

# Timothy L. Tickle, Ph.D.

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## Education:

Harvard School of Public Health (Department of Biostatistics)

September 2011-3

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

Topic included: Ovarian Tumor Genetics, Biomarker Discovery, Transcript-level Analysis.

University of North Carolina at Charlotte

August 2004

Bachelor of Science, Major: Computer Science (Cum laude)

Charlotte, NC

Research Project: Design of bioinformatics software for Ovarian Cancer Analysis.

## Research Interests:

Interested in both development and implementation of analysis infrastructure for large data sets. Experienced in applying high-throughput technology to complex diseases. Focused on applying next-generation sequencing, and microarray chip technology to basic and translational experimentation, explicitly when related to clinical studies.

## Experience:

**Postdoctoral Fellow**

Fall 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**

Fall 2007-2011

College of Computing and Informatics (UNC-Charlotte)

Charlotte, NC

- Was responsible for all work associated with the ovarian exon 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.

**Teaching Assistant**

Fall 2004-Fall 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.

**Application Developer**

Fall 2003-2004

The Vanguard Group

Charlotte, NC

- Acted as and was given the full responsibility of a Netcentric Developer.
- Developed netcentric services (web applications) from design documents.
- Participated in code reviews, presentations, unit testing, performance testing, client acceptance testing and troubleshooting.
- Lead a focus group on the creation and maintenance of automated regression suites.
- Was solely responsible for migrating the teams emailing web services to a new in-house web service.
- Coordinated and tested associated web service environment settings with database administrators.

**Honors, Awards, and Assistantships:**

International Society for Computational Biology Travel Fellowship

2012-2013

GAANN Scholars Fellowship

2009-2011

TA of the year for the College of Computing and Informatics

2008

Received the Essam El-Kwae award for student-faculty research

2005

## Invited Presentations:

Metagenomic inference and biomarker discovery for the gut microbiome in inflammatory bowel disease.	July 2013
(International Conference on Intelligence Systems for Molecular Biology)	
Surveying 16S rRNA abundance to determine sample selection for follow-up studies.	Feb 2012
(Computational Genomics Group, Dana-Faber Cancer Institute)	
Ovarian Serous Type I,II Tumor Data Set for Expression and Paracrine Signaling Investigation	Mar 2011
(Carolinas Medical Center, Cannon Research Community)	
Data Mining the Ovarian Tumor Transcriptome	Feb 2011
(UNC-Charlotte's Department of Bioinformatics and Genomics)	
Harnessing the Secrets of Life: How Bioinformatics is Changing Our World	Apr, Mar 2010
(Queens University)	
(Wingate University)	
Presented Multiple Presentations on Microarray Technology	May-Dec 2005
(UNC-Charlotte's Bioinformatics Research Group)	
(UNC-Charlotte's Computer Science Research Seminar)	
(UNC-Charlotte's Graduate Research Fair)	
Bioinformatics: A Study of Ovarian Cancer	May 2004
(Carolina's Medical Center, Molecular Biology Core Facility)	

## Professional Societies:

The International Society for Computational Biology	2010-Present
American Association of Cancer Researchers	2004-2007

## Computer Skills:

**Internet:** HTML, Dreamweaver, various emailing, internet and FTP programs

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

**Programming and Scripting Related:** JavaScript, C/C++/C#, Java (J2SE,J2EE), JDBC, Java 2D API, JSP, XML, JUnit, SQABasic, Perl (OOP), Perl DBI, Python

**Statistical Related:** SAS, R, Matlab

**Bioinformatics Related:** BLAST, TimeLogic products, OMP, Partek Genomics Suite, DataFate and other tools

**Databases:** Oracle, Postgres, SQL

**Other Applications:** Rational Rose, Visio, Websphere, PVCS Manager and Tracker, Eclipse, Rational Test Suite, Visual Studio.net, Adobe Photoshop CS4, L<sup>A</sup>T<sub>E</sub>X, bibT<sub>E</sub>X

**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

## 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.