**Figure 1**

**a.** Overview of model inputs to *inSilicoCellModel* and output as pictures of cellular distributions colored according to where cells are in the cycle.

**b.** Adaptation from Drasdo-Hohme of how the model works.

**c.** Hierarchy of the model and what can be replaced.

**Figure 2**

**a.** Multiple growth rates in boundary and no boundary (show every curve)

**b.** Show density over time in both bounded and unbounded

**Figure 3**

**a.** Points which are the real data for experiments, lines which are the model fits at different cell lengths. Cell number vs time at different dosages.

**Figure 4**

**a.** Cartoon overview of how we simulate gene expression.

**b.** Illustrating how the scaling varies between 0 to 1 for each pathway.

**c.** Pick one dosage (10 um/mL) from **Figure 3** and plot each of the effective pathways vs time for that selection. Y-axis is % of pathway activity and all pathways can be plotted together. Show difference in pathways for drug effect.

**d.** Comparison to real gene expression data along each pathway.

**Figure 5**

**a** heatmap for 2 cell types w/ & w/o boundary (pick one)

**b.** Varying mean (normal) of drug effect w/o boundary in a simulation where you would typically observe a balance in the cellular populations.

**c.** Varying SD (normal) of drug effect w/o boundary where you would typically observe a balance in the cellular populations.

**d.** gene expression