





# Who are we?

- 9 undergraduates advised by
  - 4 graduate students
  - 20 faculty from diverse departments
- 3 biologists, 2 engineers, 2 computer scientists,
- 1 physicist, and 1 biochemist.

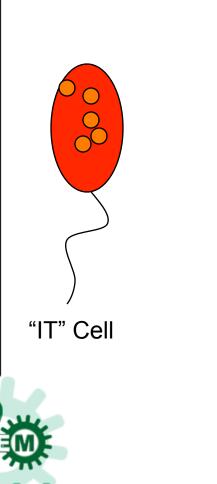


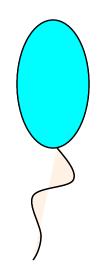


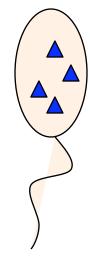




## **Bacterial Freeze Tag**

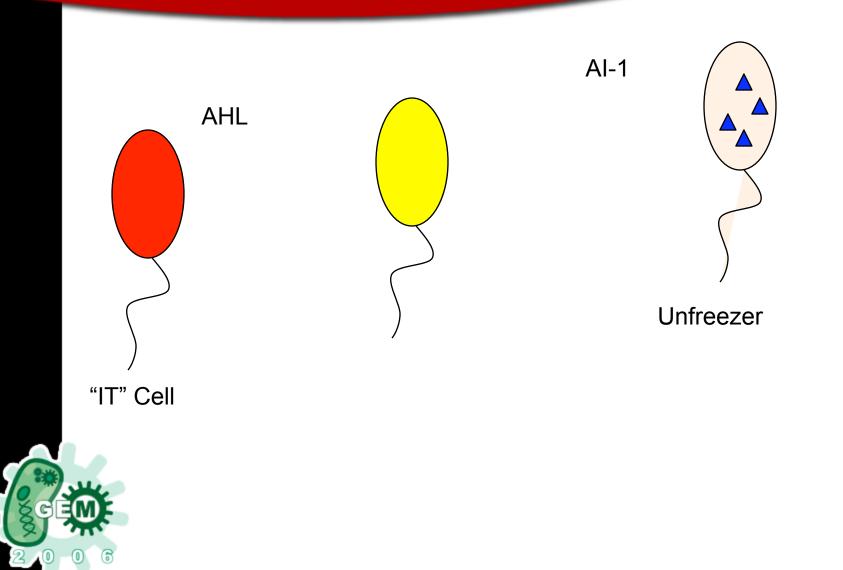




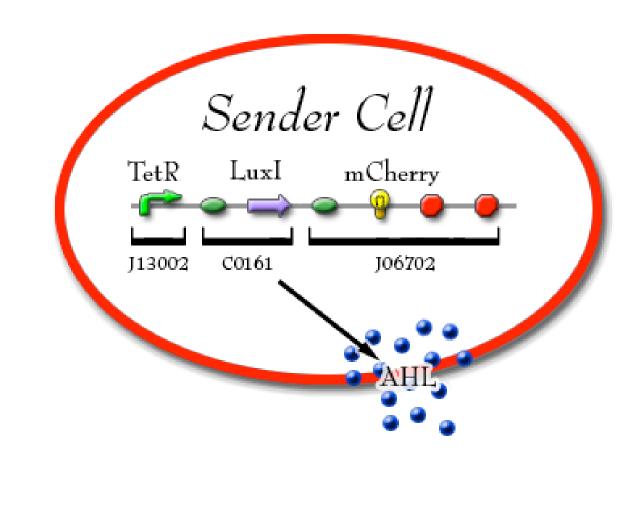


#### Unfreezer

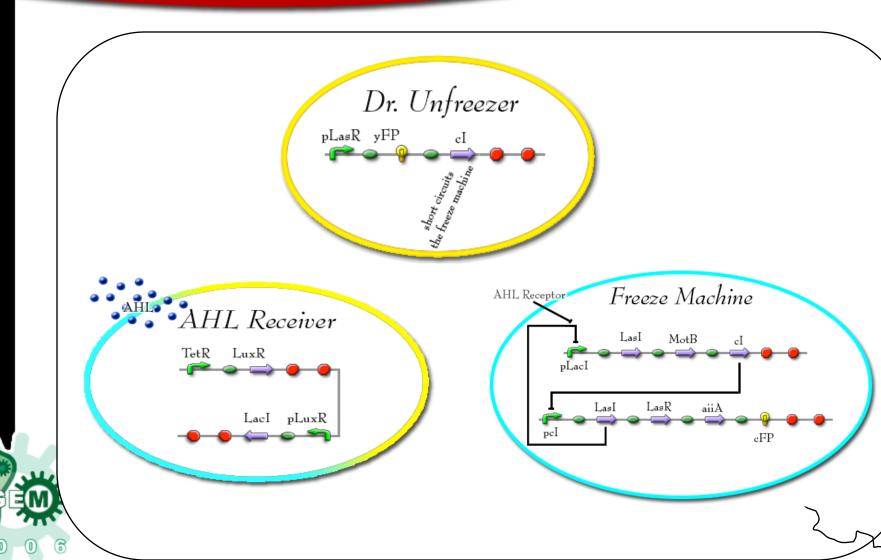
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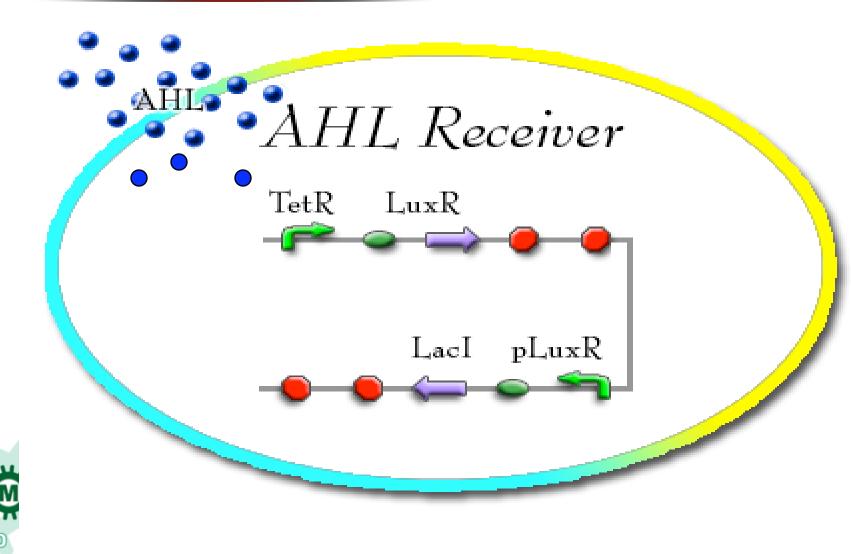


