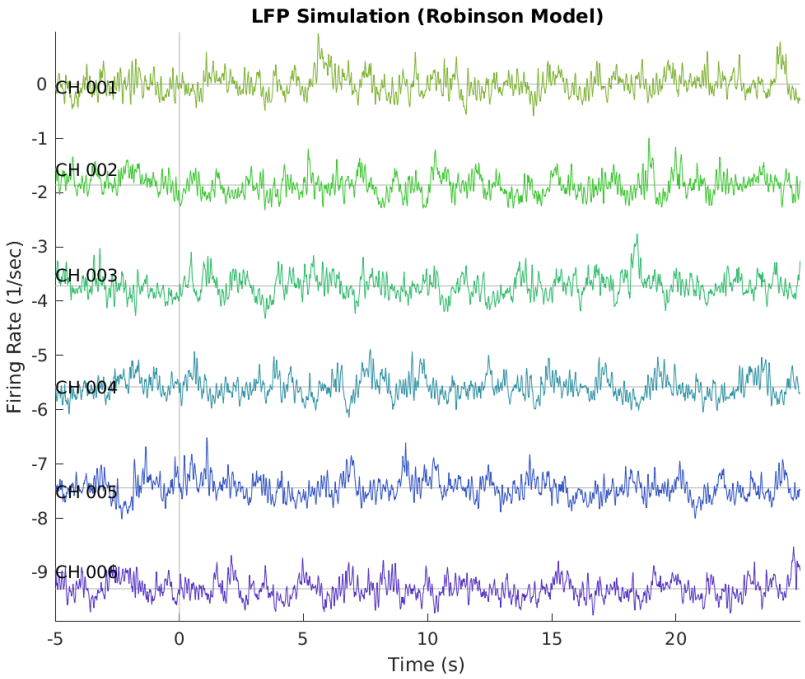
Robinson / Freyer / Hindriks Model Library Reference

Written by Christopher Thomas – January 26, 2024.



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Chapter 1

Data Structures and Additional Notes

1.1 LOOPINFO.txt

```
The synthRFH_findLoops and synthRFH_addLoopGainInfo functions return loop
information structure arrays (with one entry per loop found). These arrays
have the following fields:


From synthRFH_findLoops:

"label" is a unique identifier for the loop (the concatenation of the
  letters associated with each region in the loop's path).

"regionsvisited" is a vector containing the indices of each region in the
  loop's path. The first index is repeated as the last index.

"delay" is the propagation time for one cycle around the loop, in seconds.

"isinverting" is true if the product of the loop's edge couplings is
  negative, and false if the product is positive.

"frequency" is the loop's fundamental mode frequency in Hz (1/delay if
  non-inverting, half that if inverting).

"attenuation" is the loop's attenuation at its fundamental mode frequency
  due to low-pass effects from the alpha, beta, and gamma model parameters.
  This will be 1 if the signal is passed perfectly and less than 1 if not.



From synthRFH_addLoopGainInfo:

"cyclegainraw" is the small-signal gain from traversing once around the
  loop, without taking into account filter attenuation.
```

"cyclegain" is the small-signal gain from traversing once around the
  loop with filter attenuation taken into account.

"envelopetau" is the time constant for the growth (positive) or decay
  (negative) of the oscillation envelope. The envelope is exp(t/tau).

Optional:

"cyclegaingradient" is the gradient with respect to "intcouplings" of
  "cyclegain". This is a 4x4 matrix indexed by (destination, source)
  specifying the partial derivatives of "cyclegain" with respect to the
  coupling weights between excitatory, inhibitory, specific nucleus, and
  reticular nucleus neural populations.

(This is the end of the file.)

1.2 MODELPARAMS.txt

The synthRFH_XXX functions accept a model parameters structure with the
fields described below.

Relevant references:

(Robinson 2002)
https://journals.aps.org/pre/abstract/10.1103/PhysRevE.65.041924

(Freyer 2011)
https://www.jneurosci.org/content/31/17/6353.short

(Hindriks 2023)
https://www.nature.com/articles/s42003-023-04648-x

Sigmoid parameters (common to all):

"qmax" is the maximum firing rate (1/sec); typically 250.
"threshlevel" is the average neuronal threshold (mV); typically 15.
"threshsigma" is the standard deviation of the neuronal threshold (mV);
  typically 6.0.

Neural dynamics parameters (common to all):

"alpha" is the inverse decay time (1/sec); typically 50.

"beta" is the inverse rise time (1/sec); typically 200.
"gamma" is the inverse within-cortex propagation time (1/sec); typically 100.

Cortico-thalamic circuit parameters (for simulateNetwork):

"halfdelay_ms" is half of the round-trip cortex/thalamus loop time (ms);
  typically 40.

Additional coupling parameters (for simulateNetwork):

"noisecoupling" is the coupling weight of noise into the specific nucleus.
  Typically 0.5.
"mixturecoupling" is the coupling weight of mixed-population cortex
  excitatory signals into the cortex. Typically 0.07.

Noise generation parameters (for simulateNetwork):

"noisemean" is the mean noise signal value; typically 0.
"noisesigma" is the standard deviation of additive noise; typically 0.1.
"noisemultfactor" is "chi" in Freyer 2011/Hindriks 2023; the standard
  deviation of multiplicative noise is chi * noisesigma. Typically 0.3.

(This is the end of the file.)

Chapter 2

Function Reference

2.1 synthRFH_addLoopGainInfo.m

```
% function newloopinfo = synthRFH_addLoopGainInfo( ...
%   oldloopinfo, edgegains, edgegaingradients )
%
% This accepts a loop metadata structure array and augments each record
% with gain-related information.
%
% An empty cell array may be supplied for the gain gradients, to omit
% gradient information.
%
% "oldloopinfo" is a structure returned by synthRFH_findLoops().
% "edgegains" is a 4x4 matrix indexed by (destination, source) that contains
%   the small-signal firing rate gains between each source and destination
%   for the excitatory, inhibitory, specific nucleus, and reticular nucleus
%   neural populations.
% "edgegaingradients" is a 4x4 cell array indexed by (destination, source)
%   that contains the gradient with respect to "intcouplings" of the
%   small-signal firing rate gains in "edgegains". Passing an empty cell
%   array skips calculation of loop gain gradients.
%
% "newloopinfo" is a copy of "oldloopinfo" with the following fields added
%   to each record (per LOOPINFO.txt):
%   "cyclegainraw" is the small-signal gain from traversing once around the
%     loop, without taking into account filter attenuation.
%   "cyclegain" is the small-signal gain from traversing once around the
%     loop with filter attenuation taken into account.
%   "envelopetau" is the time constant for the growth (positive) or decay
%     (negative) of the oscillation envelope. The envelope is exp(t/tau).
%   "cyclegaingradient" is the gradient with respect to "intcouplings" of
%     "cyclegain". This is a 4x4 matrix (per "intcouplings"). If an empty
%     cell array is passed as "edgegaingradients", this field is omitted.
```

