



The Challenges of Spatial Scales in Modeling and Understanding Cardiac Fibrillation

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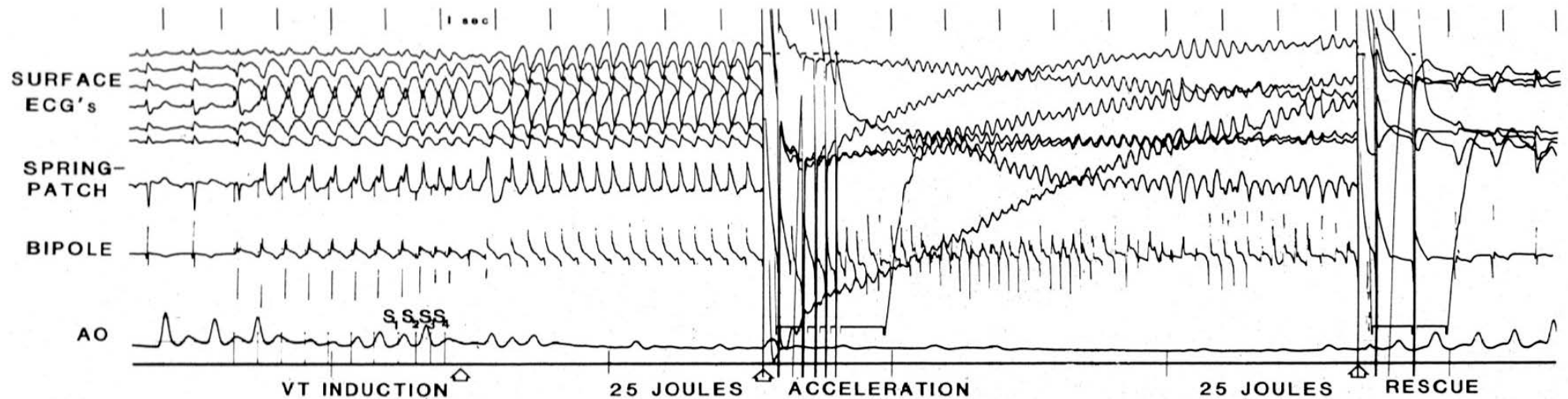
Theme

- The abrupt termination of the Cardiac Arrhythmia Suppression Trial (CAST) was the result of fatal drug effects that were not anticipated by model or experiment
- There is a rapidly growing knowledge base on the structure and function of membrane ion channels
- What is involved in providing a stronger numerical connection between the ion channel and the electrophysiology of the entire heart?
- Models of the electrical activity of the heart during cardiac fibrillation provide serve as a valuable example of just how hard this might be.



Will a particular antiarrhythmic drug alter either the fibrillation or defibrillation thresholds?

- Or... Why I use rabbit hearts as analog computers.





The Ultimate Forward Problem:

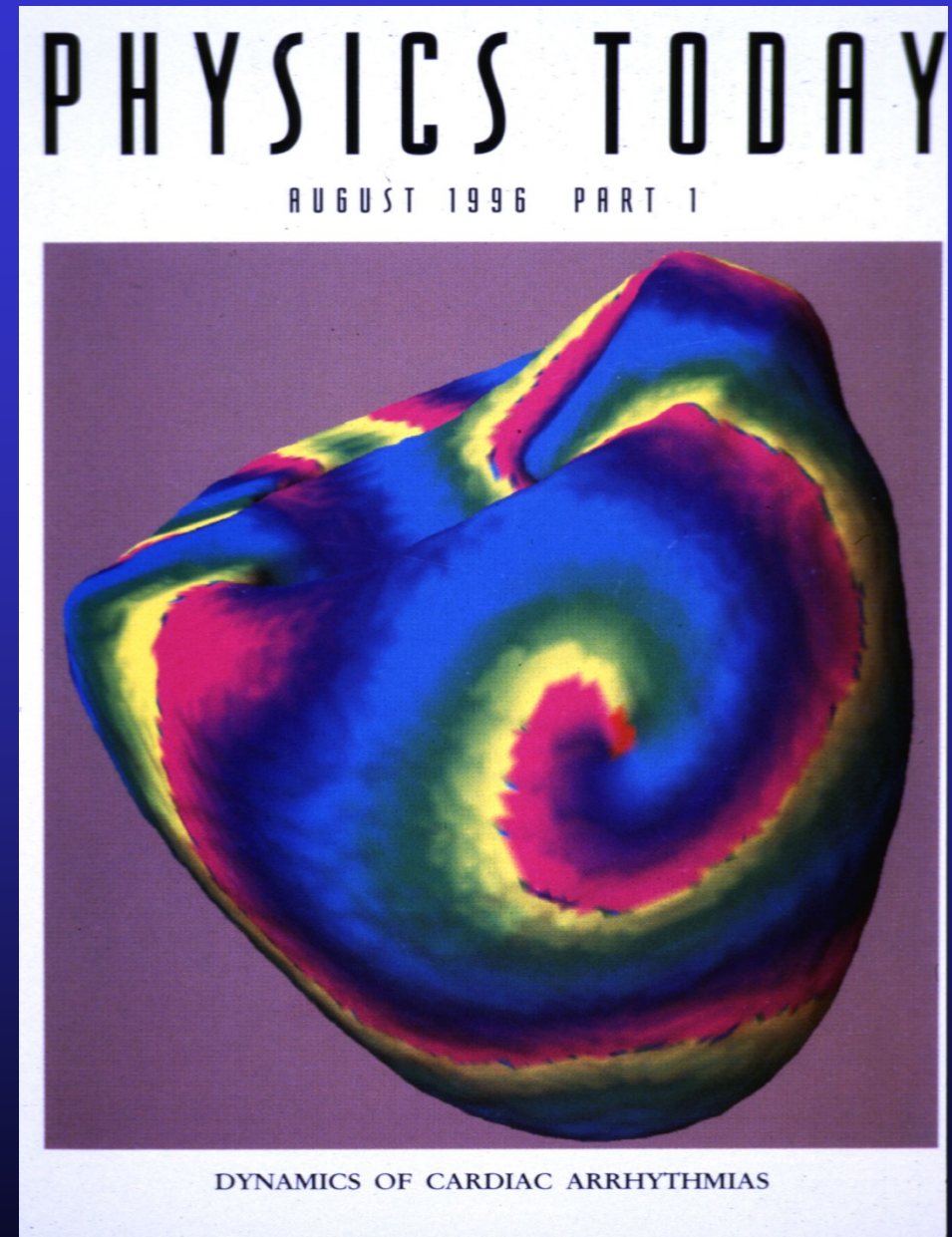
How can we use knowledge of the protein sequence for voltage-gated ion channels to predict numerically the electrocardiogram during a long episode of fibrillation?



The characteristics
of cardiac fibrillation
are set by the spatial
scale of the entire
heart

