Distribution Agreement

In presenting this thesis or dissertation as a partial fulfillment of the requirements for an advanced degree from Emory University, I hereby grant to Emory University and its agents the non-exclusive license to archive, make accessible, and display my thesis or dissertation in whole or in part in all forms of media, now or hereafter known, including display on the world wide web. I understand that I may select some access restrictions as part of the online submission of this thesis or dissertation. I retain all ownership rights to the copyright of the thesis or dissertation. I also retain the right to use in future works (such as articles or books) all or part of this thesis or dissertation.

Signature:

_____ _____

Jin Ming Date

A Bayesian Approach for Dynamic Brain Network

By

Jin Ming

Master of Science in Public Health

Emory University

Rollins School of Public Health

Department of Biostatistics and Bioinformatics

_____ [Chair's signature]

Suprateek Kundu

Committee Chair

_____ [Member's signature]

Ying Guo

A Bayesian Approach for Dynamic Brain Network

By

Jin Ming

B.A. University of Nottingham, Ningbo, China, 2014

MSPH, Emory University

Rollins School of Public Health

2016

Thesis Committee Chair: Suprateek Kundu, Ph.D

An abstract of

A thesis submitted to the Faculty of the

Rollins School of Public Health of Emory University

in partial fulfillment of the requirements for the degree of

Master of Science in Public Health

in Biostatistics

2016

Abstract

A Bayesian Approach for Dynamic Brain Network

By Jin Ming

Functional magnetic resonance imaging (fMRI) has been widely used in brain network research. Functional connectivity (FC) measures how different brain regions contact with each other. Recently there has been an increased interest in understanding the dynamic manner in the functional connectivity. Although sliding window method is still the most widely used one, because of its limitations in window size pick and interpretation, many researchers are trying to create new method. Dynamic Connectivity Regression (DCR) is a data-driven method to detect temporal change points in different brain regions. However, DCR may fail to detect some change points and is hard to detect rapid change in functional connectivity. In this paper, we introduce our Bayesian approach which combines both change point detection and Bayesian method to detect the number and positions of change points in FC simultaneously. Our method is based on the change point in precision matrix instead of the mean value of time series. Screening method like screening and ranking algorithm (SaRa) is also included in our method to increase the computation speed. Different choices of change points combinations are also provided to get an accurate estimation. Two simulation show that our method can provide a good estimation of positions when the number of change points is given. In addition, we provide an experiment data which can be used to validate our method.

A Bayesian approach for dynamic brain network

By

Jin Ming

Master of Science in Public Health

Emory University

Rollins School of Public Health

Department of Biostatistics and Bioinformatics

Thesis Committee Chair: Suprateek Kundu, Ph.D

A thesis submitted to the Faculty of the

Rollins School of Public Health of Emory University

in partial fulfillment of the requirements for the degree of

Master of Science in Public Health

in Biostatistics

2016

Acknowledgments

I would like to express my deepest gratitude to my thesis advisor, Dr. Suprateek Kundu, who gave me an opportunity to explore the dynamic brain network. Also I thank him for excellent, detailed guidance, patience and help in guiding my thesis. I really learnt a lot in this work. In addition, Dr. Ying Guo gives me a lot of help in brain imaging research and thanks for her suggestions as my thesis reader.

In addition, I would also like to show my gratitude to Phebe Kemmer (Emory University), Jordan Pierce (University of Georgia) and everyone who have helped me in my thesis.

Finally, I would thank all faculty, staff, and students in the Department of Biostatistics and Bioinformatics at the Rollins School of Public Health. I really enjoy this two years' study and what I have learnt here will change my life.

