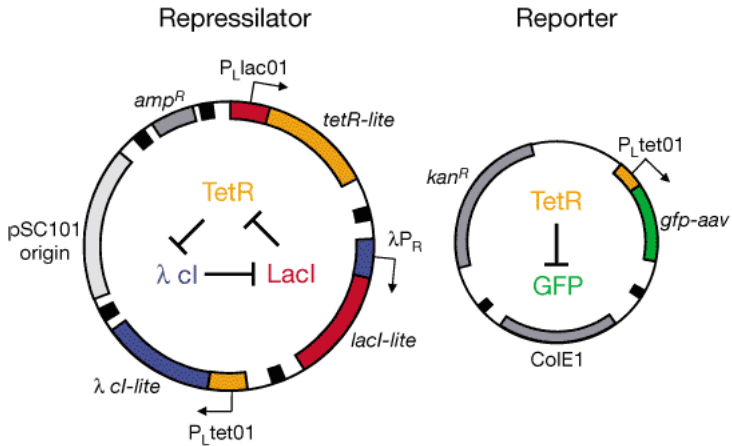# Repressilator: simulation and analysis of a synthetic oscillatory network in *E. coli*
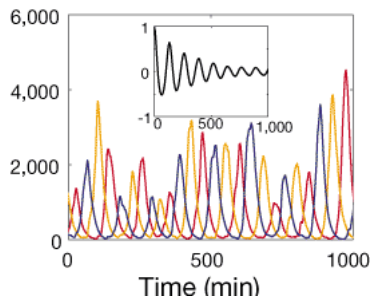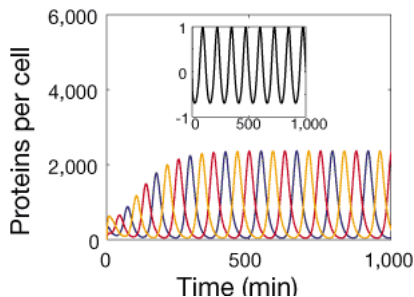
Daniel S. Standage

BCB 570

March 28, 2012

Repressilator

Repressilator

Stoichiometric matrix

$$V = \begin{bmatrix} 1 & 0 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & -1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & -1 \end{bmatrix}$$

Reactions

- transcription:

$$a_{tr}^0 + \frac{a_{tr}(K_m)^n}{(K_m)^n + I^n}$$
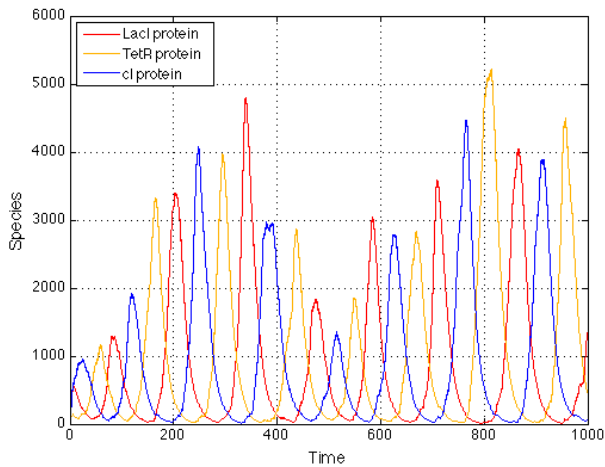
- translation:
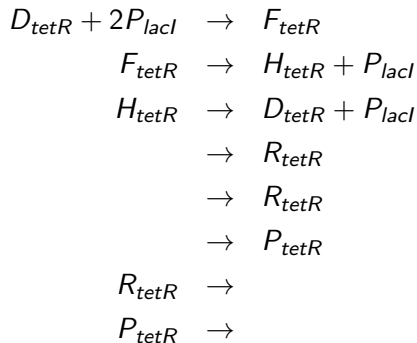
$$k_{tl} T$$

- mRNA degredation:

$$kd_t T$$

- protein degredation:

$$kd_p P$$

Simulation

Network analysis

$$
\begin{aligned}
D_{tetR} + 2P_{lacI} &\rightarrow F_{tetR} \\
F_{tetR} &\rightarrow H_{tetR} + P_{lacI} \\
H_{tetR} &\rightarrow D_{tetR} + P_{lacI} \\
&\rightarrow R_{tetR} \\
&\rightarrow R_{tetR} \\
&\rightarrow P_{tetR} \\
R_{tetR} &\rightarrow \\
P_{tetR} &\rightarrow
\end{aligned}
$$

Network analysis

- elementary flux modes: 6, 12

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Network analysis

- elementary flux modes: 6, 12
- each is an extreme pathway
- flux optimization uninformative
- minimal cut sets: 64, 1728
- simple network, not very informative

Thanks to...

- Will
- Tasos