Ryan C. Thompson, Ph. D.

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Education

2012—2019	**Ph. D. in Bioinformatics**, Skaggs Graduate School of Chemical and Biological Sciences **The Scripps Research Institute**, La Jolla, California Dissertation: *Bioinformatic analysis of complex, high-throughput genomic and epigenomic data in the context of CD4$^+$ T-cell differentiation and diagnosis and treatment of transplant rejection* Advisor: Andrew Su
2005—2009	**B. S. in Biology with High Distinction; B. A. in Mathematics** **University of Virginia**, Charlottesville, Virginia Undergraduate thesis: *Contig Farmer: A tool for extracting maximal-length contiguous Sequences from a Database of Short Sequence Reads* Advisor: Paul J. Rushton

Academic Experience

2010—2012	**Researcher, Scripps Genome Center, University of California San Diego**, San Diego, CA Advisor: Terry Gaasterland

Professional Experience

2011	**Summer Bioinformatics Internship, Informatics & IT Department, Merck & Co.**, Boston, MA Advisor: Adnan Derti
2006—2009	Summer Sailing Instructor, Raritan Yacht Club, Perth Amboy, NJ
2005—2007	Computing Advisor & Help Desk, Information, Technology, & Communication Department, University of Virginia, Charlottesville, VA

Awards & Honors

2006—2009	Echols Scholar, University of Virginia
2006	Phi Eta Sigma National Honor Society
2006	National Society of Collegiate Scholars
2005	Edward J. Bloustein Disguingished Scholar
2005	National Merit Scholar

Peer-reviewed Publications

[1] Sarah A. LaMere, **Ryan C. Thompson**, Xiangzhi Meng, H. Kiyomi Komori, Adam Mark, and Daniel R. Salomon. H3K27 Methylation Dynamics during CD4 T Cell Activation: Regulation of JAK/STAT and IL12RB2 Expression by JMJD3. *The Journal of Immunology*, 199(9):3158–3175, November 2017. `doi:10/gchc9x`.

[2] S. M. Kurian, E. Velazquez, **R. Thompson**, T. Whisenant, S. Rose, N. Riley, F. Harrison, T. Gelbart, J. J. Friedewald, J. Charette, S. Brietigam, J. Peysakhovich, M. R. First, M. M. Abecassis, and D. R. Salomon. Orthogonal Comparison of Molecular Signatures of Kidney Transplants With Subclinical and Clinical Acute Rejection: Equivalent Performance Is Agnostic to Both Technology and Platform. *American Journal of Transplantation*, 17(8):2103–2116, August 2017. `doi:10/gbp6vr`.

[3] S. A. LaMere, **R. C. Thompson**, H. K. Komori, A. Mark, and D. R. Salomon. Promoter H3K4 methylation dynamically reinforces activation-induced pathways in human CD4 T cells. *Genes & Immunity*, 17(5):283–297, July 2016. `doi:10/f97x85`.

[4] Sunitha Rangaraju, Gregory M. Solis, **Ryan C. Thompson**, Rafael L. Gomez-Amaro, Leo Kurian, Sandra E. Encalada, Alexander B. Niculescu, Daniel R. Salomon, and Michael Petrascheck. Suppression of transcriptional drift extends C. elegans lifespan by postponing the onset of mortality. *eLife*, 4(December2015):1–39, December 2015. `doi:10/ggcxmg`.

[5] S M Kurian, a N Williams, T Gelbart, D Campbell, T S Mondala, S R Head, S Horvath, L Gaber, **R Thompson**, T Whisenant, W Lin, P Langfelder, E H Robison, R L Schaffer, J S Fisher, J Friedewald, S M Flechner, L K Chan, A C Wiseman, H Shidban, R Mendez, R Heilman, M M Abecassis, C L Marsh, and D R Salomon. Molecular Classifiers for Acute Kidney Transplant Rejection in Peripheral Blood by Whole Genome Gene Expression Profiling. *American Journal of Transplantation*, 14(5):1164–1172, May 2014. `doi:10/f5xswg`.

[6] Filip Van Nieuwerburgh, **Ryan C Thompson**, Jessica Ledesma, Dieter Deforce, Terry Gaasterland, Phillip Ordoukhanian, and Steven R Head. Illumina mate-paired DNA sequencing-library preparation using Cre-Lox recombination. *Nucleic acids research*, 40(3):e24, February 2012. `doi:10/fmzd3r`.

Other Works

[7] **Ryan C. Thompson**, Terri Gelbart, Steven R Head, Phillip Ordoukhanian, Courtney Mullen, Dongmei Han, Dora M Berman, Amelia Bartholomew, Norma S Kenyon, and Daniel R Salomon. Optimizing yield of deep RNA sequencing for gene expression profiling of peripheral blood samples from cynomolgus monkeys (Macaca fascicularis). (In preparation). Institution: The Scripps Research Institute, 2019.

[8] **Ryan C. Thompson**, Sarah A. Lamere, and Daniel R. Salomon. Reproducible genome-wide epigenetic analysis of H3K4 and H3K27 methylation in naïve and memory CD4+ T-cell activation. (In preparation). Institution: The Scripps Research Institute, 2019.

[9] **Ryan C. Thompson**. *Bioinformatic Analysis of Complex , High-Throughput Genomic and Epigenomic Data in the Context of CD4+ T-Cell Differentiation and Diagnosis and Treatment of Transplant Rejection*. PhD thesis, The Scripps Research Institute, 2019.

[10] Erick R Scott, H Benjamin Larman, Ali Torkamani, Nicholas J Schork, Nathan Wineinger, Max Nanis, **Ryan C. Thompson**, Reza B. Beheshti Zavareh, Luke L Lairson, Peter G Schultz, and Andrew I. Su. RASLseqTools: Open-source methods for designing and analyzing RNA-mediated oligonucleotide Annealing, Selection, and, Ligation sequencing (RASL-seq) experiments. *bioRxiv*, 2016. `doi:10/ggcxmn`.

[11] **Ryan C. Thompson**, Paul J. Rushton, Tom W. Laudeman, and Michael P. Timko. Contig Farmer : A tool for extracting maximal-length contiguous sequences from a database of short sequence reads (Undergraduate Thesis), June 2009. Institution: University of Virginia. URL: `http://darwinawardwinner.github.io/resume/examples/UVa/contigfarmer.pdf`.

[12] **Ryan C. Thompson**. The Sources and Limits of Geometric Rigor from Euclid Through Descartes, May 2008. Institution: University of Virginia. URL: `http://darwinawardwinner.github.io/resume/examples/UVa/math-history-paper.pdf`.

Presentations and Teaching

May 8, 2018	**Guest lecturer on RNA-Seq** for Advanced Tools and Data Challenges in Bioinformatics course (Lecture & Lab). University of California, San Diego, CA
November 21, 2016	**Advanced RNA-Seq Analysis.** Schork Lab, J. Craig Venter Institute, La Jolla, CA
August 15, 2016	**RNA-seq Analysis.** Bristol-Myers Squibb, Hopewell, NJ
April 29, 2016	**Lecturer on Introductory RNA-seq Analysis** for Applied Bioinformatics and Computational Biology course. The Scripps Research Institute, La Jolla, CA
December 21, 2015	**Advanced RNA-Seq Analysis.** Bristol-Myers Squibb, Hopewell, NJ
November 13, 2015	**Advanced RNA-Seq Analysis.** The Scripps Research Institute, La Jolla, CA

Extracurricular and Volunteer Experience

2012—present	Bioconductor Project, software developer and technical support