

Vincent VanBuren, PhD  
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Systems Biology and Translational Medicine  
Texas A & M HSC College of Medicine  
702 SW HK Dodgen Loop  
Temple, TX 76504

**Rank:**

Assistant Professor

**Education:**

B.S., Biology, 1994, Cedar Crest College, Allentown, PA

Ph.D., Molecular Biology, 2002, Lehigh University, Bethlehem, PA

Postdoctoral Fellow, Bioinformatics, 2002-2006, National Institute on Aging, Baltimore, MD

**Professional Appointments:**

**Assistant Professor**, 2006-Present, Department of Systems Biology and Translational Medicine, **Texas A & M Health Science Center College of Medicine**, Temple, TX

**Teaching Performance**

**Summary for Year: 2008**

Number of hours

Lectures taught

SBTM616: Computational Systems Biology I  
Graduate level, Lecture, 4 credit hours,  
3 students

26 contact hours

**Summary for Year: 2007**

Laboratories taught

MSCI 685, Directed Studies: Medical Sciences,  
Graduate level, Laboratory, 3 credit hours,  
1 student

12 contact hours

## Summary for Year: 2006

### Lectures taught

MPHY 601, Methods in Cell Physiology, 5 contact hours  
Graduate level, Lecture, 3 credit hours, 7 students

### Course Coordination

<b>Coordinator</b> , SBTM 681, Seminar, Graduate level, 1 credit hour 2007,	Summer Summer 2008
<b>Co-Coordinator</b> , SBTM 616, Lecture, Graduate level, 4 credit hours	Fall 2008

### Curriculum and/or Course Development

Computational Systems Biology I, Member, sub-committee for curriculum development, 2007-2008. This course has been developed and was given for the first time in the fall of 2008.

Computational Systems Biology II, Member, sub-committee for curriculum development, 2007

Introduction to Systems Biology, Member, sub-committee for curriculum development, 2007

### Teaching Materials Developed

Developed a wiki for dissemination of lecture materials, readings, and coding examples for SBTM616, Computational Systems Biology I.

### Student/Trainee Supervision

Fellows/Postdoctoral/Residents/ /Visiting Scientist

**Daniel C. Jupiter, Ph.D.:** Postdoctoral Research Associate (August 2006-present)

**Hung-Chung (Joe) Huang, Ph.D.:** Assistant Research Scientist (January 2007-present)

## Graduate Student Supervision

**Hailin Chen:** first year graduate student rotation in the VanBuren lab, fall 2008.

**Jennifer Griffin:** first year graduate student rotation in the VanBuren lab, fall 2008.

## Graduate Faculty Membership

College of Medicine: Cell and Molecular Biology, Systems and Translational Biology tracks

## Research and Scholarly Activities

### Areas of research and scholarship

My work is focused in the field of computational systems biology, where computers are used in an effort to discover biological network topologies, and are used to model biological pathways to make predictions relevant to basic biology and to therapeutic applications important to human health. The field of systems biology represents a synergy between biological experimentation, biotechnological developments in generating high throughput data, and the development of computational algorithms that strive to make synthetic interpretations from the masses of data generated by these new technologies.

My early work in this area (in graduate school at Lehigh University) was in computational modeling of a macromolecular protein assembly called a microtubule, which is a structure essential for cell division. This structure's role in cell division has made it a central target of anti-cancer strategies, and my work contributed to a basic understanding of how microtubule binding agents could affect microtubule assembly properties, and thus affect their ability to function in cell division.

Following this, my postdoctoral work at the National Institute on Aging was in the area of bioinformatics, and involved analysis and annotation of cDNA (gene fragment) collections that were derived from early mouse embryos and stem cells. This work helped to provide a large well-annotated set of reagents to the research community, particularly to those interested in stem cell biology and early developmental processes. Additionally, I worked on the problem of predicting absolute mRNA abundance using a technology called DNA microarrays. Microarrays are a high throughput technology for measuring the relative abundance of mRNA in a sample as compared with a different sample. It would be a tremendous advantage if the data could be used to make predictions

about the actual number of mRNA molecules instead of a relative measure, as knowledge of actual copy number would trivialize the comparison of different experiments by different labs, and would allow for detailed modeling of mRNA population fluctuations and modeling of the regulatory influences on these molecules.

