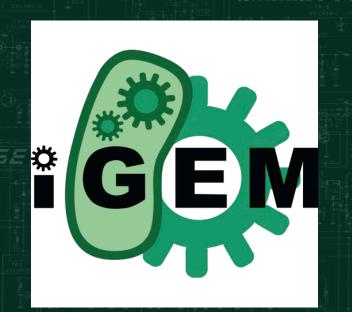
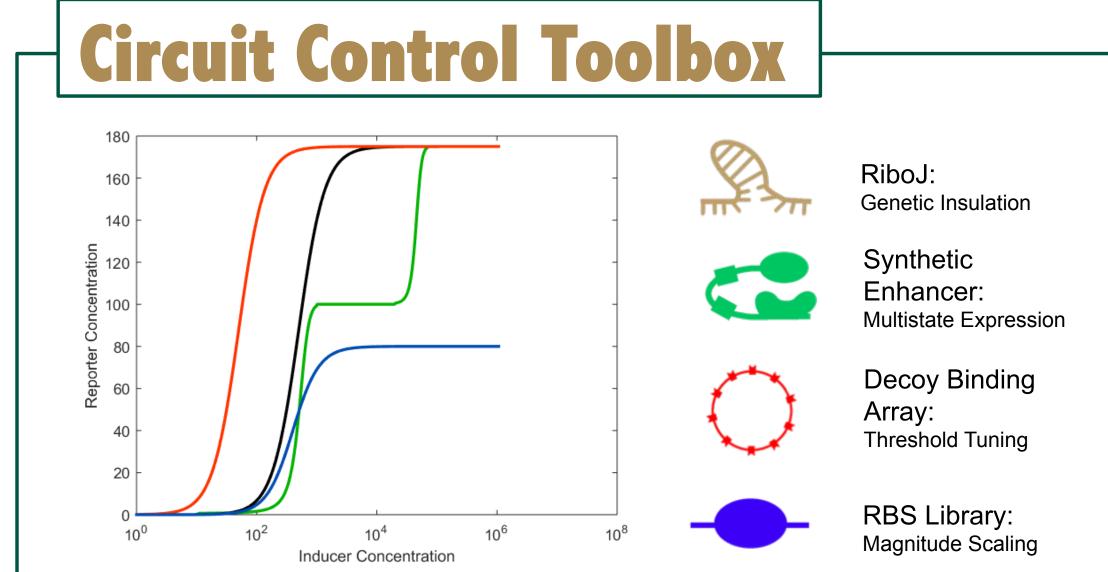


The Circuit Control Toolbox



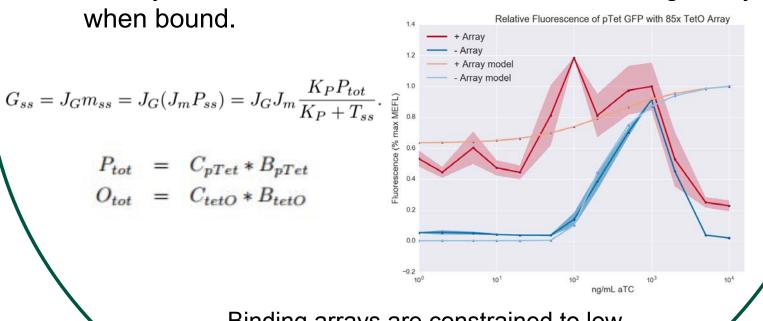
Kalen Clifton, Christine Gao, Ethan Jones, Likhitha Kolla, Joseph Maniaci, John Mitchell, Callan Monette, Adam Reiss, Andrew Halleran, Gregory D. Smith*, Margaret S. Saha**

Department of Applied Science*, Department of Biology**, College of William and Mary, Williamsburg, VA



A central problem of synthetic biology is tuning a circuit's ultimate output without disrupting its underlying function. Our Circuit Control Toolbox provides teams with a suite of orthogonal parts which can be added to the end of an arbitrary circuit to induce modular and additive effects on its transfer function, without altering the original circuit architecture.

