BJNL Matlab Toolbox User Guide

1 Introduction

The BJNL Toolbox consists of two panels, labeled BJNL and visualization, which allow application of BJNL to a dataset and visualization of the resulting estimates. This manual provides an explanation of how to use the different panels in the toolbox.

1.1 Opening the toolbox

To open the BJNL toolbox, navigate to the top level folder containing the file "BJNL.m", the user guide, and the various subdirectories. Start the toolbox either by entering:

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bjnl
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at the command prompt, or by opening BJNL.m and pressing run.

2 BJNL

The first panel of the toolbox is displayed in Figure 1. It provides the setup and implementation of the BJNL approach, as well as plots allowing the user to visualize the progress of the estimation procedure.

2.1 Setup

To start using the BJNL Toolbox, the user must:

1. Select a folder for the analysis. All output will be stored in this location.

2. Select the data for the analysis. The data must be in a .mat file in the format described in 2.1.1.

3. Select a prefix for the analysis (optional). If the user inputs a string here, all output files will start with that string.
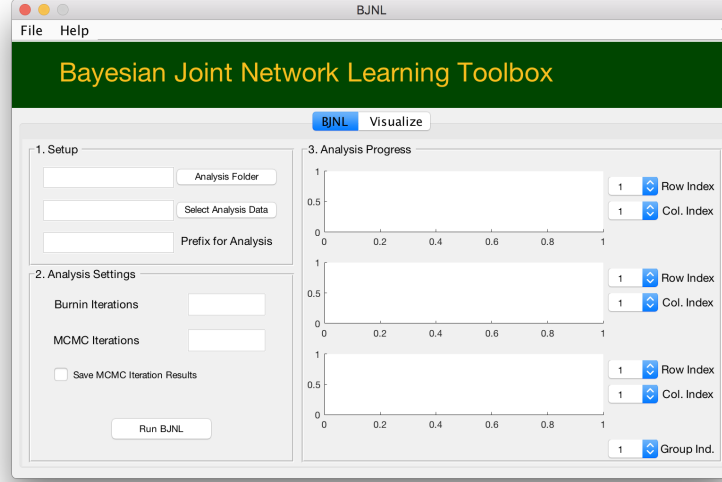
Figure 1: The BJNL panel in which the user inputs the data and runs the MCMC.

2.1.1 Data Structure

The BJNL Toolbox reads in a .mat file containing the following objects:

p The number of nodes/ROIs in the network.

N The number of groups in the analysis.

n A $N \times 1$ vector containing the number of observations in a single subject's data set for each group. For example, if each subject in Group 1 has 90 time points observed and each subject in Group 2 has 100 time points observed, then $n = [90, 100]$.

nsub A $N \times 1$ vector containing the number of subjects in each group.

SS A $p \times Np$ matrix containing the $p \times p$ covariance matrices for each group concatenated horizontally.

YY2 The $p \times max(n) \times nsub \times N$ matrix of subject level data.

z An $N \times 1$ array of platform membership. For example to compare two groups this object could be $[1, 0]$.

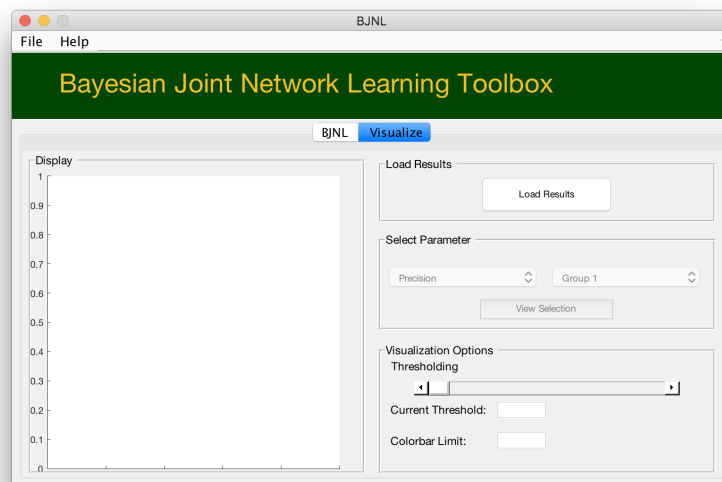Three example objects are included in the toolbox and can be found in the "examples" folder.

