

Ryan C. Thompson, Ph. D.



8656 Via Mallorca
Unit G
La Jolla, CA 92037
Phone: (908) 922-7470
Email: rct@thompsonclan.org
Website: <https://github.com/DarwinAwardWinner>

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 Distinguished 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

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

Extracurricular and Volunteer Experience

<i>2012—present</i>	Bioconductor Project, software developer and technical support
---------------------	--