As an independent investigator in the Department of Systems Biology and Translational Medicine, I have developed a research program that emphasizes reconstruction of biological networks from high-throughput data and modeling the emergent behavior of stochastic biological systems. In these efforts my research group has recently published work showing how a single X-Ray crystal structure can be used as a starting configuration in a molecular dynamics simulation, where frames of the simulation can be used to identify water clusters in the active site of an enzyme. Such water clusters are useful markers for synthesizing modified substrates that displace the stable water cluster and thus interfere with enzyme action by interacting with the active site more strongly than the unmodified substrate. This has application in the area of drug design. Previous efforts in this area required the use of multiple crystal structures; our method has a clear advantage over the laborious acquisition of crystal structures.

DNA microarrays give us data on the expression of thousands of genes in a single experiment. Although this has provided an excellent screening tool for investigators to identify genes affected by particular experimental conditions relative to other conditions, the data amassed by these experiments remain a challenge for many investigators to analyze, and data are not typically leveraged beyond the aims of the original experiment. We have created a new Web-based tool, StarNet (<http://vanburenlab.tamhsc.edu/starnet.html>), to address these issues. Briefly, we calculated Pearson correlation coefficients for all pair wise comparisons of genes across over 2000 microarrays from mouse experiments. This generated over 130 million correlation coefficients, and we made more tractable sub-distributions of the coefficients by collecting the highest (most interesting) correlations. StarNet provides a front end for visualizing correlation networks built from this data set, where the user supplies the central node (gene) for the network to be drawn. The idea of building these networks is one of "guilt by association", where gene product function may be tentatively assigned to unknown genes that have expression patterns that are similar to previously characterized genes.

The work I am pursuing in my research group is of central importance to systems biology. As we strive toward our aim of reconstructing biological networks, we will begin efforts to model the biochemical processes of these networks, and work towards experimental validation of our predictions.

## **Invited Presentations**

June 2008

*New Visual Data Mining Tools for the Systems Biology of Cancer.*  
Cancer Workshop #2, **Texas A & M Health Science Center and Texas A & M University.**

October 2007

*Visual data mining for reconstruction of transcription regulatory networks.* **Southwestern University**, Georgetown, TX.

April 2007

*Computational Systems Biology.* **Texas Bioscience Institute**, Temple, TX.

February 2007

*Simulation of Microtubule Self-Assembly Kinetics and Structure.* Department of Biomedical Engineering, **Texas A&M University**, College Station, TX..

March 2006

*Computational modeling of microtubule structure and self-assembly kinetics.* Department of Applied Sciences, **College of William and Mary**, Williamsburg, VA.

January 2006

*Preliminary studies in systems biology: reconstructing biological networks and building the Complementome.* (Temple) *Computational modeling of microtubule structure and self-assembly kinetics.* (College Station) Department of Systems Biology and Translational Medicine, College of Medicine, **Texas A&M University Health Sciences Center**, Temple, TX, and College Station, TX (2 talks).

December 2005

*Computational modeling of microtubule structure and self-assembly kinetics.* Department of Basic Medical Sciences, **College of Osteopathic Medicine of the Pacific**, Western University of Health Sciences, Pomona, CA.

June 2004

*Systems modeling and reconstruction of biological networks.* **H. Lee Moffitt Cancer Research Center**, University of Southern Florida, Tampa, FL.

May 2004

*Systems modeling: informatics infrastructure for basic research in regenerative medicine, and novel biological networks.* Department of Internal Medicine, **University of Michigan**, Ann Arbor, MI.

December 2003

*The fruits of computational biology: analysis, tools, models, and hypotheses.* Department of Biochemistry, **Robert Wood Johnson Medical School**, Piscataway, NJ.

August 2001

*Pseudomechanical simulation of microtubules and preliminary description of a full 3-D mechanical model of microtubule assembly.* Laboratory of Genetics, **National Institute on Aging, NIH**, Baltimore, MD.

October 2000

*A pseudomechanical model of microtubule dynamic instability.*  
Department of Biomedical Engineering, University of Minnesota,  
Minneapolis, MN. Department of Biomedical Engineering, **University of  
Minnesota**, Minneapolis, MN.

## **Grants**

Funded

### ***Reconstructing Biological Networks: Genetic Pathways Associated with Heart Development***

American Heart Association National Scientist Development Grant AHA  
SDG 0630263N.

