pyeemd Documentation

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This is the documentation of *pyeemd*, which is a Python wrapper for *libeemd*, a C library for performing the ensemble empirical mode decomposition (EEMD), its complete variant (CEEMDAN) or the regular empirical mode decomposition (EMD).

If you have any questions or problems with *pyeemd*, or you wish to propose enhancements, please check out the main page of libeemd. Also, if you want more detail on the inner workings of *libeemd* and/or wish to cite it in scientific work, please see the associated article published in Computational Statistics.

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1.1 Installing pyeemd

The *pyeemd* module comes with a regular Python *setuptools* installation script, so installing it should be quite straightforward. The only catch is that you first need install *libeemd*, since *pyeemd* is only a wrapper for that library. Please see the README file distributed with *libeemd* for more details.

The *pyeemd* module expects to find either a file libeamd.so in the same directory as pyeemd.py, or somewhere where *ctypes.util.find_library* will find it (most notably directories listed in the LIBRARY_PATH environment variable).

To install pyeemd please run:

```
python2 setup.py install
```

In the top-level directory of *pyeemd* (the one with setup.py).

If you want to specify an alternative installation prefix, you can do it as follows:

```
python2 setup.py install --prefix=$HOME/usr
```

1.2 Tutorial

After installing *pyeemd* as described in *Installing pyeemd* you are all set to using it with:

```
import pyeemd
```

The three main decomposition routines implemented in *pyeemd* – EMD, EEMD and CEEMDAN – are available as emd(), eemd() and ceemdan(), respectively. All these methods use similar conventions so interchanging one for another is easy.

Input data to these routines can be any kind of Python sequence that numpy can convert to an 1D array of floating point values. The output data will be a 2D numpy array, where each row of the array represents a single *intrinsic mode function* (IMF).

As an example, the *examples* subfolder of *pyeemd* contains a file ecg.csv, which contains ECG (electrocardiogram) data from the MIT-BIH Normal Sinus Rhythm Database. The data is in CSV (comma separated value) format, which can be read into Python in many ways, one of which is using numpy.loadtxt() using the appropriate delimiter:

```
from numpy import loadtxt
ecg = loadtxt("ecg.csv", delimiter=',')
```

Now we have the data in a numpy array ecg. We can quickly plot what the data looks like using matplotlib.pyplot.

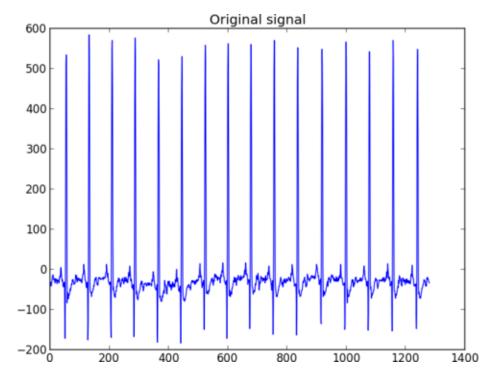


Fig. 1.1: Original ECG signal as plotted by matplotlib.pyplot.

```
from matplotlib.pyplot import plot, show, title

title("Original signal")
plot(ecg)
show()
```

The data stored in *ecg* can be decomposed with CEEMDAN using the routine ceemdan (). The only thing we need to decide is what to use as the stopping criterion for the sifting iterations. In this example we use a S-number of 4 and a maximum number of siftings of 50:

```
from pyeemd import ceemdan

imfs = ceemdan(ecg, S_number=4, num_siftings=50)
```

Now the rows of the 2D array *imfs* are the IMFs the original signal decomposes to when applying CEEMDAN. We can plot these IMFs using matplotlib.pyplot as before, but *pyeemd* also comes with an utility function plot_imfs () for easily plotting the IMFs (using matplotlib.pyplot) in separate figures.

```
from pyeemd.utils import plot_imfs

plot_imfs(imfs, plot_splines=False)
show()
```

The plot_splines=False argument prevents the plotting of the envelope curves of the IMFs, which would otherwise be shown.

This concludes our simple tutorial. For more in-depth information about the methods available in *pyeemd* please head to the *API documentation*. You can also look at example code at the examples subdirectory of *pyeemd*.

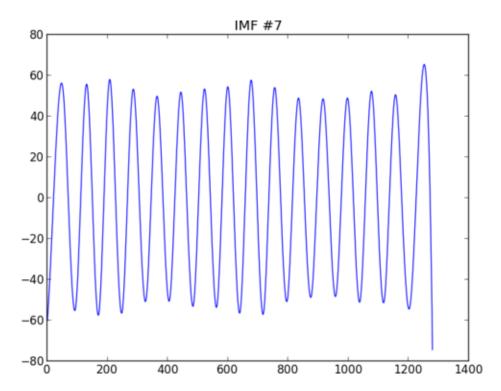


Fig. 1.2: IMF 7 extracted from ECG data with ceemdan() and plotted with plot_imfs().

How you choose to use or process the IMFs obtained by the decomposition routines is beyond the scope of this document – and beyond the scope of *pyeemd* – but you might be interested in the Hilbert transform routine offered by scipy.fftpack.hilbert().

1.3 API documentation

1.3.1 Main decomposition routines

1.3.2 Auxiliary routines

1.3.3 Utility code: pyeemd.utils

CHAPTER 2

Indices and tables

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