**Introduction**

Discuss plan:

* First step is to reduce the four-species equilibrium model described in the previous section to a two species model, in which we only track overall membrane and cytoplasmic concentrations
* The advantage of doing so is that we can use this description to describe overall membrane binding and unbinding rates as a function of overall cytoplasmic and membrane concentrations
* I will then extend this description by considering the effects of phosphorylation reactions on membrane unbinding rates, considering the possibility that monomers and dimers might respond differently to phosphorylation
* Then, after building these descriptions, I will consider the implications that dimerisation reactions might have in the context of mutual antagonism models
* As discussed in the previous section, dimerisation can impact both the amplitude of a protein’s membrane affinity, and the concentration-dependence of this affinity. To separate the impact of both, I first consider the effects of membrane affinity in mutual antagonism models with linear membrane binding kinetics. I then explore the impacts dimerisation-induced nonlinearities.

**Describing membrane binding dynamics with transition state theory**

Maybe introduce transition state theory first to justify going to two-species model?

Two-species thermodynamic model

One assumption that we can make to simplify the model is that dimerisation in the membrane and cytoplasm is fast compared to membrane exchange kinetics. This means that dimerisation equilibrium is always observed, so for a given concentration in the membrane and cytoplasm we can define instantaneous monomer and dimer concentrations. The mathematics for doing so were discussed previously in section x, and I have repeated the equations below to describe monomer and dimer concentrations at the membrane as a function of overall membrane concentration:

Where wd is defined in RT units, and concentrations in co units. As a results, we can define the overall chemical potentials of membrane and cytoplasmic protein as a function of overall membrane and cytoplasmic concentrations:

These two equations can be solved analytically at equilibrium (mum = muc) to find equilibrium membrane and cytoplasm concentrations.

Explicit description of membrane binding kinetics

**Exploring the effects of membrane lifetime in polarity models**

Model description

Threshold membrane lifetime required for symmetry breaking

Firstly, I assess the impacts of off rates on the ability of the model to polarise. I consider two regimes. Firstly, I simulate models starting from a polarised state, asking whether they can maintain polarity over the course of the simulation. Secondly, I start simulations from a uniform state, and induce a small perturbation to ask whether they can spontaneously break symmetry. Models are classed as no polarity, inducible if they can maintain polarity but not break symmetry spontaneously, and spontaneous if they break polarity spontaneously.

Low off rates strengthen pattern asymmetries

Low off rates enhance pattern robustness

**Exploring the effects of dimerisation-driven nonlinearities in polarity models**

Model description

* Separating basal and concentration-dependent effects on off rate
* Modelling aPAR to pPAR antagonism

Dimerisation can generate nonlinear antagonism

Dimerisation can amplify induced asymmetries

Implications of dimerisation in self-organising models