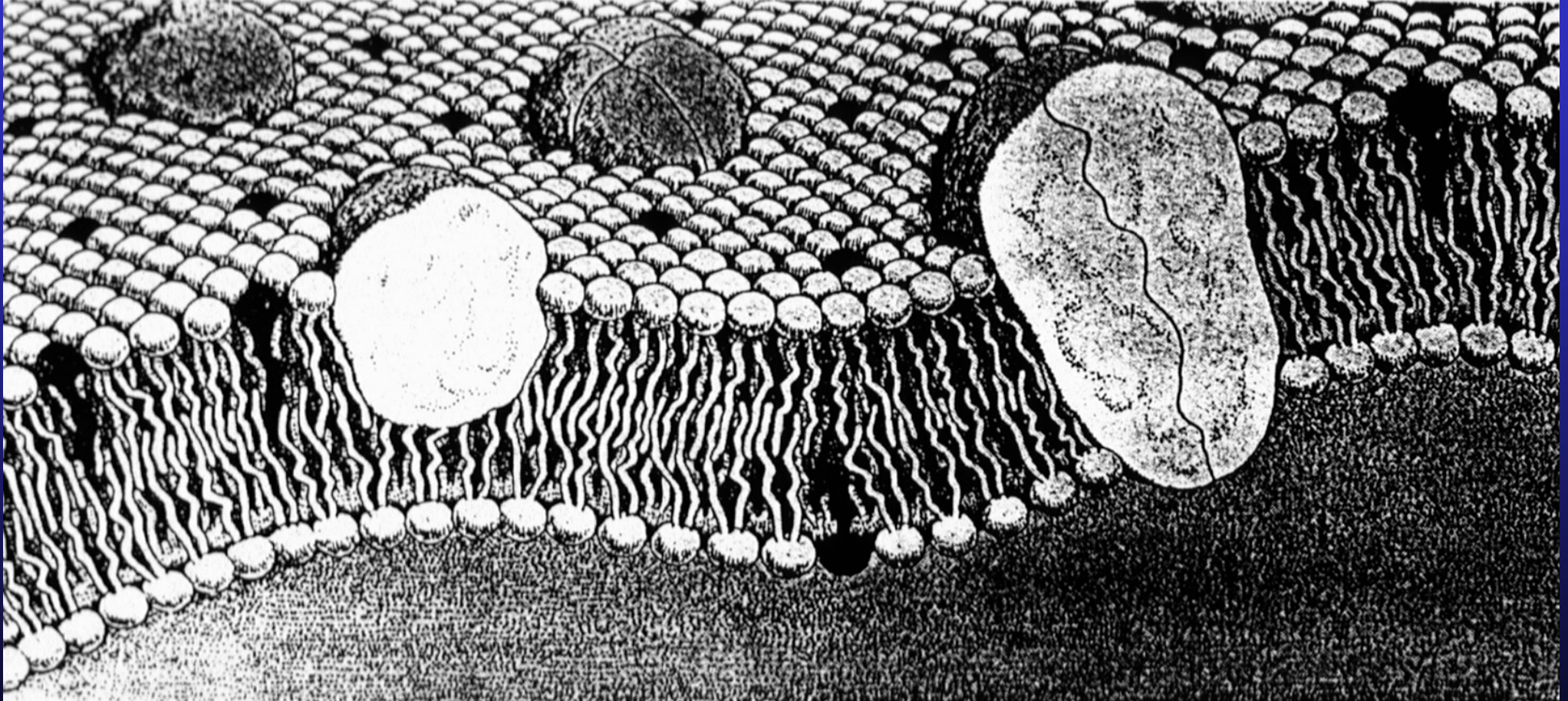
Leon Glass

TL179 BMES 2000



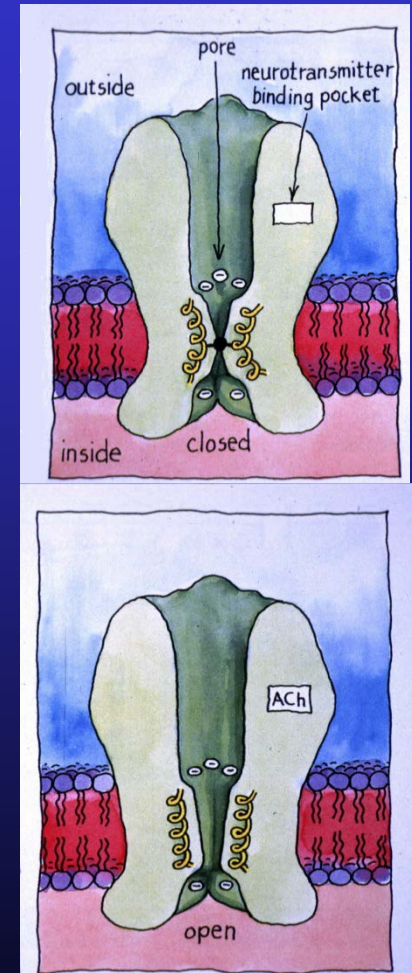
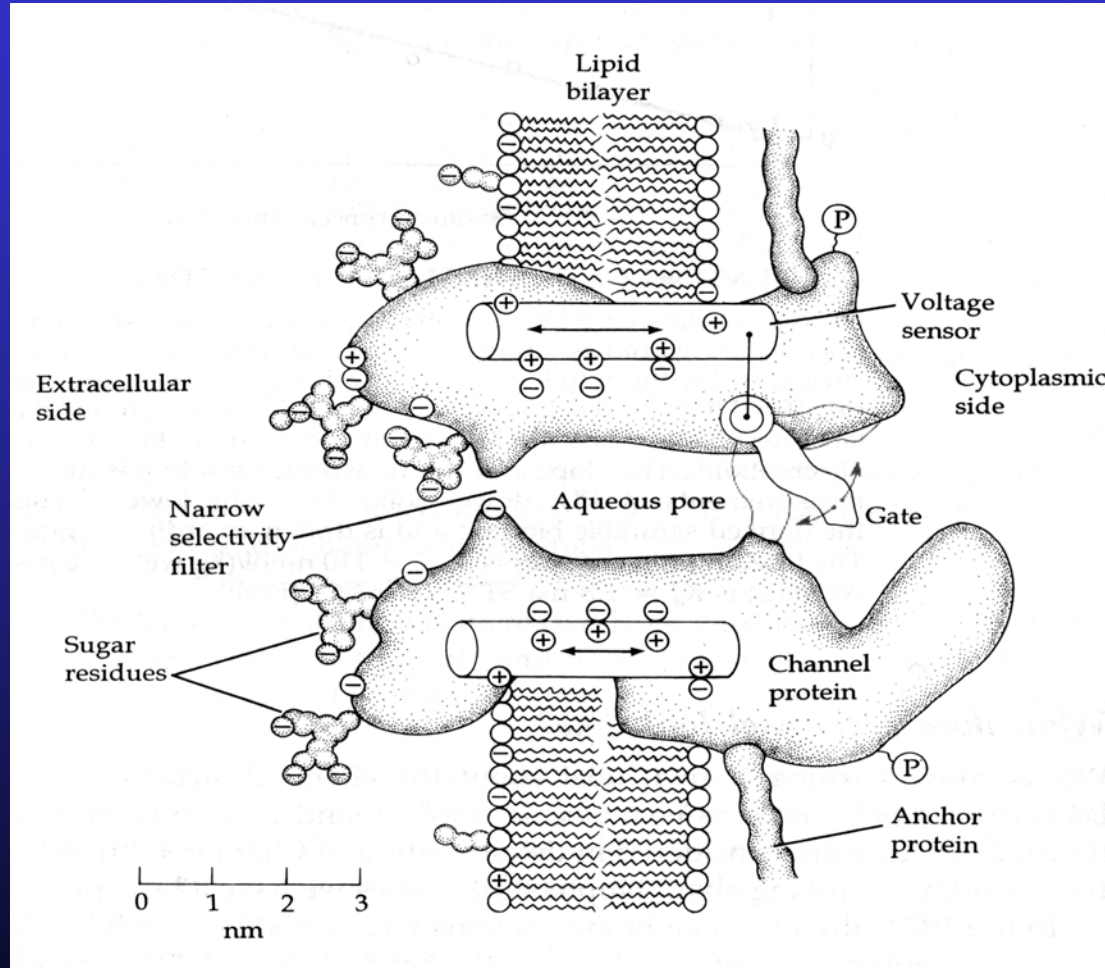
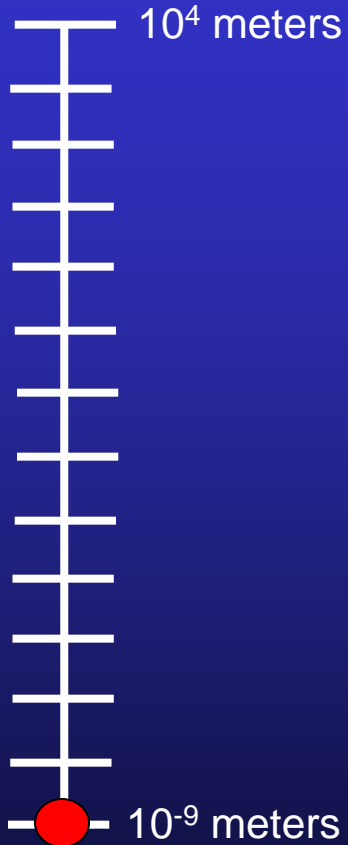


10 nanometers: Ion channels are in control



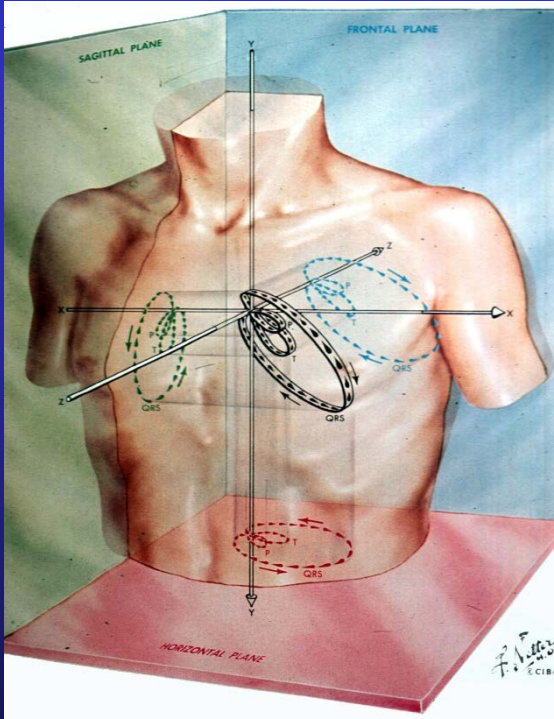


1 nanometer: Pore in a gated ion channel





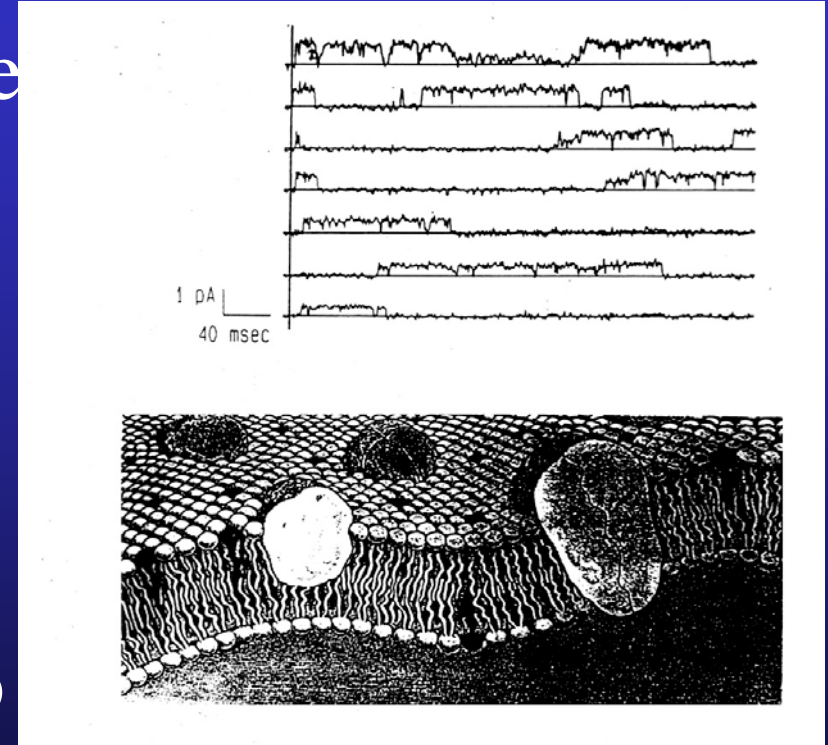
Two extremes: Models of cardiac activity



←
Einthoven triangle
and the cardiac
dipole moment

1 m, 10 sec

→
Channel kinetics
from patch clamp
10 nm, 1-10 nsec





The problem of scales:

The characteristic lengths and times in biological systems span **MANY** orders of magnitude.

- An ion channel: 10 nm ~ 1 channel/nm²
- Cardiac cell: 150 nm x 15 nm x 15 nm
500 to 30,000 channels per cell depending upon cell type
- The heart: 10 cm
4 x 10⁹ cells
2 x 10¹⁴ channels
- The body: 1 m
- **Ratio of spatial scales: 10⁸ in distance, 10²⁴ in volume**
- Channels change in 1 - 10 ns, fibrillation time scale ~10 s
- **Ratio of temporal scales: 10⁹ in time**



The Ultimate Forward Problem:

- Assume gated ion-channel protein sequence: **1 nm**
- Assume that you can compute
 - Protein structure: **1 – 10 nm**
 - Protein kinetics: **1 ns – 100 ms**
 - Channel response to antiarrhythmic drugs: **10 nm, 1 ns – 100 ms**
 - Cellular, tissue and cardiac electrodynamics: **10 mm, 10 ms**
 - Electrocardiogram: **1 m, 10 s**
 - Fibrillation and defibrillation thresholds: **1 m, 10 s**
- **What will this involve?**



Start with the DNA sequence for a potassium channel...

