CURRICULUM VITAE

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EDUCATION

2010	Physics	Ph.D.	University of Maryland, College Park
2005	Liberal Arts	B.A., Plan II Honors	University of Texas, Austin
2005	Physics	B.S., Special Honors	University of Texas, Austin

POSTDOCTORAL TRAINING

2010 –	Computational Biology	Dana-Farber Cancer Institute, Boston, MA

HONORS AND DISTINCTIONS

2006 – 2009	Full Scholarship	University of Maryland
2006 – 2009	Cancer Education Research Training Award	NIH
2005 – 2006	Excellence in Teaching Award	University of Maryland
2005	Dean's Graduate Fellow Award	University of Maryland
2005	Physics Scholarship Recipient	University of Texas
2001 – 2003	Ford Scholarship Recipient	University of Texas
2001 – 2003	Friends of Alec Scholarship Recipient	University of Texas

PROFESSIONAL SOCIETITES

2003	American Physical Society Member
2003	Sigma Pi Sigma, Lifetime Member
2002	Golden Key Honor Society Member
2002	Gamma Beta Phi Member

TEACHING EXPERIENCE

2009	Co-instructor	Hands-On Research Complex Systems Summer School, UFABC, Sao Paulo, Brazil

Prepared material for three-hour lab course on studying networks using Matlab. Sections consisted of 10-15 selected international students with various educational backgrounds. Answered questions and monitored student progress.

2006	Teaching Assistant	University of Maryland

Prepared material for and taught both study and lab sections for a course on mechanical physics for pre-med students. Sections consisted of 45-50 university students.

2005	Teaching Assistant	University of Maryland

Monitored lab work for two sections of 15-20 undergraduate physics majors. Course on data analysis.

MAJOR RESEARCH INTERESTS

My research has focused on understanding gene regulation, especially in the context of regulatory networks, initially as a graduate student and currently as a postdoc. During my graduate work I explored the network structure of the Gene Ontology while simultaneously studying protein binding in the context of epigenetic modifications via ChIP-chip and protein-binding-microarray assays. As a postdoctoral fellow, I have merged this appreciation of biological function with gene regulation. I have developed and applied a model that integrates different sources of regulatory information in order to predict a gene regulatory network. My broad research interests include regulatory networks, network structure, understanding how different types of data can be understand in a network context as well as how exploring how biological mechanisms and contexts affect regulatory network structures. My current research focuses on enhancing the understanding of gene regulation by integrating different sources of regulatory information into one model.

FUNDED GRANT PROPOSALS

"Using Networks to Assign Gene Function in Lung Disease" (1 R01 HL111759-01A1)

REVIEWER OF ARTICLES FOR:

PLoS Computational Biology
Physical Review A
BMC Bioinformatics
Frontiers in Bioscience

BIBLIOGRAPHY

Peer-reviewed Publications

1. Rozenberg JM, Bhattacharya P, Chatterjee R, **Glass K**, Vinson C. Combinatorial recruitment of CREB, C/EBPb and Jun determines activation of promoters upon keratinocyte differentiation. (in press, PLoS One, as of September 2013)

2. Black J*, Manning A*, Van Rechem C*, Kim J*, Ladd B¥, Cho J¥, Pineda C, Murphy N, Daniels D, Montagna C, Lewis P, **Glass K**, Allis C, Dyan N, Getz G, Whetstine J. Lysine Demethylase KDM4A Promotes Site Specific Copy Gain and Re-replication of Regions Amplified in Human Tumors. Cell. 2013 Jul 16. pii:S0092-8674(13)00833-7. Doi: 10.1016/j.cell.2013.06.151. [Epub ahead of print]

3. **Glass K**, Huttenhower C, Quackenbush J, Yuan GC. Passing Messages Between Biological Networks to Refine Predicted Interactions. PLoS One. 2013 May 31;8(5):e64832.

4. Baena E, Shao Z¥, Linn D¥, **Glass K**, Hamblen M, Fujiwara Y, Kim J, Saumyadipta P, Nguyen M, Zhang X, Godhino F, Bronson R, Mucci L, Loda M, Yuan GC, Orkin S, Li Z. ETV1 directs androgen metabolism and confers aggressive prostate cancer in targeted mice and patients. Genes and Development. 2013 Mar 15;27(6):683-98. PMID#23512661

5. Xu J*, Shao Z*, **Glass K**¥, Bauer D¥, Pinello L, Van Handel B, Hou S, Stamatoyannopoulos J, Mikkola H, Yuan GC, Orkin S. Developmental Stage-Specific Enhancers Control Gene Expression Programs during Human Erythropoiesis. Developmental Cell. 2012 Oct 3:S1534-5807(12)00414-5. PMID#23041383

6. **Glass K**, Ott E, Losert W, Girvan M. Implications of functional similarity for gene regulatory interactions. Journal of the Royal Society Interface. 2012 Jul 7;9(72):1625-36. PMID# 22298814

7. Warren CL, Zhao J, **Glass K**, Rishi V, Ansari A, Vinson C. Fabrication of duplex DNA microarrays incorporating methyl-5-cytosine. Lab on a Chip. 2012; 12(2):376-380. PMID# 22139143

8. Chatterjee R, Bhattacharya P, Gavrilova O, **Glass K**, Moitra J, Myakishev M, Pack S, Jou W, Feigenbaum L, Eckhaus M, Vinson C. Suppression of the C/EBP family of transcription factors in adipose tissue causes lidodystrophy. Journal of Molecular Endocrinology. 2011; 46(3):175-92. PMCID# 21321096

9. Rishi V*, Bhattacharya P*, Chatterjee R*, Rozenberg JM*, Zhao J*, **Glass K**, FitzGerald PC, Vinson C. CpG methylation of half-CRE sequences creates C/EBPα binging sites that activate some tissue-specific genes. Proc Nat Academy of Science 2010; 107(47):20311-6. PMCID# 21059933

10. Rozenburg JM, Shlyakhtenko A, **Glass K**, Rishi V, Myakishev M, FitzGerald PC, Vinson C. All and only CpG containing sequences are enriched in promoters abundantly bound by RNA polymerase II in multiple tissues. BMC Genomics 2008; 9:67. PMCID# 18252004

Evidence of Works in Progress

1. **Glass K**. Patterns and Complexity in Biological Systems: A study of Sequence Structure and Ontology-based Networks. (Thesis, published by the University of Maryland, College Park, May 2010).

2. **Glass K**, Girvan M. Annotation Enrichment Analysis: An Alternative Method for Evaluating the Functional Properties of Gene Sets. (currently under revision, manuscript available at http://arxiv.org/abs/1208.4127)

3. **Glass K**, Girvan M. Finding New Order in Biological Functions from the Network Structure of Gene Annotations. (currently under revision, manuscript available at http://arxiv.org/abs/1210.0024)

4. **Glass K**, Quackenbush J, Spentzos D, Yuan GC. *A Network Model of Angiogenesis in Ovarian Cancer.* (currently under revision, manuscript available upon request)