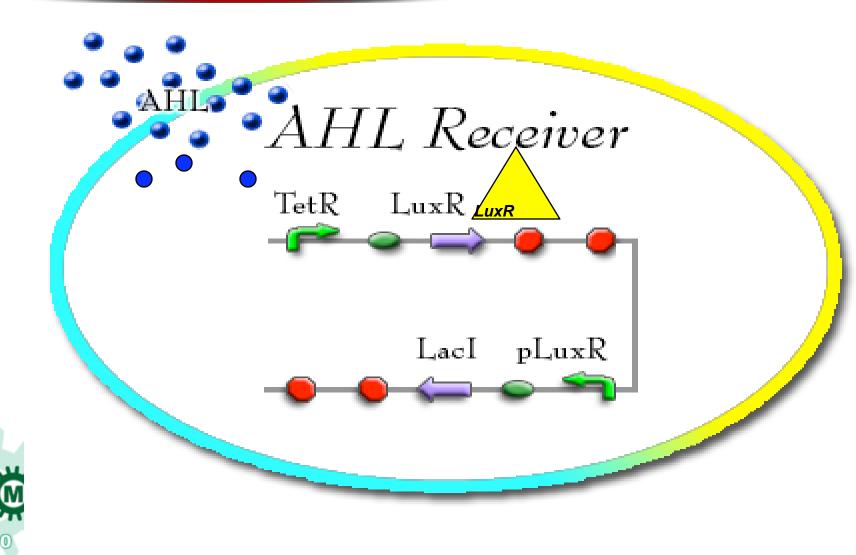
# Sender ("IT") Cell

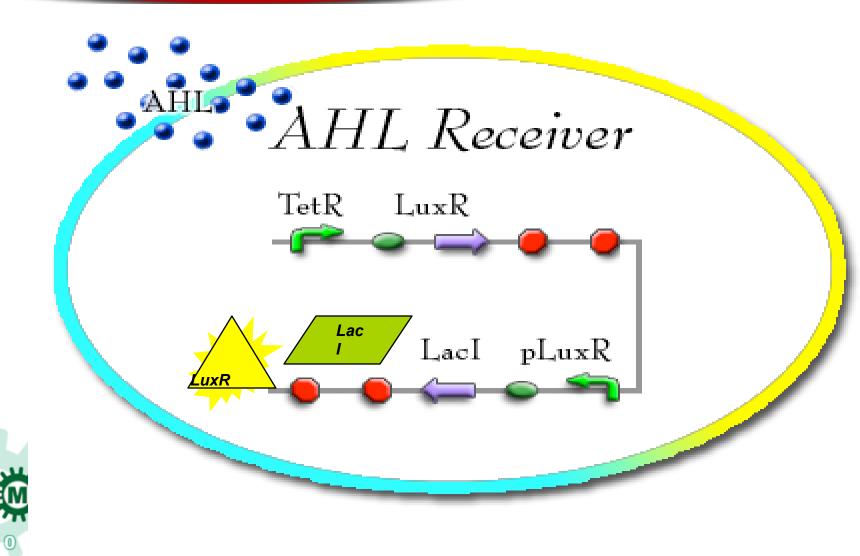


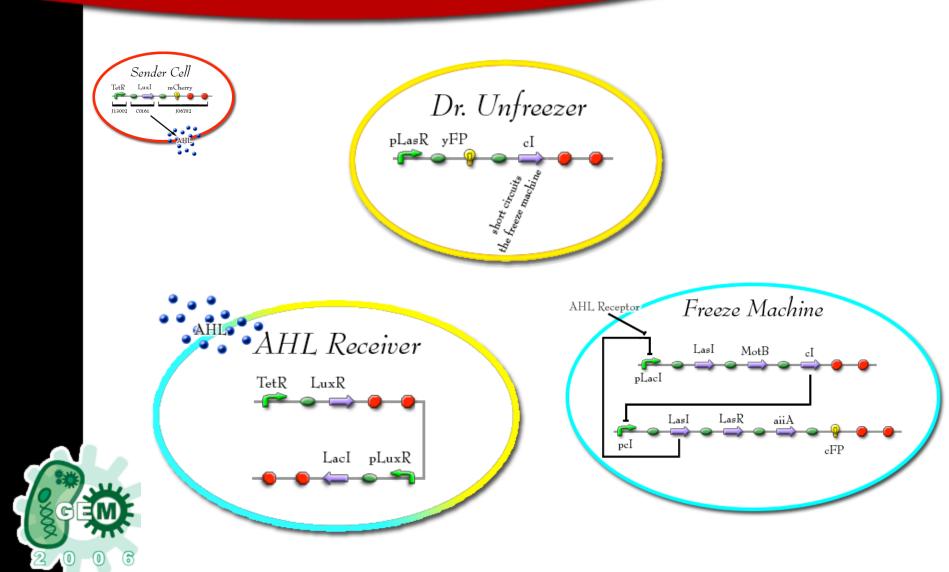


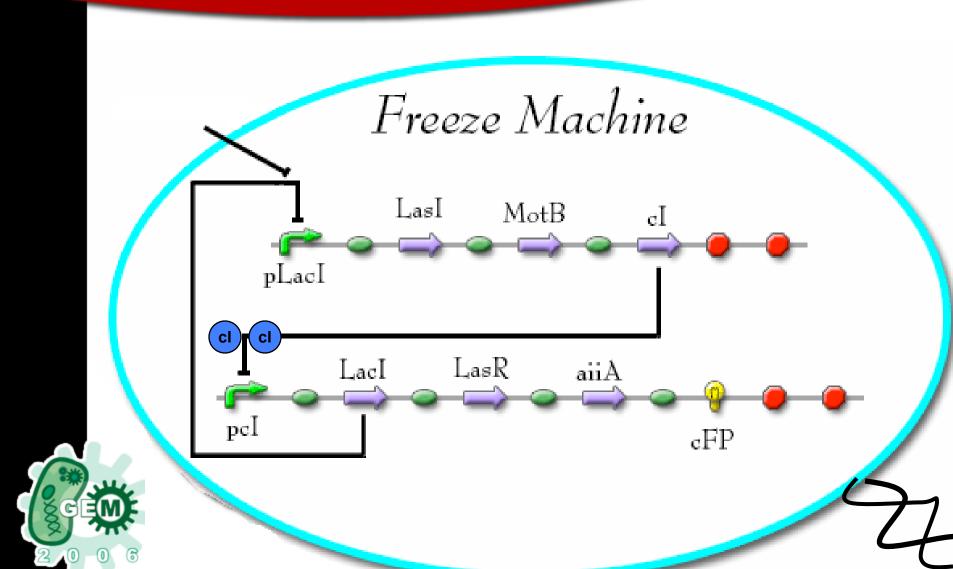


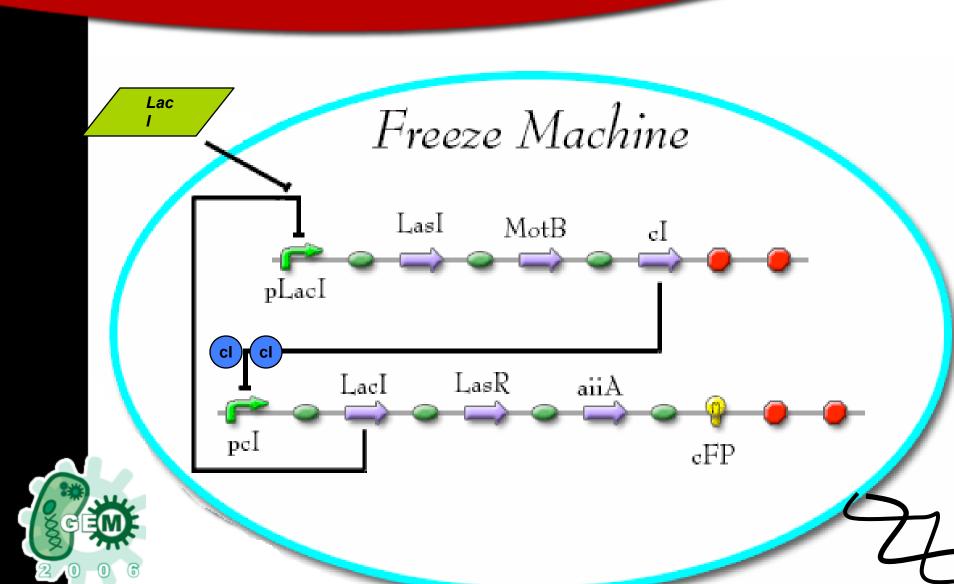


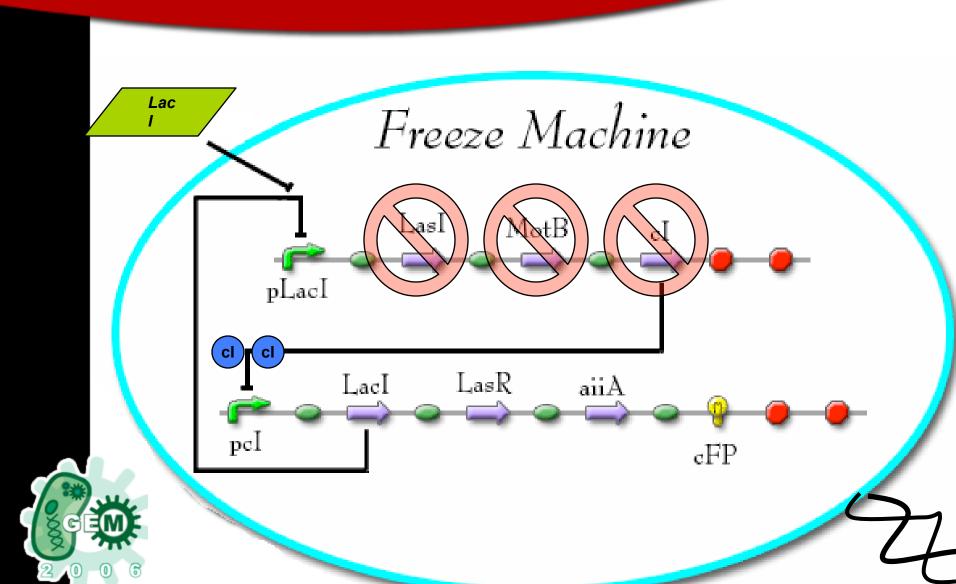


