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Optimizing Sample Size and Statistical Methods for Probabilistic Sweet Spot Mapping in Deep Brain Stimulation.

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Abstract

Deep Brain Stimulation (DBS) for movement disorders can greatly benefit from the insights provided by probabilistic mapping. This consists in the application of statistical approaches to stimulation data of multiple patients. Such analysis is influenced by the input data and chosen statistical method, hindering the generalizability of the obtained results. This study aims at determining the minimum sample size yielding stable results, and the statistical approach providing higher results consistency. Intra-operative stimulation test data of 36 patients who underwent DBS surgery for Parkinson's Disease (PD), were used to compute Probabilistic Sweet Spots (PSS). The PSS were calculated with sample sizes ranging from 4 to 36 (steps of 2) using Bayesian t-test, Wilcoxon test with False Discovery Rate correction and Wilcoxon test with nonparametric permutations correction. Calculations were repeated 10 times. Obtained PSS were compared in terms of size and position variability across sample sizes and between statistical methods. Only the PSS computed with the Bayesian t-test reached stability in all the three chosen metrics. Stability in size and centroid location was reached from a sample size of 14 patients, while the covered volume (Dice coefficient) stabilized from a sample size of 18 patients. The Bayesian t-test also provided higher results consistency with respect to the other approaches. The composition of the dataset in cohorts with <20 patients has a greater influence on the extent and location of computed PSS. Moreover, the Bayesian t-test demonstrated the highest suitability to extrapolate results from analyses involving small sample sizes.

Clinical relevance

Determining the minimum number of patients and most suitable method to calculate stable PSS is crucial for ensuring the reliability and clinical applicability of Probabilistic Mapping approaches. This ensures the generalizability of findings, allowing for a more accurate understanding of the underlying pathology. These insights can be used to refine diagnostic approaches and optimize clinical interventions, ultimately improving patient care.