BACKGROUND

DBS network mapping is a technique that correlates whole-brain normative functional connectivity profiles seeded from DBS sites with clinical improvements. The result has often been reported in form of a map of optimal connectivity, expressed by voxel-wise correlation coefficients (“R-maps”), and these maps have been reported across disorders such as Parkinson’s Disease (PD), Essential Tremor (ET) and Obsessive Compulsive Disorder (OCD). However, given intrinsic correlational structures within the functional connectome of the human brain, it remains unclear how different the profiles of R-maps could theoretically be. To probe how specific the results of DBS network mapping could potentially be for subthalamic DBS, we apply DBS network mapping to synthetic data that can systematically probe profiles for hypothetical optimal stimulation sites within the entire nucleus.

METHODS

250 synthetic volumes of tissue activated (VTA) and 1000 ground-truth spherical sweetspots were randomly and symmetrically generated across the bilateral STN. Iterating across sweetspots, based on the spatial overlap between each VTAs and the respective sweet spot, (synthetic) improvement scores were assigned to each synthetic VTA. Functional connectivity (FC) analysis was performed by seeding individual VTAs in the GSP1000 normative connectome, and R-maps were generated by correlating connectivity profiles with (synthetic) improvements. This led to 1000 R-maps, each associated with one (synthetic) sweet-spot.

RESULTS

1000 R-maps associated with each of 1000 sweetspots were subjected to a principal component analysis. Resulting principle components represent the potential 'connectivity landscape' that could result from any type of STN-DBS network mapping analysis (no matter which target, disease or clinical outcomes).

With four PCs, 98.5% of the total variance across the 1000 R-maps could be explained (PC1: 67.2%, PC2: 25.4%, PC3: 4.94%, PC4: 1%).

Spatial correlation between PCs and 1000 R-maps revealed 4 distinct patterns that could theoretically emerge from subthalamic DBS network mapping (no matter which target, disease or clinical outcomes).

CONCLUSIONS

Based on synthetic modeling, DBS network mapping seems able to reveal only four different spatial maps, which were distributed across (synthetic) optimal stimulation sites along the anterior-posterior axis of the nucleus. Our results help identify potential patterns associated with responses from DBS to the subthalamic nucleus.