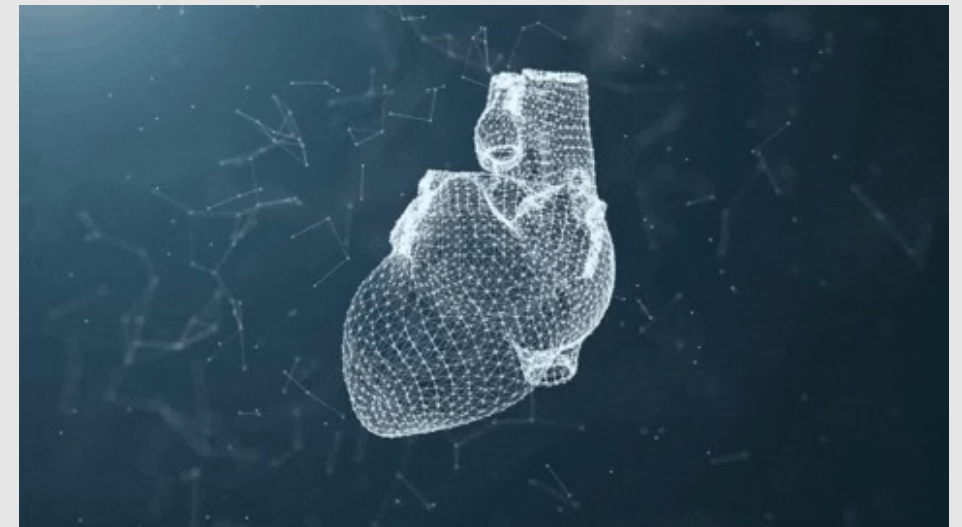
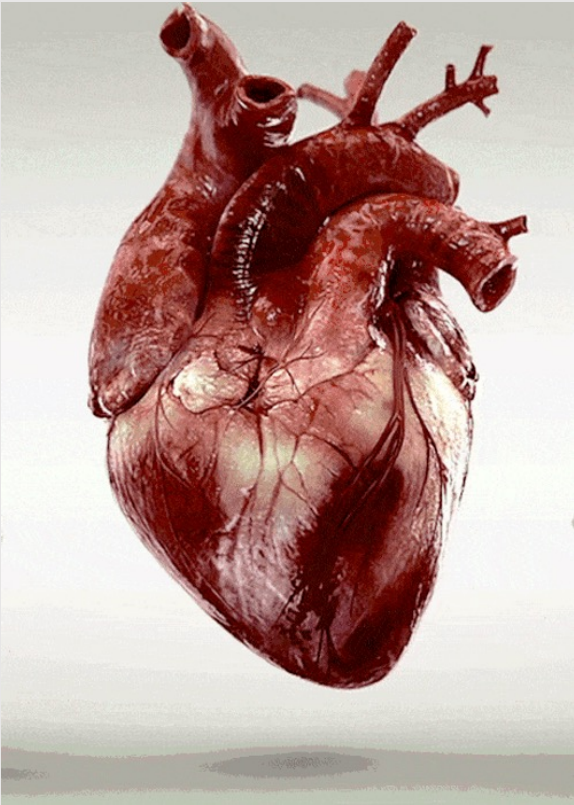


# A beginners guide to cardiac modelling

Henrik Finsberg  
Simula Summer Festival 06.06.24

**simula**

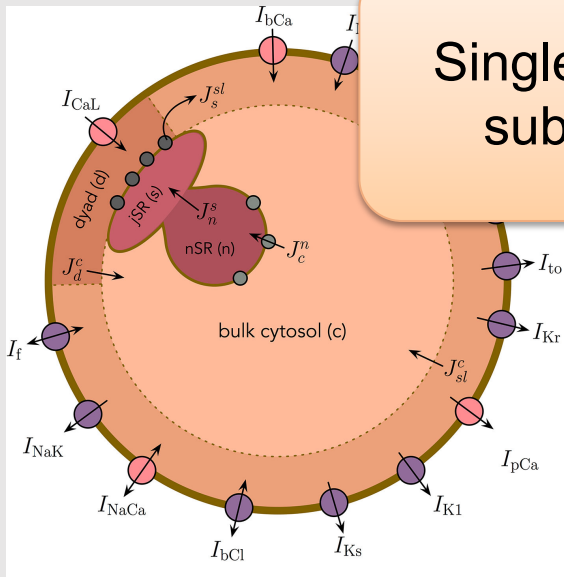
# What do you think cardiac modeling is all about?



<https://gifdb.com/gif/beating-human-heart-3d-real-animation-ndugdstfj863rnow.html>

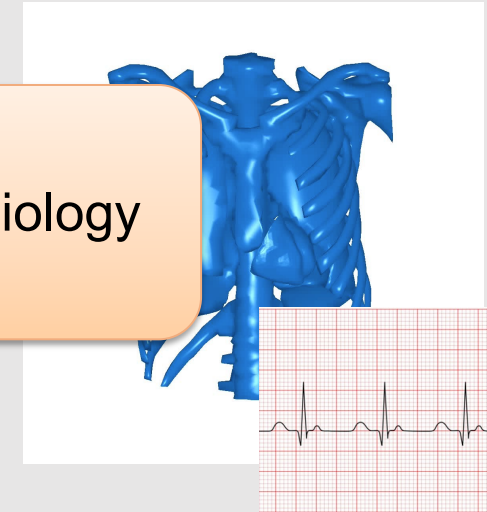
<https://insilicotrials.com/working-on-a-new-european-project-that-will-leverage-simulation-to-help-fight-cardiovascular-disease/>

Single cells (and sub-cellular)



Tveito, Jæger, Finsberg, Wall

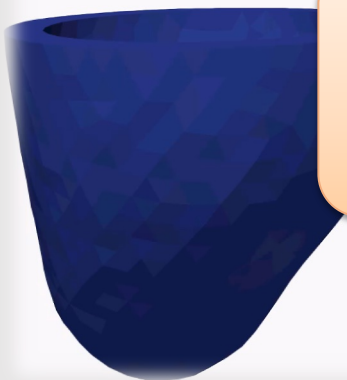
Electrophysiology



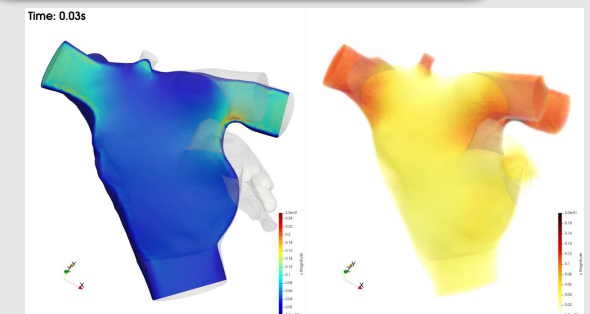
People in ComPhy are working on different aspects of cardiac modelling

Blood flow

Mechanics

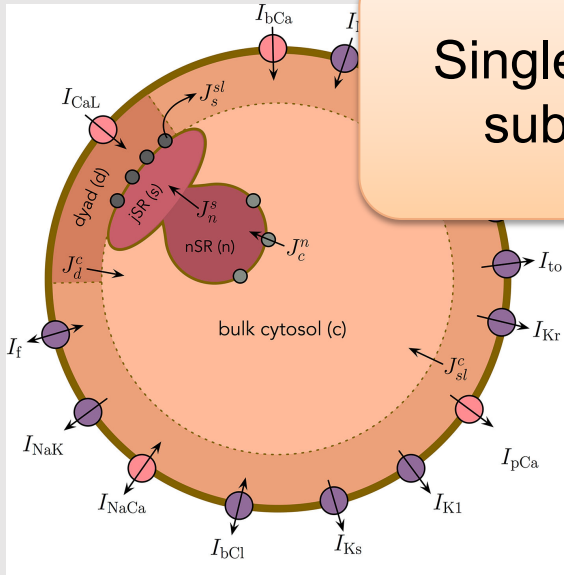


Finsberg, Sundnes, Wall



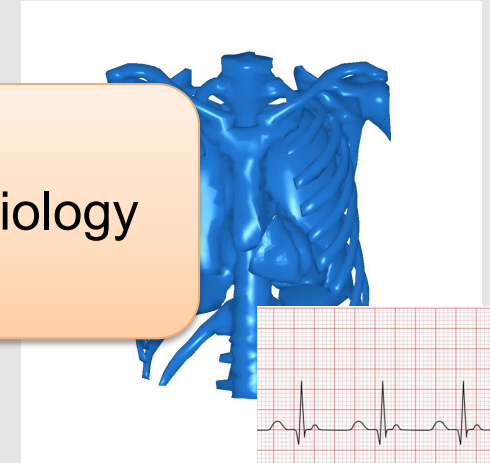
Valen-Sendstad, Khalili, Kjeldsberg

Single cells (and sub-cellular)



Tveito, Jæger, Finsberg, Wall

Electrophysiology



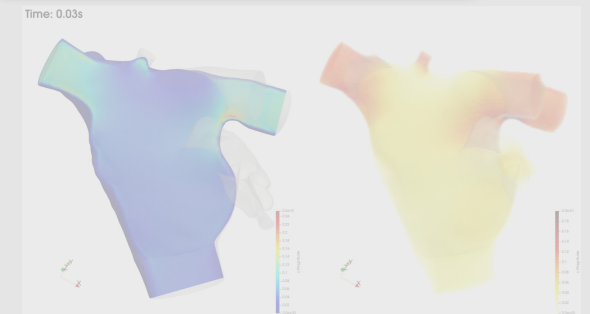
I am primarily work with cell-models, electrophysiology and mechanics

Blood flow

Mechanics



Finsberg, Sundnes, Wall



Valen-Sendstad, Khalili, Kjeldsberg

# I am not a biologist



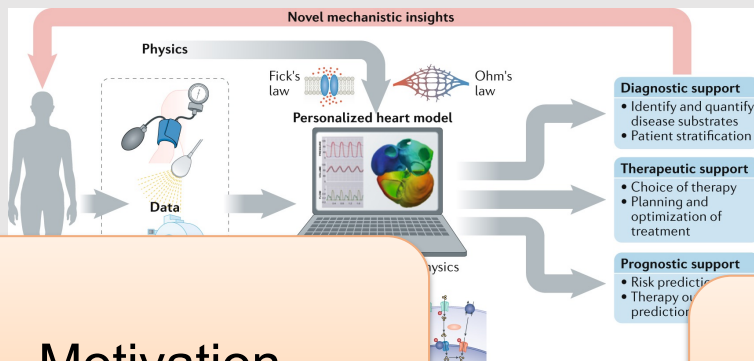
- 2014: Master: NTNU – Applied mathematics
- 2014-2017: PhD Scientific computing – Cardiac modeling (CaMO) at Simula – Patient specific computational modeling of cardiac mechanics
- 2017-2021: Research engineer
- 2021-present: Senior Research Engineer



Berkeley  
UNIVERSITY OF CALIFORNIA



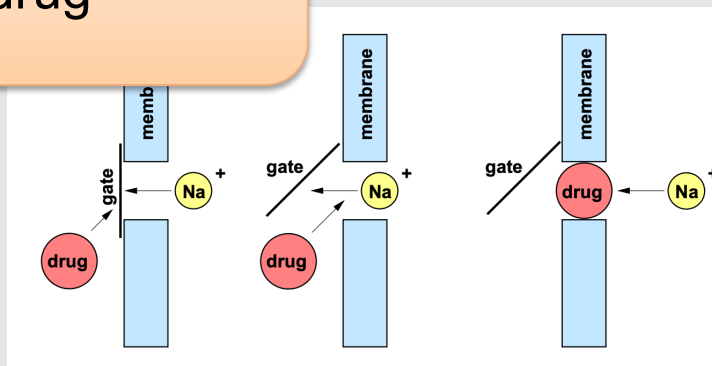
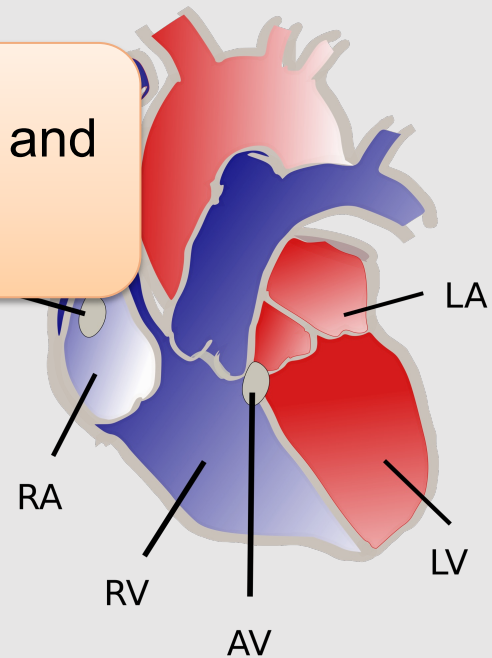
SIM  
CARDIO  
TEST



Motivation

How to model a drug

Basic anatomy and physiology



How to model the heart

Ion channel model

Cell

embed

Na<sup>+</sup>

Ca<sup>2+</sup>

SR

$$I_{Na} = g_{Na} m^3 h j (V - E_{Na})$$

$$\frac{dm}{dt} = \frac{m_{\infty}(V) - m}{\tau_m(V)}$$

$$\frac{dh}{dt} = \frac{h_{\infty}(V) - h}{\tau_h(V)}$$

$$\frac{dj}{dt} = \frac{j_{\infty}(V) - j}{\tau_j(V)}$$

$$C_m \frac{dV}{dt} + I_{ion} = I_{stim}$$

$$\chi \left( C_m \frac{dV}{dt} + I_{ion} \right) = \nabla \cdot (\sigma_i \nabla (V + \phi_e))$$

