Group-level statistics on EEG effective source connectivity

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PURPOSE

Independent component analysis (ICA) is an useful solution for EEG analysis to transform scalp channel signals into effective EEG source activities. It is particularly useful to perform multivariate causality analysis because ICA addresses issues of volume conductance and scalp mixing that make scalp channel signals highly correlated and spatially blurred. However, one of drawbacks of the use of ICA is that it complicates the group-level statistics because ICA reveals individual differences and the results are inconsistent in number of components as well as their locations. Here, we demonstrate how to address this inconsistency issue that raises in the group-level analysis. The basic concept of this solution, called Network Projection, can be found in Nima Bigdely-Shamlo's PhD dissertation.

METHOD

Subjects Participants were 45 children (26 patients with Chronic Tic Disorder, 19 healthy controls) between the ages of 8-12 years old recruited for an project ran by Dr. Sandra Loo (UCLA).

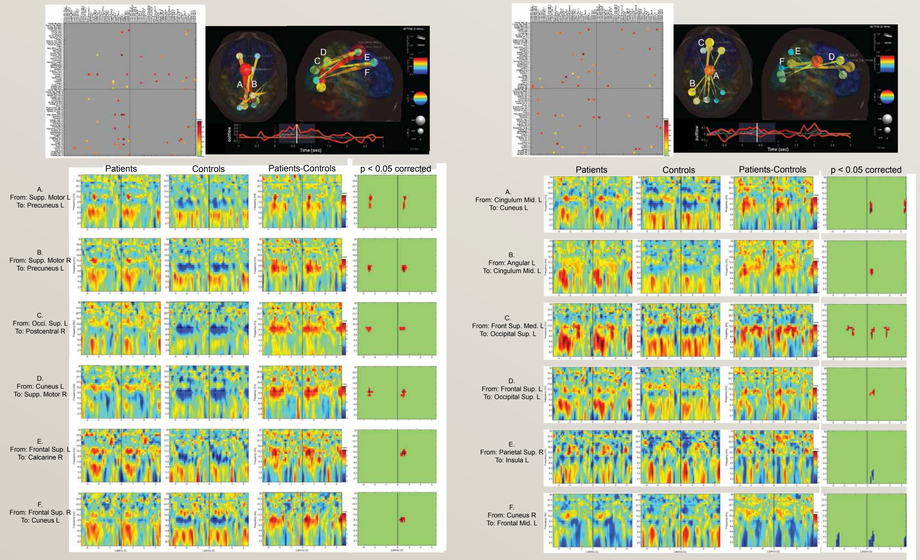
Task The subject's task was to perform an eye blink to an visual cue for every 3 seconds.

Preprocessing After cleaning using ASR [1], about 55 trails were left across all the subjects. Data were epoched to -4 to 4 second windows relative to blink cue onset. Adaptive mixture ICA (AMICA) was performed for decomposition, and only brain EEG components were selected manually (**Figure 1**).

Source Information Flow Analysis EEGLAB [2] Source Information Flow Toolbox (SIFT) [3] was used. Only top 10 ICs sorted by variance were used. Sliding window with1.5 s width was stepped every 0.1 s. Vieira-Morf was used to compute multivariate autoregressive modeling. The model order was estimated to be 9 i.e. the time lag of 90 ms. Renormalized partial directed coherence (rPDC) was computed to estimate causal information flow. 30 frequency bins were generated which was logarithmically scaled from 2 to 45 Hz.

Group-level analysis Dipole locations of all subjects were smoothed with 3-D Gaussian kernel with FWHM 14.2 mm. The cloud of dipole density was segmented into 76 anatomical AAL-defined regions [4]. The pairwise dipole density was weighted with rPDC (**Figure 2**). **This provides 76x76 connectivity matrix for each subject, thus eliminates the inconsistency problem at the group-level statistics.** The final data was 5-D matrix of 76 x 76 x 30 x 65 x 40, which is 76 x 76 = 5776 connectivity edges, each of which has 30 frequency bins x 65 time points, and for 40 subjects. The data were pre-selected: 1) Connectivity edges that has at least 60% of subjects contributes more than 0.00001 % dipole pair density. This selected 993 and 1515 edges (17% and 26%), 57% and 68% of total dipole pair density for Control and Patients, respectively; 2) The time-frequency rPDC values across subjects for the selected edges were submitted to bootstrap statistics with 10,000 iteration. For multiple comparison correction, Generalized Family-Wise Error Rate (GFWER) was used. During the bootstrap statistics, two-tailed 1-, 5-, and 10-percentile t-scores of the time-frequency map of the edge were stored for later correction across edges. For example, if 100/5776 edges were pre-selected, 10,000 surrogate values of 1-, 5-, and 10-percentile t-scores were combined into each of 10,000 x 100 distributions, and their 1-, 5-, and 10-percentile t-scores were used for global correction across all time-frequency points of all edges (**Figure 3**).

