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Non-invertibility of basal ganglia network calls for new biomarkers

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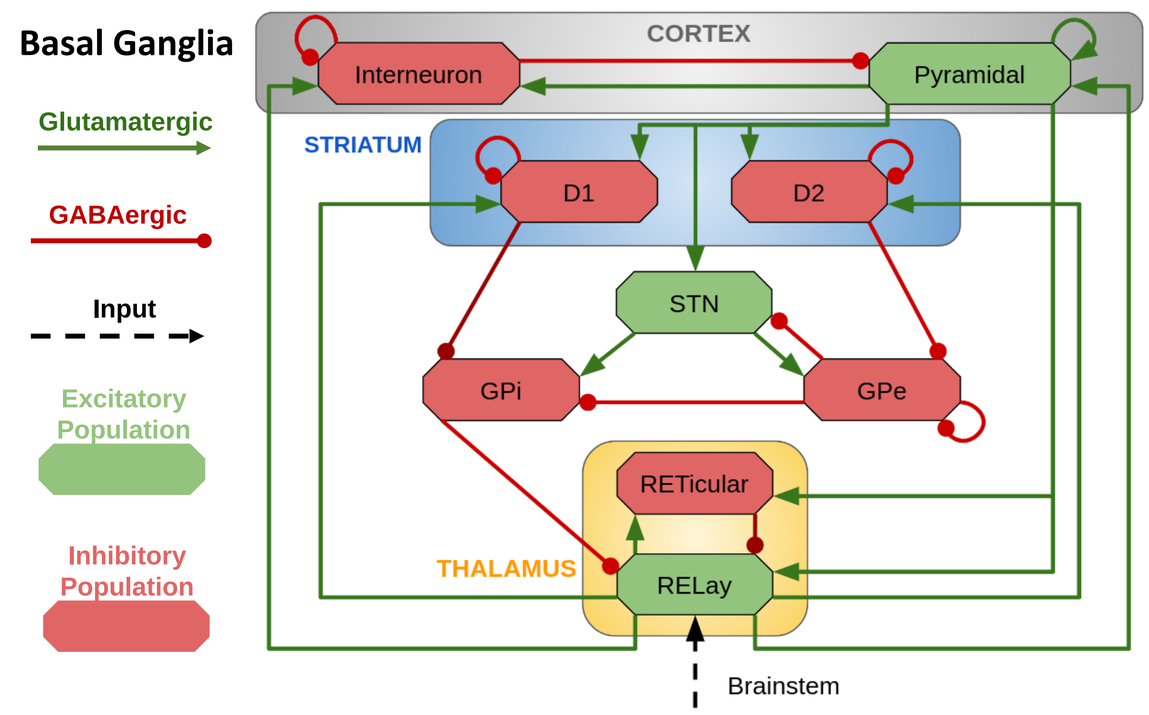
INTRODUCTION

- Mathematical models of the basal ganglia (BG) partition the parameter space based on the parkinsonian biomarkers into healthy and pathological (P-conformal)
- We show that biomarkers alone, do not constrain the high-dimensional parameters space of BG models
- Incorporation of new biomarkers or the brain recording data is a must for unique parameter extraction

MODEL



Mean-field model

- *Spatially homogeneous neural field*
- *Exponential synapses*
- *Axonal pulse attenuation without delay*
- *Noise-free input from brainstem*

Parameters

- *Parameters set according to physiological steady-state firing rates*
- *Parkinsonian state defined by varying connectivity and thresholds*
- *Sweep decay time scale to find "P-conformal" regions*