$$\nabla \cdot (\sigma_i \nabla V + (\sigma_i + \sigma_e) \nabla \phi_e) = 0$$

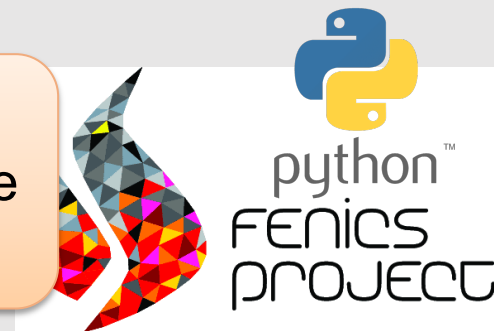
Simulated current during voltage clamp

Simulated action potential

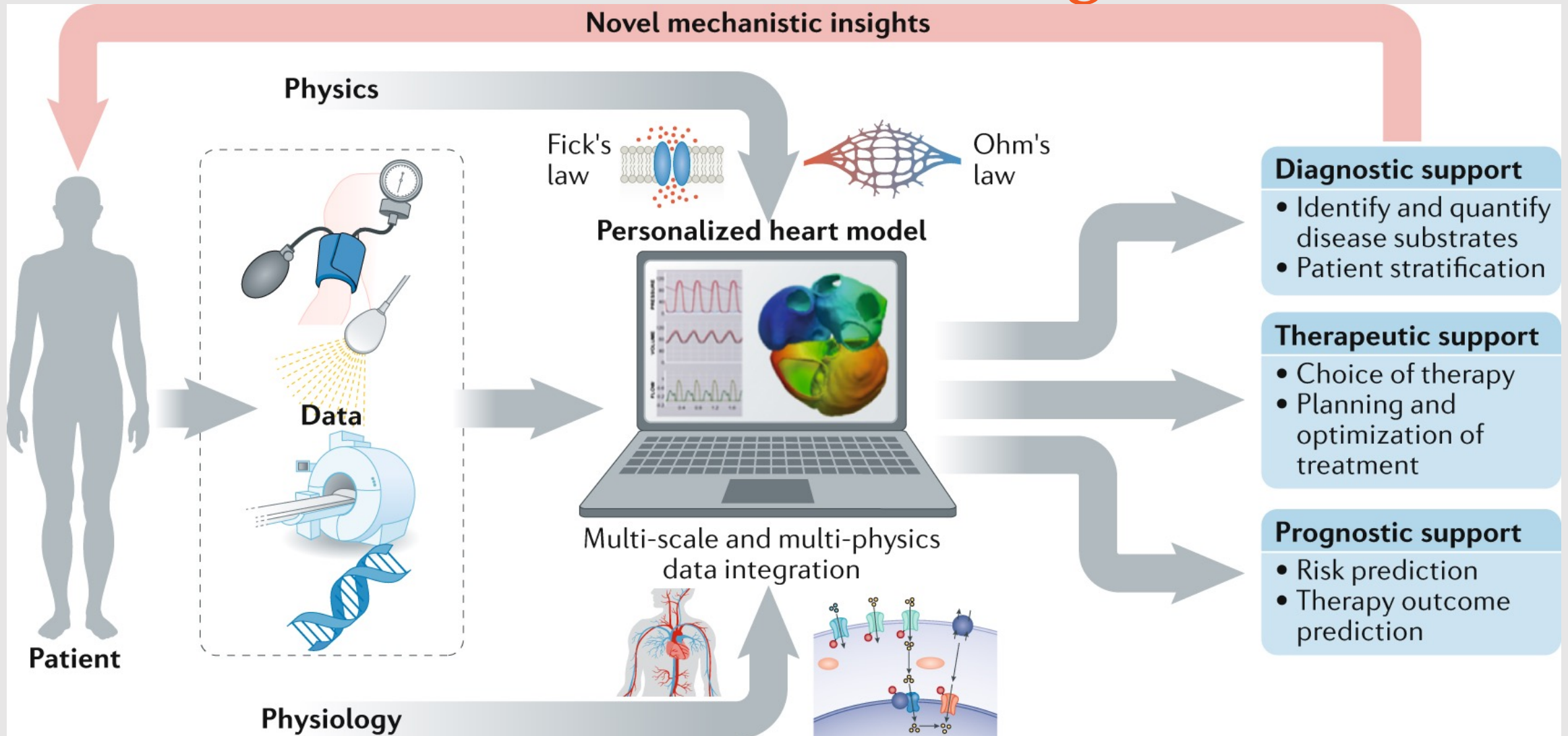
Normal propagation

Simulated arrhythmia

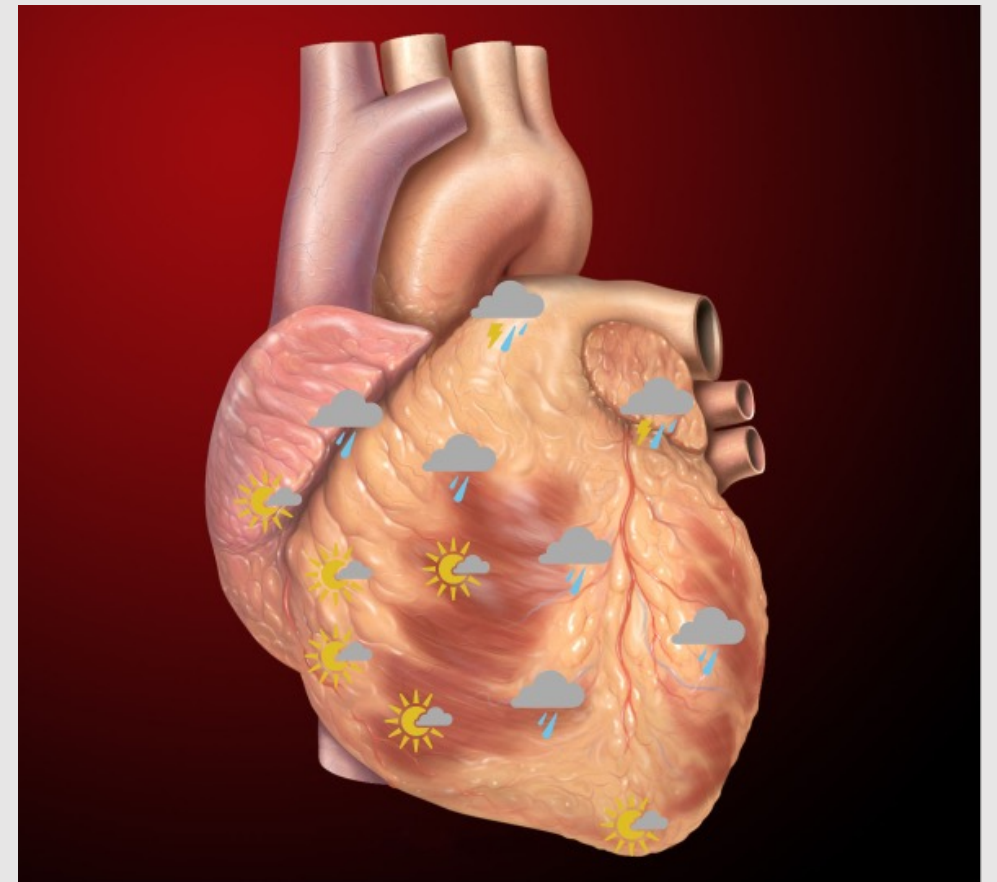
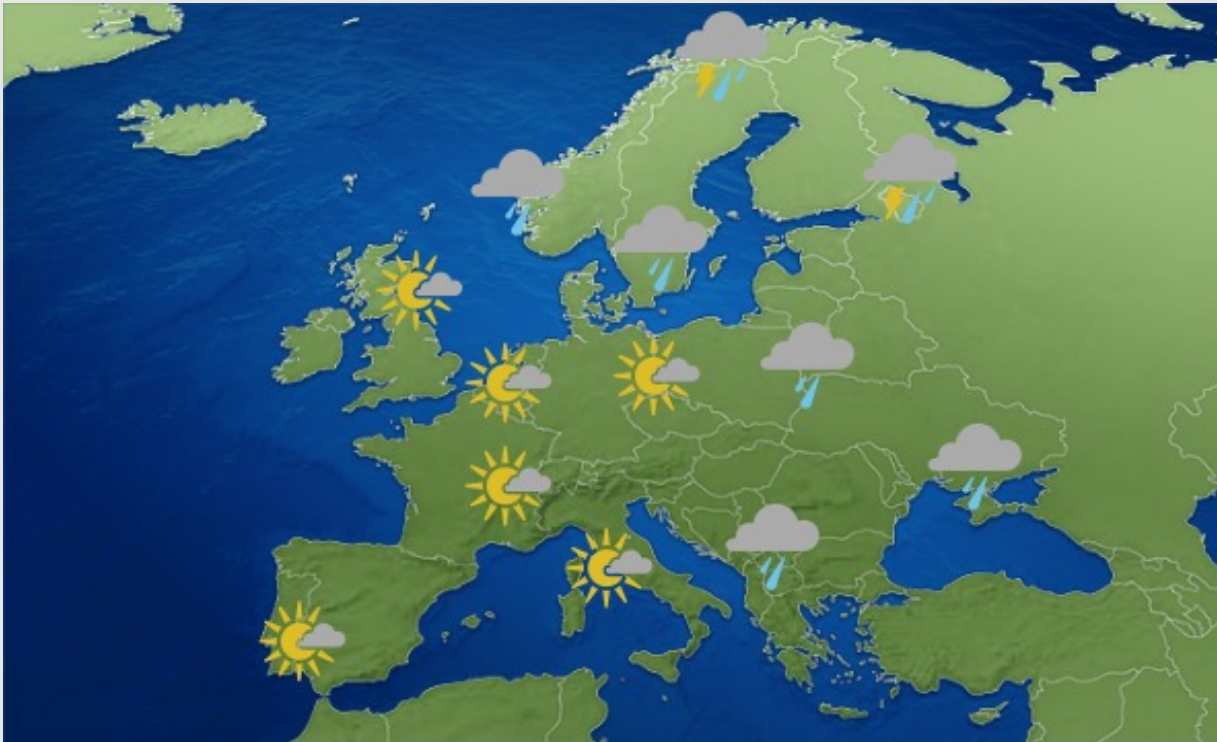
Which tools we use



# The long term goal is to use models to assist clinicians in the decision making



**We can forecast the weather, but would we be able to do the same with the heart?**



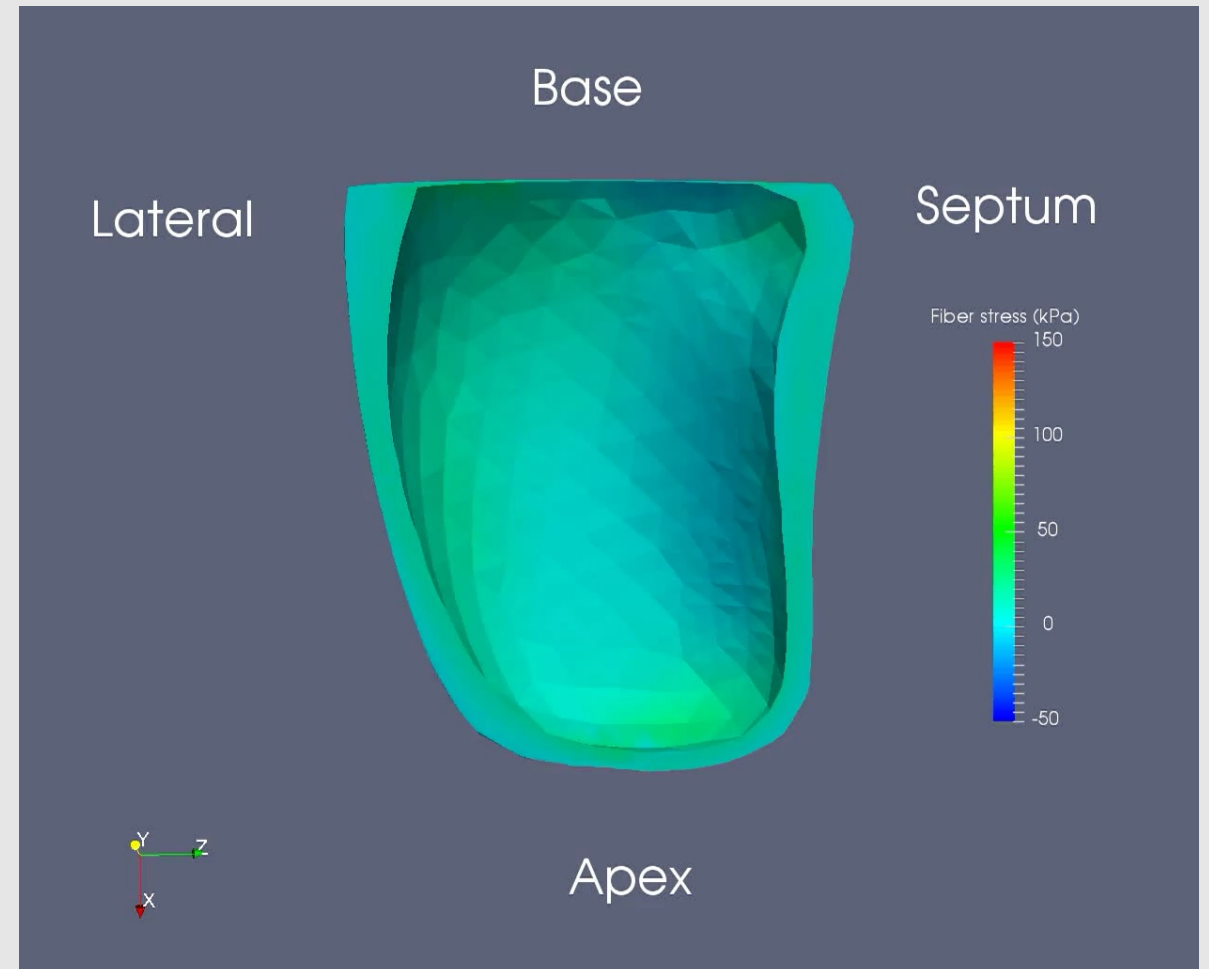


# Models can be used to compute quantities that are difficult / impossible to measure

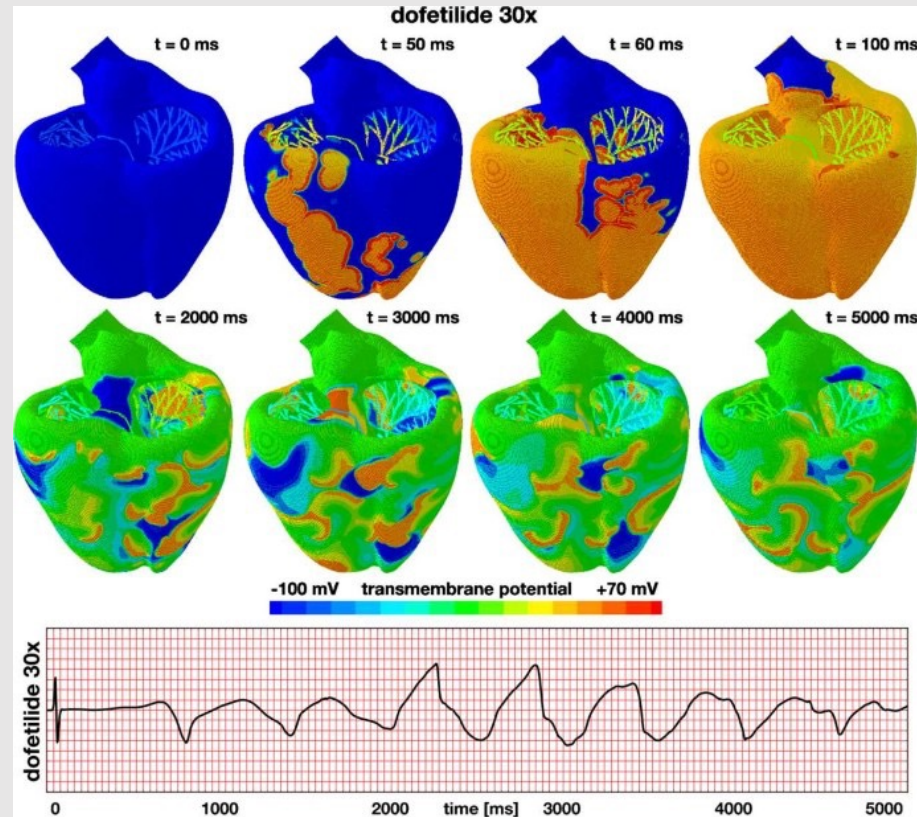
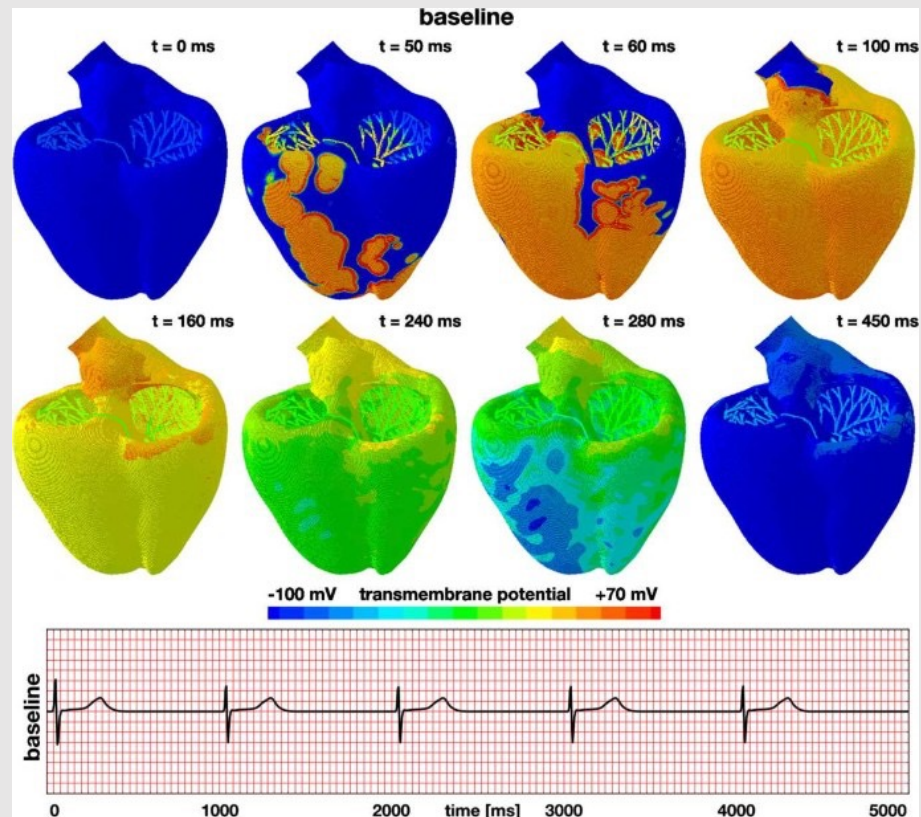
For example: forces / stresses in the heart