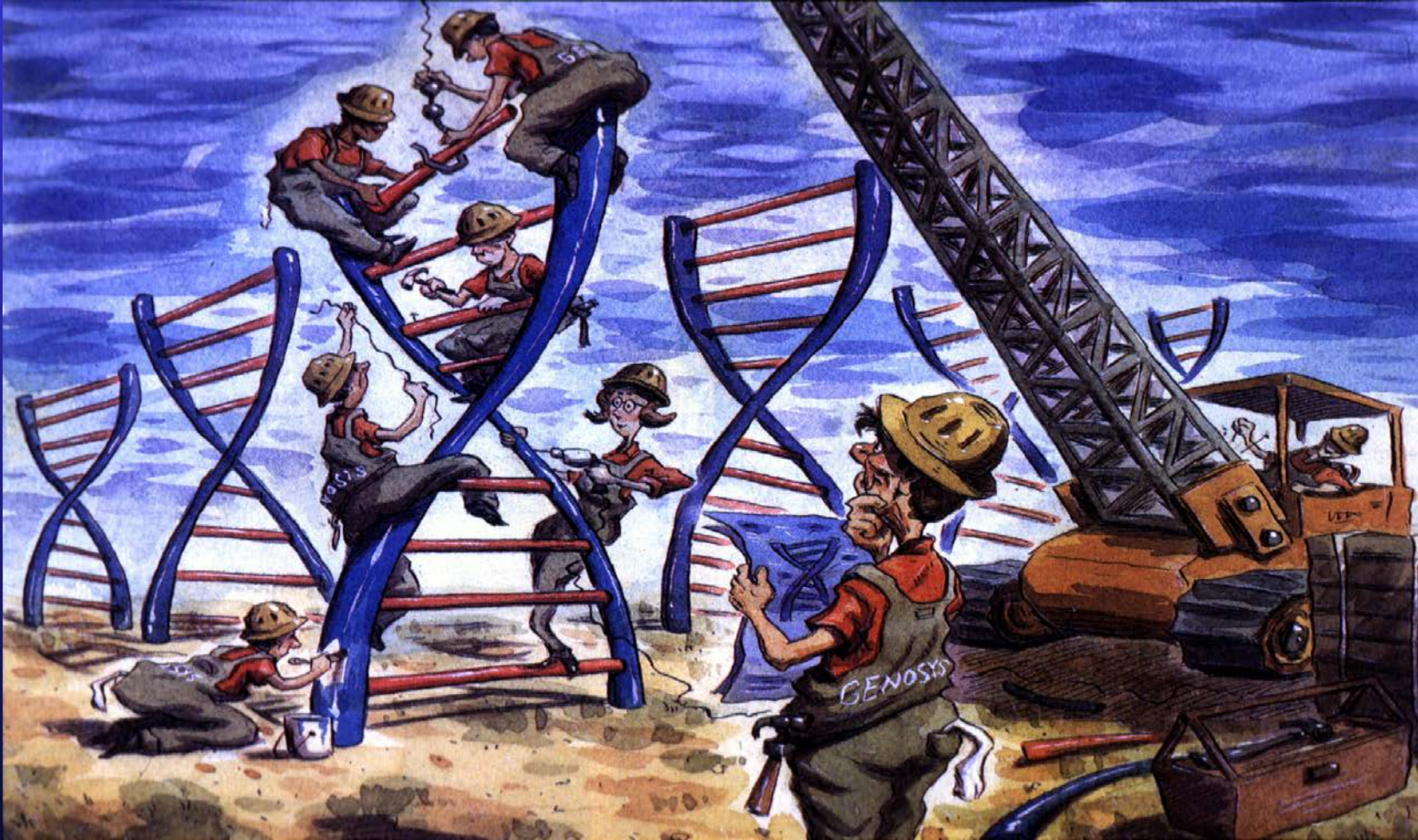
human Kv1.5

```
GCGGCCGCGCGGC'TTT'TGACGTCAGGGCCAAGCGAGGGGATCGCGCCAGCAACCCAGCTCTCCCCAGAGAGGGGCCGG
CCGACCGCTGGAGCGGAGCCTGACGCCAGGCGCCCGCGGAGCGTGAGTAGGGGGCGCGGGAGCCGGTCAGCTGGGGCGCA
GCATGCCCTCTGCTCCCGCGECATGGAGATCGCCCTGGTGCCCTGGAGAACGGCGGTGCCATGACCGTCAGAGGAGGCG
ATGAGGCCCGGGCAGGCTGCGGCCAGGCCACAGGGGGAGAGCTCCAGTGTCCTCCCGACGGCTGGGCTCAGCGATGGGCCC
AAGGAGCCGGCGCCAAAGGGGGCGCGCGCAGAGAGACGCGGACTCGGGAGTGCGGCCCTTGCCCTCCGCTGCCGGACCCGGG
AGTGCGGCCCTTGCCCTCCGCTGCCAGAGGAGCTGCCACGGCCTCGACGGCCGCTCCCGAGGACGAGGAGGAAGAAGGCG
ATCCCGGCCCTGGGCACGGTGGAGGACCAGGCTCTGGGCACGGCGTCCCTGCACCACCAGCGCGTCCACATCAACATCTCC
GGGCTGCGCTTTGAGACGCAGCTGGGCACCCCTGGCGCAGTTCCCCAACACACTCTGGGGGACCCCGCCAAGCGCCTGCC
GTACTTCGACCCCCTGAGGAACGAGTACTTCTTCGACCGCAACCGGCCAGCTTCGACGGTATCCTCTACTACTACCACT
CCGGGGGCGCCCTGCGAGGGGTCAACGTCTCCCTGGACGTGTTTCGCGGACGAGATACGCTTCTACCAGCTGGGGGACGAG
GCCATGGAGCGCTTCCGCGAGGATGAGGGCTTCATTAAAGAAGAGGAGAAGCCCTGCCCCGCAACGAGTTCCAGCGCCA
GGTGTTGGCTTATCTTCGAGTATCCGAGAGCTCTGGGTCCGCGCGGGCCATCGCCATCGTCTCGGTCTTGTTTATCTCA
TCTCCATCATCACCTTCTGCTTGGAGACCCCTGCCTGAGTTTCAGGGATGAACGTGAGCTGCTCCGCCACCCCTCCGGCGCCC
CACCAGCCTCCCGCGCCCCGCCCCCTGGGGCCAACGGCAGCGGGGTTCATGGCCCCCGCTCTGGCCCTACGGTGGCACCCGT
CCTGCCCCAGGACCTGGCCGACCCCTTCTTCATCGTGGAGACCAGTGCCTGATCTGGTTACCTTCGAGCTGCTCGTG
GCTTCTTCGCTGCCCCAGCAAGGCAGGGTTCTCCCGGAACATCATGAACATCATCGATGTGGTGGCCATCTTCCCCCTAC
TTCATCACCTTGGGCACCGAACTGGCAGAGCAGCAGCCAGGGGGCGGAGGAGGCGGCCAGAATGGGCAGCAGGCCATGTC
CCTGGCCATCTCCGAGTCATCCGCTGGTCCGGGTGTTCCGCATCTTCAAGCTCTCCCGCCACTCCAAGGGGCTGCAGA
TCTTGGGCAAGACCTTGCAGGCCCTCATGAGGGAGCTGGGGCTGCTCATCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCT
TCCAGTGCCGTCTACTTCGAGAGGCTGACAACCAGGGAACCCATTTCTCTAGCATCCCTGACGCCTTCTGGTGGGCAGT
GGTCACCATGACCACTGTGGGCTACGGGGACATGAGGCCCATCACTGTTGGGGGCAAGATCGTGGGCTCGCTGTGTGCCA
TCGCCGGGGTCTCACCATTGCCCTGCCTGTGCCCGTCATCGTCTCCAATTCAACTACTTCTACCACCGGGAACGGAT
CACGAGGAGCCGGCAGTCCCTTAAGGAAGAGCAGGGCACTCAGAGCCAGGGGGCGGGGCTGGACAGAGGAGTCCAGCGGAA
GGTCAGCGGGAGCAGGGGATCCTTCTGCAAGGCTGGGGGGACCCCTGGAGAATGCAGACAGTGCCTGAAGGGGCGAGTGCC
CCCTAGAGAAGTGTAACGTCAAGGCCAAGAGCAACGTGGACTTGCGGAGGTCCCTTTATGCCCTCTGCCTGGACACCAGC
CGGGAAACAGATTTGTGAAAGGAGATTCAAGCAGACTGGTGGCAGTGGAGTAGGGAATGGGAGGCTTCTGAACATGGATA
TCTACATTATCCGAGAGTATTTGACTCACTCCTCT
```

Courtesy of Dirk Schneiders



Assemble the proteins

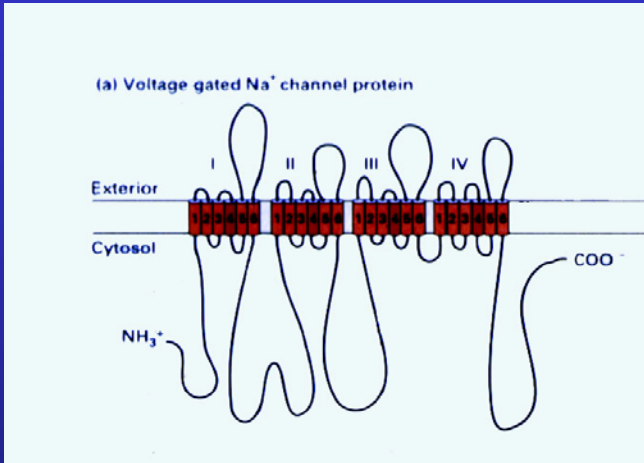




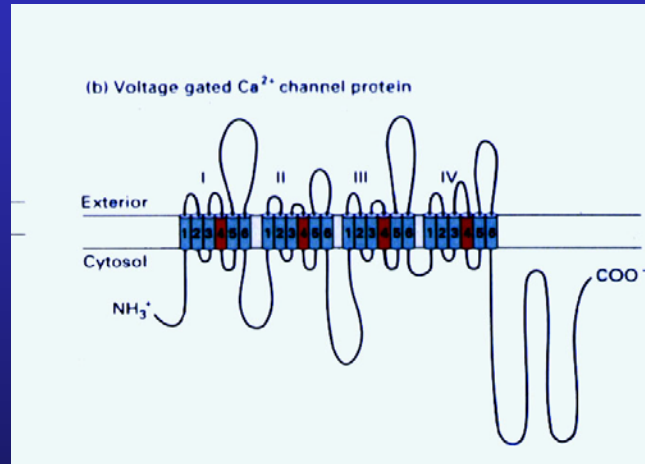
And we solve the protein folding
problem...



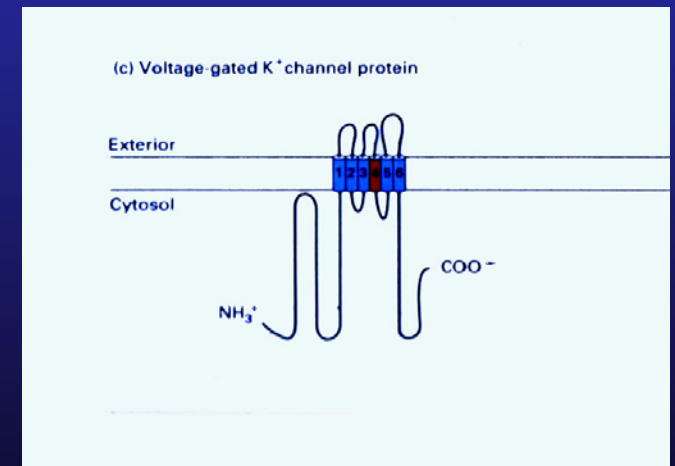
Insert the folded proteins into the membrane



