Pattern Formation of Folds in the Brain

Monica K. Hurdal
Florida State University
Department of Mathematics
Tallahassee, FL 32306-4510
mhurdal@math.fsu.edu

Abstract

The folding patterns of the brain vary across individuals in their size, depth, and location. This individual variability presents a challenge when studying and quantifying changes in brain folding patterns during development, aging, and disease. Furthermore, there are a number of biological theories that hypothesize about the mechanisms involved in the formation and location of cortical fold development, but no consensus has been reached.

In this paper we present a spatio-temporal Turing reaction-diffusion system to model folding pattern formation in the brain. A Turing system consists of two reaction-diffusion equations representing chemical morphogens. One biological hypothesis suggests that during neurogenesis intermediate progenitor (IP) cells are formed in the subventricular zone (SVZ) of the lateral ventricle (LV), leading to ridge (gyrus) and valley (sulcus) formation in the brain. We assume that folding pattern formation is driven by chemical activator and inhibitor morphogens that drive IP cell formation. We model the SVZ with a prolate spheroid surface and use exponential and logistic growth to create dynamically growing prolate spheroid domains.

We derive the mathematical equations and conditions needed to construct a growing domain Turing system that generates a genetic chemical prepattern for cortical folding. Parameters representing growth rate and domain scale are varied during numerical simulations. Altering the growth rate parameter R allows the size of the domain to be controlled, and thus the size of the SVZ and LV. Changing the domain scale parameter ω represents a change in the overall level of genetic expression of activator and inhibitor morphogens. Results demonstrate that R and ω control the complexity of the labyrinthine pattern that evolves.

We use our growing domain Turing system to model various diseases of cortical folding. Polymicrogyria is a group of cortical folding diseases where the folds of the cortex are unusually high in number and small in size. Lissencephaly is a group of diseases where cortical folds appear broader in width and fewer in number. We are able to capture various manifestations of polymicrogyria and lissencephaly by altering R and ω. For example, polymicrogyria with lateral ventricle enlargement can be modeled by increasing the value of R, resulting in a complex pattern with an increased number and width of folds. Our results demonstrate that dynamically growing domain Turing models represent an important step in improving our understanding of cortical folding pattern formation in the brain and the influence that domain growth and genetic expression can have on cortical folding.