Differential Equations in Bioscience

Simulations of Gierer-Meinhardt Model with Source Density

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- [1] Meinhardt, H. (2012) "Turing's theory of morphogenesis of 1952 and the subsequent discovery of the crucial role of local self-enhancement and long-range inhibition," *Interface focus*, 2(4), pp. 407–416.
- [2] Meinhardt, H. (1993) "A model for pattern formation of hypostome, tentacles, and foot in hydra: how to form structures close to each other, how to form them at a distance," *Developmental biology*, 157(2), pp. 321–333.
- [3] Gierer, A. and Meinhardt, H. (1972) "A theory of biological pattern formation". Kybernetik 12, 30–39

Motivation

• Morphogenesis (Turing 1952):

- Biological process allowing an organism to develop its form
- Study mechanism by which distribution of cell space occurs
- <u>Example:</u> process of embryonic development

Activator-Inhibitor Systems:

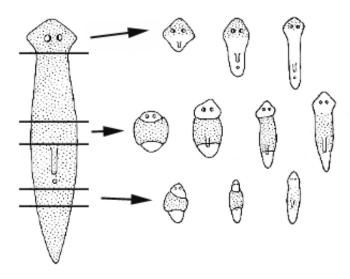
- Reaction-diffusion equations
- Explain many pattern formation processes in nature

Why do we study them?

- Polarity retention during regeneration in hydra
- Understanding congenital cardiac malformations



Schleich, Jean-Marc, Jean-Louis Dillenseger. 'Virtual Imaging for Teaching Cardiac Embryology'. *Circulation* 104.24 (2001): e134–e134. Web.

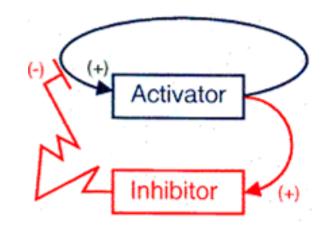


https://sites.google.com/site/flatwormsjfr2/defense-protection

Gierer-Meinhardt Model 1

Activator-Inhibitor System [1]:

- Two substances that act on each other
- Activator stimulates its own production (autocatalysis)
- Activator also produces the inhibitor
- Inhibitor represses the production of the activator



Hans Meinhardt (2006) Gierer-Meinhardt model. Scholarpedia, 1(12):1418.

D1-D2 are diffusion constants, μ - ν are decay rates, **a-b** are production rates, Δ is Laplace operator

$$\partial_t u = D_1 \Delta u + \frac{au^2}{v} - \mu u$$
$$\partial_t v = D_2 \Delta v + bu^2 - vv$$

$$\partial_t v = D_2 \Delta v + b u^2 - v v$$

activator (u), inhibitor (v) eq1

Gierer-Meinhardt Model 2

Source Density:

- Meinhardt used source density for hydra model in 1993 [1]
- It describes ability of cells to perform the autocatalytic reaction
- Higher source density increases activation concentration
- Source density gradient can determine polarity of pattern

$$\partial_t u = D_1 \Delta u + \frac{au^2}{v} S - \mu u$$

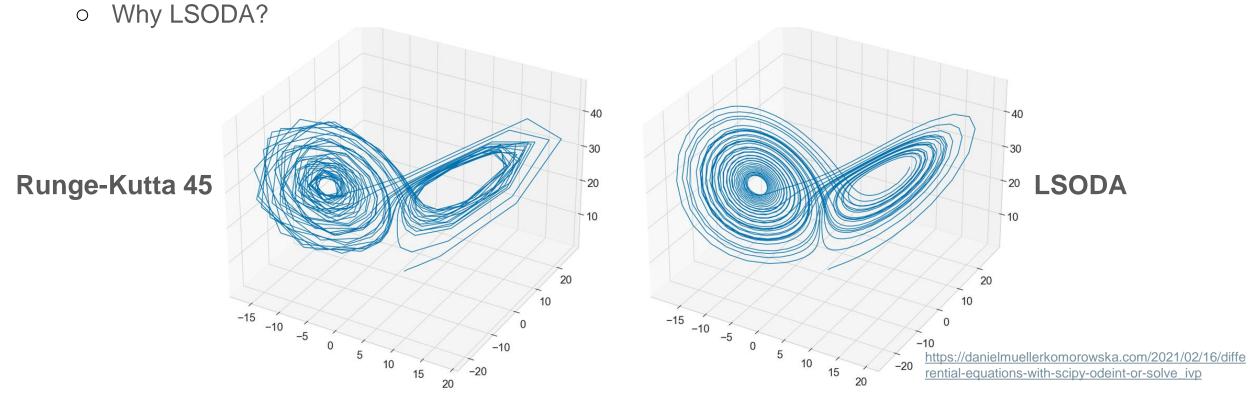
$$\partial_t v = D_2 \Delta v + bu^2 S - vv$$