Figure 2: The visualization panel.

2.2 Analysis Settings

In the analysis settings panel, the user must select the number of burnin iterations and the number of MCMC iterations. The user can also select whether or not to "Save MCMC iteration results," an option that is disabled by default. If the user selects this option, then the output file will contain the results for all parameters at every MCMC iteration, not just the final estimates, which can be useful for visualizing the posterior distributions. Note that is the dimension is large or the number of iterations is large this filesize will grow very quickly.

2.3 Analysis Progress

This panel allows the user to monitor the progress of the MCMC algorithm. The user is presented with three trace plots, one for the precision matrix, one for the covariance matrix, and one for the tau term. The dropdown menus to the right of the plots can be used to select which elements of those matrices are being viewed, as well as what group to view.

3 Visualization

The visualization panel (Figure 2) allows the user to view the estimated precision, covariance, and adjacency matrices, as well as to quickly view differences between groups. Examples of the precision matrix viewer and adjacency matrix viewer are provided in Figure 3. When viewing precision or covariance matrices,

the user can utilize the "Visualization Options" control panel to threshold the matrices by either directly inputting a cutoff value or using a slider. Additionally, the user can manually adjust the colorbar limits.
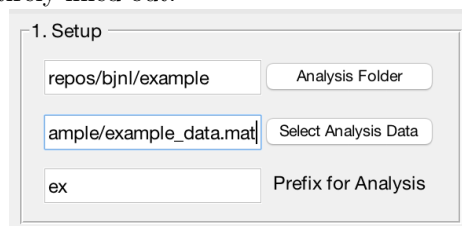
4   Example

In this section, we work through an example from start to finish using simulation data. The corresponding data is provided in the "Example" section of the BJNL folder.

Setting up the analysis

Three things are required for the analysis: an output folder, the data, and an analysis prefix.

We begin by selecting an analysis folder to which all output will be written. Clicking the "Analysis Folder" button opens a selection window. Our desired output folder is the "Example" folder, so we navigate to it and select "open."

Next, we click "Select Analysis Data" and navigate to the simulation data (stored in Examples/example data.mat). Select this to load the file. Finally, we add a prefix to the "Prefix" box. This prefix will be at the start of all output files from the analysis. At the end of the analysis setup, the first box should be entirely filled out:

Running the analysis

Moving on to the "Analysis Settings" panel, we next we input the number of burn-in iterations and the number of MCMC iterations. For our example we select 1000 and 5000. If we were interested in saving the samples from each iteration, we could also select "Save MCMC Iteration Results." However, this would result in a large file size so we leave the box unchecked for now. Clicking "Run" will start the algorithm.

We can track the analysis using the third panel. Each of the three figures will track a parameter value over the MCMC iterations. The first figure tracks elements of the precision matrix, the second tracks elements of the covariance matrix, and the third tracks variance parameters (which correspond to the spike and slab prior).