2.2 synthRFH_estimateOperatingPointExponential.m

```
% function [ firingrates potentials ] = ...
%   synthRFH_estimateOperatingPointExponential( ...
%     modelparams, intcouplings, startpotentials )
%
% This attempts to estimate the DC operating point of a Robinson neural model.
%
% Per the model guide, operating points with firing rates much less than the
% maximum are solutions to the equation:
%
% potentials = intcouplings * Q_0 * exp( potentials / sigmaprime )
%
% This function does a brute-force gradient descent search for operating
% points using "fsolve". This only finds one point; several points may
% exist.
%
% NOTE - Operating point firing rates _must_ be examined to confirm that
% they are much less than modelparams.qmax. If they are not several times
% smaller, the operating point is not correct.
%
% "modelparams" is a model parameter structure with the fields described in
%   MODELPARAMS.txt.
% "intcouplings" is a 4x4 matrix indexed by (destination,source) that
%   provides the coupling weights (in mV*s) between excitatory, inhibitory,
%   specific nucleus, and reticular nucleus neural populations.
% "startpotentials" is a vector containing cell potentials for the excitatory,
%   inhibitory, specific nucleus, and reticular nucleus populations used as
%   a starting point for further optimization. Set this to [] to call
%   synthRFH_estimateOperatingPointLinear() to generate starting potentials.
%
% "firingrates" is a vector containing firing rates for the excitatory,
%   inhibitory, specific nucleus, and reticular nucleus populations.
% "potentials" is a vector containing cell potentials for the excitatory,
%   inhibitory, specific nucleus, and reticular nucleus populations.
```

2.3 synthRFH_estimateOperatingPointLinear.m

```
% function [ firingrates potentials ] = ...
%   synthRFH_estimateOperatingPointLinear( modelparams, intcouplings )
%
% This attempts to estimate the DC operating point of a Robinson neural model.
%
% Per the model guide, operating points with firing rates much less than the
% maximum are solutions to the equation:
%
% potentials = intcouplings * Q_0 * exp( potentials / sigmaprime )
```

```
%
% This function uses a linear approximation to exp(x) to estimate operating
% points for potentials that are small compared to sigmaprime. NOTE - This
% is not a robus assumption! The operating point _must_ be examined to
% confirm that this condition holds. If it doesn't hold, the estimated
% operating point is not correct.
%
% "modelparams" is a model parameter structure with the fields described in
%   MODELPARAMS.txt.
% "intcouplings" is a 4x4 matrix indexed by (destination,source) that
%   provides the coupling weights (in mV*s) between excitatory, inhibitory,
%   specific nucleus, and reticular nucleus neural populations.
%
% "firingrates" is a vector containing firing rates for the excitatory,
%   inhibitory, specific nucleus, and reticular nucleus populations.
% "potentials" is a vector containing cell potentials for the excitatory,
%   inhibitory, specific nucleus, and reticular nucleus populations.
```

2.4 synthRFH_findLoops.m

```
% function loopinfo = ...
%   synthRFH_findLoops( modelparams, intcouplings, minweight )
%
% This examines a Robinson model coupling matrix and identifies loops.
% Loop metadata is extracted.
%
% This does not extract loop gain, since that varies with operating point.
%
% "modelparams" is a model parameter structure with the fields described in
%   MODELPARAMS.txt.
% "intcouplings" is a 4x4 matrix indexed by (destination, source) that
%   provides the coupling weights (in mV*s) between excitatory, inhibitory,
%   specific nucleus, and reticular nucleus neural populations.
% "minweight" is the threshold to use when evaluating whether a coupling
%   weight is nonzero (the absolute value must be at least "minweight").
%
% "loopinfo" is a structure array with one element per identified loop, and
%   the following fields (per LOOPINFO.txt):
%   "label" is a unique identifier for the loop (the concatenation of the
%     letters associated with each region in the loop's path).
%   "regionsvisited" is a vector containing the indices of each region in the
%     loop's path. The first index is repeated as the last index.
%   "delay" is the propagation time for one cycle around the loop, in seconds.
%   "isinverting" is true if the product of the loop's edge couplings is
%     negative, and false if the product is positive.
%   "frequency" is the loop's fundamental mode frequency in Hz (1/delay if
%     non-inverting, half that if inverting).
%   "attenuation" is the loop's attenuation at its fundamental mode
```

```
%     frequency from the alpha, beta, and gamma model parameters. This will
%     be 1 if the signal is passed perfectly and less than 1 if not.
```

2.5 synthRFH_ftWrapper_simulateNetwork.m

```
% function ftdata = synthRFH_ftWrapper_simulateNetwork( ...
%   trialcount, triggertime, poplabels, wantprogress, ...
%   duration, startup, timestep, modelparams, intcouplings, ...
%   popcount, cortexmixing, cortexdelays_ms )
%
% This is a wrapper for synthRFH_simulateNetwork().
% See that function's documentation for details.
%
% This simulates cortex and thalamus neural activity, using the model from
% Robinson 2002 with augmented input per Freyer 2011 and Hindriks 2023:
%
% https://journals.aps.org/pre/abstract/10.1103/PhysRevE.65.041924
% https://www.jneurosci.org/content/31/17/6353.short
% https://www.nature.com/articles/s42003-023-04648-x
%
% "trialcount" is the number of Field Trip trials to simulate.
% "triggertime" is the trigger offset from the start of simulation (seconds).
% "poplabels" is a cell array containing Field Trip channel names for the
%   neural populations, or {} to automatically generate channel names.
% "wantprogress" is true to write progress messages to the console, false
%   otherwise.
%
% Remaining arguments are per synthRFH_simulateNetwork().
%
% "ftdata" is a ft_datatype_raw structure containing trial data, including
%   a header (hdr) and a config structure with trial definitions (cfg.trl).
```

