

**Timothy Daniel O'Brien**  
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Vanderbilt University  
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**EDUCATION:**

- Vanderbilt University: Human Genetics PhD Program Aug 2012-Present.
- University of Washington: Bachelor of Science in Biochemistry May 2007.
- Université de Nantes: Diploma in French as a foreign language in preparation for further University Studies May 2006.

**HONORS/AWARDS:**

- Member of Tau Sigma National Honor Society (University of Washington Chapter)
- Member of "Free Radicals" Chemistry Club (University of Washington)
- Recipient of Annual Deans List Certificate (University of Washington)
- Chosen as a Student Ambassador to represent Olympia, Washington in Yashiro, Japan in the summer of 1999 to further friendly relations between these two sister cities
- First Place in the Mini-Prep purity competition at the Fred Hutchinson Cancer Research Center
- Winner of best research assistant poster at developmental biology retreat 2011 Vanderbilt University
- Poster abstract received Reviewers' Choice Award for scoring within top 10% of all poster abstracts for The American Society of Human Genetics Annual Conference (ASHG), October 2015, Baltimore, MD

**GRANTS/FELLOWSHIPS:**

- Vanderbilt University Human Genetics Training Grant T32GM080178 July 2013 – July 2015
- Vanderbilt University Center for Quantitative Sciences (CQS) travel grant award October 2014
- Vanderbilt University Graduate School travel grant award October 2015

**Pending**

- NIH/NLM National Research Service Award (NRSA) 1F31LM012353-01.  
Status: score 23 (funding line is under 30)

**SCIENTIFIC WORK EXPERIENCE:**

***Fred Hutchinson Cancer Research Center:*** November 2006 to June 2009

Research Tech I, Laboratory of ***Mark Groudine***

Under Supervision of three Post Doctoral Fellows I worked on several projects utilizing various molecular and biochemical assays and experiments including

- Gene expression analyses by generating cDNA and analyzing with qPCR
- Maintenance of Mouse and Human Cell Lines in tissue culture
- Analyses of protein-protein interactions by performing Co-IPs with western blots
- Mouse genotyping and colony maintenance
- Looking at histone modifications by performing ChIP with qPCR

- Protein-Protein interactions through a Yeast Two Hybrid Assay
- Cell-Cycle arrest experiments and cell sorting using flow cytometry
- Prepping samples for Mass Spec, Sequencing , and Microarrays

**Vanderbilt University Medical Center:** September 2009 to August 2012

Research Assistant II, Laboratory of **David M Miller**

Under minimal supervision I worked on dendritic morphogenesis of a nociceptor neuron in *C. elegans*. I performed a feeding based RNAi screen of possible targets of a transcription factor required for higher order dendritic branching in this neuron. 18 genes were discovered that are important in dendrite development and stability. One gene was further characterized for its role in the stability of dendrites in this neuron. I have learned and worked on several new procedures in this lab including

- Worm genetics and worm genotyping
- Confocal microscopy
- Microinjection of *C. elegans* to generate transgenic worms
- Cloning
- Micro particle bombardment of *C. elegans* to generate transgenic worms
- Antibody staining of worms to look at protein localization
- Fluorescent tagging of proteins to look at localization
- mRNA tagging to generate a cell-specific microarray profile

**Vanderbilt University:** August 2012 – Present

Graduate Student, Laboratory of **Zhongming Zhao**

My first project as a graduate student focused on investigating the inconsistencies between single nucleotide variants (SNVs) detected in whole exome sequencing (WES) versus RNA Sequencing (RNA-Seq) in lung cancer. I performed this analysis with a large group of collaborators within the Zhao lab and outside of Vanderbilt University. We found the overlap in SNVs called was very low (~14%) and discovered many reasons for the inconsistencies in detecting variants.

For my thesis work I am investigating the biological link between the germline and somatic genomes in lung cancer. I am interested in common genetic variants that have been found to be associated with lung cancer and how these interact with genetic mutations that occur in the lung cancer somatic tumor tissue. I am investigating this interaction using network and pathway based computational approaches. I have learned many computational approaches and analyses in my work including

- WES data analysis
- RNA-Seq data analysis
- Network analysis
- Pathway analysis
- Programming
- Cluster computing
- Statistical analysis using R

**LAB EXPERIENCE AT THE BENCH:**

- |                 |                      |                             |
|-----------------|----------------------|-----------------------------|
| •PCR            | •Western Blots       | •Confocal Microscopy        |
| •qPCR           | •Gel Electrophoresis | •Microinjection             |
| •ChIP           | •DNA/RNA Preps       | •Antibody staining          |
| •Tissue Culture | •Cloning             | •Micro particle Bombardment |
| •Plasmid Preps  | •Flow Cytometry      | •RNAi screen                |

