

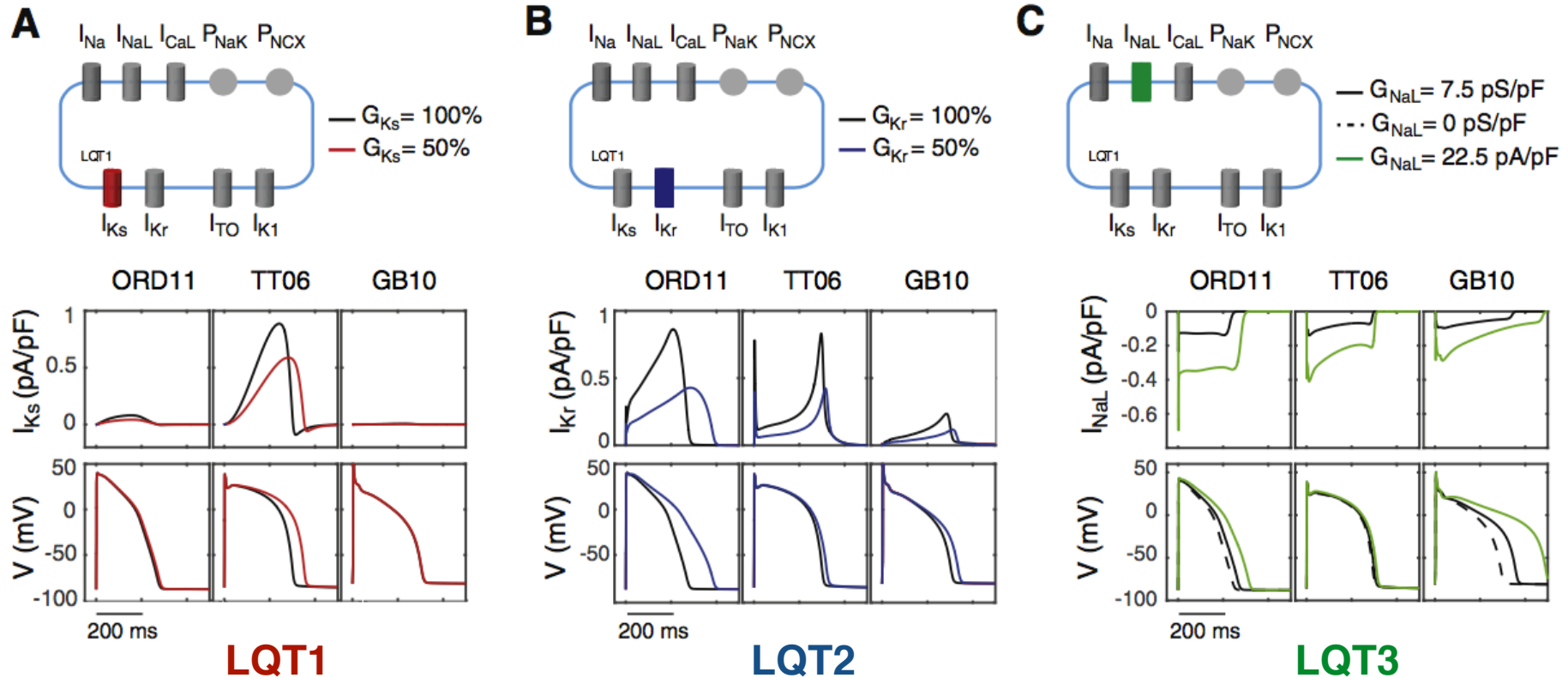
Global optimization of cardiac myocyte models

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Main question

Ionic models sometimes fail in their predictions -
can we improve models by redesigning the model
development process?

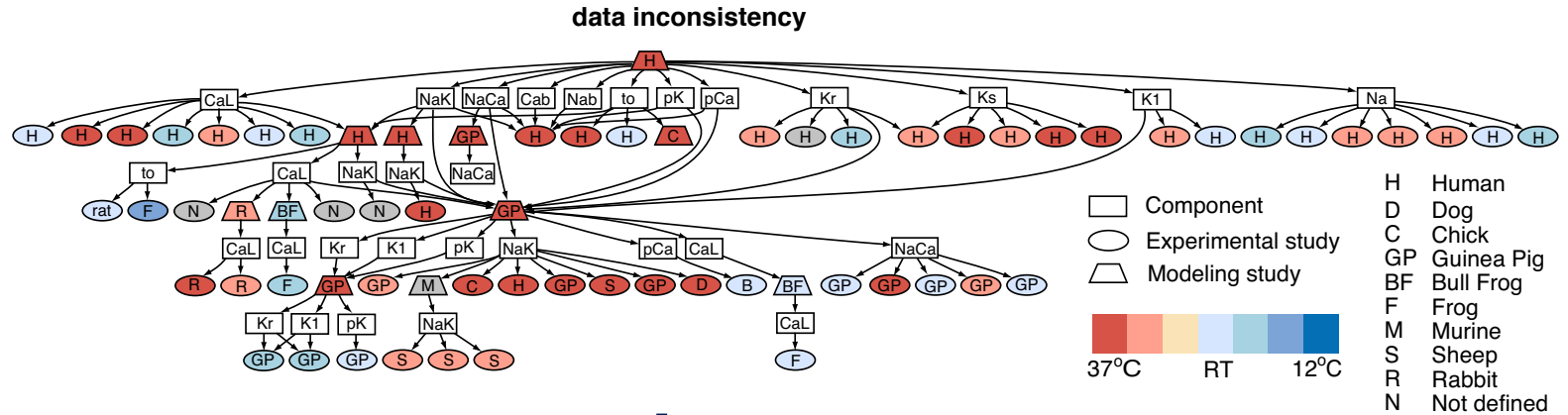
Congenital LQT simulations



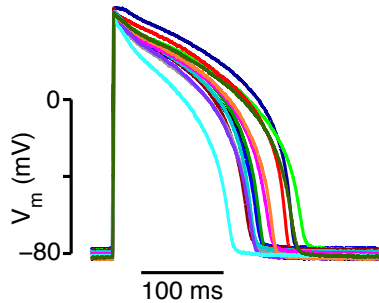
all 3 models have comparable baseline APD (~270-300ms), but differing morphology, and very different responses to simulated LQTs

difficulty that each model has representing at least some LQTs raises concerns about abilities to predict drug-induced LQT and TdP

