Robert G. Egbert

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Research interests

synthetic biology, optimizing engineered gene networks, evolvable gene networks, control systems engineering.

Education

University of Washington, Seattle, WA, USA.
Ph.D. in Electrical Engineering. August 2012.
Thesis title: Fine-tuning engineered gene regulatory networks expressed in *Escherichia coli* using hypervariable simple sequence repeats.
Thesis advisor: Eric Klavins, Electrical Engineering, UW.
Thesis committee: Ben Kerr (Biology, UW), Jennifer Nemhauser (Biology, UW), Georg Seelig (Computer Science and Engineering, UW), and Paul Wiggins (Physics/Bioengineering, UW).

Brigham Young University, Provo, UT, USA.
B.S. in Electrical Engineering. August 2003.
B.A. in Korean Studies. August 2003.

Research Experience

Research Assistant, Electrical Engineering Department, University of Washington.

- Devise and carry out research projects to construct gene networks in *Escherichia coli* that perform to meet design specifications.
- Advise graduate students and undergraduate researchers on best practices for experimental design and efficient cloning strategies.
- Assisted in building up efficient wet lab operations through core protocol development for DNA assembly and strain engineering, as well as equipment procurement for Klavins Lab.

Publications

Egbert, RG & Klavins, E (2012). Fine-tuning gene networks using simple sequence repeats. *Proc Natl Acad Sci USA doi:10.1073/pnas.1205693109*.

Jang SH, Oishi KT, Egbert RG, Klavins E (2012). "Specification and simulation of synthetic multicelled behaviors." *ACS Synth Biol* 1:365-374.

Harger M, Zheng L, Moon A, Ager C, An JH, Choe C, Lai E, Mo B, Zong D, Smith M, Egbert R, Mills J, Baker D, Swanson-Pultz I, Siegel J. "Expanding the Product Profile of a Microbial Alkane Biosynthetic Pathway." Submitted 2012.

Talks & Posters

Egbert RG "Fine-tuning engineered gene networks using simple sequence repeats." Invited talk at the Molecular Programming Project Retreat, Oxnard, CA, USA (08/2012).

Egbert RG "Predictable tuning of gene networks with simple sequence repeats." Invited talk at The 3rd International Workshop on Stochasticity in Biochemical Reaction Networks, Banff, Canada (09/2011).

Egbert RG "Tuning gene networks with simple sequence repeats." Contributed speaker at The Fifth Annual q-bio Conference on Cellular Information Processing, Santa Fe, NM, USA (08/2011).

Egbert RG, Klavins E "Tuning gene networks with simple sequence repeats in the ribosome binding site." Poster presentation at SB5.0: The Fifth International Meeting on Synthetic Biology, Stanford, CA, USA (06/2011).

Teaching

Co-instructor, Laboratory Methods in Synthetic Biology. Managed the design, assembly, and testing progress of 15 students working on five unique projects to engineer an ultrasensitive molecular detector in *E. coli*.
Co-instructor: Eric Klavins; winter 2012.

Guest lecturer for cellular and molecular biology course in Pharmaceutical Bioengineering program: "The magnetosome toolkit: porting an organelle for biofabrication of magnets to *E. coli*"
Instructor: Mark Minie; February 2012.

Course planning, Biocircuits wet lab
Instructor: Eric Klavins; spring 2010.

Teaching Assistant, Biocircuits wet lab
Instructor: Eric Klavins; spring 2009.
Link: http://soslab.ee.washington.edu/biocircuits/index.php?title=Main_Page

Advisor, UW iGEM team, 2008-2011. Specifically advised groups for Gibson Assembly toolkit and Magnetosome toolkit (see http://2011.igem.org/Team:Washington).

Honors and Awards

National Science Foundation Graduate Research Fellowship (2007-2010)
National Defense Science and Engineering Graduate Fellowship (2007, declined)
Brigham Young University Trustees Scholarship (1996-1998, 2000-2002)

Research Skills

- Engineering functional gene networks: Combinatorial plasmid (PCR, gene synthesis, Gibson assembly) and genome engineering (recombineering, MAGE) to fine-tune gene network behaviors using sequence libraries
- Cell-based experimental assays: single cell fluorescence (cytometry, time-lapse microscopy); batch culture (plate reader, solid media); and enzymatic activity (MUG for LacZ, Congo Red staining for cellulase)
- Modeling and data analysis: segmentation algorithms for time-lapse microscopy (Matlab); image processing of agar plates for colony size and fluorescence (Matlab); sequence trace analysis of evolvable sequences (Mathematica); ODE analytical models (Mathematica); and stochastic simulations (Mathematica, **gro**)

References

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