Voltage-gated Na⁺ channel



Voltage-gated Ca⁺⁺ channel

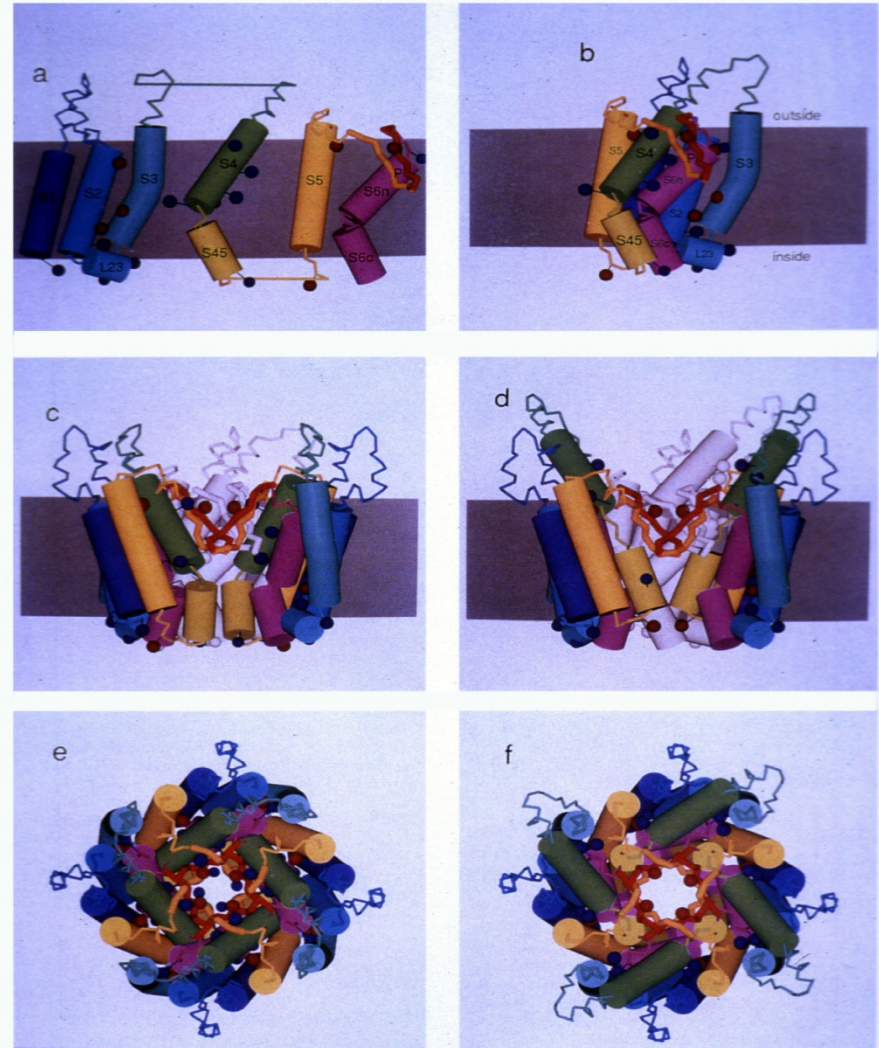


Voltage-gated K⁺ channel



Compute how the protein conformation depends upon voltage or ligand binding

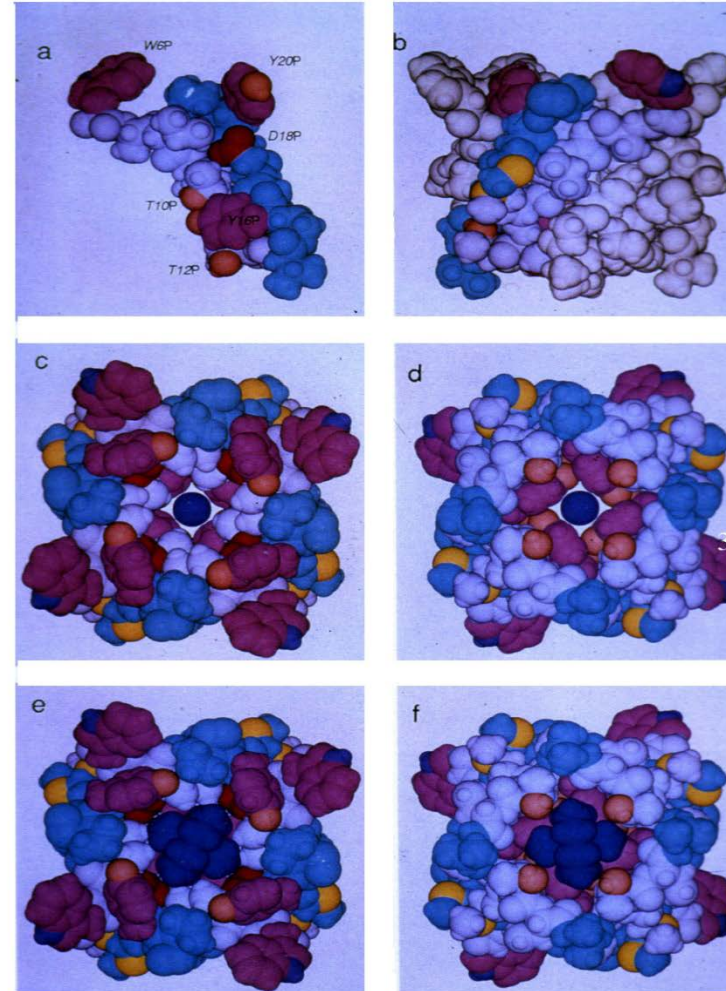
S.R. Durrell and H.R. Guy, *Biophysical Journal*, 62: Discussions 1992 238-250 (1992)





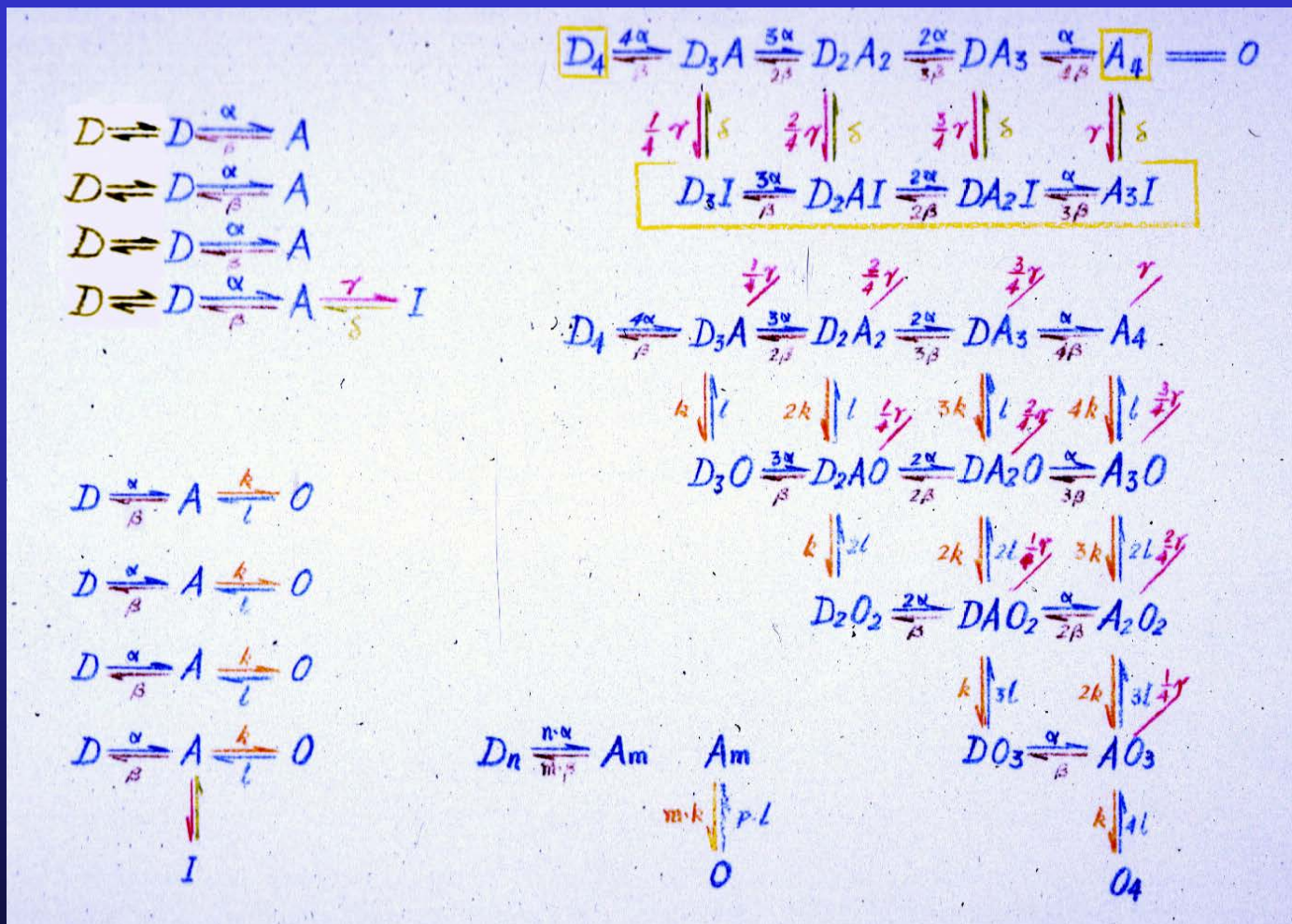
See which
drugs block
the channel

S.R. Durrell and H.R. Guy, *Biophysical Journal*, 62: Discussions 1992 238-250 (1992)





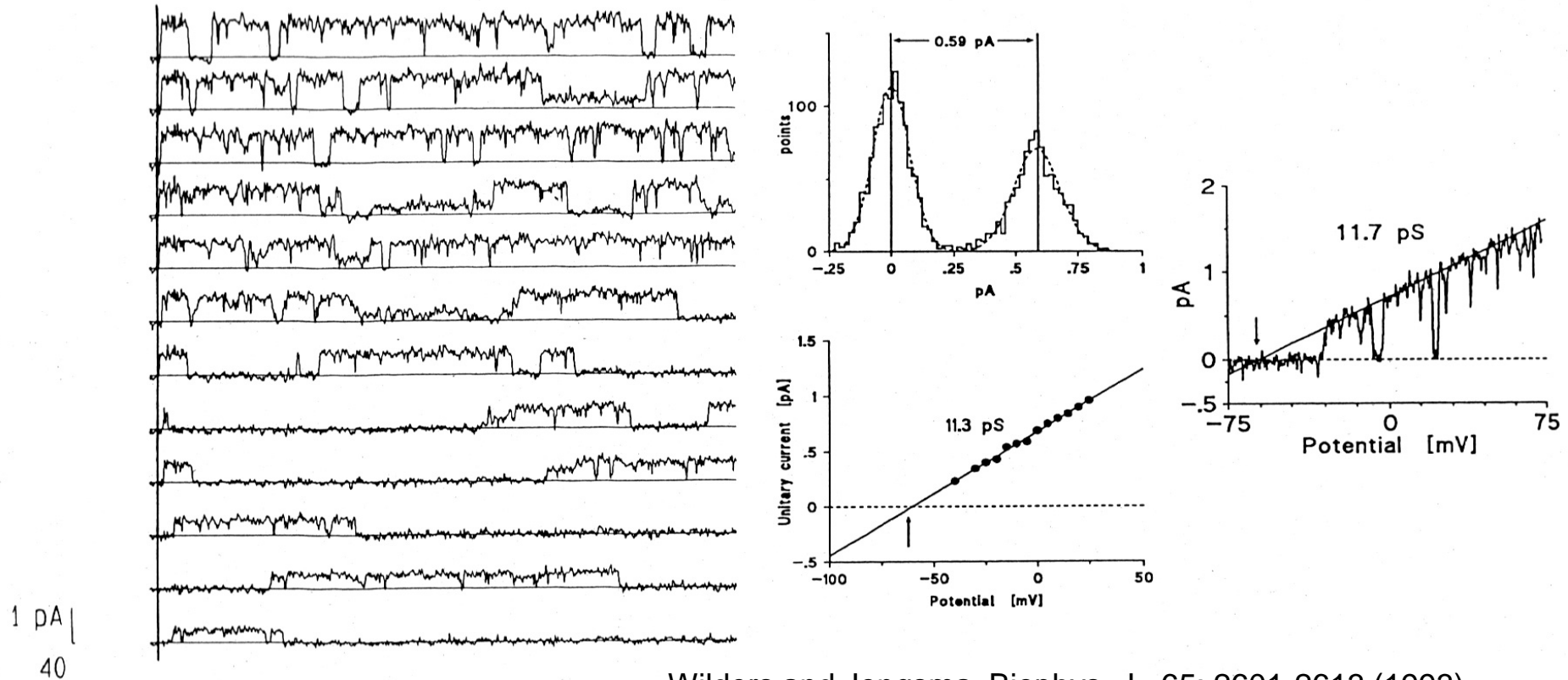
Compute the
channel
kinetics to
determine the
switching
behavior