$$\partial_t S = d\Delta S + u - \delta S$$

activator (u), inhibitor (v), source density (S) eq2

ODE Solver 1: LSODA

- LSODA: Solver for Ordinary Differential Equations
 - FORTRAN ODE solver by Hindmarsh [1] imported to python by scipy [3]
 - Switches between stiff BDF and non-stiff Adams methods [2]



- [1] A. C. Hindmarsh, "ODEPACK, A Systematized Collection of ODE Solvers," IMACS Transactions on Scientific Computation, Vol 1., pp. 55-64, 1983.
- [2] L. Petzold, "Automatic selection of methods for solving stiff and nonstiff systems of ordinary differential equations", SIAM Journal on Scientific and Statistical Computing
- [3] https://docs.scipy.org/doc/scipy/reference/generated/scipy.integrate.LSODA.html

ODE Solver 2: Adams

Adams:

- Implicit method for the numerical integration of ODEs
- Linear multistep methods, takes function and time
- \circ Replacing the integrand with polynomial that interpolates f(t,y)
- Coefficients determined by previously calculated data points

$$y'=f(t,y), \quad y(t_0)=y_0.$$
 initial value problem

$$y_{n+r} = y_{n+r-1} + h \sum_{l=1}^r \lambda_k f_{n+r-k}$$
 Adams general formula

$$\sum_{k=1}^r \lambda_k = 1$$

• h denotes time step, k denotes step size for order r, f is the function and y is the solution at time t

ODE Solver 3: BDF

- Backward differentiation formula (BDF):
 - Implicit methods for the numerical integration of ODEs
 - Linear multistep method, takes function and time
 - Approximate the derivative of function using previously computed information
 - Increasing the accuracy of the approximation

$$y'=f(t,y), \quad y(t_0)=y_0.$$
 initial value problem

$$\sum_{k=0}^s a_k y_{n+k} = h eta f(t_{n+s}, y_{n+s}),$$
 BDF general formula

h denotes time step, k denotes step size, a and β are chosen so that method achieves maximum order s, f is the function and y is the solution at time t

Code 1: Libraries

- The code was written in python 3.
- Solving differential equations:

```
import numpy as np
from scipy.integrate import solve_ivp
```

- Solve IVP function solves initial value problem for system of ODEs.
- Visualizations for simulations:

```
import matplotlib.pyplot as plt
from celluloid import Camera
```

Animating values at each instance was possible through them.

Code 2: Equations

$$\partial_t u = D_1 \Delta u + \frac{au^2}{v} S - \mu u$$

$$\partial_t v = D_2 \Delta v + bu^2 S - vv$$

$$\partial_t S = d\Delta S + u - \delta S$$

activator (u), inhibitor (v), source density (S) eq2

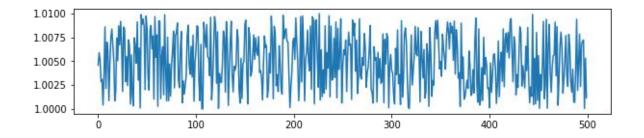
```
#activator eq2
def activator(y):
    activator = D1* delta2d(y[:dim],dx) + a*u(y)**2/v(y) * S(y) - mu*u(y)
    return(activator)

#inhibitor eq2
def inhibitor(y):
    inhibitor = D2* delta2d(y[dim:2*dim],dx) + b*u(y)**2 * S(y) - nu*v(y)
    return(inhibitor)

#source density
def source(y):
    source = d* delta2d(y[2*dim:3*dim],dx) + u(y) - delta * S(y)
    return(source)
```

Code 3: Solve ODEs

- IC is vector representation of initial state
 - Uniform Gaussian noise
 - Mean = 1
 - \blacksquare Variance = 0.01



- tc is timespan of solver i.e. it integrates from time 0 to 100
- solve_ivp takes the function, timespan and initial state and solves ODEs

```
IC = 1+0.01*np.random.rand(3*dim)
tc = [0,100]

gms_rhs = lambda t,y: [activator(y),inhibitor(y),source(y)]
sol = solve_ivp(gms_rhs,tc,IC,method='LSODA',vectorized=True)
t = sol.t
y = sol.y.T
```

