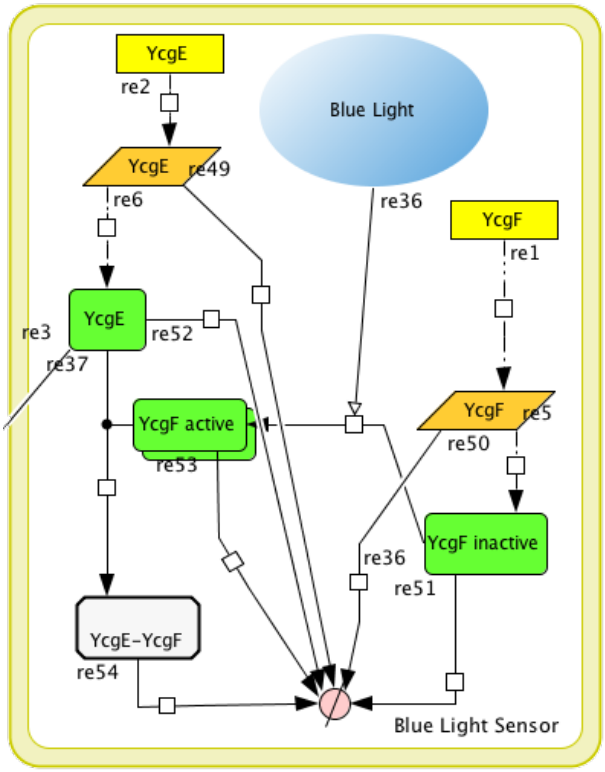
Contents

1. Model

The blue light sensor was modeled with help of the model by the iGEM team KU Leuven 2009[1]. For further details see the Papers by Tschowri [3] and Nakasone [4, 2].

The model does not take into account that the YcgE/YcgF pathway is strongly temparature dependent.

The dye output was an adaption of the model proposed in the paper by Yildirim[5]



2. Equations

$$
\begin{array}{lll}
YcgF_{mRNA} & \dot{x}_1 = & k_1 - \gamma_{mRNA} x_1 \\
YcgF_{inactive} & \dot{x}_2 = & k_3 x_1 - 2k_{dim} x_2^2 \frac{BlueLight(t)^2}{\frac{1}{4}+(BlueLight(t))^2} + 2k_{dis} x_3 - \gamma_{Protein} x_2 \\
YcgF_{dimer} & \dot{x}_3 = & 2k_{dim} x_2^2 \frac{BlueLight(t)^2}{\frac{1}{4}+(BlueLight(t))^2} - k_{bind} x_3 x_5 - k_{dis} x_3 + k_{ubind} x_6 - \gamma_{Protein} x_3 \\
YcgE_{RNA} & \dot{x}_4 = & k_2 - \gamma_{mRNA} x_4 \\
YcgE_{Protein} & \dot{x}_5 = & k_4 x_4 - k_{bind} x_3 x_5 + k_{ubind} x_6 - \gamma_{Protein} x_5 \\
YcgE.YcgF_{complex} & \dot{x}_6 = & -k_{ubind} x_6 + k_{bind} x_3 x_5 \\
lacZ_{mRNA} & \dot{x}_7 = & \alpha_M \left(1 - \frac{\left(\frac{x_5}{K3}\right)^{n_l}}{1+\left(\frac{x_5}{K3}\right)^{n_l}} \right) - \gamma_M x_7 \\
\beta - Galactosidase & \dot{x}_8 = & \alpha_B x_7 - \gamma_B x_8 \\
dye & \dot{x}_9 = & \alpha_A x_8
\end{array}
$$

