

machine learning in drug development

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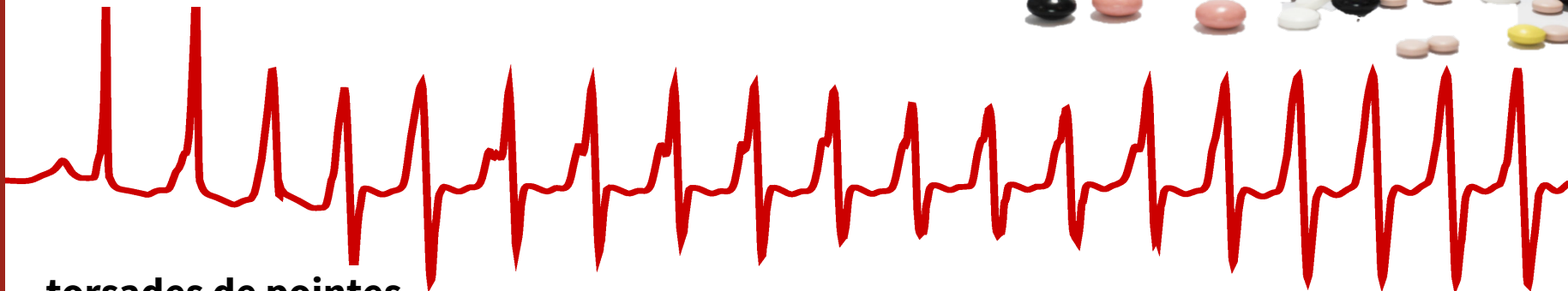
advania



drug development



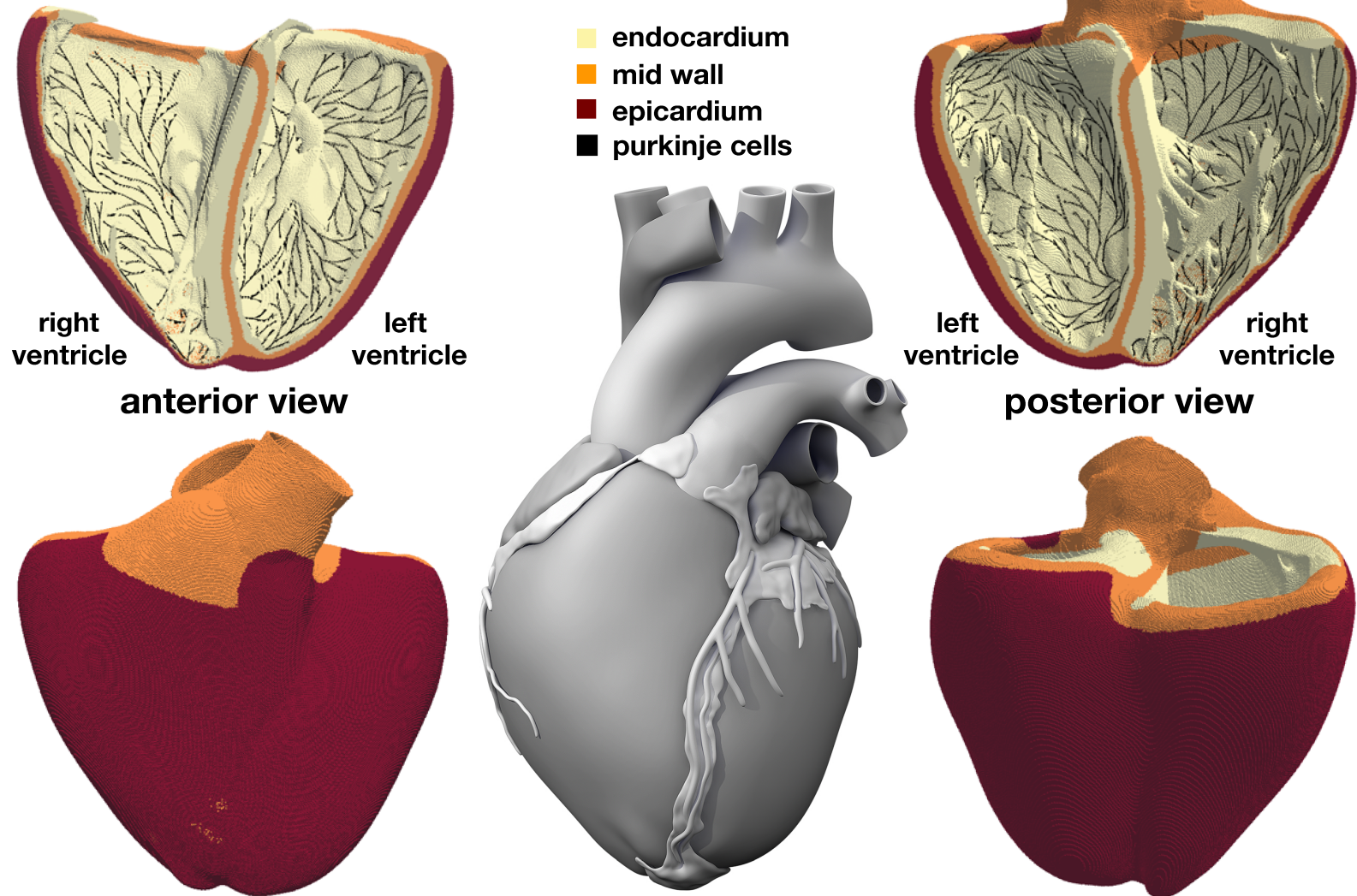
- numerous drugs have **serious side effects on the heart**
- gold standard safety test **action potential** and **QT interval** lengths
- criteria are **non-specific** / useful drugs are **falsely screened out**
- new drug - average cost **\$2.5 billion** / average time **> 10 years**
- CiPA initiative by FDA – **new paradigm for drug safety evaluation**



torsades de pointes

colatsky et al. [2016], crumb et al. [2016], gintant et al. [2016], johannesen et al. [2014], mirams et al. [2011], sager et al. [2014], stockbridge et al. [2013], wang et al. [2017], vincente et al. [2016,2018]

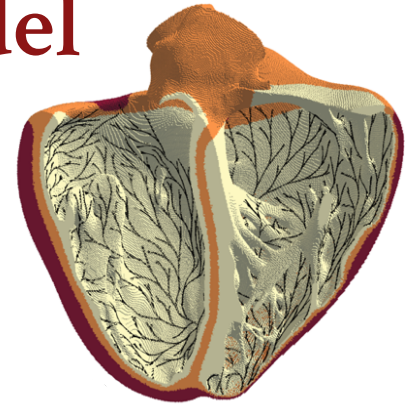
organ model - the living heart



spatial discretization: 0.3mm, 7M linear hexahedral elements, 8M nodes, 250M internal variables; temporal discretization: 0.005ms, 1M steps, 5 beats.

sahli costabal, hurtado, kuhl [2016], <https://github.com/fsahli/fractal-tree>

tissue model - monodomain model



- monodomain model - **action potential**

$$\dot{\phi} = \text{div}(\mathbf{D} \cdot \nabla \phi) + f^{\phi}$$

- flux term - second order **conductivity tensor**

$$\mathbf{D} = D_{\text{iso}} \mathbf{I} + D_{\text{ani}} \mathbf{f} \otimes \mathbf{f}$$

- source term - **ionic currents**

$$f^{\phi} = -I_{\text{ion}}/C_m \quad \text{with} \quad I_{\text{ion}} = I_{\text{ion}}(\phi, \mathbf{q}(\phi); t)$$

