DRIFTER TOOLBOX

An SPM toolbox for removing periodic noise in fMRI data

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Short Description

This SPM toolbox is an implementation of the DRIFTER algorithm [1], which is a Bayesian method for physiological noise modeling and removal allowing accurate dynamical tracking of the variations in the cardiac and respiratory frequencies by using Interacting Multiple Models (IMM), Kalman Filter (KF) and Rauch-Tung-Striebel (RTS) smoother algorithms.

The frequency trajectories can be either estimated from reference signals (e.g., by using pulse meters and respiratory belts), or if the time resolution allows, directly from the fMRI signal. The estimated frequency trajectory is used for accurate model based separation of the fMRI signal into activation, physiological noise and white noise components using Kalman filter and RTS smoother algorithms. This separation is done for each voxel in the image separately. The basic idea of the method is to build a stochastic model for each component of the signal: the cleaned BOLD signal (including haemodynamical effects) is a relatively slowly varying signal, cardiac and respiration induced noise components are stochastic resonators with multiple harmonics, and the rest of the signal is white noise.

To get started using the DRIFTER toolbox, the user is required to specify at least the following parameters for the data section:

- EPI files : the fMRI data files
- TR : Repetition time (in ms)

And for each reference signal:

- Reference signal data
- Sampling interval
- List of possible frequencies

The physiological noise components are usually cardiac- and respiration-induced signals. However, the toolbox is not limited to these two in any way. Furthermore, the toolbox interface lets the user modify virtually every parameter in the estimation process. The default setup is not optimized for any particular purpose, and the user is encouraged to test the effects and abilities of the toolbox for the particular data at hand.

For further details on the toolbox, refer to the article [1].

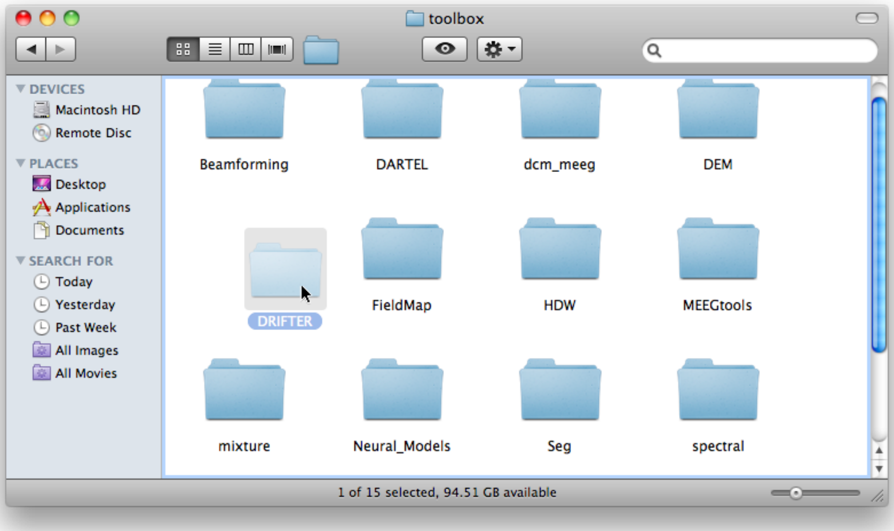
References:

1 Särkkä, S., Solin, A., Nummenmaa, A., Vehtari, A., Auranen, T., Vanni, S., and Lin, F.-H. (2012). Dynamical retrospective filtering of physiological noise in BOLD fMRI: DRIFTER. NeuroImage, 60:1517-1527.

System Requirements

The toolbox has been tested under Matlab 2011b and SPM8. On a computer with 8 Gb RAM running Ubuntu. The toolbox should run as well under Windows and Intel Macs without problems.

