Electronic Supplementary Material (ESI) for Molecular BioSystems.

Supplementary material

Supplementary figures

Gillespie algorithm

Transform the parameter θ to the stochastic parameter $\tilde{\theta}$ (e.g. [39]). Let the system be in state ν at time t.

(1) First, calculate the sum over all v_j:

$$\chi_0(\eta, \tilde{\theta}) = \sum_{j=1}^{r} v_j(\nu, \tilde{\theta}).$$

(2) The stochastic time step is

$$\tau = -\frac{1}{\chi_0(\nu(t), \tilde{\theta})} \log\ u_1,$$

with a uniformly distributed random number $u_1 \sim U((0,1])$.

(3) For the determination of the move, choose $\mu \in \mathbb{N}$ such that

$$\sum_{j=1}^{\mu-1} \frac{v_j(\nu, \tilde{\theta})}{\chi_0(\eta, \tilde{\theta})} \ < u_2 \ \leq \ \sum_{j=1}^{\mu} \frac{v_j(\eta, \tilde{\theta})}{\chi_0(\eta, \tilde{\theta})}$$

is fulfilled with another uniformly distributed random number $u_2 \sim U((0,1])$.

(4) Realize the reaction r_μ by updating the numbers of the involved species in the move and increase the time by τ. Go to (1) and repeat until the desired end time.

Figure A1: Gillespie algorithm

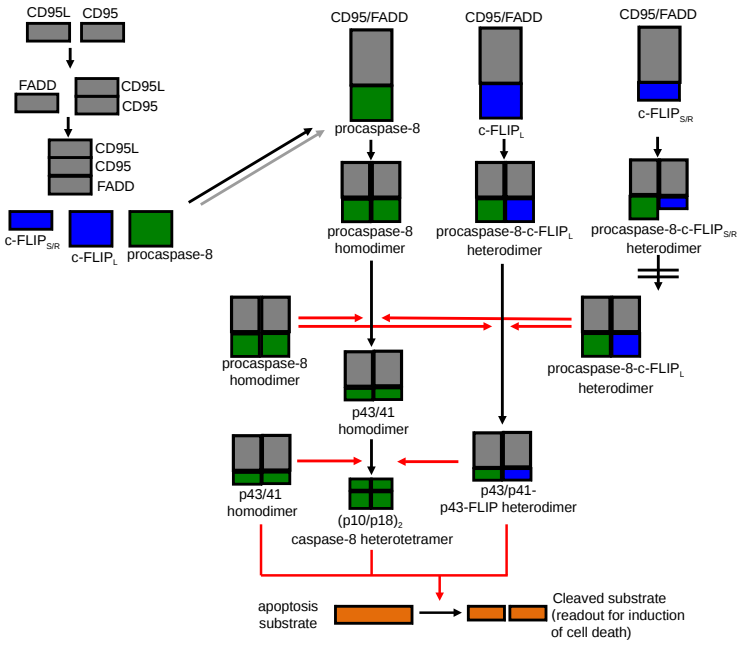

Figure A2: The topology of the mathematical model. CD95, CD95L, and FADD are depicted in gray, the long and short isoforms of c-FLIP in blue, and procaspase-8 as well as its cleavage products in green. At the DISC procaspase-8 homodimers, procaspase-8/c-FLIP$_L$ dimers and procaspase-8/c-FLIP$_{S/R}$ dimers are formed. Red arrows indicate catalytic processing. (Adapted from [7]).