Model development limitations

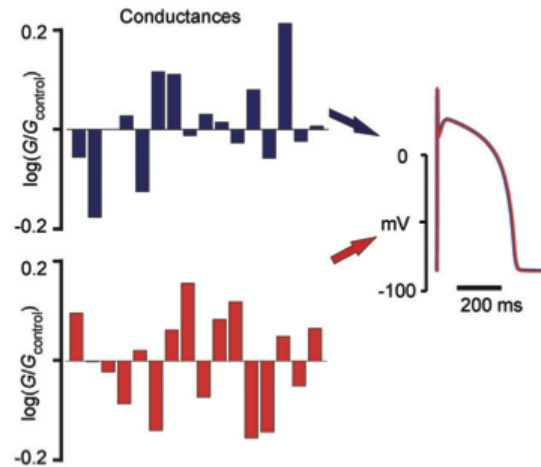


cell-to-cell variability

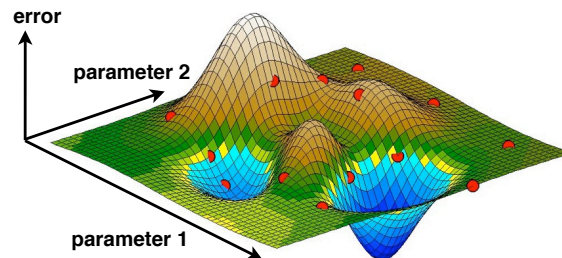


generic models with limited ability to reproduce specific complex dynamics

simple dynamics and non-uniqueness

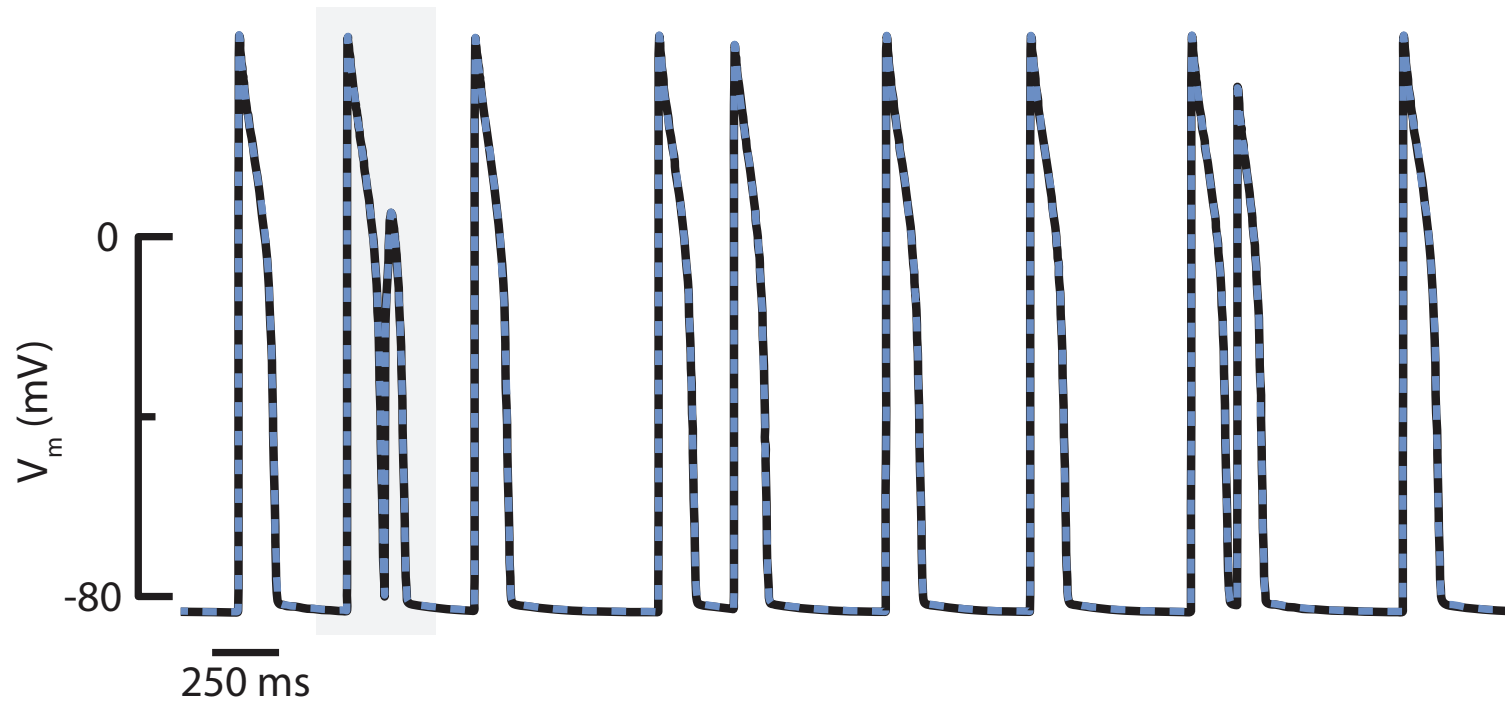


manual tuning



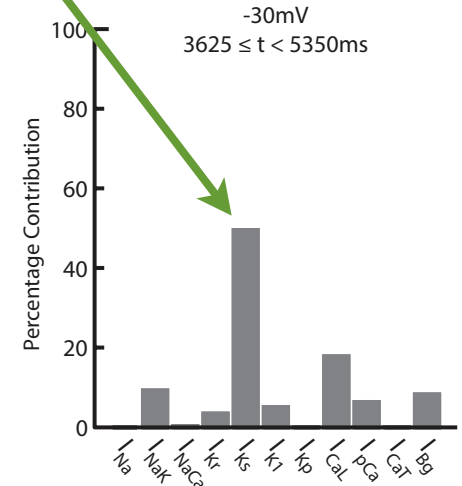
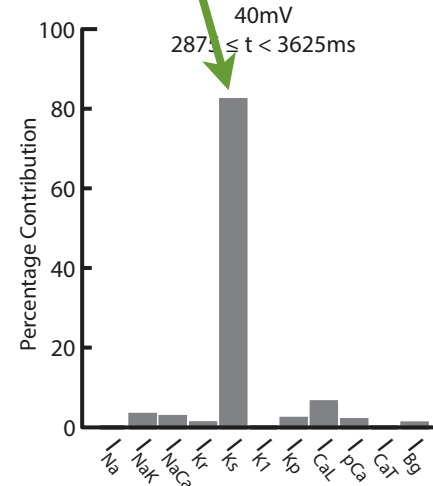
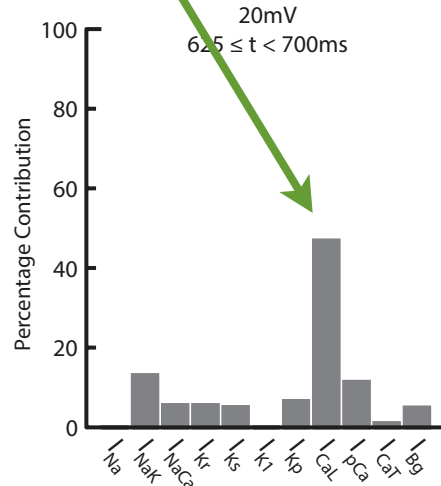
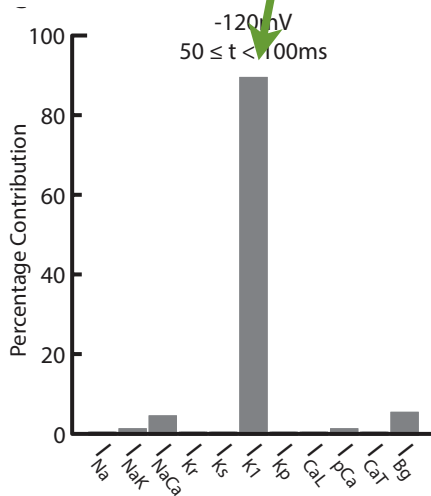
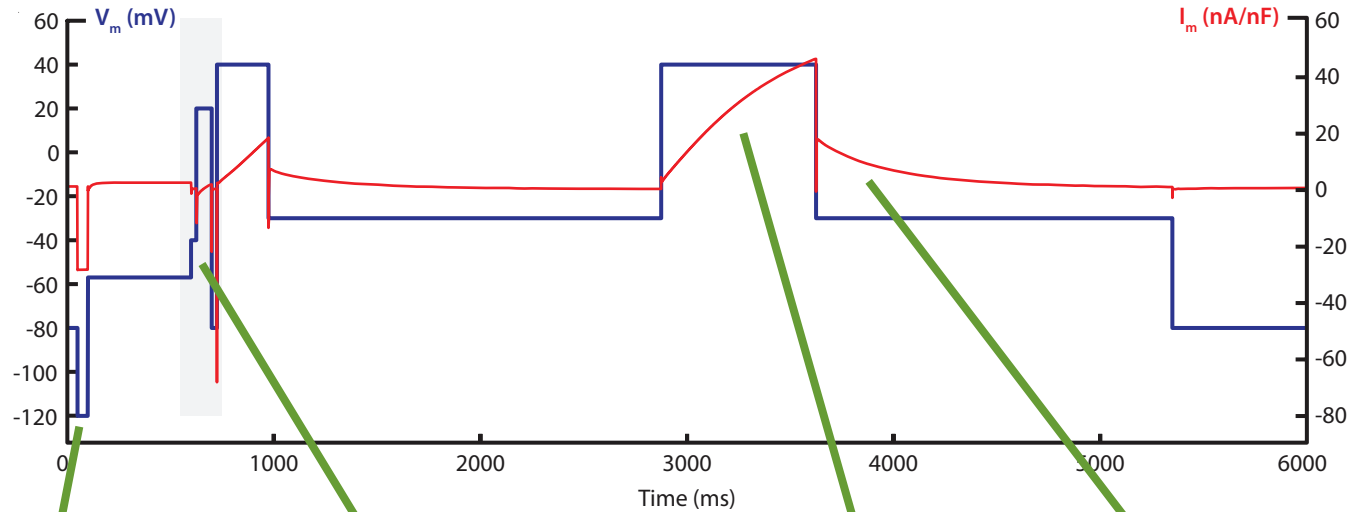
one information-rich data + global optimization approach

1. Use APs obtained during irregular pacing

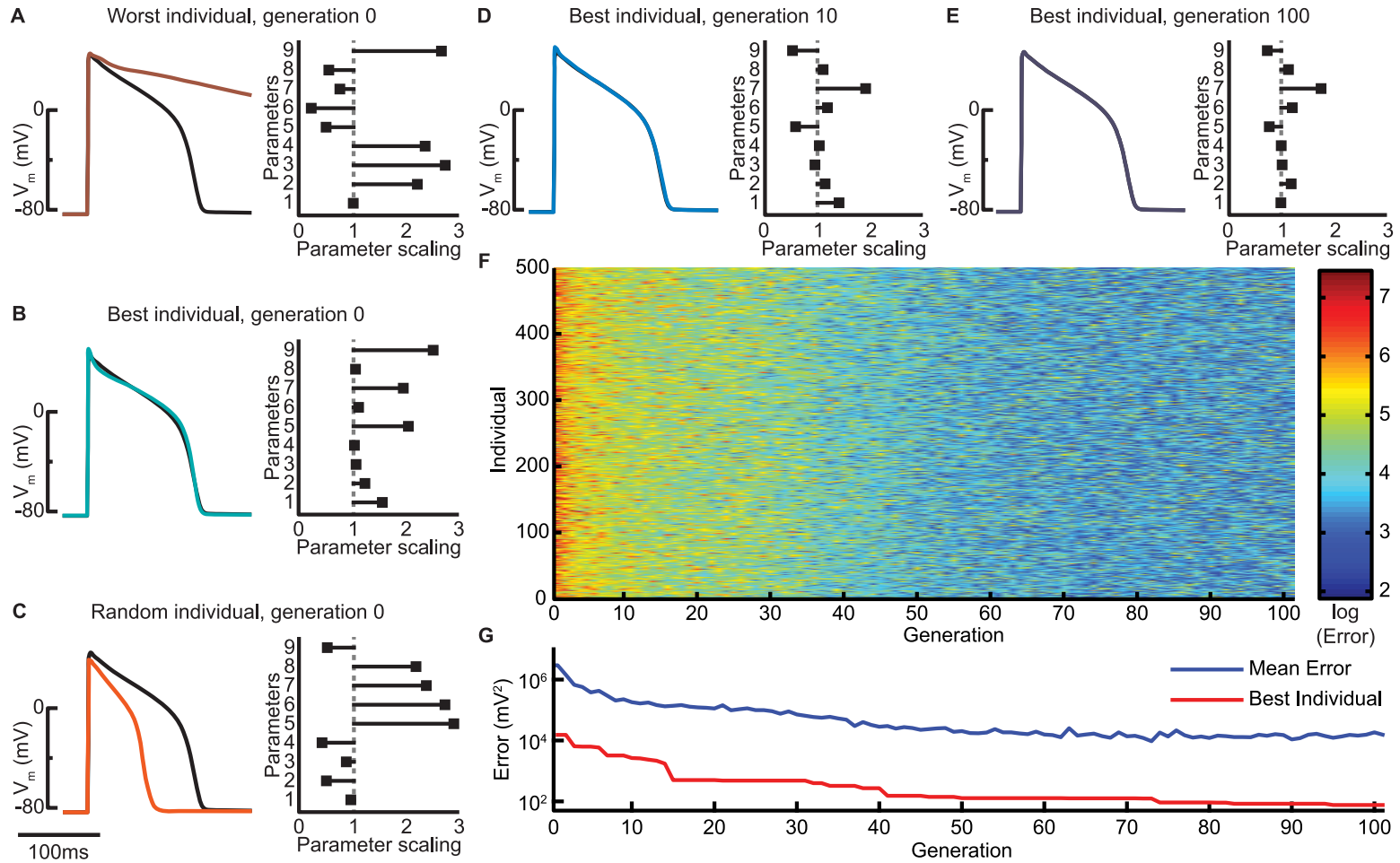


2. How about incorporating voltage-clamp data?

Can carefully designed voltage-clamp protocols inform model building?