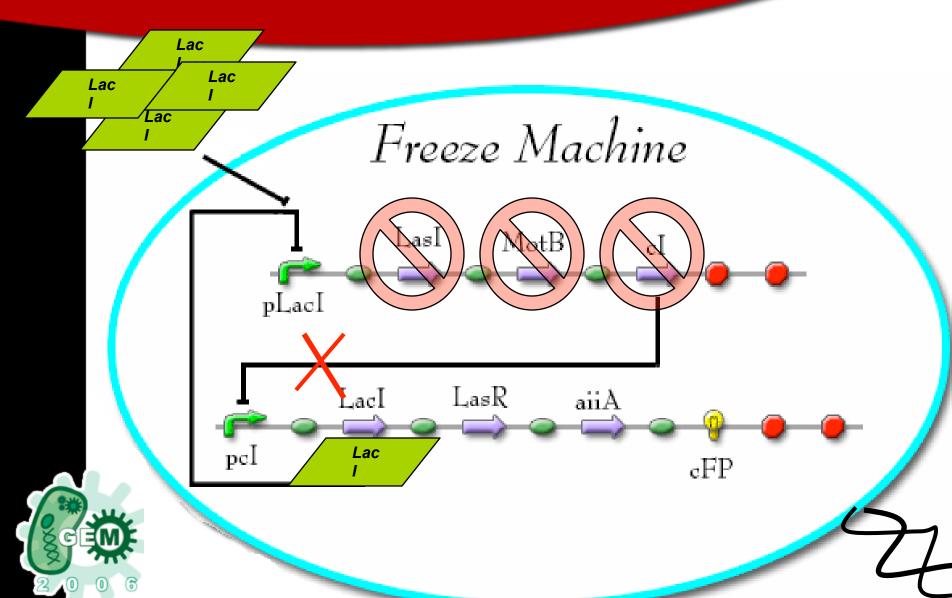


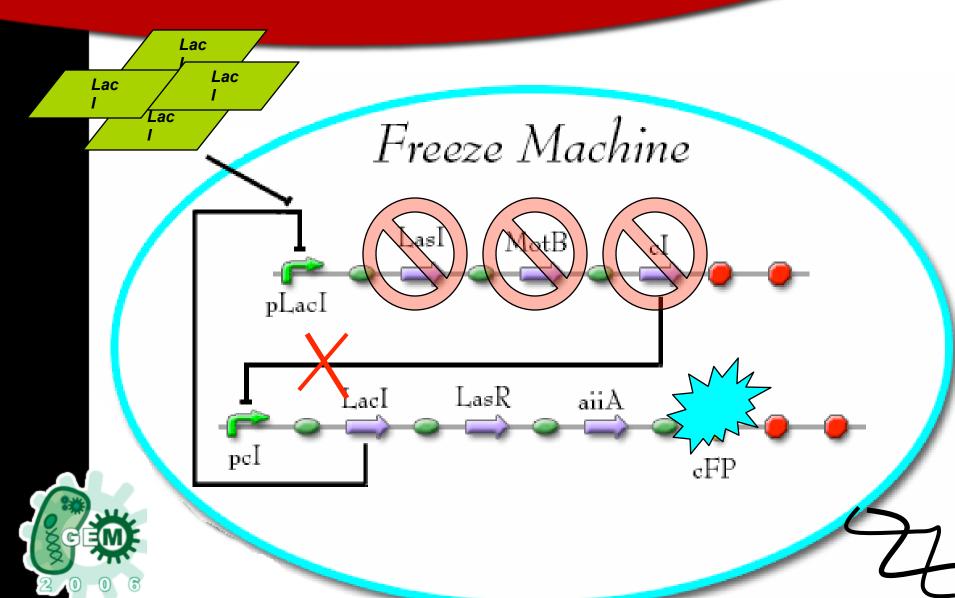


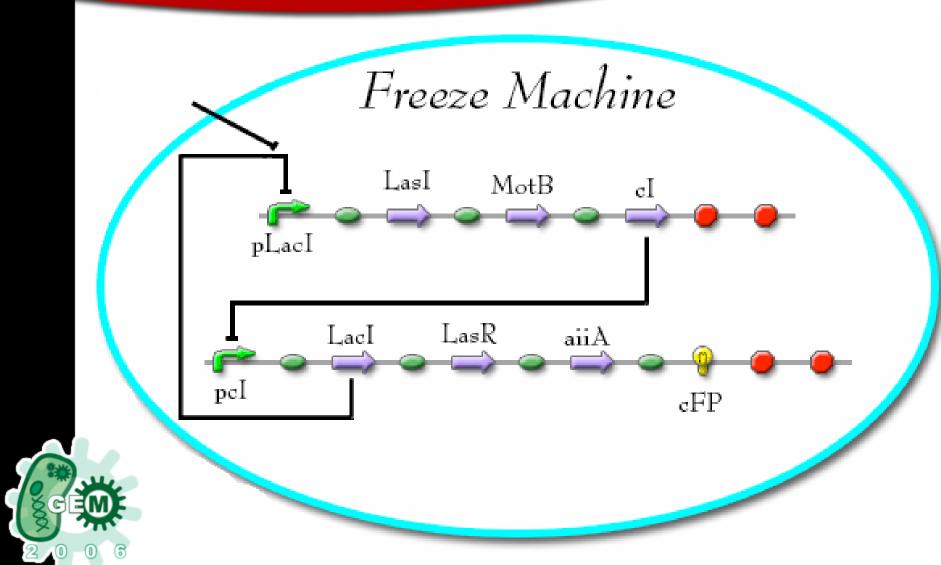


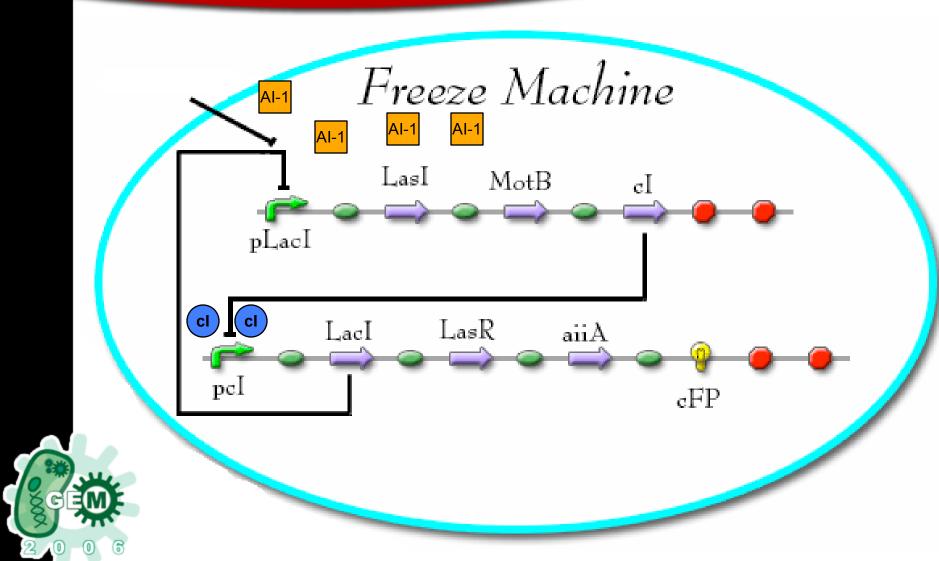


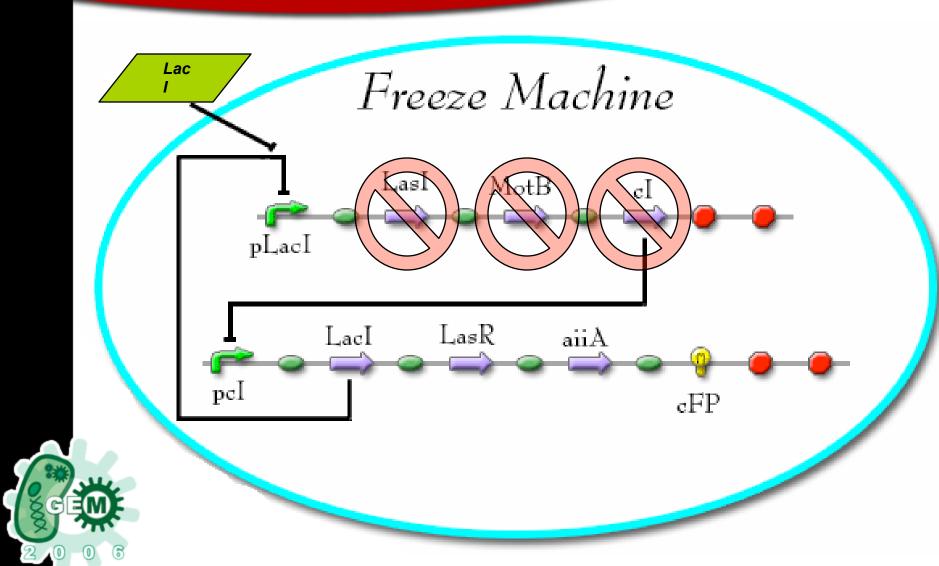


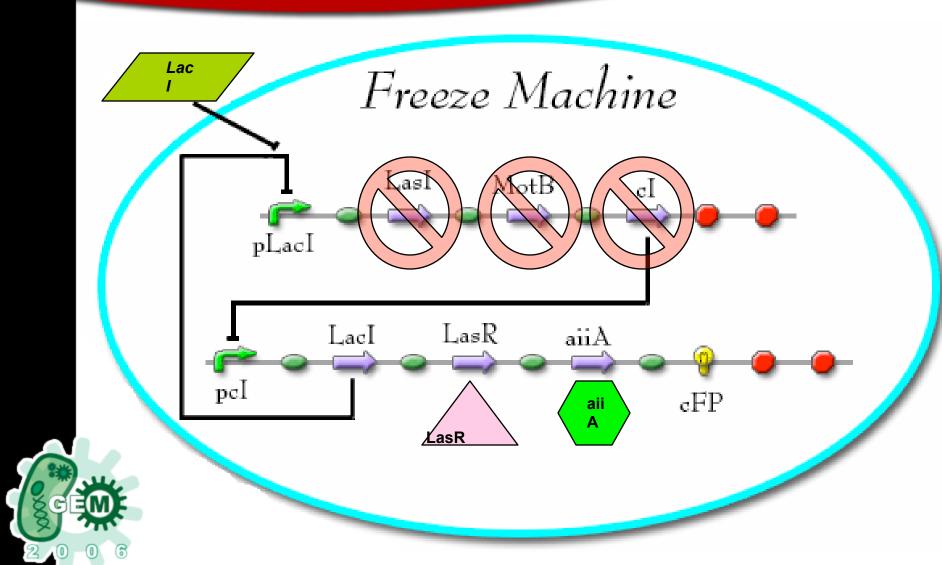