Table of Contents

1. Introduction

Functional magnetic resonance imaging (fMRI) is a prominent non-invasive technique for studying brain activity. It measures the bold oxygenation level dependent (BOLD) signal as a correlation of neural activity. fMRI has been widely used for brain activity study because of its high spatial resolution and temporal resolution compared with other methods(Hutchison et al., 2013). Traditional researches implicitly assumed that the functional connectivity (FC) of brain was temporal static(Friston, 2011). However, this assumption has been questioned recently(Friston, 2011; Hutchison et al., 2013; Thompsona et al., 2014). Dynamic functional connectivity has been proposed as an extension of traditional FC that the statistical interdependence of different brain regions or signals may not be stable over time(Calhoun, Miller, Pearlson, & Adali, 2014; Cribben, Haraldsdottir, Atlas, Wager, & Lindquist, 2012; Hutchison et al., 2013; Lindquist, Xu, Nebel, & Caffo, 2014). The main problems of dynamic functional connectivity study using fMRI data are the high dimensional of data and its low signal-to-noise ratio(Allen et al., 2014). Normally there are over ten thousand of voxels and hundreds of time points for each single subject. And even after pre-processing, the noise may not be completely eliminated.(Hutchison et al., 2013; Lindquist et al., 2014)

Recently there are some studies in this area and the most popular one is sliding window analysis(Allen et al., 2014). In sliding window analysis, a time window of fixed length is selected to calculate the FC metric of different voxels. The presence of reproducible or

transient patterns of region-to-region correlation can be detected in this method. Normally, the correlation coefficients of different region of interests are calculated as the metric of function connectivity. However, based on the complexity of fMRI data, there are some limitations and concerns of sliding window analysis(Hindriks et al., 2016; Hutchison et al., 2013). First of all, it is difficult to interpret the existence of variability alone. Because of the low signal-to-noise ratio, the reliability of results is in query. The similar results through slicing window method can be replicated by a randomly generated white noise data. Secondly, the choice of window size, or length of time points, is hard to decide. Larger window size may permit robust estimation of FC and resolve the lowest frequencies of interest in signal. However, it may also ignore the potential interesting transients in functional connectivity. In contrast, smaller window size can capture possible transients but may fail to generate a good estimation of functional connectivity. Now most researches use 20-60 time points as potential window size.

There are also some other innovative methods for the study of dynamic functional connectivity. As mentioned before, one key limitation of sliding-window analysis is the choice of window size. The time-frequency analysis is one way to solve this problem. It can be applied to estimate the coherence and time shift between two different time series as a function of both time and frequency(Chang, 2011). By using the wavelet transform (WTC), it can provide a rich picture of the coherence across multiple time scales. However, the vast amount of information produced by a WTC analysis presents changelings when multiple subjects and brain regions are involved. Single-volume co-activation patterns(Liu

& Duyn, 2013), repeating sequences of BOLD activity(Majeed et al., 2012), and ICA are also being used in this area(Calhoun et al., 2014).

In 2012, Dr. Martin Lindquist et al(Cribben et al., 2012; Cribben, Wager, & Lindquist, 2013) generate one new method for dynamic functional connectivity study. This Dynamic Connectivity Regression (DCR) combined change point detection and graphical models into fMRI study. This DCR method can be used to detect temporal change points in functional connectivity and estimate the relationship between different regions of interests between two consecutive temporal change points. However, one problem of this method is that it can only detect the change in mean value of fMRI data. In fact, it is the functional connectivity of different voxels, or regions of interests, change over time instead of the mean value of each voxel. In addition, we think partial correlation, or precision matrix, is a better metric to show the functional connectivity of different ROIs than pairwise correlation matrix. Based on this understanding, we build our new dynamic change point method, which can be used to detect the number and position of change points in partial correlation matrix. And then our method can estimate the dynamic functional connectivity of each time bin through fMRI data.

2. Methods

The goal of our method is to detect temporal change point in functional connectivity of ROIs and then estimate a graph of different ROIs between consecutive temporal change

points. The method is based on multi subjects and we assume that they share same or similar dynamic functional connectivity and change points.

