

Timothy L. Tickle, Ph.D.

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TIMOTHYLTICKLE@GMAIL.COM

Education:

Harvard School of Public Health (Department of Biostatistics) September 2011-Present
Postdoctoral Fellow (Curtis Huttenhower Lab) Boston, MA

University of North Carolina at Charlotte May 2011
Doctor of Philosophy in Bioinformatics and Computational Biology Charlotte, NC
Dissertation: “Data Mining the Serous Ovarian Tumor Transcriptome”.
Topic included: Ovarian Tumor Genetics, Biomarker Discovery, Transcript-level Analysis.

University of North Carolina at Charlotte August 2004
Bachelor of Science: Computer Science Charlotte, NC
Research Project: Design of bioinformatics software for Ovarian Cancer Analysis.

Wake Forest University May 1999
Bachelor of Science: History, Education Winston-Salem, NC

Research Interests:

Experienced in applying high-throughput technology to complex diseases. Interested in both designing and implementing analysis infrastructure and software systems for bioinformatics analysis. Focused on applying next-generation sequencing, and microarray chip technology to basic and translational experimentation, explicitly when related to clinical studies.

Peer Reviewed Publications:

T. L. Tickle, N. Segata, L. Waldron, U. Weingart, and C. Huttenhower, “Two-stage microbial community experimental design,” *ISME Journal*, 2013.

N. Segata, D. Boernigen, T. L. Tickle, X. C. Morgan, W. S. Garrett, and C. Huttenhower, “Computational metagenomics for microbial community studies,” *Molecular Systems Biology*, vol. 9, 2013.

H. Sokol, T. Tickle, X. Morgan, D. Gevers, K. Devaney, D. Ward, J. Reyes, S. Shah, N. LeLeiko, S. Snapper, A. Bousvaros, J. Korzenik, B. Sands, R. Xavier, and C. Huttenhower, “Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment,” *Genome Biology*, vol. 13, no. R79, 2012.

T. L. Tickle, *Data Mining the Serous Ovarian Tumor Transcriptome*. PhD thesis, University of North Carolina at Charlotte, 2011.

Z. Mostafavi, T. Tickle, J. Zhang, K. Bennett, J. Vachris, M. Spencer, M. T. Mostafavi, and D. Tait, “Correlation analysis of hox, erbb and igfbp family gene expression in ovarian cancer,” *Cancer Investigation*, vol. 26, pp. 990–998, 2008.

A. Fodor, T. Tickle, and C. Richardson, “Towards the uniform distribution of null p values on affymetrix microarrays,” *Genome Biology*, vol. 8, no. 5, 2007.

Research Experience:

Postdoctoral Fellow

2011-Present

Department of Biostatistics (Harvard University, Curtis Huttenhower Lab) Boston, MA

- Responsible for the development and validation of methodology and software for translating metagenomics studies to human diseases.
- Assist in and lead clinical study analysis in microbial biomarker associations with genetic, environmental, and host phenotypes.
- Responsible for adhering to software development practices including versioning, regression/unit testing, lab coding standards, and code reviews.
- Provide documentation, establish a web presence, and support software users.
- Write scientific reports and create custom visualizations.
- Mentor students, lab members, and visiting scientists on analysis and tool use.

Research Assistant

2007-2011

College of Computing and Informatics (UNC-Charlotte) Charlotte, NC

- Was responsible for all work associated with the ovarian tumor transcriptome study. Solely performed all wet-lab protocols and dry-lab analysis.
- Developed and performed wet lab protocols including: sample preparation and storage; tissue staining; pathology evaluation; cryosectioning; laser capture microdissection; immunohistochemistry; RNA extraction, and isolation; and cDNA generation, amplification, and preparation for Affymetrix GeneChip Human Exon 1.0 ST Arrays.
- Participated in training other team members and interns in various wet lab protocols.
- Performed associated analysis and developed software and database solutions.

Instructor

2010

Introduction to Bioinformatics (UNC-Charlotte) Charlotte, NC

- Acted as the instructor of record. Was solely responsible for designing and teaching the first undergraduate introductory bioinformatics class.
- Designed and delivered all lectures and associated presentations.
- Developed assessment activities including testing, review sessions, labs, and homework.