Installing



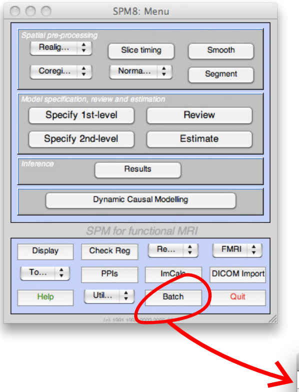
Download the latest verison of the toolbox as a ZIP file. Unzip the file. Copy the `DRIFTER` folder to your SPM `toolbox` folder that can be found directly under your `SPM` path. SPM should now recognize the DRIFTER toolbox once you start the application in Matlab.

License and Referring

Please cite the *DRIFTER Reference Paper* [1] when you have used DRIFTER for data analysis in your study.

Basic Usage

The figures below demonstrate how to access the toolbox functionalities through the graphical user interface in SPM. Only some parameters are obligatory and the toolbox can be configured in a couple of easy steps.



The toolbox can be accessed graphically through the SPM batch utility editor.

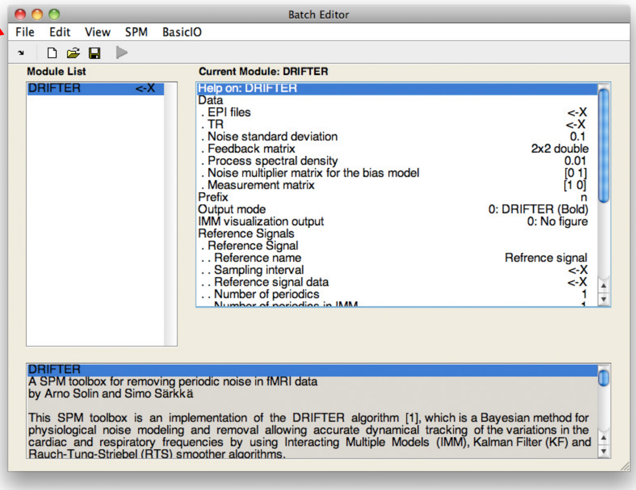
Choose "SPM → Tools → DRIFTER" in the toolbar menu to access the toolbox setup.

At minimum the following settings have to be specified:

- EPI files - the fMRI data files
- TR - Repetition time (in ms)

And for each reference signal:

- Sampling interval
- Reference signal data
- List of possible frequencies



Two types of error warning messages have been implemented:

- A warning is thrown if the Nyquist frequency is met (the TR is long) and there are unnecessary many harmonics being estimated. Fix this by modifying the N parameter of the reference signals.
- If the reference goes havoc at some timepoint (e.g. due the subject's actions), it is possible that the IMM estimations looses track of the signal. This can result in singular marices and the estimation returning null data. Try modifying the list of frequencies or check the quality of the reference signals.

All Options

The toolbox setup is divided in three: (i) General Estimation Parameters, (ii) EPI Data Parameters, and (iii) Reference Signal Parameters. The names are more or less self-explanatory; the general parameters defining the general setup, the epidata defining the fMRI data related parameters, and the refernce signal parameters defining the setup for each reference signal.

Below all the parameters are explained in some detail. For more mathematical details refer to the article Särkkä et al. (2012). For each parameter both the *full name* in the user interface is shown and the *short name* for batch usage. The *default value* is specified and a *brief description* is presented.

General Estimation Parameters

Option	Description
Output mode `mode` *0: DRIFTER (Bold)*	Choose data output mode. Either only the cleaned bias BOLD signal is returned or alternatively also the noise is added back to the output (i.e. only the periodic components are removed). The RETROICOR method is also included for comparison (see Glover et al. (2000) for details).
Prefix `prefix` *n*	File name prefix for output files.
IMM visualization output `visual` *0*	Choose '1: Save figure' to save a visualization of the IMM estimation results. The figure is saved under the current path as a PNG file.

EPI Data Parameters

Option	Description
Feedback matrix `BF` *[0 1;0 0]*	Feedback matrix for the bias model of the bold signal. The default value corresponds to a Wiener velocity model which assumes that the signal try to continue in the same direction as on the previous step.