2.1 Problem setup

Assume there are N subjects. For each single subject, the dataset we are going to work with is a $T \times V$ matrix with

$$\tilde{y}_t = (y_{t1}, y_{t2}, \dots, y_{tV}) \qquad t = 1,2, \dots, T$$

Here we assume that there are V voxels and overall T time points. In addition, we assume that the partial correlations of V voxels are changed in some fixed time points. Suppose there are K change points and the partial correlations of voxels between any two consecutive change points are fixed. So there are K+1 bins and the partial correlation matrix between any two consecutive bins have some differences. The K change points are:

$$0 = t_0^* < t_1^* < \cdots < t_K^* < T$$

Under this setting, $\tilde{y}_t$ is a multivariate normal distribution with k change points:

$$\tilde{y}_t \sim \sum_{k=1}^{K} N(\eta_t \tilde{\mu}, \Sigma_k)\, I(t_{k-1}^* < t \le t_k^*)$$

Here I is the indicator function of t value, which belongs to time points t_{k-1}^* (not included) to t_k^* (included), or equivalent, in k`s bin. η_t is a scaling factor and is not affected by dataset. In addition, $\eta_t \in [0,1]$. $\tilde{\mu}$ is the a $1 \times V$ vector corresponding to the common mean of these V voxels. In addition, Σ_k, which is also the most important part, is the covariance matrix of V voxels in time bin k, which means in time period $(t_{k-1}^*, t_k^*]$. We assume that Σ_k follows Inverse-Wishart distribution as following:

$$\Sigma_k \sim W^{-1}(d\, I_V, b) \quad d \sim Gamma(a_d, b_d)$$

$b, a_d \; and \; b_d$ are fixed parameters. The main reason to use Inverse-Wishart distribution is that we don't need to make any assumption about the underlying dynamic functional connectivity, or graph(Kundu, n.d). We are going to use these N $\tilde{y}_t$ to estimate all K change points and K+1 covariance matrix and corresponding precision matrix, which shows the functional connectivity in each bin. Before introducing our method, I will briefly introduce some supporting theoretical foundation that are required for the development of our method. These include change point method and screening method.

2.2 Change points method

The problem of change points detection has been widely studied in various fields including statistics, biostatistics, engineering and economics(Eckley, Fearnhead, & Killick, 2011). Bhattcharya(Bhayyacharya, 1994) made an overview of this area. In his paper, there is a linear array of independent observations $Y_1, Y_2, \dots, Y_n$, whose distribution is going to change after Y_τ for some $1 < \tau < n$. The target is to detect and estimate change point, Y_τ. In 2003,Elliott (Elliott & Shope, 2003) combined Bayesian method with change point detection method to estimate the effect of a Graduated Driver`s Licensing Program in Michigan, U.S. All these methods were set for change detection in mean value of observations. However, there were only few methods used for detection of change points in covariance or precision matrix(Barnett & Onnela, 2014; Galeano & Pena, 2007). In addition, in normal case, both the number and the position of change points need to be estimated. And theoretically all time points are potential candidate for a change point, which makes the problem high-dimensional and computationally complexity(Barnett & Onnela, 2014; Chen & Gupta, 1997; Elliott & Shope, 2003; Wied & Galeano, 2013).

2.3 Screening method

As mentioned above, the huge number of potential candidate for a change point makes it hard in computation. In fMRI study, normally there are over 200 time points. Suppose there are 3 change points, for example, the number of possible combinations is over one million. So it is essential to shrink the sample pool of possible change points, which is the motivation of screening method. Screening is closely related to change point detection because the purpose of these two methods are similar in some cases(By Tracy Ke, Jiashun Jin, 2011). Niu and Zhang(Niu & Zhang, 2012) combined change points detection and screening method then created the screening and ranking algorithm (SaRa) for DNA copy number detection. Their assumption is that global screening is less efficient because time point Y_{100} may provide little information for the estimation of true value of Y_{10} if there is some change. A neighborhood around a change point can provide sufficient information for the detection.