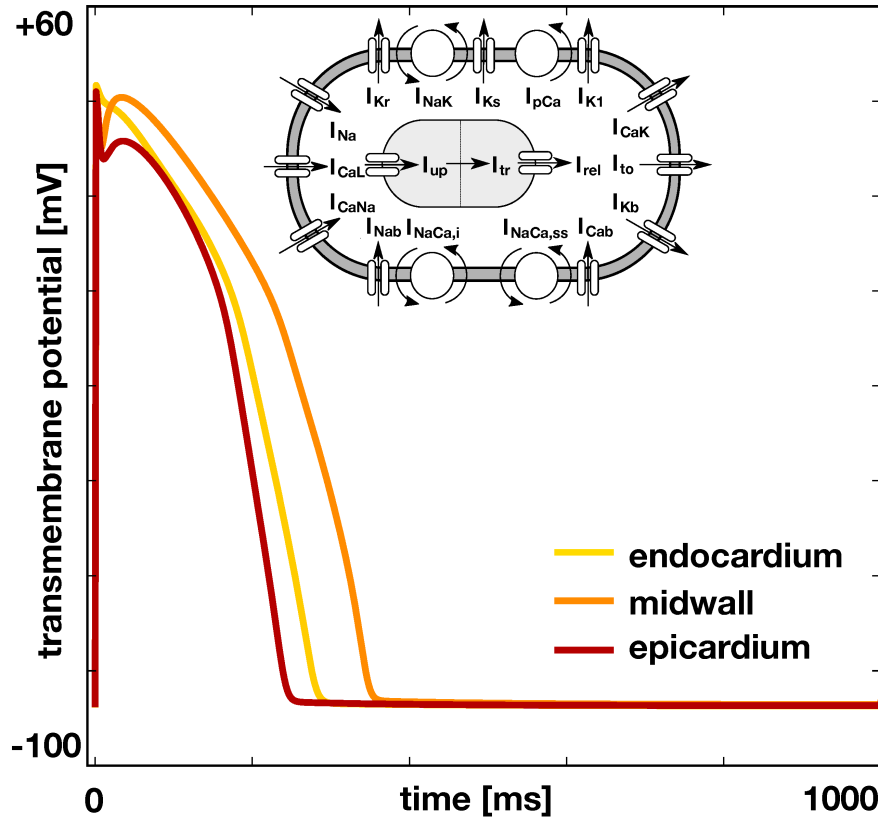
- ordinary differential equations for **state variables**

$$\dot{\mathbf{q}} = \mathbf{g}(\phi, \mathbf{q}(\phi); t)$$

- ventricular cells - **o'hara rudy model** - 15 currents / 39 state variables
- purkinje cells - **stewart model** - 14 currents / 20 state variables

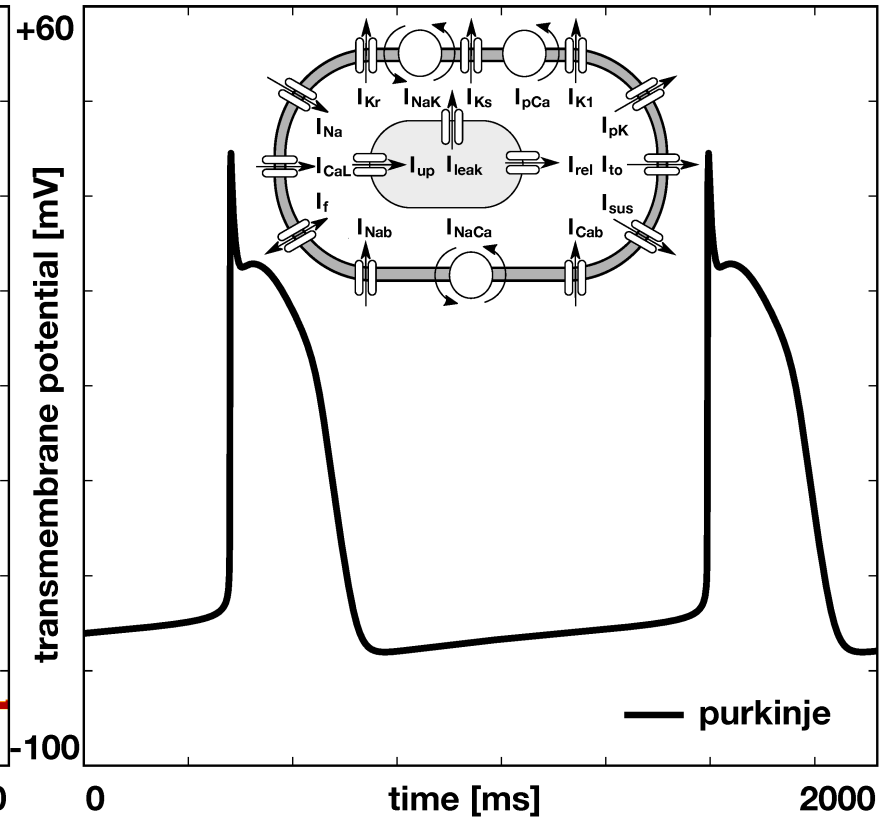
cell model - ventricular and purkinje cells

ventricular cells



$$\begin{aligned}
 I_{ion} = & I_{CaL} + I_{Na} + I_{Cab} + I_{Nab} \\
 & + I_{Kr} + I_{Ks} + I_{K1} + I_{to} \\
 & + I_f + I_{sus} \\
 & + I_{NaK} + I_{pCa} + I_{pK} + I_{NaCa}
 \end{aligned}$$

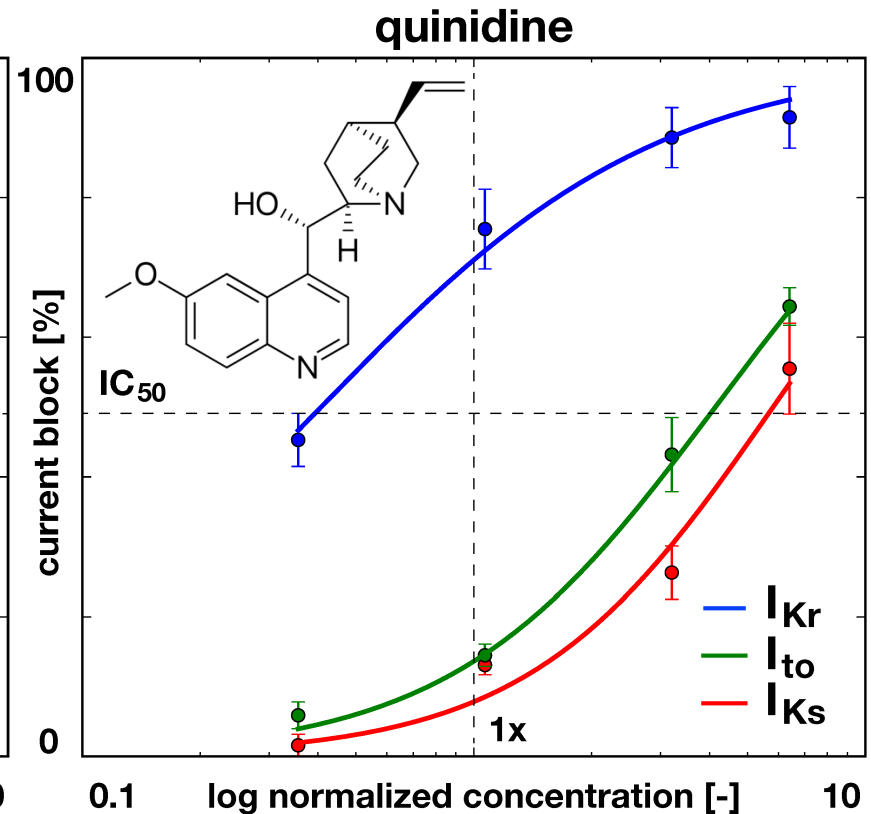
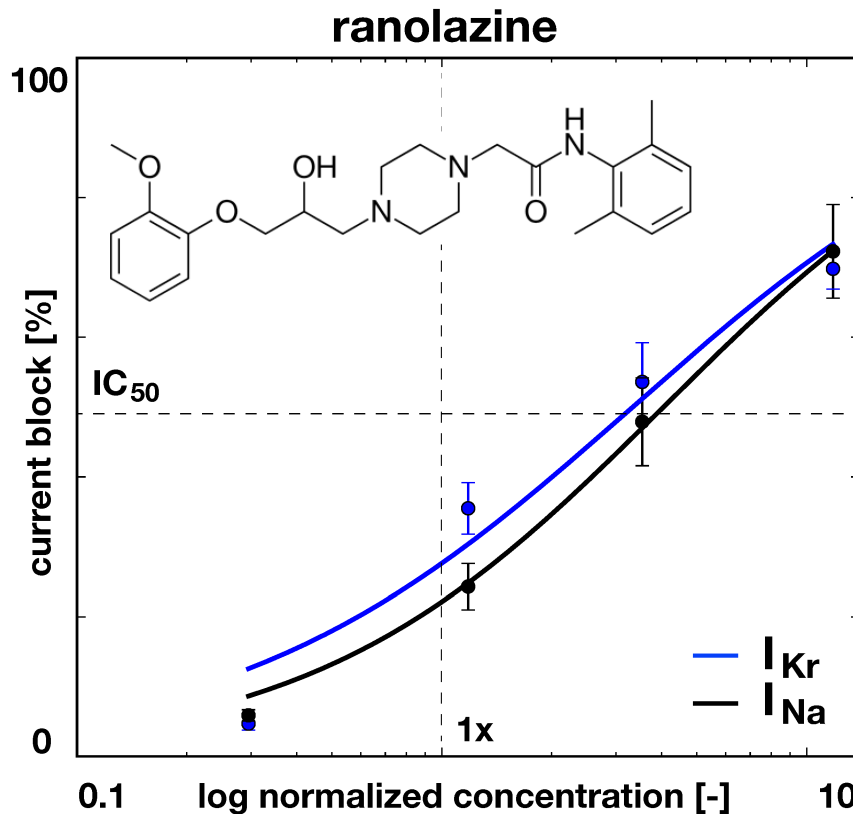
purkinje cells