RESULTS



For both left and right figures, the top left panel shows 76-by-76 connectivity matrix with statistically significant results (GFWER p<0.05, u=10, minimum cluster size k=5); the top right panel shows a frame from a movie pointing to a latency where statistically significant information flows are maximal in the healthy subjects; the bottom paneles shows representative edges (rows) for patients (left column), controls (second from left), their difference (third from left), and significance mask (right column). The results showed that the envelopes of information flows in control subjects showed typical time course, while that in patients was less structured and disturbed.

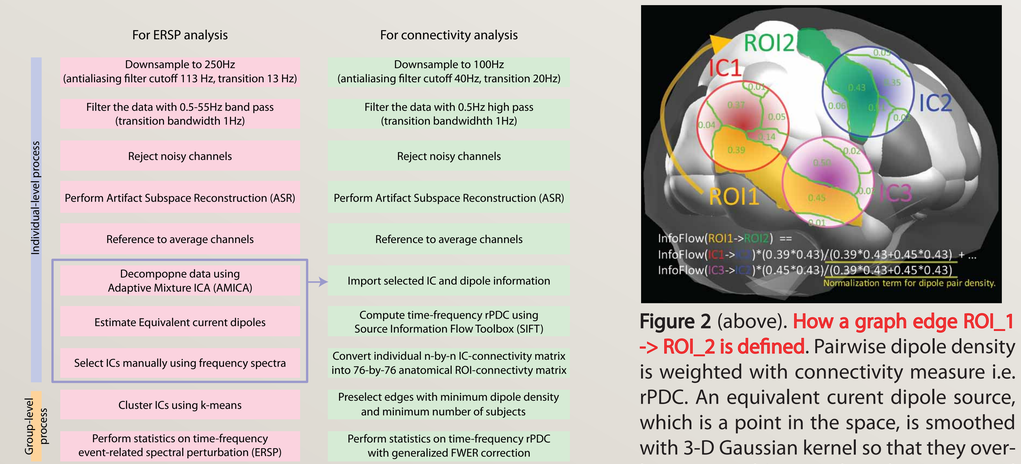


Figure 1 (above). Preprocessing pipeline for the scalp channel signal.

Figure 2 (above). **How a graph edge ROI_1 -> ROI_2 is defined.** Pairwise dipole density is weighted with connectivity measure i.e. rPDC. An equivalent curent dipole source, which is a point in the space, is smoothed with 3-D Gaussian kernel so that they overlap across subjects and can be segmented into pre-defined anatomical ROIs.

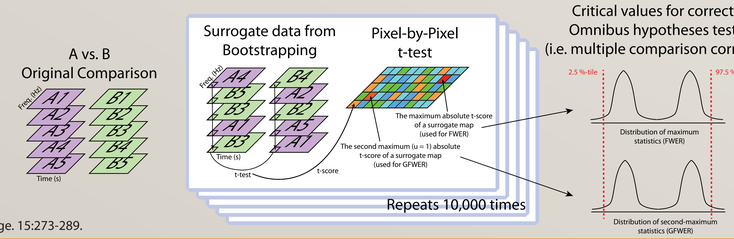


Figure 3 (left). Schematics of generalized family-wise error rate (GFWER) correction. Near-maximum statistics of bootstrap surrogate data is saved for every iteration to generate a distribution, whose critical values can be used to correct multiple tests.

CONCLUSION

We demonstrated that a collection of individualized information flows across ICA-decomposed effective EEG sources can be integrated into a 5-D structure which allows straightforward group-level statistics. It has been a common practice that after some processing, IC activations are projected to scalp channels again to ensure consistency across subjects. However, mixing ICs contradicts the purpose of ICA to address issues of volume condactance and scalp mixing. The merit of the proposed solution is that it does not need, in any way, to project ICs to channels while addressing individual differences.

The data used here was presented as a separate poster with a focus on clinical significance. Abstract Title: Neural connectivity and cortical activation in chronic tic disorders. Session Title: Movement Disorders. Session Number: 311. Session Time: 11/14/2016 8:00-9:00 AM. Posterboard Number: M12. Contact: ktung117@gmail.com

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