Measurement matrix `BH` *[1 0]*	The measurement matrix for the bias model defines the observation of the bold signal bias process.
Noise multiplier matrix for the bias model `BL` *[0;1]*	The noise multiplier matrix for the bias model defines how the noise affects the bias evolution.
Process spectral density `BQ` *0.01*	The process spectral density for the bias model represents the continuous time noise in the bold signal
TR `tr` *[]*	(Required) Interscan interval, TR, (specified in milliseconds). This is the time between the plane scans (typically 100-4000 ms).
Noise standard deviation `sd` *0.1*	Estimate of measurement noise standard deviation.
EPI files `files`	(Required) Select the (fMRI) scans for this session. They all must have identical dimensions/orientation/voxel size etc.

Reference Signal Parameters

Option	Description
Feedback matrix `BF` *[0 1;0 0]*	Feedback matrix for the IMM bias model of the external signal. The default value corresponds to a Wiener velocity model.
Measurement matrix for the bias model `BH` *[1 0]*	The measurement matrix for the bias model defines the observation of the bold signal bias process.
Noise multiplier matrix for the bias model `BL` *[0;1]*	The noise multiplier matrix for the bias model defines how the noise affects the bias evolution.
Process spectral density for the bias model `BQ` *0.01*	The process spectral density for the bias model represents the continuous time noise in the bold signal

Number of periodics `N` *1*	(Required) The total number of periodics (fundamental + harmonics) that are estimated from the fMRI data.
Number of periodics in IMM `Nimm` *1*	The total number of periodics (fundamental + harmonics) that are estimated during the IMM stage where the frequency trajectory is estimated from the reference signal.
Reference signal data `data` *[]*	Reference signal data as a 1xN vector sampled the specified resolution and spanning the same time interval as the (fMRI) scans. If no data is supplied, the method uses the averaged fMRI data.
Sampling interval to downsample to `downdt` *0.1*	The sampling interval (in seconds) to downsample the reference signal to. Considerable speed-up can be achieved in this way as often the fMRI TR » the reference dt.
Sampling interval `dt` *[]*	(Required) The sampling interval, dt, of the reference signal (in seconds).
Sampling interval `dt` *[]*	(Required) The sampling interval, dt, of the reference signal (in seconds).
Array of possible frequencies in bpm `freqlist` *[]*	An array of possible frequencies in beats per minute (e.g. 40:120). The interacting Markov chain model uses these for finding the frequency trajectory in the external signal
Frequency time series `frequency` *[]*	Alternatively a frequency time series spanning over the same time interval as the scans can be defined.
Reference name `name` *'Refrence signal'*	Reference signal name (e.g. 'External cardiac' signal). This information can be provided for debugging puposes.
Overall transition probability `poverall` *0*	Transition probability between all steps of frequencies (i.e. the probability of a jump from e.g. 70 bpm to 80 bpm).
Markov chain transition probability `ptrans` *0.01*	Transition probability between consecutive steps of frequencies (i.e. the probability of a jump from e.g. 70 bpm to 71 bpm).

Resonator process noise spectral density `qr` *0.01*	The resonator process noise spectral density defines the continuous-time variation of the resonator signals. Adjust primarily this parameter to control the behavior of the periodic signals.
Reference Signals `refdata`	Specify reference signal – e.g. pulse or respiration.
Noise standard deviation `sd` *0.1*	Estimate of measurement noise standard deviation in the IMM model.

SPM Batch Example

The toolbox can easily be used in batch mode. It creates an SPM batch job structure which can be run using the normal `spm_jobman` method in SPM. Below a basic example of the toolbox use is demonstrated. Refer to the more advanced settings above to modify the `job` structure.