$$\begin{aligned}
 I_{ion} = & I_{CaL} + I_{Na} + I_{CaNa} + I_{CaK} \\
 & + I_{Cab} + I_{Nab} + I_{Kb} \\
 & + I_{Kr} + I_{Ks} + I_{K1} + I_{to} \\
 & + I_{NaK} + I_{pCa} + I_{NaCa,i} + I_{NaCa,ss}
 \end{aligned}$$

o'hara, virag, varro, rudy [2011], stewart, aslanidi, noble, noble, boyett, zhang [2009]

drug model - ranolazine and quinidine



- calculate **ionic current**
- two-parameter **Hill-type model**
- calculate drug-specific block

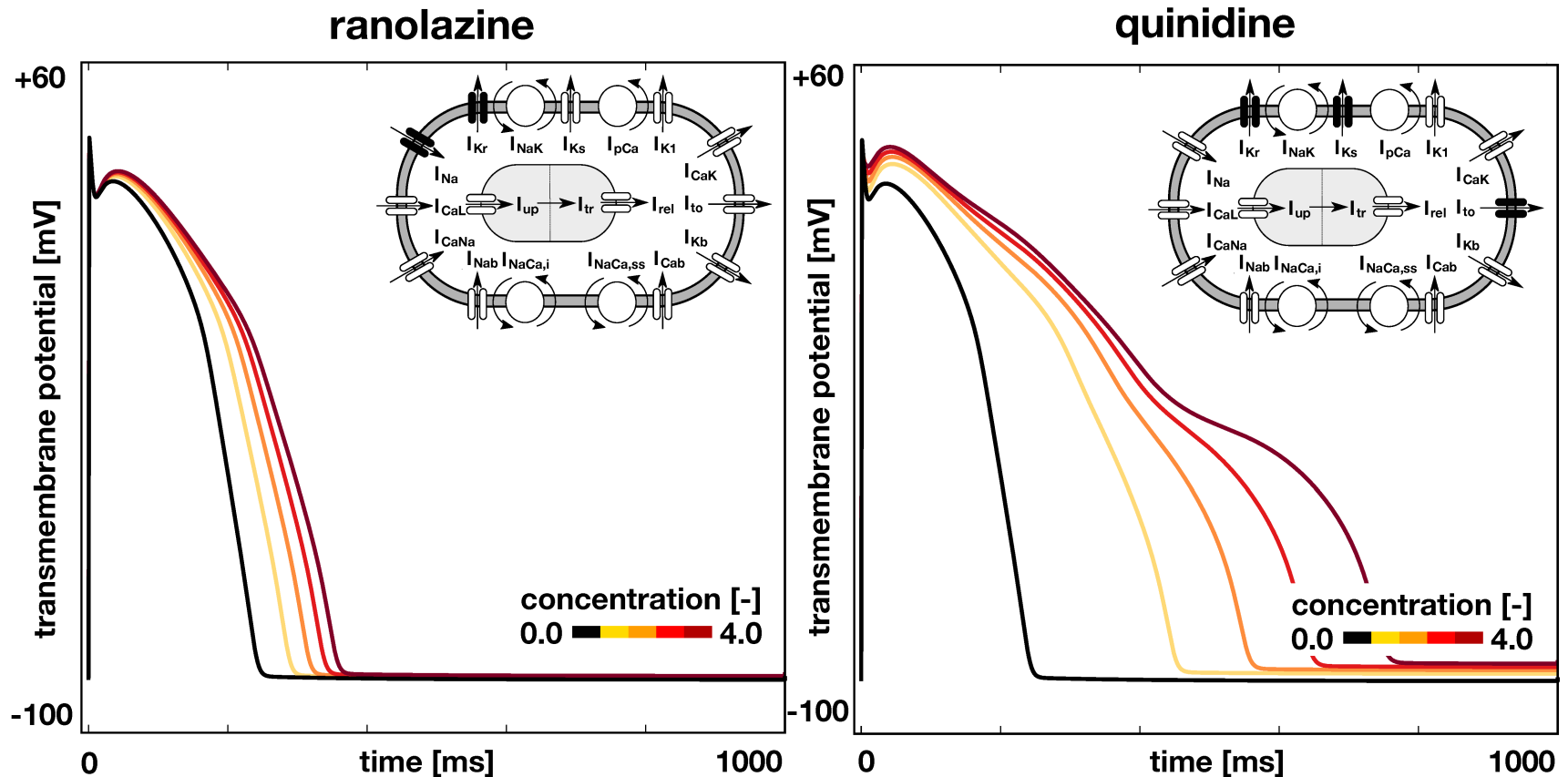
$$I_{ion} = I_{ion}(\phi, q(\phi); t)$$

$$\beta = C^h / [IC_{50}^h + C^h]$$

$$I_{drug} = [1 - \beta] I_{ion}$$

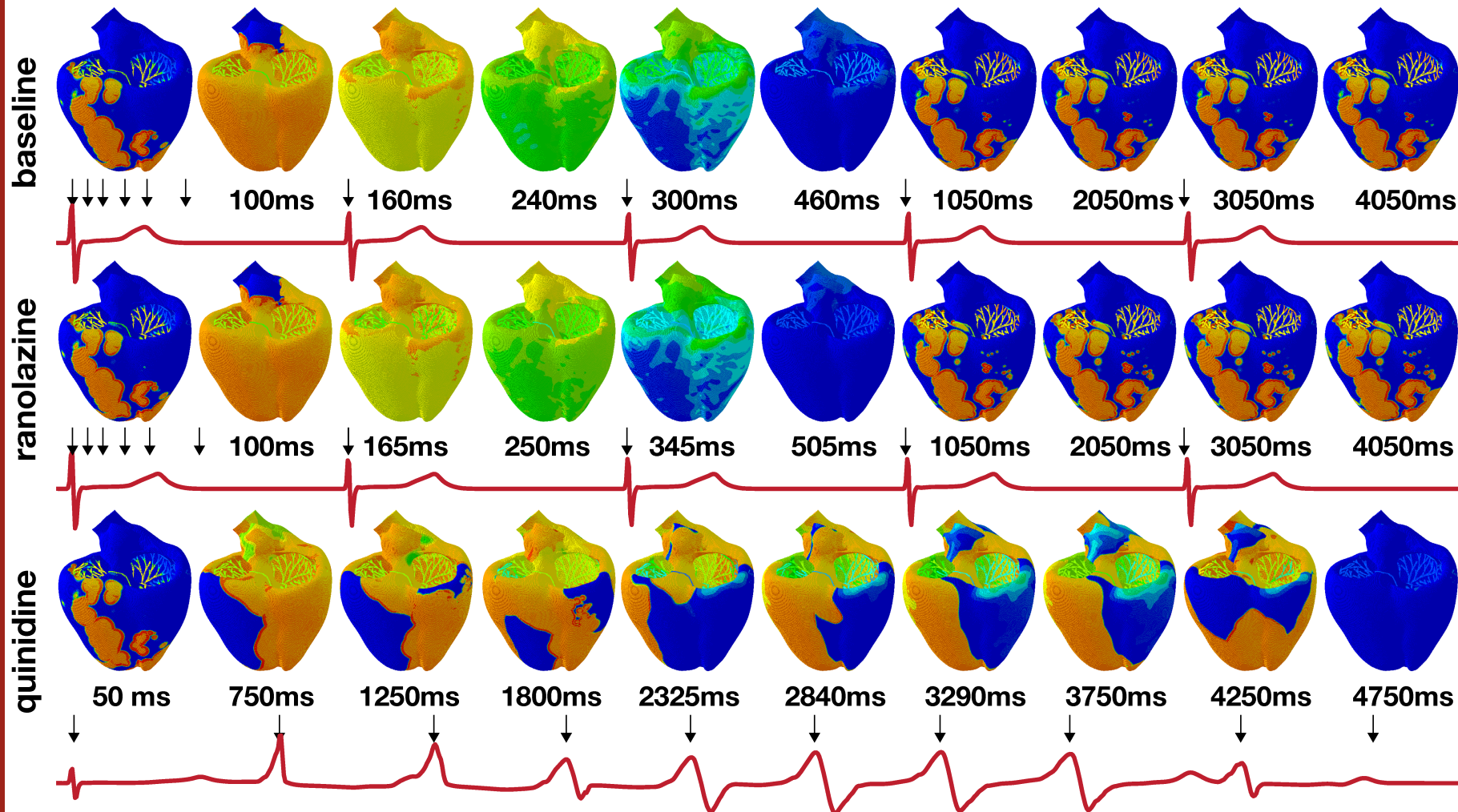
mirams, cui, sher, fink, cooper, heath, mc mahon, gavaghan, noble [2011], colatsky, fermini, gintant, pierson, sager, sekino, strauss, stockbridge[2016], crumb, vicente, johannesen, strauss[2016]