2.4 Dynamic Change point method

In our method, we are going to estimate the number and the position of change points, and then estimate the dynamic functional connectivity in different time bins. There are K $T \times V$ matrix $\tilde{y}_t$ given as input data. In addition, a minimal distance between two change points, d, is needed for functional connectivity estimation. In our method we assume this minimal distance to be 10, which means that there are at least 10 time points between any two consecutive change points. However, this number can be changed under different situation and the impact of it is limited and will be showed in simulation part. The general steps of our method is as follows:

First of all, we use modified SaRa method to get a potential pooling for change points. As there are V voxels, we use modified SaRa for each voxel to get a potential pooling of time points and then make the union of them all. The purpose is to get all possible change points into our potential pool. We want to make sure that all true change points are in this final potential pool and some false positive is acceptable. For each voxel v $(v = 1,2, \dots, V)$ we calculate local measure D_{vt} at each time point $t = 1,2, \dots, T$ as:

$$D(vt) = \left| \frac{1}{h} \sum_{i=t}^{t+h-1} y_{iv} - \frac{1}{h} \sum_{i=t-h}^{t-1} y_{iv} \right|, \qquad h \leq d$$

here, h is a parameter of the length of neighborhood, or the number of time points being used for D. The first and last h time points are assumed to have 0 D measure because they don't have enough time points to calculate this measure.

After getting all $D(vt)$ values, we rank them in all local neighborhood as stated in Niu and Zhang(2012)`s paper and pick up the local maximal $\acute{D}(vt)$.

$$\acute{D}(vt) \geq D(v\acute{t}) \quad for\ all\ \acute{t} \in [t-h, t+h]$$

Let LM be the set of all time of local maxims. We finally pickup a subset S of LM through a thresholding rule. Then we get a pool of all possible values of change points, S.

Then we run Markov chain Monte Carlo (MCMC). We first estimate the number of change points. We assume that there may be at most 5 change points. Then we need to get the possibility of each number of change points. Based on the assumption that each combination of change points has same weight, we sample the number of change points.

Then we sample the location of change points. The posterior distribution of each combination of change points is as follows:

e.g. suppose there are k possible change points $t^* = (t_1^* \dots t_k^*)$, and the number of points in each bin are $(n_1, \dots, n_{k+1})$ separately, where $\sum_{i=1}^{k+1} n_i = T$, then we get $k+1$ different matrix for each time bin, denoted as $B_1, \dots, B_{k+1}$, the dimensions of each bin are $n_1 \times V, \dots, n_{k+1} \times V$ correspondingly. We take average of the B matrix for all N subjects to become the new B matrix. After that we calculate the correlation matrix and corresponding determinant, denoted as $u_1, \dots, u_{k+1}$,of that correlation matrix of each time bin. Then the posterior distribution of this combination of change points is:

$$p(Y|t^*) = \prod_{i=1}^{k+1} \{\log\left(\Gamma\left(0.5\times(30+n_i)\right)\right) + 0.5\times(30+n_i)\times u_i\}$$

Over thousands of time of iteration in MCMC, we get thousands of estimations of number of change points and corresponding positions. Here we used two different methods to get the final estimation of both number and position of change points. In the first method, we try to make our decision of change points based on the frequency of different combinations. In this method, we pick up two combinations that showed up most times. The main reason for us to pick up two combinations is that we found in some cases the show up time of these two combinations are quite close. And we want to make sure that our method could correctly find out the true number of change points and corresponding positions. In the second method, we want to make our decision by combining all information through our MCMC process. We first calculate the show up number of different change points. Then for the most frequent one, we calculate the mean value of positions.

After we get the estimation of both number and positions of change points through the process described above, the dataset is separated into several different bins. Then we get the estimation of precision matrix, as well as partial correlation, in each time bin based on the corresponding voxel values in that time bin. As we set the minimal value of time length in each time bin, we have enough time points to get a reasonable precision and correlation matrix.

2.5 Dynamic Connectivity Regression (DCR) method

In this section, we are going to briefly introduce Dynamic Connectivity Regression (DCR) method, which is also the main competing method. DCR method works as following: First of all, they calculate covariance matrix of all ROIs using full time length. Then they use Bayesian Information Criteria (BIC) to get a sample precision matrix with minimal BIC. This minimal value of BIC is recorded. Afterwards, they split the full time length into two consecutive parts and calculated the combined BIC based on the previous two steps. If some split points have the minimal combined BIC over all possible combinations and this combined BIC is lower than the recorded full BIC, then this time point is chosen as the split time point and the full time length is successfully separated into two parts. This DCR procedure continues by using the same method above until each separate time length can not be split any further. Finally, the chosen split time and corresponding graph in each time bins are calculated. When testing for multiple subjects, like N subjects, and each of them have a $T \times V$ matrix of fMRI data. DCR will combine all these matrices by row to generate a big $NT \times V$ and then use use the procedure described above.