3. Use genetic algorithm



```
def getSolutionCosts (navigationCode):
```

```
    fuelStopCost = 15
```

```
    extraComputationCost = 8
```

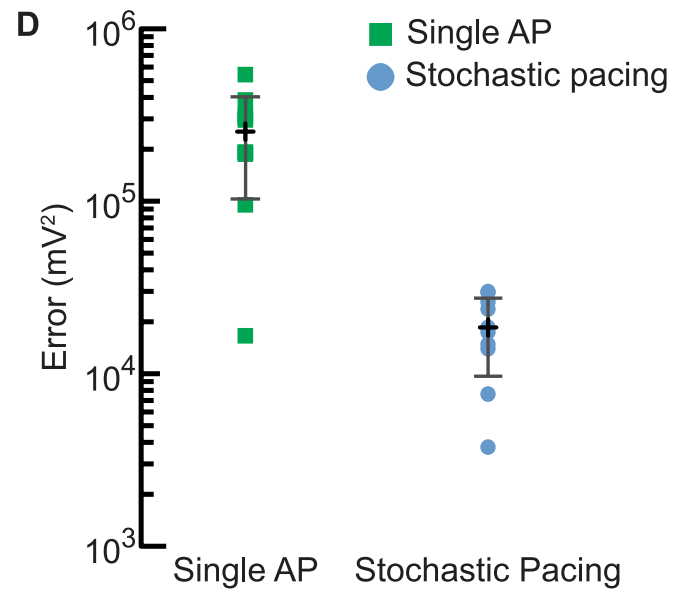
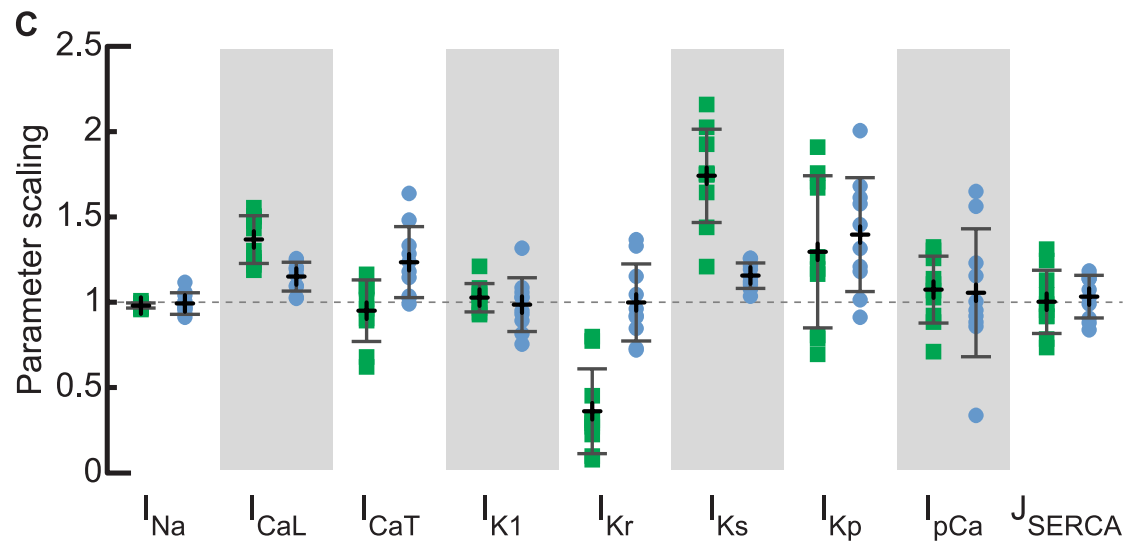
```
    thisAlgorithmBecomingSkynetCost = 999999999
```

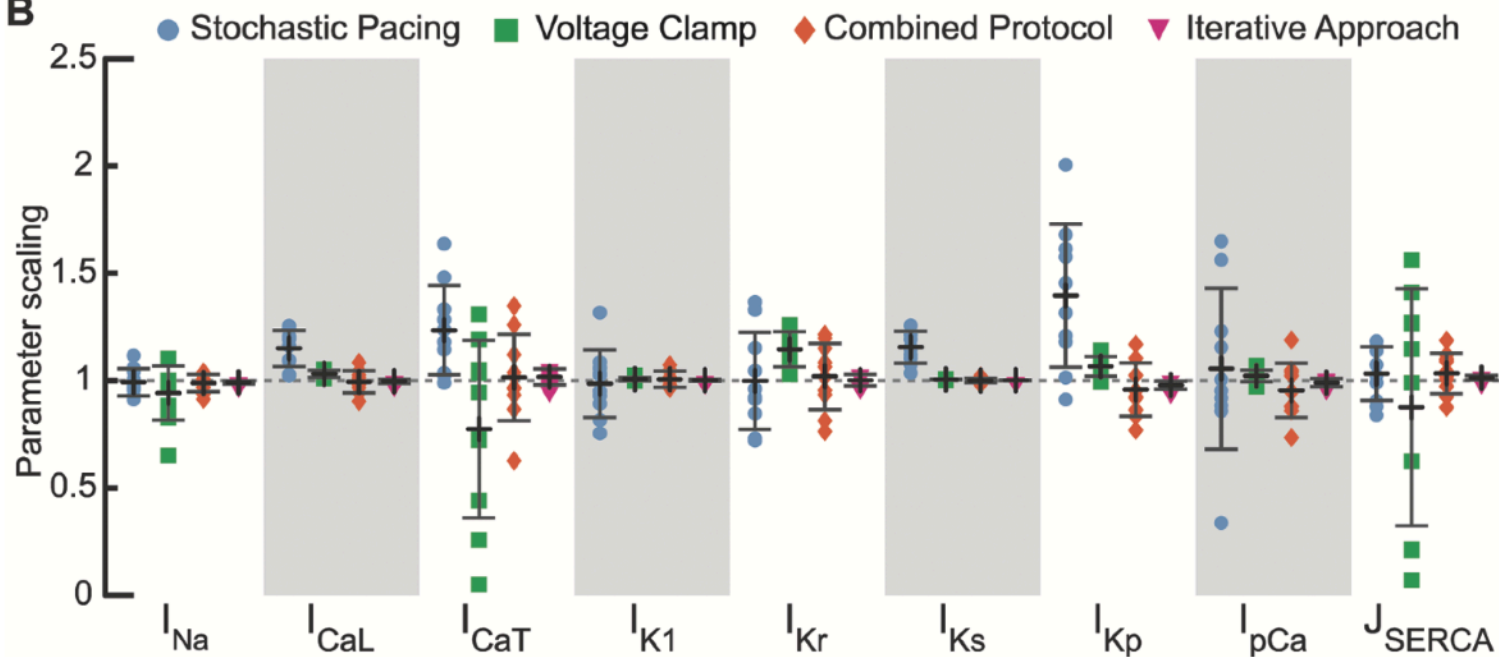
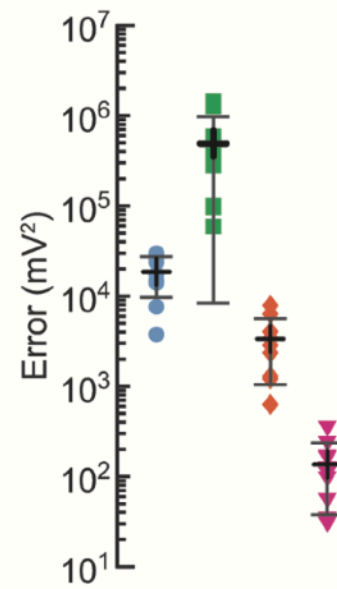
```
    waterCrossingCost = 45
```



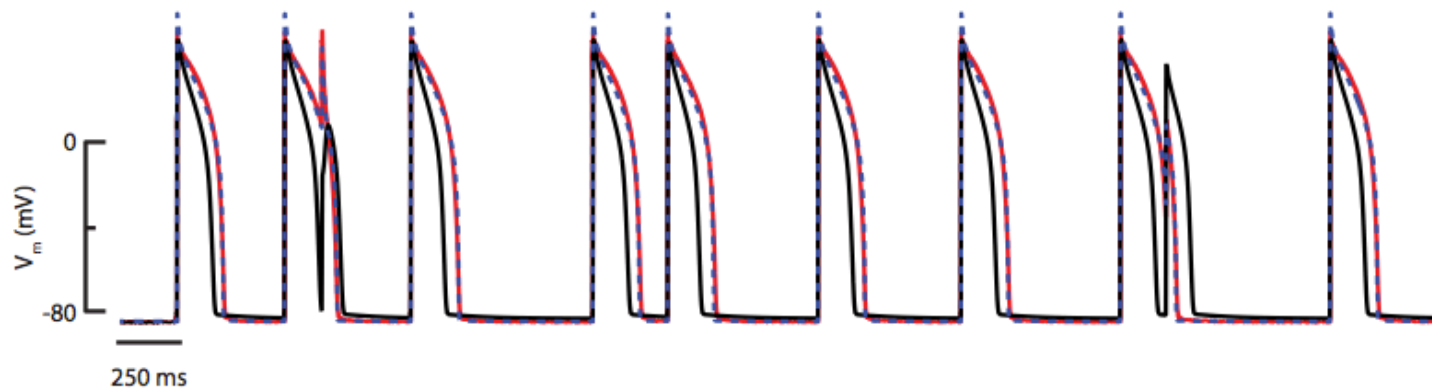
GENETIC ALGORITHMS TIP:

ALWAYS INCLUDE THIS IN YOUR FITNESS FUNCTION

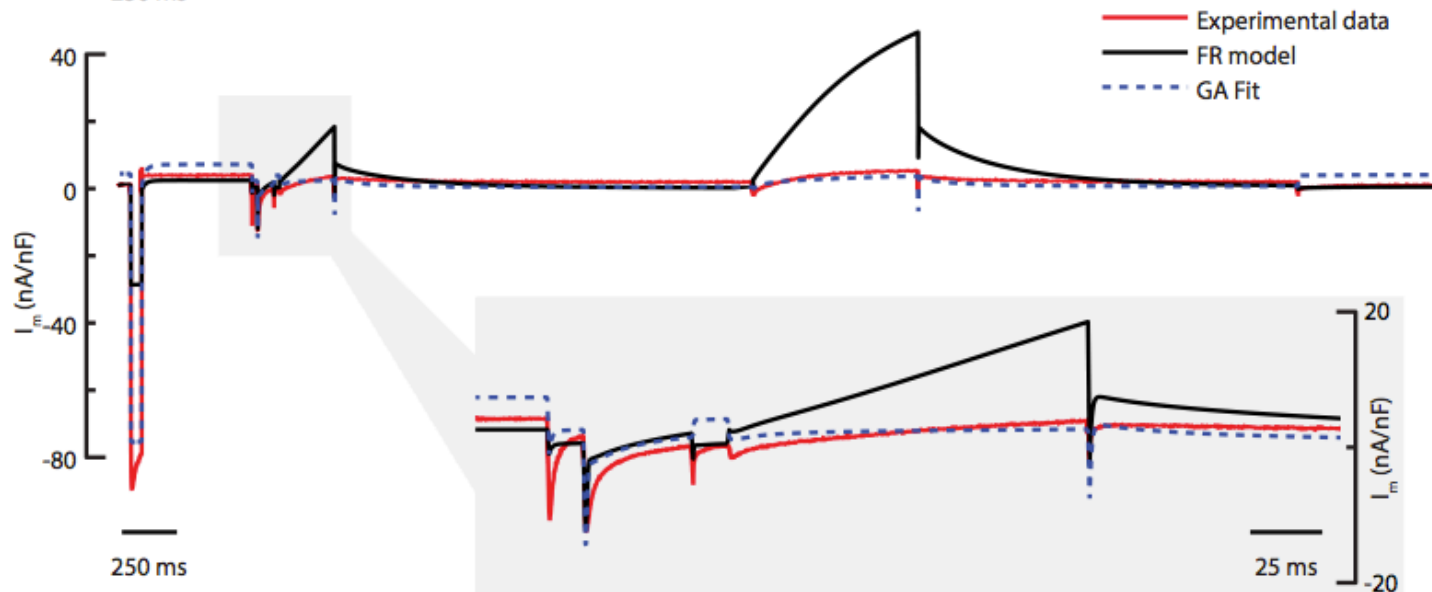


B**C**

Fitting current and voltage clamp *in vitro* data

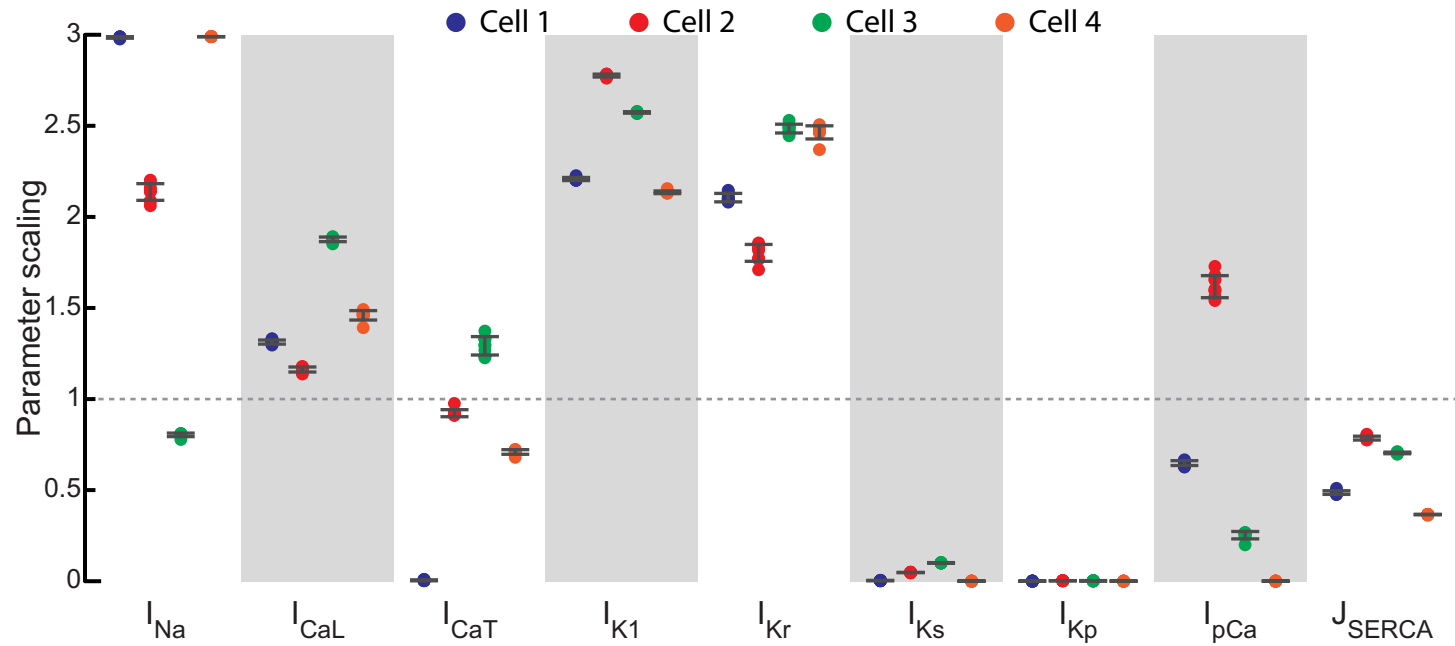


Stochastic
pacing

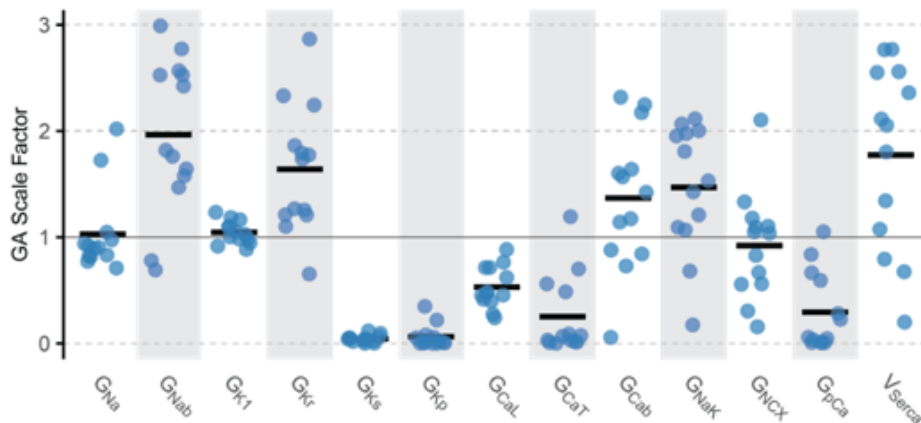
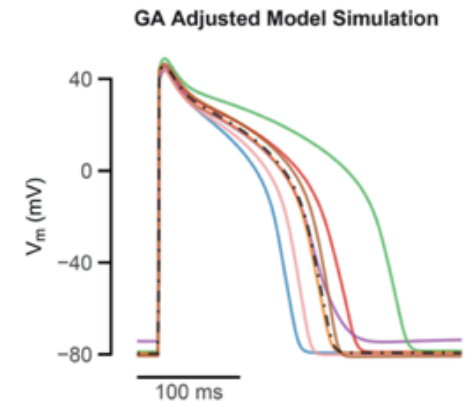
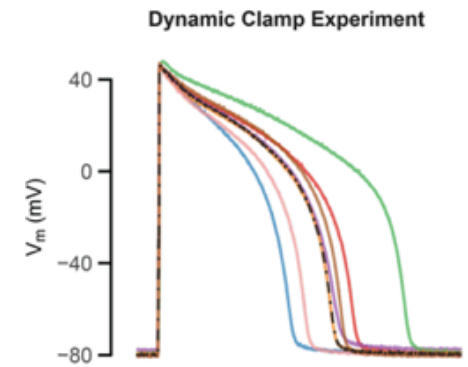
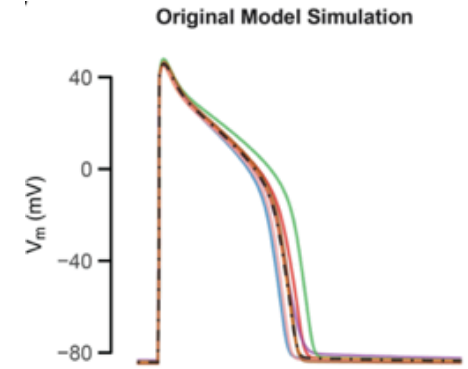
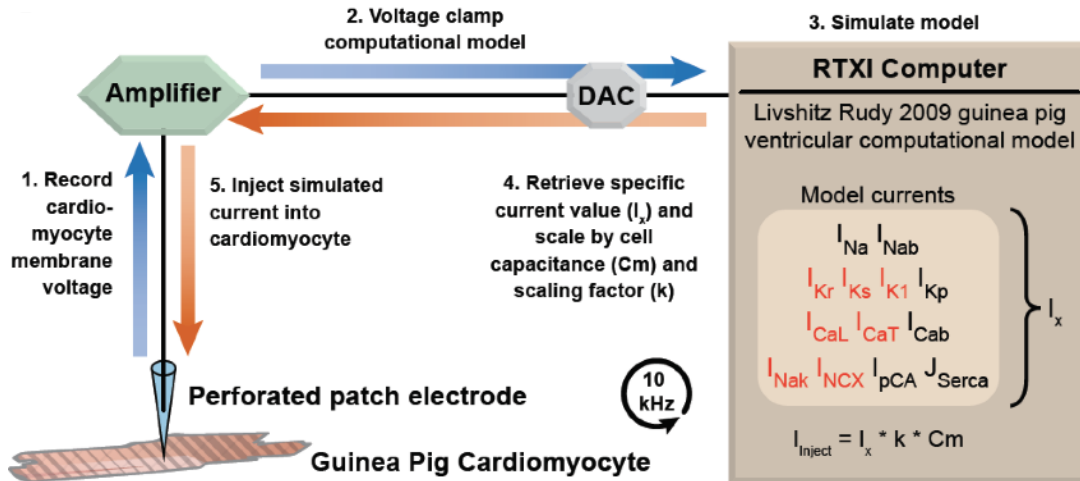