Courtesy of Dirk Schneiders



Compute the time-dependent channel conductance

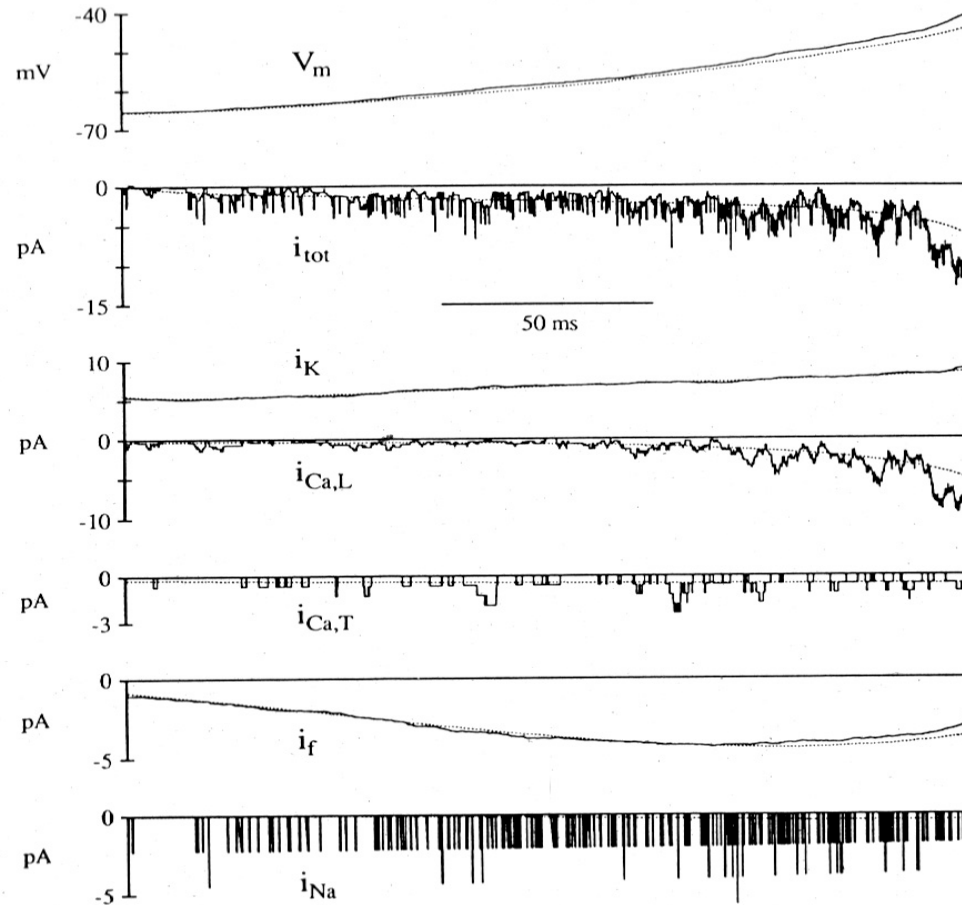


Wilders and Jongsma, Biophys. J., 65: 2601-2613 (1993)



Stochastically activate the channels

R. Wilders and H.J. Jongsma, *Biophysical J.*, 65: 2601-2613 (1993)

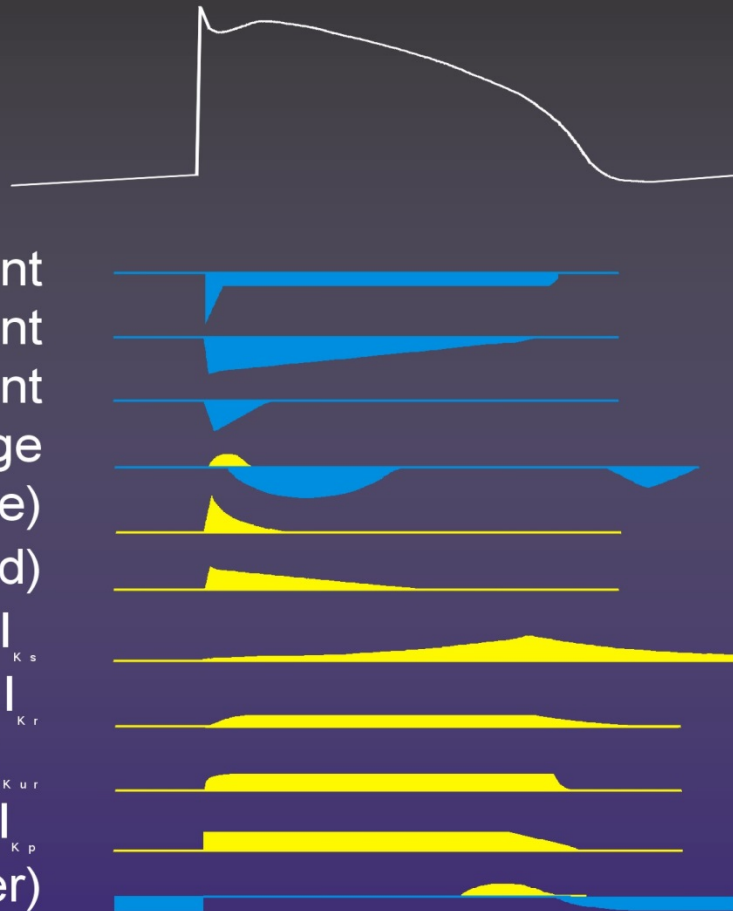


Describe the channel currents in terms of a Hodgkin-Huxley-like model such as Luo-Rudy I or II

Courtesy of Dan Roden

Current

sodium current
L-type calcium current
T-type calcium current
Na-Ca exchange
 I_{TO1} (4-AP-sensitive)
 I_{TO2} (Ca-activated)
 I_{Ks}
 I_{Kr}
 I_{Kur}
 I_{Cl} or I_{Kp}
 I_{K1} (inward rectifier)
 I_{KACh} ; I_{KATP}
 I_h (pacemaker current)



Probable clone

H1, SCN5A*

✓*

✓

Na-Ca exchanger

Kv4.3 (?1.2, 1.4, 1.5, 2.1, 4.2)*?

--

KvLQT1 + minK (IsK)

HERG + MiRP1

Kv1.5

CFTR, TWIK (?others)

Kir2.x

Kir3.1/3.4; Kir6.x/SUR

hCNG

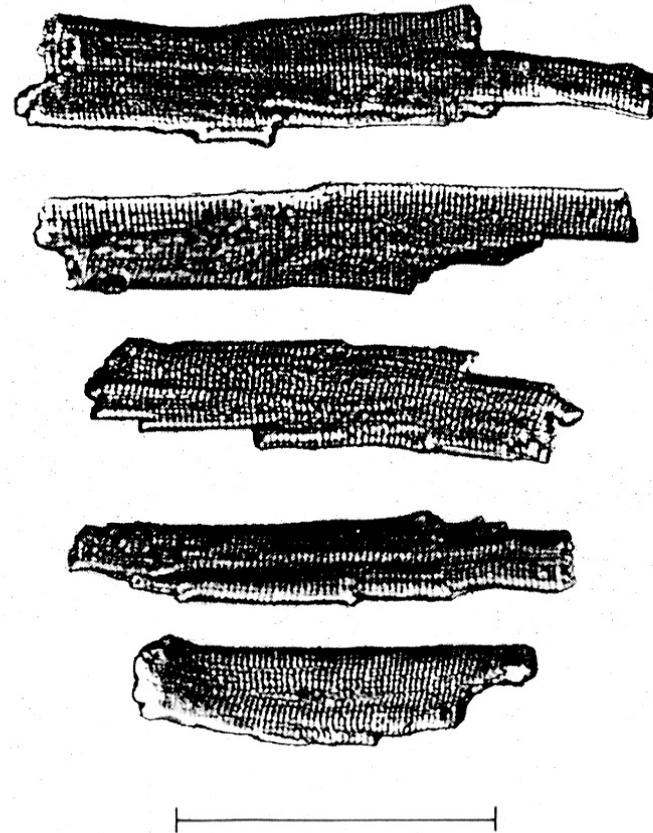
*+sub-units 20

TL179 BMES 2000



Sprinkle the channels and their currents onto a family of virtual cardiac cells

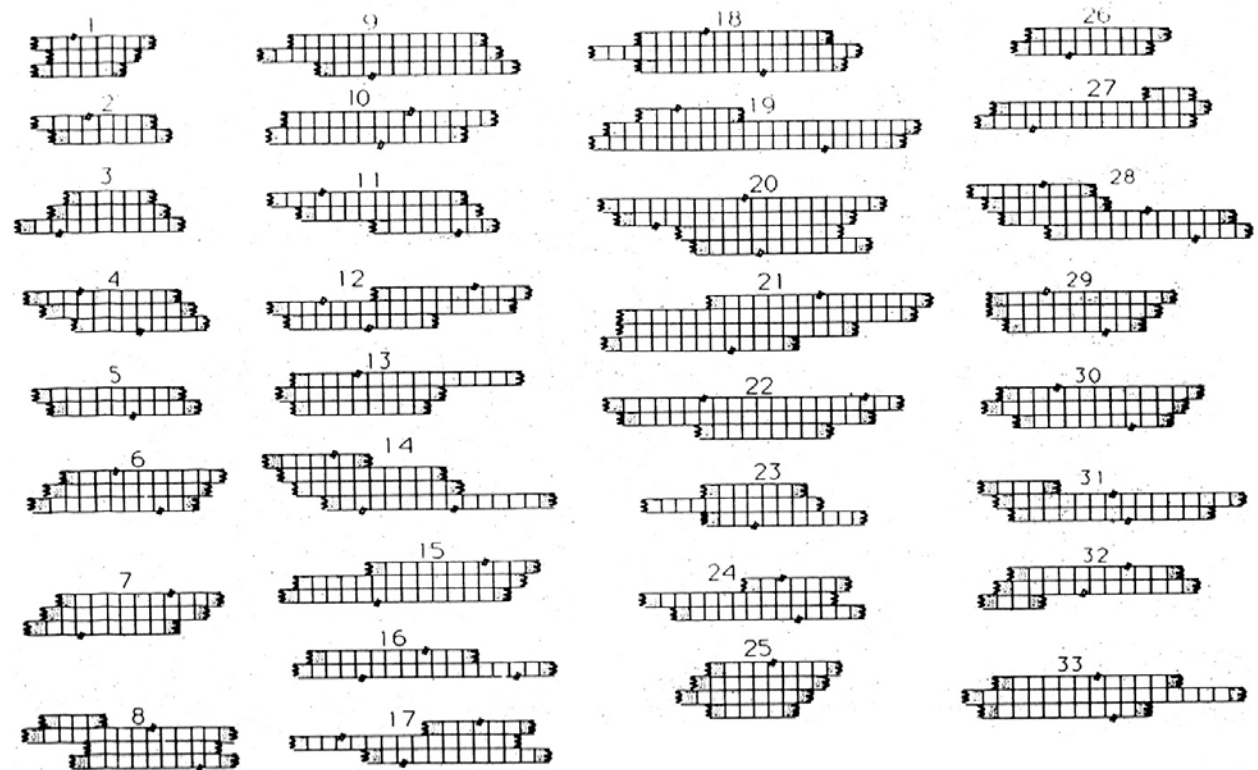
M.S. Spach and J.F. Heidlage, in *High Performance Computing in Biomedical Research*, T.C. Pilkington *et al.*, Eds., (CRC, Boca Raton, 1993) pp 289-317