drug model - effects on the cell level

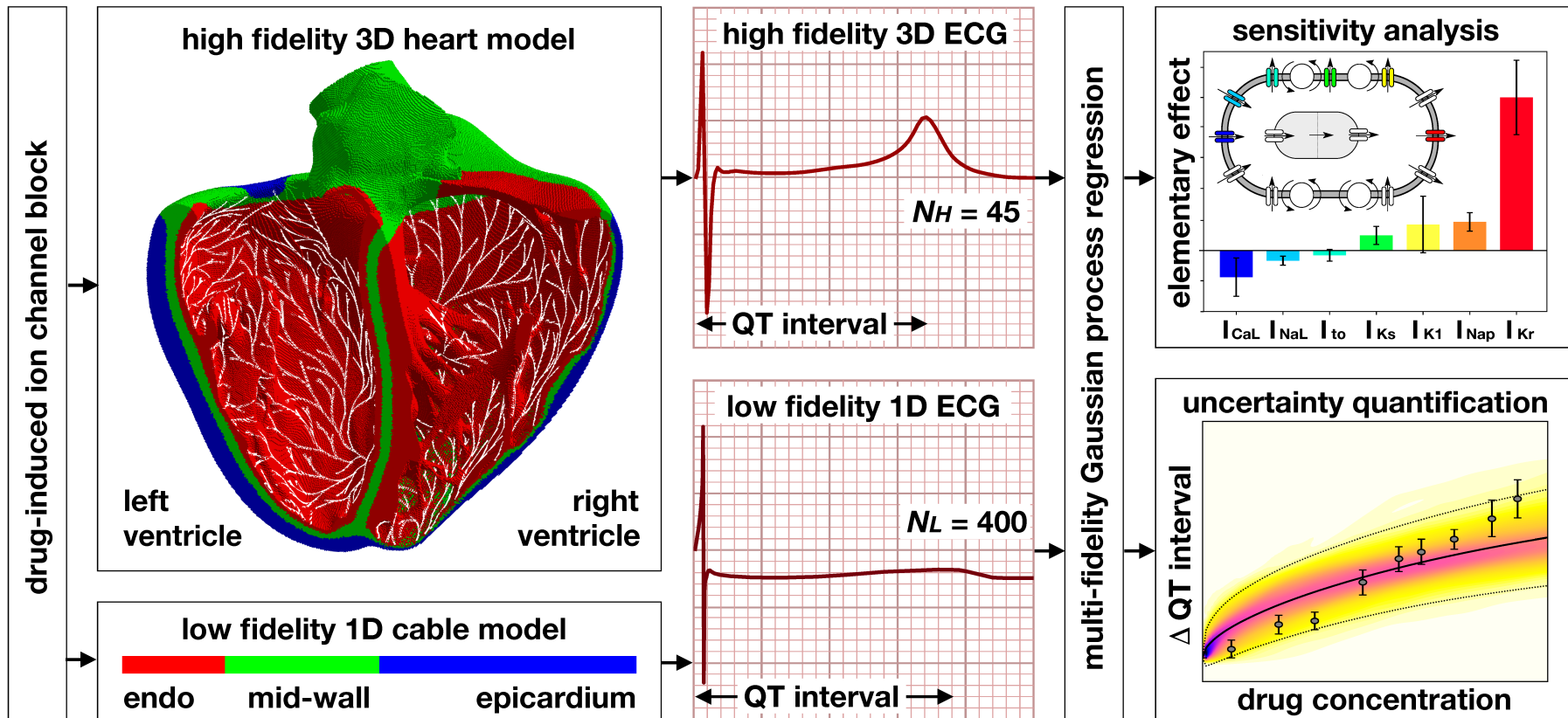


- **ranolazine** chronic angina drug
- blocks I_{Kr} and I_{Na}
- **mildly prolongs** APD and QT
- **low** torsades de pointes **risk**
- **quinidine** antiarrhythmic agent
- blocks I_{Kr} and I_{Ks} and I_{to}
- **severely prolongs** APD and QT
- **high** torsades de pointes **risk**

drug model - effects on the organ level

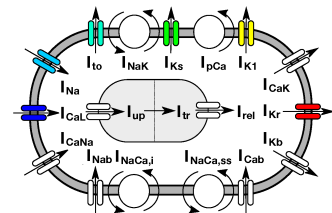
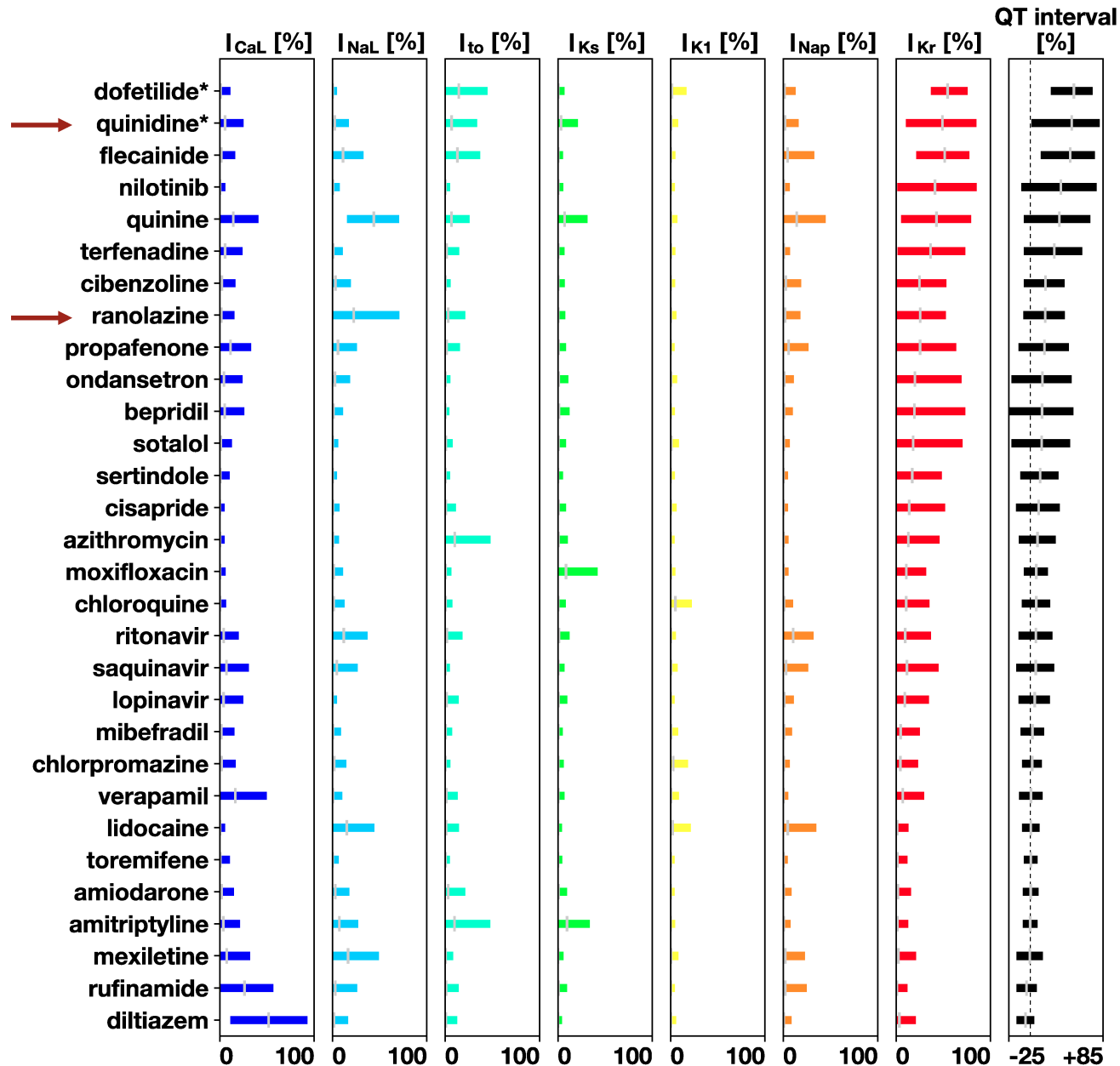