2.6 synthRFH_getEdgeGainGradients.m

```
% function edgegaingradients = synthRFH_getEdgeGainGradients( ...
%   modelparams, intcouplings, firingrates, rategradients )
%
% This function calculates the gradient of the small-signal gains of each
% network edge in a Robinson neural model with respect to the internal
% coupling matrix, at a specified operating point.
%
% This assumes firing rates that are much less than the maximum rate, and
% assumes that the gradients of the firing rates are already known.
%
% "modelparams" is a model parameter structure with the fields described in
%   MODELPARAMS.txt.
```

```
% "intcouplings" is a 4x4 matrix indexed by (destination, source) that
%   provides the coupling weights (in mV*s) between excitatory, inhibitory,
%   specific nucleus, and reticular nucleus neural populations.
% "firingrates" is a vector specifying the operating point firing rates of
%   excitatory, inhibitory, specific nucleus, and reticular nucleus neural
%   populations.
% "rategradients" is a cell array with 4 cells, containing gradient matrices
%   with respect to "intcouplings" for the excitatory, inhibitory, specific
%   nucleus, and reticular nucleus firing rates.
%
% "edgegaingradients" is a 4x4 cell array indexed by (destination, source)
%   that contains the gradient with respect to "intcouplings" of the
%   small-signal firing rate gains between each source and destination for
%   the excitatory, inhibitory, specific nucleus, and reticular nucleus
%   neural populations.
```

2.7 synthRFH_getEdgeGains.m

```
% function edgegains = synthRFH_getEdgeGains( ...
%   modelparams, intcouplings, firingrates )
%
% This function estimates the small-signal gain of each network edge in a
% Robinson neural model, at a specified operating point.
%
% "modelparams" is a model parameter structure with the fields described in
%   MODELPARAMS.txt.
% "intcouplings" is a 4x4 matrix indexed by (destination, source) that
%   provides the coupling weights (in mV*s) between excitatory, inhibitory,
%   specific nucleus, and reticular nucleus neural populations.
% "firingrates" is a vector specifying the operating point firing rates of
%   excitatory, inhibitory, specific nucleus, and reticular nucleus neural
%   populations.
%
% "edgegains" is a 4x4 matrix indexed by (destination, source) that contains
%   the small-signal firing rate gains between each source and destination
%   for the excitatory, inhibitory, specific nucleus, and reticular nucleus
%   neural populations.
```

2.8 synthRFH_getModelParamsFreyer.m

```
% function [ modelparams intcouplings ] = synthRFH_getModelParamsFreyer()
%
% This returns model and coupling parameters for use with
% synthRFH_stepCortexThalamus() and related functions.
%
% Values are the ones used in Freyer 2011 (Table 1):
```

```
% https://www.jneurosci.org/content/31/17/6353.short
%
% These have slightly adjusted alpha and beta time constants and
% substantially different coupling weights vs Robinson 2002.
%
% No arguments.
%
% "modelparams" is a model parameter structure with the fields described
%   in MODELPARAMS.txt.
% "intcouplings" is a 4x4 matrix indexed by (destination,source) that
%   provides the coupling weights (in mV*s) between excitatory, inhibitory,
%   specific nucleus, and reticular nucleus neurons.
```

2.9 synthRFH_getModelParamsHindriks.m

```
% function [ modelparams intcouplings ] = synthRFH_getModelParamsHindriks()
%
% This returns model and coupling parameters for use with
% synthRFH_stepCortexThalamus() and related functions.
%
% Values are the ones used in Hindriks 2023:
% https://www.nature.com/articles/s42003-023-04648-x
% https://github.com/Prejaas/amplitudecoupling
%
% These are identical to the Robinson 2002 values, except with a smaller
% noise coupling coefficient.
%
% No arguments.
%
% "modelparams" is a model parameter structure with the fields described
%   in MODELPARAMS.txt.
% "intcouplings" is a 4x4 matrix indexed by (destination,source) that
%   provides the coupling weights (in mV*s) between excitatory, inhibitory,
%   specific nucleus, and reticular nucleus neurons.
```

2.10 synthRFH_getModelParamsRobinson.m

```
% function [ modelparams intcouplings ] = synthRFH_getModelParamsRobinson()
%
% This returns model and coupling parameters for use with
% synthRFH_stepCortexThalamus() and related functions.
%
% Values are the ones used in Robinson 2002 (Table 1):
% https://journals.aps.org/pre/abstract/10.1103/PhysRevE.65.041924
%
% No arguments.
```

```
%
% "modelparams" is a model parameter structure with the fields described
%   in MODELPARAMS.txt.
% "intcouplings" is a 4x4 matrix indexed by (destination,source) that
%   provides the coupling weights (in mV*s) between excitatory, inhibitory,
%   specific nucleus, and reticular nucleus neurons.
```

2.11 synthRFH_getOperatingPointGradient.m

```
% function [ rategradients potentialgradients ] = ...
%   synthRFH_getOperatingPointGradient( ...
%     modelparams, intcouplings, testpotentials, couplingstep, zerohandling )
%
% This function attempts to estimate the gradient of the DC operating point
% of a Robinson neural model with respect to the internal coupling matrix.
%
% This assumes firing rates that are much less than the maximum rate. Per the
% model guide, operating points under these conditions are solutions to:
%
% potentials = intcouplings * Q_0 * exp( potentials / sigmaprime )
%
% The gradient of this function is evaluated numerically, by perturbing the
% coupling matrix and finding operating points for each perturbed version.
%
% "modelparams" is a model parameter structure with the fields described in
%   MODELPARAMS.txt.
% "intcouplings" is a 4x4 matrix indexed by (destination, source) that
%   provides the coupling weights (in mV*s) between excitatory, inhibitory,
%   specific nucleus, and reticular nucleus neural populations.
% "testpotentials" is a vector containing cell potentials for the excitatory,
%   inhibitory, specific nucleus, and reticular nucleus populations at the
%   test point to analyze. This is used as the starting point for the
%   operating point search.
% "couplingstep" is a scalar indicating the amount by which each coupling
%   value should be perturbed when evaluating the gradient numerically. This
%   should be much smaller than the magnitude of nonzero coupling values.
% "zerohandling" is 'all' to compute the gradient with respect to all
%   coupling values, and 'nonzero' to compute the gradient with respect to
%   all coupling values with magnitudes larger than "couplingstep" (storing
%   NaN as the gradient for coupling values that are smaller than this).
%
% "rategradients" is a cell array with 4 cells, containing gradient matrices
%   with respect to "intcouplings" for the excitatory, inhibitory, specific
%   nucleus, and reticular nucleus firing rates.
% "potentialgradients" is a cell array with 4 cells, containing gradient
%   matrices with respect to "intcouplings" for the excitatory, inhibitory,
%   specific nucleus, and reticular nucleus cell potentials.
```