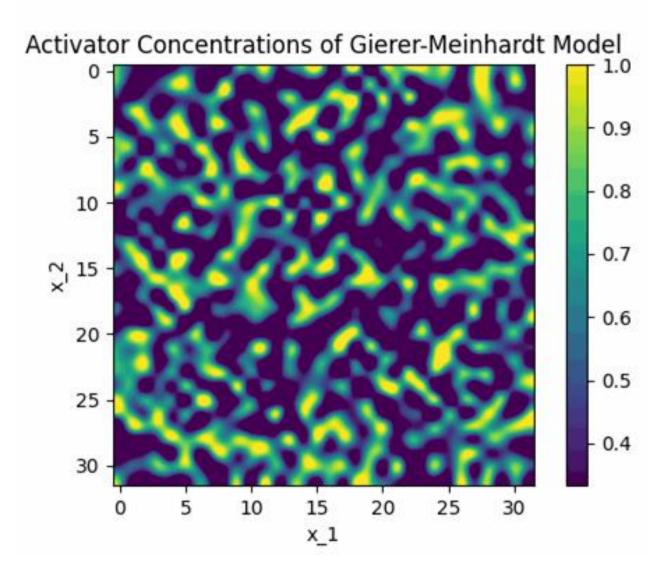
Code 4: Visualization

- Loop through the solutions for each instance
- plt.imshow creates 2D surface plot of solution
- Camera captures current slice of result using snap function
- animate function arranges all snaps of instances into a gif file

```
fig = plt.figure(dpi=100)
camera = Camera(fig)

for i in range(len(y)):
   image = y[i,:dim].reshape((N,N))
   image = minmax_scale(image)
   plt.imshow(image,interpolation='sinc',vmin=np.max(image)/3)
   plt.xlabel('x_1')
   plt.ylabel('x_2')
   plt.title('Activator Concentrations of Gierer-Meinhardt Model')
        camera.snap()
   plt.colorbar()
   animation = camera.animate()
   animation.save('simulation3.gif', writer='pillow', fps=60)
```

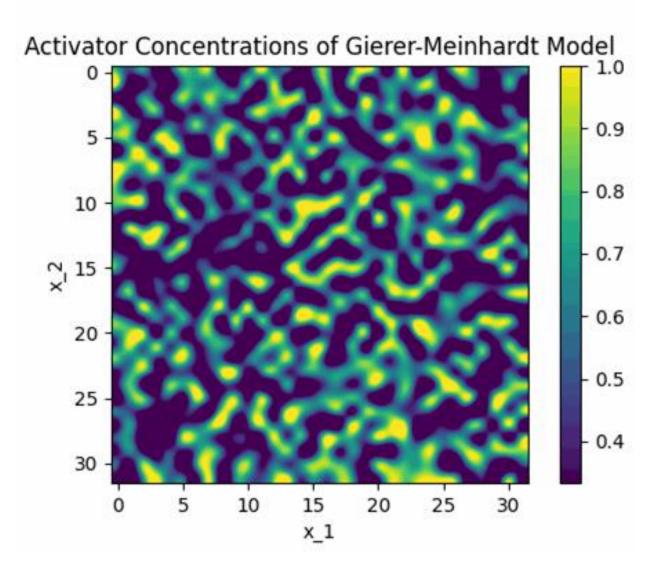
Simulation 1: eq2



T = 012 norm value: 15.8821 - 0.8 - 0.7 - 0.6 - 0.5 T = 10012 norm value: 5.5459 - 0.9 - 0.8 10 - 0.7 ~, 15 - 0.6 25 25 10 x_1