## **LAB EXPERIENCE COMPUTATIONAL:**

### Computer languages and computational biology analysis tools

- Linux
- Python
- Bash
- Awk
- R
- Supercomputer cluster computing
- Samtools
- BWA
- FASTQC
- Picard
- GATK
- MuTect
- VarScan
- TopHat
- Bedtools
- PLINK
- Tabix
- vcftools
- Cytoscape
- WebGestalt
- DAVID

### Bioinformatics and computational biology experience

- Whole exome sequencing analysis
- RNA sequencing analysis
- Network analysis
- Pathway analysis
- GWAS quality control
- SNP functional analysis
- eQTL enrichment analysis
- Epigenomic analysis
- biological pathway modeling

## **SELECTED UPPER LEVEL UNDERGRADUATE AND GRADUATE SCHOOL COURSES:**

Biochemistry, Biochemistry Lab, Physical Chemistry, Medical Virology, Chemical Separation Techniques, Inorganic Chemistry, Akkadian I, Akkadian II, Bioregulation I, DNA Structure and Topology, Intro to Structural Biology, Molecular basis of Microbial Pathogenesis, Applied Bioinformatics, The RNA World, Cancer Systems Biology, Human Genetics I, Tutorials in Human Genetics, Principles in Modern Biostatistics, Human Genetics II, Applied Linear Regression

## **LANGUAGES AND ADDITIONAL SKILLS:**

- Near fluency in French (1 year university and 1 year study abroad in Nantes, France)
- Near fluency in Spanish (4 years high school and 1 summer study abroad in Morelia, Mexico).
- Basic conversation skills in Polish (2 semesters university)
- Basic reading and writing skills in Akkadian (2 semesters university)
- Microsoft Word, Microsoft Excel, Microsoft PowerPoint
- Basic use of: RNAfold, Panther, UN-SCAN-IT gel 6.1, ImageQuant 5.2, WinMDI 2.9, SDS 2.2.2, PYSB, STATA
- Adobe Photoshop, Adobe Illustrator, Image J

## **CONFERENCE PRESENTATIONS:**

Poster presentation at the International Conference on Intelligent Biology and Medicine (ICIBM), November 2015, Indianapolis, IN.

Poster presentation\* at The American Society of Human Genetics (ASHG) Annual Conference, October 2015, Baltimore, MD. **\*Poster abstract selected as a Reviewers' Choice Abstract**

Poster presentation at 14th Annual UT-KBRIN Bioinformatics Summit, March 2015, Buchanan, TN. (listed online under name of senior author Zhongming Zhao).

Poster presentation at The American Society of Human Genetics Annual Conference (ASHG), October 2014, San Diego, CA.

## **INVITED TALKS:**

Presentation at the Vanderbilt University Genetics Retreat, February 2016, Nashville, TN.

Presentation to the Thoracic disease, Research, Epidemiology, Assessment, and Treatment (TREAT) Lung Cancer Program at Vanderbilt University, March 2016, Nashville, TN.

## **PUBLICATIONS:**

**O'Brien TD**, Jia P, Xia J, Saxena U, Jin H, Vuong H, Kim P, Wang Q, Aryee MJ, Mino-Kenudson M, Engelman JA, Le LP, Iafrate AJ, Heist RS, Pao W, Zhao Z. Inconsistency and features of single nucleotide variants detected in whole exome sequencing versus transcriptome sequencing: A case study in lung cancer. *Methods*, Volume 83, 15 July 2015, Pages 118-127.

\*Cody J. Smith, \***Timothy O'Brien**, Marios Chatzigeorgiou, W. Clay Spencer, Elana Feingold-Link, Steven J. Husson, Sayaka Hori, Shohei Mitani, Alexander Gottschalk, William R. Schafer, David M. Miller III. Sensory Neuron Fates Are Distinguished by a Transcriptional Switch that Regulates Dendrite Branch Stabilization, *Neuron*, Volume 79, Issue 2, 24 July 2013, Pages 266-280.

**\*These authors contributed equally**

Smith, C.J., Watson, J.D., Spencer, W.C., **O'Brien, T.**, Cha, B., Albeg, A., Treinin, M., Miller, D.M., 3rd, 2010. Time-lapse imaging and cell-specific expression profiling reveal dynamic branching and molecular determinants of a multi-dendritic nociceptor in *C. elegans*. *Dev Biol* 345, 18-33.

## **In Preparation**

**O'Brien TD**, Jia P, Zhao Z. Defining the regulatory roles of common genetic variants associated with three subtypes of lung cancer identifies shared and distinct genetic signatures of disease.

## **MENTORING EXPERIENCE:**

- Mentored an undergraduate on my research project for the spring/summer of 2012. Miller Lab, Vanderbilt University
- Mentored an IGP rotation student on my research project in the fall of 2011. Miller Lab, Vanderbilt University

## **VOLUNTEER EXPERIENCE:**

- International Conference on Intelligent Biology and Medicine (ICIBM) 2013.
- Vanderbilt University Brain Blast 2010, 2011, 2012.
- Tutor at AVID college prep program at Metro Nashville public schools 2009
- Seattle Emergency Housing Jan 2004-April 2004.