We can change which element is being viewed using the dropdown menus on the right side of the panel, and we can control which group's parameters are
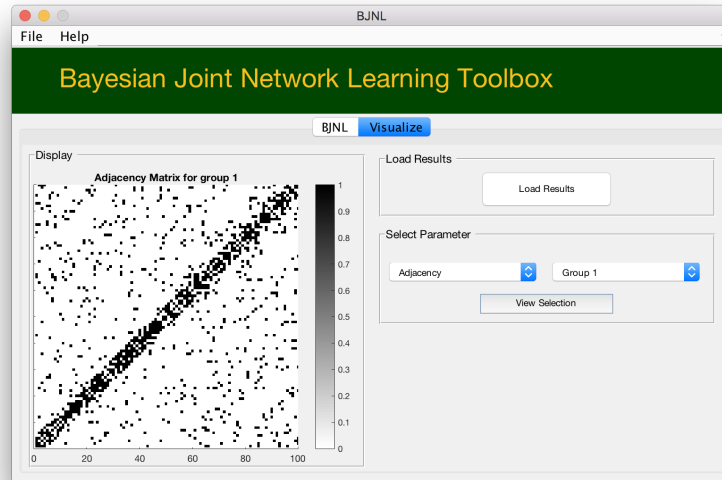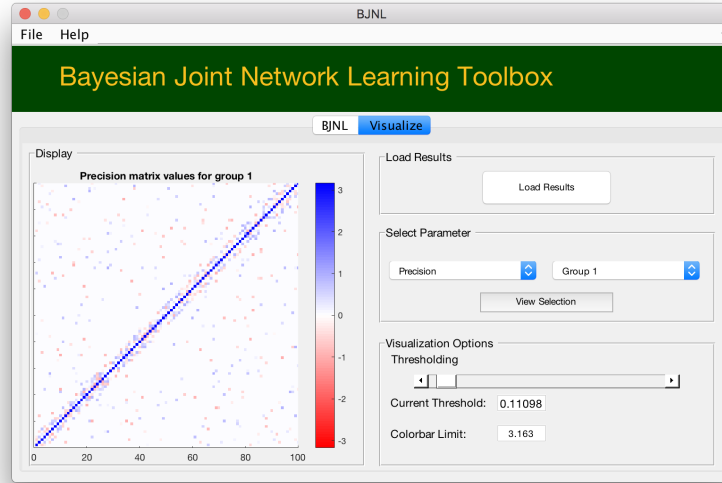
Figure 3: Examples of the visualization panel in which the user can view the estimated precision, covariance, and adjacency matrices for each group, as well as the differences between the two groups. The first panel displays the viewer output for the precision matrix and the second panel displays output for the adjacency matrix.

being viewed using the group dropdown menu at the bottom of the screen (see below).
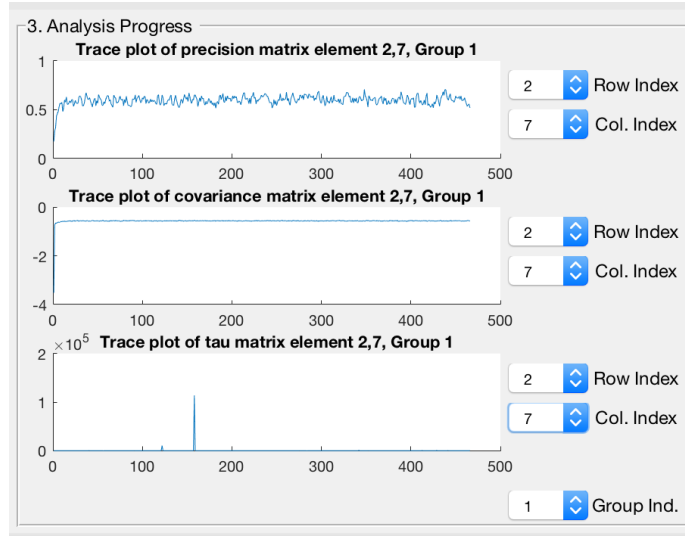
Visualizing results

After the algorithm terminates, the results are available in the second panel of the toolbox. To load the results, click on the "Load Results" button and navigate to the output folder. There will be a file there titled "ex_mcmc_results.mat" (in general the form is prefix_mcmc_results.mat). We select this file and can then visualize our output.

We can select between the precision, partial correlation, and adjacency matrices for each group using the "Select Parameter" panel. The results can then be viewed using the "View Selection Button." The figure on the left side of the GUI will then load the requested result. We can also threshold the result using the slider in the window. For example, the precision matrix output thresholded at 0.5 is provided below.