using machine learning in drug development

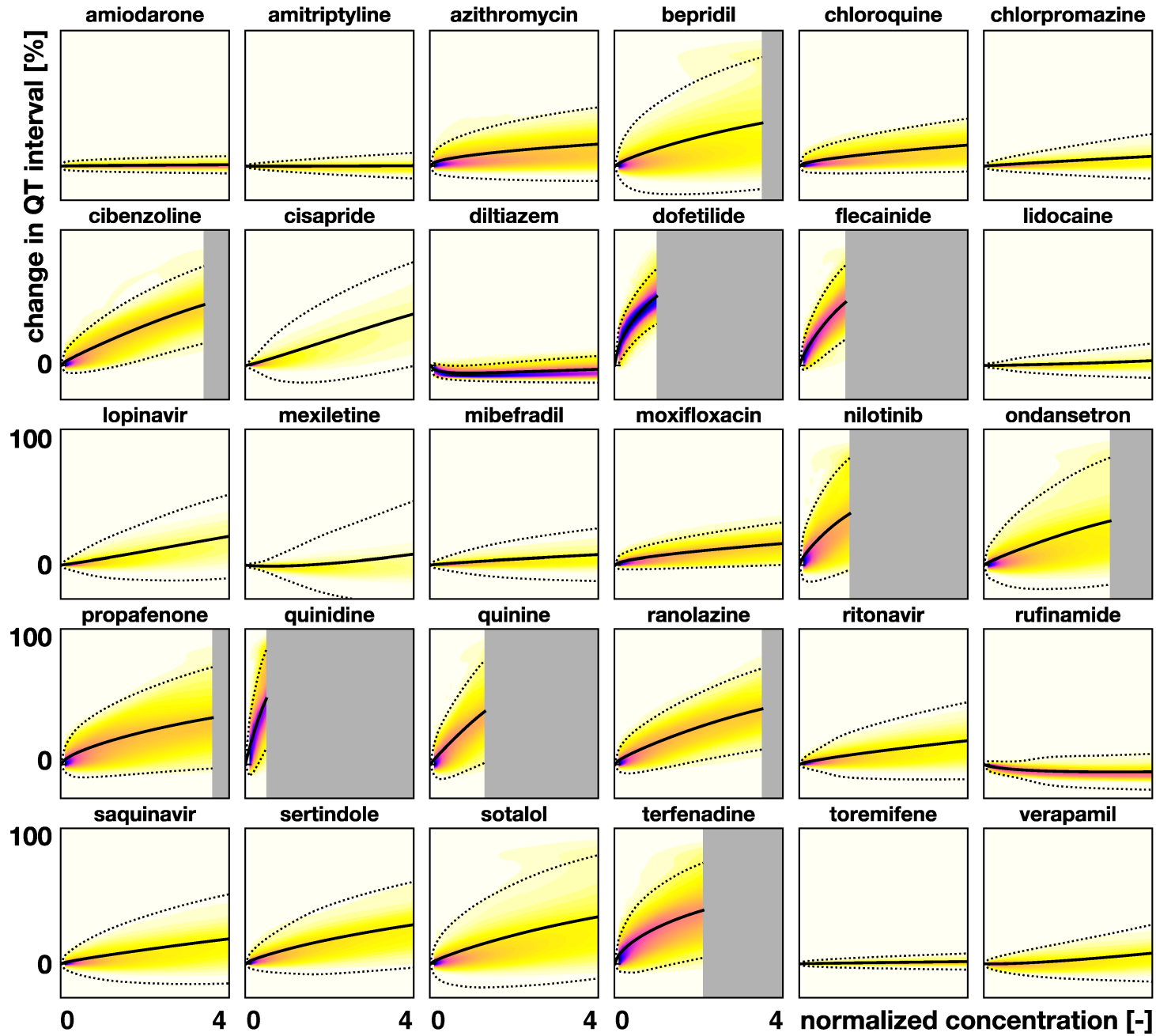


characterizing effect of 30 drugs on the QT interval using gaussian process regression, surrogate model for sensitivity analysis and uncertainty quantification

