The Structure, Function, and Evolution of Biological Systems

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Mileyko et al.
Positive feedback equations with implicit dependence on copy number

- $x$ are monomers (unactivated), $y$ are dimers (activated)
- $d_0$ are occupied states and $d_1$ are unoccupied
- $m$ is mRNA, $\sigma$ is transcription, $\gamma_p$ is degradation
- $k_\pm$ is binding/unbinding, $\kappa_\pm$ is coupling/uncoupling for dimers
- $N = d/C$ is copy number
Toggle Switch

\[
\begin{align*}
\dot{x}_i &= 2\kappa_+ y_i - 2\kappa_- x_i^2 + \sigma m_i - \gamma_i x_i \\
\dot{y}_i &= -\kappa_- y_i + \kappa_+ x_i^2 + k_- d_{i+1} - k_+ d_{0,i+1} y_i \\
\dot{d}_{0,i} &= k_- d_i - k_+ d_{0,i} y_{i+1} \\
\dot{d}_i &= -k_- d_i + k_+ d_{0,i} y_{i+1} \\
\dot{m}_i &= \alpha_i d_{0,i} + \beta_i d_i - \gamma_m m_i,
\end{align*}
\]
Repressilator

\[ \begin{align*}
\dot{x}_i &= 2\kappa_- y_i - 2\kappa_+ x_i^2 + \sigma m_i - \gamma_p x_i \\
\dot{y}_i &= -\kappa_- y_i + \kappa_+ x_i^2 + k_- d_{i+1} - k_+ d_{0,i+1} y_i \\
\dot{d}_{0,i} &= k_- d_i - k_+ d_{0,i} y_{i+2} \\
\dot{d}_i &= -k_- d_i + k_+ d_{0,i} y_{i+2} \\
\dot{m}_i &= \alpha d_{0,i} - \gamma_m m_i
\end{align*} \]
Positive feedback equations with implicit dependence on copy number

\begin{align*}
\dot{x} &= 2\kappa_+ y - 2\kappa_+ x^2 + \sigma m - \gamma_p x \\
\dot{y} &= -\kappa_- y + \kappa_+ x^2 + k_+ d_y - k_- d_y \\
\dot{d}_0 &= k_- d_y - k_+ d_0 \\
\dot{d}_x &= k_+ d_0 y - k_+ d_y \\
\dot{m} &= \alpha d_0 + \beta d_y - \gamma_m m,
\end{align*}
Quasi steady state approximation (QSSA)

In the end, they really look at cases of equilibrium and steady states without details about relative time scales.
Positive feedback solutions using quasi steady state approximation (QSSA)

\[
y = c_p x^2,
\]
\[
d_1 = d \frac{c_p c_d x^2}{1 + c_p c_d x^2},
\]
\[
d_0 = \frac{d}{1 + c_p c_d x^2},
\]
\[
m = \frac{d}{\gamma_m} \frac{\alpha + \beta c_p c_d x^2}{1 + c_p c_d x^2}
\]
Equilibrium concentration with copy number

\[ N = \frac{\bar{u}(1 + \bar{u}^2)}{\hat{\alpha} + \hat{\beta}\bar{u}^2}. \]

Transition in copy number occurs at

\[ \bar{u}^2 = \frac{1 - 3a \pm \sqrt{(1 - 3a)^2 - 4a}}{2}. \]

Vary numbers of whole motifs, not of nodes within motif
Condition for transition

\[(1 - 3a)^2 - 4a > 0.\]
Plot of transition with copy number
Transition in oscillations as well
Physical values of parameters

mate kinetic values common for the four motifs are as follows: $\kappa_+/\kappa_- = 10^7$ M$^{-1}$, $k_+/k_- = 10^7$ M$^{-1}$, $\sigma = 0.5$ min$^{-1}$, $C = 10^{-9}$ M, $\gamma_m = 0.1$ min$^{-1}$.
Kinetic values specific for each of the motifs are:

Positive feedback: $\alpha = 0.025$ min$^{-1}$, $\beta = 1.7$ min$^{-1}$, $\gamma_p = 0.05$ min$^{-1}$.

Bistable feedback: $\alpha_1 = 0.1$ min$^{-1}$, $\beta_1 = 2.4$ min$^{-1}$, $\gamma_1 = 0.08$ min$^{-1}$, $\alpha_2 = 0.8$ min$^{-1}$, $\beta_2 = 0.01$ min$^{-1}$, $\gamma_2 = 0.06$ min$^{-1}$.

Toggle switch: $\alpha_1 = 10.12$ min$^{-1}$, $\beta_1 = 0.22$ min$^{-1}$, $\gamma_1 = 0.08$ min$^{-1}$, $\alpha_2 = 5.2$ min$^{-1}$, $\beta_2 = 0.52$ min$^{-1}$, $\gamma_2 = 0.06$ min$^{-1}$.

Repressilator: $\alpha = 2$ min$^{-1}$, $\gamma_p = 0.08$ min$^{-1}$.
Stouffer and Bascompte
Equations for motifs and food webs

\[ \frac{dB_i}{dt} = r_i G_i B_i - x_i B_i + x_i B_i \sum_{j=\text{prey}} y_i F_{ij} - \sum_{k=\text{pred}} \frac{x_k y_k B_k F_{ki}}{e_{ki}} \]

Density dependence

\[ G_i = 1 - \sum_{j=\text{prod}} \frac{B_j}{K} \]

Type 2 functional response

\[ F_{ij} = \frac{w_{ij} B_j}{B_0 + \sum_{k=\text{prey}} w_{ik} B_k} \]
Scaling of terms with mass

Choose time scale of 1

Mass-specific metabolic rate

\[ r_i = 1 \]

\[ x_i = \frac{a_x}{a_r} \left( \frac{M_i}{M_b} \right)^{-1/4} \]

Consumption rate relative to metabolic rate

\[ y_i = \frac{a_y}{a_x}, \]

Very particular choice of parameter values. Out to 4 decimal. Likely means there results are extremely sensitive. Connectance is low and size is medium.
Persistence of motifs

more frequent

less frequent

(a)

Tri-trophic Omnivory Exploitive competition Apparent competition

(b)

Fraction of persistent modules

(c)

Timesteps

Fraction of persistent modules
Contribution of motifs to whole web persistence

Persistence is measured as fraction of species that persist after a specified number of time steps.
Contribution of motifs to whole web persistence
Conclusions and questions

Motif persistence is not tied to web persistence

Most common motifs are tied to web persistence

Are there larger motifs where persistence in isolation and persistence of whole web do match? If so, those motifs might be the real building blocks.

Do webs with different patterns of motifs that imply less persistence have greater short term robustness?

How do prey selection and dynamics of motifs and motif representation change in time? What does this mean for the results?