

# BioSigKit

Contents of **BioSigKit**:

```
BioSigKit          - ===== BioSigKit =====
Demo              - ===== Demo ===== %%
RunBioSigKit      - ===== This Function initiates BioSigKit ===== %%
```

**BioSigKit** is both a directory and a function.

```
===== BioSigKit =====
BioSigKit is a set of useful signal processing tools that are either
developed by me personally or others in different fields of biosignal
processing. BioSigKit is a wrapper with a simple visual interface that
gathers this tools under a simple easy to use platform. This tool might
be only used for non-commercial, academic, research and learning
purposes.

% ===== How to start =====
example:: obj = BioSigKit(Sig, Fs, Gr)
Where:::
Sig: is the signal
Fs : Sample Rate
Gr : Flag for showing the interface or not
Then you can call any subroutine
% ====List Of Subroutines that you can call for QRS detection =====
----- Algorithm ----- How to Call -----
(1) Pan-Tompkins Algorithm :      obj.PanTompkins
(2) Phase Space Reconstruction :  obj.PhaseSpaceAlg
(3) RST State-Machine :          obj.StateMachine
(4) Filter Bank:                  obj.FilterBankQRS
(5) MTEO qrstAlg:                 obj.MTEO_qrstAlg
(6) AMPD:                         obj.AMPD_PAlg
% ==== List of all subroutines for ACC, EMG and etc processing =====
(7) Activity Detection Hilbert:    obj.Env_hilbert
----- Inputs ----- %
Smooth_window : Length of smoothing window in nr of sample
threshold_style : Set 0 for Automatic, Set 1 for Manual
DURATION : The number of samples for signal to be above
threshold to be considered active
----- Output ----- %
alarm : Pattern of activities
----- Demo ----- %
v = repmat([.1*ones(200,1);ones(100,1)],[10 1]);           % generate true variance profile
obj.sig = sqrt(v).*randn(size(v));
obj.Env_hilbert;
-----
(8) Comp Mobility and Complexity:  obj.ComputeHjorthP
-----
(9) Posture detection 3 Chann ACC: obj.ACC_Act
----- Inputs ----- %
obj.sig : 3 axis Accelerometer signal where, each row is an axis
and each column a sample (e.g. (3,:))
obj.Fs : Sampling frequency of the Accelerometer
----- Output ----- %
output : adaptively filtered ACC channels based on activity
state : activity level (0:steady,1:walking,2:joggin)
EE : Energy Expenditure over 1 min (or length sig)
F : Bandpass filter in Hz
SMA : Signal Magnitude area
-----
(10) PsuedoCorr template matching : obj.TemplateMatch
----- Inputs ----- %
template : A template in the form of a vector, the length of
```

```

the template should be smaller than the signal.
lag : a lag in terms of nr of samples to move the template,
it should be smaller than the length of the template
----- Outputs ----- %
PsC_s : template matching score in range [0,1].
best_lag: the lag that gave the highest correlation score.
-----
(11)ECG derived respiration :      obj.EDR_comp
-----
(12)ACC derived respiration :      obj.ADR_comp
% ===== General Projective, linear and nonlinear filterings ===== %%
(13)Real-time neural PCA:          obj.neural_pca
----- Inputs ----- %
X : Multi-channel signal, each row represents a channel and
each column a sample.
nPCA: Number of PCAs to extract
nit: Number of iterations to go through the whole signal
T : Learning rate in range [0,1], default:0.9
----- Outputs ----- %
EigVec: Eigen vectors
PC : PCs
Eigval : Eigenvalues
-----
(14)Adaptive Filtering:            obj.adaptive_filter
      * RLS : Recursive Least Squares Filter
      * ALE : Adaptive Line Enhancer (Delayed Filter)
      * VLAE : Variable Leaky Adaptive Line Enhancer
      * NLMS_ecg : Normalized Least Mean Squares filter for artifcat
      removal in ECG based on 3 channel Accelerometer recordings
----- Inputs ----- %
type: type of the filter (numeric):
      (1) RLS : Recursive Least Squares Filter
      (2) ALE : Adaptive Line Enhancer (Delayed Filter)
      (3) VLAE : Variable Leaky Adaptive Line Enhancer
      (4) NLMS_ecg : Normalized Least Mean Squares filter for
      artifcat removal in ECG based on 3 channel Accelerometer
      recordings
ref: Reference signal:
      * For RLS filter it is single channel (1*N)