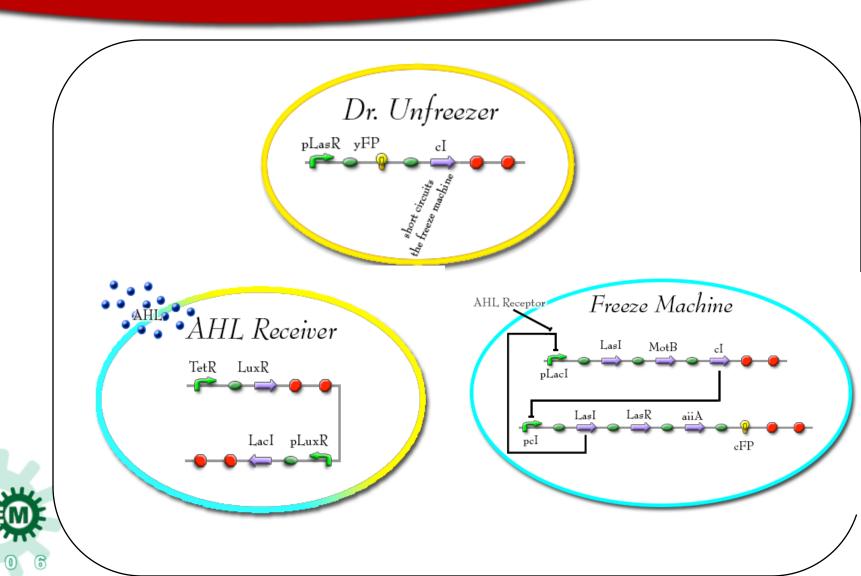


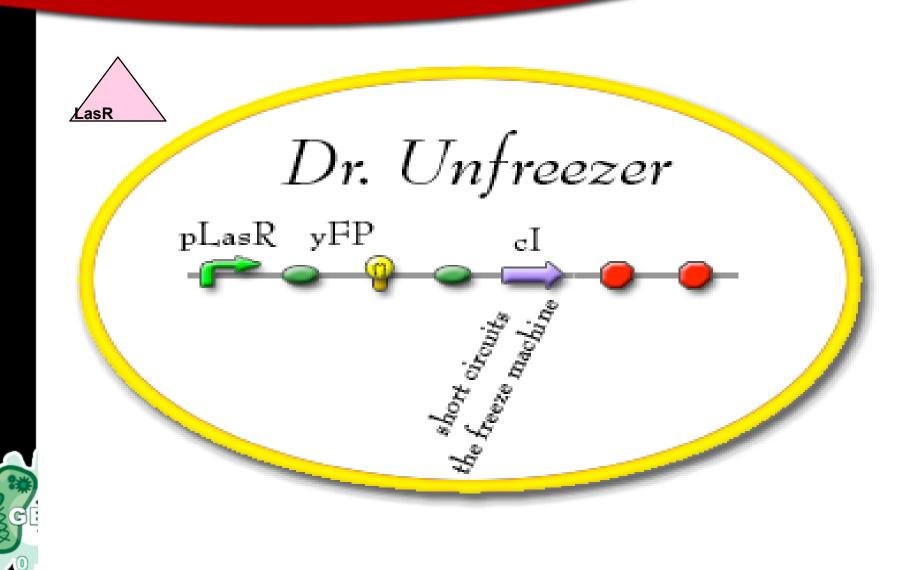


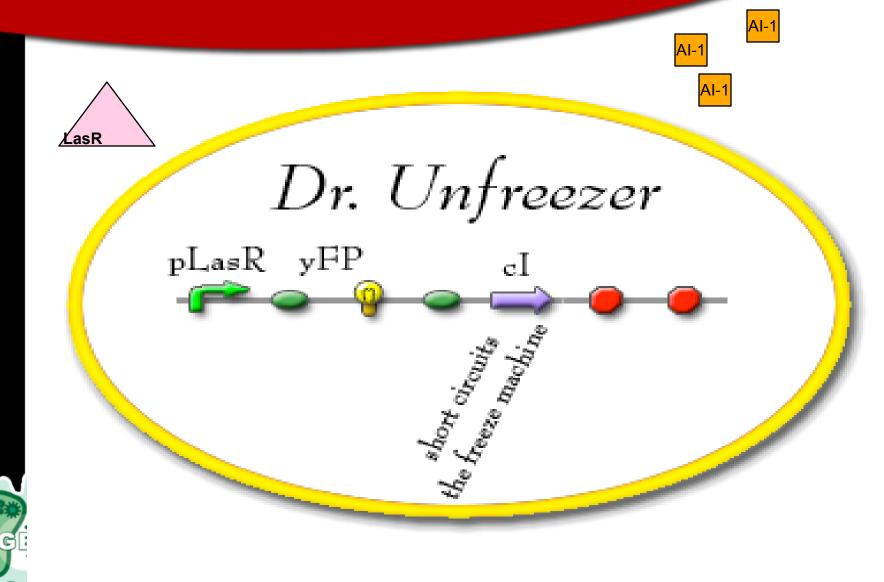


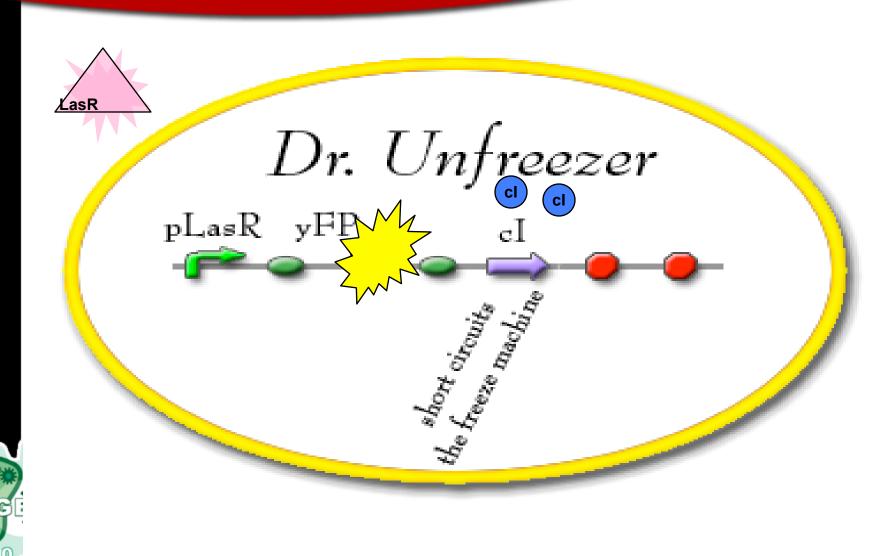


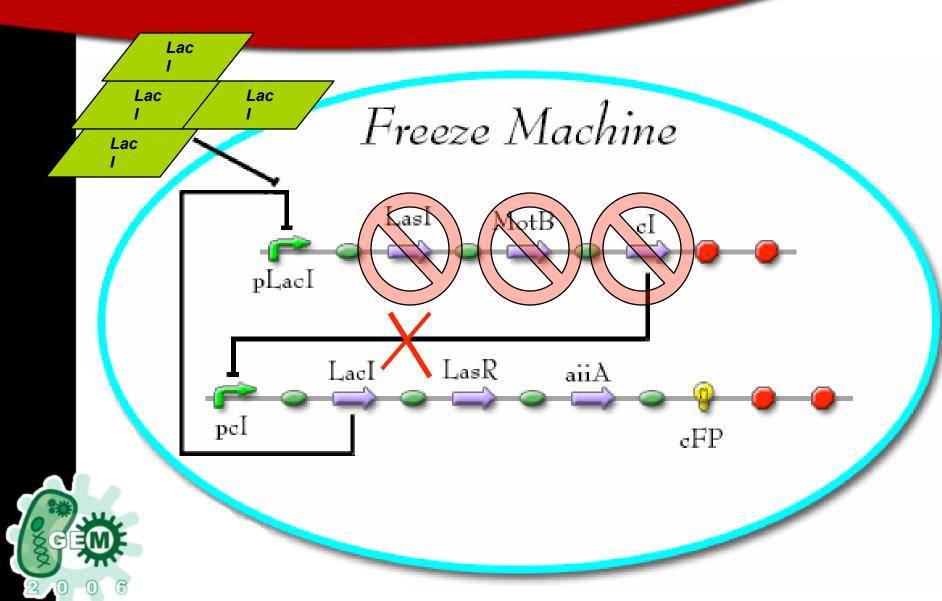


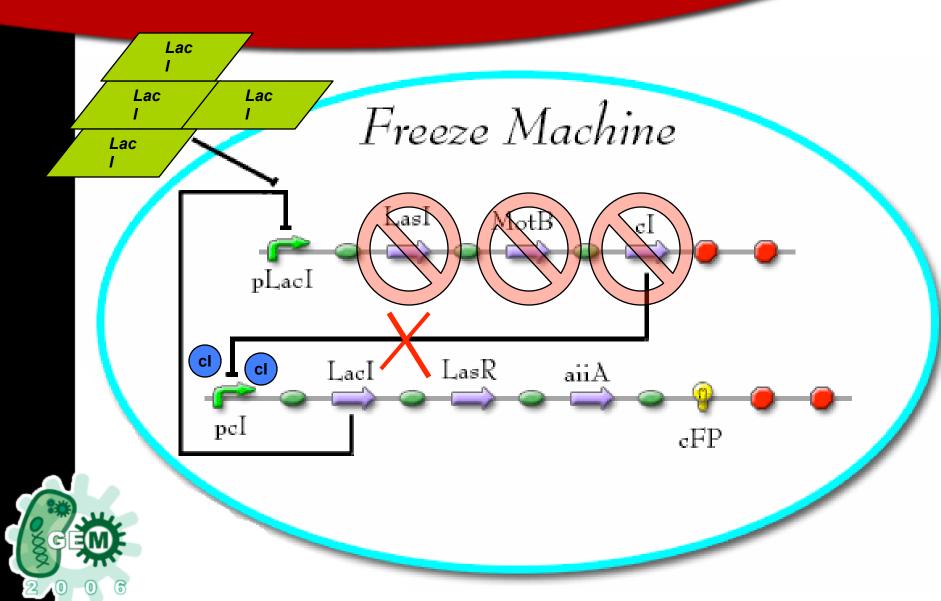