Validation is hard

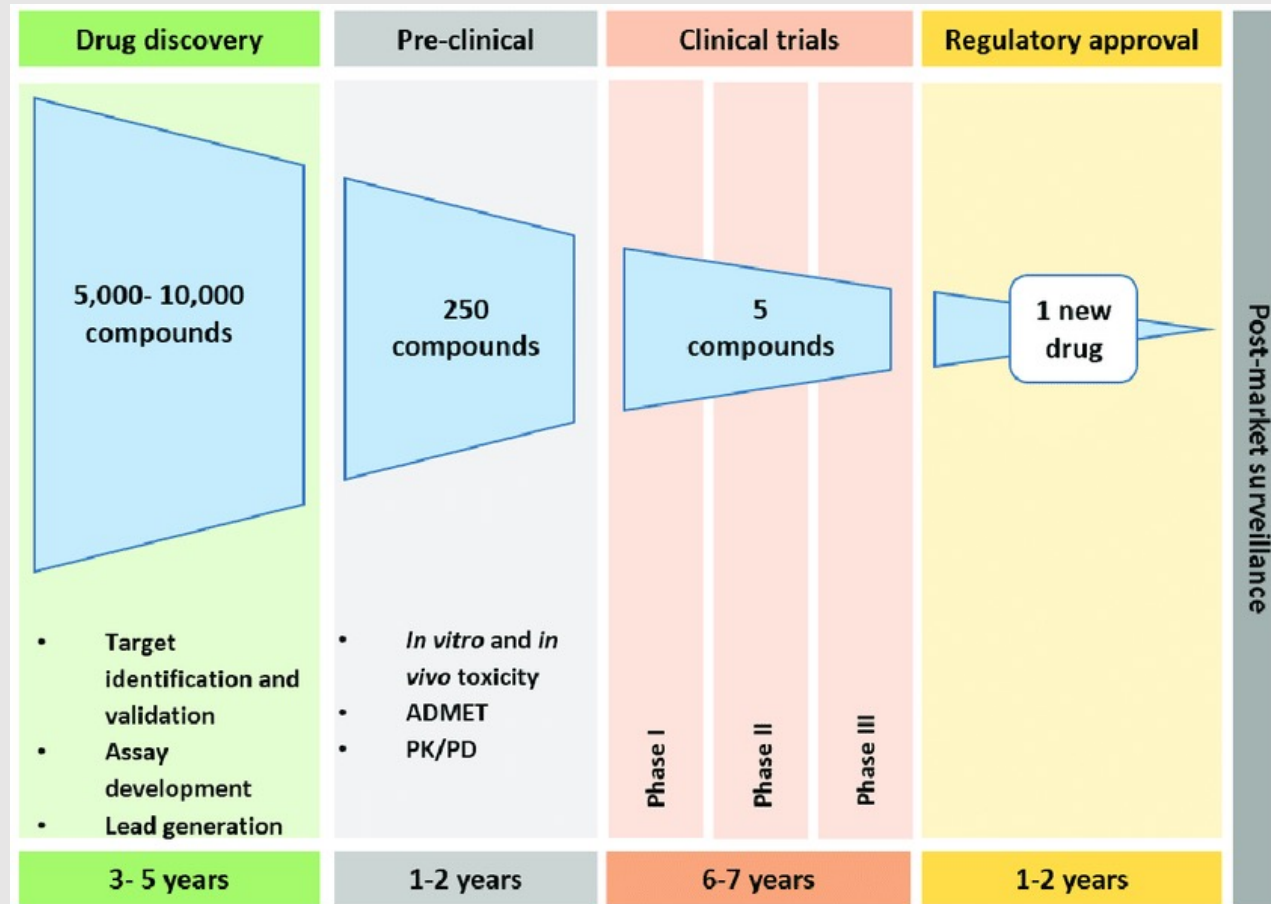
Development of new biomarkers



# Models can be used to test if a drug is safe / efficient

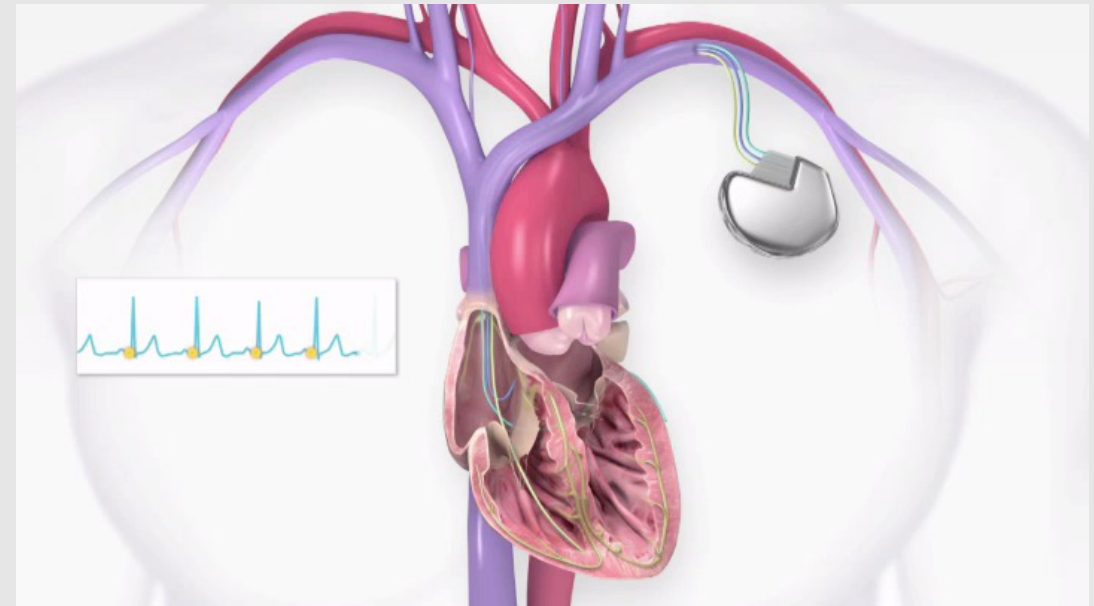
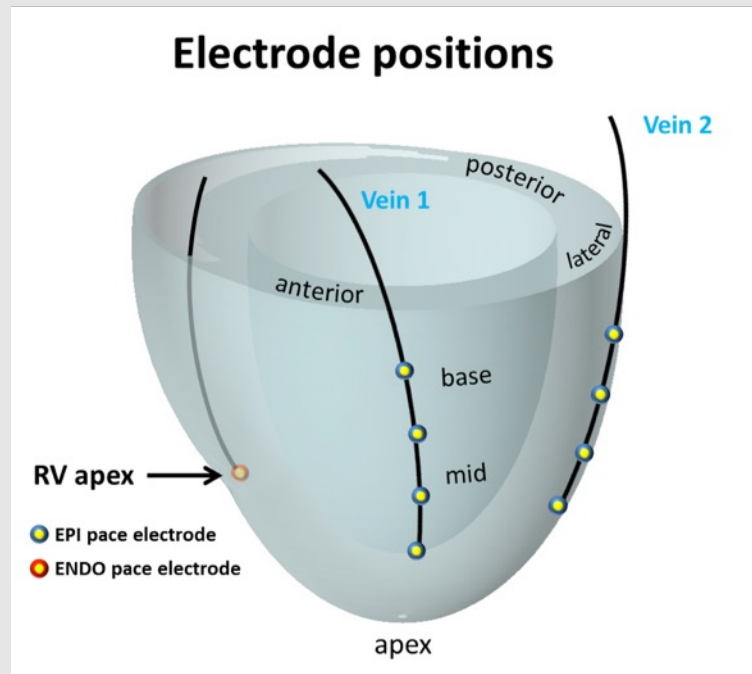


# Development of drugs is a costly and time consuming process



# Models can be used to test different therapies and optimize treatment

- Find optimal electrode positions for pacemakers



# The heart has four chambers

SA: Sino Atrial node

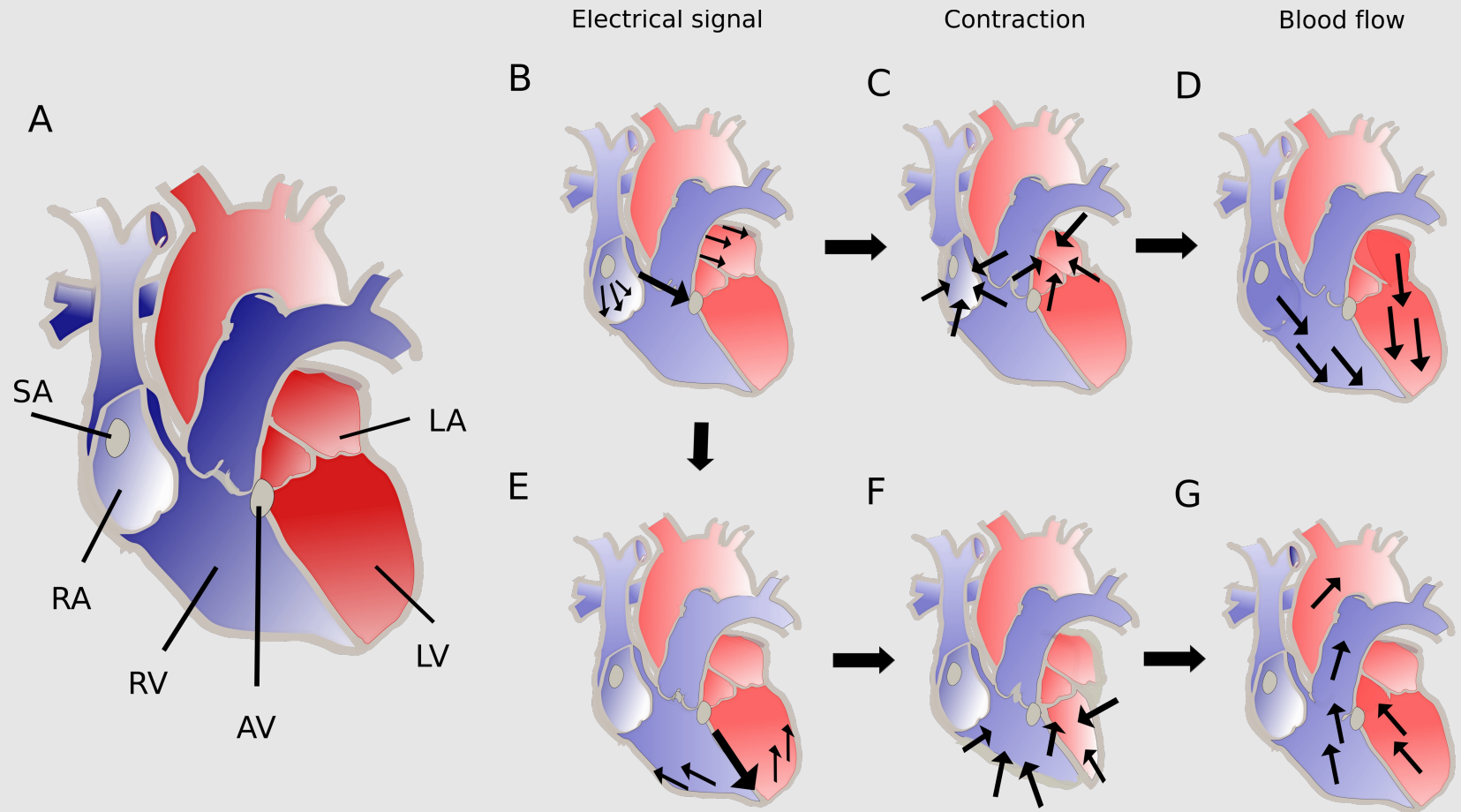
AV: Atrioventricular node

RA: Right Atrium

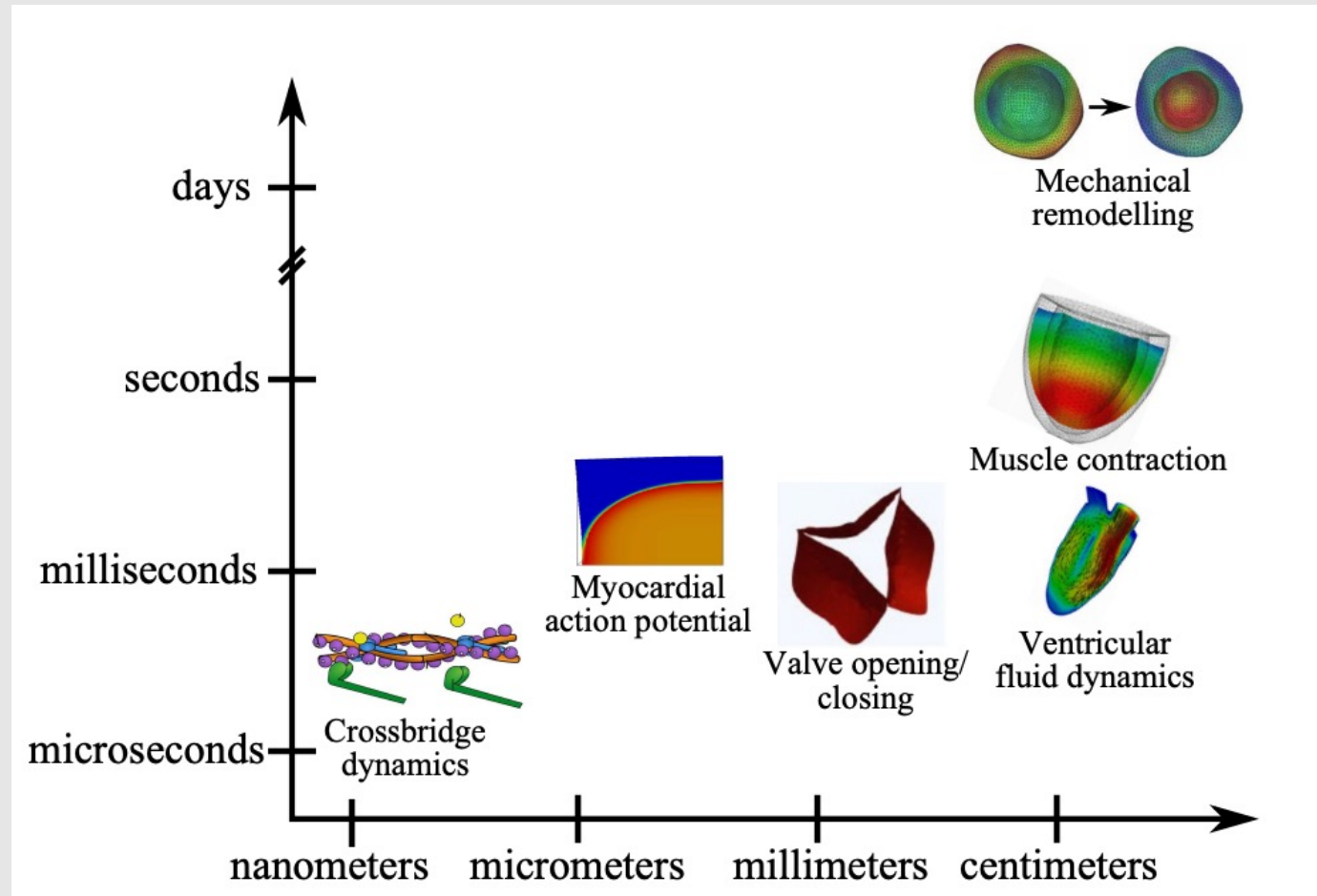
RV: Right ventricle

LA: Left Atrium

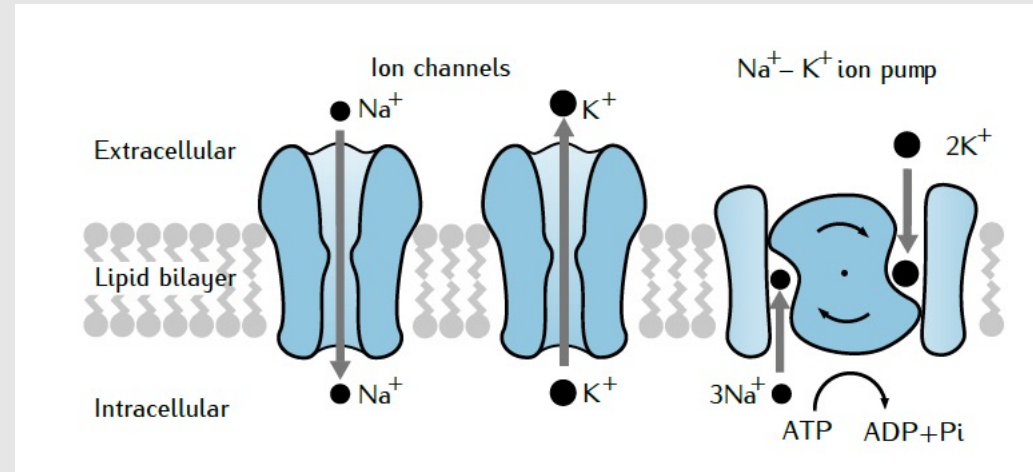
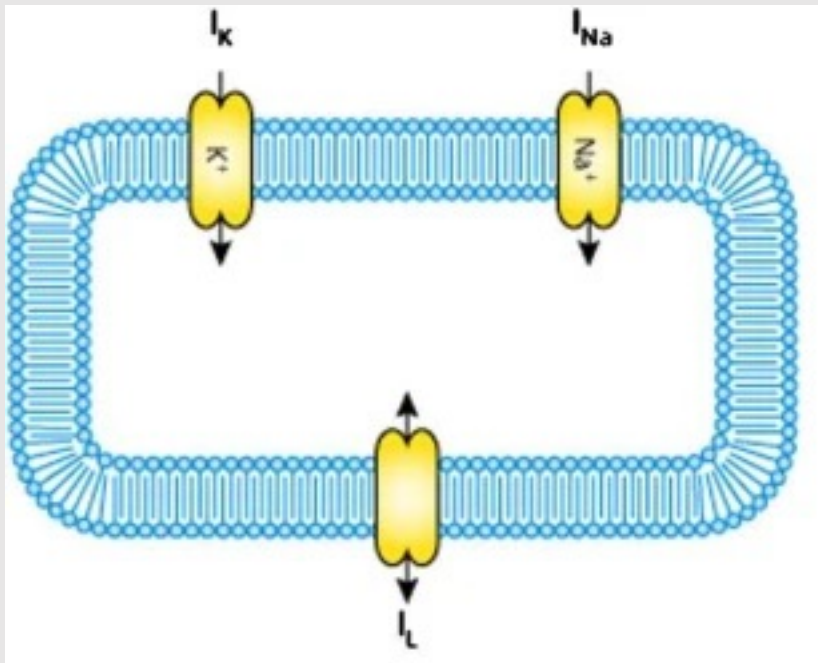
LV: Left ventricle