Divide each
cell into a
numerically
stable subunit

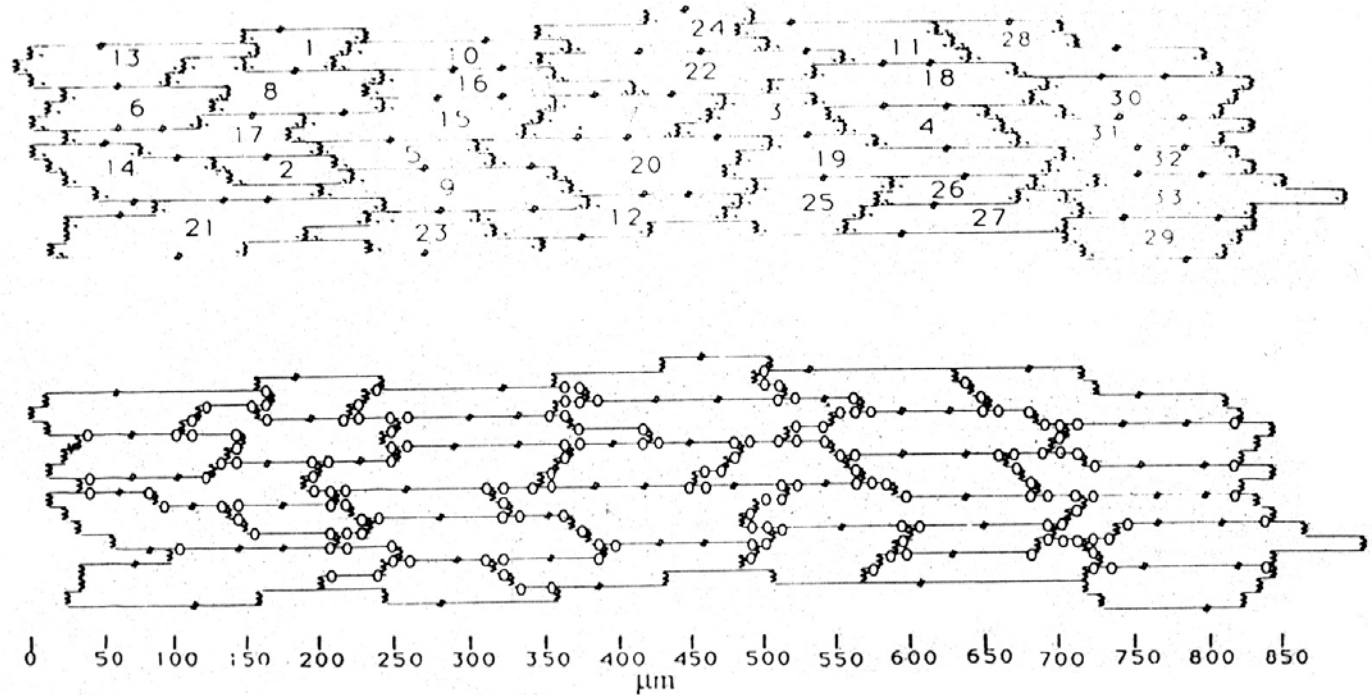
M.S. Spach and J.F. Heidlage, in *High Performance Computing in Biomedical Research*, T.C. Pilkington *et al.*, Eds., (CRC, Boca Raton, 1993) pp 289-317





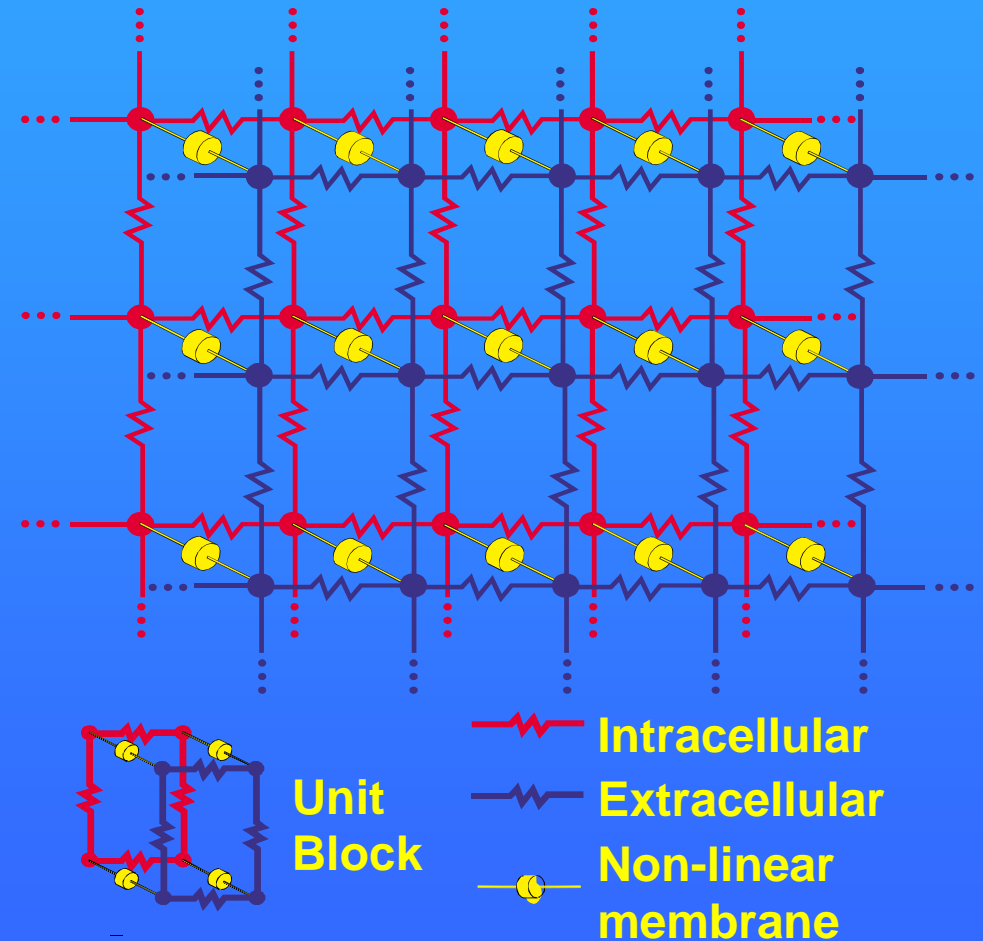
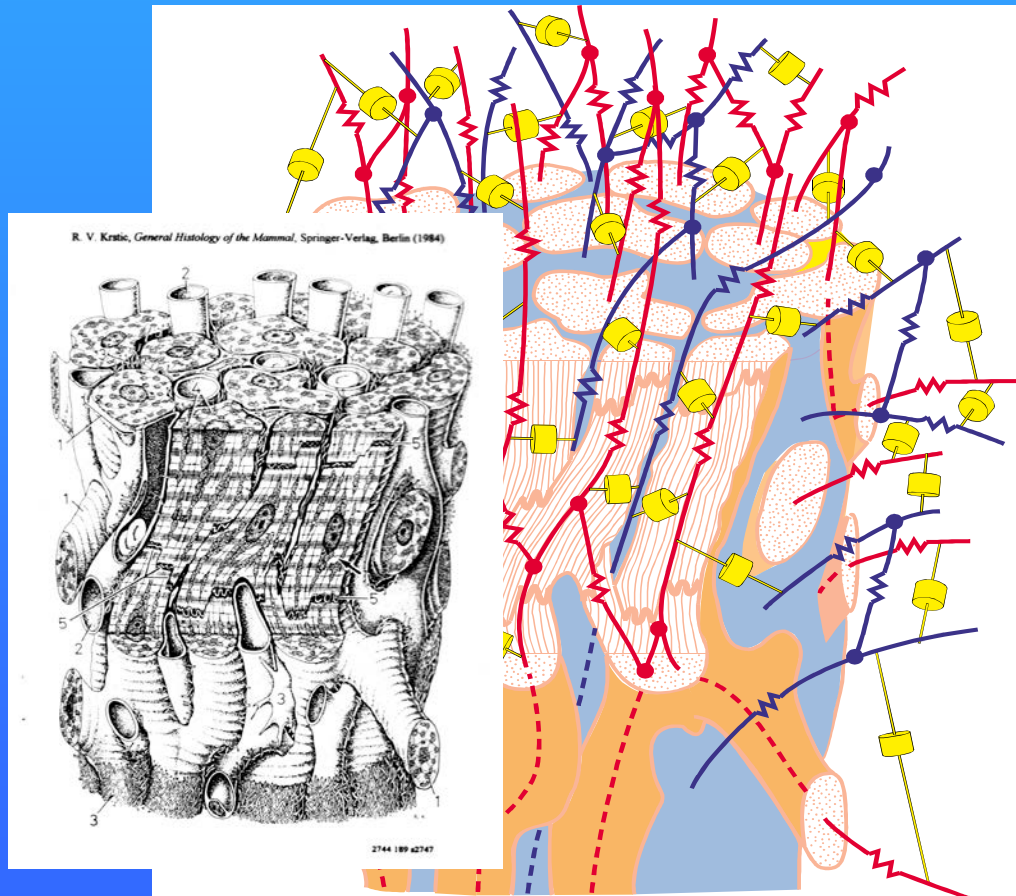
Assemble the cells into small regions of cardiac tissue

M.S. Spach and J.F. Heidlage, in *High Performance Computing in Biomedical Research*, T.C. Pilkington *et al.*, Eds., (CRC, Boca Raton, 1993) pp 289-317