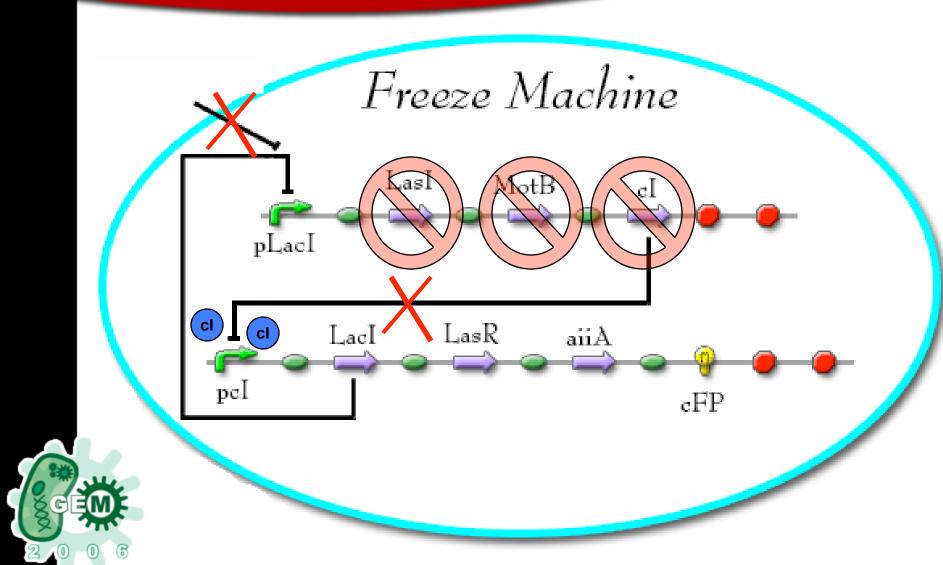


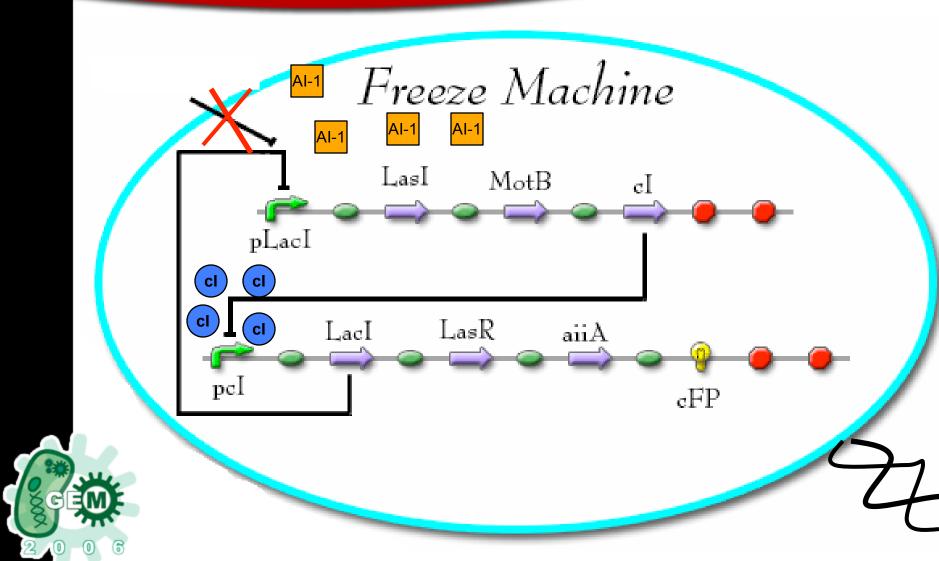












### The Tri-stable Toggle Switch



# The Tri-stable Toggle Switch

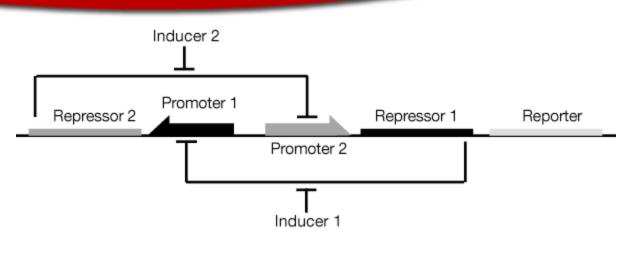
# Construction of a genetic toggle switch in *Escherichia coli*

