

MODEL SEGMENTATION CLOCK NETWORK PARAMETERS AND INITIAL CONDITIONS

Parameters:

Notch loop

| Parameter | Description | Value |
|-------------|---|--------------------------------|
| v_{sN} | Maximum rate of Notch synthesis | 0.23 nM/min |
| v_{dN} | Maximum rate of Notch degradation | 2.82 nM/min |
| K_{dN} | Michaelis constant for Notch degradation | 1.4 nM |
| k_c | Rate constant for Notch cleavage | 3.45 min ⁻¹ |
| v_{dNa} | Maximum rate of cytoplasmic NICD degradation | 0.01 nM/min |
| K_{dNa} | Michaelis constant for cytoplasmic NICD degradation | 0.001 nM |
| v_{dNan} | Maximum rate of nuclear NICD degradation | 0.1 nM/min |
| K_{dNan} | Michaelis constant for nuclear NICD degradation | 0.001 nM |
| K_{IF} | Threshold constant for inhibition of Notch cleavage by Lfng | 0.45 nM |
| K_{aDL} | Delta signaling threshold constant for Notch cleavage | 0.035 nM |
| k_{t1} | Rate constant for NICD entry into nucleus | 0.1 min ⁻¹ |
| k_{t2} | Rate constant for NICD exit from the nucleus | 0.1 min ⁻¹ |
| v_{Nap} | Maximum fraction of NICD phosphorylated | 1.0 |
| K_{pN} | Threshold constant for Gsk3β-mediated NICD phosphorylation | 2.5 nM |
| v_{sF} | Maximum rate of Lfng transcription | 3.24 nM/min |
| K_A | Threshold constant for activation of Lfng gene by NICD | 0.05 nM |
| v_{mF} | Maximum rate of Lfng mRNA degradation | 1.92 nM/min |
| K_{dmF} | Michaelis constant for Lfng mRNA degradation | 0.768 nM |
| k_{sF} | Rate constant for Lfng protein synthesis | 0.3 min ⁻¹ |
| v_{dF} | Maximum rate of Lfng protein degradation | 0.39 nM/min |
| K_{dF} | Michaelis constant for Lfng protein degradation | 0.37 nM |
| v_{sDMDF} | Maximum rate of DMF transcription | 0.497 nM/min |
| K_{aNDMF} | Michaelis constant for Notch activation of DMF | 0.05 nM |
| v_{dmDMF} | Maximum rate of DMF mRNA degradation | 0.314 nM/min |
| K_{dmDMF} | Michaelis constant for DMF mRNA degradation | 0.4 nM |
| K_{sDMF} | Rate constant for translation of DMF | 0.1047 min⁻¹ |
| v_{dDMF} | Maximum rate of DMF protein degradation | 0.209 nM/min |
| K_{dDMF} | Michaelis constant for DMF protein degradation | 0.5 nM |
| k_{sDL} | Rate constant for Delta protein synthesis | 0.75 min⁻¹ |
| MDL | Concentration of Delta mRNA | 0.5 nM |
| K_{Nan} | Michaelis constant for NICD stimulation of Delta translation | 0.04 nM |
| k_{tDL} | Rate constant for Delta protein transport to membrane | 0.5 min⁻¹ |
| v_{dDLc} | Maximum rate of Delta protein degradation in cytoplasm | 0.5 nM/min |
| K_{dDLc} | Michaelis constant for Delta protein degradation in cytoplasm | 0.5 nM |
| v_{dDLm} | Maximum rate of Delta protein degradation on membrane | 0.5 nM/min |
| K_{dDLm} | Michaelis constant for Delta protein degradation on membrane | 0.5 nM |
| K_{DL} | Threshold constant for Delta signaling | 0.08 nM |
| ϵ | Scaling factor for Notch loop | 0.43 |

Parameters in **bold** are additions to the Goldbeter-Pourquié model.

Wnt loop

| Parameter | Description | Value |
|-----------|---|----------------------------|
| a_1 | Rate constant for Gsk3 β -Axin2 binding | 1.8 nM $^{-1}$ min $^{-1}$ |
| d_1 | Rate constant for Gsk3 β -Axin2 dissociation | 0.1 min $^{-1}$ |
| v_{sB} | Maximum rate of β -catenin synthesis | 0.087 nM/min |
| k_{t3} | Rate constant for β -catenin entry into the nucleus | 0.7 min $^{-1}$ |
| k_{t4} | Rate constant for β -catenin exit from the nucleus | 1.5 min $^{-1}$ |
| V_{MK} | Maximum rate of Gsk3 β -mediated β -catenin phosphorylation | 4.5 nM/min |
| K_t | Total Gsk3 β concentration | 3.0 nM |
| K_{ID} | Threshold constant for Dsh inhibition of β -catenin phosphorylation | 0.5 nM |
| K_1 | Michaelis constant for β -catenin phosphorylation | 0.28 nM |
| V_{MP} | Maximum rate of β -catenin dephosphorylation | 1.0 nM/min |
| K_2 | Michaelis constant for β -catenin dephosphorylation | 0.03 nM |
| k_{d1} | Rate constant for unphosphorylated β -catenin degradation | 0.0 min $^{-1}$ |
| k_{d2} | Rate constant for phosphorylated β -catenin degradation | 7.062 min $^{-1}$ |
| v_0 | Basal rate of Axin2 transcription | 0.06 nM/min |
| v_{MB} | Maximum rate of β -catenin activated Axin2 transcription | 1.64 nM/min |
| K_{aB} | Threshold constant for β -catenin activation of Axin2 | 0.7 nM |
| v_{md} | Maximum rate of Axin2 mRNA degradation | 0.8 nM/min |
| K_{md} | Michaelis constant for Axin2 mRNA degradation | 0.48 nM |
| v_{MXa} | Maximum rate of Xa activated Axin2 transcription | 0.5 nM/min |
| K_{aXa} | Threshold constant for Xa activation of Axin2 | 0.05 nM |
| K_{sAx} | Rate constant for Axin2 translation | 0.02 min $^{-1}$ |
| v_{dAx} | Maximum rate of Axin2 protein degradation | 0.6 nM/min |
| K_{dAx} | Michaelis constant for Axin2 protein degradation | 0.63 nM |
| θ | Scaling factor for Wnt loop | 1.12 |