3. Simulation

3.1 simulation design

To assess the performance of dynamic change point method, a series of simulations was performed. All simulations are based on multiple subjects, which is also the target dataset of our method. These two simulations are used to test the ability of our method to detect the real locations of change points when the number of change points are given. DCR method is also used in each simulation as a comparison method with our method. As this paper only gives a simplify version of the whole method, our simulations are based on fixed number of change points. More simulations will be provided in the future.

For each subject, we generate a dataset with 200 time points and 15 region of interests (ROIs). This is the representative of real data that we may face in fMRI study. We believe that it is unrealistic to assume a completely different functional connectivity of each time bin in the fMRI time series. It may be more reasonable to assume that there are some functional connectivity changes from one bin to the next. Based on this assumption, we generate our simulated data as the following: we first generate a completely random precision matrix (or functional connectivity) for the first bin. For the precision matrices in the following time bins, each time there are some edges changed from the previous precision matrix while all the others keep the same. After the generation of all precision matrices, a 200×15 matrix is generated by precision matrix as the time line we are going to test. In addition, as we are dealing with multiple subjects, in each simulation, we set

there are 25 subjects in total and all of them share the same number and position of change points.

For two simulations, we assume that there are only two change points and we want to test whether our method could detect these two change points. As stated above, there are 15 ROIs and 200 time points. In the first simulation, we set real change points to be 65 and 160. It is a normal case and each bin have over 40 time points to estimate the functional connectivity. In the second simulation, the real change points are time 25 and time 95. The first time bin has only 25 time points and our minimal length of each bin is set to 20. We want to test the ability of detecting rapid change in time.

3.2 Experimental data

In this section, we are going to talk about one real data analysis. The data was taken from Jordan et al`s (2016) research in cognitive control of saccade task. Saccade tasks are frequently used in study of cognitive control. There are two kinds of saccade tasks, prosaccades (rapid eye movements towards a stimulus) and antisaccades (movements to the mirror image location of a stimulus). In this study, one task consisted of repeating blocks of prosaccades, antisaccades, and fixation is provided. There were 30 right-handed, health participants (mean age = 19.5 years, SD (standard deviation) = 3.7 years) and 10 of them are males. All participants had no experience of major psychiatric disorders or substance abuse and metal implants. The blocked task consisted of repeating 20 second blocks of fixation, 10 prosaccade trials and 10 antisaccade trials. The fixation within the saccade blocks lasted for 500 ms before each trial. In conclusion, this is a circulation of

10s of prosaccade trials and 10s of antisaccade trails with fixation before each trail. Based on previous studies, the blood oxygenation level dependent functional magnetic resonance imaging (BOLD fMRI) will be stronger in prosaccade trails than antisaccade trails. The main purpose of using this block design study is to validate our method by correctly detecting the change point.

4. Results

Figure 1A shows the result of first simulation. By choosing two combinations of change points showed up most times, our method could give an estimation close enough to real change point position. There are totally 342 possible change points combinations in our method and both of these two mood combinations show up over 20 times out of 5000 iterations in MCMC. The estimation of mean value is also close to the real change point position. In contrast, for DCR method, as there are 25 subjects, there should be 75 change points for the enlarged 5000×15 matrix. However, it could only detect 43 change points. In addition, the mood estimation of DCR method does not works better than our method.

Real Change Point Position	Estimation of Change Point Position by our method			DCR (mood value of each change point)
	Mood 1	Mood 2	Mean	
65	62	63	69	69
160	164	161	156	164

Figure 1A.

Result of simulation 1. There are two change points (time 65 and 160) out of all 200-time length. We assume that we know there are only two change points. Mood 1 is the combination of change points that show up most times. Mood 2 is the combination of change points that show up second most times. Mean is the mean estimation of position over all MCMC procedure. DCR method provide the mood estimation of each change point.