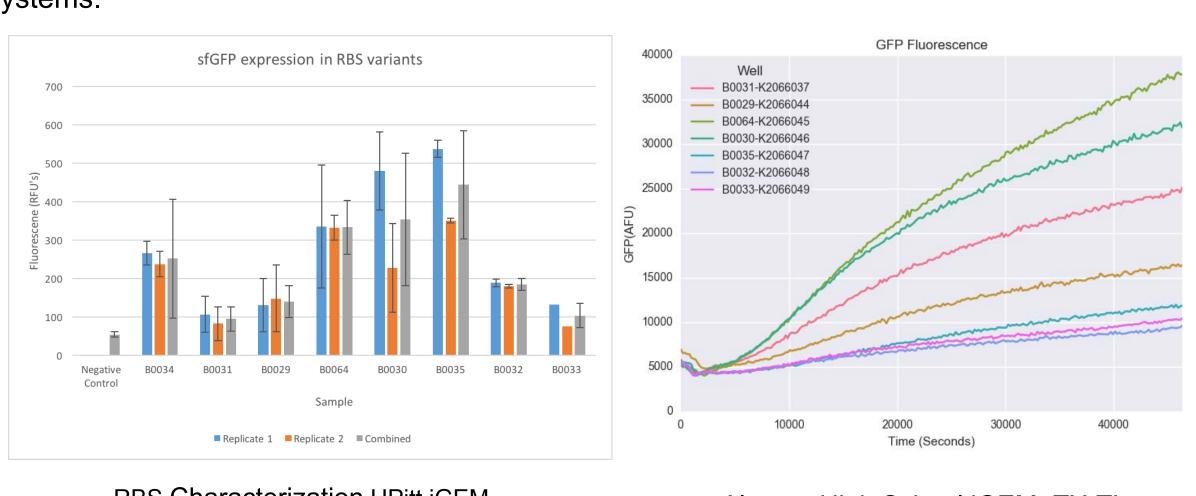
We developed a mathematical model parameterized by physiological values for Toolbox parts. Our kinetic ODE model of a basic GFP-expression system includes constitutively expressed TetR inhibiting GFP expression. Model accounts for the presence of decoy TetO arrays, and activity of aTC, which disables TetR's DNA-binding ability



Binding arrays are constrained to low copy models as a high copy introduces intrinsic metabolic strain.

Collaborations

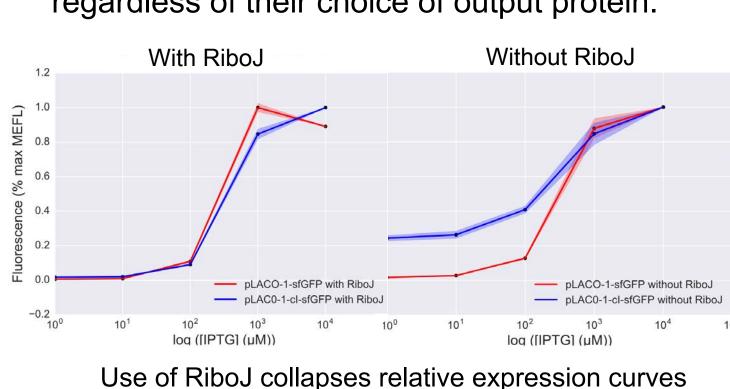
We collaborated with UPitt and Alverno's iGEM teams to characterize RBS strength in cellfree systems. We sent blinded versions of our RBS characterization devices to University of Pittsburgh and Alverno High School's iGEM team, who characterized the devices in S30 and TX-TL, respectively. Both teams' results were generally consistent with ours and previous characterization efforts, but the B0064 RBS was found to be stronger in both cell-free systems



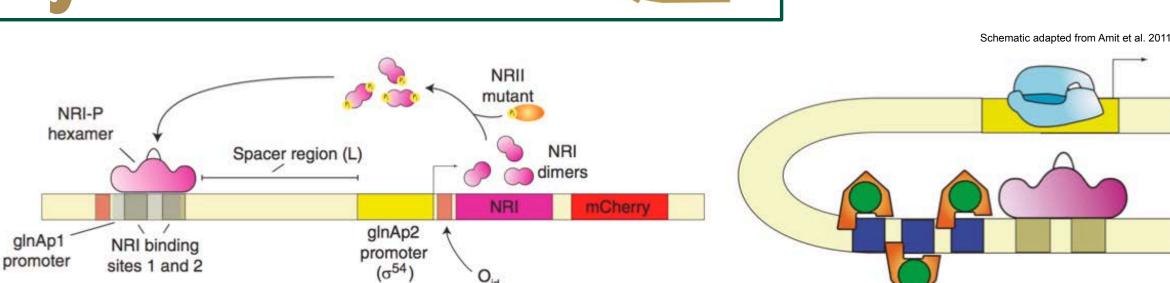
RBS Characterization UPitt iGEM-S30 system

Alverno High School iGEM- TX-TL

The self cleaving ribozyme RiboJ standardizes the 5' UTR of the transcript, causing the normalized transfer functions of circuit components to be invariant to the choice of protein coding sequence⁴. This insulation ensures that our Toolbox and its modifications are applicable to arbitrary genetic circuits, regardless of their choice of output protein.