FGF loop

| Parameter | Description | Value |
|---------------|--|------------------|
| Ras_t | Total concentration of Ras protein | 2.0 nM |
| V_{MaRas} | Maximum rate of Ras activation | 4.968 nM/min |
| K_{aFaf} | FGF8 threshold constant for activation of Ras | 0.5 nM |
| K_{aRas} | Inactive Ras threshold constant for activation of Ras | 0.103 nM |
| V_{MdRas} | Maximum rate of Ras activation | 0.41 nM/min |
| K_{dRas} | Michaelis constant for Ras inactivation | 0.1 nM |
| ERK_t | Total concentration of ERK protein kinase | 2.0 nM |
| V_{MaErk} | Maximum rate of Ras-mediated ERK activation | 3.3 nM/min |
| K_{aErk} | Inactive ERK threshold constant for ERK activation | 0.05 nM |
| K_{cDusp} | Rate constant for inactivation of ERK | 1.35 min $^{-1}$ |
| K_{dErk} | Michaelis constant for inactivation of ERK | 0.05 nM |
| X_t | Total concentration of factor X | 2.0 nM |
| V_{MaX} | Maximum rate of ERK-mediated X activation | 1.6 nM/min |
| K_{aX} | Threshold constant for ERK-mediated X activation | 0.05 nM |
| V_{MdX} | Maximum rate of X inactivation | 0.5 nM/min |
| K_{dX} | Michaelis constant for X inactivation | 0.05 nM |
| $V_{MsMDusp}$ | Maximum rate of Dusp6 transcription | 0.9 nM/min |
| K_{aMDusp} | Threshold constant for X-activated Dusp6 transcription | 0.5 nM |
| $V_{MdMDusp}$ | Maximum rate of Dusp6 mRNA degradation | 0.5 nM/min |
| K_{dMDusp} | Michaelis constant for Dusp6 mRNA degradation | 0.5 nM |
| k_{sDusp} | Rate constant for Dusp6 translation | 0.5 min $^{-1}$ |

| | | |
|---------------|--|---------------|
| V_{dDusp} | Maximum rate of Dusp6 protein degradation | 2.0 nM/min |
| K_{dDusp} | Michaelis constant for Dusp6 protein degradation | 0.5 nM |
| v_{DuspX} | Fraction of Dusp6 transcription solely regulated by X | 0.2 |
| $v_{DuspDMF}$ | Fraction of Dusp6 transcription under regulation by DMF | 0.8 |
| K_{IMDusp} | Threshold constant for DMF-mediated inhibition of Dusp6 | 0.3 nM |
| v | Scaling factor for FGF8 loop | 0.328 |

Parameters in **bold** are additions to the Goldbeter-Pourquié model.

Initial variable values:

Notch loop

| Variable | Description | Value |
|----------|--|------------------|
| N | Notch in the membrane | 0.0552 nM |
| N_a | Activated Notch | 0.8095 nM |
| N_{an} | Activated Notch in the nucleus | 0.0039 nM |
| N_{ap} | Phosphorylated Notch | 0.0013 nM |
| MF | Lunatic Fringe mRNA | 0.003 nM |
| F | Lunatic Fringe protein | 0.0006 nM |
| $MDMF$ | Delta Modification Factor mRNA | 0.0011 nM |
| DMF | Delta Modification Factor protein | 0.0003 nM |
| DL_c | Delta protein in the cytoplasm | 0.0138 nM |
| DL_m | Delta protein on the membrane | 0.0058 nM |

Variables in **bold** are additions to the Goldbeter-Pourquié model.

Wnt loop

| Variable | Description | Value |
|----------|---------------------------------|-----------|
| K | Free Gsk3 protein | 1.2252 nM |
| B | β -catenin | 0.9118 nM |
| B_p | Phosphorylated β -catenin | 0.0171 nM |
| B_N | Nuclear β -catenin | 0.4324 nM |
| Max | Axin2 mRNA | 7.7560 nM |
| A | Axin2 protein | 0.1076 nM |
| AK | Axin2-Gsk3 complex | 1.7747 nM |

FGF loop

| Variable | Description | Value |
|----------|----------------------------------|-----------|
| Ras_a | Activated Ras protein | 1.9912 nM |
| ERK_a | Activated ERK protein | 1.9780 nM |
| X_a | Activated transcription factor X | 1.9777 nM |
| $MDusp$ | Dusp mRNA | 2.9054 nM |
| $Dusp$ | Dusp protein | 0.7692 nM |