Subcortical structures in resting state fMRI: uncovering functional networks involving deep-brain structures using non-local mean denoising at 1.5T′

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PURPOSE

In functional magnetic resonance imaging (fMRI), it is challenging to detect and validate activations in key sub-cortical areas such as the thalamus, given their poor SNR due to susceptibility artifacts caused by partial volume effects of surrounding tissues (GM/WM interface). This is especially true on relatively low-field clinical MR systems (e.g. 1.5 T). One way to overcome this situation is by using a spatial denoising technique used in structural MRI and more recently in diffusion and functional MRI called non-local means (NLM) denoising [1]. Here, we build on these task-related fMRI results by investigating whether NLM can also help in identifying functional networks involving subcortical structures in resting state fMRI at 1.5 T.

METHODS

We previously collected 4 separate fMRI datasets in 22 healthy subjects using a standard echo-planar imaging (EPI) sequence [1]: 35 axial image slices, 64 × 64 matrix, TR/TE 2730/40 msec, voxel size 3.438 × 3.438 × 4.2 mm. Data were acquired in a box-car format, with subjects alternating between baseline and task conditions via short auditory cues (30 sec rest, eyes closed, and 20 sec task, repeated 5 times and ending with a rest epoch, total of 4 min and 40 sec). Tasks were (1) a left (FTL) and (2) right (FTR) rapid alternating finger tapping sequence and (3) an eyes open-closed (EOC) sequence. We also obtained a (4) resting-state fMRI (RS) for functional network analysis. The preprocessing of all datasets, described thoroughly in a previous work [1], was done using AFNI [2]. The task-based activation maps were obtained following the NLM preprocessing pipeline, thought RS analysis was carried out using both Gaussian smoothing (GS) and NLM for comparison purpose: GS consisted of slice timing and motion correction, 5 mm gaussian spatial smooth and band-pass temporal filtering (0.008 to 0.1 hz). For the NLM pipeline, we replaced the GS with NLM denoising (Rician noise compensation), implemented in Dipy [4,5]. We combined the resulting activation maps of FTL and FTR to create a symmetric map of finger tapping activation (FT), which was then registered to the RS dataset using ANTS [1,3]. We used these maps to create regions of interest (ROIs) to initiate seed-based RS correlations maps: since there are 13 seeds for FT and 3 for EOC, each subject has 13 FT and 3 EOC seed RS-maps. In order to remove the bias from seed location, the seed and its surrounding area were excluded for each seed RS-maps. We then define the task-based RS networks by averaging all seed RS-maps related to a task. This process was repeated for every subject, for both the GS and NLM pipeline. The mean network of all subjects is finally computed for both pipelines.

