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SIMULATION OF SPIRAL WAVES IN ATRIAL FIBRILLATION

Aim:

To simulate and visualize spiral waves in atrial fibrillation.

Objectives:

1. To simulate spirals arising in atrial fibrillation
2. Implementation of a monodomain reaction-diffusion model in 2-D using MATLAB

Apparatus:

1. Laptop/desktop
2. MATLAB

Theory:

Atrial fibrillation (AFib) is an irregular and often very rapid heart rhythm. An irregular heart rhythm is called an arrhythmia. AFib can lead to blood clots in the heart. The condition also increases the risk of stroke, heart failure and other heart-related complications. Spiral wave fronts, known to cardiologists as cardiac rotors, are responsible for heart arrhythmias. The modeling of the path of the spiral will ultimately assist in understanding why arrhythmias occur and how to treat them.

A monodomain reaction-diffusion model is a mathematical and computational framework used to describe the spatiotemporal dynamics of biological systems, particularly in the context of excitable tissues such as cardiac tissue. The equations for the monodomain reaction-diffusion model in 2-D are a variant of the Fitzhugh-Nagumo equations modified to simulate the cardiac action potential. The progression of the two normalized state variables, membrane voltage (v) and recovery (r), is computed across a 128 x 128 spatial domain and across time. This function simulates spiral waves, which are hypothesized to underlie reentrant tachycardia. The spiral waves can be initiated by two different cardiac pacing methods:

- Two-point stimulation where a point stimulus is delivered in the center of the

domain followed by another point stimulus on the partially refractory wake of the first wave of excitation.

- Cross-field stimulation where a stimulus is applied to the left domain boundary causing a plane wave.

  As this wave travels across the domain, a second stimulus is applied to the bottom boundary of the domain.

Methodology:

Simulation Parameters:

1. Number of columns in the spatial domain (ncols): 128
2. Number of rows in the spatial domain (nrows): 128
3. Duration of simulation (dur): 25000 time steps
4. Grid size (h): 2.0
5. Time step (dt): 0.15
6. Amplitude of external current (Iex): 30
7. Anisotropy factor (mu): 1.0
8. Conductances (Gx, Gy): 1.0 (Gy is adjusted based on anisotropy)
9. FHN model parameters:
    - a: 0.13
    - b: 0.013
    - c1: 0.26
    - c2: 0.1
    - d: 1.0

Stimulation Protocols:

1. Two-point stimulation:
    - First stimulus: Point stimulus in the center of the domain
    - Second stimulus: Point stimulus on the partially refractory wake of the first wave of excitation
2. Cross-field stimulation:
    - First stimulus: Applied to the left domain boundary, causing a plane wave
    - Second stimulus: Applied to the bottom boundary of the domain as the wave travels

Simulation Procedure:

- Initialize the spatial domain with membrane voltage (v) and refractoriness (r) arrays.
- Set up the initial stimulus current pattern based on the chosen stimulation protocol (Two-point or Cross-field).
- Configure the simulation environment, including the colormap, figure window, and user interface for quitting.
- Enter the time loop for the simulation:
    - Update external stimuli at specified time steps.
    - Compute spatial derivatives and integrate the model equations using finite difference and explicit Euler methods.
    - Visualize the evolving membrane voltage using a grayscale colormap.
    - Save every 500th frame to create a movie for later analysis.
    - Terminate the simulation when the specified duration is reached or when user input indicates termination.
- This function accepts only one input argument, StimProtocol, which can be either the numerical values '1' (for two-point stimulation) or '2' (for cross-field stimulation).