Synthetic Enhancer

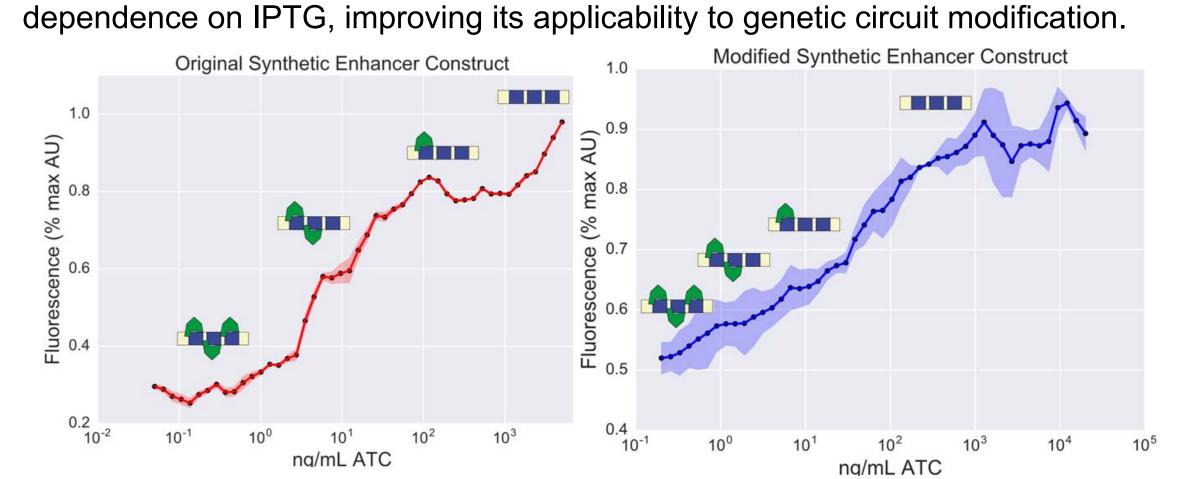


A new iGEM backbone

standard designed for

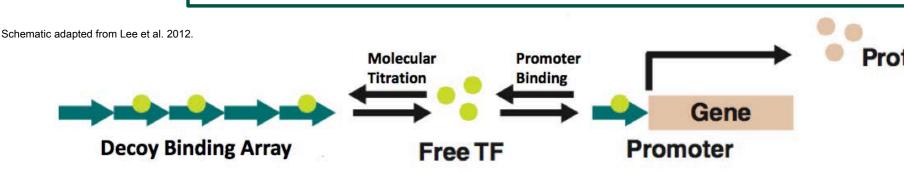
Gibson Assembly

The synthetic enhancer construct allows genes to exhibit multi-state transfer functions where each state corresponds to a distinct number of proteins bound to a binding cassette in the spacer region. We improved on the synthetic enhancer construct by combining its essential components into one plasmid and removing its