2.12 synthRFH_getRegionInfo.m

```
% function [ indices_lut names_lut ]  = synthRFH_getRegionInfo()
%
% This returns metadata associating each region simulated by the Robinson
% 2002 model with a row/column index, a pretty name, and abbreviated names.
%
% No arguments.
%
% "indices_lut" is a structure with the following fields:
%   "cortex_excitatory" is the row/column index corresponding to excitatory
%     neurons in the cortex.
%   "cortex_inhibitory" is the row/column index corresponding to inhibitory
%     neurons in the cortex.
%   "thalamus_specific" is the row/column index corresponding to "specific
%     nucleus" neurons in the thalamus (also called the relay population).
%   "thalamus_reticular" is the row/column index corresponding to "reticular
%     nucleus" neurons in the thalamus.
%
% "names_lut" is a structure array indexed by region number, with the
%   following fields (all character vectors):
%   "title" is a verbose plot-safe name.
%   "label" is a terse filename-safe and plot-safe name.
%   "letter" is a capital letter.
%   "lutfield" is the name of the corresponding field in "indices_lut".
```

2.13 synthRFH_getSigmoid.m

```
% function firingrate = synthRFH_getSigmoid( ...
%   potential, maxrate, threshlevel, threshdeviation )
%
% This converts a cell-body potential (V in Robinson's model) to a firing
% rate (Q in Robinson's model).
%
% This is described in eq. 1 of Robinson 2002:
% https://journals.aps.org/pre/abstract/10.1103/PhysRevE.65.041924
% And in terms of sigma, not sigma-prime, in eq. m4 of Freyer 2011:
% https://www.jneurosci.org/content/31/17/6353.short
%
% "potential" is the cell body potential (V) to convert. This may be a
%   vector or matrix, to convert several potentials.
% "maxrate" is the maximum firing rate (Q_max).
% "threshlevel" is the average neuron threshold (theta).
% "threshdeviation" is the standard deviation of the average neuron threshold
%   (sigma - not sigma prime!).
%
% "firingrate" is the resulting firing rate (Q, or S(V)).
```

2.14 synthRFH_getSigmoidDerivative.m

```
% function dQdV = synthRFH_getSigmoidDerivative( ...
%   potential, maxrate, threshlevel, threshdeviation )
%
% This gets the derivative of the Robinson 2002 activation function with
% respect to cell-body potential, for a given potential.
%
% "potential" is the cell body potential (V) to evaluate the derivative at.
%   This may be a vector or matrix, to evaluate several potentials.
% "maxrate" is the maximum firing rate (Q_max).
% "threshlevel" is the average neuron threshold (theta).
% "threshdeviation" is the standard deviation of the average neuron threshold
%   (sigma - not sigma prime!).
%
% "dQdV" is the derivative of the firing rate with respect to potential,
%   at the specified potential.
```

2.15 synthRFH_getSigmoidInverse.m

```
% function potential = synthRFH_getSigmoidInverse( ...
%   firingrate, maxrate, threshlevel, threshdeviation )
%
% This converts a firing rate (Q in Robinson's model) back to a cell-body
% potential (V in Robinson's model), performing the inverse of
% synthRFH_getSigmoid().
%
% "firingrate" is the firing rate (Q, or S(V)). This may be a vector or
%   matrix, to convert several firing rates into potentials.
% "maxrate" is the maximum firing rate (Q_max).
% "threshlevel" is the average neuron threshold (theta).
% "threshdeviation" is the standard deviation of the average neuron threshold
%   (sigma - not sigma prime!).
%
% "potential" is the cell body potential (V).
```

2.16 synthRFH_makeFTDataFromMatrices.m

```
% function ftdata = synthRFH_makeFTDataFromMatrices( ...
%   wavedata, samprate, trigoffsetsamps, trigtimes, labelprefix )
%
% This builds a ft_datatype_raw structure containing supplied waveform data.
%
% "wavedata" is either a Nchans x Nsamples x Ntrials matrix or a cell array
%   with Ntrials cells, each containing a Nchans x Nsamples matrix.
```

```
% "samprate" is the sampling rate.
% "trigoffsetsamps" specifies when the trigger time is within each trial.
%   This is 0 if the first sample in the trial is at the trigger, positive
%   if a later sample in the trial is the trigger, and negative if the
%   trigger occurred before the first sample in the trial.
% "trigtimes" is a vector with trigger times for each trial. This is used for
%   constructign trial definitions. If necessary, an offset is added to
%   guarantee that all samples have positive indices in the global data.
%   Specify [] to automatically build trigger times for trial definitions.
% "labelprefix" is a character vector containing a prefix to use when
%   constructing channel labels.
%
% "ftdata" is a ft_datatype_raw structure containing trial data. This
%   includes a header and a config structure with cfg.trl.
```

2.17 synthRFH_optimizeCouplings.m

```
% function [ bestcouplings besterr ] = synthRFH_optimizeCouplings( ...
%   modelparams, startcouplings, loopinfo, loopgoals, ...
%   taulimit, bestfactor, maxprobes )
%
% This attempts to optimize the internal coupling weights of a Robinson
% neural model to modify the loop gains to meet a specified set of
% constraints.
%
% This works via brute-force gradient descent (using "fsolve").
%
% Note that the output coupling matrix follows the constraints described
% in Robinson 2002, Freyer 2011, and Hindriks 2023: The nu_ix weights are
% set to the same values as the nu_ex weights, and the weights that are
% zero in the references are set to be zero here.
%
% "modelparams" is a model parameter structure with the fields described in
%   MODELPARAMS.txt.
% "startcouplings" is a 4x4 matrix indexed by (destination,source) that
%   provides the coupling weights (in mV*s) between excitatory, inhibitory,
%   specific nucleus, and reticular nucleus neural populations.
% "loopinfo" is a loop metadata structure returned by synthRFH_findLoops().
% "loopgoals" is a Nx2 cell array. Each row contains a loop label in the
%   first column and a goal keyword in the second column. Goal keywords are
%   'biggest', 'grow', 'decay', or 'dontcare'. Loops with positive tau less
%   than the specified limit are growing, loops with negative tau with
%   absolute value less than the specified limit are decaying, and a growing
%   loop is "biggest" if its tau is smaller than all other growing tau
%   values by the specified factor. Loops not listed default to 'dontcare'.
% "taulimit" is the longest time constant (in seconds) that an envelope may
%   have to be counted as "growing" or "decaying". Typically 1.0 or less.
% "bestfactor" is the factor by which the "best" loop's tau must be smaller
```

```
%   than all other growing tau values. Typically 1.2-1.5.
% "maxprobes" is the maximum number of probes to make, or [] or NaN for the
%   default number (about 1400).
%
% "bestcouplings" is a perturbed version of "startcouplings" that produces
%   the desired loop behaviors.
% "besterr" is the error value associated with "bestcouplings". This is in
%   the range 0..1, with 0 being perfect and 1 being terrible.
```