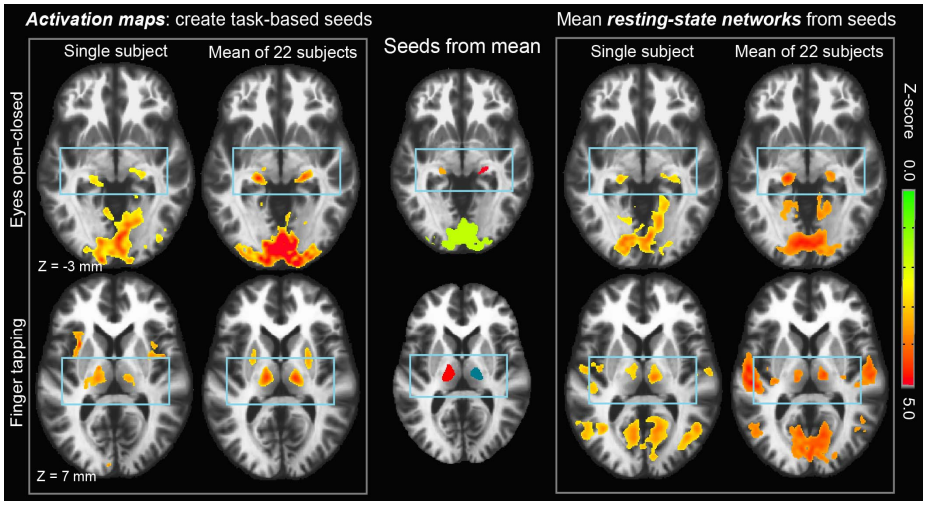

FIG. 1: TASK vs NETWORK. Comparison of mean and single-subject activation maps and resting state networks obtained using task-based seed points. Each resulting network is obtained by computing the mean of all seed-based networks (3 seeds for EOC, 13 for FT).

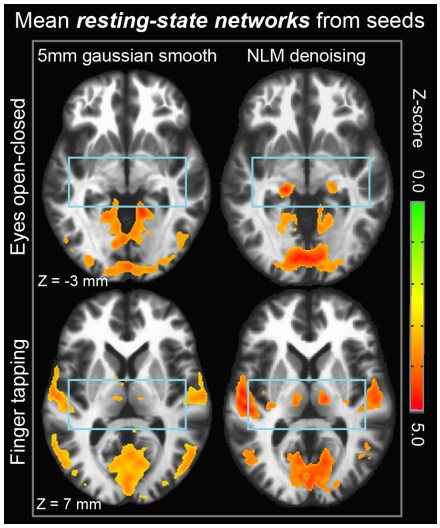

FIG. 2: GAUSSIAN vs NLM. Comparaison of resting-state networks obtained by the Gaussian pipeline and by non-local mean denoising. NLM easely integrates thalamic activity in corresponding networks.

RESULTS

Fig. 1 shows the NLM activation maps for EOC and FT in a single representative subject and the group-average (left). The ROIs used for seed-based RS analysis (middle) and resulting task-based RS networks are also shown (right). Fig.2 illustrates the difference between the group average of the Gaussian and NLM task-based RS networks obtained for both task.

DISCUSSION & CONCLUSION

The comparison between the task activation in the occipital region and the thalamus for the EOC task, shown in Fig.1 for both for the single-subject and the mean average, illustrates how well NLM can recover the LGN part of the thalamus into the EOC network: in fact, the similarity between the network-based activation and the task-based activation (Fig.1 left vs right) validates the efficiency of the method. Fig.2 demonstrates how the Gaussian smooth is not sufficient to uncover these areas as opposed to NLM. The same can be interpreted from the FT task. For both tasks, additional ROIs are uncovered outside of the thalamus (Fig.1-2); during cognitive task, only parts of one or multiple networks are activated, defining our seed points, while in resting state the whole networks containing the seed points are uncovered. By example, on Fig.1 for the FT task, the activation seen on the RS network images is part of two known functional networks, motor and sensory (according to Neurosynth [6]), while in the FT task activation map the lateral areas where not solicited. In addition, Fig.2 shows that even if seeds are located in the thalamus, in the GS pipeline, the signal is interpreted as noise in this area and cannot be correlated to their corresponding network, as opposed the NLM pipeline. This technique can be extended to non-task related analysis by using anatomically-defined ROIs (e.g. freesurfer); using known functional network (default, sensory, motor, etc.) cortical ROIs as seed points, we could easily uncover additional related regions in sub-cortical areas. Hence, this approach would better isolate the functional networks of the brain, especially in deep-brain areas, using unsupervised resting-state acquisitions on clinical 1.5 T scanners. This could be useful in clinical studies where localization of sub-cortical networks is required in patients unable to preform motor/cognitive tasks.

REFERENCES

[1] Bernier et al., Front. Hum. Neuro., 2014 [2] Cox et al., JBI, 1996 [3] Avants et al., PICSL, 2009 [4] Coupe et al., IEEE trans. Med. Im., 2008 [5] Garyfallidis et al., Front. In Neuroinf., 2014 [6] Yarkoni1et al., Nature, Methods, 2011