Voltage
clamp

Parameter estimation for individual myocytes



another information-rich data + global optimization approach - dynamic clamp

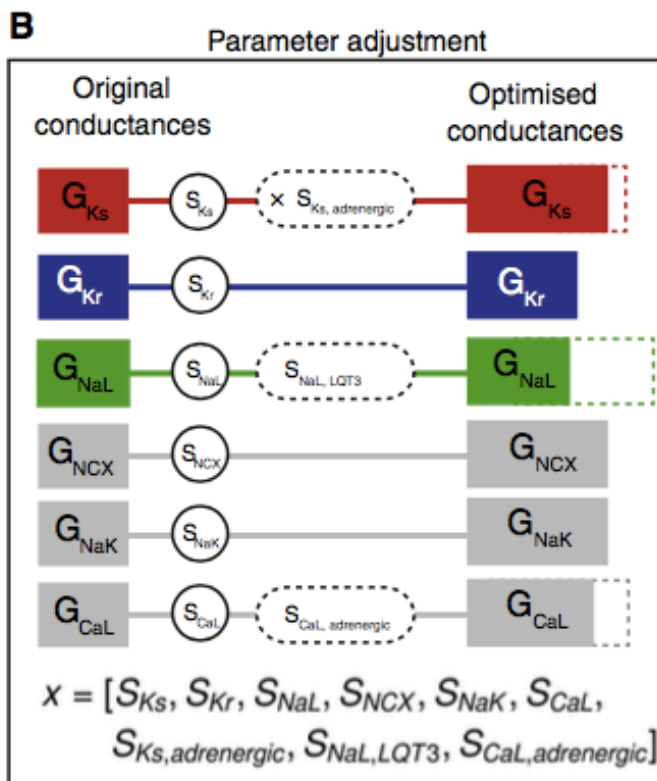
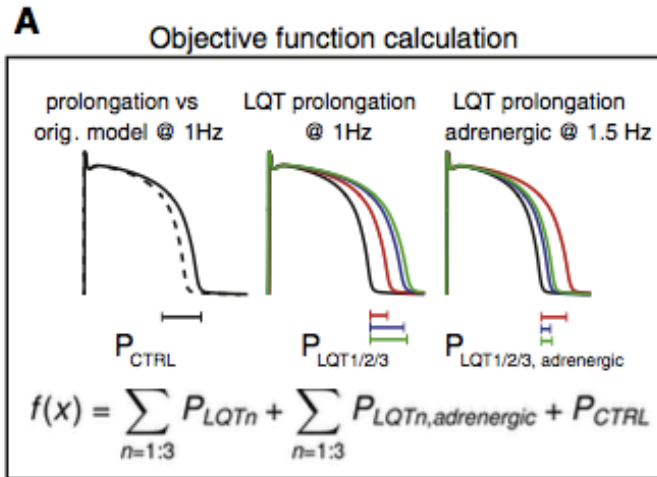


+/- 40% →

Current applied:

- $-I_{Kr}$ $-I_{K1}$ $-I_{CaT}$ $-I_{NCX}$
- $+I_{Ks}$ $+I_{CaL}$ $+I_{NaK}$ \dots Baseline

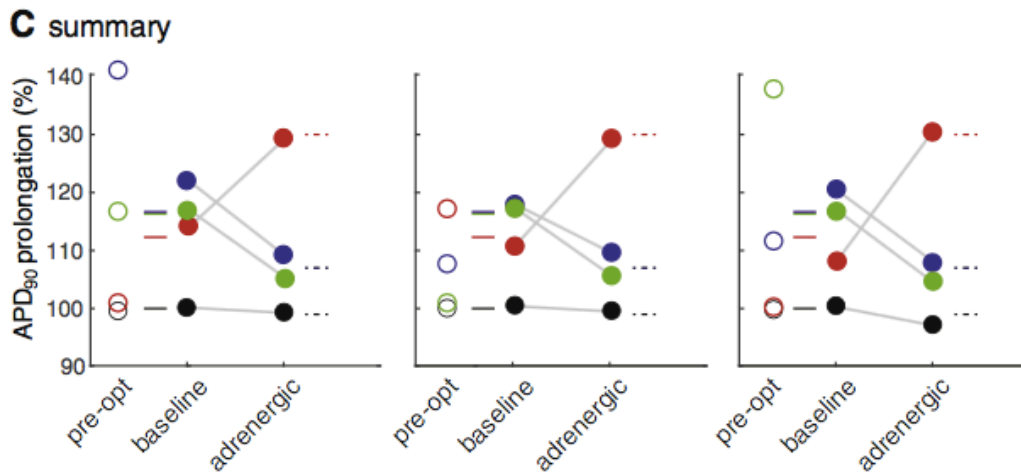
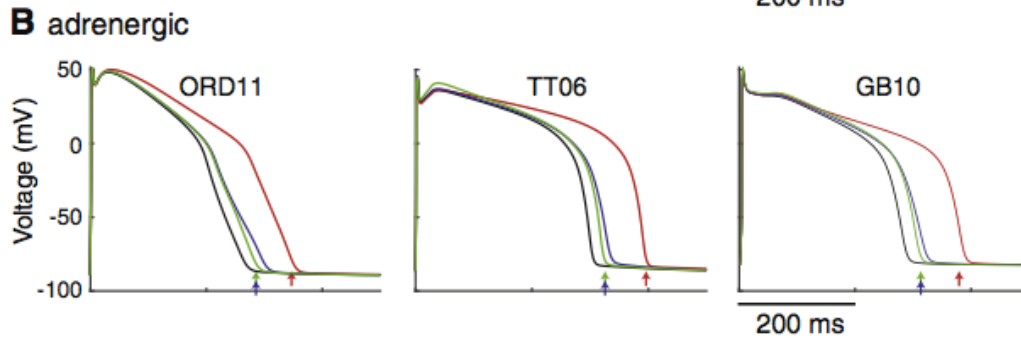
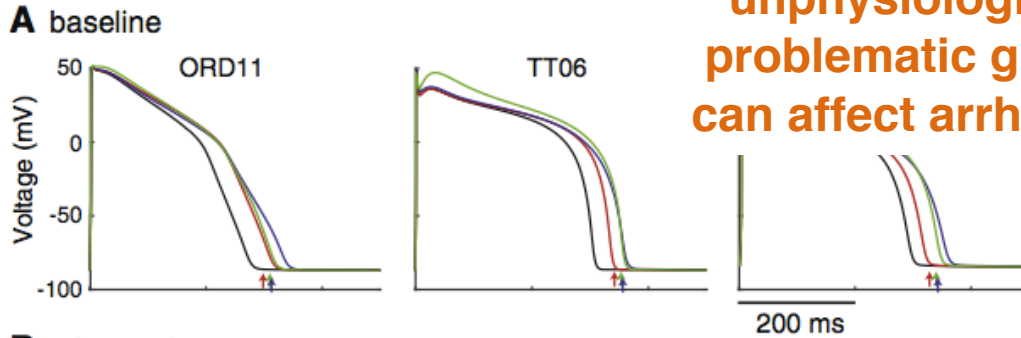
and another information-rich data + global optimization approach



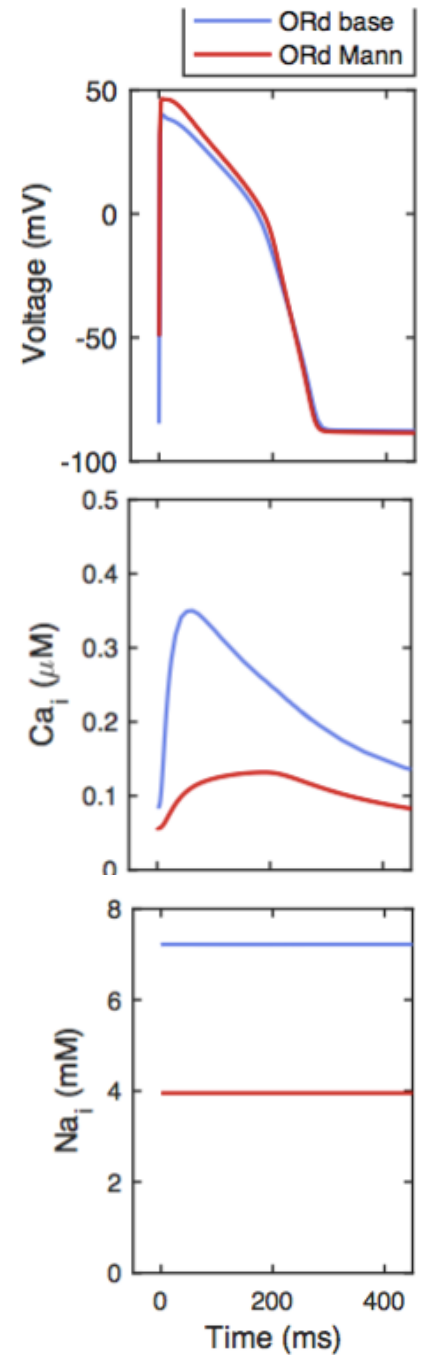
“In-silico models of cardiac electrophysiology have the potential to be tremendously useful in complementing traditional preclinical drug testing studies. However, our results demonstrate they should be carefully validated and optimized to clinical data before they can be used for this purpose.”

it works!