2.18 synthRFH_simulateNetwork.m

```
% function firingrates = synthRFH_simulateNetwork( ...
%   duration, startup, timestep, modelparams, intcouplings, ...
%   popcount, cortexmixing, cortexdelays_ms )
%
% This simulates cortex and thalamus neural activity, using the model from
% Robinson 2002 with augmented input per Freyer 2011 and Hindriks 2023:
%
% https://journals.aps.org/pre/abstract/10.1103/PhysRevE.65.041924
% https://www.jneurosci.org/content/31/17/6353.short
% https://www.nature.com/articles/s42003-023-04648-x
%
% This simulates N populations of excitatory and inhibitory neurons in the
% cortex, and N populations of neurons in the specific and reticular nuclei
% in the thalamus (per Freyer 2011). Excitatory neuron populations in the
% cortex interact with each other, per Hindriks 2023.
%
% NOTE - This uses the forward Euler method for evolving system state.
% This is numerically stable if and only if the time step is much smaller
% than the time scales of any system dynamics. Make this much smaller than
% you think you need to.
%
% NOTE - If multiple durations are specifies, various parameters _may_ be
% specified for each epoch rather than globally. This is optional; any
% parameters that are not specified per-epoch are duplicated as needed.
%
% "duration" is the number of seconds to simulate. NOTE - This may be a
%   vector, specifying several successive durations which may have
%   different simulation parameters.
% "startup" is the number of seconds to simulate before the duration to
%   allow the simulation to settle/converge. This is typically 2-5 seconds.
% "timestep" is the amount of time to advance the simulation during each
%   sample, in seconds. NOTE - This must be much smaller than system
%   dynamics timescales!
% "modelparams" is a structure specifying model tuning parameters, per
%   MODELPARAMS.txt. NOTE - If "duration" is a vector, this may optionally
%   be a struct array specifying different parameters for each epoch.
% "intcouplings" is a 4x4 matrix indexed by (destination,source) that
```

```
%   provides the coupling weights (in mV*s) between excitatory cortex
%   neurons (1), inhibitory cortex neurons (2), specific nucleus neurons (3),
%   and reticular neurons (4). Typical coupling range from -2 to +2.
%   NOTE - If "duration" is a vector, this may optionally be a 4x4xN matrix
%   specifying different couplings for each epoch.
% "popcount" is the number of neural populations to simulate (Npop).
% "cortexmixing" is a Npop x Npop matrix indexed by (destination,source)
%   that specifies the internal communication mixing of excitatory neurons
%   in the cortex. After mixing, these then get weighted by (scalar)
%   modelparams.mixturecoupling before integration as neural inputs. Set
%   this to [] to omit internal cortex communication/mixing.
%   NOTE - The typical mixture coupling weight in MODELPARAMS.txt assumes that
%   the cortex mixing matrix has rows normalized so that the absolute values
%   of each row's elements sums to 1 (or a value close to 1).
%   NOTE - If "duration" is a vector, this may optionally be a Npop x Npop x N
%   matrix specifying different mixing weights for each epoch.
% "cortexdelays_ms" is a Npop x Npop matrix indexed by (destination,source)
%   that specifies the internal communication delays of excitatory neurons
%   in the cortex, in milliseconds. Set this to [] to omit internal cortex
%   communication/mixing.
%   NOTE - If "duration" is a vector, this may optionally be a Npop x Npop x N
%   matrix specifying different delays for each epoch.
%
% "firingrates" is a 4 x Npop x Nsamples matrix containing firing rates
%   for excitatory cortex neurons (1), inhibitory cortex neurons (2),
%   specific nucleus neurons (3), and reticular neurons (4). The excitatory
%   cortex neuron firing rates are gamma-damped, per Robinson 2002.
```

2.19 synthRFH_stepCortexThalamus.m

```
% function statefuture = synthRFH_stepCortexThalamus( modelparams, ...
%   timestep, statepresent, statepast, intcouplings, extrates, extcouplings )
%
% This generates the future state of a cortico-thalamic loop given the
% present state, using the model from Robinson 2002 with augmented input
% per Freyer 2011 and Hindriks 2023:
%
% https://journals.aps.org/pre/abstract/10.1103/PhysRevE.65.041924
% https://www.jneurosci.org/content/31/17/6353.short
% https://www.nature.com/articles/s42003-023-04648-x
%
% This simulates N populations of excitatory and inhibatory neurons in the
% cortex, and N populations of neurons in the specific and reticular nuclei
% in the thalamus (per Freyer 2011). Population bins are independent of
% each other (communication is handled by the caller).
%
% NOTE - This uses the forward Euler method for evolving system state.
% This is numerically stable if and only if the time step is much smaller
```

```
% than the time scales of any system dynamics. Make this much smaller than
% you think you need to.
%
% "modelparams" is a structure with the following fields (as described in
%   MODELPARAMS.txt):
%   "qmax" is the maximum firing rate (1/sec); typically 250.
%   "threshlevel" is the average neuronal threshold (mV); typ. 15.
%   "threshsigma" is the standard deviation of the neuronal threshold (mV);
%     typically 6.0.
%   "alpha" is the inverse decay time (1/sec); typically 50.
%   "beta" is the inverse rise time (1/sec); typically 200.
%   "gamma" is the inverse within-cortex propagation time (1/sec); typ. 100.
% "timestep" is the amount of time to advance the simulation by (in seconds).
%   NOTE - This must be much smaller than system dynamics timescales!
% "statepresent" is a structure with the following fields:
%   "potentials" is a 4xN matrix containing Ve_k, Vi_k, Vs_k, and Vr_k from
%     the Robinson model.
%   "velocities" is a 4xN matrix containing the approximate first time
%     derivative of "potentials".
%   "cortexrates" is a 1xN matrix containing the gamma-damped firing rate
%     of cortex excitatory neurons (phi_e).
%   "cortexvelocities" is a 1xN matrix containing the approxmate first time
%     derivative of "cortexrates".
% "statepast" is a structure with the same fields as "statepresent", taken
%   from a past stimulation step. This should be delayed by the one-way
%   cortex/thalamus communication time (one half of the round-trip delay).
% "intcouplings" is a 4x4 matrix indexed by (destination,source) that
%   provides the coupling weights (in mV*s) between excitatory cortex
%   neurons (1), inhibitory cortex neurons (2), specific nucleus neurons (3),
%   and reticular nucleus neurons (4). Typical couplings range from -2 to +2.
% "extrates" is a MxN matrix containing the firing rates of M external inputs
%   to the system. These may represent noise (as with Freyer 2011) or
%   cross-coupled activity within the cortex (as with Hindriks 2023).
%   This may be empty (M = 0).
% "extcouplings" is a 4xM matrix indexed by (destination,source) that
%   provides the coupling weights (in mV*s) between the internal model
%   neurons (destinations) and the system's external inputs (sources).
%   This may be empty (M = 0).
%
% "statefuture" is a copy of "statepresent" advanced by one time step.
```