Listing 1: The file `demo_drifter.m` and the data used in this example are all available on the toolbox web page.

```
%% DEMO_drifter - Example usage of the DRIFTER toolbox
%
% Description:
%   This file demonstrates the use of the DRIFTER method in SPM. It
%   uses data files that are available for download on the toolbox
%   web page. Refer to the toolbox documentation for further details.
%
% See also:
%   http://the.url.to/the/documentation.of.the.toolbox
%
% Version:
%   updated 20110826
%
% Copyright:
%   Arno Solin, 2011

%% Set up

  % Make sure SPM is in your path (Must be changed!!!)
  addpath /path/to/spm8

  % Initialize SPM defaults
  spm('Defaults','fMRI');
  spm_jobman('initcfg'); % useful in SPM8 only

  % Load filenames using SPM built-in functions
  f = spm_select('FPListRec','demodata/','^d.*\.img$');

  % Load reference signal data (respiration, cardiac),
  % both sampled at dt=0.001 s
  load references.mat


%% Preliminary stuff

  % Here you can do some preliminary fixing of the data. Such as
  % - REALIGN
  % - COREGISTER
  % - SEGMENT
  % - ... (not necessarily prior to using DRIFTER)

  % Help on these can be found e.g. in the SPM documentation file.


%% Use the new toolbox

%  METHOD SPECIFICATION
```

```
    % Choose in which mode to run the method (0 = DRIFTER with all noise
    % removed, 1 = DRIFTER with only physiological noise removed,
    % 2 = a RETROICOR implementation)
    jobs{1}.spm.tools.drifter.mode = 1;

    % Choose with which prefix to output the data
    jobs{1}.spm.tools.drifter.prefix = 'n';

    % Assign the EPI fMRI data files (as we have not done anything prior to
    % this, we use the original data files loaded into f)
    jobs{1}.spm.tools.drifter.epidata.files = f;

    % The  Interscan interval, TR, (specified in milliseconds)
    jobs{1}.spm.tools.drifter.epidata.tr = 100;

  % REFERENCE 1: The cardiac signal

    % Signal name (for debugging)
    jobs{1}.spm.tools.drifter.refdata(1).name     = 'Cardiac Signal';

    % Assign the reference data that was loaded earlier
    jobs{1}.spm.tools.drifter.refdata(1).data     = cardiac;

    % Set the sampling interval of the reference signal (dt=0.001)
    jobs{1}.spm.tools.drifter.refdata(1).dt       = 1/1000;

    % To speed up the estimation we downsample the signal
    jobs{1}.spm.tools.drifter.refdata(1).downdt   = 1/10;

    % List of possible frequencies for this phenomenon (in beats per min)
    jobs{1}.spm.tools.drifter.refdata(1).freqlist = 60:120;

    % Number of periodics to estimate (fundamental + number of harmonics)
    jobs{1}.spm.tools.drifter.refdata(1).N        = 3;

    % There is no need to estimate as many periodics while finding the
    % frequency. Therefore we use only the fundamental here.
    jobs{1}.spm.tools.drifter.refdata(1).Nimm     = 1;

  % REFERENCE 2: The respiration signal (see above for details)
    jobs{1}.spm.tools.drifter.refdata(2).name     = 'Respiratory Signal';
    jobs{1}.spm.tools.drifter.refdata(2).data     = respiration;
    jobs{1}.spm.tools.drifter.refdata(2).dt       = 1/1000;
    jobs{1}.spm.tools.drifter.refdata(2).downdt   = 1/10;
    jobs{1}.spm.tools.drifter.refdata(2).freqlist = 10:70;
    jobs{1}.spm.tools.drifter.refdata(2).N        = 4;
    jobs{1}.spm.tools.drifter.refdata(2).Nimm     = 1;

  % RUN THE JOB (either in interactive mode or as a batch job)
    %spm_jobman('interactive',jobs);
    spm_jobman('run',jobs);


  %% Further analysis

    % Now you have the cleaned data stored on disk with the prefix specified
    % above. Hereafter the data can be analyzed in various ways with e.g. the
    % default functionalities provided by SPM.
    % See the SPM documentation for help.
```

An Example of Running DRIFTER Without SPM

The toolbox can also be run without SPM by calling the `drifter` function in Matlab. Make sure the DRIFTER code folder is in your path before calling the function. The function takes to input arguments: a **data** structure that defines the data that is used, and a **refdata** cell array defining the periodic components that will be estimated. The structure fields are the same as in the 'EPI Data Parameters' and 'Reference Signal Parameters' as earlier. The function returns similar structures, with all estimation parameters and results.