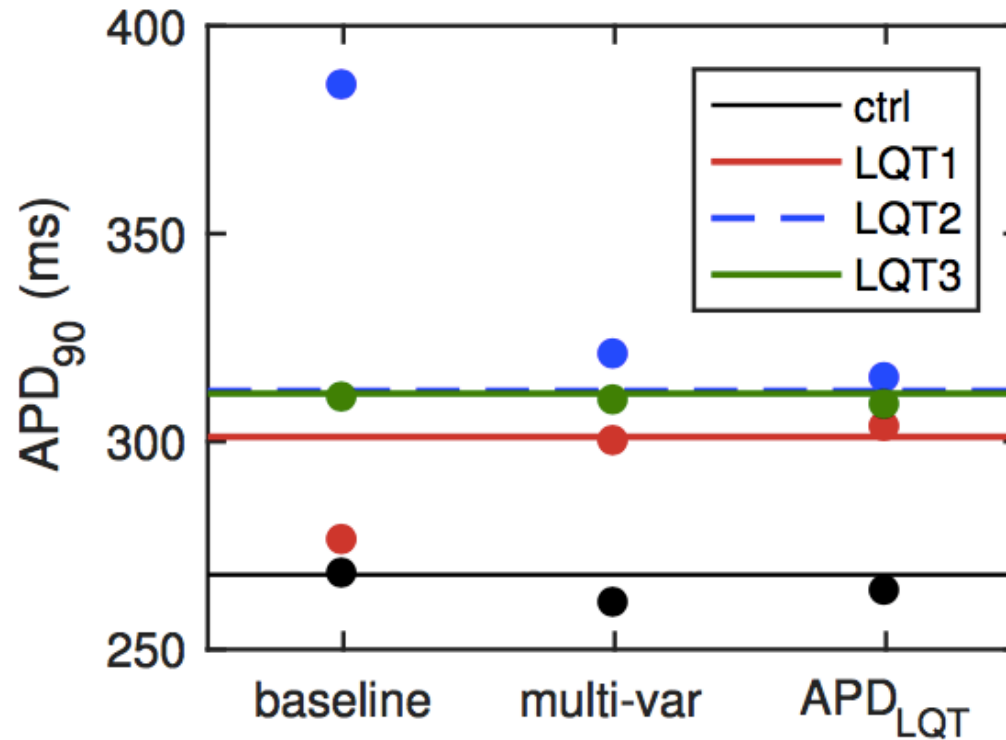
except, in the process, $[Ca^{2+}]_i$ and $[Na^+]_i$ becomes unphysiological, which is problematic given that both can affect arrhythmogenesis



LQT1
LQT2
LQT3

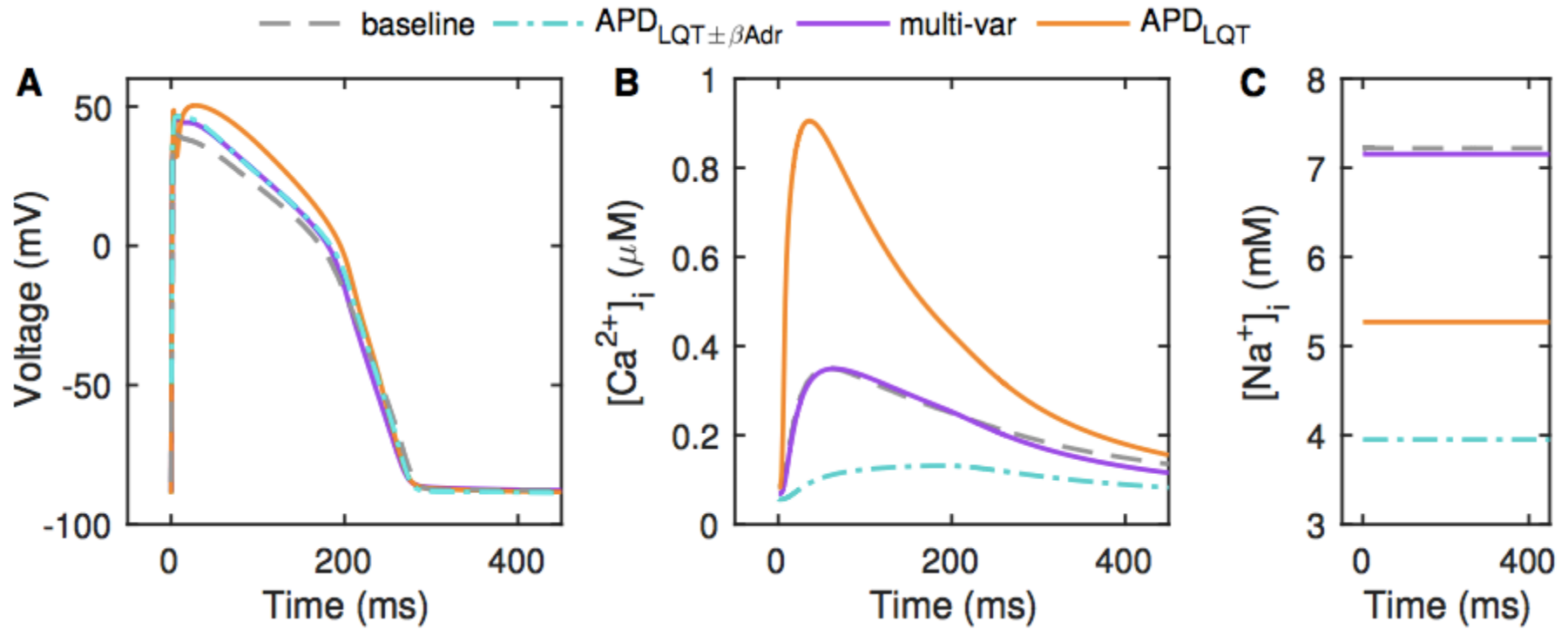


add optimization constraints on $[Na]_i$ and $[Ca^{2+}]_i$



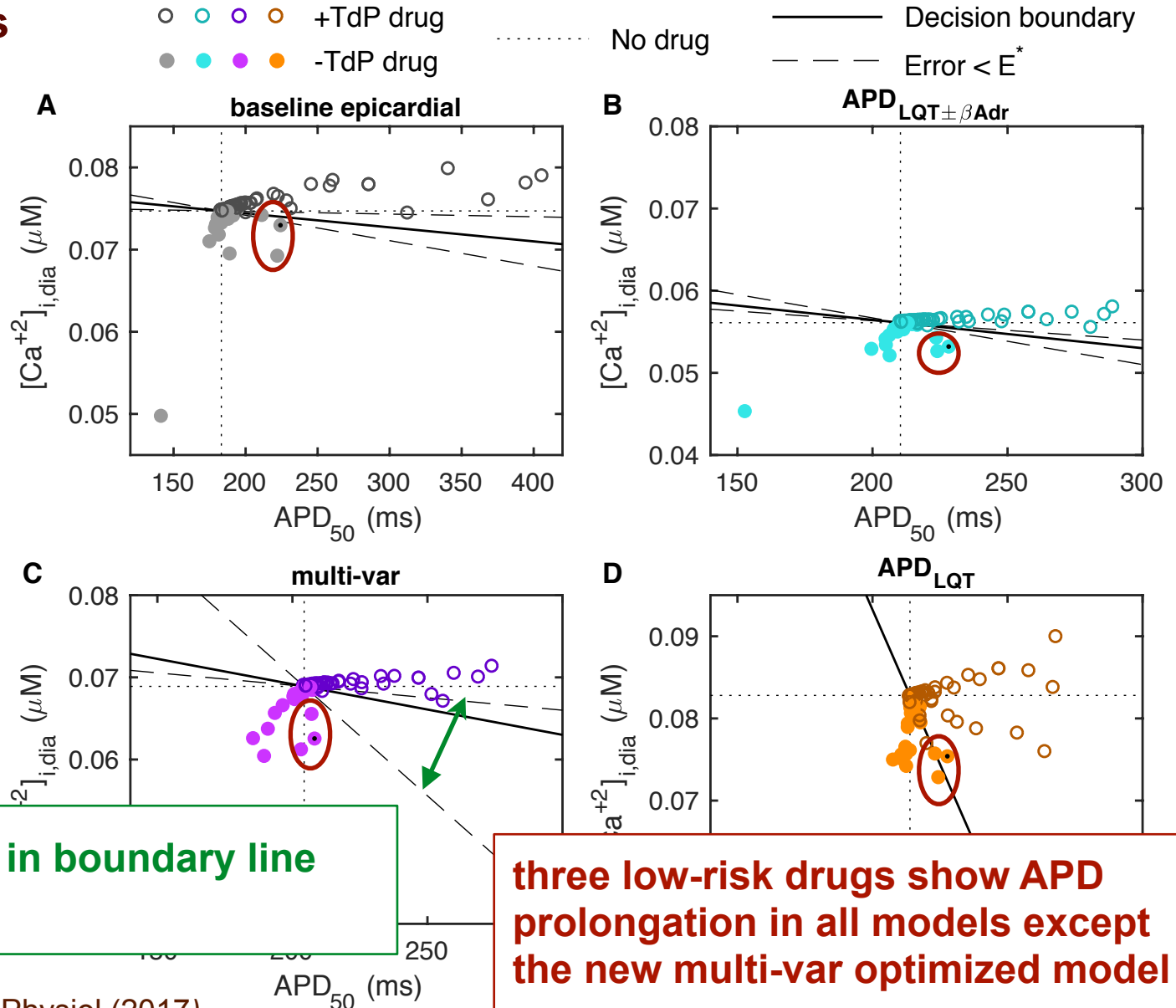
- **Baseline:** published ORd
- **APD_{LQT} :** optimized to APD errors for LQTs
- **multi-var:** optimized to APD errors, plus penalized solutions with $[Na^+]_i$ and $[Ca^{2+}]_i$ outside physiological values

constraint solution: discard models with unphysiological $[Na^+]_i$ and $[Ca^{2+}]_i$ during global optimization