Chapter 3

Sample Code

3.1 do_analyze_robinson.m

```
% Example Code - Analysis of behavior of the Robinson/Freyer/Hindriks model.
% Written by Christopher Thomas.


%
% Libraries and folders.


% Generated files get put in this folder.

outdir = 'output';


% Library paths.

% NOTE - These are specific to my test system; as long as you have the
% SynthRobinson library path and the Field Trip library path set up, you can
% remove these.
addpath('../../library');
addpath('../../../../neurolab/fieldtrip/fieldtrip-latest');


% Field Trip setup.

evalc('ft_defaults');
ft_notice('off');
ft_info('off');
ft_warning('off');
```

```
%
% Configuration.


% Pick a model to test.

model_name = 'hindriks';
%model_name = 'freyer';


% Switch for measuring operating points by simulation. This takes time.

want_sim = true;

sim_duration_secs = 30;
sim_startup_secs = 2;
sim_samprate = 10000;


% Loop detection. Any coupling weight smaller than this is treated as zero.

minweight = 0.01;


% Joint optimization of loop gains by adjusting coupling weights.

want_adjust_weights = false;

adjust_taulimit = 1.0;
adjust_bestfactor = 1.2;

% Default is 200 * paramcount, or about 1400.
% Set NaN or [] to keep the default.
%adjust_maxprobes = 100;
adjust_maxprobes = 10000;

% Joint optimization goal depends on the model.
if strcmp('hindriks', model_name)
  % Test perturbing Hindriks.
  adjust_goals = { 'ES', 'grow' };
else
  % Test perturbing Freyer.
  adjust_goals = { 'ES', 'biggest' };
% adjust_goals = { 'ES', 'decay' };
end


% Flags for reporting gradient measurements to console.

tattle_rate_gradients = false;
```

```
tattle_edge_gradients = false;
tattle_loop_gradients = false;



%
% Set up models and get metadata.

if strcmp('hindriks', model_name)
  disp('-- Using Hindriks 2023 model parameters.');
  [ modelparams intcouplings ] = synthRFH_getModelParamsHindriks();
else
  disp('-- Using Freyer 2011 model parameters.');
  [ modelparams intcouplings ] = synthRFH_getModelParamsFreyer();
end

regioncount = size(intcouplings,1);

[ indices_lut names_lut ] = synthRFH_getRegionInfo();
labels_from_indices = { names_lut.title };
letters_from_indices = { names_lut.letter };



%
% Get operating points by various methods.


% Simulation.

if want_sim

  disp('-- Measuring operating point by simulation.');
  tic;

  % Only simulate one population with no cross-coupling.
  popcount = 1;

  allrates = synthRFH_simulateNetwork( ...
    sim_duration_secs, sim_startup_secs, 1 / sim_samprate, ...
    modelparams, intcouplings, popcount, [], [] );

  allpotentials = synthRFH_getSigmoidInverse( allrates, ...
    modelparams.qmax, modelparams.threshlevel, modelparams.threshsigma );


  % NOTE - This assumes unimodal signals!
  % Signals that switch between several behaviors may give bad estimates.

  oprates = [];
```

```
  oppotentials = [];
  for ridx = 1:regioncount
    oprates(ridx,1) = mean(mean( allrates(ridx,:,:) ));
    oppotentials(ridx,1) = mean(mean( allpotentials(ridx,:,:) ));
  end


  durstring = helper_makePrettyTime(toc);
  disp([ '-- Simulation finished in ' durstring '.' ]);

  ratemsg = 'Real rates:              ';
  potmsg =  'Real potentials:        ';
  for ridx = 1:regioncount
    ratemsg = [ ratemsg sprintf('  %s: %.1f /sec', ...
      letters_from_indices{ridx}, oprates(ridx)) ];
    potmsg = [ potmsg sprintf('   %s: %.2f mV', ...
      letters_from_indices{ridx}, oppotentials(ridx)) ];
  end

  disp(ratemsg);
  disp(potmsg);

end


% Linear approximation.
% NOTE - This might wander outside the range of valid solutions!

[ oprates oppotentials ] = ...
  synthRFH_estimateOperatingPointLinear( modelparams, intcouplings );

ratemsg = 'Linear rates:            ';
potmsg =  'Linear potentials:      ';
for ridx = 1:regioncount
  ratemsg = [ ratemsg sprintf('  %s: %.1f /sec', ...
    letters_from_indices{ridx}, oprates(ridx)) ];
  potmsg = [ potmsg sprintf('   %s: %.2f mV', ...
    letters_from_indices{ridx}, oppotentials(ridx)) ];
end

disp(ratemsg);
disp(potmsg);


% Exponential approximation.
% NOTE - Fsolve works by black magic, so there are no guarantees about
% which solution it'll find out of the valid ones.

[ oprates oppotentials ] = ...
  synthRFH_estimateOperatingPointExponential( ...
```

```
    modelparams, intcouplings, [] );

ratemsg = 'Exponential rates:       ';