# The heart is operating on different spatial and temporal scales

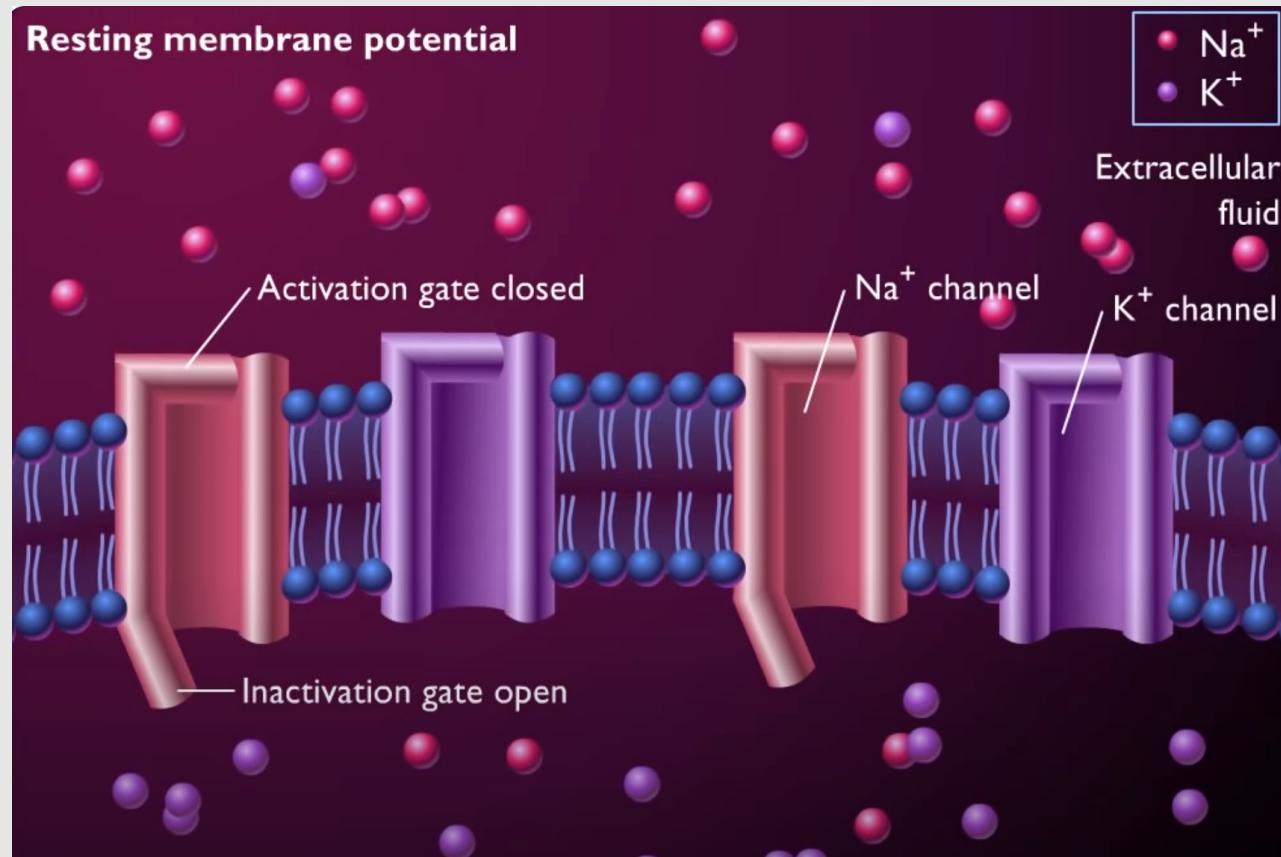


# A cell consists of two spaces separated by a membrane



Ions can flow through specialized channels that can open and close in response to changes in voltage

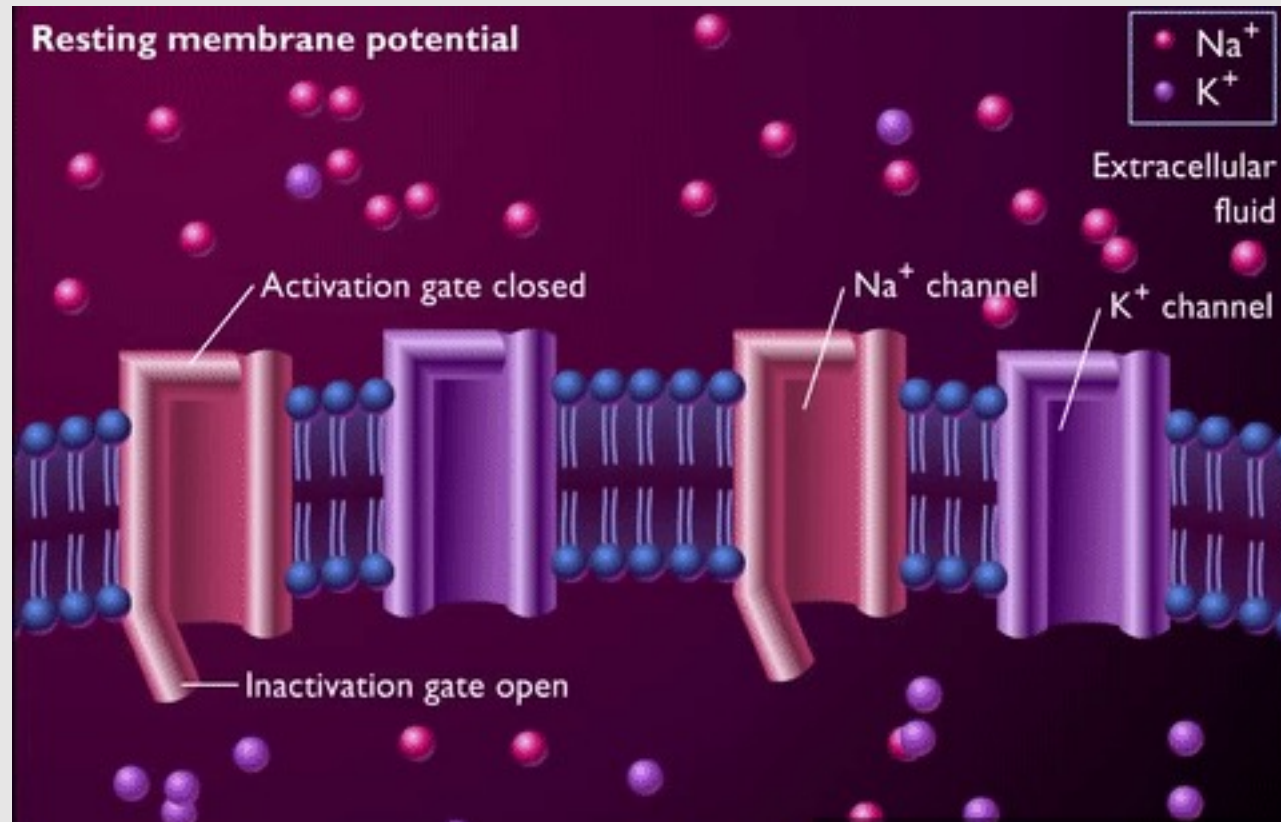
# A single ion channel can be open or closed by one or more gates



[https://www.youtube.com/watch?v=kxnb\\_TSqmFY&t=2s](https://www.youtube.com/watch?v=kxnb_TSqmFY&t=2s)



# A single ion channel can be open or closed by one or more gates



[https://www.youtube.com/watch?v=kxnb\\_TSqmFY&t=2s](https://www.youtube.com/watch?v=kxnb_TSqmFY&t=2s)

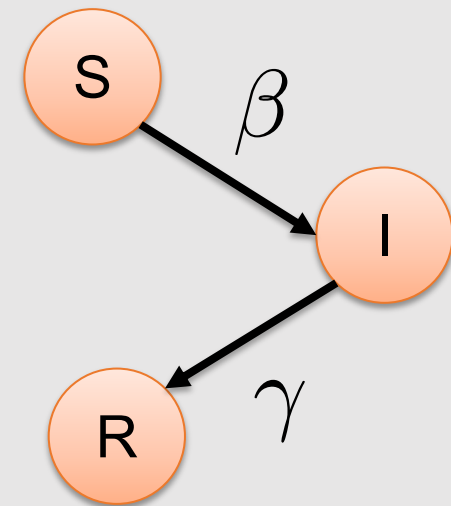
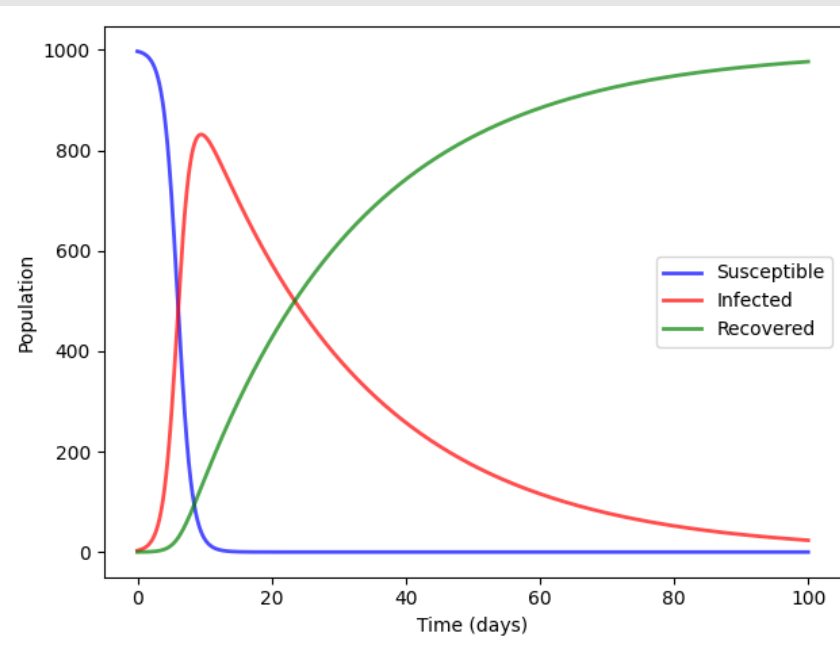
# We can model a single cardiac cell using a system of ordinary differential equations (ODE)

- An system of ordinary differential equation described how a variables changes over time
- For example a pandemic (using the SIR model)

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$



# To solve the ODEs we use General Ode TRANslator (Gotran(x))

- Domain Specific Language (DSL) for ODEs
- Describe ODEs in DSL
- Generate code in different programming languages for solving

<https://github.com/finsberg/gotranx>

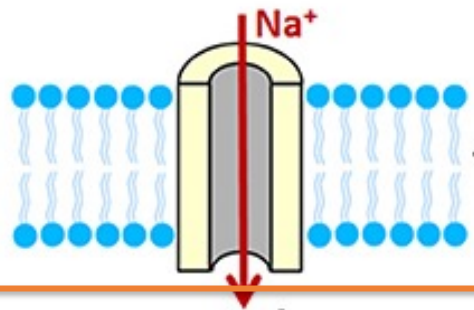
<https://github.com/ComputationalPhysiology/gotran>

```
sandbox > sir > sir ode
1  parameters(
2      beta=0.001,
3      gamma=0.04
4  )
5
6  states(
7      S=997,
8      I=3,
9      R=0
10 )
11
12 dS_dt = -beta * S * I
13 dI_dt = beta * S * I - gamma * I
14 dR_dt = gamma * I
```

# Typical state variables are ionic concentrations, state that controls channel opening and the voltage

Total current through one channel

Ion channel model



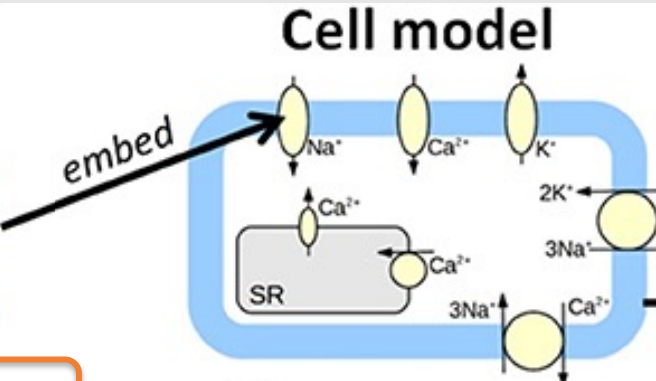
$$I_{Na} = g_{Na} m^3 h j (V - E_{Na})$$

$$\frac{dm}{dt} = \frac{m_{\infty}(V) - m}{\tau_m(V)}$$

$$\frac{dh}{dt} = \frac{h_{\infty}(V) - h}{\tau_h(V)}$$

$$\frac{dj}{dt} = \frac{j_{\infty}(V) - j}{\tau_j(V)}$$

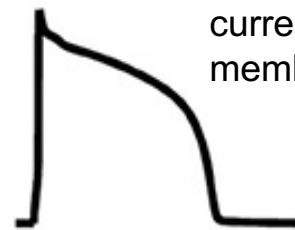
Variables determining whether a channel is open or closed



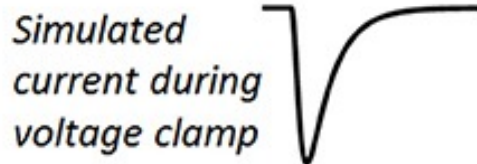
$$C_m \frac{dV}{dt} + I_{ion} = I_{stim}$$

Conservation of charge

Sum of all currents across membrane



Simulated action potential



Simulated current during voltage clamp

# How can we determine model parameters?

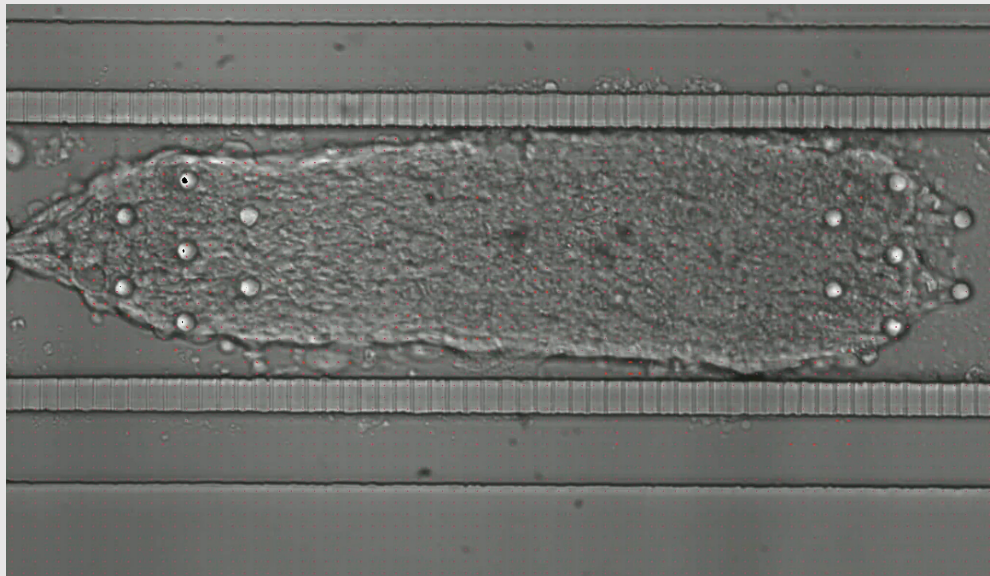
- For example we need to determine the conductance for each channel

$$I_{\text{Na}} = g_{\text{Na}} m^3 h j (V - E_{\text{Na}})$$

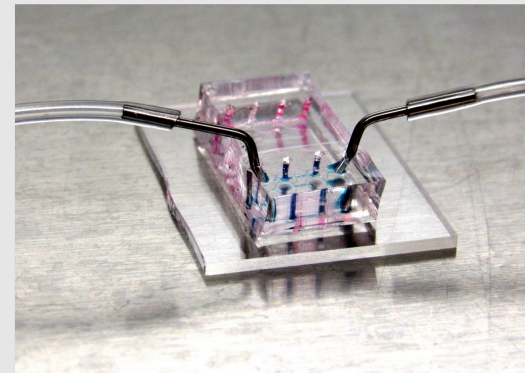
# We can use data from optical measurements



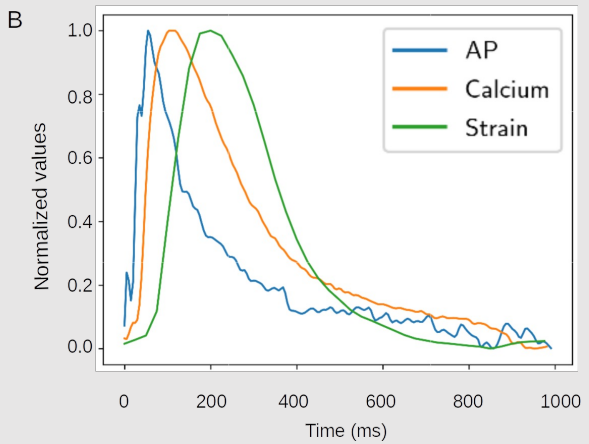
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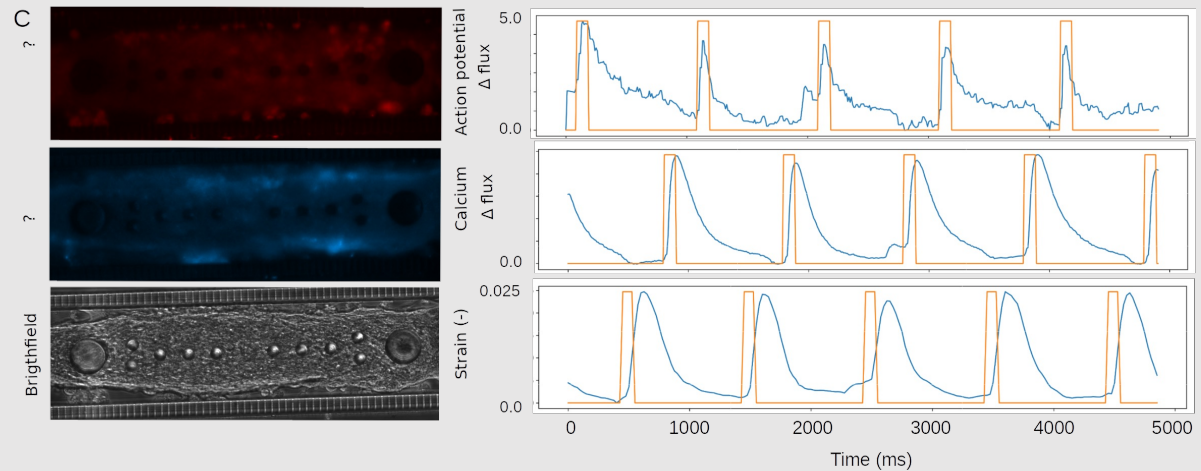
A