Total direct and indirect costs: \$260,000

Dates of grant period: October 2006 – September 2010

Role: Principle Investigator

## **Manuscript Review**

Journals Refereed; Book/Chapter Review

Plant Physiology

Physics Letters A

## **Grant Reviews**

Study Section, Review Panel, Special Emphasis Panel

**NSF Review Panelist**, October 2006.

**NSF Review Panelist**, June 2008.

**Invited NSF Review Panelist (but could not participate due to  
conflict of interest)**, November 2008.

## **Professional and Scholarly Societies**

American Heart Association  
American Society for Cell Biology  
American Society for the Advancement of Science  
International Society for Computational Biology  
Life Sciences Society  
Sigma Xi

## **Institutional Service to the HSC**

### Component Committees

February 2007-Present

**Member, Pre- and Post-doctoral Training Program Assessment and Revision Committee**, Department of Systems Biology and Translational Medicine, Texas A&M HSC, Temple, TX.

February 2007-September 2008

**Chair, Faculty Oversight Committee for the Departmental Microarray Laboratory**, Department of Systems Biology and Translational Medicine, Texas A&M HSC, Temple, TX.

August 2006-February 2007

**Member, Faculty Oversight Committee for the departmental Microarray Core Facility**, Department of Systems Biology and Translational Medicine, Texas A&M HSC, Temple, TX.

August 2006-present

**Member, Faculty Committee for Biocomputing**, Department of Systems Biology and Translational Medicine, Texas A&M HSC, Temple, TX.

### Other Component Service

September 2006-September 2008

**Director, SBTM Microarray Laboratory**, Department of Systems Biology and Translational Medicine, Texas A&M HSC, Temple, TX.

August 2006-August 2007

**Seminar Coordinator, Cardiovascular Research Institute**, Texas A&M HSC, Temple, TX.

August 2007-Present

**Seminar Coordinator, Department of Systems Biology and Translational Medicine**, Texas A&M HSC, Temple, TX.

### HSC Committees

December 2007-Present

**Member, Graduate Admissions Committee**, Graduate School of Medical Sciences, Texas A&M HSC, Temple / College Station, TX.

## Publications

### Refereed Papers

1. **VanBuren, V.**, Odde, D.J., Cassimeris, L. (2002) *Estimates of Lateral and Longitudinal Bond Energies within the Microtubule Lattice*. **Proc Natl Acad Sci USA**, 99(9): 6035-40.

2. **VanBuren, V.**, Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Martin, P.R., Stagg, C.A., Bassey, U.C., Aiba, K., Hamatani, T., Kargul, G.J., Luo, A.G., Kelso, J., Hide, W., Ko, M.S.H. (2002) *Assembly, Verification, and Initial Annotation of the NIA Mouse 7.4K cDNA Clone Set*. **Genome Research**, 12:1999-2003.

3. Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y., **VanBuren, V.**, Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C., Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L., Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S., Nagaraja, R., Boheler, K.R., Taub, D., Longo, D.L., Schlessinger, D., Keller, J., Klotz, E., Kelsoe, G., Umezawa, A., Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L.M., Curci, A., D'Urso, M., Kelso, J., Hide, W., and Ko, M.S.H. (2003) *Transcriptome analyses yield gene sets correlated with developmental potential in mouse stem cells and early embryos*. **PLoS Biology**, 1(3): 410-419.

4. Carter, M.G., Piao, Y., Dudekula, D.B., Qian, Y., **VanBuren, V.**, Sharov, A.A., Tanaka, T.S., Martin, P.R., Bassey, U.C., Stagg, C.A., Aiba, K., Hamatani, T., Ko, M.S.H. (2003) *The NIA Mouse cDNA Project: Building a Gene Catalog of Mouse Stem Cells and Early Embryos*. **CR Biologies**, 326 (10-11): 931-940.

5. Hamatani T, Falco G, Carter MG, Akutsu H, Stagg CA, Sharov AA, Dudekula DB, **VanBuren V**, Ko MS. (2004) *Age-associated alteration of gene expression patterns in mouse oocytes*. **Hum Mol Genet**. 13 (19): 2263-2278. [Aug 18 Epub ahead of print].

6. **VanBuren, V.**, Cassimeris, L., Odde, D.J. (2005) *A mechanochemical model for microtubule structure and self-assembly kinetics*. **Biophysical Journal** 89:2911-2926. [June 10 Epub ahead of print]

\* **New and Notable commentary:** Schek, H.T. III, and Hunt A.J. (2005) *Microtubules: Mechanical meets chemical*. **Biophysical Journal** 89:2909-2910.

