We used the two member MAPK scaffold model (cite PNAS paper) as a basis for our model with the following alterations. First, RAF (MAPKKK) dynamics were removed and a basal level of RAF activation was assumed. Second, we spacially partition the cell into "front" and "back" compartments, each with subcellular regions of cytoplasm, membrane and vesicles. Scaffold is capable of recycling through those three subcellular regions and is initially only cytoplasmic. MAPK components are cytoplasmic however they can be recruited to vesicle scaffolds, which can further catalyze the creation of dually phosphorylated MAPK.

Translocation of cytoplasmic scaffold to the membrane occurs at a rate proportional to dose.

Simulation was carried out through temporal integration of the sytem to steady state. until a specific toleracen. Because of convergence issues, instead of using numerical root finding

X-p phosphorylation, X

$$\mathrm{p3}(0) = (\mathrm{p3bSmem}(0)(t) + \mathrm{p3a}) \left(\frac{1 - \mathrm{p3d}}{e^{\mathrm{p3f}(\mathrm{Smem}(0)(t) - \mathrm{p3e})} + 1} + \mathrm{p3d} \right) \qquad (1)$$