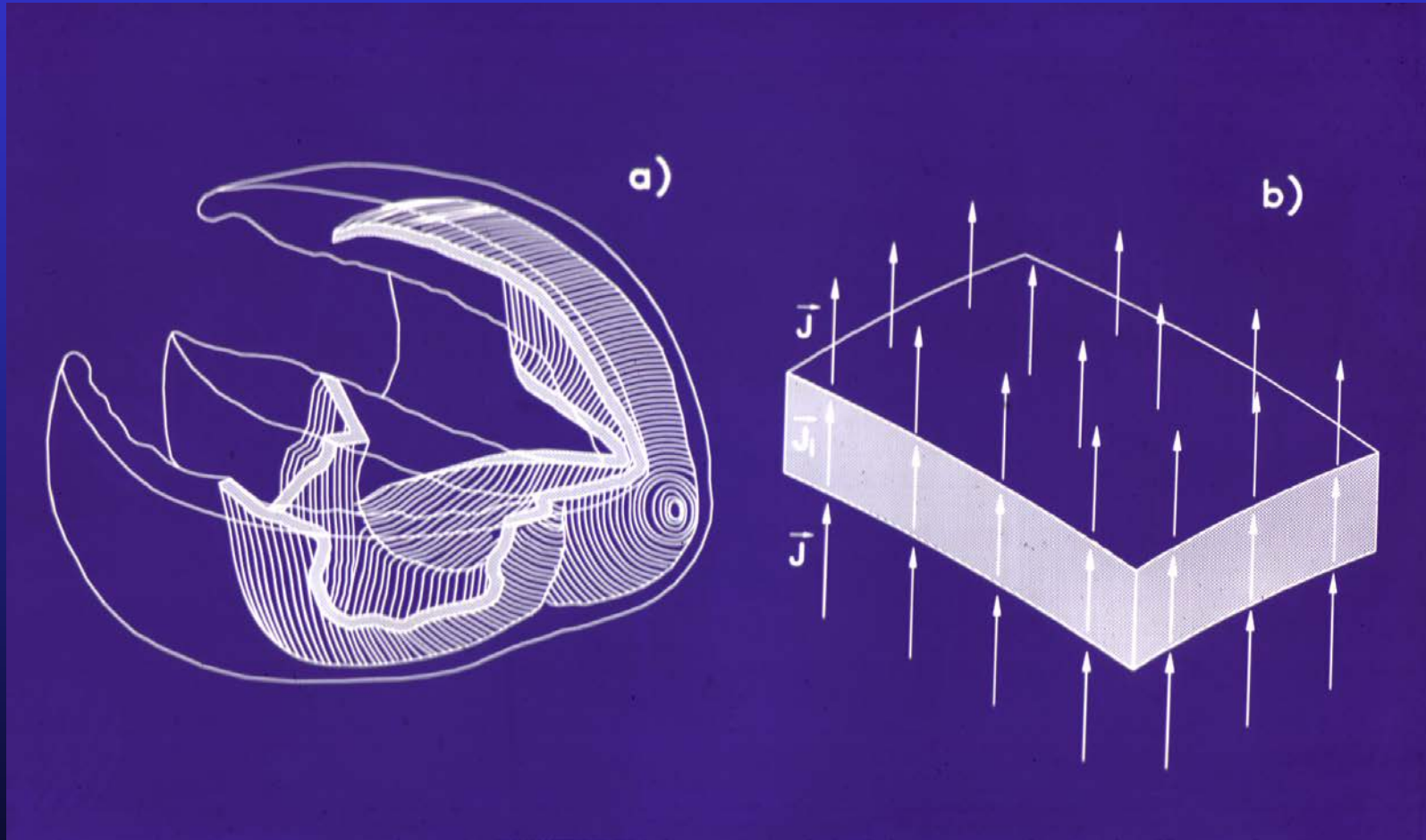


Include the three-dimensional cable properties of the anisotropic cardiac syncytium





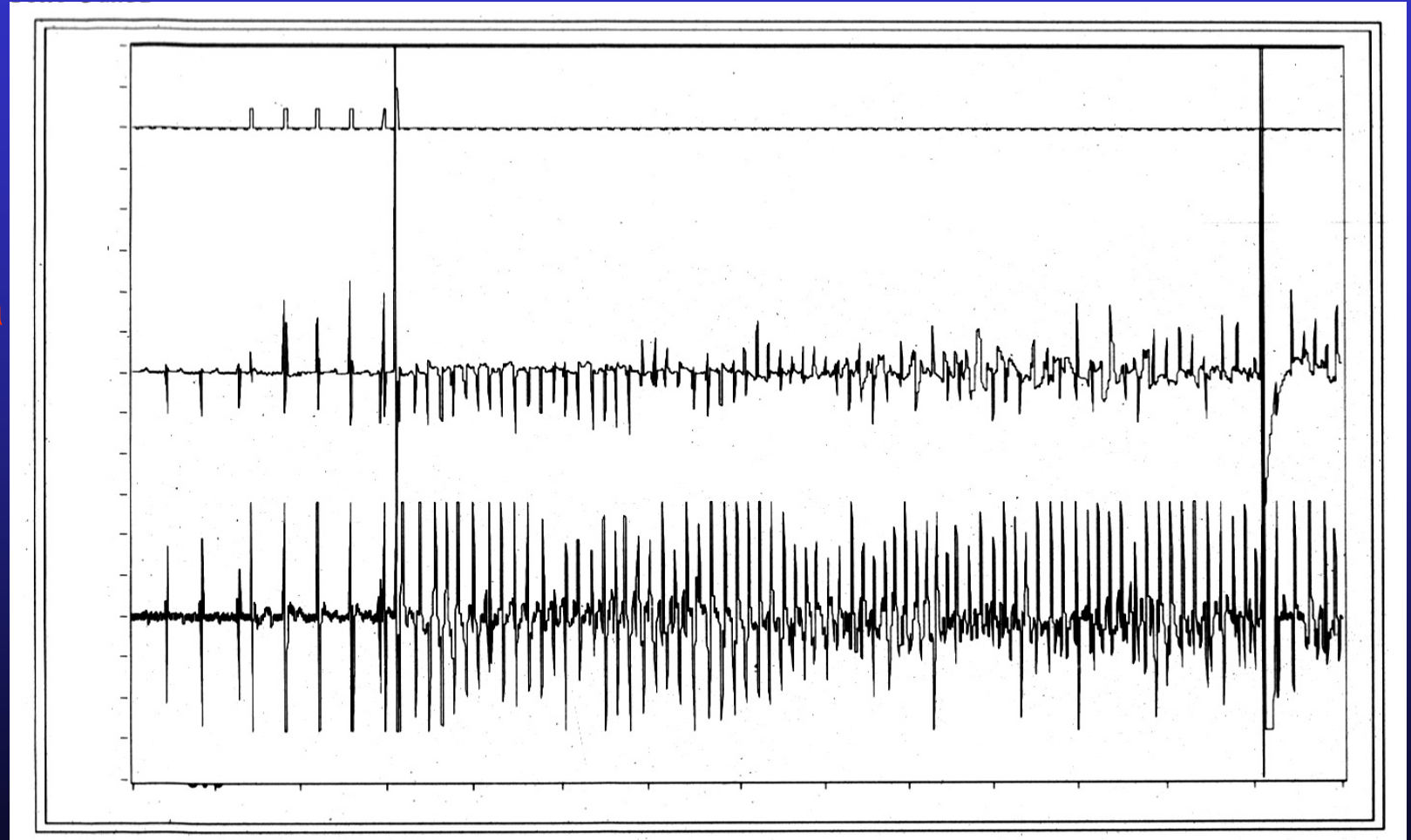
Assemble the regions into a whole heart





Compute 10 seconds of fibrillation ...

Traces of
experimental data





The computer
runs forever....

Look at the
model

81 free parameters
for each volume
element in the
model

<i>Potentials</i>	(2)
V_i, V_e	
<i>Anisotropy tensors</i>	(3 × 6 = 18)
conductivity, stress, strain	
<i>Volume fractions</i>	(3)
$\text{vol}_e/\text{vol}_i, \text{vol}_{sr}/\text{vol}_i, \text{area}_m/\text{vol}_i$	
<i>Concentrations</i>	(12)
$[\text{Na}^+]_i, [\text{Na}^+]_e, [\text{K}^+]_i, [\text{K}^+]_e, [\text{K}^+]_{\text{cleft}},$ $[\text{Cl}^-]_i, [\text{Cl}^-]_e, [\text{Ca}^{+2}]_i, [\text{Ca}^{+2}]_e, [\text{Ca}^{+2}]_{sr},$ $[\text{ATP}]_i, [\text{ACh}]_e, [\text{H}^+]_i, [\text{H}^+]_e$	
<i>Currents with activation and inactivation</i>	(6 × 3 = 18)
$I_{\text{Na}}, I_{\text{Ca}}, I_{\text{Ca,Na}}, I_{\text{Ca,K}}, I_{\text{rel}}, I_{\text{Cl,Ca}}$	
<i>Currents with activation</i>	(7 × 2 = 14)
$I_{\text{K1}}, I_{\text{Kp}}, I_{\text{K}}, I_{\text{ns,Na}}, I_{\text{ns,K}}, I_{\text{tr}}, I_{\text{stretch}}$	
<i>Steady-state currents</i>	(7)
$I_{\text{Ca,b}}, I_{\text{Na,b}}, I_{\text{leak}}, I_{\text{k,ATP}}, I_{\text{k,ACh}}, I_{\text{k,PC}}, I_{\text{k,AA}}$	
<i>Pumps</i>	(7)
$I_{\text{NaK}}, I_{\text{p(Ca)}}, I_{\text{up}}, I_{\text{NaCa}}, I_{\text{ATPCa}}, I_{\text{HK}}, I_{\text{HCl}}$	
Total	81

2791 188 s2794



The Problem of Scale: Numerical Models

- Divide each cardiac cell into 10 segments:
 4×10^{10} segments/heart
- At least 50 currents and other variables/segment
 2×10^{12} variables/heart
- $5 \mu\text{s}$ /timestep: 2×10^6 timesteps/10s of fibrillation
- 4×10^{18} equations to solve ... micromoles
- 46,000 years on a 25 MFLOP workstation
- 10 years on 1200 100 MFLOP workstations
- 1 year on a 1 TFLOP workstation
- At 100 bytes/segment, 4 Tbytes of memory or disk to store the model

Cherry, Greenside, Henriquez PRL 2/7/00: Whole-heart, minimal adaptive mesh LR1 estimated 10^{-5} real time with a 533 MHz DEC α ; 70x increase with a 100-parallel computer.



Discussion

- Whole-heart cardiac models involve brute-force solution of partial differential equations, using either HH-type models (LR, etc), or eikonal equations
- At present, there are few if any numerical, theoretical, or analytic connections between the molecular description of the channel and either HH-type or eikonal models



Solutions to the *Ultimate Forward Problem*

- Develop efficient multiscale/mesoscale models to span the full range of space and time
 - Molecular dynamics vs. statistical mechanics vs. thermodynamics
 - Eikonal equations for the wave front properties
 - Direct physiological determination of eikonal equation parameters
- An isolated rabbit heart: **a self-assembling, multivariable, multistate, massively parallel, non-linear analog computer**
 - Solves $\sim 10^{17}$ equations/second at \$30/hour
 - Requires improved programming techniques
 - Requires improved readout of the answer



Characterizing the Cardiac State

What do you do with all the data?

- Ontological failure: “The phenomena you are interested in requires elements or laws outside of the set you have been given.”
- Epistemological Failure: “You have enough elements and the laws do apply, but you yourself cannot understand the explanation that they provide.”

