

Thin filament regulation – Run example

The code calculates (1) the dynamics of myosin binding to actin filaments in a solution, and (2) the “titration”. Equilibrium is reached by stochastic transitions of tropomyosin between the states blocked, closed and open, and myosin transition between unbind, bind, and rigid states.

- (1) Select an output file;
- (2) Setup the parameters on the text-boxes. The first box indicate the number of block of 7 monomers per actin fiber and the second box indicate the number of fibers. Thus the total number of possible binding sites are $7 \times \text{BOX1} \times \text{BOX2}$. Next choose the time step and the total time of the simulation. Note that a too small time step increase the CPU time, and a too large add errors, thus at the bottom of the page there is a button which suggest a time step. We strong recommend do not select a time step greater than the suggest time. Smaller time steps are always welcome. In the next 8 boxes is possible to select all rates constants. The molar concentration of actin can be selected at box 13;
- (3) Select the type of simulation between (a) time course and (b) titration. For time course you have to add the myosin concentration while for titration you have to add the initial and the final concentration of myosin and the number of steps between them. The number of steps will determine the accuracy of the titration curve;
- (4) The last text box is the random seed. The random seed can be changed to have different stochastic process. The same random seed with the same parameters will reproduce exactly the same result. However, the overall result should be very similar, almost identical, for different random seeds in a large system;
- (5) Then press run to run;
- (6) Press graphs to see results (several data files, with header, are also stored in the same directory);

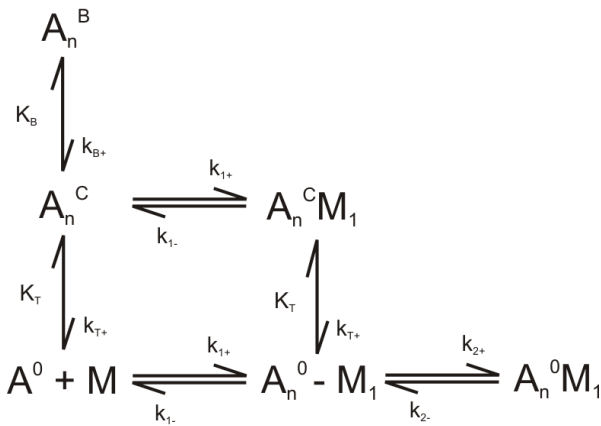
Time course frame:

The screenshot shows the 'Thin Filament Regulation' software interface in 'Time Course' mode. The window title is 'Thin Filament Regulation'. The interface includes several input fields and buttons. The 'Output File' field is set to 'C:\Documents and Settings\Aleksandra\My Documents\Output'. The 'The Number of Actin7.TmTn Units [#]' is 100, and 'The Number of Tm Chains per Fiber [#]' is 2. The 'Time Step [s]' is 0.0001, and 'Total Time [s]' is 20. The 'Equilibrium Constant Between the Blocked and Closed States (Kb)' is 0.3, 'Forward Rate Constant Between the Blocked and Closed States (Kb+)' is 300, 'Equilibrium Constant Between the Closed and Open States (Kl)' is 0.2, 'Forward Rate Constant Between the Closed and Open States (Kl+)' is 200, 'Forward Rate Constant of Myosin Weak Binding (k1+ [1/(M*s)])' is 2e6, 'Backward Rate Constant of Myosin Weak Binding (k1- [1/s])' is 10, 'Forward Isomerization Rate Constant (k2+ [1/s])' is 1000, and 'Backward Isomerization Rate Constant (k2- [1/s])' is 5. The 'Molar Concentration of Actin [uM]' is 0.05. The 'Type of Simulation' is set to 'Time Course'. At the bottom, there are fields for '(For Titration) Molar Concentration of Myosin Initial / Final / # of Steps [uM / uM / #]' with values 0, 0.25, and 500, and a 'Random Seed' field with value 0.182700. Buttons for 'Suggest Times', 'Graphs', and 'Run' are visible. The status bar at the bottom left shows 'Ready'.

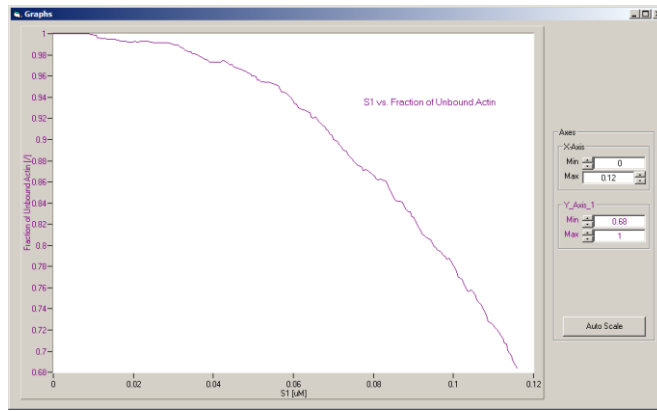
Titration frame:

The screenshot shows the 'Thin Filament Regulation' software interface in 'Titration' mode. The window title is 'Thin Filament Regulation'. The interface includes several input fields and buttons. The 'Output File' field is set to 'C:\Documents and Settings\Aleksandra\My Documents\Output'. The 'The Number of Actin7.TmTn Units [#]' is 100, and 'The Number of Tm Chains per Fiber [#]' is 2. The 'Time Step [s]' is 0.0001, and 'Total Time [s]' is 20. The 'Equilibrium Constant Between the Blocked and Closed States (Kb)' is 0.3, 'Forward Rate Constant Between the Blocked and Closed States (Kb+)' is 300, 'Equilibrium Constant Between the Closed and Open States (Kl)' is 0.2, 'Forward Rate Constant Between the Closed and Open States (Kl+)' is 200, 'Forward Rate Constant of Myosin Weak Binding (k1+ [1/(M*s)])' is 2e6, 'Backward Rate Constant of Myosin Weak Binding (k1- [1/s])' is 10, 'Forward Isomerization Rate Constant (k2+ [1/s])' is 1000, and 'Backward Isomerization Rate Constant (k2- [1/s])' is 5. The 'Molar Concentration of Actin [uM]' is 0.05. The 'Type of Simulation' is set to 'Titration'. At the bottom, there are fields for 'Molar Concentration of Myosin [uM]' with value 0.25, and a 'Random Seed' field with value 0.182700. Buttons for 'Suggest Times', 'Graphs', and 'Run' are visible. The status bar at the bottom left shows 'Ready'.

Used constant rates scheme:



Typical titration graphical result:



Typical histogram of the occupancy of myosin in the actin filament. The y-axes of each column indicate the fraction of tropomyosin is occupied with 1, 2, ... or 7 myosins. Typical time course graphical output is on the right side (picture below)