B



C

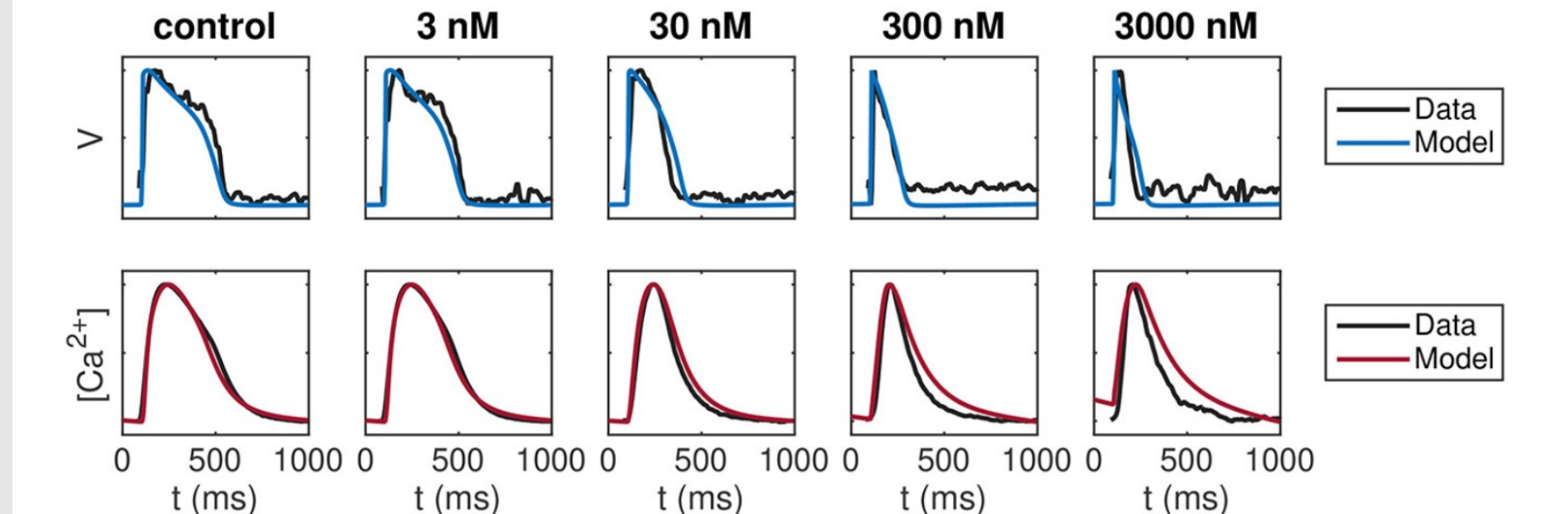


We can measure the membrane potential and calcium concentration inside the cell using optics

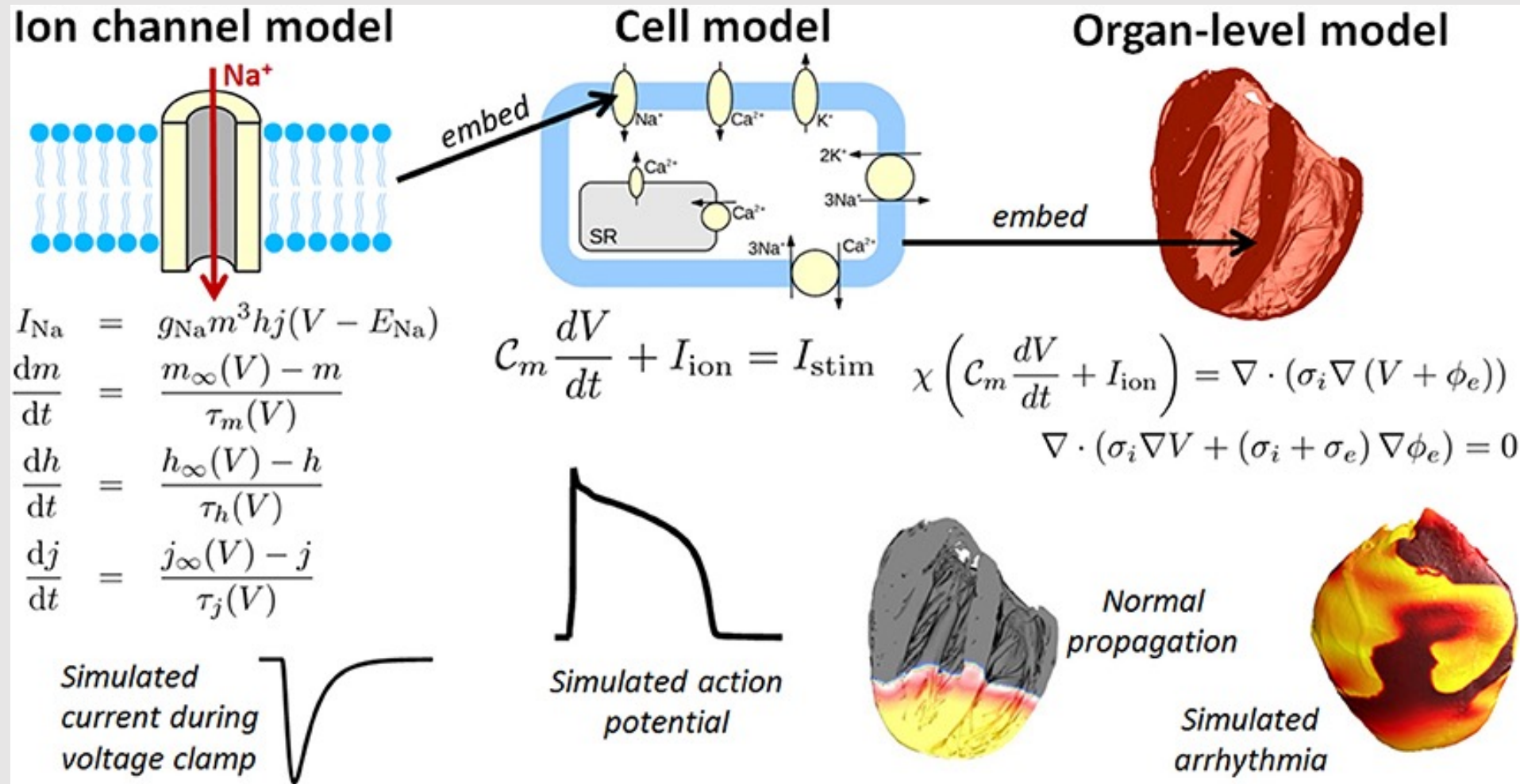
# We select a few parameters in the model and tune them to fit data

$$I_{\text{Na}} = g_{\text{Na}} m^3 h j (V - E_{\text{Na}})$$

**C** Comparison between data and fitted model

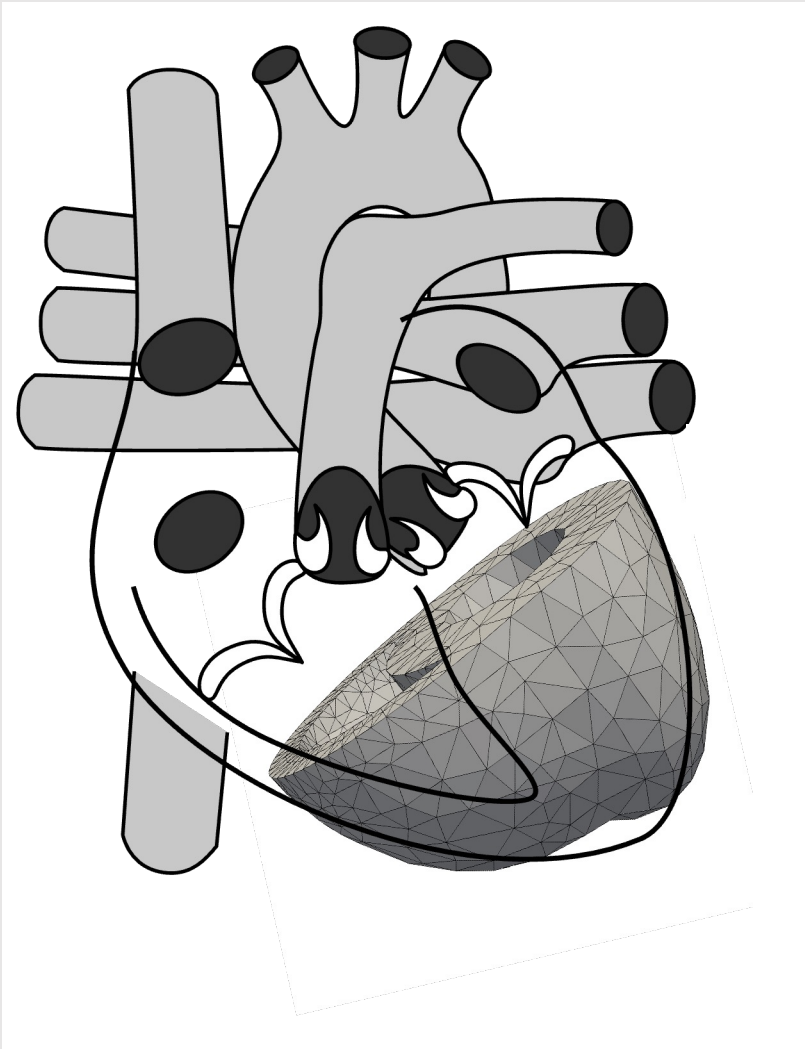


# We embed the cell model into the organ-level model by having one different cell in each point

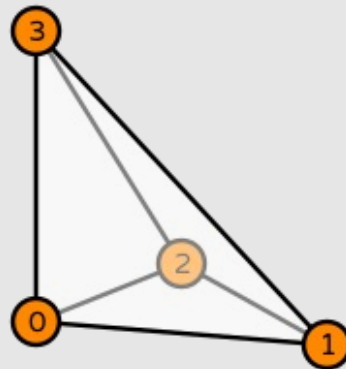




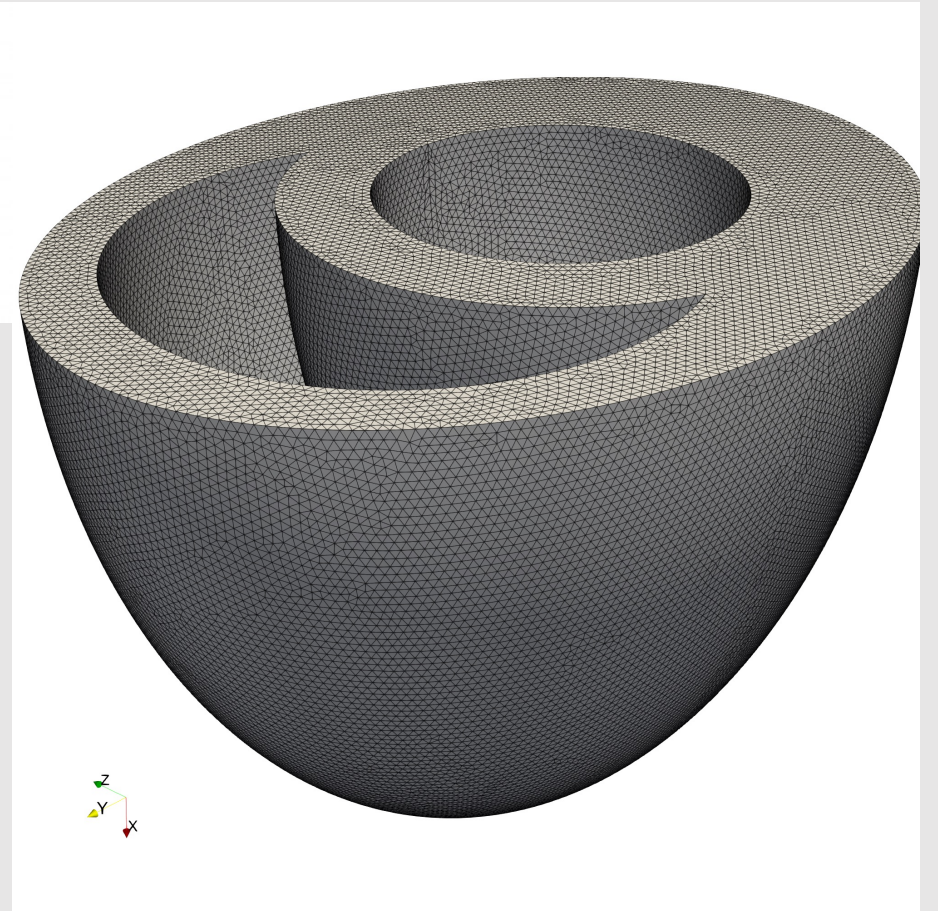
# We discretize the geometry into tetraheadra and assign one heart cell to each node



<https://gmsh.info>

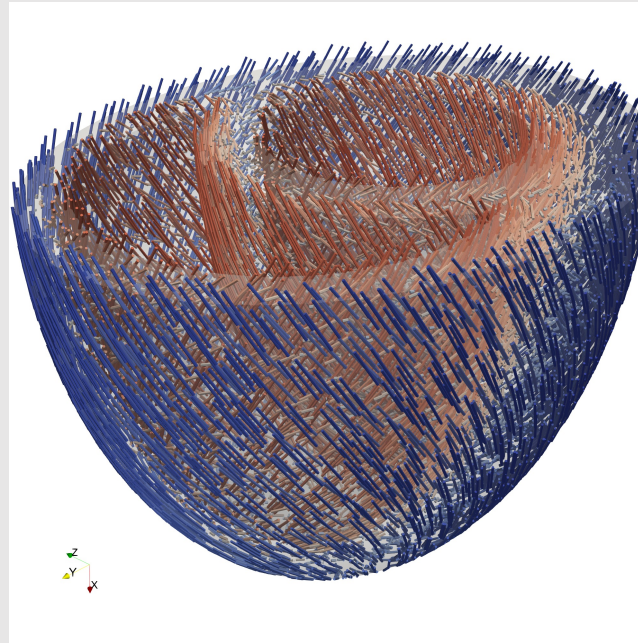
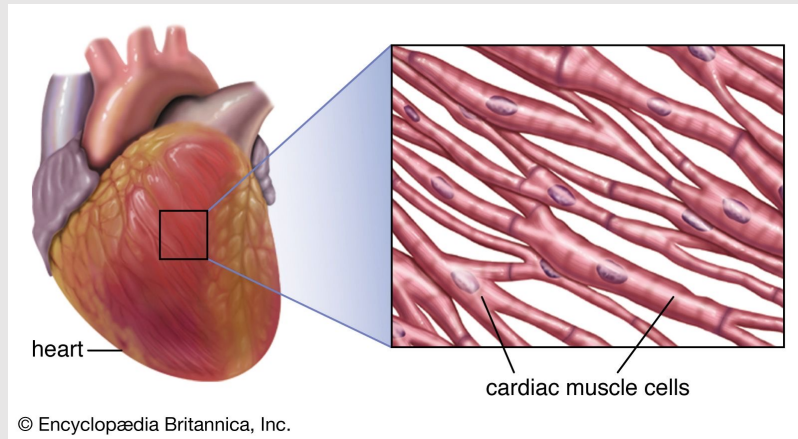


<https://defelement.com/elements/laqrage.html>



[https://github.com/ComputationalPhysiology/cardiac\\_geometries](https://github.com/ComputationalPhysiology/cardiac_geometries)

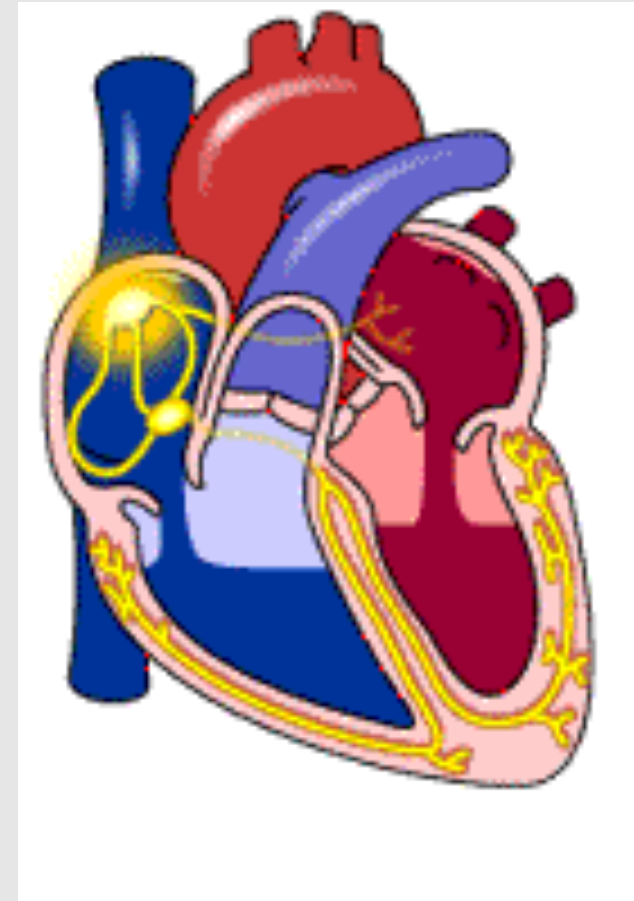
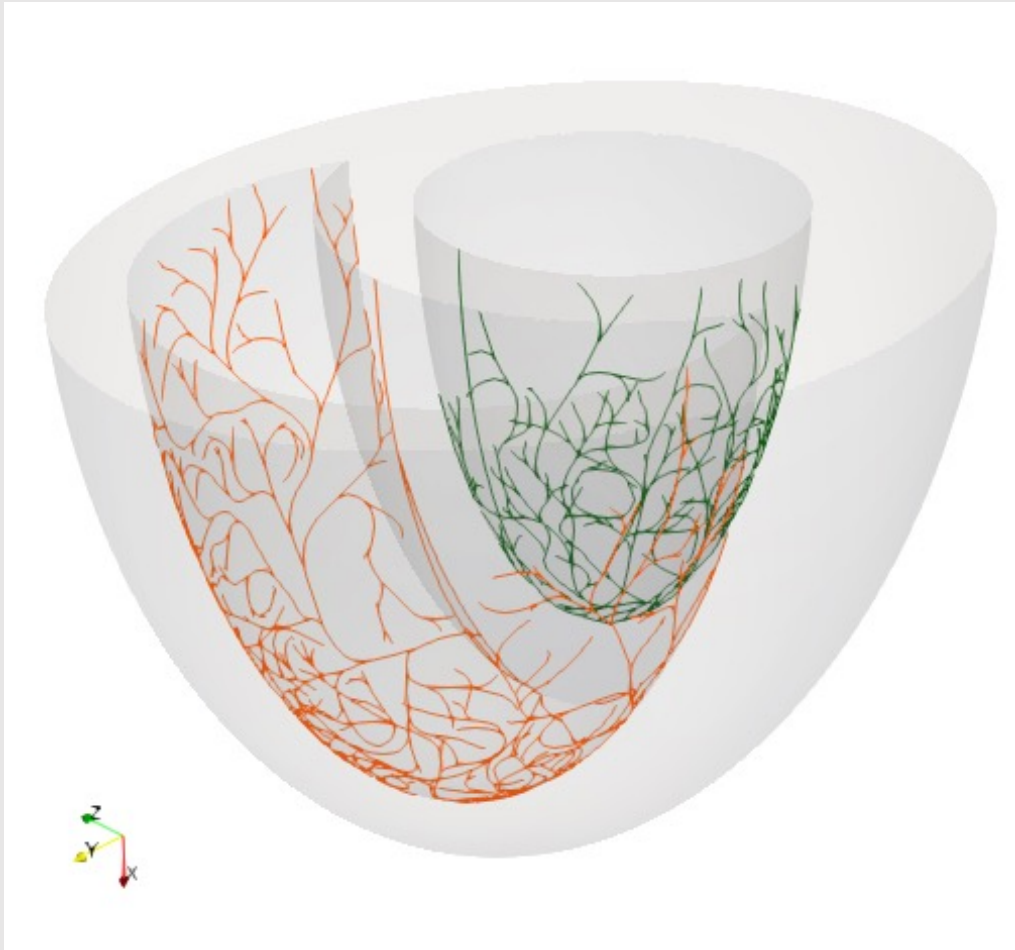
# We also need vectors that assigns the direction of the muscle fibers in the heart



