MVARX Demo

March 20, 2018

0.1 Simulate MVARX Data

In the following we use mvarx_data_gen to simulate a train of MVARX data.

First of all we load MVARX model parameters we estimated from past results.

```
In [1]: % load MVARX models estimated from Chang, et al. Front Hum Neurosci. 2012; 6: 317.
        load('mdl_cltd.mat', 'mdl_F3_FA_5m')
```

Then we set the model dimension and model parameters.

```
In [2]: m_ori = size(mdl_F3_FA_5m.Aw, 1);    % number of channel in the original model
        m = 3;    % number of channels we will be using in this simulation
        p = 3;    % MVARX AR order
        l = 10;   % MVARX feedforward length
```

```
In [3]: col_set = kron(ones(1, m), 1:p) + kron(0:m_ori:m_ori*(p-1), ones(1, m));
        A = mdl_F3_FA_5m.Aw(1:m, col_set);      % MVARX A matrix
        B = mdl_F3_FA_5m.Bw(1:m, 1:l);          % MVARX B matrix
        Q = 25 * mdl_F3_FA_5m.Qw(1:m, 1:m);     % MVARX Q matrix
```

Here we scale A properly so that A is stable and the time series don't blow up.

```
In [4]: while ~is_stbl(A)
            A = A * 0.9;
        end
```

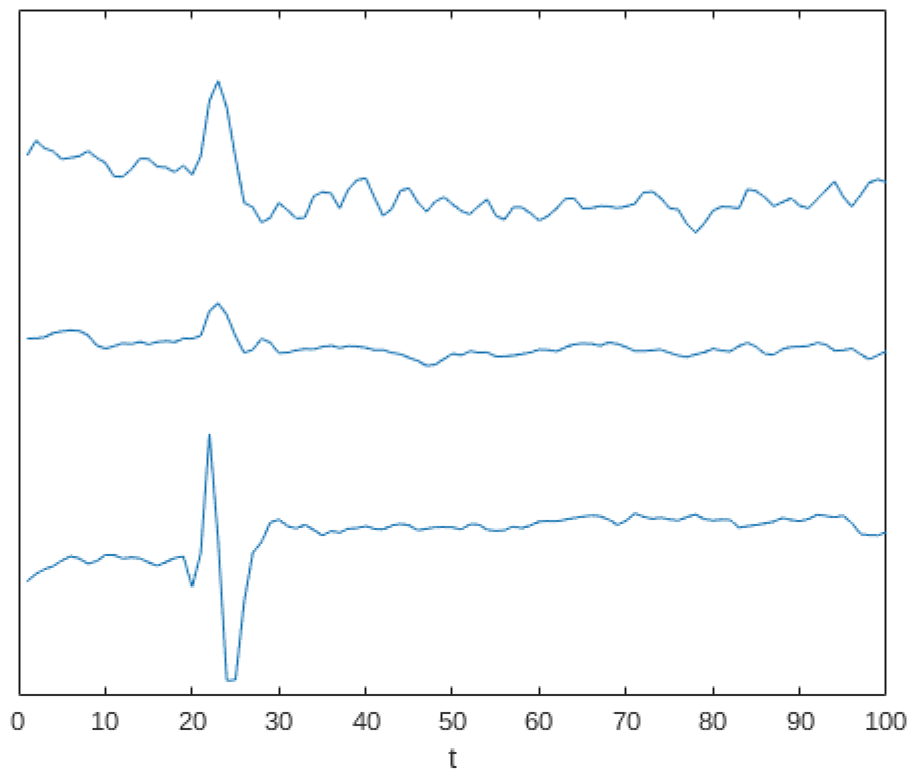
We use a train of 100 samples of stimulation input with the actual input being inserted at 20th sample.

```
In [5]: u = [zeros(1, 19), 1, zeros(1, 80)];  % train of stimulation
```

```
In [6]: X = mvarx_data_gen(A, B, Q, u);
```