Timothy S. Gardner\*†, Charles R. Cantor\* & James J. Collins\*†

\* Department of Biomedical Engineering, † Center for BioDynamics and ‡ Center for Advanced Biotechnology, Boston University, 44 Cummington Street, Boston, Massachusetts 02215, USA



# The Tri-stable Toggle Switch



A Bi-stable Toggle Switch

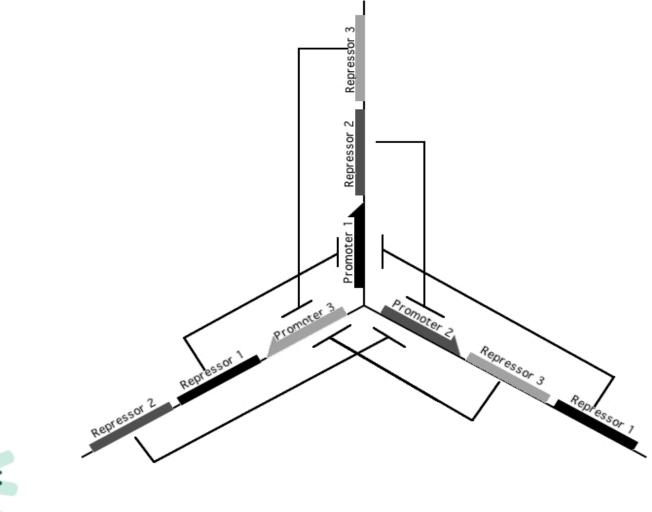
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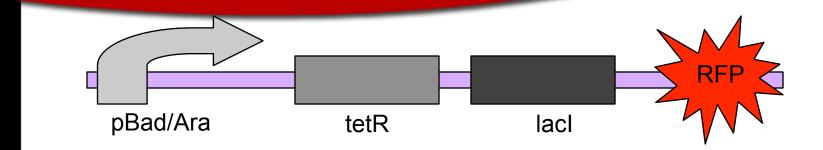


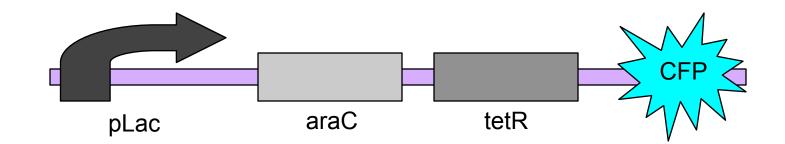
#### A Tristable Toggle Switch

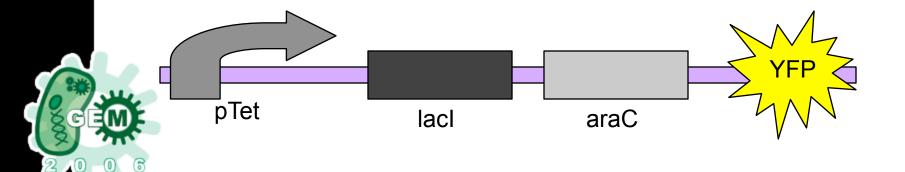




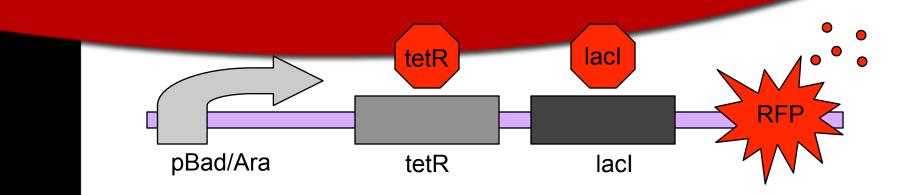
#### Let's watch in practice...

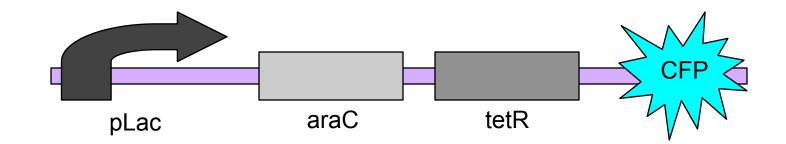


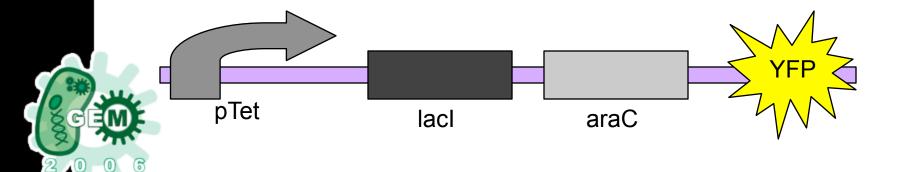




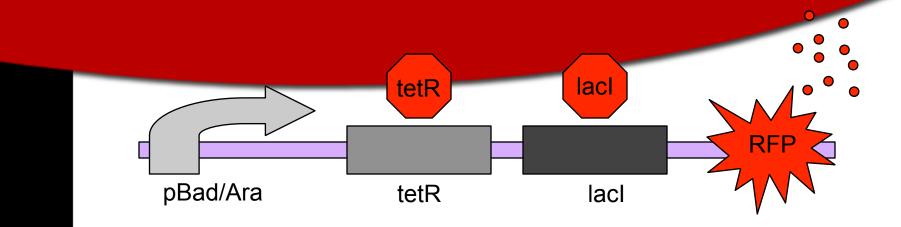
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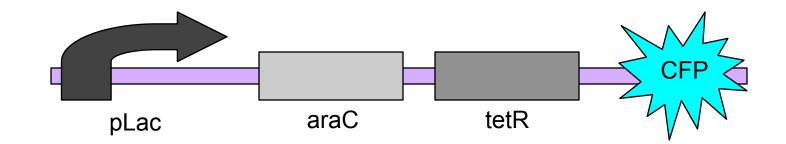


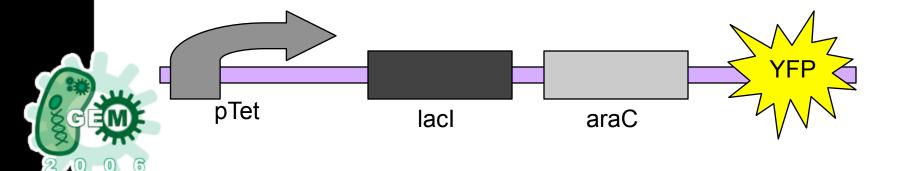




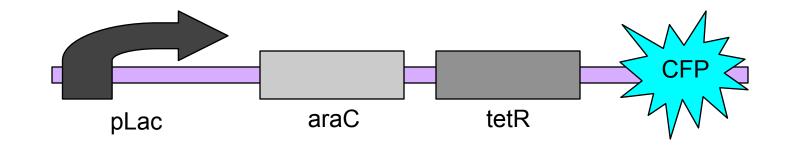
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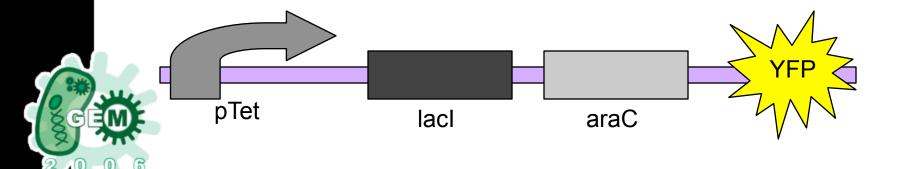




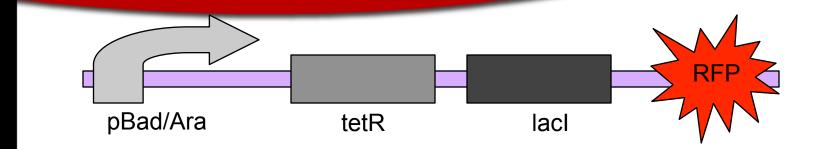


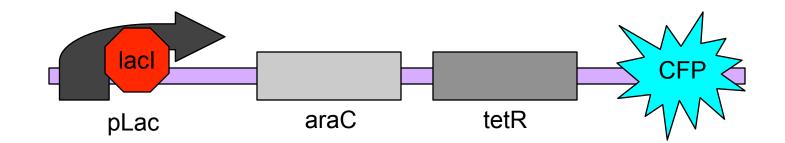
# Let's watch in practice... Without interruption, this state is stable.