Listing 2: The file `demo_drifter_no_SPM.m` is available on the toolbox web page.

```
%% DEMO_drifter_no_SPM - Example usage of the DRIFTER toolbox without SPM
%
% Description:
%   This file demonstrates the use of the DRIFTER method without SPM.
%   Feel free to play around with the parameters (the defaults are
%   returned by the method). Refer to the toolbox documentation for
%   further details about possible parameters.
%
% See also:
%   http://becs.aalto.fi/en/research/bayes/drifter/
%
% Version:
%   updated 2012-04-17
%
% Copyright:
%   Arno Solin, 2011-2012

%% Add the toolbox path

  % Add the DRIFTER folder to your MATLAB path (Must be changed!!!)
  addpath /path/to/DRIFTER


%% Make artificial data

  % We simulate very simple artificial data fopr one reference signal,
  % and a one-dimensional brain signal with both white noise and periodic
  % noise.

  % Define parameters of the artificial data
  dt      = 0.1;           % Sampling rate (in seconds)
  T       = 0:dt:100;      % Time instants
  f       = 72 / 60;       % 72 beats per minute, constant frequency

  % Make reference data with fundamental signal + one harmonic
  ref_data   = 1*sin(1*2*pi*f*T) + ...
               2*cos(2*2*pi*f*T);

  % Make true slow brain signal
  brain_data = cumsum(0.05*randn(size(T)));

  % Make simulated brain data (random walk + oscillators)
  true_data =  brain_data + ...
               .2*sin(1*2*pi*f*T) + ...
               .1*cos(2*2*pi*f*T);
```

```
  % Add noise to true data
  obs_data = true_data + 0.05*randn(size(true_data));


%% Set up DRIFTER and run it

  % Provide two structures: "data" and "refdata" such that
  data.data = obs_data;
  data.dt = dt;

  % And for each reference signal
  refdata{1}.dt = dt;
  refdata{1}.freqlist = 60:90; % Vector of possible frequencies in bpm
  refdata{1}.data = ref_data;  % NOTE: If this is left out, the data.data
                               % is used.

  % Run DRIFTER
  [data,refdata] = drifter(data,refdata);

  % All the parameters are now visible in the structures
  % 'data' and 'refdata'.

%% Visualize result

  % The following code is only for providing a visual interpretation
  % of the estimation results. Three figures are shown:
  % (1) the brain signal (the true signal, a noisy observation of it,
  % the DRIFTER estimate, and the DRIFTER estimate with the measurement
  % noise added back to it), (2) The estimated periodic noise component,
  % (3) The stimated frequency trajectory.

  figure(1); clf
  subplot(2,2,[1 2]); hold on
    plot(T,brain_data,'--k', ...
         T,squeeze(data.data),'-g', ...
         T,squeeze(data.estimate),'-b', ...
         T,squeeze(data.estimate+data.noise),'-r')
    legend('True data','Observed data','Estimate','Estimate+white noise')
    title('\bf Results'); xlabel('Time [s]');
  subplot(223); hold on
    plot(T,squeeze(refdata{1}.estimate),'-b')
    title([refdata{1}.name ' Estimate'])
    xlabel('Time [s]');
  subplot(224); hold on
    plot(T,refdata{1}.FF,'-b')
    ylim([min(refdata{1}.freqlist) max(refdata{1}.freqlist)])
    title([refdata{1}.name ' Frequency'])
    xlabel('Time [s]'); ylabel('Freq (bpm)')
```