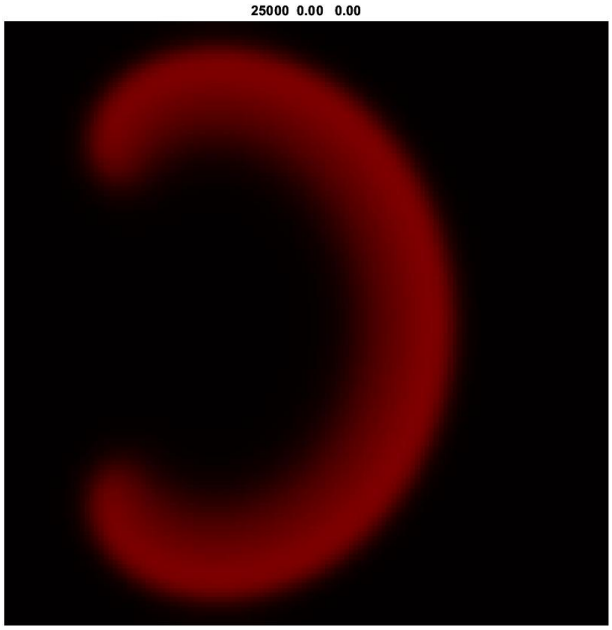
Code:

```
function SpiralWaves(StimProtocol)
ncols=128;
nrows=128;
dur=25000;
h=2.0;
h2=h^2;
dt=0.15;
Iex=30;
mu=1.0;
Gx=1; Gy=Gx/mu;
a=0.13; b=0.013; c1=0.26; c2=0.1; d=1.0;
v=zeros(nrows,ncols);
r=v;
% Set initial stim current and pattern
iex=zeros(nrows,ncols);
if StimProtocol==1
   iex(62:67,62:67)=Iex;
else
   iex(:,1)=Iex;
end
% Setup image
ih=imagesc(v); set(ih,'cdatamapping','direct')
colormap(hot); axis image off; th=title('');
```

```
set(gcf,'position',[500 600 256 256],'color',[1 1 1],'menubar','none')

% Create 'Quit' pushbutton in figure window
uicontrol('units','normal','position',[.45 .02 .13 .07], ...
   'callback','set(gcf,"userdata",1)',...
   'fontsize',10,'string','Quit');
n=0;
k=0;
done=0;
n1e=20;
switch StimProtocol
   case 1          % Two-point stimulation
      n2b=3800;
      n2e=3900;
   case 2          % Cross-field stimulation
      n2b=5400;
      n2e=5420;
end
while ~done

   if n == n1e
      iex=zeros(nrows,ncols);
   end

   if n == n2b
      switch StimProtocol
         case 1
            iex(62:67,49:54)=Iex;
         case 2
            iex(end,:)=Iex;
      end
   end

   if n == n2e
      iex=zeros(nrows,ncols);
   end


      vv=[[0 v(2,:) 0];[v(:,2) v v(:,end-1)];[0 v(end-1,:) 0]];

   vxx=(vv(2:end-1,1:end-2) + vv(2:end-1,3:end) -2*v)/h2;
   vyy=(vv(1:end-2,2:end-1) + vv(3:end,2:end-1) -2*v)/h2;
   dvdt=c1*v.*(v-a).*(1-v)-c2*v.*r+iex+Gx*vxx+Gy*vyy;
   v_new=v + dvdt*dt;


   drdt=b*(v-d*r);
   r=r + drdt*dt;
   v=v_new; clear v_new
```

```
    m=1+round(63*v); m=max(m,1); m=min(m,64);

    set(ih,'cdata',m);
    set(th,'string',sprintf('%d  %0.2f   %0.2f',n,v(1,1),r(1,1)))
    drawnow

    % Write every 500th frame to movie
    if rem(n,500)==0
       k=k+1;
       mov(k)=getframe;
    end

    n=n+1;
    done=(n > dur);
    if max(v(:)) < 1.0e-4, done=1; end
    if ~isempty(get(gcf,'userdata')), done=1; end
end

if isunix, sep='/'; else sep='\'; end
[fn,pn]=uiputfile([pwd sep 'SpiralWaves.avi'],'Save movie as:');
if ischar(fn)
    video_file = VideoWriter(fullfile(pn, fn), 'Motion JPEG AVI');
    video_file.Quality = 75;
    open(video_file);
    writeVideo(video_file, mov);
    close(video_file);

else
    disp('User pressed cancel')
end
close(gcf)
```

Output:



Conclusion:

In this simulation study, a two-dimensional Monodomain reaction-diffusion model based on the Fitzhugh-Nagumo equations has been utilized to investigate the dynamics of spiral waves in atrial fibrillation. The model successfully captures the spatiotemporal evolution of membrane voltage (v) and recovery (r) across a 128 x 128 spatial domain. The model visually encapsulates the progression of spiral waves over time, offering a dynamic representation of the underlying mechanisms.