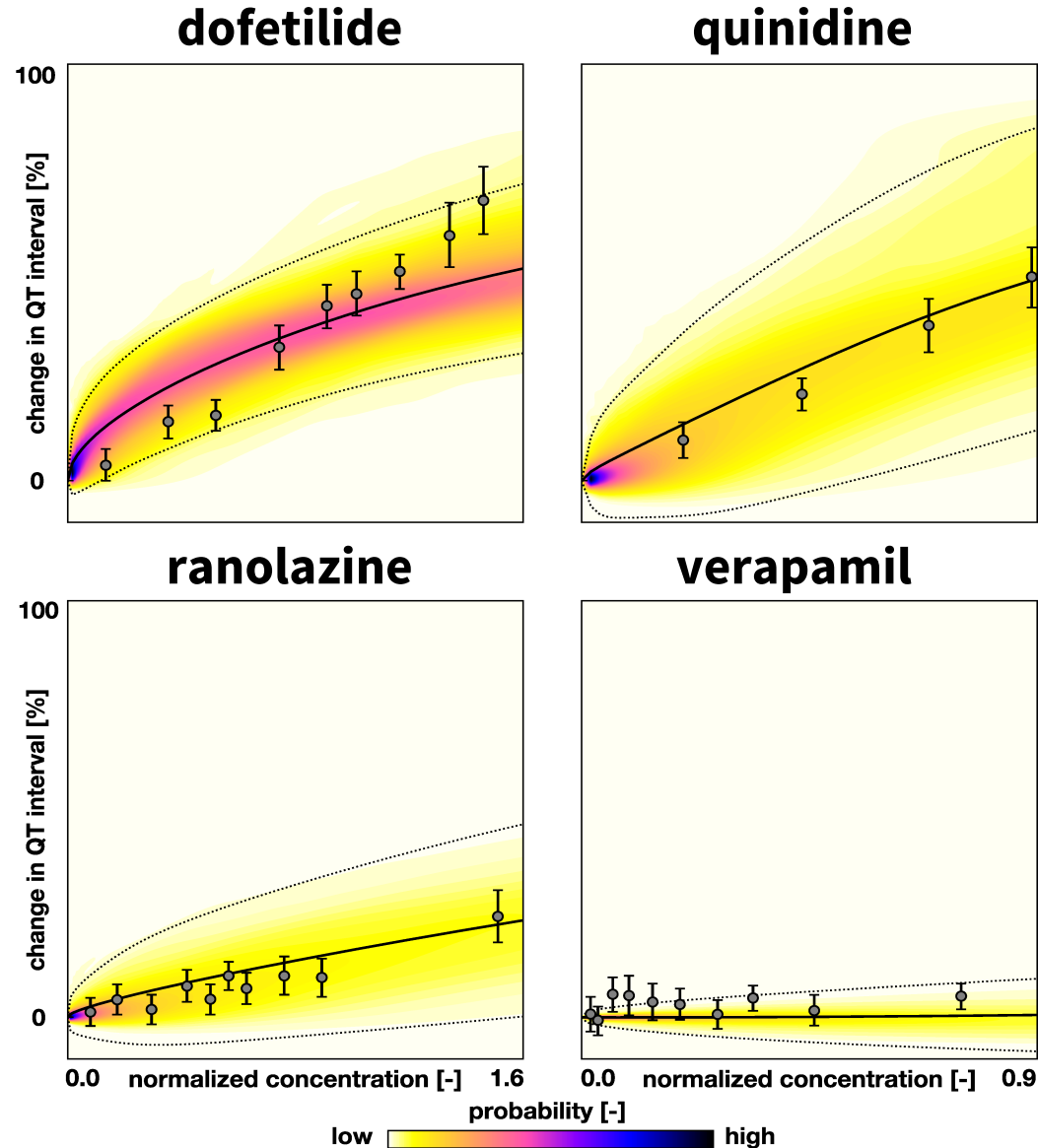
uncertainty quantification for 30 drugs



uncertainty quantification for 30 drugs

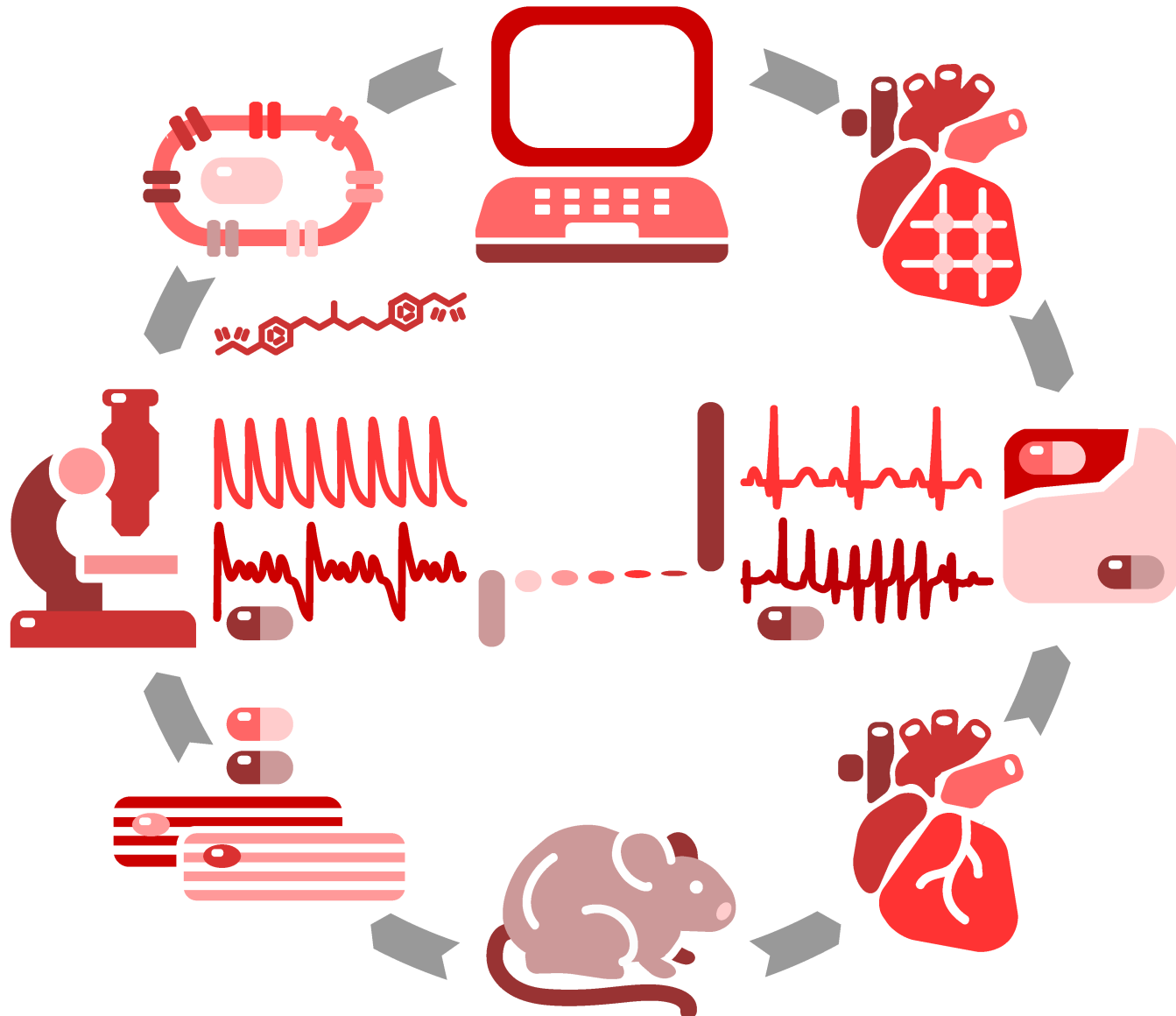


validation of uncertainty quantification

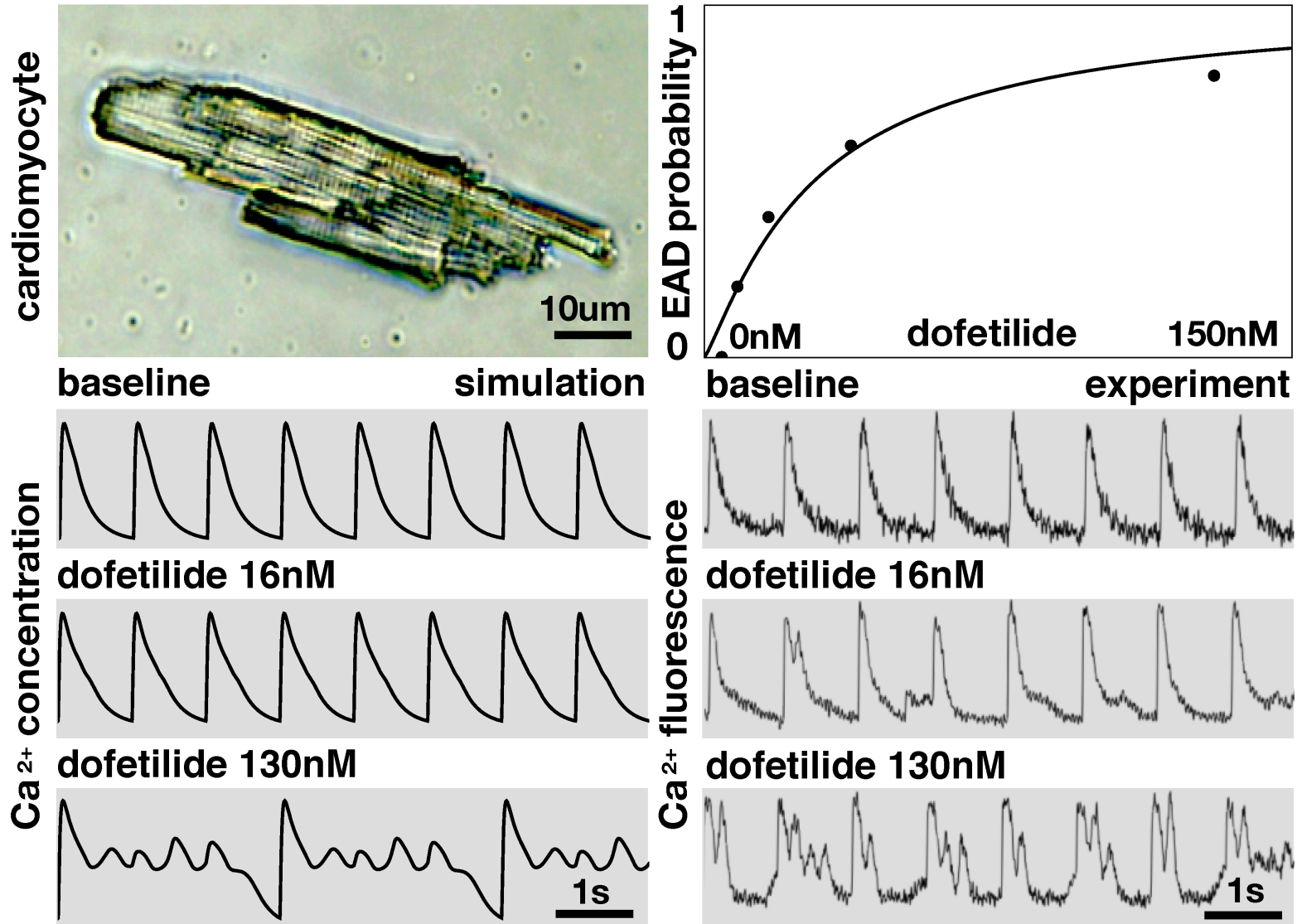


validation of QT interval change for drugs dofetilide, quinidine, ranolazine, and verapamil data from randomized clinical trial, error bars 95% confidence; johannesen et al. [2014]

