Abstract
Recently, Hidden Markov Models (HMM) have been used for the identification of spike sources in Parkinson’s disease treatment. Usual classification criteria consists in maximum a posteriori rule (MAP) for the recognition of the correct class. However, classification could be improved using proximity analysis, transforming matrices of Markov process to another space where similarities and differences are better revealed. The authors present the proximity analysis approach using HMM for the identification of spike sources (Thalamo and Subthalamo, Gpi and GPe). Results show that proximity analysis improves recognition performance for about 4% over traditional approach.

Keywords
Parkinson’s Disease, hidden markov models, proximity analysis, principal component analysis.