'D1', 0.0002, 'D2', 0.01, 'a', 1, 'b', 1, 'mu', 0.5, 'nu', 1, 'd', 0, 'delta', 1

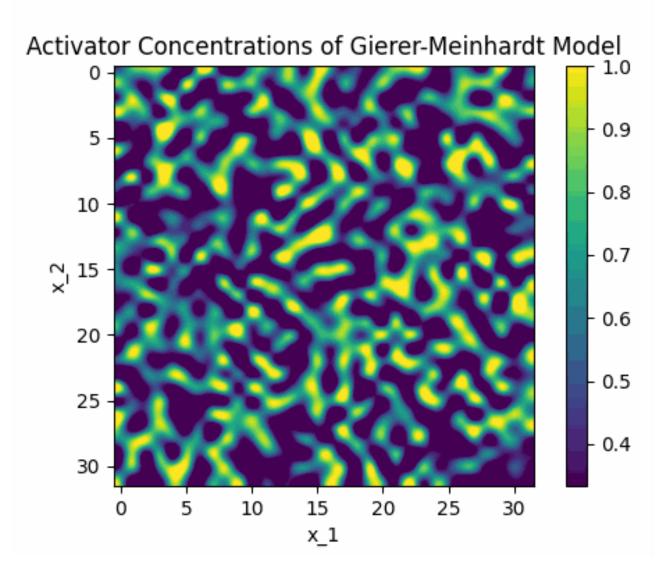
Simulation 2: eq2

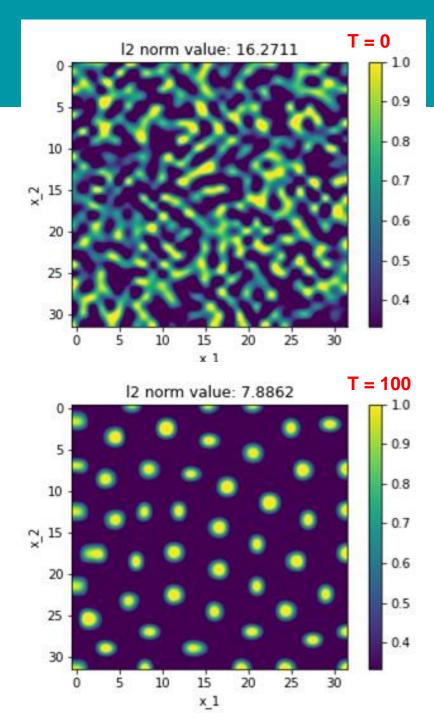


T = 012 norm value: 16.2426 0.9 - 0.8 - 0.7 - 0.6 0.5 10 15 T = 10012 norm value: 4.0991 0.9 - 0.8 - 0.7 ∾, 15 × 0.6 20 0.5 25 0.4 30 20 25