Below we show waterfall plot of the three channels.

```
In [7]: wf_shift = (0:-20:(m-1)*(-20))';
        plot((X + wf_shift(:, ones(1, 100)))', 'Color', [31,120,180] / 255);
        set(gca, 'ytick', '')
        xlabel('t')
```



Now generate 20 epochs/trials of MVARX data.

```
In [8]: n_epoch = 20;
        X = cell(1, n_epoch);
        for i = 1:n_epoch
            X{i} = mvarx_data_gen(A, B, Q, u);
        end
```

```
In [9]: % create a 1-by-20 cell, each cell is the train of stimulation for the epoch
        u = num2cell(repmat(u, 1, 1, n_epoch), [1, 2]);
```

0.2 Estimate Model

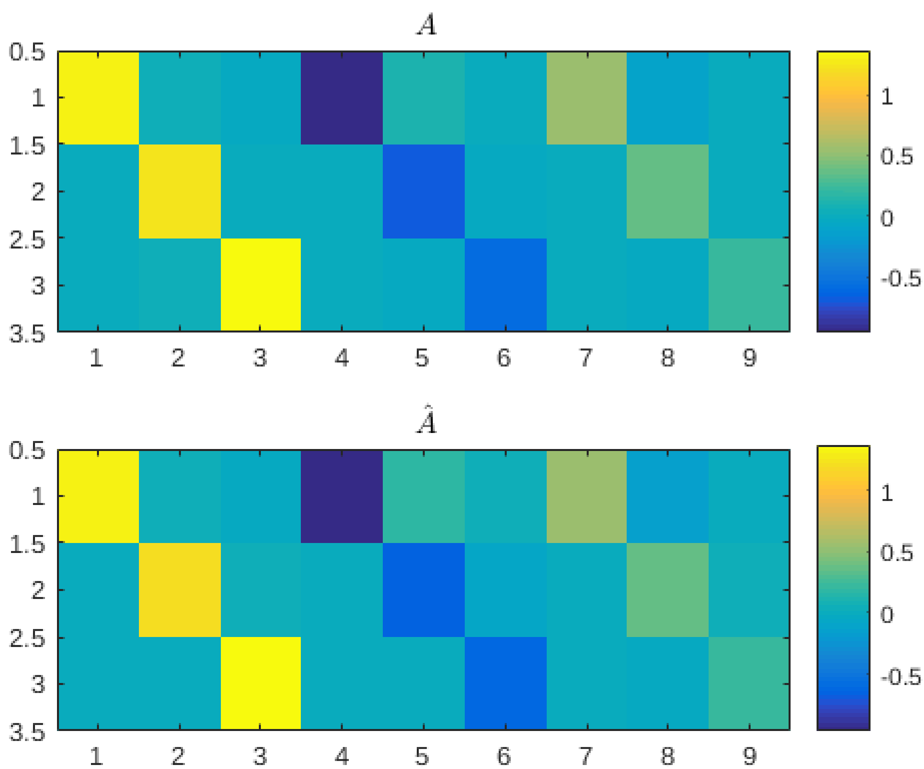
Secify the model dimensions of the model we would like to estimate.

```
In [10]: p = 3;
         l = 10;
```

```
In [11]: [A_hat, B_hat, Q_hat, W, n_spl] = mvarx_fit(X, u, p, l);
```

Now we show that the estimated A matrix A_hat is similar to the original A matrix.