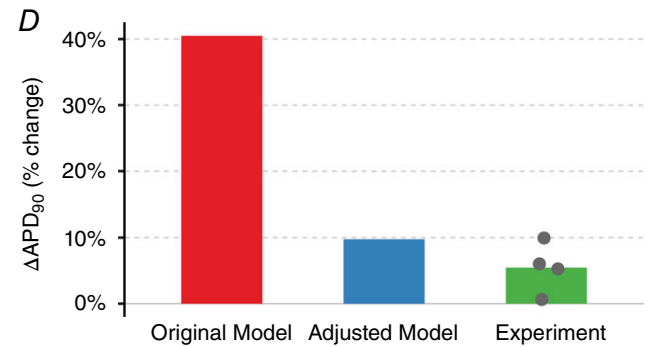
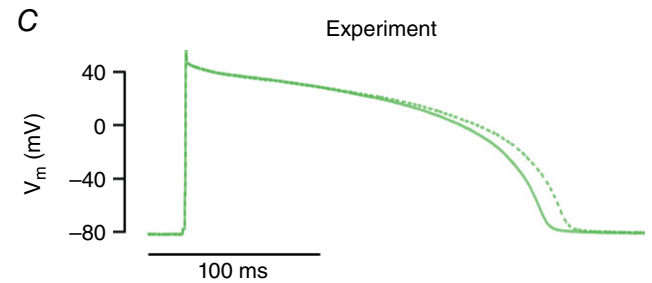
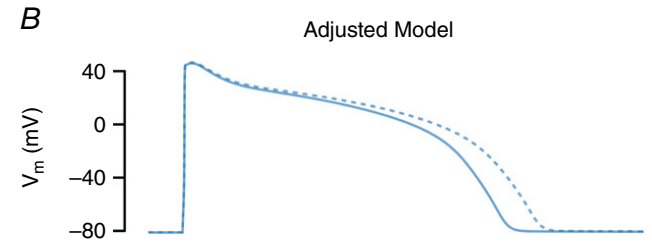
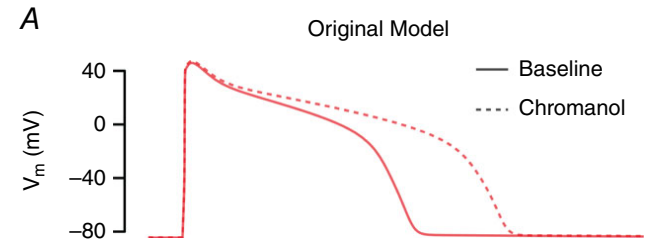
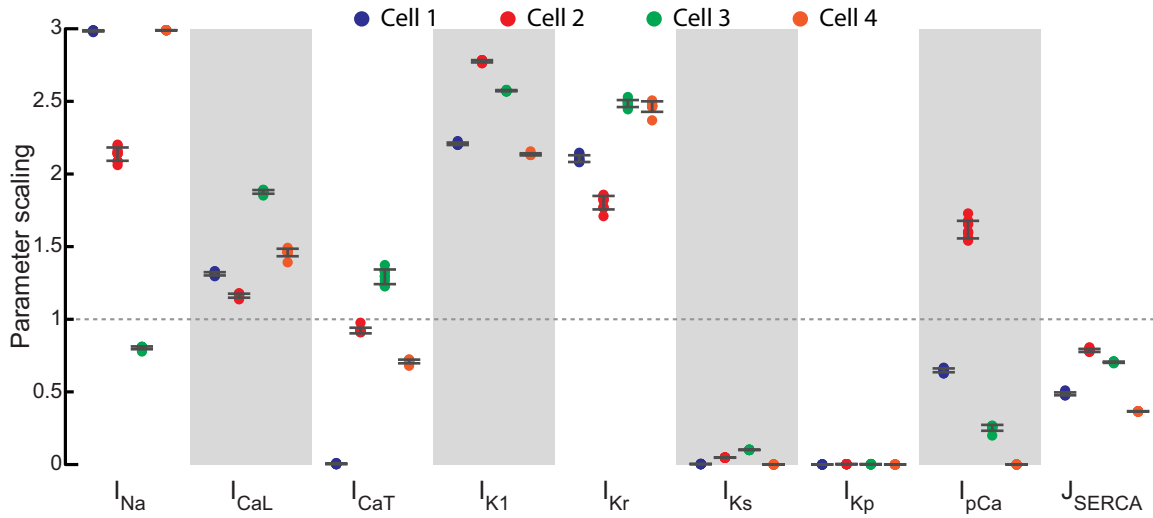


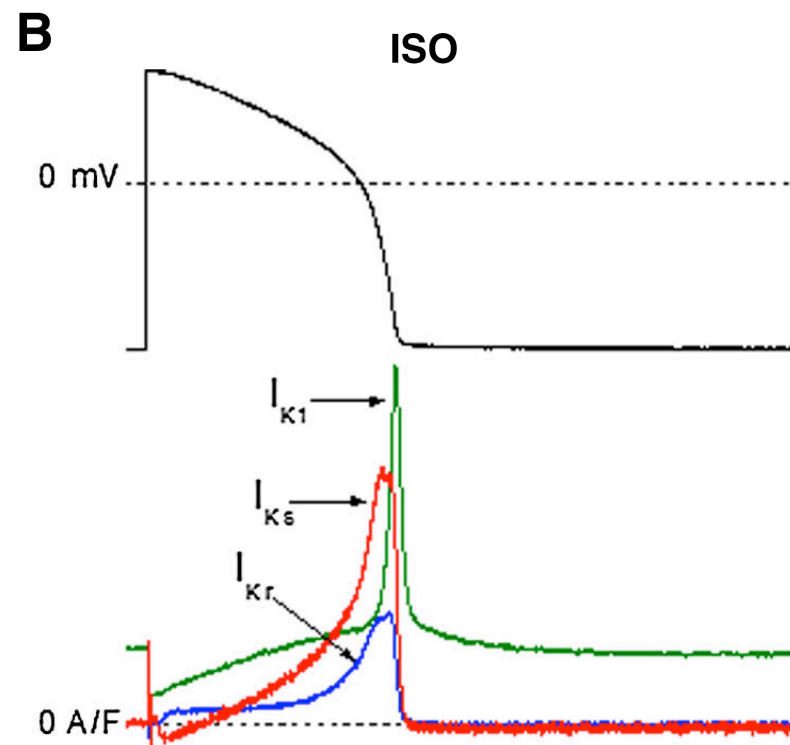
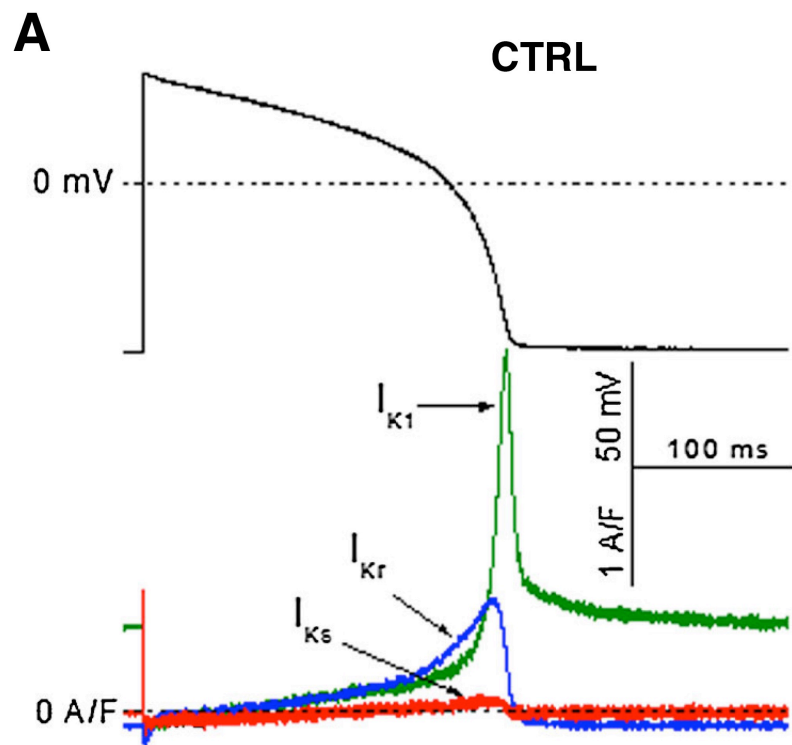
model with more physiological constraints is better at separating TdP risk drugs

tested 86 I_{Kr} , I_{CaL} , I_{Na} blockers as in Lancaster & Sobie (*Clin. Pharm. Therap.* 2016)



