Ryan C. Thompson, Ph. D.

8656 Via Mallorca
Unit G
La Jolla, CA 92037

Email: rct@thompsonclan.org
Website: https://github.com/DarwinAwardWinner
Phone: (908) 922–7470

Summary

- Accomplished, experienced computational biologist with deep knowledge of biology, mathematics, statistics, and programming.

- 12 years of bioinformatics experience answering a wide range of complex biological questions through analysis of large NGS- and microarray-based whole transcriptome and epigenetic data sets.

- Focus on sound statistical analysis, effective data visualization and communication, and making expert knowledge and successful analysis methods available as re-usable software tools.

- Supportive team member and experienced mentor with a strong ability to help others connect biological, statistical, and computational understanding.

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

Research Experience

Salomon & Su Labs, The Scripps Research Institute   La Jolla, CA   2012—2019

Contact: Dr. Andrew Su, asu@scripps.edu

- Created an open source, reproducible workflow to analyze a large multi-omics next-gen sequencing dataset of 220 RNA-seq and ChIP-seq samples to reveal coordinated changes in histone marks and gene expression during CD4$^+$ T-cell activation as well as epigenetic convergence between naive and memory cells after activation [1, 3, 8].
  Links: Reproducible workflow, Slides, Example results and visualizations

- Significantly improved cross-validated performance of machine learning classifier for identifying biomarkers of transplant rejection by developing appropriate single-sample microarray normalization procedures [5], including training a custom set of frozen RMA normalization vectors. Classifier is currently being developed into a clinical test for transplant dysfunction.
  Links: fRMA example code & plots, Classifier Method Write-up

- Performed a comprehensive comparative evaluation of over 20 subtly different statistical models for differential methylation in Illumina 450k arrays, selecting a model that best explained the observed sources and trends of variation in the data, including cross-domain application of a method originally designed for RNA-seq data.
  Link: Example diagnostic plots

- Evaluated and optimized cost and performance of custom protocol for RNA-seq of human and primate blood samples while minimizing nuisance globin reads. Increased yield of useful reads nearly 2-fold [7].
  Link: Example results

- Mentored 3 coworkers from both biology and programming backgrounds in learning bioinformatics.

Summer Internship, Informatics IT, Merck & Co.   Boston, MA   2011

Contact: Adnan Derti, adnan.derti@gmail.com

- Built a transcriptome assembly and quantification pipeline using Cufflinks, including fully-automated cluster job control for high-throughput reproducible analysis, and presented a conceptual overview of Cufflinks' assembly and quantification algorithms to help the team understand Cufflinks.
  Link: Presentation Slides

- Assisted in a molecular genetics study to evaluate peformance of two variant calling algorithms in detection of causal mutations in antibiotic-resistant bacterial genomes.

Gaasterland Lab, UCSD Bioinformatcs   La Jolla, CA   2010—2012

Contact: Terry Gaasterland, gaasterland@ucsd.edu

- Designed and implemented Deloxer, a critical software step in a new Illumina mate-pair sequencing protocol using Cre recombination. Deloxer is publishedand now in use in several labs around the world [6].
  Links: Documentation; Code

- Performed a molecular genetics study to find potential causal mutations for fatal iron overload disease in critically endangered black rhinoceros by *de novo* assembly of transcriptomes for black rhino and closely-related white rhino. Developed a custom pipeline to match up ortholog gene pairs, discover single-nucleotide differences between them, and functionally annotate these differences, and delivered a list of potential causal variants to collaborators for follow-up.
  Link: Example results

- Helped design & implement one of the first large-scale high-throughput exome sequencing pipelines for SNP discovery and functional annotation, including QC and validation of on-target coverage depth and reproducibility of coverage.
  Links: Example 1; Example 2; Example 3

- Analyzed miRNA target predictions using GO & KEGG grouping to identify target pathways of autophagy-related miRNAs for biological validation.
  Link: Example results

Timko Lab, U. of Virginia Biology   Charlottesville, VA   2007—2009

Advisor: Paul J. Rushton

- Undergraduate thesis: Designed and implemented Contig Farmer, an algorithm for efficient selective contig assembly starting from "seed" sequences of interest, and used Contig Farmer to accelerate transcription factor gene discovery in cowpea and tobacco shotgun genomic sequence data [11].

- Investigated transcription factors mediating plant stress response using expression microarray time-course, and refined the custom microarray design using data from previous runs to identify and eliminate uninformative probes, yielding an improved design for future studies.
  Link: Code

- Acted as translator between biological researchers and computational analysts to help match computational solutions to biological problems.
  Link: Presentation Slides

Skills

Computing Skills R/Bioconductor, Python, Perl, Lisp, Java, C#, C++; Git version control; Remote UNIX system administration & software compilation, computing cluster job management & parallel computation
Public code: https://github.com/DarwinAwardWinner
Stack Overflow profile: http://stackoverflow.com/users/125921

  - Active member of the Bioconductor community since 2012 and contributing developer for several packages.
    Links: Support Profile; Packages: BiocParallel, ChIPPeakAnno, MyGene

Statistics, Machine Learning, & Data Analysis Multi-omics NGS & microarray analysis, multi-factor linear and generalized linear regression, experimental design and parametrization, empirical Bayesian methods, predictive modeling of clinical outcomes, machine learning classifier training & validation, survival analysis, data visualization & presentation, reproducible research practices

Wet Lab: PCR, molecular cloning, recombinant protein purification, epitope mapping, site-directed mutagenesis, 2D gels, real-time PCR, and associated data analysis

Languages: English: native speaker; German: written and spoken

Other Work Experience

2005—2007	Help Desk & Computing Advisor, U. Va. IT Dept.	Charlottesville, VA
2006—2009	Summer Sailing Instructor, Raritan Yacht Club	Perth Amboy, NJ

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