<https://github.com/finsberg/ldrb>

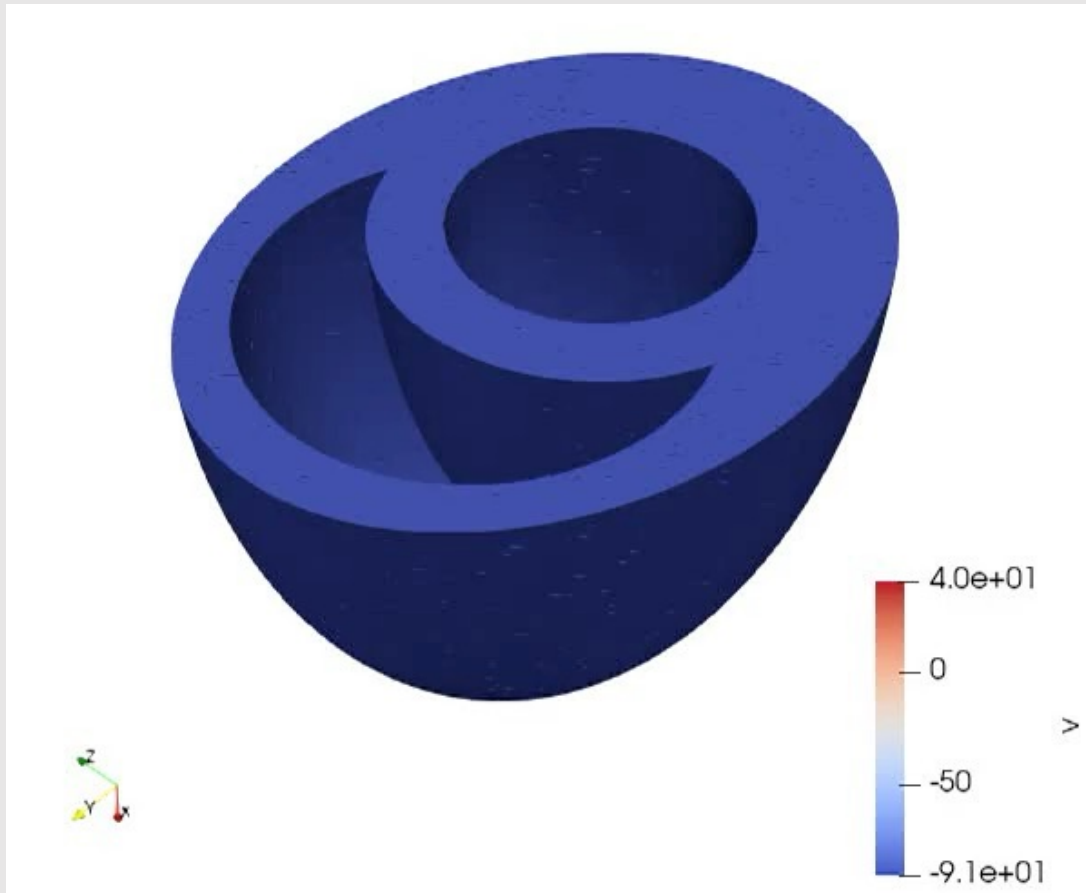
- Electrical current travels faster along the fibers
- Heart tissue is stiffer along the fibers
- The tissue contracts in the direction of the fibers

The heart tissue is stimulated by specialized cells (called purkinje cells) where the conduction is faster



<https://github.com/finsberg/fractal-tree>

# Now we can simulate the electrical propagation



README MIT license

## fenics-beat

A simplified version of `cbcbeat` for running cardiac electrophysiology simulations.

- Source code: <https://github.com/finsberg/fenics-beat>
- Documentation: <https://finsberv.github.io/fenics-beat>

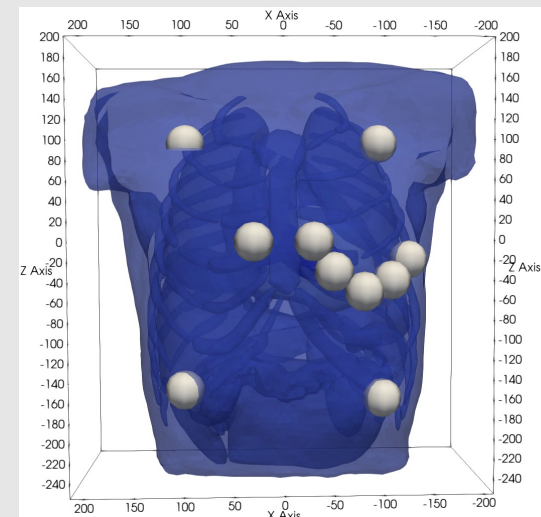
### Install

You can install the library with pip

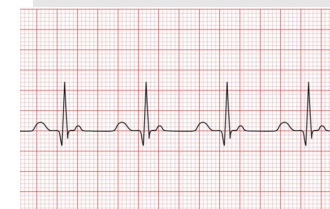
```
python3 -m pip install fenics-beat
```

### Getting started

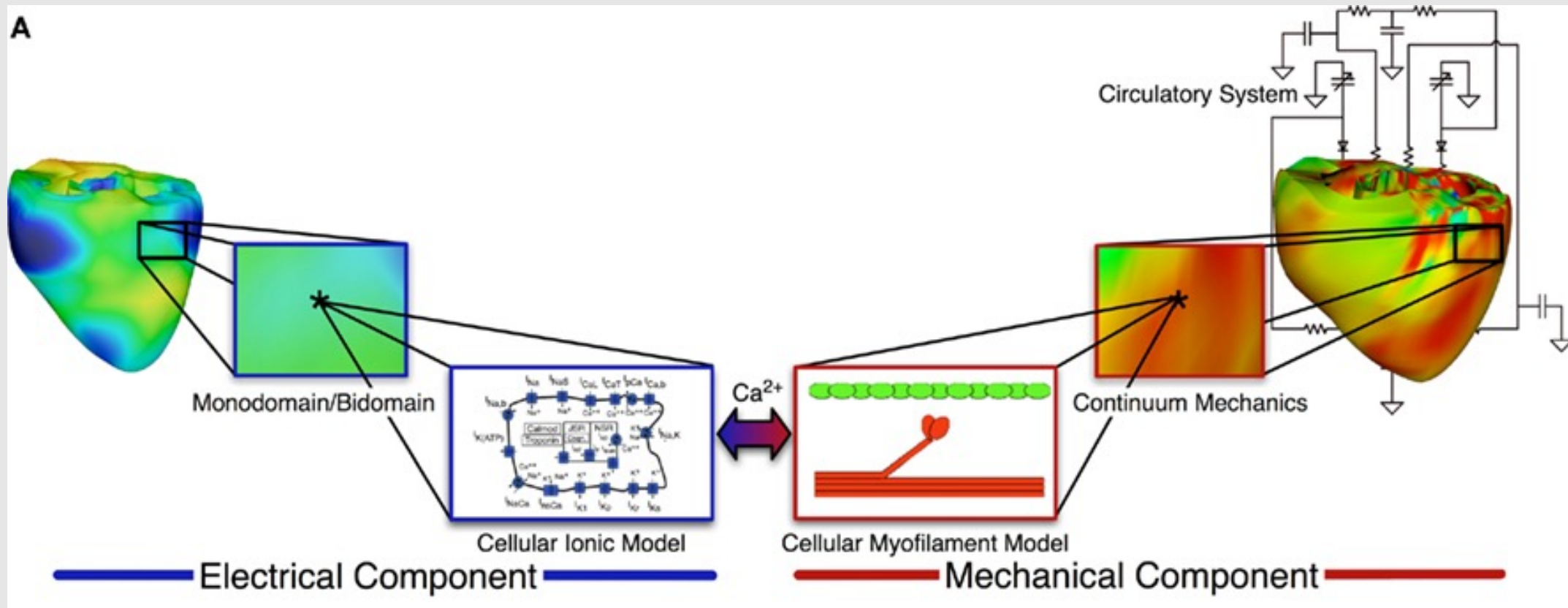
<https://github.com/finsberg/fenics-beat>



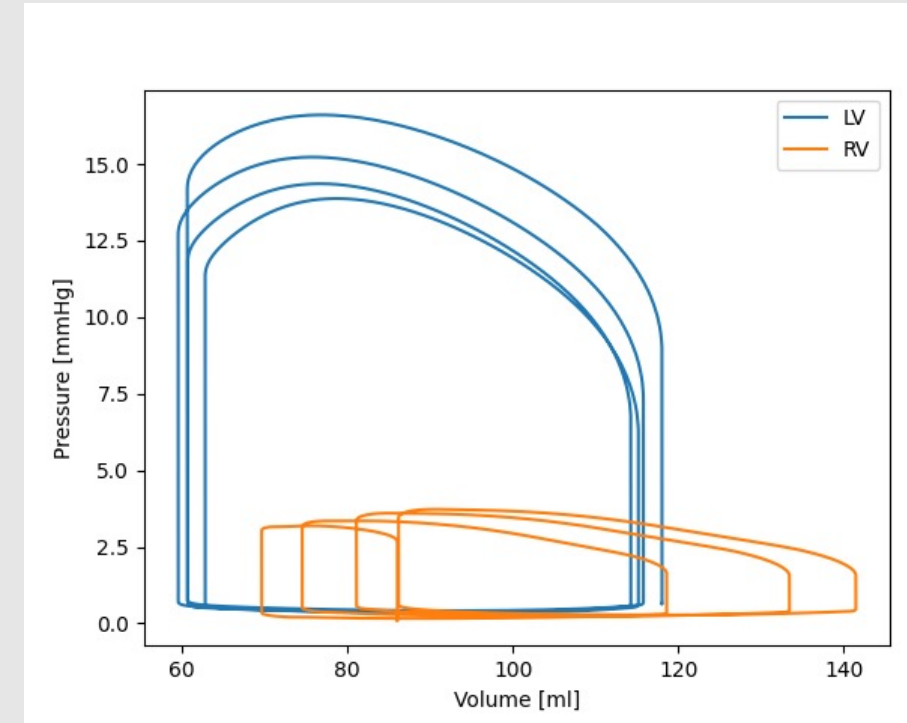
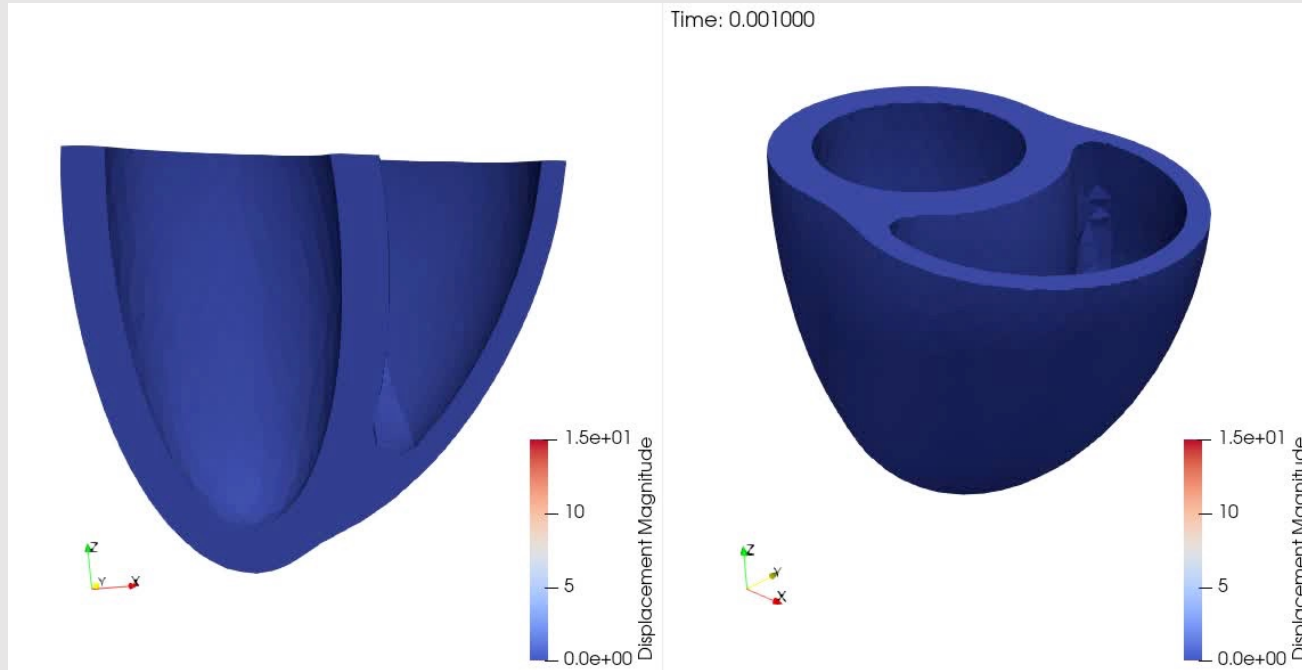
And Compute ECG



# From the electrical model we can compute the calcium concentration which drives the mechanics



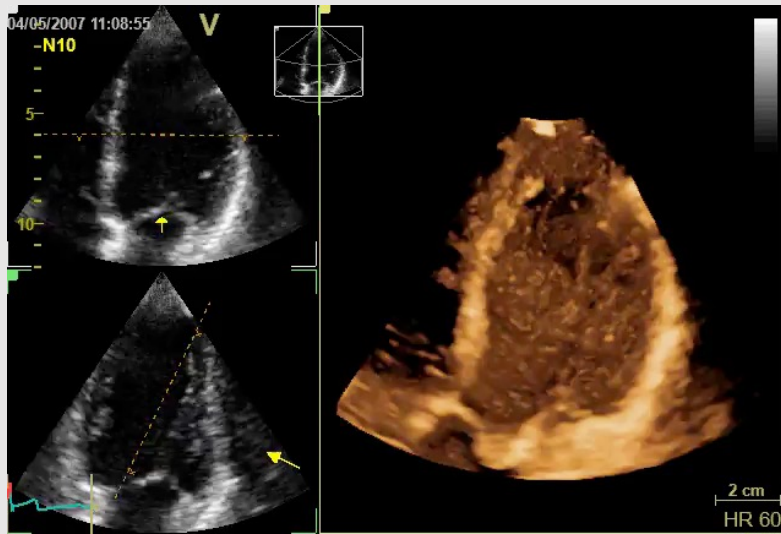
# And we can use this to simulate a beating heart



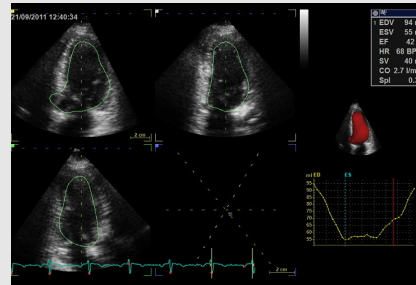
<https://github.com/marchirschvogel/ambit/tree/master>  
<https://github.com/finsberg/pulse>