3. Parameters

Parameter	Value	Unit	Name	Source
k_1	1.54e-3	$\frac{1}{s}$	max transcription rate YcgF	[1]
k_2	0.848e-3	$\frac{1}{s}$	max transcription rate YcgE	[1]
k_3	0.167	$\frac{1}{s}$	max translation rate YcgF	[1]
k_4	0.167	$\frac{1}{s}$	max translation rate YcgE	[1]
k_{dim}	0.008	$\frac{1}{s}$	dimerization rate YcgF	[1]
k_{dis}	0.0058	$\frac{1}{s}$	dissociation rate YcgF dimer	[1]
k_{bind}	100	$\frac{1}{s}$	binding rate YcgF dimer to YcgE	[1]
k_{ubind}	1	$\frac{1}{s}$	unbinding rate YcgF.YcgE	[1]
γ_{mRNA}	2.3105e-3	$\frac{1}{s}$	degradation mRNA YcgE/YcgF	[1]
$\gamma_{Protein}$	1.9254e-5	$\frac{1}{s}$	degradation rate Protein YcgE/YcgF	[1]
$K3$	600	nM	response param. YcgE,lacZ	guessed
α_M	$\frac{0.997}{60}$	$\frac{nM}{s}$	max transcription rate lacZ	[5]
α_B	$\frac{1.661e-5}{60}$	$\frac{1}{s}$	max translation rate lacZ	[5]

Parameter	Value	Unit	Name	Source
α_A	$\frac{20}{60}$	$\frac{1}{s}$	enzymatic reaction rate	[5]
γ_M	$\frac{0.411}{60}$	$\frac{1}{s}$	degradation lacZ mRNA	[5]
γ_B	$\frac{8.331e-4}{60}$	$\frac{1}{s}$	degradation β-Galactosidase	[5]