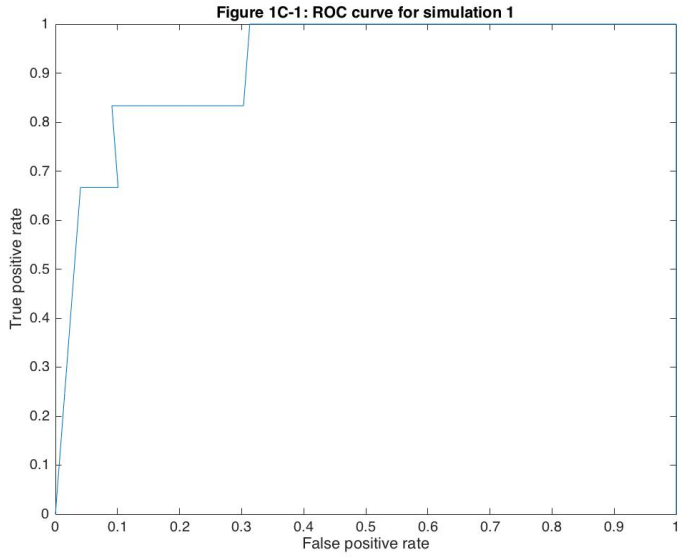
Figure 1B shows the result of the second simulation. Simulation 2 is used to test the ability of our method to detect the fast change, where there are only 25 time points in the first bin. Mood 1 provides a quite good estimation of both position, although mood 2 and mean estimation has a higher value for the first position of change point. For DCR method, there should be 25 changes at first change position (time 25). However, it could only detect 4 times of this change position and the value is much higher than the real value. It shows that there maybe some problem for DCR method to detect fast changes or short time periods in some time bins.

Real Change Point Position	Estimation of Change Point Position by our method			DCR (mood value of each change point)
	Mood 1	Mood 2	Mean	
65	22	32	36	29
160	96	94	96	94

Figure 1B.

Result of simulation 2. There are two change points (time 25 and 95) out of all 200-time length. We assume that we know there are only two change points. Mood 1 is the combination of change points that show up most times. Mood 2 is the combination of change points that show up second most times. Mean is the mean estimation of position over all MCMC procedure. DCR method provide the mood estimation of each change point.

Another goal of our method is to provide an estimation of dynamic functional connectivity, Figure 1C is the receiver operating characteristic (ROC) curve of simulation 1 and simulation 2. ROC curve is generated based on comparing true precision matrix with our estimated precision matrix based on mood1 estimation of change points. The value under ROC are 0.9192 and 0.7318 respectably. Thus our method can give an accurate estimation of the dynamic functional connectivity.



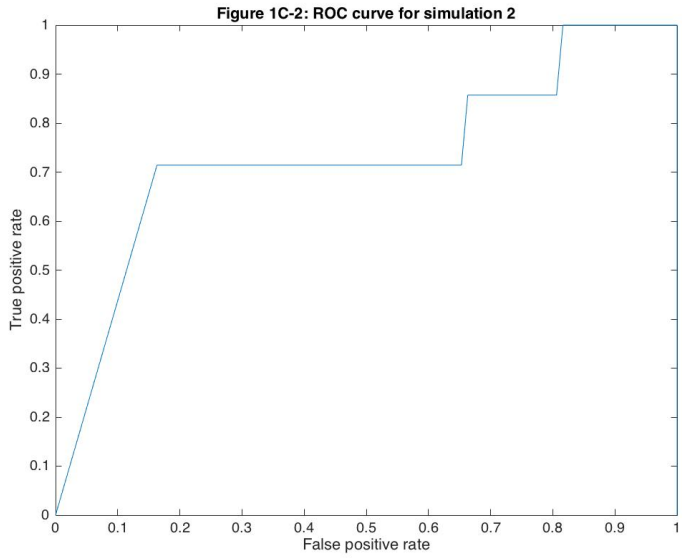


Figure 1C.