      * For NLMS_ECG filter it should be 3 Channel
      Accelerometer (3*N)
obj.Sig: input signal to clean (single channel vector)
order : order of the filter (for VLAE and ALE also delay)
lambda : learning rate(0<= lambda <=1, usually close to 1)
----- Outputs ----- %
output: cleaned signal
error_sig : error signal
-----
(15)Nonlinear phasespace filtering: obj.nonlinear_phase_filt
----- Method ----- %
Employs nonlinear phasespace filter to clean up the signal. This
method is very strong and even able to extract foetal ecg from
single channel maternal recordings. Please refer to examples of
BioSigKit for further details.
----- Inputs ----- %
sig : Signal to be analyzed (single channel)
t : Number of samples for computing delayed phase space (def: 1)
d : Embedding dimension to consider (def: 50)
m : dimension of null space (def: 49)
r : number of nearest neighbors to consider
(normally a large number def: length(sig)/4)
----- Output ----- %
output : Cleaned Signal
----- example ----- %
output = projective(foetal_ecg(:,2), 1, round(Fs/5), round(Fs/6.25), 1500);
(16)Teager-Keiser energy operator: obj.TK_comp

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## Class Details

Superclasses	<a href="#">handle</a>
Sealed	false
Construct on load	false

**Constructor Summary**

<a href="#">BioSigKit</a>	----- Check Inputs -----%
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**Property Summary**

<a href="#">ACC</a>	3 channel ACC
<a href="#">Alg</a>	Alg type from interface
<a href="#">FreqValHolder</a>	Holds SampFreq from interface
<a href="#">Fs</a>	Sample Freq
<a href="#">Gr</a>	Flag for showing the interface
<a href="#">LoadedSig</a>	Loaded Sig
<a href="#">PhasePeriod</a>	Phase Period Used for Phase Space
<a href="#">PlotResult</a>	Verbose results of each algorithm
<a href="#">Results</a>	Struct holding results
<a href="#">ScalogramL</a>	Scalogram Length
<a href="#">Sig</a>	Signal
<a href="#">SigView</a>	Signal View Axis
<a href="#">Status</a>	Loader
<a href="#">complexity</a>	Complexity based on Hjorth Param
<a href="#">mobility</a>	mobility based on Hjorth
<a href="#">panel</a>	Main Visualization Panel
<a href="#">path_alg</a>	Path of Algorithm
<a href="#">slashchar</a>	OS dependent /
<a href="#">statsC</a>	Holding Stats

**Method Summary**

	<a href="#">ACC_Act</a>	----- Inputs ----- %
	<a href="#">ADR_comp</a>	----- Method -----%
	<a href="#">AMPD_PAIg</a>	
protected	<a href="#">BioSigKitPanel</a>	===== Sets up BioSigKit GUI ===== %%
	<a href="#">ComputeHjorthP</a>	----- Hjorth Parameters ----- %
	<a href="#">EDR_comp</a>	----- Method ----- %
	<a href="#">Env_hilbert</a>	----- Inputs ----- %
	<a href="#">FilterBankQRS</a>	
	<a href="#">ImportSig</a>	
	<a href="#">MTEO_qrstAlg</a>	
	<a href="#">PanTompkins</a>	
	<a href="#">PhaseSpaceAlg</a>	
	<a href="#">ResetStats</a>	
	<a href="#">RunAlg</a>	
	<a href="#">StateMachine</a>	
	<a href="#">TK_comp</a>	----- Outputs -----%
	<a href="#">TemplateMatch</a>	----- Inputs ----- %
	<a href="#">UpdateFig</a>	
	<a href="#">adaptive_filter</a>	----- Inputs -----%
	<a href="#">addListener</a>	Add listener for event.
	<a href="#">delete</a>	Delete a handle object.
	<a href="#">eq</a>	== (EQ) Test handle equality.
	<a href="#">findobj</a>	Find objects matching specified conditions.
	<a href="#">findprop</a>	Find property of MATLAB handle object.

	<a href="#">ge</a>	>= (GE) Greater than or equal relation for handles.
	<a href="#">gt</a>	> (GT) Greater than relation for handles.
Sealed	<a href="#">isvalid</a>	Test handle validity.
	<a href="#">le</a>	<= (LE) Less than or equal relation for handles.
	<a href="#">lt</a>	< (LT) Less than relation for handles.
	<a href="#">ne</a>	~= (NE) Not equal relation for handles.
	<a href="#">neural_pca</a>	----- Inputs ----- %
	<a href="#">nonlinear_phase_filt</a>	----- Method ----- %
	<a href="#">notify</a>	Notify listeners of event.
	<a href="#">visualizeResults</a>	----- First the Figure ----- %

### Event Summary

<a href="#">ObjectBeingDestroyed</a>	Notifies listeners that a particular object has been destroyed.
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