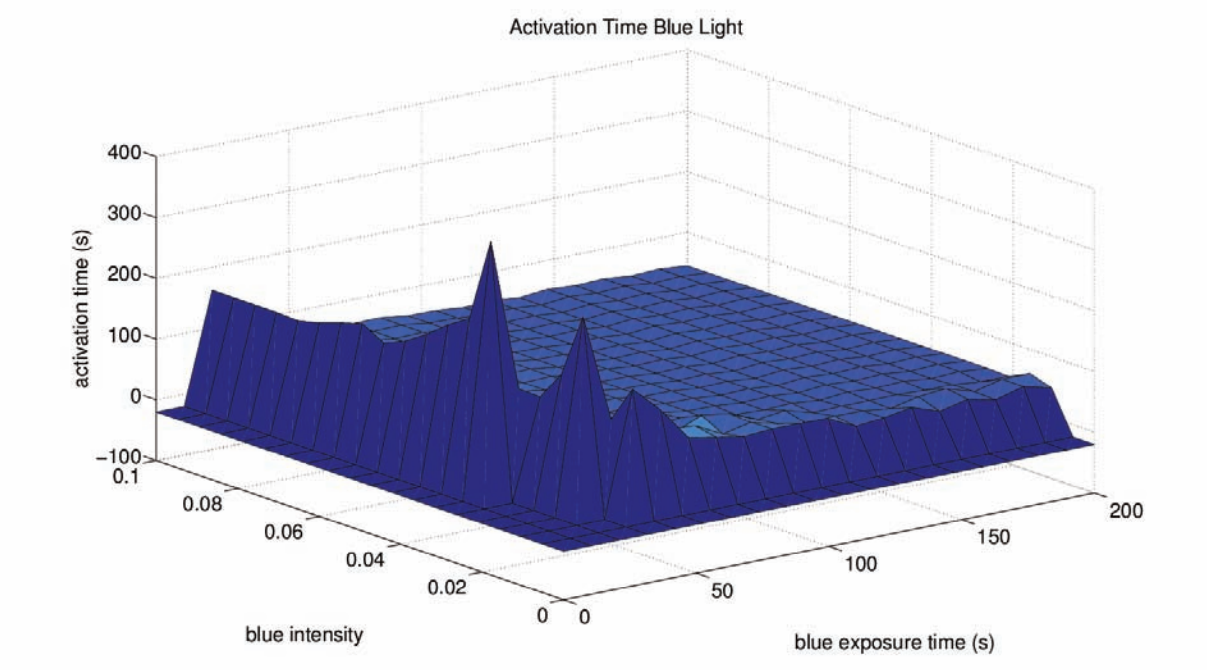
4. Initial Data

Name	Variable	Initial Value	Comment	Source
$YcgF_{mRNA}$	x_1	$\frac{k_1}{\gamma_{mRNA}}$	steady state	
$YcgF_{inactive}$	x_2	$\frac{k_3}{\gamma_{Protein}}\frac{k_1}{\gamma_{mRNA}}$	steady state	
$YcgF_{dimer}$	x_3	0		
$YcgE_{mRNA}$	x_4	$\frac{k_2}{\gamma_{mRNA}}$	steady state	
$YcgE$	x_5	$\frac{k_4}{\gamma_{Protein}}\frac{k_2}{\gamma_{mRNA}}$	steady state	
$YcgE.YcgF$	x_6	0		
$lacZ_{mRNA}$	x_7	0		
$\beta - Galactosidase$	x_8	0		
dye	x_9	0		

5. Simulation

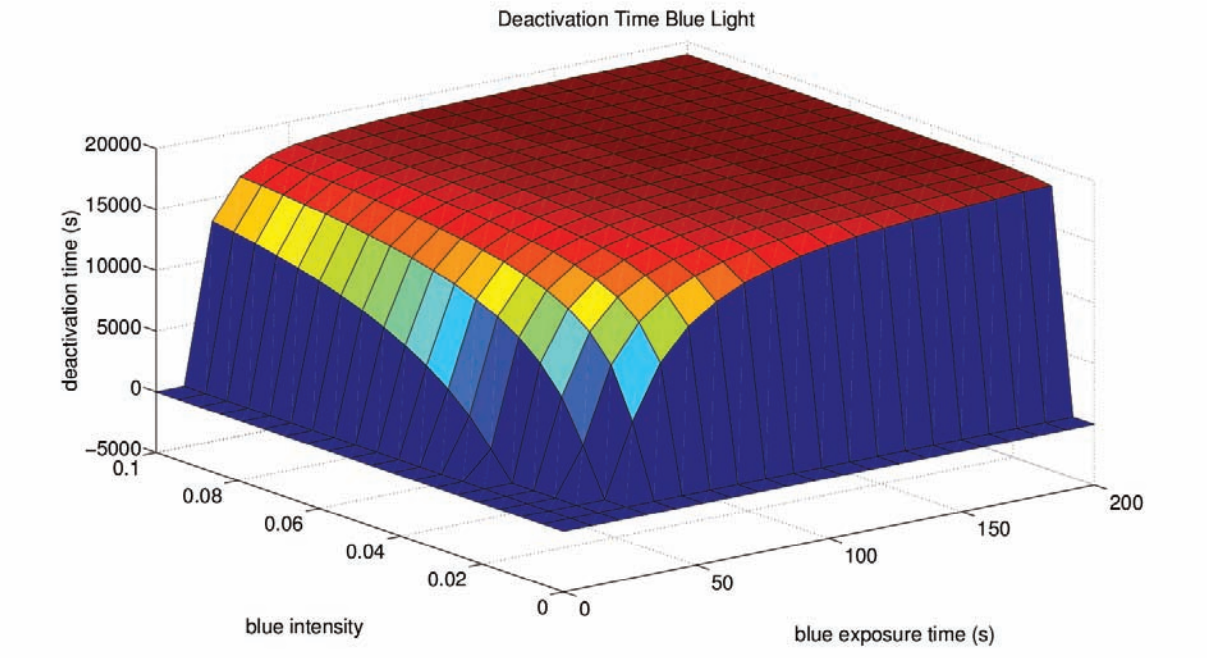
The goal of the simulation was to investigate the dependence of the of the activation time and deactivation time as well as the output of dye on the irradiation time and the irradiation intesity.

The range of both were adapted such that further increase would lead to no qualitative change.



We see that the activation time only depends on the exposure time, not on the intensity which should **not** coincide with the real world behavior.