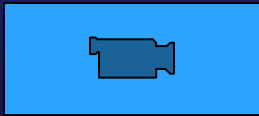
D Bray, TIBS 22, pp 325-326 (1997)



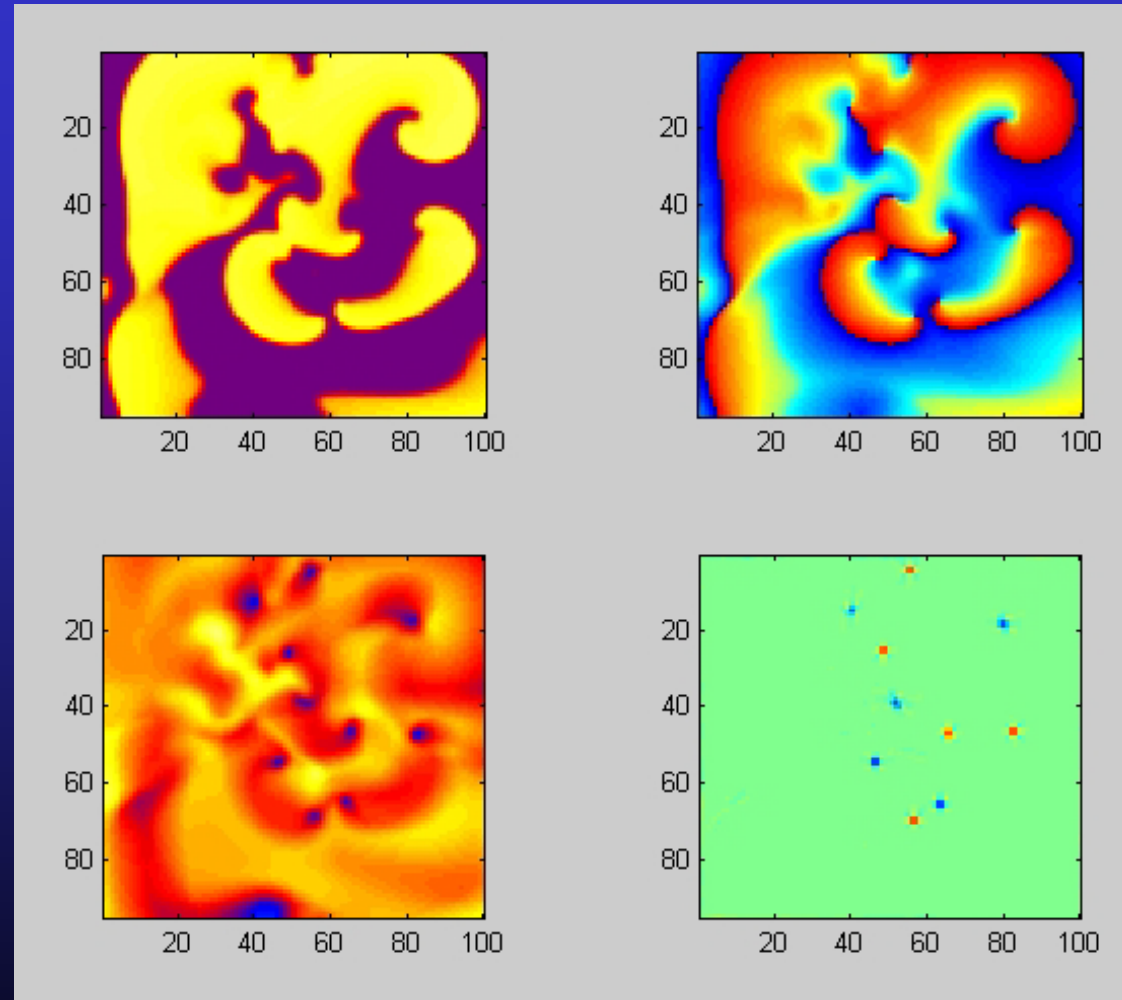
Visualizing Fibrillation

V_m Phase

Variance Curl



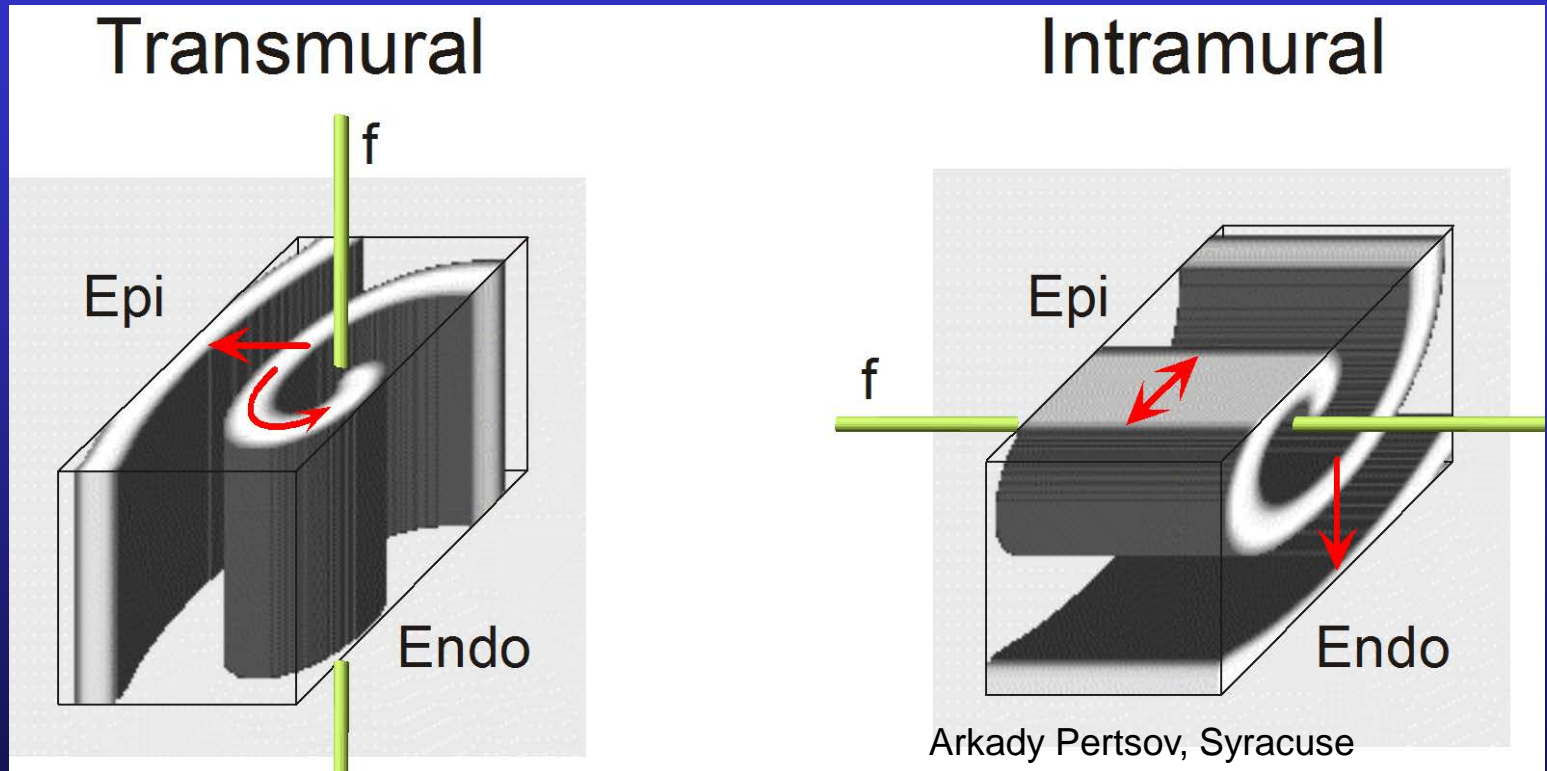
Vm_Var_Phase_Curl.mp4





And the Third Dimension...

Spiral VS Scroll Waves

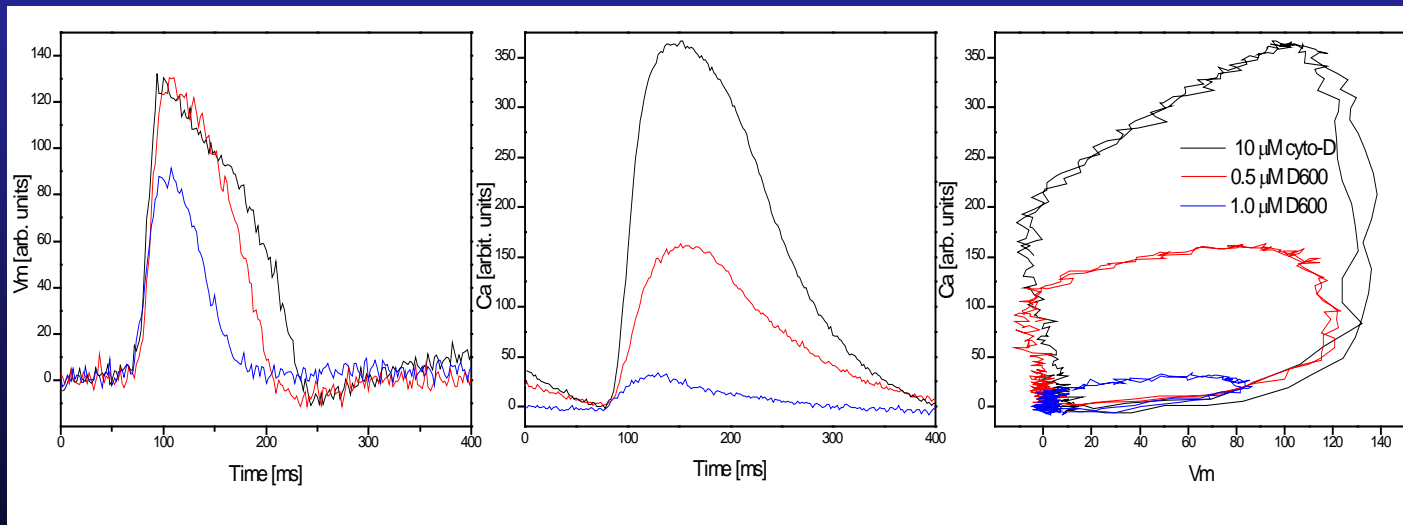
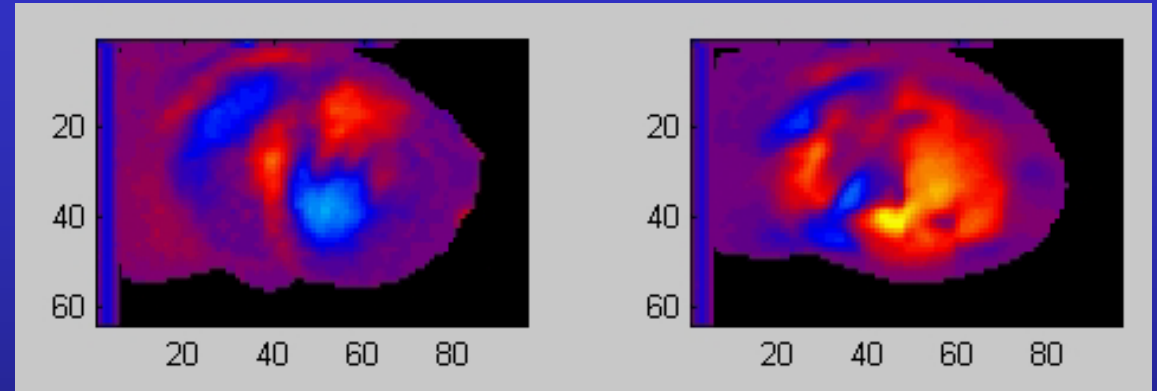


- Transmural waves can exist in 2-D (thin) or 3-D (thick)
- Intramural waves require ~ 1 cm wall thickness



Understanding Cardiac Dynamics

V_m & Ca^{++}
vs.
Methoxyverapamil
(D-600)



Vm_Ca.mp4



Questions