$$
\begin{aligned}
\frac{d([x1])}{dt} &= -(p1 \cdot [x1] \cdot [x2]) \\
\frac{d([x2])}{dt} &= -(p1 \cdot [x1] \cdot [x2]) \\
\frac{d([x3])}{dt} &= -(p2 \cdot [x3] \cdot [x7]) \\
\frac{d([x4])}{dt} &= -(p3 \cdot [x4] \cdot [x8]) \\
\frac{d([x5])}{dt} &= -(p4 \cdot [x5] \cdot [x8]) \\
\frac{d([x6])}{dt} &= -(p5 \cdot [x6] \cdot [x8]) \\
\frac{d([x7])}{dt} &= +(p1 \cdot [x1] \cdot [x2]) - (p2 \cdot [x3] \cdot [x7]) \\
\frac{d([x8])}{dt} &= +(p2 \cdot [x3] \cdot [x7]) - (p3 \cdot [x4] \cdot [x8]) - (p4 \cdot [x5] \cdot [x8]) \\
&\quad -(p5 \cdot [x6] \cdot [x8]) + 4 \cdot (0.5 \cdot p13 \cdot [x16] \cdot [x16]) + 2 \cdot (p14 \cdot [x15] \cdot [x16]) \\
\frac{d([x9])}{dt} &= -2 \cdot (p6 \cdot [x9] \cdot [x9]) + (p3 \cdot [x4] \cdot [x8]) \\
&\quad -(p7 \cdot [x9] \cdot [x10]) - (p8 \cdot [x9] \cdot [x11]) \\
\frac{d([x10])}{dt} &= +(p4 \cdot [x5] \cdot [x8]) - (p7 \cdot [x9] \cdot [x10]) \\
\frac{d([x11])}{dt} &= +(p5 \cdot [x6] \cdot [x8]) - (p8 \cdot [x9] \cdot [x11]) \\
\frac{d([x12])}{dt} &= -(p12 \cdot [x15] \cdot [x12]) - (p11 \cdot [x16] \cdot [x12]) - (p9 \cdot [x13] \cdot [x12]) \\
&\quad +(p7 \cdot [x9] \cdot [x10]) - 2 \cdot (0.5 \cdot p10 \cdot [x12] \cdot [x12]) \\
\frac{d([x13])}{dt} &= -(p12 \cdot [x15] \cdot [x13]) - (p11 \cdot [x16] \cdot [x13]) - (p10 \cdot [x12] \cdot [x13]) \\
&\quad -2 \cdot (0.5 \cdot p9 \cdot [x13] \cdot [x13]) + (p6 \cdot [x9] \cdot [x9]) \\
\frac{d([x14])}{dt} &= +(p8 \cdot [x9] \cdot [x11]) \\
\frac{d([x15])}{dt} &= +(p12 \cdot [x15] \cdot [x12]) + (p11 \cdot [x16] \cdot [x12]) \\
&\quad +(p9 \cdot [x13] \cdot [x12]) + 2 \cdot (0.5 \cdot p10 \cdot [x12] \cdot [x12]) \\
\frac{d([x16])}{dt} &= +(p12 \cdot [x15] \cdot [x13]) + (p11 \cdot [x16] \cdot [x13]) + (p10 \cdot [x12] \cdot [x13]) \\
&\quad +2 \cdot (0.5 \cdot p9 \cdot [x13] \cdot [x13]) - 2 \cdot (0.5 \cdot p13 \cdot [x16] \cdot [x16]) - (p14 \cdot [x15] \cdot [x16]) \\
\frac{d([x17])}{dt} &= +2 \cdot (0.5 \cdot p13 \cdot [x16] \cdot [x16]) + (p14 \cdot [x15] \cdot [x16])
\end{aligned}
$$

Figure A3: Model equations

$$
\begin{aligned}
\text{mf1} &= 2 \cdot [\text{x17}] \\
\text{mf2} &= 2 \cdot [\text{x16}] + [\text{x15}] \\
\text{mf3} &= [\text{x4}] + [\text{x9}] + [\text{x12}] + 2 \cdot [\text{x13}] + [\text{x14}]
\end{aligned}
$$

Figure A4: Measurement functions

Supplementary tables

name	abbreviation	component	initial molecule number
CD95Ligand	CD95L	x_1	1 400 050
CD95	CD95R	x_2	209348
FADD		x_3	146807
procaspase-8	C8	x_4	265269
c-FLIP$_L$	FL	x_5	329.641
c-FLIP$_S$	FS	x_6	411.938
CD95L bound to CD95	CD95RL	x_7	0
FADD bound to CD95/CD95L	CD95FADD	x_8	0
procaspase-8 bound to the DISC via FADD	FADDC8	x_9	0
c-FLIPL bound to the DISC via FADD	FADDFL	x_{10}	0
c-FLIPS bound to the DISC via FADD	FADDFS	x_{11}	0
procaspase-8 homodimer	C8heterodimer	x_{12}	0
C8homodimer		x_{13}	0
procaspase-8/ c-FLIP$_S$ heterodimer	C8FSdimer	x_{14}	0
heterodimer of p43/p41 procaspase-8 and p43-FLIP	p43heterodimer	x_{15}	0
homodimer of p43/p41 procaspase-8	p43homodimer	x_{16}	0
active caspase-8	p18	x_{17}	0

Table A1: Components, names and initial concentrations

Figure A5: **Good fit parameters:** All parameters that lead to an objective function value that is no more than 100% worse than the best fit; open as separate file: tab-estimates.pdf