

## Example: 2D FitzHugh-Nagumo model

File: sample/FHN2D.isml

This example solves FitzHugh-Nagumo monodomain model two dimensionally.

This model solves the electrical activity in a cell and constitutes with two equations. First equation (1) describes the course of excitation and second equation (2) calculates recovery. Here,  $u(t,x,y)$  is a normalized transmembrane potential and  $v(t,x,y)$  is a dimensionless time-dependent recovery variable. We consider the model equations

$$\frac{\partial u}{\partial t} = \varepsilon \nabla \cdot \nabla u + \lambda(v - u(1 - u)(u - \theta)) \quad (1)$$

$$\frac{\partial v}{\partial t} = \alpha u - \beta v \quad (2)$$

for  $t > 0$  and  $\mathbf{u} = (u, v)^T \in (0,1)^2$ , with parameters:  $\varepsilon = 0.01$ ,  $\lambda = -100$ ,  $\theta = 0.25$ ,  $\alpha = 0.16875$  and  $\beta = 1.0$ . Here,  $\varepsilon$  is an excitation constant and  $\lambda$  is an excitation decay constant, and  $\theta$  represents the normalized threshold potential value and  $\alpha$  is a dimensionless time-dependent recovery variable and  $\beta$  is a recovery decay constant.

The initial values are given by the following smooth data

$$u = \frac{1}{1 + e^{-50(\sqrt{u^2 + v^2} - 0.1)}} \quad \text{and} \quad v = 0 \quad (3)$$

and homogeneous Neumann boundary conditions are applied. The problem is solved on the unit rectangular square  $(0,1)^2$  from 0 to 5 in time with a uniform grid mesh as is shown in Fig. 1.

These equations are solved by finite element method solver FreeFem++. FreeFem++ code of “freefem.edp” is generated from insilicoML file of “FHN2D.isml”.

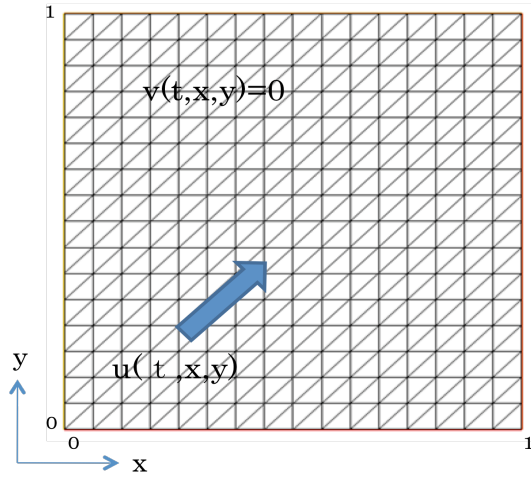


Fig. 1: Square uniform mesh (16x16)

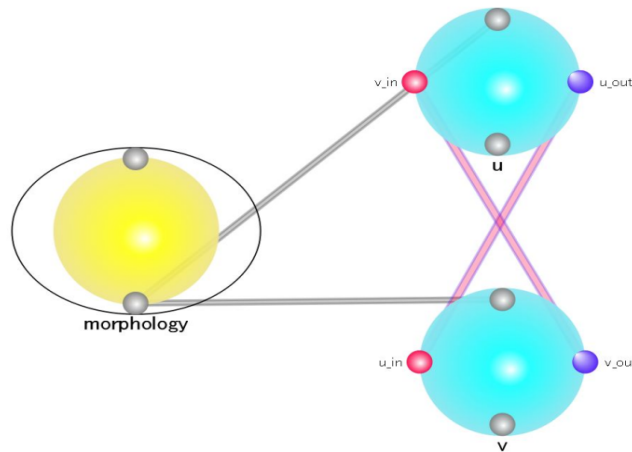


Fig. 2: insilicoML model

*insilicoML* model is shown in Fig. 2. This model has three modules which are named as “morphology”, “u” and “v”. “morphology” module defines the mesh shape of Fig. 1. Morphology primitive, “regular-rectangle”, is used for the definition. “u” module solves a first equation (1) and “v” module solves second equation (2). The “morphology” module has a output port from which morphology information is given to “u” and “v” modules via structure edge. Module “u” and “v” have another two ports  $u_{out}$  and  $v_{in}$  for “u” module, and  $u_{in}$  and  $v_{out}$  for “v” module. Both  $u_{out}$  and  $u_{in}$  ports are linked via “u” edge and  $v_{in}$  and  $v_{out}$  ports are linked via “v” edge. First equation (1) is solved only for state variable  $u$  and new  $u$  is sent to “v” module via “u” edge and second equation (2) is solved only for state variable  $v$  and new  $v$  is sent to “u” module via “v” edge. Some results are shown in the following Figures.

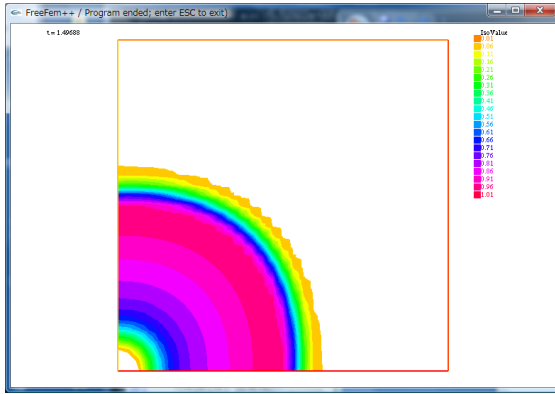


Fig. 3:  $u(t,x,y)$   $t=1.5$  (36x36 grid)

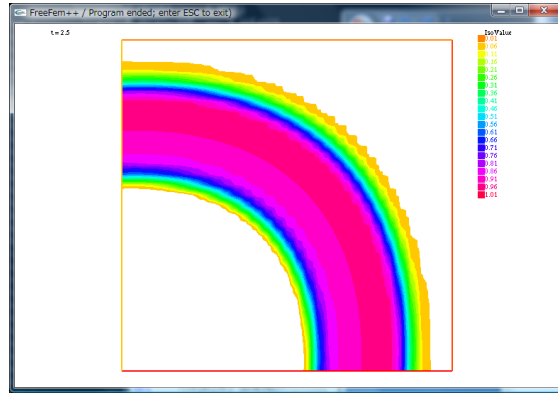


Fig. 4:  $u(t,x,y)$   $t=2.5$  (36x36 grid)

Reference.

“A Multilevel Adaptive Approach for Computational Cardiology”, W. Ying, Duke University, 2005.