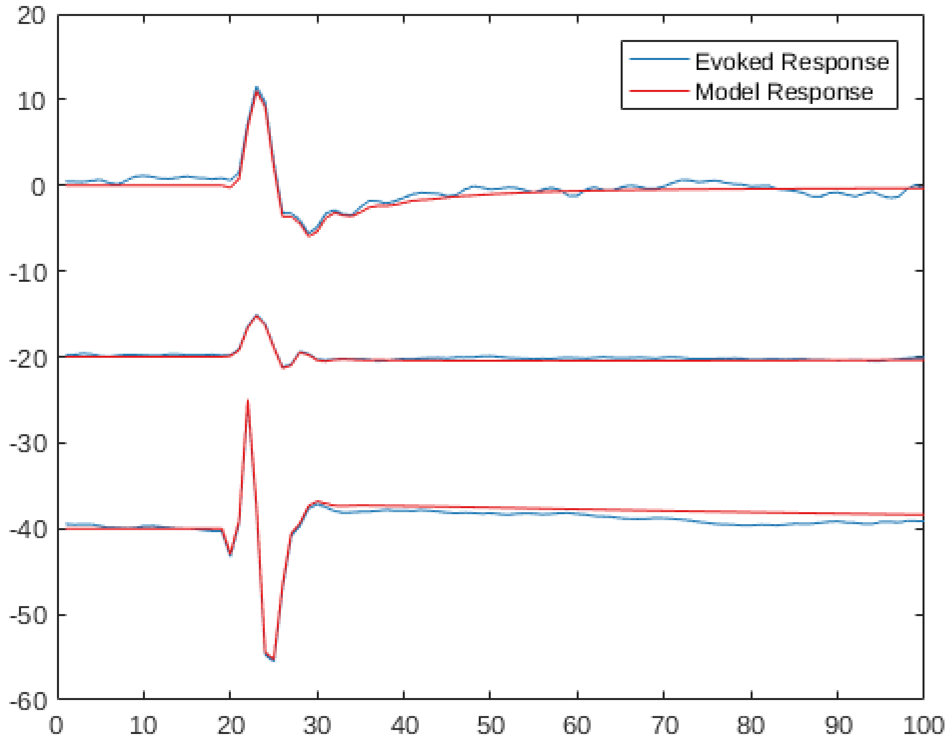
```
In [12]: cmin = min([A_hat(:); A(:)]);
         cmax = max([A_hat(:); A(:)]);
         subplot(211); imagesc(A, [cmin, cmax]); title('$A$', 'Interpreter', 'latex'); colorbar;
         subplot(212); imagesc(A_hat, [cmin, cmax]); title('$\hat A$', 'Interpreter', 'latex');
```



We can also generate model response with mvarx_data_gen.

```
In [13]: evoked_response = mean(reshape(cell2mat(X), m, size(u{1},2), []), 3);
         model_response = mvarx_data_gen(A_hat, B_hat, [], u{1}, 'evoked', true);
```

```
In [14]: wf_shift = (0:-20:(m-1)*(-20))';
         h1 = plot((evoked_response + wf_shift(:, ones(1, 100)))', 'Color', [31,120,180] / 255);
         h2 = plot((model_response + wf_shift(:, ones(1, 100)))', 'Color', [227,26,28] / 255);
         legend([h1(1), h2(1)], {'Evoked Response', 'Model Response'})
```



0.3 Check Residual Whiteness

In the output values of mvarx_residual_whiteness, H is the hypothesis statistics, which under H_0 (the residual is uncorrelated), should be a standard normal random variable. P is the p-value, which is computed as 2 * (1 - normcdf(abs(H)).

```
In [15]: [H, p] = mvarx_residual_whiteness(W{1})
```

```
H =

    0.5067


p =

    0.6124
```

There are five kernel functions ('kernel') available: 'TR' (Truncated), 'BAR' (Bartlett (default)), 'DAN', (Daniell), 'PAR' (Parzen), 'QS' (Quadratic-Spectral).

There are also five available memory length L ('L') for the statistics: '2', '3', 'log', 'n_to_point2' (default), 'n_to_point3'.

```
In [16]: [H, p] = mvarx_residual_whiteness(cell2mat(W), 'kernel', 'PAR', 'L', 'log')


H =

   -2.4129


p =

    0.0158
```