'D1', 0.0002, 'D2', 0.01, 'a', 2, 'b', 1, 'mu', 1, 'nu', 2, 'd', 2, 'delta', 1.5

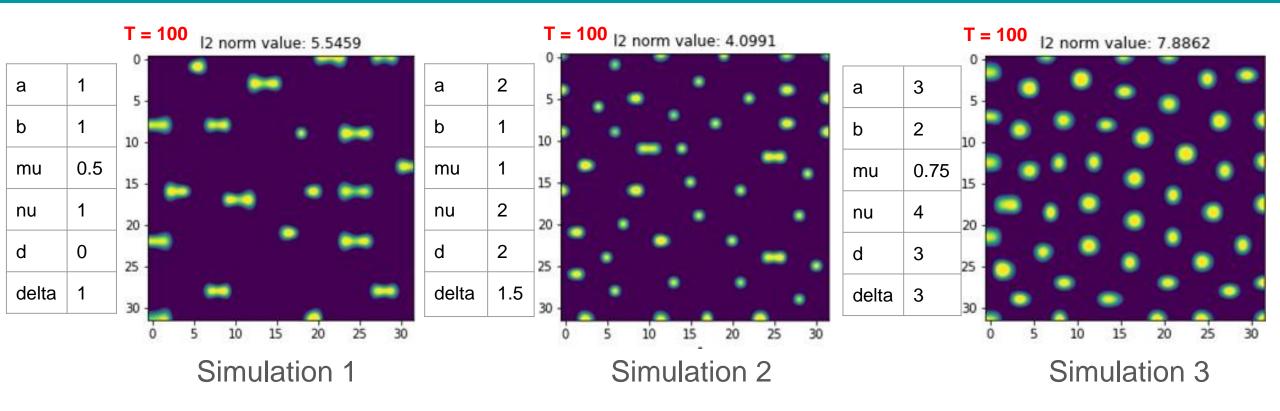
Simulation 3: eq2





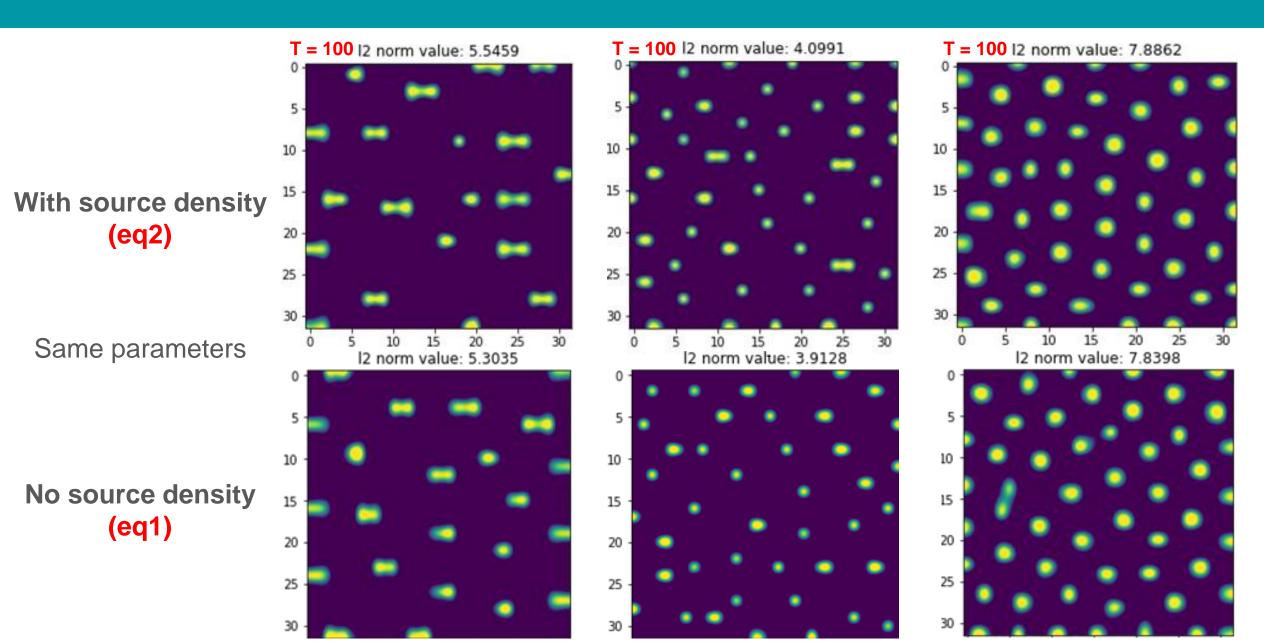
'D1', 0.0002, 'D2', 0.01, 'a', 3, 'b', 2, 'mu', 0.75, 'nu', 4, 'd', 3, 'delta', 3

Results 1: eq2



- Comparison of the systems at their final pattern
- D1 and D2 values were 0.0002 and 0.01 for all
- L2 norm tending to 0 indicates reaching the steady state
 - values did not go lower when increasing tf from 100 to 300

Results 2: Comparison



Results 3: Slight changes

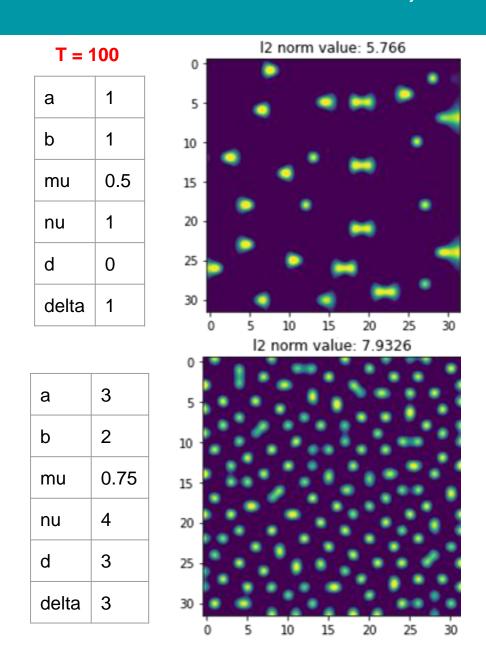
- Experimenting with slightly different equation:
 - Source density impact is higher
 - However the difference is not major
 - Compared to eq1 and eq2

$$\partial_t u = D_1 \Delta u + \begin{bmatrix} \frac{au^2}{v} & -\mu u \\ \frac{au^2}{v} & -\nu v \end{bmatrix} S$$

$$\partial_t v = D_2 \Delta v + \begin{bmatrix} bu^2 & -\nu v \\ \frac{au^2}{v} & -\nu v \end{bmatrix} S$$

