TABLE 1. Description of the input concentrations and of the program output.
See "**Model Reactions**" for parameter definitions and [1] for more details.

Concentration	**Description**
$[ATP]$	Concentration of ATP
$[ADP]$	Concentration of ADP
$[Pi]$	Concentration of inorganic phosphate
$[P]$	Concentration of free profilin (not bound to G-actin)

Variable	**Description**
A_c	Actin critical concentration. At steady state, A_c is equal to the total concentration of free monomeric actin (sum of all nucleotide forms): $A_c = [T] + [D + [I] + [A]$ (see "**Model Reactions**")
k_{ON}	net rate of polymerization per filament or steady state flux of the subunit exchange: $k_{ON} = k_{OFF}$
g_f	Fraction of filament ends free (not bound to profilin, sum of all nucleotide forms)
k_1	$= k_{Pi+} \cdot [Pi]$
k_2	$= k_{Pi-}$

Fractions of different nucleotide forms in the free monomeric actin pool

r_A	$= [A] / [A_c]$	fraction of the form A in the free monomeric actin pool
r_T	$= [T] / [A_c]$	fraction of the form T in the free monomeric actin pool
r_I	$= [I] / [A_c]$	fraction of the form I in the free monomeric actin pool
r_D	$= [D] / [A_c]$	fraction of the form D in the free monomeric actin pool

Acceleration factors

S_H	$= r_{He} \cdot (1 + r_H \cdot [P] / K_{dbT})$
S_{Pi}	$= r_{Pie} \cdot (1 + r_{Pi} \cdot [P] / K_{dbI})$
S_A	$= (1 + r_{A+} \cdot [P] / K_{dA}) = (1 + r_{A-} \cdot [P] / K_{dbA})$
S_T	$= (1 + r_{T+} \cdot [P] / K_{dT}) = (1 + r_{T-} \cdot [P] / K_{dbT})$
S_I	$= (1 + r_{I+} \cdot [P] / K_{dI}) = (1 + r_{I-} \cdot [P] / K_{dbI})$
S_D	$= (1 + r_{D+} \cdot [P] / K_{dD}) = (1 + r_{D-} \cdot [P] / K_{dbD})$

Factors defining binding of profilin the barbed ends of the corresponding type

q_A	$= (1 + [P] / K_{dbA})$
q_T	$= (1 + [P] / K_{dbT})$
q_I	$= (1 + [P] / K_{dbI})$
q_D	$= (1 + [P] / K_{dbD})$

Critical concentrations for pure forms

A_{cA} critical concentrations for pure *A* form: $A_{cA} = k_{A-} / k_{A+}$
A_{cT} critical concentrations for pure *T* form: $A_{cT} = k_{T-} / k_{T+}$
A_{cI} critical concentrations for pure *I* form: $A_{cI} = k_{I-} / k_{I+}$
A_{cD} critical concentrations for pure *D* form: $A_{cD} = k_{D-} / k_{D+}$

Fractions of different nucleotide forms in the free barbed ends pool

g_T fraction of the uncapped ATP-bound ends in the uncapped (free) ends pool
g_D fraction of the uncapped ADP-bound ends in the uncapped pool
g_I fraction of the uncapped ADP-Pi-bound ends in the uncapped pool
g_A fraction of the uncapped nucleotide-free ends in the uncapped pool

Model variables

(see [1] for details and the other output variables including indexed factors *f*, *C*, and *U*)

$\alpha = S_H + g_f^{-1} \cdot \lambda / (1 - \lambda)$;
$\beta = S_{Pi} + g_f^{-1} \cdot \delta / (1 - \delta)$;

$\lambda = 1 - (k_H / (2 \cdot k_{ON})) \cdot ((1 + 4 \cdot k_{ON} / k_H)^{1/2} - 1)$
$\delta = 1 - ((k_1 + k_2) / (2 \cdot k_{ON})) \cdot ((1 + 4 \cdot k_{ON} / (k_1 + k_2))^{1/2} - 1)$

$\gamma = k_2 \cdot (S_{Pi} - S_H) / (k_H - k_1)$
$\psi = k_1 / (k_1 + k_2)$
$\varphi = (k_H - k_1) / (k_H - (k_1 + k_2) = (1 + k_2 / (k_H - (k_1 + k_2))$

N_{iter} number of iterations used to achieve desired accuracy

Please check for updates: we plan to update our output for a more user-friendly list - more relevant to the physical properties of actin filament and polymerization mechanisms

1. Yarmola, E.G., Dranishnikov, D.A. and Bubb, M.R. 2008. Effect of Profilin on Actin Critical Concentration: A Theoretical Analysis. *Biophys. J.* 95: 5544–5573.