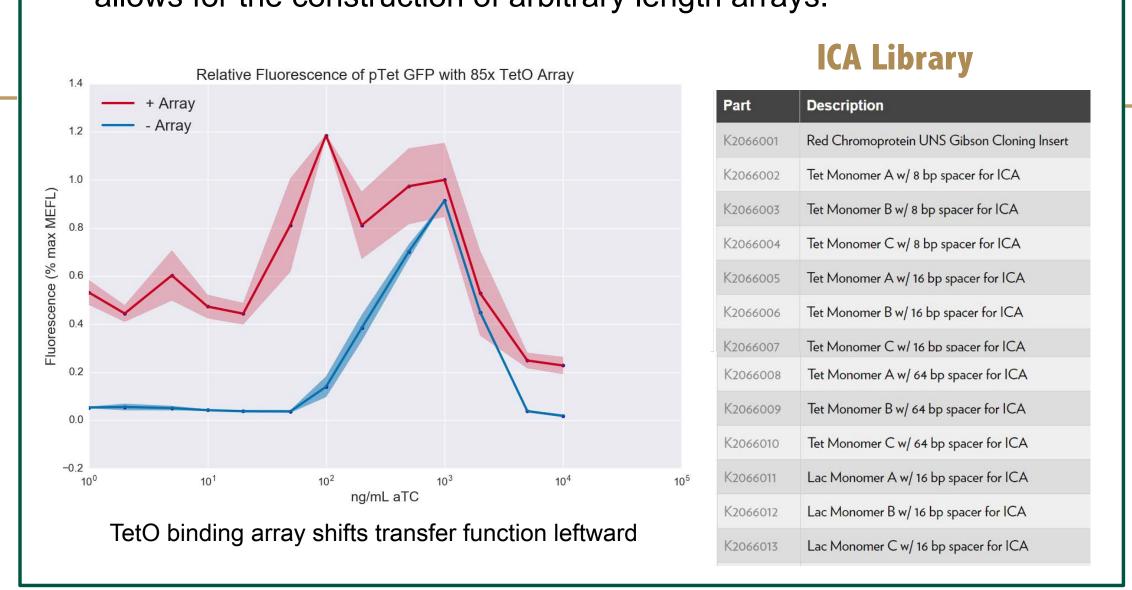


Original plasmids were a gift from the Amit Lab. Modified plasmid contains enhancer and helper circuits on a single UNS backbone

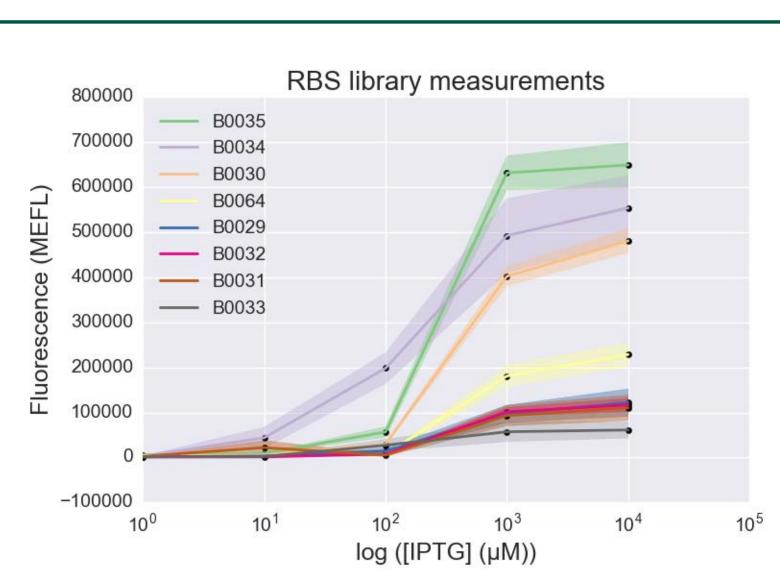
Decoy Binding Array



Transcription Factors can be titrated out using Decoy Binding Arrays. This titration shifts the threshold of a given transfer function, allowing for tuning of the sensitivity of a given circuit to an arbitrary transcription factor. The magnitude of the shift is determined by the number of binding sites, and our ICA library allows for the construction of arbitrary length arrays.



RBS Characterization —



We characterized the community library of RBSs using a standardized reporter construct that is driven by an inducible promoter and contains RiboJ upstream of the RBS sequence. This device allows for characterization of RBS strength over a dynamic range of transcriptional activity while also standardizing the 5' UTR of the transcript through RiboJ insulation to remove the influence of promoter choice on the results of the characterization.



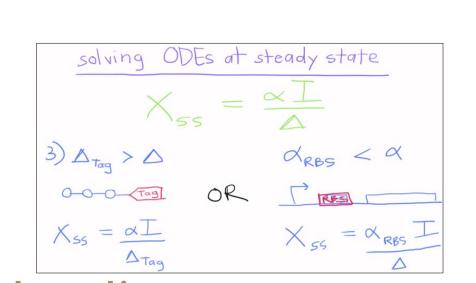
Building With Biology Workshop

We held a science workshop targeted at at local children and their parents, where we performed scientific activities and discussed our questions and concerns with GMOs



CRISPR/Cas9 Forum

We invited the Williamsburg community to discuss the implications and ethics of genome editing in bioremediation, medicine. agriculture, and biotechnology.