Plot of Pressure vs Volume  
inside the two chambers

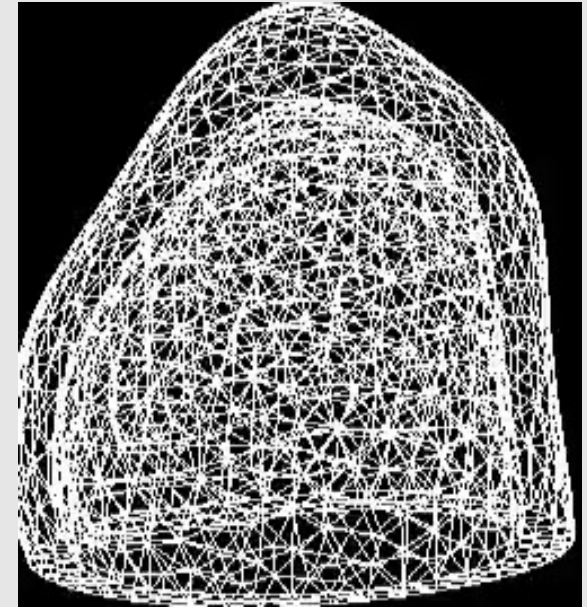
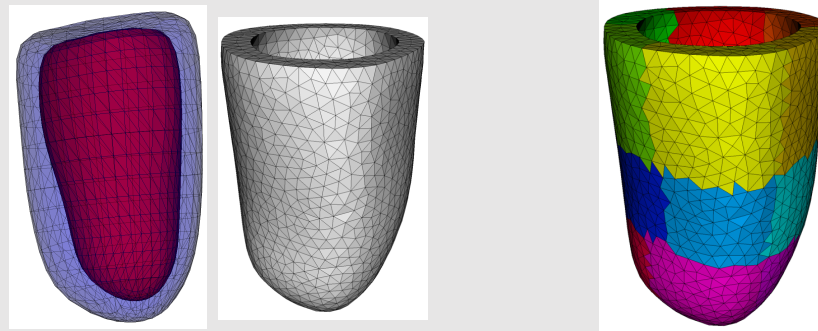
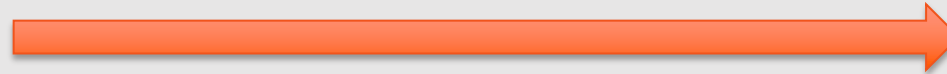
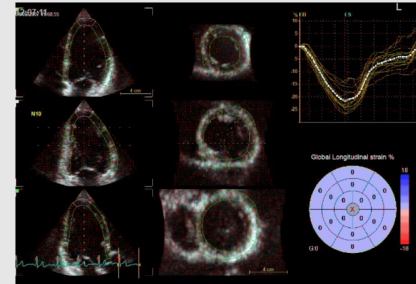
# My PhD was about building patient specific computational models of the heart



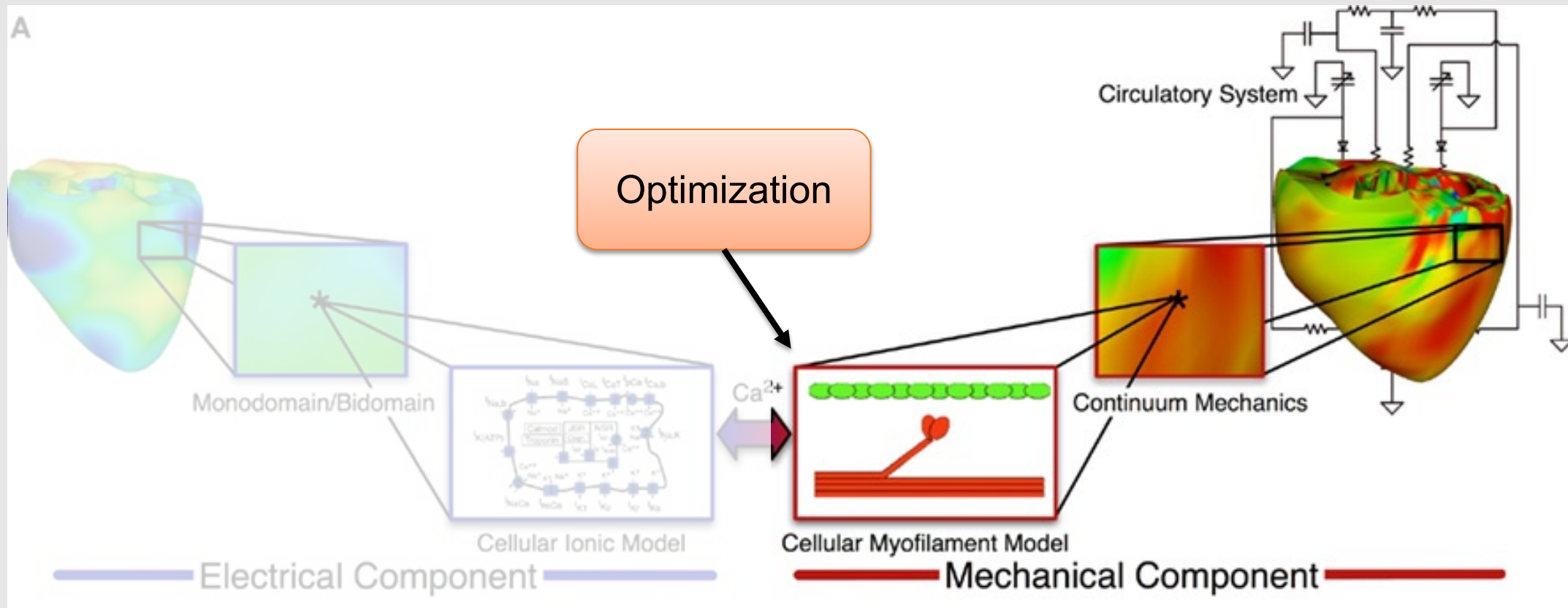
Volume



Regional strain

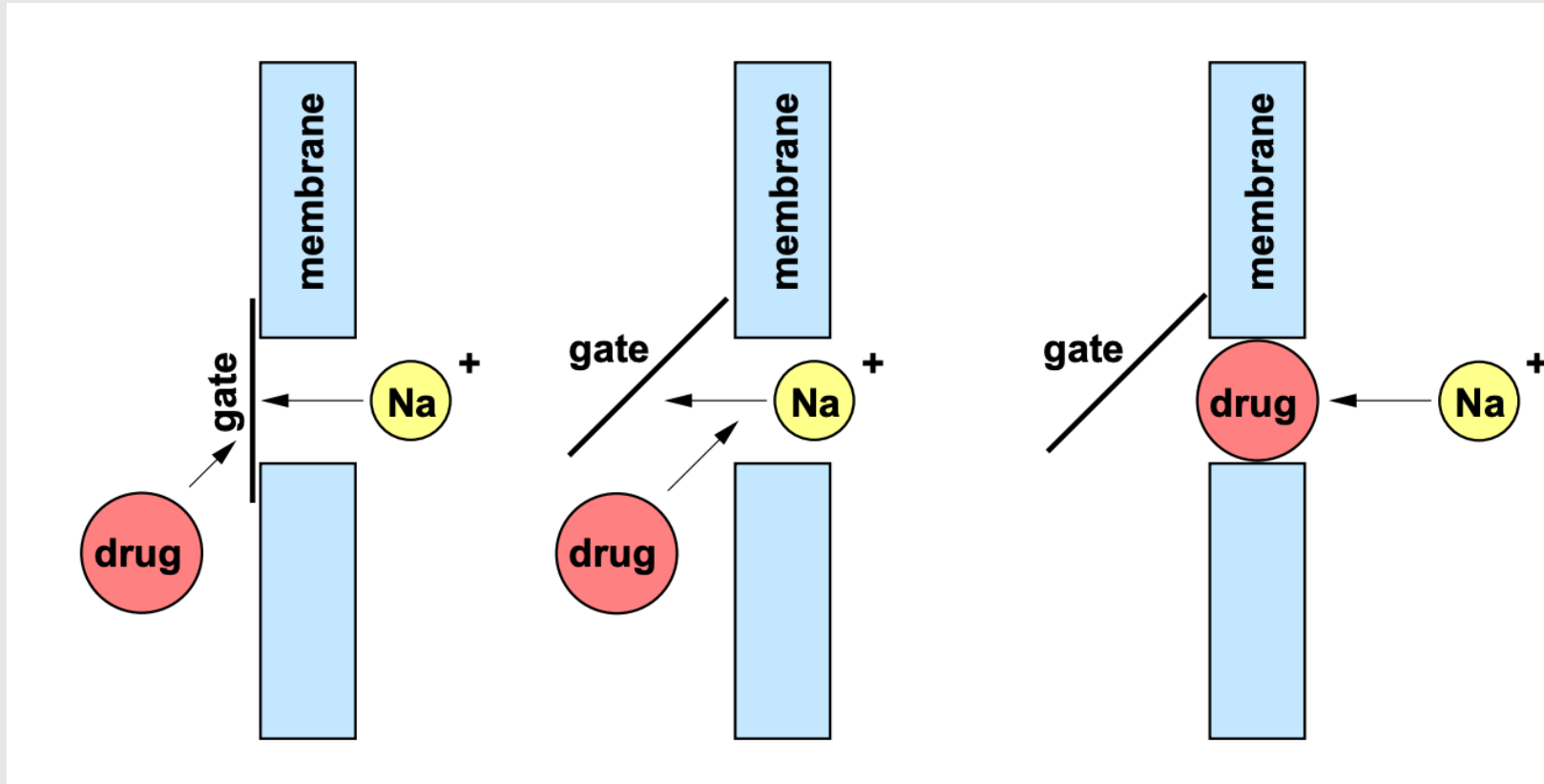


In that case we used optimization to find how much contraction we needed to fit the data



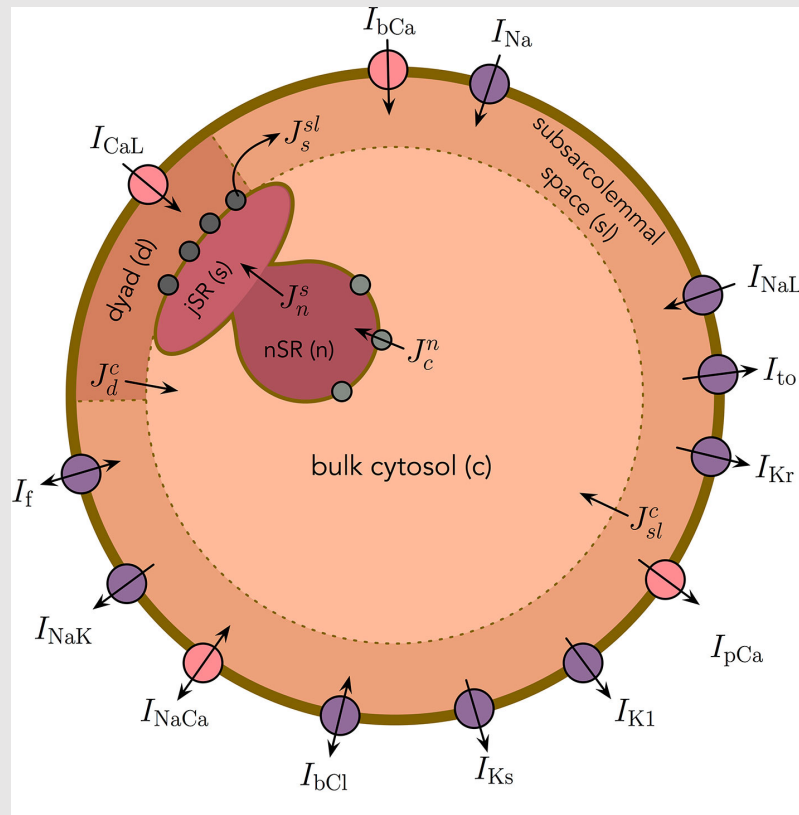


# To model a drug effect we can block one of these channels



Starmer, C. Frank. "How antiarrhythmic drugs increase the rate of sudden cardiac death." *International Journal of Bifurcation and Chaos* 12.09 (2002): 1953-1968.

# To model a drug effect we can block on of these channels



### Ion channel model

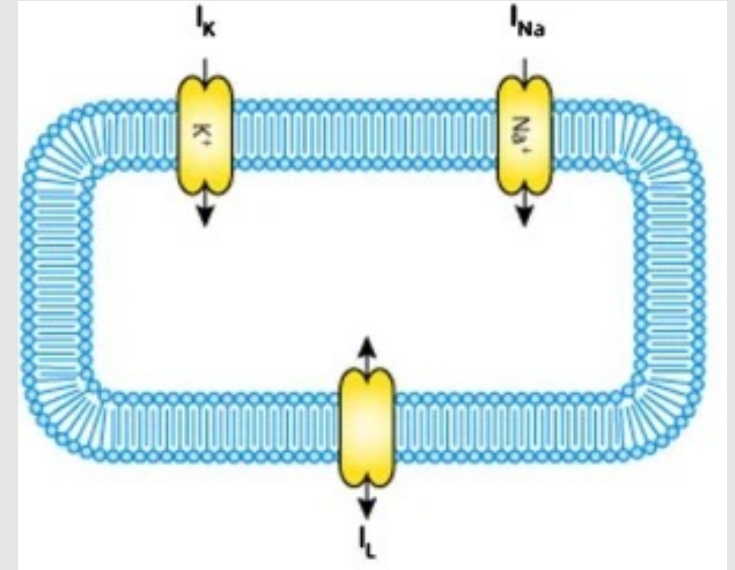
$$I_{Na} = g_{Na} m^3 h j (V - E_{Na})$$

$$\frac{dm}{dt} = \frac{m_{\infty}(V) - m}{\tau_m(V)}$$

$$\frac{dh}{dt} = \frac{h_{\infty}(V) - h}{\tau_h(V)}$$

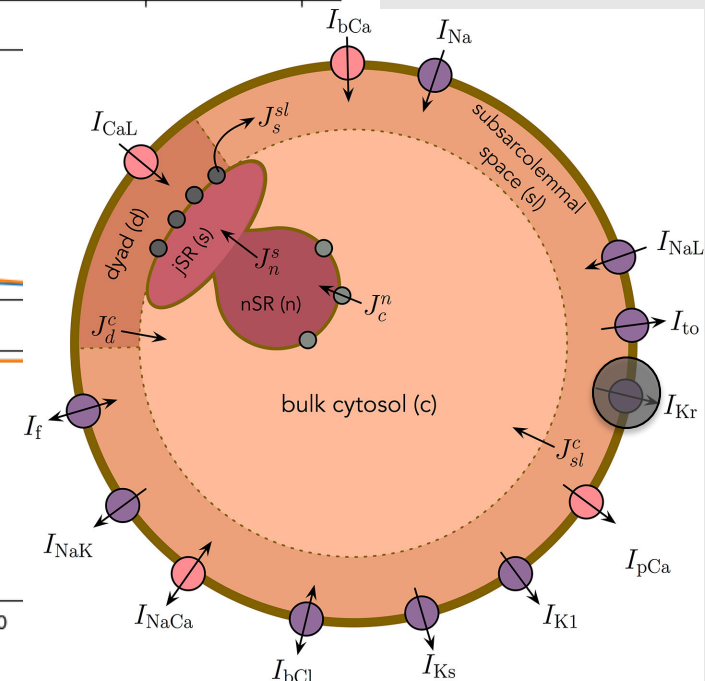
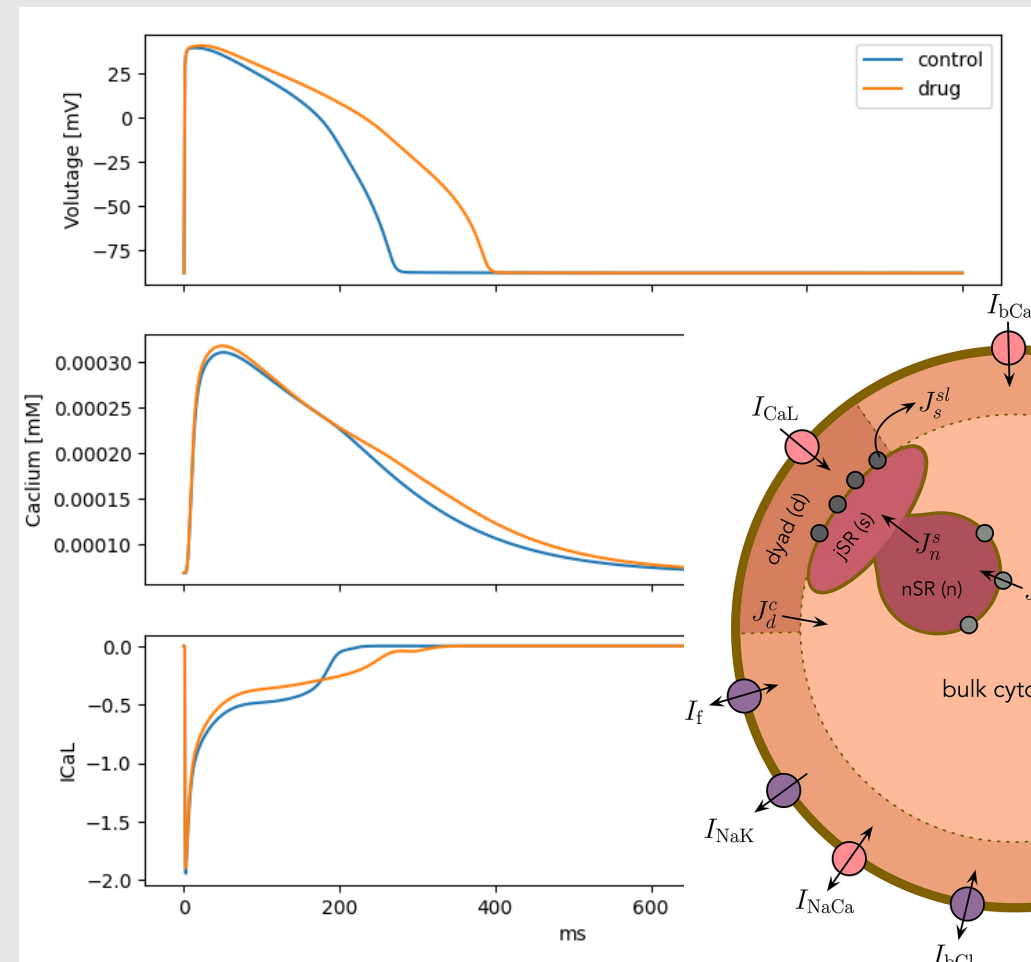
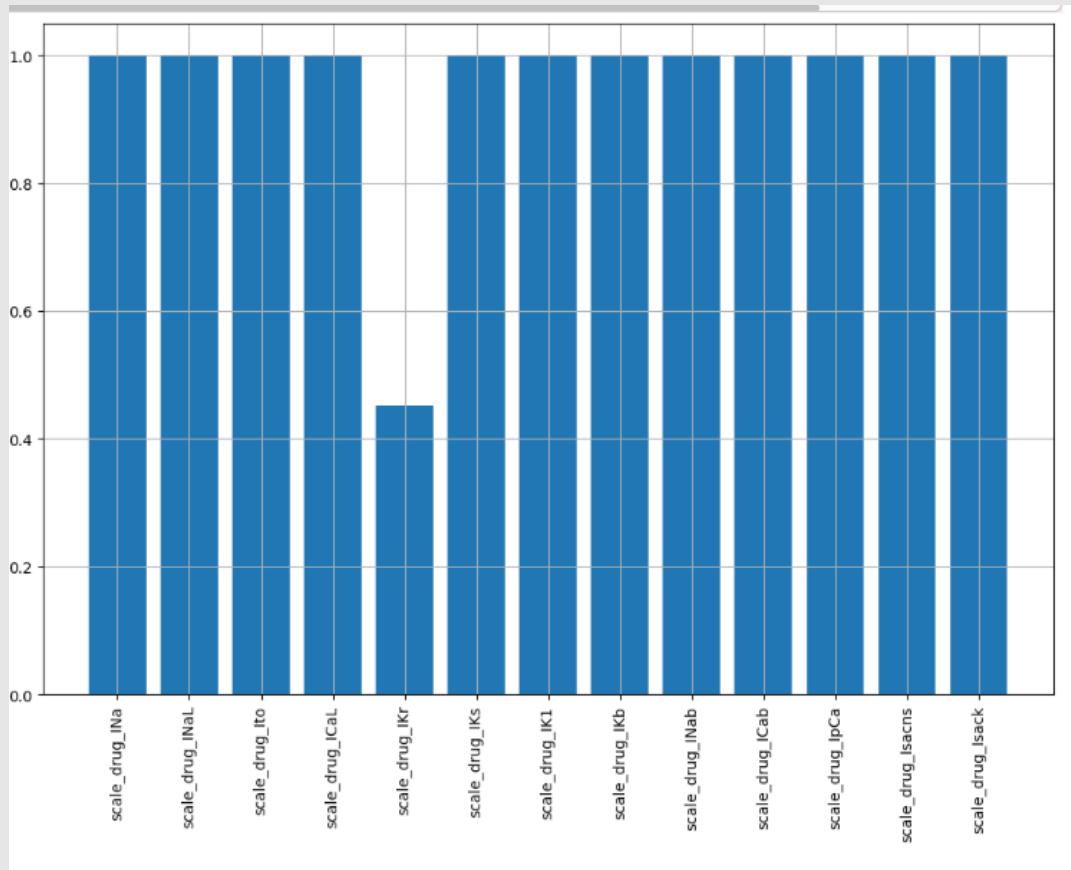
$$\frac{dj}{dt} = \frac{j_{\infty}(V) - j}{\tau_j(V)}$$