7. Carter, M.G., Sharov, A.A., **VanBuren, V.**, Dudekula, D.B., Carmack, C.E., and Ko, M.S.H. (2005) *A mouse whole-genome oligonucleotide microarray platform for transcript copy number estimation*. **Genome Biology** 6:R61.

8. Huang, H.C., Jupiter, D., Qiu M., Briggs, J.M., **VanBuren, V.** (2008) *Cluster analysis of hydration waters around the active sites of bacterial alanine racemase using a 2-ns MD simulation*. **Biopolymers** 89(3) 210-219 (\* **Featured on the journal cover, see attachment**).

9. Jupiter DC, **VanBuren V** (2008) *A Visual Data Mining Tool that Facilitates Reconstruction of Transcription Regulatory Networks*. **PLoS ONE** 3(3): e1717. doi:10.1371/journal.pone.0001717 (\* **Highly accessed online with >1000 views**).

#### Abstract

1. **VanBuren, V.**, Odde, D.J., Cassimeris, L. (1999) *Modeling Tube Tops: A Model for Tubulin-Tubulin Interactions in Microtubule Statics and Dynamics*. *Mol Biol Cell* 10(S): 376a.

2. **VanBuren, V.**, Cassimeris, L., Odde, D.J. (2000) *Static Modeling of Microtubular Structures*. *Mol Biol Cell* 11(S): 357a.

3. **VanBuren, V.**, Yoshikawa, T., Hamatani, T., Ko, M.S.H. (2003) *Probe Design for Large-Scale Molecular Biology Applications*. *IEEE CSB Proceedings (CSB2003)*. 502-503.

4. U. Chowdhury, **V. VanBuren**. *SBTM Microarray Laboratory: An overview of operations*. Cardiovascular Research Institute Annual Retreat 2006, College Station, TX.

5. E.J. Lee, H.-C. Huang, **V. VanBuren**. *SBTM Microarray Laboratory: An overview of operations*. Cardiovascular Research Institute Annual Retreat 2007, Temple, TX.

6-8. H. Huang, D. Jupiter, J. M. Briggs, **V. VanBuren**. *Identification of Conserved Water Sites in Bacterial Alanine Racemase for Drug Design*.

Poster presented at:

- Computational Systems Bioinformatics 2007, University of California - San Diego, San Diego, CA, IEEE CSB Proceedings (CSB2007)
- Cardiovascular Research Institute Annual Retreat, 2007, Temple, TX
- American Society for Cell Biology. 2007 Annual Meeting, Abstract 1402, Washington, D.C.

9-11. D. Jupiter, **V. VanBuren**. *StarNet: Visual Data Mining for Inferring Gene Regulatory Networks in Mouse Cardiac Development*.

Poster presented at:

- Computational Systems Bioinformatics 2007, University of California - San Diego, San Diego, CA, IEEE CSB Proceedings (CSB2007)
- Cardiovascular Research Institute Annual Retreat, 2007, Temple, TX
- American Society for Cell Biology. 2007 Annual Meeting, Abstract 1211, Washington, D.C.

12. . H.-C.Huang, D.C. Jupiter, **V. VanBuren**. *Identification of Genetic Switches and Biomarkers via the Gene Expression Profiles of Microarray Data*.

- BIOT 2008, Arlington TX.

## Book Chapters

1. **VanBuren, V.** and Ko, M.S.H. (2005) Regulation of genome activity and genetic networks in mammals (invited book chapter). *Mammalian Genomics*. CAB International Publishing, Cambridge, Massachusetts. 201-220.
2. **VanBuren, V.** and Ko, M.S.H. (2005) Principles and applications of embryogenomics (invited encyclopedia section). *Encyclopedia of Molecular Cell Biology and Molecular Medicine*. Wiley-VCH, Berlin. 529-556.

## Manuscripts Already Submitted

1. Daniel Jupiter, Jessica Sahutoglu, and **Vincent VanBuren**. TreeHugger: A new test for enrichment and depletion of GO Terms. Submitted to **INFORMS Journal on Computing**.
2. H. Wayne Sampson, Christopher D. Chaput, Jason Brannen, Robert A. Probe, , Kayla J. Bayless, Alaina C. Dearman, **Vincent J. VanBuren**. *Alcohol Consumption During the Inflammatory Stage of Fracture Healing Appears to Increase Chemotaxis and Cell Migration, Decrease Cell Cycle Progression and Proliferation, and Increase Development: A Microarray Analysis of Gene Expression*. Submitted to **Alcohol**.