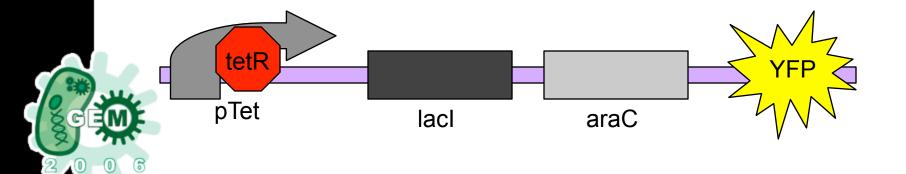




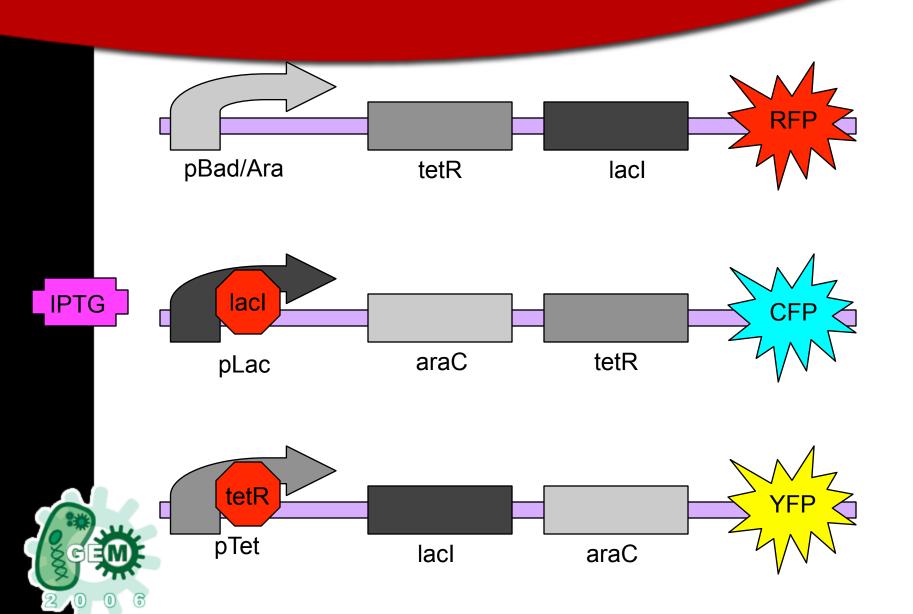
#### But we can induce a change with IPTG...



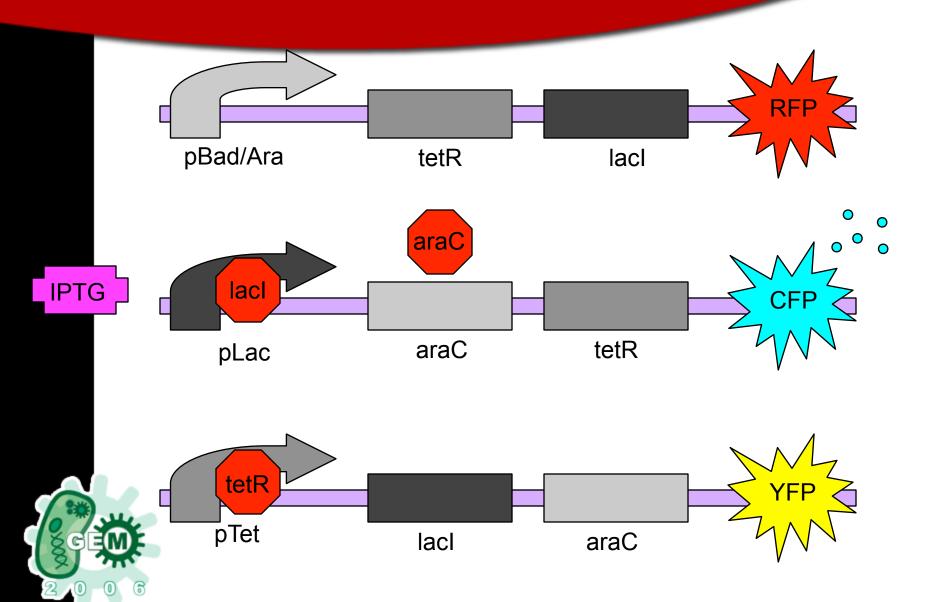




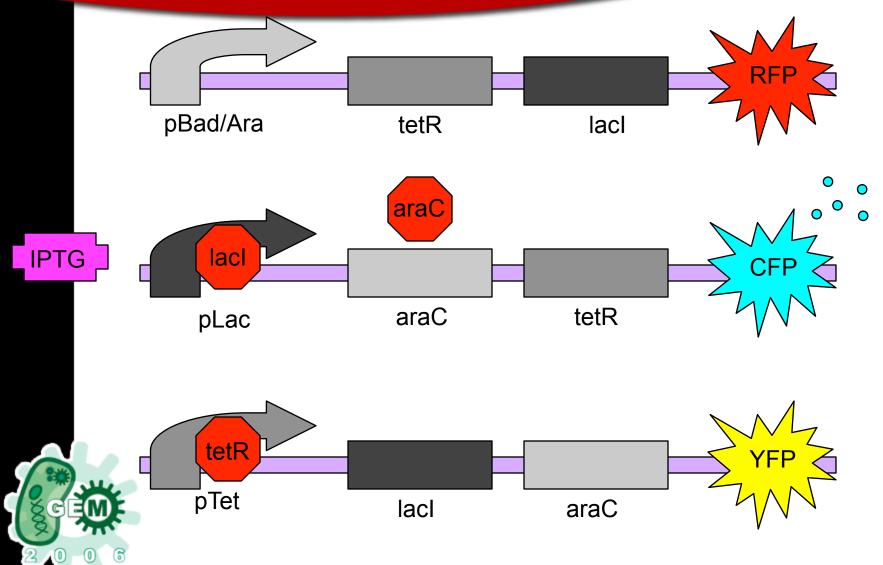
#### But we can induce a change with IPTG...



But we can induce a change with IPTG... Without interruption, *this* state is stable.



But we can induce a change with IPTG... Without interruption, *this* state is stable. We could have induced the pBad/Ara pathway with arabinose or the pTet pathway with tetracycline.



## Modeling

#### Deterministic Model based on:

"Prediction and measurement of an autoregulatory genetic module." Isaacs et al. PNAS 2003

And

"A Bottom-Up Approach to Gene Regulation." Guido et al. Nature 2006



**Basic Idea** 

Fast reactions – "merizations" and operator binding events•equilibrium equations

Slow reactions – transcription, translation, degradation

differential equations

Combine these equations with an equation for total molecule in the system based on plasmid copy number

Manipulate these equations to derive an expression for the evolution of protein monomers/time

Fast reactions – k's on order of seconds

Ex:  $k_{11}/V$  $L + L \rightarrow \mathbb{R} L_{2}$  $k_{_{-1L}}$  $k_{21}/V$  $L + L_2 \rightarrow \mathbb{R} L_3$  $k_{_{-2L}}$  $k_{3L}/V$  $L + L_3 - R L_4$  $k_{_{-3L}}$  $k_{_{4I}}/V$  $D_{0L} + L_4 - B D_{1L}$  $k_{-4L}$ 