potmsg =  'Exponential potentials: ';
for ridx = 1:regioncount
  ratemsg = [ ratemsg sprintf('  %s: %.1f /sec', ...
    letters_from_indices{ridx}, oprates(ridx)) ];
  potmsg = [ potmsg sprintf('   %s: %.2f mV', ...
    letters_from_indices{ridx}, oppotentials(ridx)) ];
end

disp(ratemsg);
disp(potmsg);


% NOTE - We're keeping the exponential operating point for later use.



%
% Get loop information.


disp('-- Loop analysis:');

loopinfo = synthRFH_findLoops( modelparams, intcouplings, minweight );
edgegains = synthRFH_getEdgeGains( modelparams, intcouplings, oprates );
loopinfo = synthRFH_addLoopGainInfo( loopinfo, edgegains, {} );

[ looptext looptable ] = helper_makePrettyLoopTable(loopinfo);

disp(looptext);
save( [ outdir filesep 'loop-info-' model_name '.mat' ], ...
  'looptable', '-v7.3' );

disp('-- Finished loop analysis.');



%
% Gradient analysis.


disp('-- Computing gradients of potentials and firing rates.');

gradstep = 0.01;
zerohandling = 'nonzero';

[ rategrad potgrad ] = ...
  synthRFH_getOperatingPointGradient( ...
```

```
    modelparams, intcouplings, oppotentials, gradstep, zerohandling );

save( [ outdir filesep 'rate-gradients-' model_name '.mat' ], ...
  'rategrad', 'potgrad', '-v7.3' );

if tattle_rate_gradients

  disp('Firing rate gradients around exponential operating point:');

  for ridx = 1:regioncount
    disp([ '.. ' labels_from_indices{ridx} ':' ]);
    disp(rategrad{ridx});
  end

  disp('Potential gradients around exponential operating point:');

  for ridx = 1:regioncount
    disp([ '.. ' labels_from_indices{ridx} ':' ]);
    disp(potgrad{ridx});
  end

end


disp('-- Computing gradients of edge and loop gains.');

% We already have edge gains themselves from the loop analysis.
% Get the edge gain gradients.

edgegaingradients = synthRFH_getEdgeGainGradients( ...
  modelparams, intcouplings, oprates, rategrad );

% Add edge gain gradient information to the loop table.
% This computes loop gain gradients, storing in 'cyclegaingradient'.
loopinfo = synthRFH_addLoopGainInfo( loopinfo, edgegains, edgegaingradients );

edgesvalid = (abs(intcouplings) >= minweight);

save( [ outdir filesep 'edge-loop-gradients-' model_name '.mat' ], ...
  'edgegaingradients', 'edgesvalid', 'loopinfo', '-v7.3' );


if tattle_edge_gradients

  disp('-- Edge gains around exponential operating point:');

  disp(edgegains);

  disp('-- Edge gain gradients around exponential operating point:');
```

```
  for dstidx = 1:regioncount
    for srcidx = 1:regioncount
      if edgesvalid(dstidx, srcidx)

        disp([ '.. ' labels_from_indices{dstidx} ' <-- ' ...
          labels_from_indices{srcidx} ...
          sprintf( ' (gain %.3f):', edgegains(dstidx,srcidx) ) ]);
        disp(edgegaingradients{dstidx,srcidx});

      end
    end
  end

end


% Report loop gain gradients.

if tattle_loop_gradients

  disp('-- Loop gain gradients around exponential operating point:');

  for lidx = 1:length(loopinfo)
    thisrec = loopinfo(lidx);

    disp([ '.. Loop "' thisrec.label '" gain gradient:' ]);
    disp(thisrec.cyclegaingradient);
  end

end


disp('-- Finished gradient calculations.');



%
% Tune the model if requested.

if want_adjust_weights

  disp('-- Adjusting coupling weights.');
  tic;

  disp('.. Initial couplings:');
  disp(intcouplings);

  [ intcouplings opterr ] = synthRFH_optimizeCouplings( ...
    modelparams, intcouplings, loopinfo, adjust_goals, ...
    adjust_taulimit, adjust_bestfactor, adjust_maxprobes );
```

```
  disp('.. Final couplings:');
  disp(intcouplings);

  if (opterr > 0.1)
    disp(sprintf( '###  Optimization failed! Final error:  %.3f', opterr ));
  else
    % FIXME - Diagnostics.
    disp(sprintf( '.. Optimization succeeded. Final error:  %.3f', opterr ));
  end

  durstring = helper_makePrettyTime(toc);
  disp([ '-- Finished adjusting coupling weights (' durstring ').' ]);


  disp('-- Revised loop analysis:');

  loopinfo = synthRFH_findLoops( modelparams, intcouplings, minweight );
  edgegains = synthRFH_getEdgeGains( modelparams, intcouplings, oprates );
  loopinfo = synthRFH_addLoopGainInfo( loopinfo, edgegains, {} );

  [ looptext looptable ] = helper_makePrettyLoopTable(loopinfo);

  disp(looptext);

  disp('-- End of revised loop analysis.');
end



%
% This is the end of the file.
```

