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Does the regulation of local excitation-inhibition balance aid in recovery of functional connectivity? A computational account

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Abstract

Computational modeling of the spontaneous dynamics over the whole brain provides critical insight into the spatiotemporal organization of brain dynamics at multiple resolutions and their alteration to changes in brain structure (e.g. in diseased states, aging, across individuals). Recent experimental evidence further suggests that the adverse effect of lesions are visible on spontaneous dynamics characterized by changes in resting state functional connectivity and its graph theoretical properties (e.g. modularity). These changes originate from altered neural dynamics in individual brain areas that are otherwise poised towards a homeostatic equilibrium