Fisher-Kolmogorov equations for neurodegenerative diseases

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1 Introduction

The objective of this project is to apply various numerical methods to solve the Fisher-Kolmogorov equations, which are used to model the spread of misfolded proteins in the brain, a process associated with numerous neurodegenerative diseases.

1.1 Fisher-Kolmogorov equation

$$\begin{cases} \dfrac{\partial c}{\partial t} - \nabla \cdot (D \nabla c) - \alpha c(1-c) = 0 & \text{in } \Omega \\ D \nabla c \cdot \mathbf{n} = 0 & \text{on } \partial\Omega \\ c(t=0) = c_0 & \text{in } \Omega \end{cases}$$

c: concentration of the misfolded protein in a zone of the brain ($0 \leq c \leq 1$)
α: constant of concentration growth
D: diffusion coefficient of the misfolded protein.
It can be isotropic (a scalar) or anisotropic (a square matrix).
In case of anisotropic coefficient the term can be computed as:

$$\underline{\mathrm{D}} = d^{\mathrm{ext}} \underline{\mathrm{I}} + d^{\mathrm{axn}} (\mathbf{n} \otimes \mathbf{n})$$

where d^{ext} is the extracellular diffusion term, d^{axn} is the axonal diffusion term and $\mathbf{n}$ the direction of axonal diffusion. Usually extracellular diffusion is slower than axonal diffusion: $d^{\mathrm{ext}} < d^{\mathrm{axn}}$.

The Fisher-Kolmogorov equation is a **diffusion-reaction** equation with a nonlinear forcing term that can be used to model population growth. In this case it is used to model the spreading of proteins in the brain.

1.2 Mesh

The mesh we used is a 3D representation of the human brain.

2 Methods

List and description of the implemented methods with numerical analysis.

2.1 1D implementation

2.1.1 Stability and Accuracy

2.1.2 Algorithm

2.2 Fully explicit

2.2.1 Stability and Accuracy

2.3 Semi-implicit

2.3.1 Stability and Accuracy

2.4 Fully implicit

2.4.1 Stability and Accuracy

Stability and accuracy analysis of the implemented methods.

3 Results and algorithmic comparation

Results of the project for all the implemented algorithms and graphs.