validation on cell and organ levels

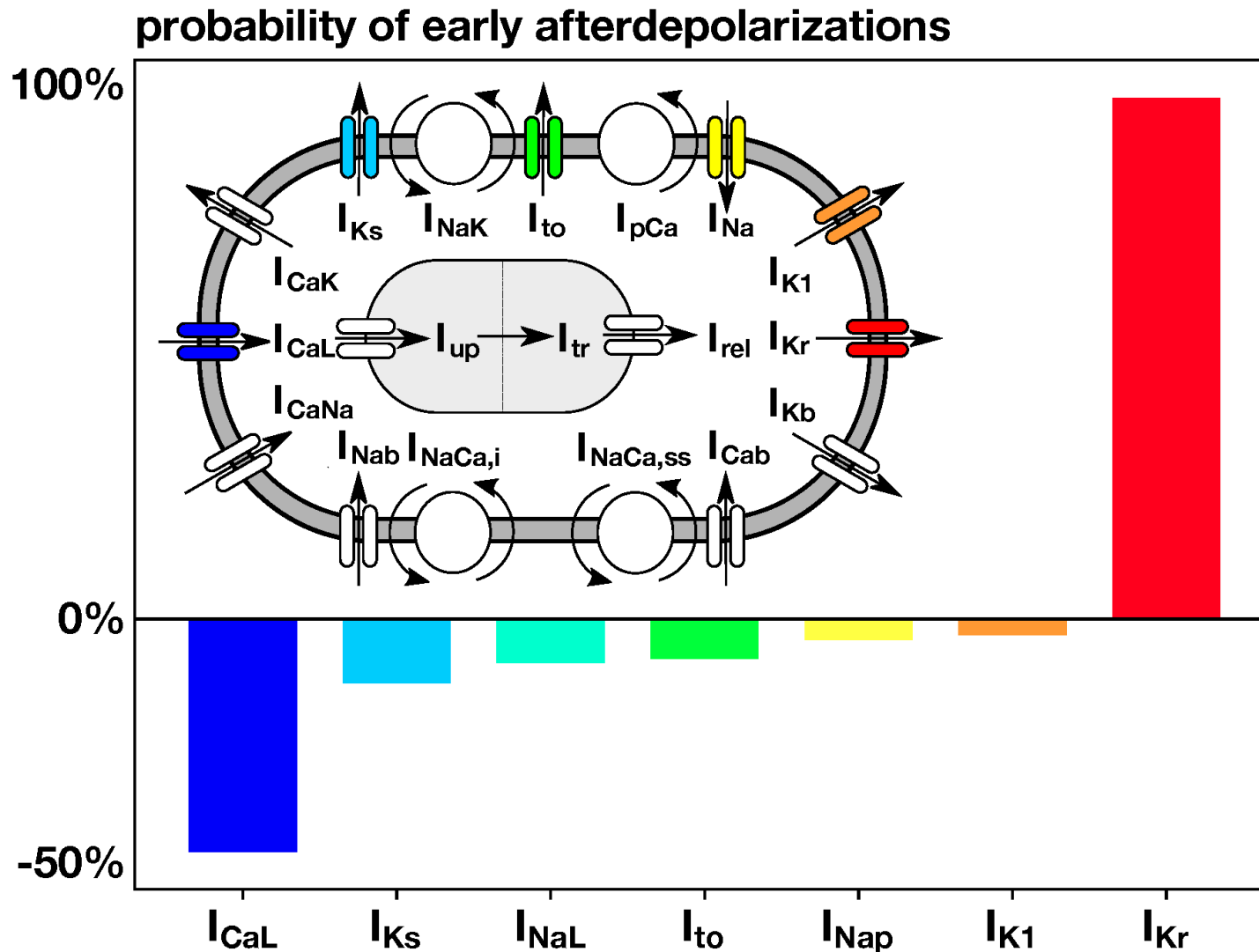


cell level validation - early afterdepolarizations



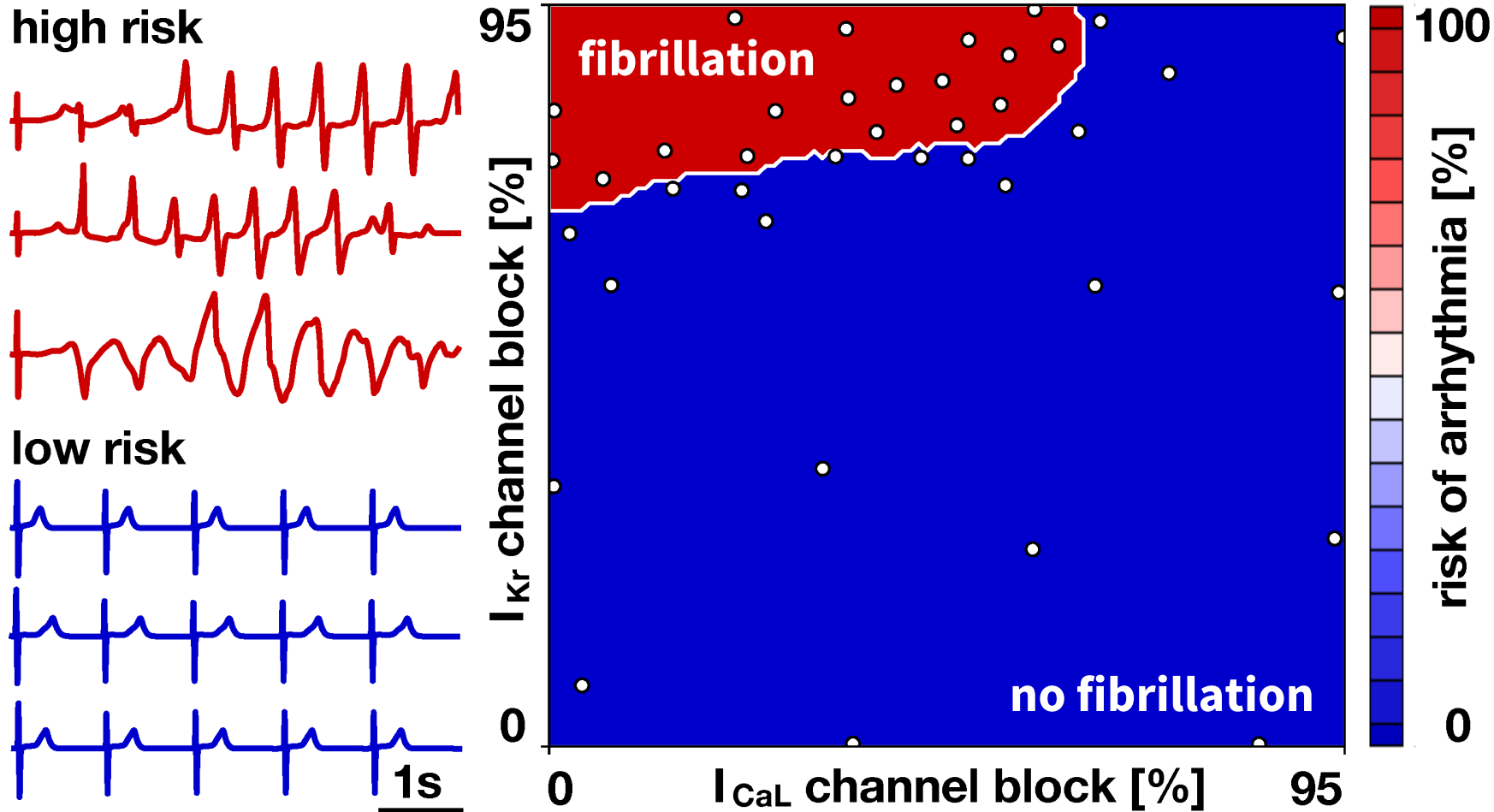
early afterdepolarizations. simulation and isolated rat cardiomyocytes at dofetilide concentrations of 4nM, 8nM, 16nM, 38nM, 130nM (n=6 cells each).

