. The FFT method is generally faster than using inner products.

scale_down : bool

If true, linearly scale down all coefficients such that the magnitude of the high-frequency coefficients are reduced the most.

Returns **u** : numpy.ndarray

Generated signal.

bionet.utils.trig_poly.gen_trig_poly_2d

`bionet.utils.trig_poly.gen_trig_poly_2d(Sx, Sy, dx, dy, c)`

Construct a 2D trigonometric polynomial.

Parameters **Sx** : float

Period of signal along the X-axis.

Sy : float

Period of signal along the Y-axis.

dx : float

Resolution along the X-axis.

dy : float

Resolution along the Y-axis.

c : tuple or numpy.ndarray

X-axis and Y-axis trigonometric polynomial orders or an array of Dirichlet coefficients with shape $(2*M_y+1, 2*M_x+1)$.

Returns **S** : numpy.ndarray

Generated signal.

Notes

This function uses the FFT to generate the output signal.

See http://fourier.eng.hmc.edu/e101/lectures/Image_Processing/node6.html for an example of a DFT of a real 2D discrete signal.

bionet.utils.trig_poly.get_dirichlet_coeffs

`bionet.utils.trig_poly.get_dirichlet_coeffs(u, dt, M, method='fft')`

Compute the Dirichlet coefficients of a trigonometric polynomial.

Parameters **u** : numpy.ndarray

Input signal.

dt : float

Time resolution (s).

M : int

Trigonometric polynomial order.

method : {'fft', 'inner'}

Method to use when computing coefficients. The FFT method is generally faster than using inner products.

Returns `am` : `numpy.ndarray`

Array of $2M+1$ Dirichlet coefficients.

Notes

Assumes that u is defined over times $dt \cdot \text{arange}(0, \text{len}(u))$ and that $dt \cdot \text{len}(u)$ is equal to the period of the trigonometric polynomial.

`bionet.utils.trig_poly.scale_down_coeffs`

`bionet.utils.trig_poly.scale_down_coeffs(am)`

Scale down Dirichlet coefficients.

Parameters `am` : `numpy.ndarray`

Array of Dirichlet coefficients of a real trigonometric polynomial. Must be of odd length.

Returns `am_new` : `numpy.ndarray`

Array of scaled coefficients; the highest frequency coefficients are scaled down the most.

4.2.10 Video I/O Classes and Routines

```
ReadVideo
WriteFigureVideo
WriteVideo
video_capture
```

Publications

The Time Encoding and Decoding Toolkit implements algorithms from the following publications:

- [1] A.A. Lazar, **Time Encoding with an Integrate-and-Fire Neuron with a Refractory Period**, *Neurocomputing*, Vol. 58-60, pp. 53-58, Jun. 2004
- [2] A.A. Lazar and L.T. Toth, **Perfect Recovery and Sensitivity Analysis of Time Encoded Bandlimited Signals**, *IEEE Transactions on Circuits and Systems-I: Regular Papers*, Vol. 51, No. 10, pp. 2060-2073, Oct. 2004
- [3] A.A. Lazar, **Multichannel Time Encoding with Integrate-and-Fire Neurons**, *Neurocomputing*, Vol. 65-66, pp. 401-407, Jun. 2005
- [4] A.A. Lazar, E.K. Simonyi, and L.T. Toth, **Fast Recovery Algorithms of Time Encoded Bandlimited Signals**, *IEEE International Conference on Acoustics, Speech and Signal Processing*, Vol. 4, pp. 237-240, Philadelphia, PA, Mar. 19-23, 2005
- [5] A.A. Lazar, **A Simple Model of Spike Processing**, *Neurocomputing*, Vol. 69, pp. 1081-1085, Jun. 2006
- [8] A.A. Lazar and E.A. Pnevmatikakis, **Faithful Representation of Stimuli with a Population of Integrate-and-Fire Neurons**, *Neural Computation*, Vol. 20, No. 11, pp. 2715-2744, Nov. 2008
- [10] A.A. Lazar, E.K. Simonyi, and L.T. Toth, **An Overcomplete Stitching Algorithm for Time Decoding Machines**, *IEEE Transactions on Circuits and Systems-I: Regular Papers*, Vol. 55, No. 9, pp. 2619-2630, Oct. 2008
- [12] A.A. Lazar and E.A. Pnevmatikakis, **Consistent Recovery of Sensory Stimuli Encoded with MIMO Neural Circuits**, *Computational Intelligence and Neuroscience, Special Issue on Signal Processing for Neural Spike Trains*, Feb. 2010

Authors & Acknowledgments

This software was written and packaged by Lev Givon, currently at the Bionet Group ¹ at Columbia University.

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- Yevgeniy B. Slutskiy
- Robert J. Turetsky

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- Robert J. Turetsky
- Yiyin Zhou

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Change Log

8.1 Release 0.7.1 - (Under Development)

- Add pip installation information.
- Replace `distribute_setup` with `ez_setup`.
- Change name to Time Encoding and Decoding Toolkit.
- Fix various demos.
- Change to PEP 440 version numbering.
- Use ReadTheDocs theme in HTML docs.

8.2 Release 0.07 - (August 8, 2012)

- Merge with utils toolkit.
- Add docs for merged utilities.
- Improve finding of includes/libraries needed to build bpa extension.
- Download distribute for package installation if it isn't available.

8.3 Release 0.062 - (September 19, 2011)

- Improve precision of IAF encoders.
- Fix signs in delayed IAF example.
- Add decoders that use the trigonometric polynomial approximation.
- Add more PyCUDA decoder implementations.

8.4 Release 0.061 - (November 24, 2010)

- Add docs for PyCUDA-based functions.
- Update installation information.

- Update copyright information.

8.5 Release 0.06 - (September 17, 2010)

- Add SISO PyCUDA-based IAF TEM/TDM implementations.
- Fix encoder resampling.
- Update docs.

8.6 Release 0.051 - (June 9, 2010)

- Eliminate various unnecessary loops and summations.

8.7 Release 0.05 - (June 1, 2010)

- Add documentation.
- Add more efficient concurrent IAF encoder.
- Fix bug in MIMO spline interpolation decoders.

8.8 Release 0.04 - (April 19, 2010)

- Improve docstrings, use numpy docstring conventions.
- Add IAF interpolation spline decoding algorithms.
- Add coupled IAF encoding and decoding algorithms.
- Add MIMO delayed IAF encoding and decoding algorithms.

8.9 Release 0.03 - (November 12, 2009)

- Accelerate IAF decoder implementations.
- Add IAF population decoding algorithm.
- Add IAF real-time decoding algorithm.
- Clean up demos.
- Facilitate installation on x86_64 Linux.

8.10 Release 0.021 - (October 23, 2009)

- Clean up real-time algorithm implementations.
- Make time array construction consistently use a fixed time step.

8.11 Release 0.02 - (June 26,2009)

- Add real-time encoding and decoding algorithms.
- Add ASDM population decoding algorithms.
- Make code more readable.

8.12 Release 0.011 - (May 08, 2009)

- Change package name to Time Encoding and Decoding Toolbox.

8.13 Release 0.01 - (May 08, 2009)

- First public release.

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