

Matlab baby monitoring code - overview

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May 9, 2007

The main aspects of the original code used for this research are outlined here. Many other helper functions also exist which are not described. These functions work with Matlab v6.5 or higher, though the data file is saved in v7 (compressed) format.

1 Top level scripts

<code>chooseexperiment</code>	Select an experiment from list and run it. Includes short demonstrations and long runs.
<code>runexperiment</code>	Rerun the last experiment.
<code>runxfactorexperiments</code>	Run X-factor experiments in thesis (long!).
<code>zoomplot</code>	Show panning, zooming chart with inferences and gold standard annotation.

Experiment settings files are all held in the same directory, with the prefix ‘`exp_`’. These files can be edited or copied in order to add or remove factors, specify different training/test babies, usage of cross-validation, whether to save inferences to disk, whether to use EM etc.

Ancillary scripts

<code>factors2statespace</code>	Full switching state-space model from individual factors.
<code>factors2meancov</code>	Full FHMM model from individual factors.
<code>globalconstants</code>	IDs of observed channel names, factors and inference types.
<code>globalsettings</code>	Global settings for all experiments.
<code>preprocessing_and_setup</code>	Preprocess data and set up factorial model structure.
<code>training_and_inference</code>	Train the model, make inferences and evaluate.
<code>train_*</code>	Fit models for normal and factor dynamics.

2 Statistical functions

<code>ar2statespace</code>	Convert AR process to state space form.
<code>arima2ar</code>	Integrated AR process to AR.
<code>arspectrum</code>	Power spectrum of an AR process.
<code>aryw</code>	Learn AR coefficients using Yule-Walker equations.
<code>autocov</code>	Autocovariance of a univariate sequence.
<code>chainindex2state</code>	Cross-product index of a switch setting from factor settings.
<code>convertdiscontinuities</code>	Correct quantisation effects.
<code>factoriseposteriors</code>	Factorise cross-product inferences.
<code>fhmexact</code>	FHMM inference.
<code>hiddenarima</code>	Learn hidden ARIMA model.
<code>hiddenrelativear</code>	Learn state space with two hidden AR components.
<code>kalmanll</code>	Likelihood and innovations of a Kalman filter given data.
<code>kfdd</code>	Kalman Filter Diagnostic Dashboard.
<code>learnxf</code>	Update X-factor parameters with EM.
<code>mavg</code>	Moving average with different window functions.
<code>pacf</code>	Partial autocorrelation of a univariate sequence.
<code>rocintervals</code>	Calculate ROC statistics given ground truth.
<code>samplestatespace</code>	Draw a sample from a state space model.
<code>skf_adf</code>	SKF inference with Gaussian sum approximation.
<code>skf_rbpf</code>	SKF inference with Rao-Blackwellised particle filtering.
<code>stateindex2chain</code>	Factor settings from cross-product switch setting index.

3 Data format

The data used in the experiments is contained in the file `15days.mat`. The struct array `data` has two fields, `raw` and `preprocessed`, each of which is a cell array with elements representing each of the 15 babies. These elements are also struct arrays, with fields containing the raw physiological data for each baby, and other information such as gestation and anonymised identifiers.

The struct array `intervals` contains annotations provided by the clinical experts. For example, `intervals.BloodSample{3}` contains an array of times for which a blood sample was thought to have occurred for baby 3. This is an $n \times 2$ matrix in which each row represents `[start_index stop_index]` for a particular episode of blood sampling. Indices are relative to the start of the 24 hour monitoring period.