Ex: Dimer formation

Trimer

formation

Equilibrium equations

 $l_2 = \frac{k_{1L}}{k_{1L}} l^2$ 

 $l_3 = \frac{\kappa_{2L}}{k \dots V} l_2 l$ 

Tetramer formation

 $l_4 = \frac{k_{3L}}{k} l_3$ 

Operator binding

 $d_{1L} = \frac{k_{4L}}{k_{4L}} l_4 d_{0L}$ 

 $\alpha_L \eta_{LT} k_{tL}$ 

 $D_{1L} \longrightarrow \mathbb{R} \quad D_{1L} + T$ 

Slow reactions – k's on order of minutes

unbound 
$$D_{0L} \longrightarrow D_{0L} +$$

Transcription and translation of TetR from unbound and bound pLacl promoters

bound

**Differential equations** 

Ex:

$$\frac{dZ_{T}}{dt} = \eta_{AT}\beta_{A}(d_{0A} + d_{1A} + \alpha_{A1}d_{2A} + \alpha_{A2}d_{1AA} + \alpha_{A3}d_{2AA}) + \eta_{LT}\beta_{L}(d_{0L} + \alpha_{L}d_{1L}) - \gamma_{T}T$$

T

 $\alpha_L \eta_{LT} k_{tL}$ 

 $D_{1L} \longrightarrow \mathbb{R} \quad D_{1L} + T$ 

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Transcription and translation of TetR from unbound and bound pLacl promoters

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**Differential equations** 

Ex:

$$\frac{dZ_{T}}{dt} = \left[ \eta_{AT} \beta_{A} \left( d_{0A} + d_{1A} + \alpha_{A1} d_{2A} + \alpha_{A2} d_{1AA} + \alpha_{A3} d_{2AA} \right) + \eta_{LT} \beta_{L} \left( d_{0L} + \alpha_{L} d_{1L} \right) - \gamma_{T} T \right]$$

TetR created by pBAD promoter

 $\alpha_L \eta_{LT} k_{tL}$ 

 $D_{1L} \longrightarrow \mathbb{R} \quad D_{1L} + T$ 

Slow reactions – k's on order of minutes

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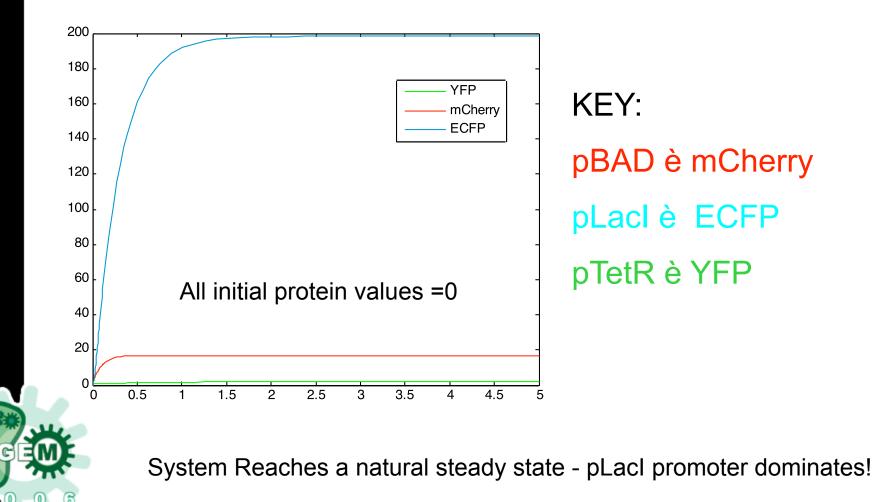
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$$\frac{dZ_{T}}{dt} = \eta_{AT}\beta_{A}(d_{0A} + d_{1A} + \alpha_{A1}d_{2A} + \alpha_{A2}d_{1AA} + \alpha_{A3}d_{2A}) + \eta_{LT}\beta_{L}(d_{0L} + \alpha_{L}d_{1L}) - \gamma_{T}T$$

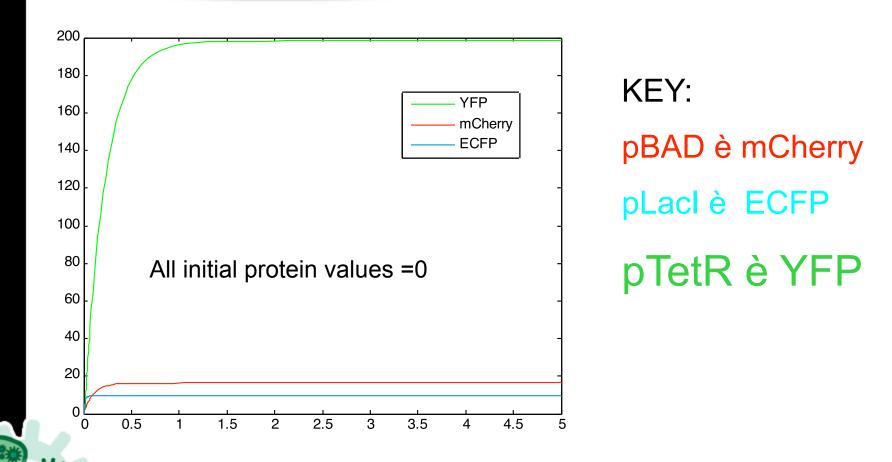
T

TetR created by pLacl promoter

#### Prediction – no inducer



#### **Prediction - Tetracycline**



Model CONFIRMS our hypothesis in the presence of tetracylcine!

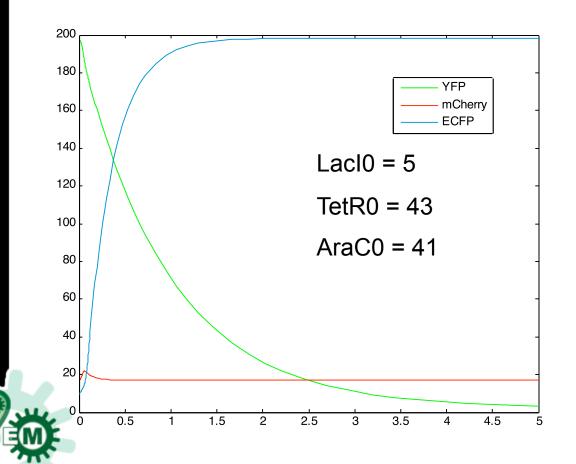
#### Test for stability

Will the tri-stable switch work...?

- Plug in final protein concentrations from induced state into inducer-less system
- Test whether state remains stable



#### Test for stability

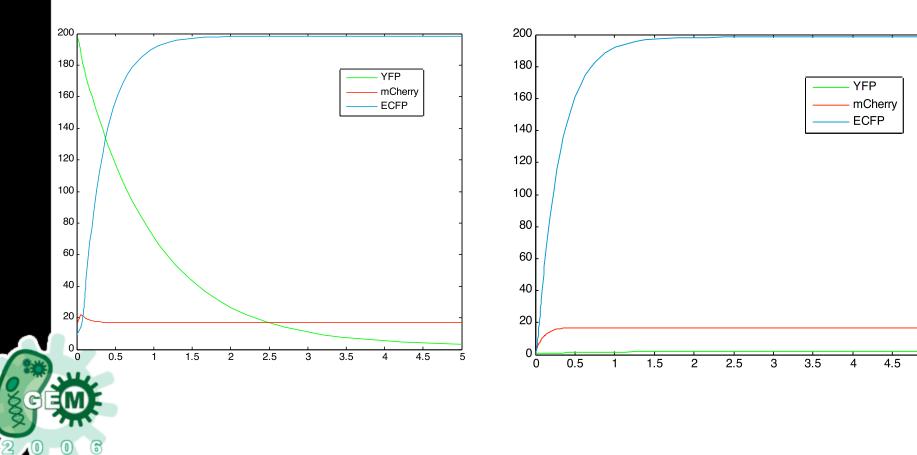


KEY: pBAD è mCherry pLacl è ECFP pTetR è YFP

# System switches back to natural steady state!

pTetR stability test

Natural steady state



## Future

- Experimentally obtain more appropriate model parameters
- Run parameter scans for tri-stability
  - Potentially identify proper regulatory elements and or tinkering required to for tri-stability
- Add stochastic variation to the model



## Conclusions

- Tri-stable Toggle Switch
  - Our model predicts that a tri-stable switch given our experimental setup will be unable to reach a stable state following transient induction
- Freeze-tag
  - Theoretically shows an interesting biological circuit which uses cell-cell communication with a bi-stable circuit to create a novel observable interaction
  - Circuit complexity may jeopardize the efficiency of the system by causing a build-up of various proteins.
    Modifications of the circuit may be required to circumvent such effects.

## Special thanks to:

- Gary Wessel
- Tayhas Palmore
- Alex Brodskey
- Nicola Neretti
- Karen Haberstroh
- David Targan
- Ruth Simmons
- Houseknecht lab @ Pfizer
- Sir Josiah Carberry