I_{Ks} in GP ventricular myocytes





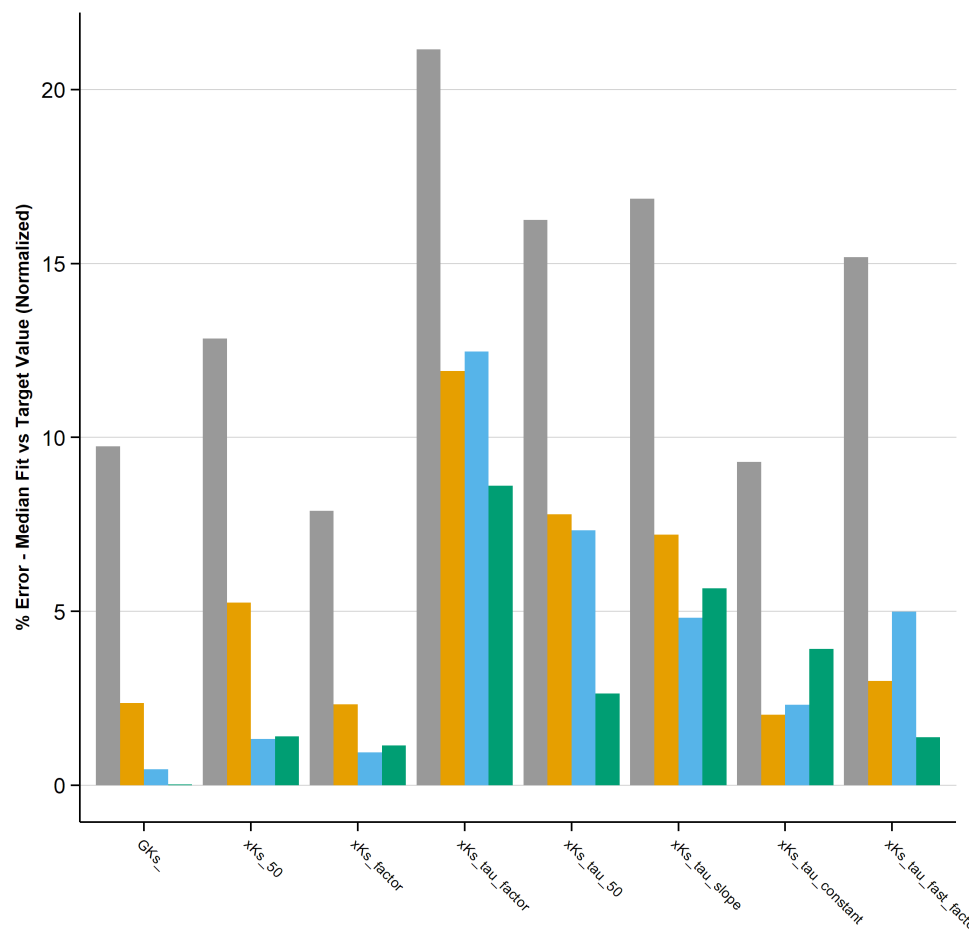
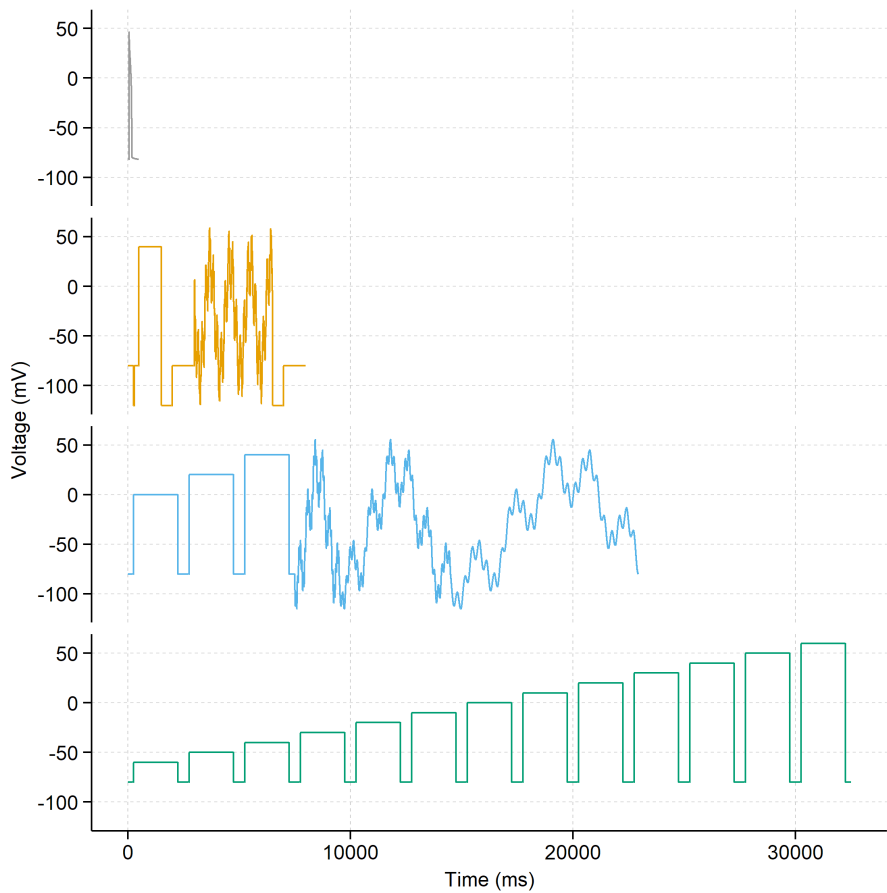
Questions

- What is the ratio of the delayed rectifier currents in the guinea pig?
- How does this ratio vary with β -adrenergic stimulation?

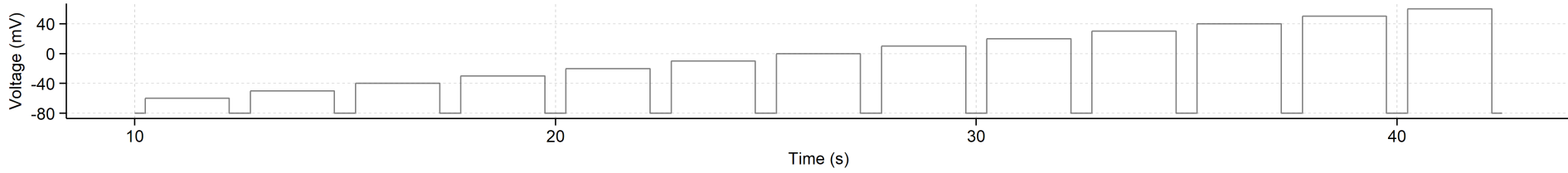
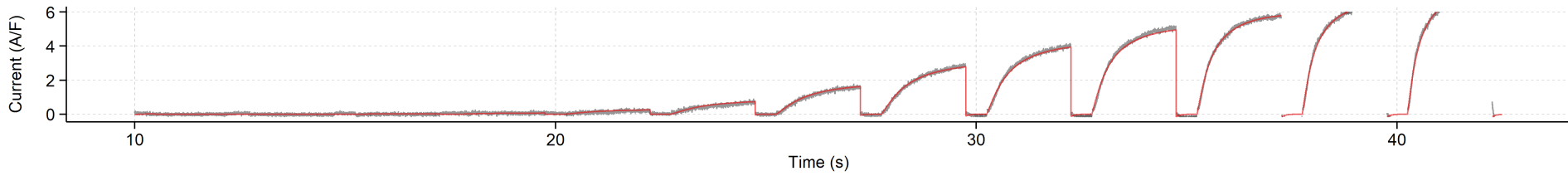
Approach

- Use computational modeling to identify a voltage clamp protocol that allows for accurate parameterization of the formulations of I_{Ks} and I_{Kr}
- Develop and perform *in vitro* experiment to gather current-specific information

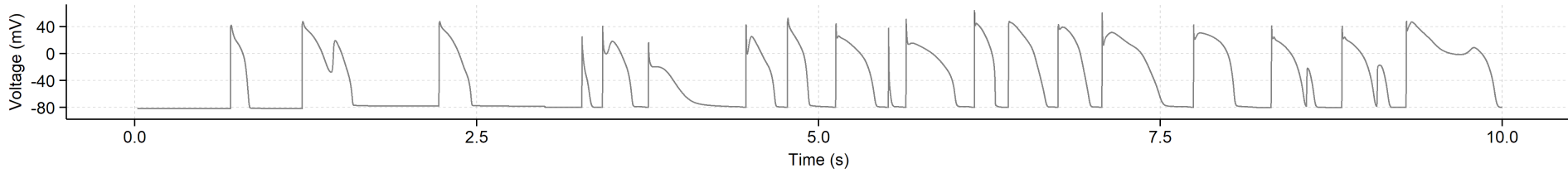
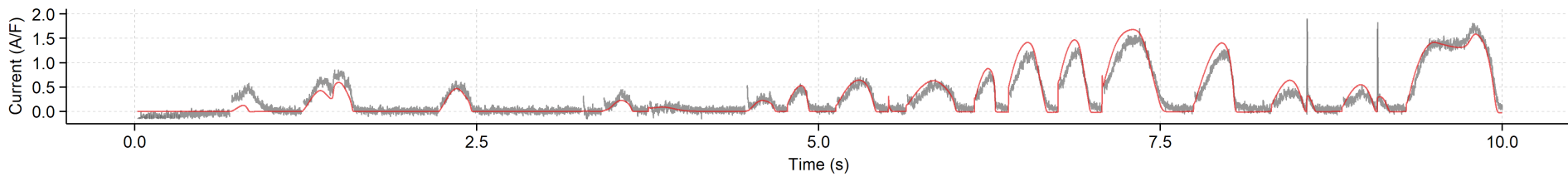
I_{Ks} protocol testing



GA fit



Validation



conclusions and next steps

- rich data are needed in cardiac myocyte model optimization
- optimization to such data can generate models with higher accuracy - including for predictions of drug-induced cardiotoxicity
- extend +TdP / -TdP drug segmentation using
 - population-of-models approach
 - tissue simulations
- I_{Ks}/I_{Kr} protocols and levels
- Add Ca transient measurements to optimization objective
- Use cell-specific models to study cellular heterogeneity

Acknowledgements



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