ROC curve based on simulation 1 and simulation 2.

5. Discussion

In this thesis, we introduce a new Bayesian method to detect both number and positions of change points in dynamic fMRI data, and then to estimate the dynamic functional connectivity. Compared with other methods to detect dynamic functional connectivity, our method is based on the change in precision matrix, or functional connectivity, of fMRI data. Most dynamic functional connectivity methods now assume that there is change in the mean value of dataset and they are trying to capture this change in mean. There was no method dealing with change in functional connectivity, or precision matrix directly. In addition, it assumed that all subject share same location of change points and the functional connectivity share some similarity between any two consecutive time bins. Although many other methods assumed mostly different functional connectivity for any two time bins.

Based on the simulation, our method can successfully detect the position of change point when the number of change points is given. Although the positions of change points are not the same with real position, in most cases the difference is less than 3 time points. In addition, compared with DCR method, which is another change point detection method used for dynamic functional connectivity. Our method works much better to detect all change points and can better handle short time bins situation. In addition, in terms of estimating dynamic functional connectivity. Our method works quite well and can detect correct edge.

However, there are also some limitations for our method. First of all, we provide two different methods to choose final change points. The mood method works better than mean one. However, just as mentioned above, the final choice of combination of change points are in a close neighborhood of real value. It would be better if we could choose the true value of combination. Secondly, in the simulation of our work, we have only tried the cases where we know the number of change points. When the number of change points is unknown, the performance of our method still need to be check. Thirdly, although our method works better than DCR in detecting the true value of change points. It takes longer time than DCR method. For simulation 1, DCR method takes about 1 minute and our method takes about 10 minutes. This only consider the two change point case. If more change points are being considered, the computation time will even increase more. The effectiveness of computation still need to be improved. Finally, our method based on the assumption that all patients share the same dynamic functional connectivity and change points. This is also a normal assumption for most paper in the area of dynamic functional connectivity. However, whether this assumption is correct still needs to be verified.

This works is just a simplified version of our method to detect change points based precision matrix. In the future, we are going to do more real data analysis and extend our method for more possible numbers of change points. And we will try to estimate the number and position of change points simultaneous. In addition, to data, we have tried at most 20 ROIs. In terms of dealing with more complicated data, the number of ROIs need to be increased. Besides, the assumption of same change points among all subjects will be tested also.

In sum, our method of Bayesian approach to detect dynamic brain networks is capable to detect position of change points when the number of change points is given. Compared with most other dynamic functional connectivity methods, it can directly work with precision matrix instead of mean value of each voxel. In addition, the limit assumption of data makes this method suitable in other areas including economy, finance, and engineering.

Reference:

Allen, E. A., Damaraju, E., Plis, S. M., Erhardt, E. B., Eichele, T., & Calhoun, V. D. (2014). Tracking whole-brain connectivity dynamics in the resting state. *Cerebral Cortex*, *24*(3), 663–676. http://doi.org/10.1093/cercor/bhs352

Barnett, I., & Onnela, J.-P. (2014). Change Point Detection in Correlation Networks. *Nature Publishing Group*, (2), 23. http://doi.org/10.1038/srep18893

Bhayyacharya, P. K. (1994). Some Aspects of Change-Point Analysis, *23*(1980).

By Tracy Ke, Jiashun Jin, J. F. (2011). Covariance Assited Screening and Estimation, *72*(2), 181–204. http://doi.org/10.1038/nature13314.A

Calhoun, V. D., Miller, R., Pearlson, G., & Adali, T. (2014). The Chronnectome: Time-Varying Connectivity Networks as the Next Frontier in fMRI Data Discovery. *Neuron*, *84*(2), 262–274. http://doi.org/10.1016/j.neuron.2014.10.015

Chang, C. (2011). Time-frequency dynamics of resting-state brain connectivity measured with fMRI, *50*(1), 81–98. http://doi.org/10.1016/j.neuroimage.2009.12.011.Time-frequency

Chen, J., & Gupta, a. K. (1997). Testing and locating variance changepoints with application to stock prices. *Journal of the American Statistical Association*, *92*(438), 739–747. http://doi.org/10.2307/2965722