$$\partial_t S = d\Delta S + u - \delta S$$

activator (u), inhibitor (v), source density (S) eq3



Results 4: Saturation

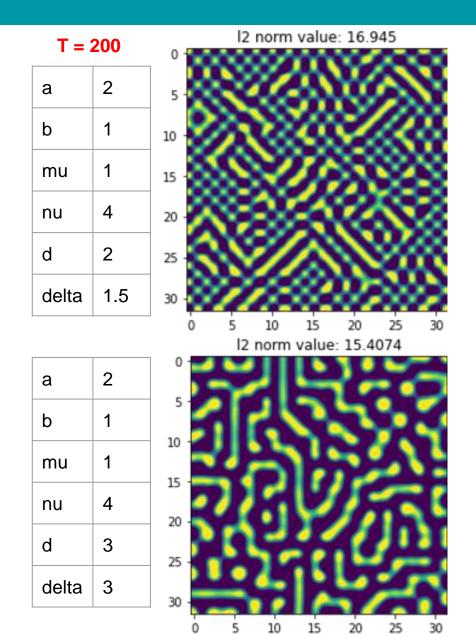
- For the case of saturation of the activator [1]:
 - Replacing u² with u²/(1+ku²)
 - \circ K = 0.002
 - Gives rise to striped and checkered patterns
 - Steady state not reached within T=200

$$\partial_t u = D_1 \Delta u + \left\{ \frac{au^2}{v(1+ku^2)} - \mu u \right\} S$$

$$\partial_t v = D_2 \Delta v + \left\{ bu^2 - vv \right\} S$$

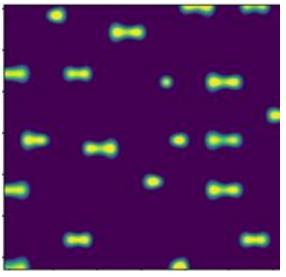
$$\partial_t S = d\Delta S + u - \delta S$$

activator (u), inhibitor (v), source density (S) eq4

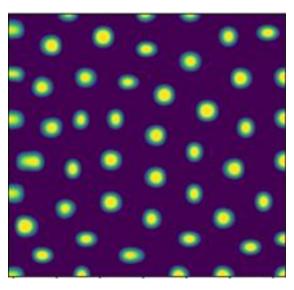


[1] Li, Y., Wang, J., & Hou, X. (2017). Stripe and spot patterns for the Gierer–Meinhardt model with saturated activator production. In Journal of Mathematical Analysis and Applications (Vol. 449, Issue 2, pp. 1863–1879)

Patterns in Nature

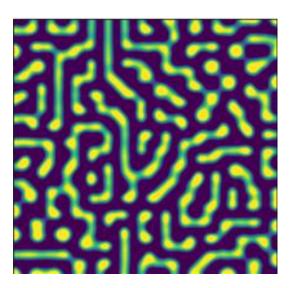














https://nl.pinterest.com/pin/418553359100200002/

Discussion

- Time overhead (google colab):
 - Simulations took between 30 to 60 seconds when T=100
 - Animation took approximately 30 seconds

- Not much noticeable difference between eq1 and eq2
- Some difference was noticed in eq3
- Major difference in eq4 when activator saturated

- Source density in simulations:
 - Seems not very effective for eq1, eq2
 - However very effective in case of eq3, eq4
 - Systems were most affected by μ and ν

Thank you for your time!

Questions?



Github: link to code

Appendix: delta2d function and params

```
N = 32
dim = N**2
dx = 1/(N-1)
D1 = 0.0002
D2 = 0.01
a = 3
b = 2
mu = 0.75
nu = 4
d = 3
delta = 3
```

params

```
def delta2d(y,dx):
 y = y.reshape(-1,1)
 N = int(np.sqrt(len(y)))
 U = np.reshape(y,(N,N))
 Ur = np.hstack([U[:,1:],U[:,-1].reshape(-1,1)])
 Ul = np.hstack([U[:,0].reshape(-1,1), U[:,:-1]])
 Ut = np.vstack([U[0,:].reshape(-1,1).T, U[:-1,:]])
 Ub = np.vstack([U[1:,:], U[-1,:].reshape(-1,1).T])
 dU = (Ur+Ul+Ut+Ub - np.multiply(4,U))/dx**2
 dy = dU.ravel().reshape(-1,1)
  return(dy)
```

delta2D computes the finite difference approximation of the Laplace operator with Neumann boundary conditions in the 2D squared domain.