**Assembly A**
- Filamin binding to filamin (strong)
- Filamin excludes both tropomyosin and α-actinin
- Filamin binding competes with myosin-II

**Assembly B**
- Actin filaments binding to tropomyosin (strong)
- Tropomyosin excludes filamin and allows α-actinin to bind only to plus end
- Tropomyosin encourages myosin-II binding

Result:
- Network of cross-linked actin filaments
- Bundle of contractile actin filaments
\[
\frac{\partial F}{\partial t}(\theta,t) = D \frac{\partial^2 F}{\partial \theta^2} + \gamma B - \beta F(\theta) \int_{-\pi}^{\pi} K(\theta - \theta') B(\theta') d\theta' \\
\frac{\partial B}{\partial t}(\theta,t) = -\gamma B + \beta B(\theta) \int_{-\pi}^{\pi} K(\theta - \theta') F(\theta') d\theta'
\]

\[
K(\theta) \geq 0, \quad K(\theta) = K(-\theta), \quad \int_{-\pi}^{\pi} K(\theta) d\theta = 1
\]

\[
\int_{-\pi}^{\pi} [F(\theta) + B(\theta)] d\theta = 2\pi A = \text{const}
\]

\[
F = \tilde{F}, \quad B = \tilde{B}, \quad \gamma \tilde{B} - \beta \tilde{F} \tilde{B} = 0,
\]

\[
\tilde{F} = \frac{\gamma}{\beta}, \quad \tilde{B} = A - \frac{\gamma}{\beta}
\]
\[ F = F + fe^{\lambda t}e^{ik\theta}, \quad B = B + be^{\lambda t}e^{ik\theta}, \quad K(\theta) = \sum_{0}^{\infty} \hat{K}(k)e^{ik\theta}, \quad \hat{K}(0) = 1 \]

\[ \lambda f = -Dk^2f + \gamma b - \beta F\hat{K}(k)b - \beta Bf \]

\[ \lambda b = -\gamma b + \beta B\hat{K}(k)f + \beta Fb \]

\[
\begin{vmatrix}
(\lambda + Dk^2 + \beta B) & (\beta F\hat{K}(k) - \gamma) \\
-\beta B\hat{K}(k) & (\lambda + \gamma - \beta F)
\end{vmatrix} = \begin{vmatrix}
(\lambda + Dk^2 + \beta B) & \gamma(\hat{K}(k) - 1) \\
-\beta B\hat{K}(k) & \lambda
\end{vmatrix} = 0
\]

\[ \lambda^2 + (Dk^2 + \beta B)\lambda + \beta B\hat{K}(k)(\hat{K}(k) - 1) = 0 \]

\[ \lambda(k) = 0.5 \left(-\left(Dk^2 + \beta B\right) \pm \sqrt{(Dk^2 + \beta B)^2 - 4\beta B\hat{K}(k)(\hat{K}(k) - 1)}\right) \]

\[ \lambda(k) > 0 \text{ at } \hat{K}(k)(\hat{K}(k) - 1) < 0 \]
single hump, $\phi = \pi/4$

double hump, $\phi = \pi/6$

double hump, $\phi = \pi/4$
Problems with the model:
Always unstable no matter how many crosslinkers. This can be fixed by term like \( \beta F(\theta) \int_{-\pi}^{\pi} K(\theta - \theta') F(\theta') d\theta' \) but this makes the model not robust. No spatial behavior. No actin turnover. No quantitative data.

Qualitative predictions are kind of clear without modeling. Diffusion in reality is extremely slow. However, pretty interesting mathematics.
1. Extracellular stimuli

2. Produce active GTPases & PIP2

3. Activate WASp/Scar

4. Activate Arp2/3 complex to initiate new filaments

5. Barbed ends elongate

6. Growing filaments push membrane forward

7. Capping protein terminates elongation

8. Aging

9. ADF/cofilin severs & depolymerizes ADP-filaments

10. Profilin catalyzes exchange of ADP for ATP

11. Pool of ATP-actin bound to profilin

12. LIM-kinase inhibits ADF/cofilin
\[ \psi \approx 67^\circ, \sigma \approx 12^\circ \]

\[ V_{\text{fil}} = \delta k_{\text{on}} MP_\delta = V_{\text{protr}} \cos \phi \]

\[ P_\delta = p_0 / \cos \phi, \quad p_0 = V_{\text{protr}} / \delta k_{\text{on}} M \]

\[ \phi < \theta = \arccos p_0 \]

Capping takes place with rate \( cP_\delta = cp_0 / \cos \phi \)

\[ \theta < \psi / 2 - \text{nothing!} \]

\[ \psi / 2 < \theta < \psi \]

More than 4 orientations cannot exist when \( \psi > 60^\circ \)

\[ \psi < \theta \]
\[
\frac{\partial n}{\partial t}(\phi, t) = -\frac{cp_0}{\cos \phi} n(\phi, t) + \\
\frac{a}{\int_{-\theta}^{\theta} n(\phi, t) \, d\phi} \int_{-\theta}^{\theta} \left( \exp \left[ -\frac{(\phi' + \psi - \phi)^2}{2\sigma^2} \right] + \exp \left[ -\frac{(\phi' - \psi - \phi)^2}{2\sigma^2} \right] \right) n(\phi', t) \, d\phi'
\]
What is great about this model? Both theory and experiment. Quantitative, not only qualitative statements. Qualitative statement is non-trivial. Assumptions are simple, clear and spelled out. Mathematics is nice.
- Where modeling is needed and where it’s not needed
- Look for quantitative data; order of magnitude estimates (example with k_on)
- Available and free parameters, experiments, much useless and wrong and irrelevant information
- Modeling as a jigsaw puzzle
- What are the appropriate math methods; what other knowledge is needed
- Qualitative models (cartoons) at the end of bio papers
- How to read bio paper (which journals, intro, discussion, results, materials and methods); knowing what is happening
- Two tiers of math biology plus numerics
- Writing math bio papers: structure, where to send, how to respond to reviewers
- How to give talks to mixed audiences (where to present, structure, do not apologize)
- How, when and where to write grants; first do something
- Problem with bio jargon; combination of very precise use of words with vagueness
- Stay universal (favorite technique) or focus on a sub-field

- Biomath is a very social science; how to find and communicate to collaborators
- Different culture and mentality in biology