Study

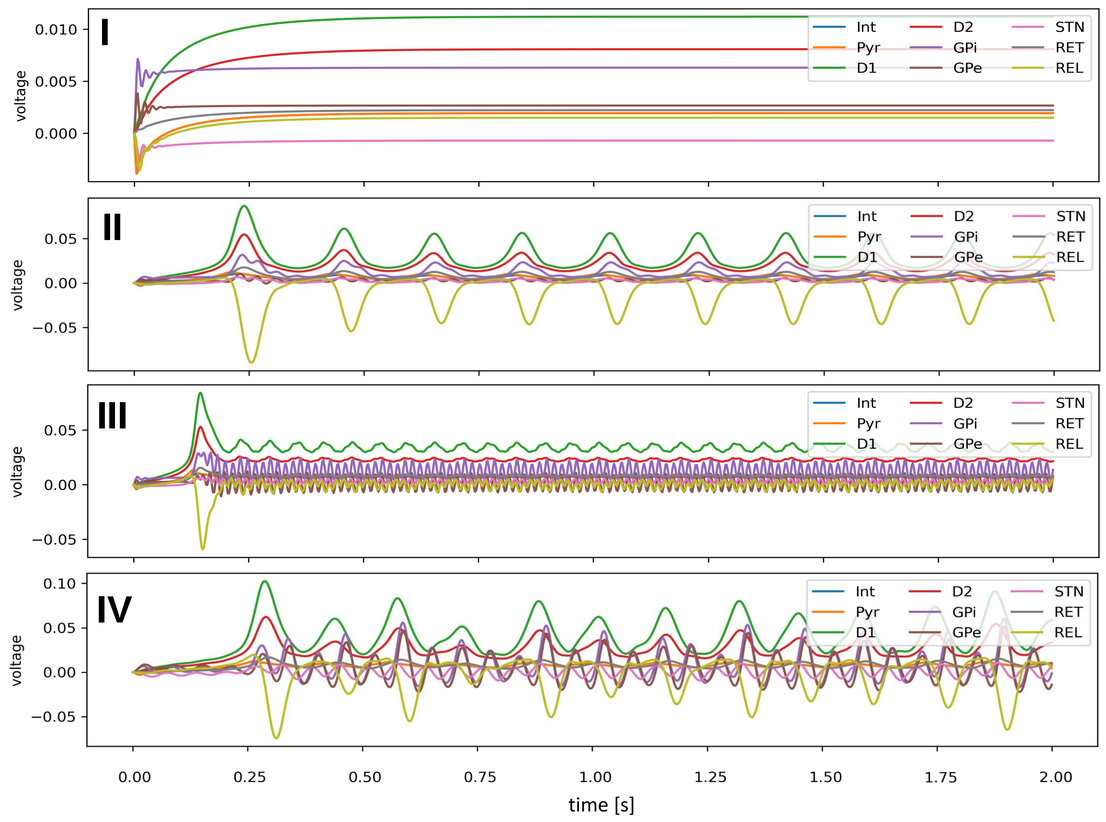
- *Sweep decay time scale (τ_d)*
- *Investigate the pathological to healthy beta power ratio*
- *Parameters consistent with the beta excess biomarker (ratio >1) are marker as "P-conformal"*

$$\textit{P-conformal} = \left(\frac{P_\beta^{parkin}}{P_\beta^{healthy}} > 1\right) \qquad P_\beta = \int_{12\ Hz}^{30\ Hz} PSD(f)df$$