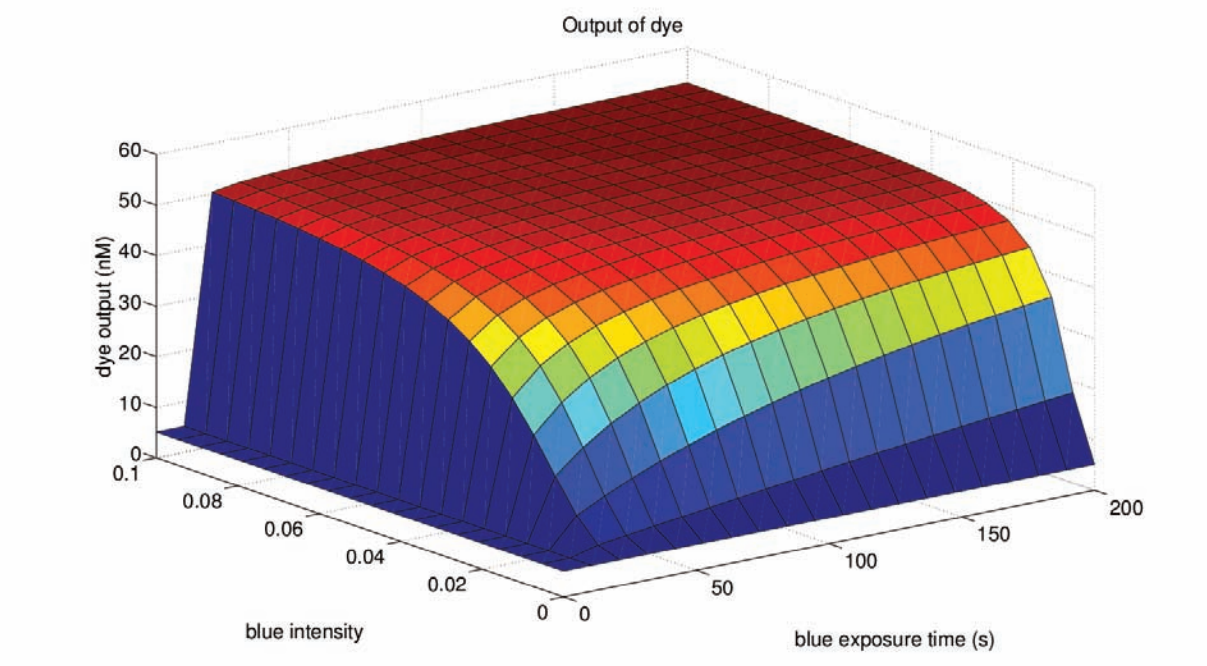
The deactivation time is defined as the timespan that the mRNA concentration needs to again drop below the threshold of $0.5nM$ after expiration of the exposure time.



We see that the deactivation time reaches its upper bound quite fast with respect to both intensity and exposure time. This is due to the fact that the reaction is quite fast and

that the two steady states of the bistable behavior are affected by neither intensity nor exposure time. Hence more time is needed to dephosporelate all OmpR and drop the mRNA concentration below the threshold.

The final point of interest is the total output of dye. For this the value of $x_{10}(40000)$ was used. Although this might not be the final output of the system, it should be a rough approximation.



Again the output reaches its steady state quite fast in respect to both variables for the same reasons as stated above.

6. Conclusion

We can observe that the system reaches its steady states quite fast for sufficiently high intensity and exposure time. For our final system the deactivation time defines the minimum recommended time between two single excitation of focused points. Hence maximum intensity and minimal exposure time is desirable.

References

1. KU Leuven 2009, *Blue light receptor: Modeling*, 2009.
2. Yusuke Nakasone, Taka-aki Ono, Asako Ishii, Shinji Masuda, and Masahide Terazima, *Temperature-sensitive reaction of a photosensor protein ycgf: Possibility of a role of temperature sensor*, Biochemistry **49** (2010), no. 10, 2288–2296, PMID: 20141167.
3. Tschowri, Natalia and Busse, Susan and Hengge, Regine, *The BLUF-EAL protein YcgF acts as a direct anti-repressor in a blue-light response of Escherichia coli*, Genes and Development **23** (2009), no. 4, 522–534.
4. Y. Nakasone and T. Ono and A. Ishii and S. Masuda and M. Terazima , *Trans. Dim. and Conf. Change of a BLUF Protein YcgF*, Journal of the American Chemical Society **129** (2007), no. 22, 7028–7035.

5. N Yildirim, M Santillan, D Horike, and MC Mackey, *Dynamics and bistability in a reduced model of the lac operon*, CHAOS **14** (2004), no. 2, 279–292 (English).