3.2 do_synth_robinson.m

```
% Example Code - Data synthesis using the Robinson/Freyer/Hindriks model.
% Written by Christopher Thomas.


%
% Libraries and folders.


% Generated files get put in this folder.

outdir = 'output';
```

```
% Library paths.

% NOTE - These are specific to my test system; as long as you have the
% SynthRobinson library path and the Field Trip library path set up, you can
% remove these.
addpath('../../library');
addpath('../../../../neurolab/fieldtrip/fieldtrip-latest');


% Field Trip setup.

evalc('ft_defaults');
ft_notice('off');
ft_info('off');
ft_warning('off');



%
% Configuration.


% Number of trials per test configuration.
trialcount = 10;

% Trial duration before and after "stimulation".
% Signal perturbations take about 1 second to settle after parameter changes.
trial_secs_before = 5;
trial_secs_after = 10;


% Sampling rates and filter parameters.
% Remember that we're generating firing rates, not an LFP. This pretty much
% _is_ rectified multi-unit activity.
samprate_sim = 10000;
samprate_mua = 2000;
mua_lowpass = 50; % Hz.


% Simulation parameters.

chancount = 4;

sim_startup_secs = 2;

% Explicity set this, rather than keeping the Hindriks baseline value.
% 0.07 gets us strong power spectrum peaks at harmonics, not just the
% fundamental mode, but can also go unstable and stay at the maximum rate.
mixture_coupling_coeff = 0.06;
```

```
% Factor by which to increase v_es when boosting activity. This is very
% sensitive; raising 1% or decreasing 2% has a very visible effect.
mua_enhance_coeff_factor = 1.01;
mua_suppress_coeff_factor = 0.98;

% Mixing is already gamma-delayed, so an extra delay isn't necessary.
mixing_delays_ms = zeros(chancount, chancount);


% Mixing matrices for various test cases.

% We have to keep each population's input consistent between cases, since
% behavior is very sensitive to it. Do this by having rows sum to consistent
% values but take contributions from different population distributions.

% Everything couples to everything. All links bidirectional.
mixing_matrix_uniform = ...
[ 0     0.333 0.333 0.333 ; ...
  0.333 0     0.333 0.333 ; ...
  0.333 0.333 0     0.333 ; ...
  0.333 0.333 0.333 0     ];

% 1-2 and 3-4, bidirectional.
mixing_matrix_routing_A = ...
[ 0 1 0 0 ; ...
  1 0 0 0 ; ...
  0 0 0 1 ; ...
  0 0 1 0 ];

% 1-4 and 2-3, bidirectional.
mixing_matrix_routing_B = ...
[ 0 0 0 1 ; ...
  0 0 1 0 ; ...
  0 1 0 0 ; ...
  1 0 0 0 ];

% 1-2-3-4-1, bidirectional.
mixing_matrix_loop_bidirectional = ...
[ 0   0.5 0   0.5 ; ...
  0.5 0   0.5 0   ; ...
  0   0.5 0   0.5 ; ...
  0.5 0   0.5 0   ];

% 1->2->3->4->1, directional.
mixing_matrix_loop_ascending = ...
[ 0 0 0 1 ; ...
  1 0 0 0 ; ...
  0 1 0 0 ; ...
  0 0 1 0 ];
```

```
% 1<-2<-3<-4<-1, directional.
mixing_matrix_loop_descending = ...
[ 0 1 0 0 ; ...
  0 0 1 0 ; ...
  0 0 0 1 ; ...
  1 0 0 0 ];



%
% Generate and save the synthetic trials.


% Get baseline simulation parameters.

[ modelparams_baseline intcouplings_baseline ] = ...
  synthRFH_getModelParamsHindriks;

% Override the default mixture coupling.
modelparams_baseline.mixturecoupling = mixture_coupling_coeff;


% Set up two epochs (before and after stimulation).

durationlist = [ trial_secs_before, trial_secs_after ];

modelparams = modelparams_baseline;
modelparams(2) = modelparams_baseline;

intcouplings = intcouplings_baseline;
intcouplings(:,:,2) = intcouplings_baseline;

% We never change this, so just make the original dual-epoch.
mixing_delays_ms(:,:,2) = mixing_delays_ms(:,:,1);



% Build test cases using two different baselines: uniform, and bidirectional
% loop.

% Uniform isn't actually that useful as a baseline, but include it anyways.
% The bidirectional loop is equal to the two routing states superimposed
% and to the two directed loop cases superimposed, so it's a better baseline.

baselinematrices = ...
  { mixing_matrix_uniform, mixing_matrix_loop_bidirectional };
baselinelabels = { 'unibase', 'loopbase' };
baselinetitles = { 'uniform', 'bidirected loop' };

muafactors = [ 1.0, mua_enhance_coeff_factor, mua_suppress_coeff_factor ];
```

```
mualabels = { 'baseline', 'strong', 'weak' };
muatitles = { 'baseline', 'stronger', 'weaker' };

mixcasematrices = { mixing_matrix_routing_A, mixing_matrix_routing_B, ...
  mixing_matrix_loop_ascending, mixing_matrix_loop_descending };
mixcaselabels = { 'routeA', 'routeB', 'loopup', 'loopdown' };
mixcasetitles = { 'routing state A', 'routing state B', ...
  'ascending loop', 'descending loop' };

[ idxlut namelut ] = synthRFH_getRegionInfo();

totaltime = 0;

for baseidx = 1:length(baselinematrices)

  disp([ '== Generating cases with ' baselinetitles{baseidx} ' baseline.' ]);

  mixing_matrix = baselinematrices{baseidx};
  mixing_matrix(:,:,2) = mixing_matrix(:,:,1);


  % Generate different strengths of MUA response. This includes the baseline.

  ves_baseline = intcouplings(idxlut.cortex_excitatory, ...
    idxlut.thalamus_specific, 2);

  for caseidx = 1:length(muafactors)
    disp([ '-- Generating ' muatitles{caseidx} ' MUA response.' ]);
    tic;

    intcouplings(idxlut.cortex_excitatory, idxlut.thalamus_specific, 2) = ...
      ves_baseline * muafactors(caseidx);

    ftdata = synthRFH_ftWrapper_simulateNetwork( ...
      trialcount, trial_secs_before, {}, true, ...
      durationlist, sim_startup_secs, 1 / samprate_sim, modelparams, ...
      intcouplings, chancount, mixing_matrix, mixing_delays_ms );

    fname = [ outdir filesep 'mua-' baselinelabels{baseidx} ...
      '-' mualabels{caseidx} '.mat' ];
    helper_writeFTData( fname, ftdata, modelparams, intcouplings, ...
      mixing_matrix, mixing_delays_ms, mua_lowpass, samprate_mua );

    totaltime = totaltime + toc;
    durstring = helper_makePrettyTime(toc);
    disp([ '.. Elapsed time: ', durstring ]);
  end

  % Restore the original couplings.
  intcouplings(:,:,2) = intcouplings(:,:,1);
```

```
  % Generate different routing states. Baseline is already covered.

  for caseidx = 1:length(mixcasematrices)
    disp([ '-- Generating response with ' mixcasetitles{caseidx} ...
      ' mixing.' ]);

    mixing_matrix(:,:,2) = mixcasematrices{caseidx};

    ftdata = synthRFH_ftWrapper_simulateNetwork( ...
      trialcount, trial_secs_before, {}, true, ...
      durationlist, sim_startup_secs, 1 / samprate_sim, modelparams, ...
      intcouplings, chancount, mixing_matrix, mixing_delays_ms );

    fname = [ outdir filesep 'mua-' baselinelabels{baseidx} ...
      '-' mixcaselabels{caseidx} '.mat' ];
    helper_writeFTData( fname, ftdata, modelparams, intcouplings, ...
      mixing_matrix, mixing_delays_ms, mua_lowpass, samprate_mua );

    totaltime = totaltime + toc;
    durstring = helper_makePrettyTime(toc);
    disp([ '.. Elapsed time: ', durstring ]);
  end

  % Restore the original mixing matrix.
  mixing_matrix(:,:,2) = mixing_matrix(:,:,1);

end

disp('== Finished generating cases.');

durstring = helper_makePrettyTime(totaltime);
disp([ '== Total elapsed time: ', durstring ]);



%
% Helper Functions


% This writes a Field Trip dataset and auxiliary metadata to a matlab file.
% The Field Trip dataset is filtered and downsampled before writing.

function helper_writeFTData( fname, ftdata_mua, modelparams, intcouplings, ...
  mixing_matrix, mixing_delays_ms, lowpass_corner, resample_rate )

  % Field Trip configuration structures.
  ftconfig_filt = struct( 'lpfilter', 'yes', 'lpfilttype', 'but', ...
    'lpfreq', lowpass_corner, 'feedback', 'no' );
```

```
  ftconfig_resample = struct( 'resamplefs', resample_rate, ...
    'detrend', 'no', 'feedback', 'no' );

  % Extract native-rate information that we want to keep.
  % NOTE - We know that synthRFH_makeFTDataFromMatrices() provides these.
  origheader = ftdata_mua.hdr;
  origconfigtrl = ftdata_mua.cfg.trl;

  % Filter and downsample.
  ftdata_mua = ft_preprocessing( ftconfig_filt, ftdata_mua );
  ftdata_mua = ft_resampledata( ftconfig_resample, ftdata_mua );

  % Save data and metadata.
  save( fname, 'ftdata_mua', 'origheader', 'origconfigtrl', ...
    'modelparams', 'intcouplings', 'mixing_matrix', 'mixing_delays_ms', ...
    '-v7.3' );

end



%
% This is the end of the file.
```