*Simulated current during voltage clamp*

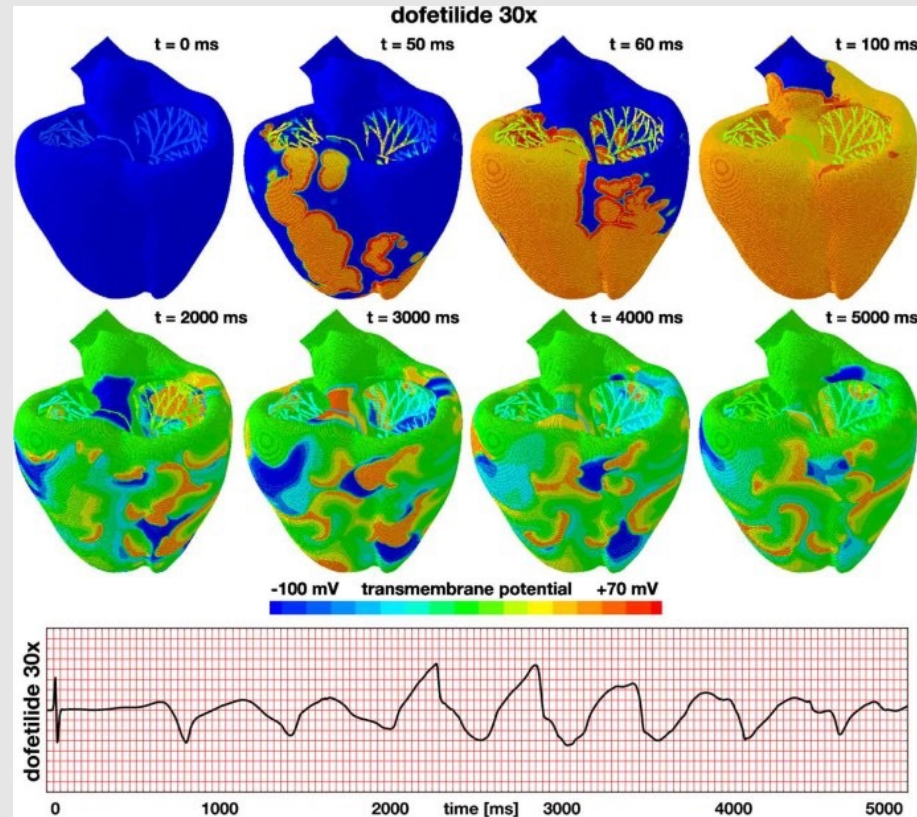
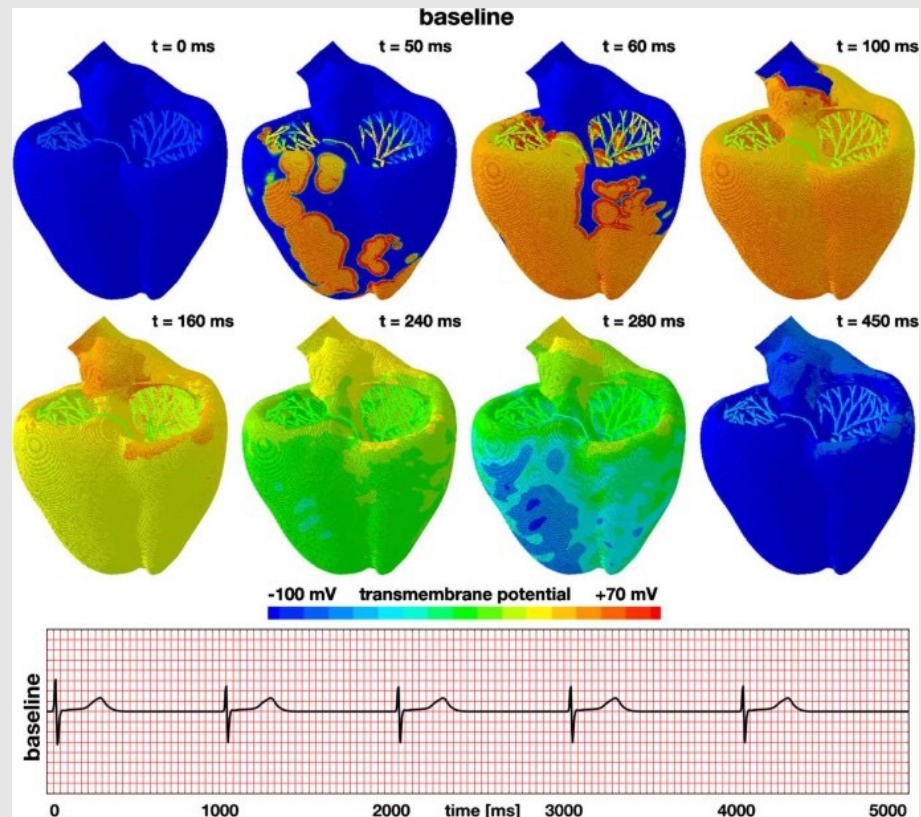


# Modeling drug effect in a single cell modelling

Drug that block a single channel



# Now you can model a drug effect by simply changing a parameter in the cell model and rerunning the simulation



# The equations are solved with FEniCS (dolfinx / dolfin)



$$a(u, v) = L(v) \quad \forall v \in \hat{V}.$$

$$a(u, v) = \int_{\Omega} \nabla u \cdot \nabla v \, dx,$$
$$L(v) = \int_{\Omega} f v \, dx.$$

```
a = ufl.dot(ufl.grad(u), ufl.grad(v)) * ufl.dx
L = f * v * ufl.dx
```

```
from dolfinx.fem.petsc import LinearProblem
problem = LinearProblem(a, L, bcs=[bc], petsc_options={"ksp_type": "preonly", "pc_type": "l
uh = problem.solve()
```

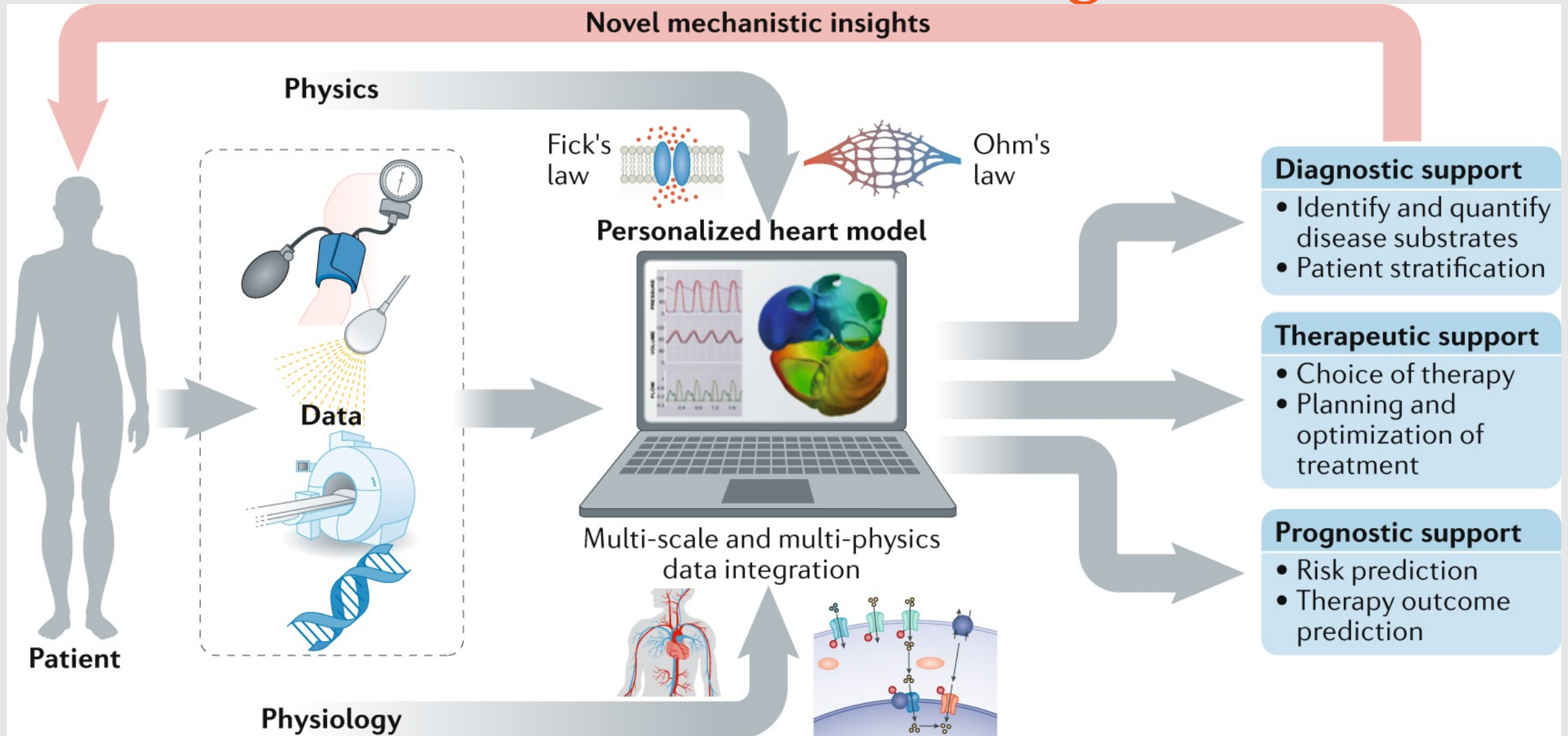
FEniCS is a library for solving partial differential equations with the finite element method

<https://fenicsproject.org>

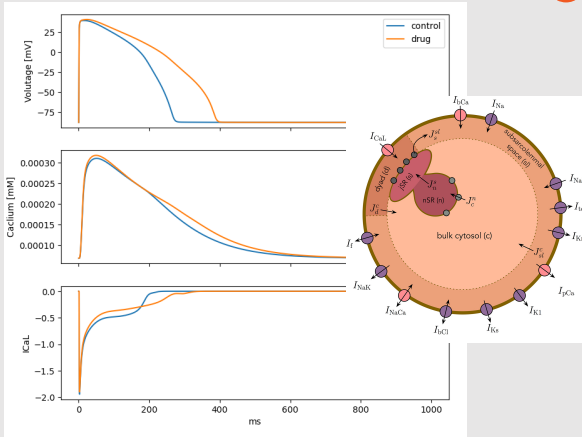
<https://jsdokken.com/dolfinx-tutorial/>

Presentation earlier  
today by Jørgen

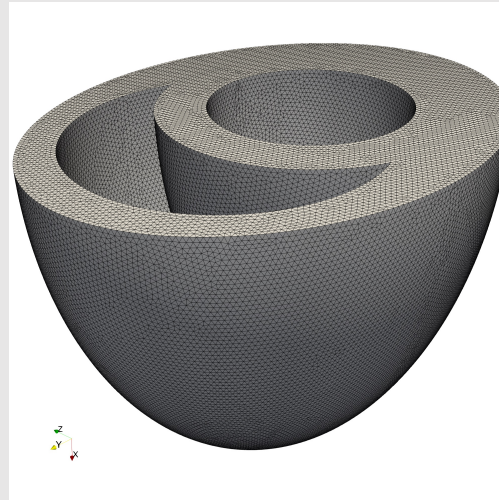
# The long term goal is to use models to assist clinicians in the decision making



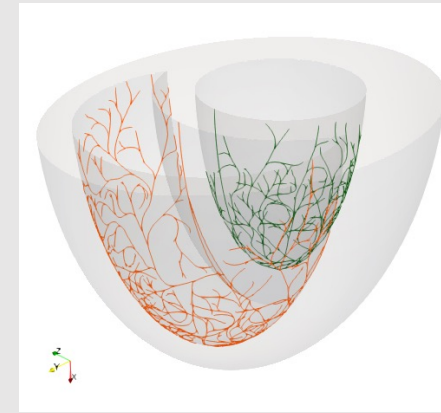
# Summary



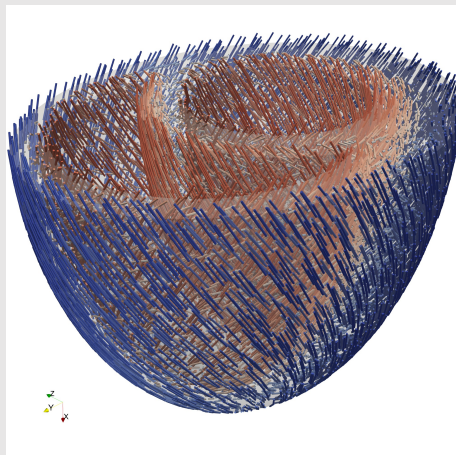
<https://github.com/finsberg/gotranx>



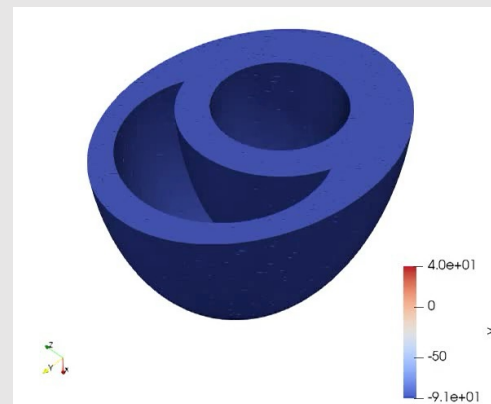
[https://github.com/ComputationalPhysiology/cardiac\\_geometries](https://github.com/ComputationalPhysiology/cardiac_geometries)



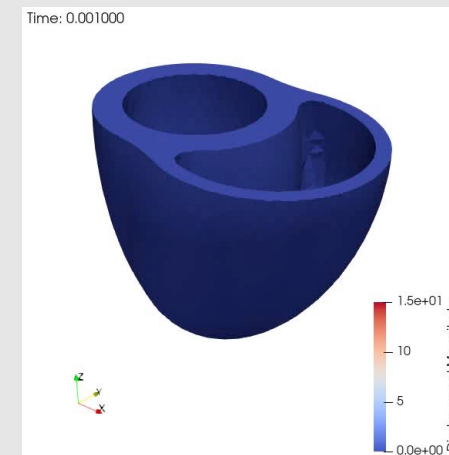
<https://github.com/finsberg/fractal-tree>



<https://github.com/finsberg/lrb>



<https://github.com/finsberg/fenics-beat>



<https://github.com/finsberg/pulse>