1. I'd like to give a talk under the title of "Statistical models …" I would like to dedicated to Professor Yanai of St. Luke College of Nursing for his longstanding dedication in research, friendship, and mentorship. Specifically,I'dlike to discuss two such models, both of which have been recently developed in our quantitative psychology lab at McGill. Both models are based on structural equation models (SEM), currently very popular in psychology and other social sciences.
2. So let me start with a brief introduction to SEM. We often collect multivariate data to characterize objects of our concern from a variety of perspectives. We may have some idea about how those variables are related. SEM essentially tries to assess how plausible our hypotheses are in the light of empirical data. It existed in different guises for long time, e.g., path analysis in sociology and simultaneous equation methods in econometrics. One important ingredient was added to the methodology when it was brought into psychometrics, i.e., latent variables (hypothetical constructs) were introduced to simplify the relationships among observed variables.
3. Here is an example of SEM that I often use to teach SEM. This was taken from an introductory text by Prof. Toyoda of Waseda Univ. There are 4 food variables measuring average daily intakes of CAL, meat, alchohol, and milk products, which are highly correlated with each other. So we think there must be something common underlying all of these variables. Let's call it tentatively the "western style diet (D)." There are also two variables related to the mortality rate by cancer (lower intestine and rectum cancers). They are also highly correlated, and so again we think there must be something common underlying these variables. Let's call it the "proness to cancer in lower digestive organs (C)." We have two LVs, and we may assume that (D) affects (C), i.e., high scores on (D) will incur high rates of death by cancer in LDO. There are two kinds of models involved; one representing the relationships between observed and LV, called the measurement models, and the other specifying the relationships between LVs, called structural models. (SEM always consist of these two kinds of models.) If we fit the data, we get estimates of regression coefficients, indicating the strength of influence from one variable to another. I'd like you to look at this number, .98, indicating that that more than 95% of the variability in (D) can be explained by (D). This is indeed amazing, but wait a minute. Can we unequivocally interpret the result as indicating that (D) is bad for your health because it increases the chance of dying by cancer? Another totally different interpretation is also possible: (D) is good and so it makes people live longer, long enough to die by cancer. This points to an intrinsic limitation of this methodology you always have to keep in your mind when you use it. The model considers only six those variables; there could be a host of other

variables, such as overall wealth, average life span, accessibility to health care systems, etc. that may be able to explain away at least some of the high predictability of (C) by (D).

4. We use this SEM idea to construct methods of analysis of fMRI data. These methods are useful to reveal how functionally specialized areas interact and how these interactions depend on changes of experimental context. Here is an example of analyzing effective connectivity. First, a number of specific brain regions are selected based on a hypothesis about their importance in completing a given task. Here, V1, V5, and SPC are selected. The selected brain areas are called regions of interest, in short, ROIs. And then, their directional relationships in response to cognitive tasks are modeled and tested. In the framework of SEM, we have observed variables which are the records of activations (BOLD signals) in voxels in ROIs, representative variations of which are captured by LV corresponding to the ROIs. The relationships between the observed variables (voxel activations) and the LVs (ROIs) are captured by measurement models. The relationships between the ROIs (LVs) are captured by structural models.
5. Here are the functional neuroimaging data. Five BOLD signals in each of the three ROIs are presented as functions of time. These are observed variables. It can be seen that although there is a bit of variability among the voxels in each ROI, there is also some common variability across voxels within a ROI. This common variability is deemed representative of neuronal activities in the ROI, and is represented as a latent variable.
6. Structural models not only capture contemporaneous effects among ROIs (which are all bidirectional in this case), but also time-lagged effects (the effects of activations in a ROI at previous time points on the current activations), and possibly some stimulus effects given during the data collection. The dotted curves indicate autoregressive (time-lagged) effects, and u_j's indicate stimulus effects. There are two kinds of stimulus effects; u_1 directly affects ROi_1 (\gamma_1), while u_2 and u_3 affects connections from ROI_1 (V1) to ROI_2 (V5), and from ROI_3 (SPC) to ROI_2 (V5), respectively. The latter are called modulating effects of stimuli, and are captured by interactions between the stimuli and LVs (ROIs).
7. If we put them in the form of equations, we have …. There are 3 measurement equations corresponding to the 3 ROIs (LVs), and 3 structural equations representing all the features that I just described.
   These are the contemporaneous bidirectional effects.
   These are the time-lag effects (which make the model dynamic; Matrix S_1 will be explained shortly.)
   This is the direct effect of u_1.
   These are the modulating effects of u_2 and _u_3.

8. This describes what S_1 is like. It basically defines the (time-lagged) effect of t -1 on t. (The S_j for any j >1 can be defined similarly.)
9. Here is an illustration of the stimulus effect. A stimulus is given at two specific time points, which are convolved with hemodynamic response function to create this function (done by a routine provided in SPM) which serves as a direct input to the SEM.
10. Hemodynmic functions corresponding to the three stimuli are depicted here. (Visual stimulus, some of them are with motion, and some with attention prompt).
11. To summarize the features of the structural models used in the present study:
12. Model fitting: Parameters in the entire model (both measurement and structural) are estimated in such a way that the errors in prediction are as small as possible.
13. We use the bootstrap method to assess the reliability of estimated parameters. One problem in using a standard bootstrap method is that the observations are serially correlated. To circumvent the problem, we use the MMBB method in which we resample blocks of observations instead of individual observations.
14. Here are the results of analysis:
    6 contemporaneous effects – all significant
    Only 1 time lagged effect is significant out of 3
    The direct effect of u_1 on V1 is significant
    Neither of the two modulating effects of stimuli (u_2 and u_3) are significant.
15. To confirm the results of stimulus effects are sensible, we present time series for stimuli, ROIs, and their interactions:
16. Here I another example. example demonstrates that our approach can fit as complex model as this (unlike other predecessors). There are 7 ROIs, which are assumed contemporaneously and bidirectionally affected with each other, and in which time–lag effects of order 1 of ROIs on themselves. No stimulus effects.
17. Here are the results. Some assumed effects were not significant. This example is to demonstrate that our method can fit a model as complex as this unlike its predecessors (e.g., unified SEM, extended unified SEM).
18. There are several advantages with the method presented so far:
19. There are also some limitations as well:
20. By the latent interaction we mean this. We initially thought this would complicate the algorithm considerably, but it has turned out to be quite simple.
21. Multiple subjects – Why?
22. Multiple subjects

23. Second model (GCANO) -- Model features; some explanations for multiple-set canonical correlation analysis(?)
24. The bootstrap method: More straightforward
25. An example data set
26. Multiple-group structure – equality constraints
27. Analyses
28. Result 1 (One group, 30 subjects): These are the activations at 7 ROIs most representative of all subjects. All ROIs are simultaneously excited and de-excited. Not so exciting a result for us.
29. Result 2 (Multiple groups; 15 subjects in each of the two groups; completely separate analyses): ROIs activations are almost entirely different across the groups, except perhaps ROI4 (CL-R). Correlations are still high among ROIs within the groups. The schizophrenic group is more variable, and a bit heterogeneous than normal control.
30. We applied the second order PCA to the 14 ROIs (7 in each of the 2 groups) extracted in the second analysis. As we briefly remarked, ROI4 in the schizophrenic group is more highly correlated with the 7 ROIs in the normal group.
31. \gamma_4 equated across groups.
32. Future prospects
33. Acknowledgement
34. Thank you for your attention!