Modeling Dementia
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Neurodegeneration will undoubtedly become a major challenge in medicine and public health caused by demographic changes worldwide. More than 45 million people are living with dementia today and this number is expected to triple by 2050. Recent studies have reinforced the hypothesis that the prion paradigm, the templated growth and spreading of misfolded proteins, could help explain the progression of a variety of neurodegenerative disorders. However, our current understanding of prion-like growth and spreading is rather empirical. Here we show that a physics-based reaction-diffusion model can explain the growth and spreading of misfolded protein in a variety of neurodegenerative disorders. We combine the classical Fisher-Kolmogorov equation for population dynamics with anisotropic diffusion and simulate misfolding across representative sections of the human brain and across the brain as a whole. Our model correctly predicts amyloid-beta deposits and tau inclusions in Alzheimer's disease, alpha-synuclein inclusions in Parkinson's disease, and TDP-43 inclusions in amyotrophic lateral sclerosis. To reduce the computational complexity, we represent the brain through a connectivity-weighted Laplacian graph created from 418 brains of the Human Connectome Project. Our brain network model correctly predicts the key characteristic features of whole brain models at a fraction of their computational cost. Our results suggest that misfolded proteins in various neurodegenerative disorders grow and spread according to a universal law that follows the basic physical principles of nonlinear reaction and anisotropic diffusion. Our simulations can have important clinical implications, ranging from estimating the socioeconomic burden of neurodegeneration to designing clinical trials and pharmacological intervention.