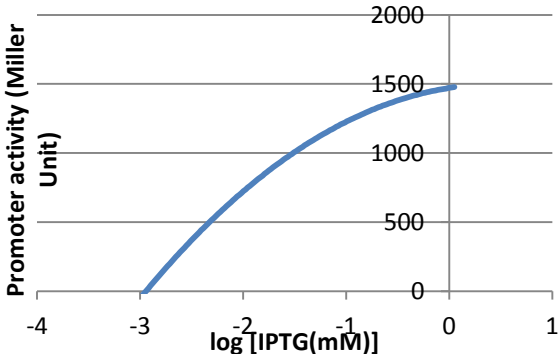
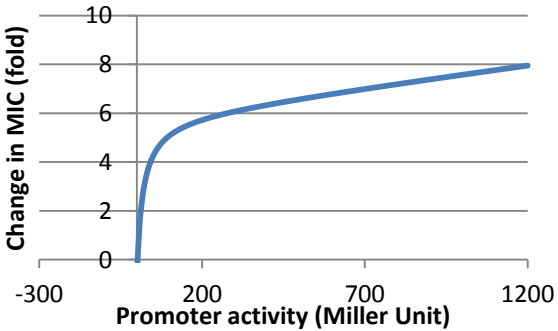
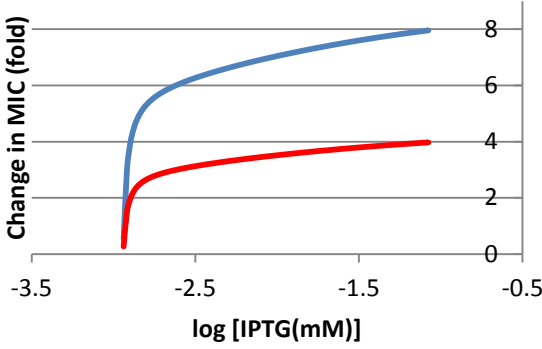
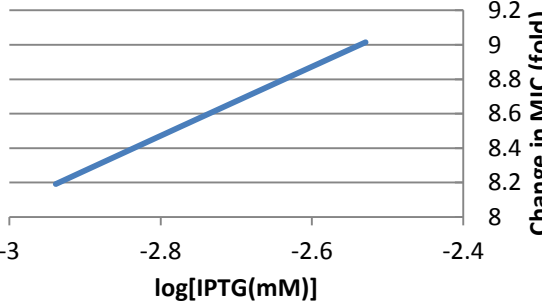


## Collaboration

We are glad to cooperate with HKUST on modeling the hypothetical behavior of *bcr* gene if driven by a *lac* or T7 promoter. *bcr* is a membrane protein that actively pumps out a variety of substrates from the cell, notably being antibiotics such as tetracycline and kanamycin. Hence, expression of *bcr* leads to antibiotic resistance. The collaboration was made because of the similarity between halorhodopsin and *bcr* - both are active cell membrane transporters, and our familiarity with such scenario.

## Modeling results

<p>1. <i>lac</i> promoter activity vs. IPTG</p>	 <p>The graph plots Promoter activity (Miller Unit) on the y-axis (0 to 2000) against log [IPTG(mM)] on the x-axis (-4 to 1). A blue curve shows a sigmoidal increase in activity as IPTG concentration increases, starting near zero at log [IPTG(mM)] = -3 and reaching approximately 1500 Miller Units at log [IPTG(mM)] = 0.</p>	<p>Curve fitting using one-site total binding model from experimental data [4], [5].</p>
<p>2. Activity of native promoter [1] of <i>bcr</i> (<i>acrAp+acrBp</i>) vs. change in MIC  (Blue - Tetracycline)</p>	 <p>The graph plots Change in MIC (fold) on the y-axis (0 to 10) against Promoter activity (Miller Unit) on the x-axis (-300 to 1200). A blue curve shows a sigmoidal increase in MIC fold as promoter activity increases, starting at 0 for negative promoter activity and reaching approximately 8 fold at 1200 Miller Units.</p>	<p>Curve fitting using one-site total binding model from experimental data [3], [6].</p>

<p>3. Change in MIC vs. IPTG (lac promoter construct)</p> <p>(Blue - Tetracycline; Red - Kanamycin)</p>		<p>By substituting the result of the 1<sup>st</sup> graph to the 2<sup>nd</sup> graph.</p>
<p>4. Change in MIC (effect of using other promoters)</p>	<p>BBa_K568003 (T7 promoter)</p> 	<p>By promoter activity data from [7] and feed into the 2<sup>nd</sup> graph.</p>

## Assumptions

- Steady-state approximation: bacteria were already transformed with the *plac+bcr* construct and are undergoing or have undergone the exponential phase, before exposing to the antibiotics.
- The inclusion of *plac* does not alter the metabolism in any other ways except expression of *bcr*.
- The addition of IPTG does not affect the bacteria in any other ways except inducing *plac*.

## Major insights and highlights from modeling results

- Only a small amount of IPTG is required to induce the *bcr* to the extent where the bacteria shows antibiotic resistance similar to that seen in the wild type. However, further increase in IPTG has a much weaker effect on the strength of antibiotic resistance. This is probably due to the toxicity of antibiotics other than their main mode of action, at higher concentrations.

## Reference

- [1] RegulonDB  
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- [3] Increased expression of the multidrug efflux genes *acrAB* occurs during slow growth of *Escherichia coli*  
FEMS Microbiology Letters Volume 207, Issue 1, pages 91–95, January 2002
- [4] [http://www.expressys.com/main\\_applications.html](http://www.expressys.com/main_applications.html)
- [5] [http://partsregistry.org/Part:BBa\\_R0010:Experience](http://partsregistry.org/Part:BBa_R0010:Experience)
- [6] Analysis of a Complete Library of Putative Drug Transporter Genes in *Escherichia coli*  
J Bacteriol. 2001 October; 183(20): 5803–5812.
- [7] [http://2011.igem.org/Team:TU\\_Munich/lab/results](http://2011.igem.org/Team:TU_Munich/lab/results)