

Timothy L. Tickle, Ph.D.

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Education:

Harvard School of Public Health (Department of Biostatistics)

September 2011-3

Postdoctoral Fellow

Boston, MA

Advisor: Curtis Huttenhower

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

Charlotte, NC

Major: Computer Science

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.

Peer Reviewed Publications:

Research Experience:

Postdoctoral Fellow

Fall 2011-Present

Department of Biostatistics (Harvard University)

Boston, MA

Curtis Huttenhower Lab

Responsible for the development and validation of methodology and infrastructure 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, code reviews, supporting users, maintaining a web presence, and providing source code and Galaxy interfaces for public use.
- 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 (excluding chip hybridizations performed at an off-site core facility).

- 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.
- Managed ordering and storage of all associated reagents.
- Participated in training other team members and interns in various wet lab protocols.
- Formulated analysis and quality control protocols for exon data.
- Developed software and database solutions to perform exon analysis.

Teaching Assistant

Fall 2004-2007

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 (excluding chip hybridizations performed at an off-site core facility).

- 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.
- Managed ordering and storage of all associated reagents.
- Participated in training other team members and interns in various wet lab protocols.
- Formulated analysis and quality control protocols for exon data.
- Developed software and database solutions to perform exon analysis.

Application Developer

Fall 2003-2004

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 (excluding chip hybridizations performed at an off-site core facility).

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. (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) (Wingate University)	Apr, Mar 2010
Presented Multiple Presentations on Microarray Technology (UNC-Charlotte's Bioinformatics Research Group) (UNC-Charlotte's Computer Science Research Seminar) (UNC-Charlotte's Graduate Research Fair)	May-Dec 2005
Bioinformatics: A Study of Ovarian Cancer (Carolina's Medical Center, Molecular Biology Core Facility)	May 2004

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^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