Cribben, I., Haraldsdottir, R., Atlas, L. Y., Wager, T. D., & Lindquist, M. A. (2012). Dynamic connectivity regression: Determining state-related changes in brain connectivity. *NeuroImage*, *61*(4), 907–920. http://doi.org/10.1016/j.neuroimage.2012.03.070

Cribben, I., Wager, T. D., & Lindquist, M. a. (2013). Detecting functional connectivity change points for single-subject fMRI data. *Frontiers in Computational Neuroscience*, *7*(October), 143. http://doi.org/10.3389/fncom.2013.00143

Eckley, I. A., Fearnhead, P., & Killick, R. (2011). Analysis of Changepoint Models. *Bayesian Time Series Models*, (January), 205–224. http://doi.org/10.1017/CBO9780511984679.011

Elliott, M. R., & Shope, J. T. (2003). Use of a Bayesian changepoint model to estimate effects of a graduated driver's licensing program. *Journal of Data Science*, *1*(1), 43–63.

Friston, K. J. (2011). Functional and effective connectivity: a review. *Brain Connectivity*, *1*(1), 13–36. http://doi.org/10.1089/brain.2011.0008

Galeano, P., & Pena, D. (2007). Covariance changes detection in multivariate time series. *Journal of Statistical Planning and Inference*, *137*(1), 194–211. http://doi.org/10.1016/j.jspi.2005.09.003

Hindriks, R., Adhikari, M. H., Murayama, Y., Ganzetti, M., Mantini, D., Logothetis, N. K., & Deco, G. (2016). Can sliding-window correlations reveal dynamic functional connectivity in resting-state fMRI? *NeuroImage*, *127*, 242–256. http://doi.org/10.1016/j.neuroimage.2015.11.055

Hutchison, R. M., Womelsdorf, T., Allen, E. A., Bandettini, P. A., Calhoun, V. D., Corbetta, M., … Chang, C. (2013). NeuroImage Dynamic functional connectivity : Promise , issues , and interpretations. *NeuroImage*, *80*, 360–378. http://doi.org/10.1016/j.neuroimage.2013.05.079

Kundu, S. (n.d.). Efficient Bayesian Regularization for Graphical Model Se- lection, 1–

24. Unpublished

Lindquist, M. A., Xu, Y., Nebel, M. B., & Caffo, B. S. (2014). Evaluating dynamic bivariate correlations in resting-state fMRI: A comparison study and a new approach. *NeuroImage*, *101*, 531–546. http://doi.org/10.1016/j.neuroimage.2014.06.052

Liu, X., & Duyn, J. H. (2013). Time-varying functional network information extracted from brief instances of spontaneous brain activity. *Proceedings of the National Academy of Sciences of the United States of America*, *110*(11), 4392–7. http://doi.org/10.1073/pnas.1216856110

Majeed, W., Magnuson, M., Hasenkamp, W., Schwarb, H., Schumacher, E. H., Barsalou, L., & Keilholz, S. D. (2012). Spatiotemporal dynamics of low frequency BOLD fluctuations in rats and humans, *54*(2), 1140–1150. http://doi.org/10.1016/j.neuroimage.2010.08.030.Spatiotemporal

Niu, Y. S., & Zhang, H. (2012). the Screening and Ranking Algorithm To Detect Dna Copy Number Variations. *The Annals of Applied Statistics*, *6*(3), 1306–1326. http://doi.org/10.1214/12-AOAS539SUPP

Thompsona, G. J., Merritta, M. D., Pana, W.-J., Magnusona, M. E., Groomsa, J. K., Jaegerb, D., … Garth. (2014). Neural correlates of time-varying functional connectivity in the rat, 1–28. http://doi.org/10.1016/j.neuroimage.2013.07.036.Neural

Wied, D., & Galeano, P. (2013). Monitoring correlation change in a sequence of random variables. *Journal of Statistical Planning and Inference*, *143*(1), 186–196. http://doi.org/10.1016/j.jspi.2012.06.007