RESULTS

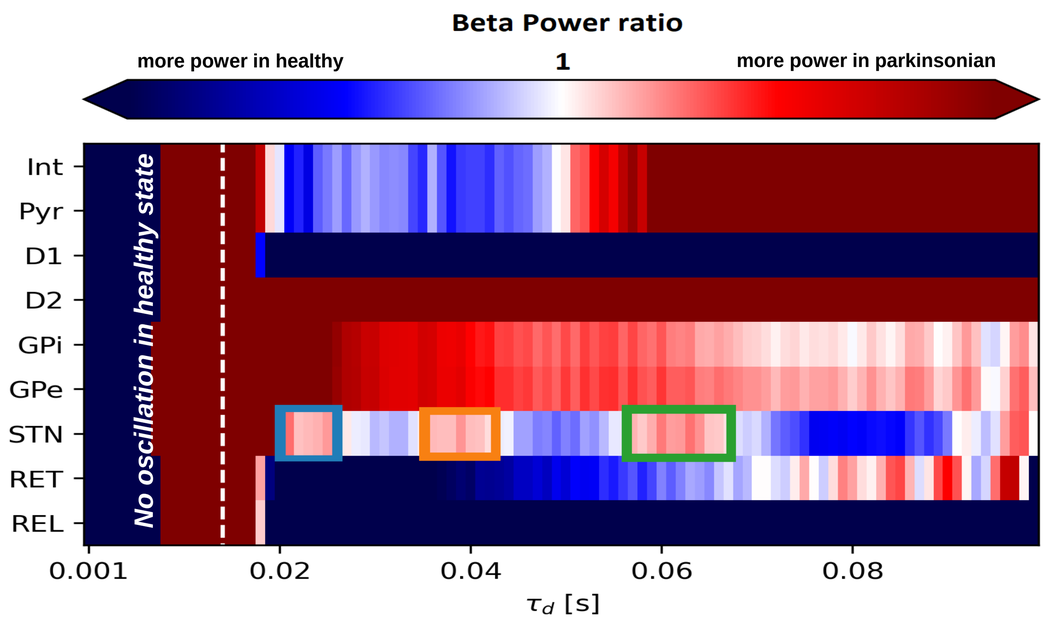
A. Existence of multitude of P-conformal parameters with dynamically different behavior

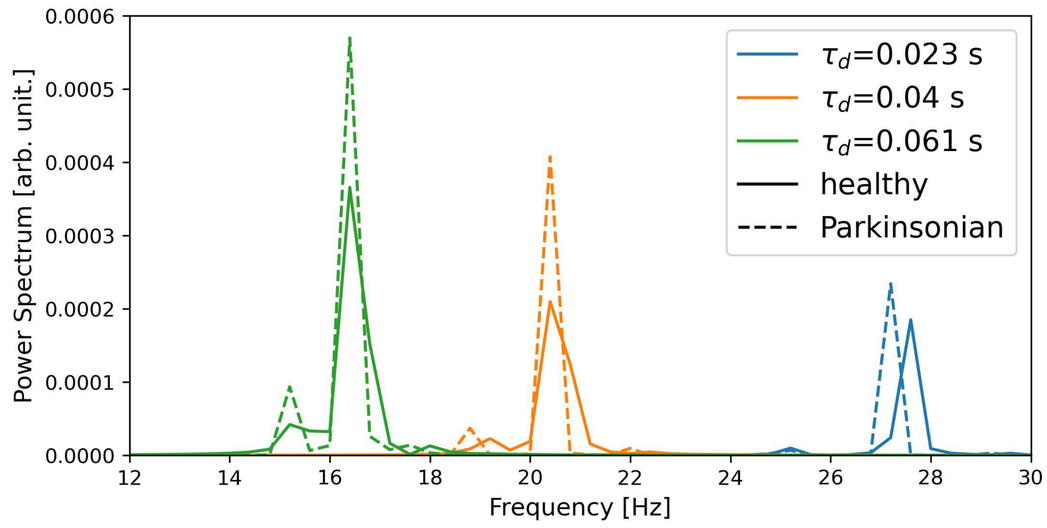
I. Steady-state → [1,2], this work
II. Unimodal oscillation → [3], this work
III. Multimodal oscillation → this work
IV. Chaotic → this work



B. Multitude of P-conformal parameter regions

- May be discerned based on number of modes, peak frequency, or additional biomarkers (e.g. cross-correlation)
- Utilizing brain recordings is necessary to extract parameters





FUTURE WORK & ACKNOWLEDGMENT

- Implementation of the axonal delays
- Use EEG/ECoG recordings and Bayesian inversion to estimate parameters systematically

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