Supplement 1: Model Prediction Accuracy Metric

Description

The model prediction accuracy used as the result of all UQ simulations in this study was the same as that used in the original study by Tan *et al.* [1], which compared model predictions of the results of input-output, input-intermediate and inhibition experiments to published findings. Each experimental finding was classified statistically as either a significant change or no significant change in a specific measurement represented by a model output or intermediate node in response to a single input stretch stimulus or a single input stimulus plus an inhibitor of a single network component. Significantly changed measurements were further classified as increased or decreased. To compare these experimental outcomes with model predictions, the same combination of input stimulus and inhibition was applied to the model, and the change in measured intermediate or output node value was classified as increased, decreased or no-change based on a constant threshold value with a default of 5% as used in the original report. Below, we summarize this accuracy measure formally.

Definitions

N_+: Number of correctly predicted experiments
N_T: Total number of validation experiments (174)
P: Parameters sampled
ΔS: Node activity change after perturbation in model simulation
E: Experiment measurement (1: Increased, 0: No Change, -1: Decreased)
A: Accuracy

Implementation

$$\begin{aligned} N_{+,P} &= \sum_{i}^{N_T}(E_i == 1\&\Delta S_i >= 0.05)|(E_i == -1\&\Delta S_i <= -0.05)|(E_i == 0\&|\Delta S_i| < 0.05) \\ A_P &= \frac{N_{+,P}}{N_T} \end{aligned}$$

References

1. Philip M Tan, Kyle S Buchholz, Jeffrey H Omens, Andrew D McCulloch, and Jeffrey J Saucerman. Predictive model identifies key network regulators of cardiomyocyte mechano-signaling. *PLoS Computational Biology*, 13(11):e1005854, 2017.