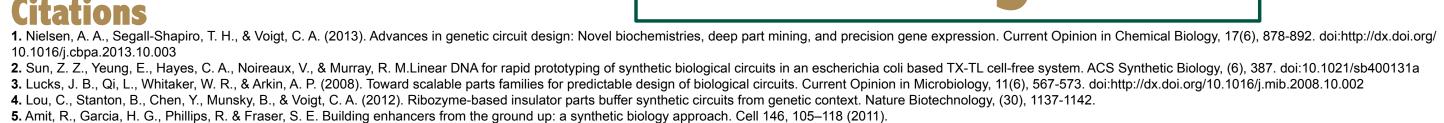


Learnsynbio.org

into the classroom.

We built a website to host our instructional videos and educational materials to introduce high school students to the ideas in Synthetic Biology, with a focus on integrating mathematical modeling. We collaborated with high school teachers to ensure the easy integration of our materials

- Built and characterized the Circuit Control Toolbox, which allows future teams to have precise, modular control over their circuits' behavior with targeted, orthogonal modifications that are applicable to arbitrary circuits.
- The Toolbox contains 118 parts on the UNS backbone standard, including: A library of monomers to build binding arrays of arbitrary length.
 - A standardized RBS characterization device for rigorous measurement of RBS effects over dynamic gene expression levels.
 - An improved synthetic enhancer construct designed for compatibility with gene circuit integration.
 - Created a website, LearnSynBio.org, designed to promote and teach synthetic biology to high school students with an explicit focus on integrating mathematical modeling.



6. Brewster, R. C., Weinert, F. M., Garcia, H. G., Song, D., Rydenfelt, M., & Phillips, R. (2014). The transcription factor titration effect dictates level of gene expression. Cell, 156(6), 1312. doi:10.1016/j.cell.2014.02.022 7. Castillo-Hair, S. M., Sexton, J. T., Landry, B. P., Olson, E. J., Igoshin, O. A., & Tabor, J. J. (2016). FlowCal: A user-friendly, open source software tool for automatically converting flow cytometry data from arbitrary to calibrated units. ACS synthetic

8. Daniel, R., Rubens, J. R., Sarpeshkar, R., & Lu, T. K. (2013). Synthetic analog computation in living cells. Nature, 497, 619-623. doi:doi:10.1038/nature12148 9. Milo, R., Phillips, R., & Orme, N. (2015). Cell biology by the numbers. Garland Science 10. Nielsen, A. A., Segall-Shapiro, T. H., & Voigt, C. A. (2013). Advances in genetic circuit design: Novel biochemistries, deep part mining, and precision gene expression. Current Opinion in Chemical Biology, 17(6), 878-892. doi:http://dx.doi.org/

11. Pothoulakis, G., Ceroni, F., Reeve, B., & Ellis, T. (2014). The spinach RNA aptamer as a characterization tool for synthetic biology. ACS Synthetic Biology, 3(3), 182-187. doi:10.1021/sb400089c 12. So LH, Ghosh A, Zong C, Sepu'Iveda LA, Segev R, Golding I. General properties of transcriptional time series in Escherichia coli. Nat Genet. 2011 Jun43(6):554-60 13. Torella, J. P., Boehm, C. R., Lienert, F., Chen, J., Way, J. C., & Silver, P. A. (2014). Rapid construction of insulated genetic circuits via synthetic sequence-guided isothermal assembly. Nucleic Acids Research, 42(1), 681-689. doi:doi:10.1093/nar/

14. Briggs, A. W., Rios, X., Chari, R., Yang, L., Zhang, F., Mali, P., & Church, G. M. (2012). Iterative capped assembly: rapid and scalable synthesis of repeat-module DNA such as TAL effectors from individual monomers. Nucleic Acids Research, 15. Harnessing mutagenic homologous recombination for targeted mutagenesis in vivo by TaGTEAM. Finney-Manchester SP, Maheshri N. *Nucleic Acids Res. 2013 Mar* 7. 10.1093/nar/gkt150 PubMed 23470991 16. Lee, T., & Maheshri, N. (2012). A regulatory role for repeated decoy transcription factor binding sites in target gene expression. *Molecular Systems Biology, 8.* doi:10.1038/msb.2012.7

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