VAG tool documentation

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This is an update summary of VAG signal processing scripts used in the article *Spectral Analysis on Vibroartrographic Signal of Total Knee Arthroplasty*. There are two issues intended to solve in this version:

- Break the file allocation dependency. Former script use file allocation convention to run script properly, *i.e.*, the new data set need to be place in the correct directory, for example, .../../data/.
- Use R library for plotting. ggplot library provides a publication-quality plotting library and is open source (in progress).

The overview of all code and folder structure is shown below:

```
vag-tool
    doc // documentation latex source code
    lib // external library used to write up the script
    cdfa
    gsl-2.2.1
    libeemd
    README
    src // code written in this project
    signal_to_imfs
    signal_to_imfs_all
    remove_spike
    script_dfa.sh
    use_dfa
    use_dfa_all
```

Installation

Prerequisite is scientific python and r which can be easily installed on Debian linux with the command:

\$ sudo apt-get install build-essential python-pip3 python3 ipython3 r-base \$ pip install numpy scipy matplotlib

Then copy the folder vag-tool to your computer. In order to make command line know the new script, we have to export the new path to the folder, which can be done easily by:

\$ export PATH=\$PATH:/path/to/vag-tool/src/

Additionally, we can add this line to the .bash_profile or .bashrc to make this line execute every time we attend the terminal session.

Usage

EEMD with libeemd

For IMFs, EEMD algorithm take a single time signal located at path, in_path and output the set of IMF to the output directory out_dir. In case multiple input files, there is a script called signal_to_imfs_all which replace path to input file, in_path with path to input directory in_dir

```
$ signal_to_imfs in_path out_dir\\
$ signal_to_imfs_all in_dir out_dir
```

DFA

After downloading library DFA and make process, there will be an executable dfa. This exececutable can be used directly one by one to create DFA pairs but not very convenient when we would like to process over the directory so that script_dfa.sh is introduced.

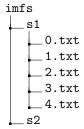
The parameter α is calculated from DFA pairs. Each IMFs is composed back with the alpha criterion, for example, $\alpha > 0.5$. Both steps (1) obtain α of each IMF (2) composite the IMFs back due to alpha criterion are done with use_dfa_and use_dfa_all.

Working example

Let assume there are the data at directory sample:

\$ signal_to_imfs_all sample/ imfs/

and finally out put to the folder imfs



__0.txt

__1.txt

__2.txt __3.txt __4.txt