Teaching Assistant

2004-2007

College of Computing and Informatics (UNC-Charlotte) Charlotte, NC

ITCS 3050 (Intro to Bioinformatics), ITCS 6160 (Programming for Biologists), ITCS 2181(Computer Logic & Design), ITCS 3183 (Hardware Systems Design), ITCS 3181/5141 (Computer Organization & Architecture) and ITCS 3650/3651 (Senior Projects).

- Taught classes on programming and class related software.
- Held lab sessions, office hours, and weekly tutoring sessions.

Honors, Awards, and Assistantships:

International Society for Computational Biology Travel Fellowship	2012 and 2013
GAANN Scholars Fellowship	2009-2011
UNC-Charlotte Biotechnology Conference Finalist	2010
TA of the year for the College of Computing and Informatics	2008
Received the Essam El-Kwae award for student-faculty research	2005
Graduated <i>Cum Laude</i> from the University of North Carolina at Charlotte	2004
Graduated <i>Cum Laude</i> from Wake Forest University	1999

Invited Presentations (recent):

Microbial biomaker inference in metadata rich studies. (Genomics Retreat, Dana-Farber Cancer Institute)	November 2013
Metagenomic inference and biomarker discovery for the gut microbiome in inflammatory bowel disease. (International Conference on Intelligence Systems for Molecular Biology)	July 2013
Surveying 16S rRNA abundance to determine sample selection for follow-up studies. (Computational Genomics Group, Dana-Faber Cancer Institute)	Feb 2012
Ovarian Serous Type I,II Tumor Data Set for Expression and Paracrine Signaling Investigation. (Carolinas Medical Center, Cannon Research Community)	Mar 2011
Data Mining the Ovarian Tumor Transcriptome. (UNC-Charlotte's Department of Bioinformatics and Genomics)	Feb 2011
Harnessing the Secrets of Life: How Bioinformatics is Changing Our World. (Queens University and Wingate University)	Apr, Mar 2010

Guest Lecturing:

Mentor Graphics Tutorial (Computer Systems Lab and Recitation; UNC-Charlotte)	Sept 2010
Microarray Technology (Bioinformatics; Davidson College)	Apr 2010
Unit Testing in Python (Bioinformatics Programming I; UNC-Charlotte)	Mar 2010
Mentor Graphics Tutorial (Computer Architecture/Hardware Design; UNC-Charlotte)	Sept 2009
Unit Testing in Python (Bioinformatics Programming I; UNC-Charlotte)	Nov 2009

Public Data Sets Developed:

Serous ovarian benign tumor and type II carcinoma data set for expression and paracrine signaling investigation (GEO# GSE29156).

Professional Societies:

The International Society for Computational Biology
American Association of Cancer Researchers

2010-Present
2004-2007

Computer Skills:

Operating Systems: Windows (current), Mac OS (desktop and server), Linux (Ubuntu)

Programming and Scripting Related: C/C++/C#, Java (SE, EE), JDBC, Java 2D API, JSP, JUnit, XML, JSON, Python, NumPy, mply, matplotlib, PyUnit, PyCogent, Biopython, R

Bioinformatics Related: 16S amplicon and whole microbial metagenomics analysis, BLAST, Bowtie2, metaPhlan, HUMAnN, LefSe, and other Huttenhower tools

Databases: Oracle, Postgres, SQL

Other Applications: Bitbucket / mercurial, Eclipse, Inkscape, L^AT_EX, bibT_EX

Algorithms: Support Vector Machines (SVMs), Gradient Boosting, Multivariate Regression, K-medoids, Multiple Factor Analysis, Principle Components Analysis (PCA), Principle Coordinates Analysis (PCoA), Nonmetric Multidimensional Scaling (NMDS), Hierarchical Clustering

Wet Lab Skills:

Antibody Based: Immunohistochemistry

Laser Capture Microdissection: Manual (PixCell IIe) and Automated (ArcturusXTTM); cut and capture, cryosectioning

General Molecular Biology Techniques: Purification columns, affinity beads, RNA (extraction, isolation), cDNA (isolation, amplification), Nanodrop, Bioanalyzer

Human Study Specific: Human tissue and fluid (serum) preparation for tissue bank, familiar with ovarian tumor pathology

Next Generation Sequencing: cDNA library construction, emulsion PCR (emPCR)

Microarray Related: ST-cDNA conversion, cDNA fragmentation and labeling, sample preparation for Affymetrix GeneChip Human Exon 1.0 ST Arrays using NuGEN products

Staining: Hematoxylin and eosin, HistoGene