## Coupled PDEs with Initial Solution from Data in COMSOL 4

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## Outlines

- Model Description
- Two Approaches
- Initial Data Input As Data File
- Results


## Problem Statement

We consider an example from mathematical biology, the FitzHugh-Nagumo equations:

$$
\begin{aligned}
C_{t}-\nabla \cdot\left(D_{\mathrm{eff}} \nabla C\right) & =C(C-\alpha)(1-C)-\beta v, \\
v_{t} & =\epsilon(C-\gamma v),
\end{aligned}
$$

It is a reduced system of coupled time-dependent reaction-diffusion equations with:

- Square domain $\Omega=(0,150) \times(0,150) \subset \mathbb{R}^{2}$ in units of micrometers ( $\mu \mathrm{m}$ ).
- No-flow boundary conditions $\mathbf{n} \cdot\left(D_{\text {eff }} \nabla C\right)=0$ for all $(x, y) \in \partial \Omega$.
- The initial conditions are given by data in txt files that specify the values of $C(x, y, 0)=C_{0}(x, y)$ and $v(x, y, 0)=v_{0}(x, y)$ on a $50 \times 50$ mesh of $\bar{\Omega}$.
- The physiological parameters of the problem are $D_{\text {eff }}=1$, $\alpha=\beta=0.1, \gamma=0.2$, and $\epsilon=0.07$.


## Two Approaches for Coupled PDEs

The idea of the first approach is to model each PDE equation in the system separately and then couple them together.

- Each equation in the coupled system of PDEs is represented by one Physics, each need to set up source term, boundary condition, and initial condition.
- This method is convenient with smaller systems of PDE, or PDEs with different structure.

The idea of the second approach is to use only One Physics by using the matrix form of coefficients.

- In this case, Diffusion Coefficient is a diagonal $2 \times 2$ matrix with 1 and 0 on diagonal. The source term is a $2 \times 1$ vector with $f_{1}=C(C-\alpha)(1-C)-\beta v$ and $f_{2}=\epsilon(C-\gamma v)$.
- The initial condition is in the form of a $2 \times 1$ vector with $C_{0}(x, y)$ and $v_{0}(x, y)$.
- This method suits the situation that we have multiple PDEs with similar shape.

COMSOL calculated identical results with both approaches.

## Setting up Initial Conditions from Data Files

- The initial condition profiles for the excitation variable, $C_{0}(x, y)$, and recovery variable, $v_{0}(x, y)$, are provided in two separate txt files.
- We use Global Definitions and then Interpolation Function to create functions from our data file.
- Enter the name of the appropriate interpolation function as the initial value. at tab Coefficient Form PDE
- The benefit of using this function is our data does not have to agree with the mesh, see Fig 1.
- The plots are 2D Plot Group with Height Expression
- Figure shows how excitation is induced and then it proceeds into the resting part of the domain. This physiological process is characterized by the visual appearance of a double spiral wave.

(a) $t=0 \mathrm{~s}$
(e) $t=200 \mathrm{~s}$


(b) $t=50 \mathrm{~s}$

(f) $t=250 \mathrm{~s}$

(c) $t=100 \mathrm{~s}$

(g) $t=300 \mathrm{~s}$

(d) $t=150 \mathrm{~s}$

(h) $t=350 \mathrm{~s}$


## Three-dimensional view of the excitation variable $v$ at different times

- Figure shows a recovery variable controls the local recovery of the excitation.

(a) $t=0 \mathrm{~s}$

(e) $t=200 \mathrm{~s}$

(b) $t=50 \mathrm{~s}$

(f) $t=250 \mathrm{~s}$

(c) $t=100 \mathrm{~s}$

(g) $t=300 \mathrm{~s}$

(d) $t=150 \mathrm{~s}$

(h) $t=350 \mathrm{~s}$


## Two-dimensional view of the excitation variable $C$ at different times

- Figure depicts the two-dimensional view of the excitation variable, where one can easily see the curl pattern.

(a) $t=0 \mathrm{~s}$

(e) $t=200 \mathrm{~s}$

(b) $t=50 \mathrm{~s}$

(f) $t=250 \mathrm{~s}$

(c) $t=100 \mathrm{~s}$

(g) $t=300 \mathrm{~s}$

(d) $t=150 \mathrm{~s}$

(h) $t=350 \mathrm{~s}$


## Conclusion

- We solved the coupled system of PDEs with two approaches, they gave the same results.
- COMSOL read initial conditions from Data files, then used interpolation to work with different mesh.