cell level sensitivity analysis - ion channels



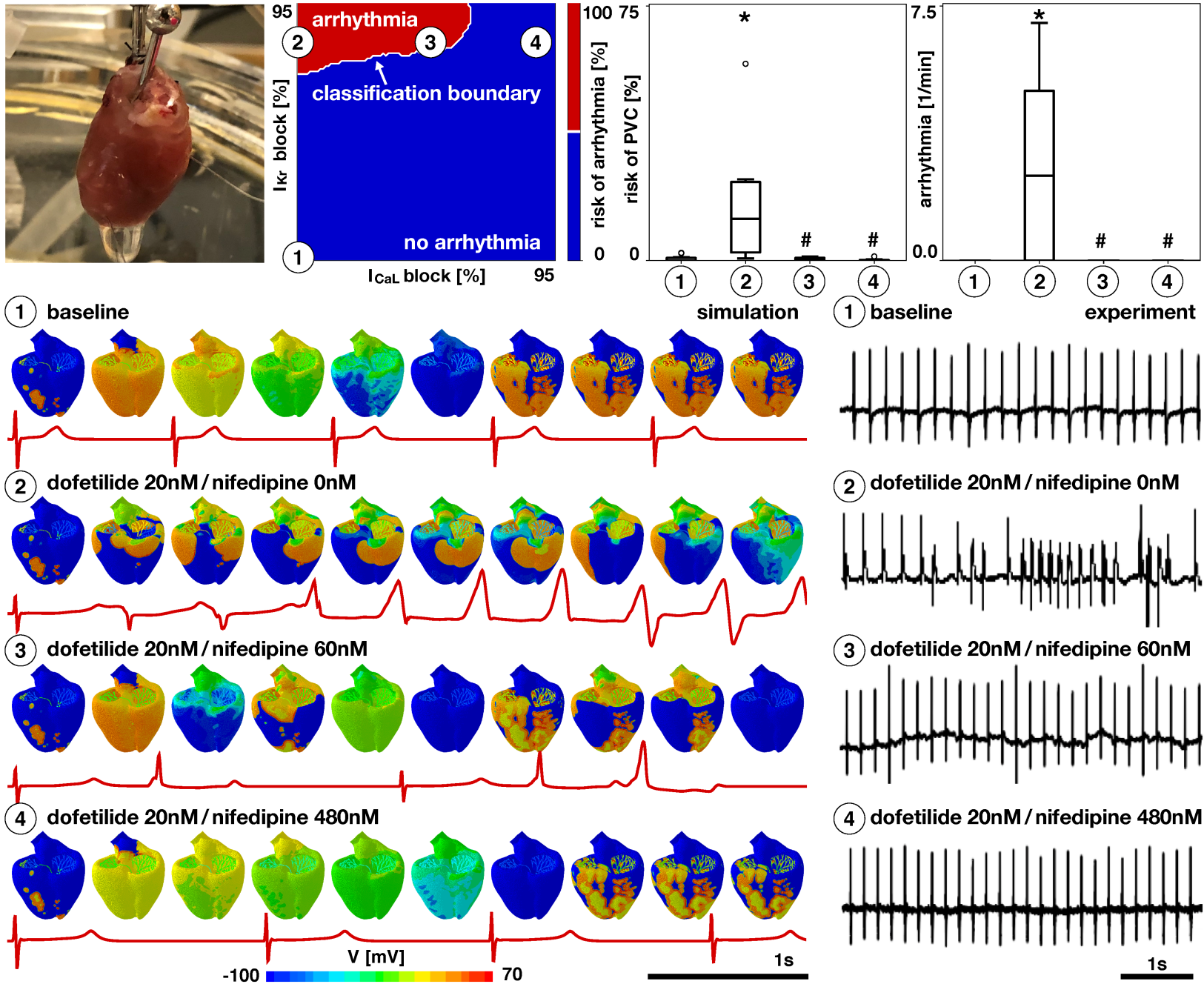
n = 500 single cell simulations > EAD > logistic regression > marginal effects.
 blocking I_{Kr} and I_{CaL} increases and reduces risk of early afterdepolarizations

new pro-arrhythmic risk classifier

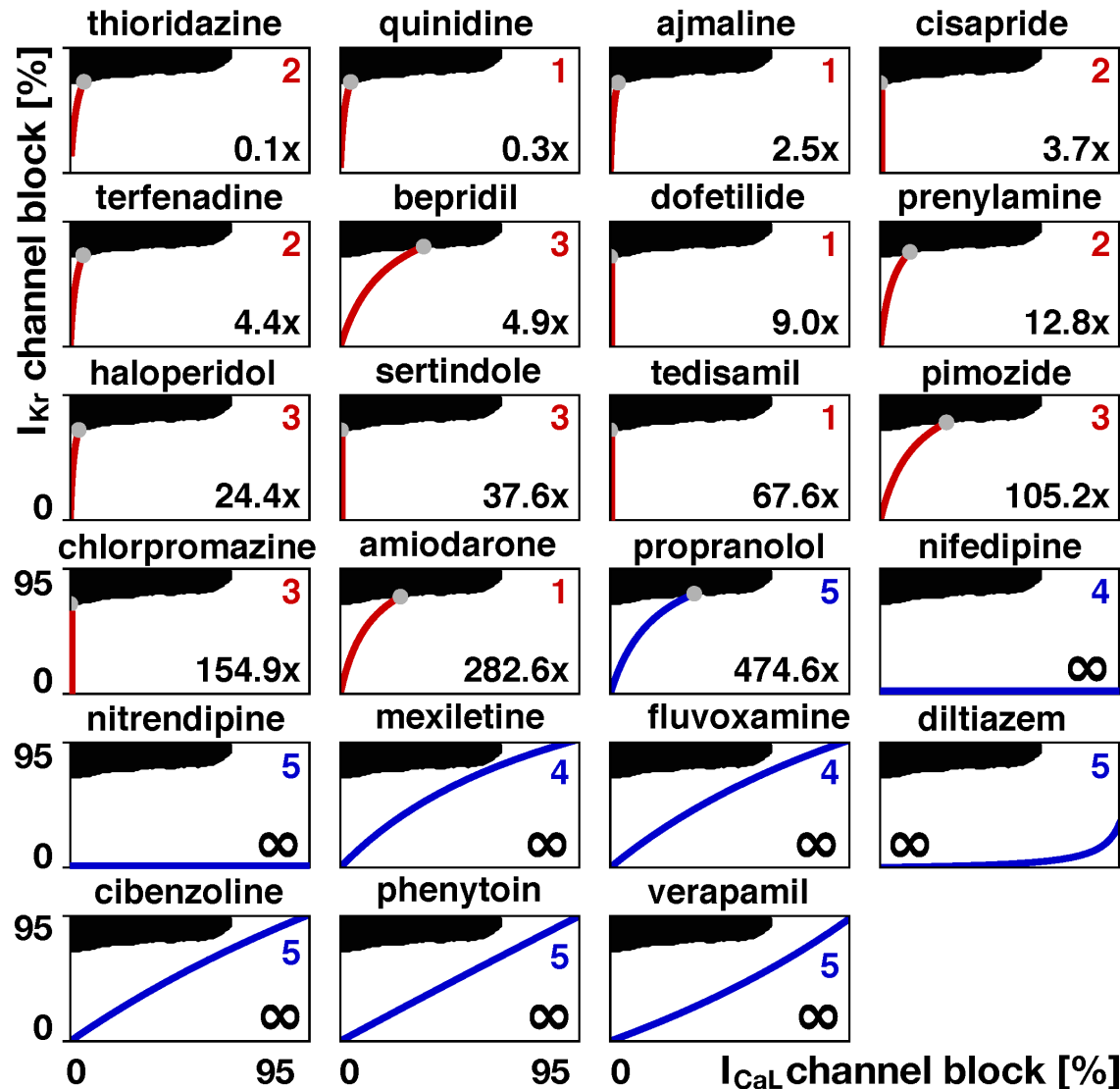


particle learning method to sample classification boundary within I_{Kr} / I_{CaL} space, gaussian process classifier, adaptively sample of point of maximum entropy, create $n = 10$ samples from latin hypercube design, sample $n = 30$ samples adaptively

organ level validation - arrhythmogenic risk

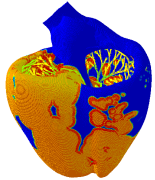


new paradigm for drug safety evaluation?

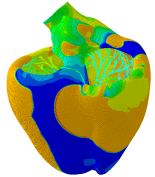


risk stratification of 23 drugs using our pro-arrhythmic risk classifier. numbers x indicate critical concentration; 1-5 risk category; red = torsadogenic, blue = safe.

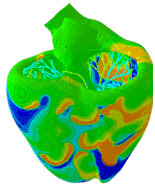
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multi fidelity **gaussian process regression** - sensitivities I_{CaL} / I_{Kr}



uncertainty quantification – effect of variations on **QT interval**



gaussian process **classification** – risk classifier in **polypharmacy**

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NSF CAREER award the virtual heart
BioX interdisciplinary seed grant 2018



HYPERION RESEARCH

INNOVATION AWARD 2017



advania



Stanford University