Abhinav Nellore

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My computational biology group develops and deploys software that rapidly and uniformly analyzes many thousands of high-throughput sequencing samples on large computer clusters. Our primary focus is RNA sequencing (RNA-seq) data. We often use tools in the Hadoop ecosystem, and we often perform analyses in the cloud with Amazon Web Services. Together with collaborators at Johns Hopkins University, we are also developing tools that search the processed outputs of our analysis pipeline Rail-RNA, which we regularly run on archived RNA-seq samples from the Sequence Read Archive (SRA). These tools will allow investigators to find archived samples with expression patterns similar to newly sequenced samples, giving them insight into the contexts of features of interest like variants, fusions, and alternative isoforms.

Employment

DEPTS. OF *BIOMEDICAL ENGINEERING* AND *SURGERY*   **NOV 2016-PRESENT**
OREGON HEALTH AND SCIENCE UNIVERSITY (PORTLAND, OR)
ASSISTANT PROFESSOR

DEPTS. OF *BIOSTATISTICS* AND *COMPUTER SCIENCE*   **2013-2016**
JOHNS HOPKINS UNIVERSITY (BALTIMORE, MD)
POSTDOCTORAL SCHOLAR BETWEEN LABS OF BEN LANGMEAD AND JEFF LEEK
I developed scalable software in **Python** called Rail-RNA for integrative analysis of thousands of RNA sequencing samples. Visit http://rail.bio for more information.

DEPT. OF *HUMAN GENETICS*   **2012-2013**
UNIVERSITY OF CALIFORNIA, SAN FRANCISCO (SAN FRANCISCO, CA)
POSTDOCTORAL SCHOLAR, JUN S. SONG'S LAB
I participated in writing software for identifying nucleosome positions from MNase-seq data (NSeq) and performing quality control of ChIP-seq data (CHANCE) in **Java** and **Matlab**, respectively. I also did published research involving 1) the mechanisms underlying the development of melanoma, and 2) lncRNAs in neural stem cells of mice.

JIFF, INC. (PALO ALTO, CA)   **2011**
MOBILE APP DEVELOPER

I coded part of JiffPad (language: **Objective-C**), an iPad app that helps doctors create teaching materials for their patients. JiffPad was presented at TechCrunch Disrupt SF 2011's Startup Battlefield and was available in the App Store through 2012.

PRINCETON CONSULTANTS (PRINCETON, NJ)   **2010-2011**
SENIOR ASSOCIATE

NetJets is a fractional jet company; instead of buying their own jets and hiring their own flight crews, NetJets customers buy fractions of crewed jets and make flight reservations shortly before takeoff. This poses a large-scale optimization problem: how can one schedule flights and assign crews to minimize operational costs? I maintained software written in **Java** and **C#** that solves this problem.

Education

DOCTOR OF PHILOSOPHY, PHYSICS (STRING THEORY)   **2010**
PRINCETON UNIVERSITY (PRINCETON, NJ)

Thesis: Applications of the gauge/gravity duality
Adviser: Steven S. Gubser

BACHELOR OF SCIENCE, PHYSICS   **2005**
UNIVERSITY OF MARYLAND, COLLEGE PARK

Thesis: Quantizing exotic states in *SU(3)* soliton models
Adviser: Thomas D. Cohen
GPA: 3.925 (graduated with high honors)

Awards

Postdoctoral Poster Award (for NSeq), UCSF Biomedical Sciences, 2012
Princeton University Department of Physics Teaching Award, 2010
Princeton University Centennial Fellowship, 2005-2010
National Defense Science and Engineering Graduate Fellowship (NDSEG), 2005-2008

Talks and posters

1. *Realigning TCGA RNA-seq data from CGC with Rail-RNA on Amazon Elastic MapReduce*, Seven Bridges luncheon, ASHG, October 2016 (**talk**)

2. *Rail-RNA: scalable analysis of RNA-seq splicing and coverage*. HiTSeq, ISMB, July 2016 (**talk**)

3. *Scalable analysis and search of thousands of human RNA-seq samples*. Biology of Genomes, Cold Spring Harbor Lab, May 2016 (**poster**)

4. *Scalable analysis and search of thousands of human RNA-seq samples*. Computational Biology Program, OHSU, April 2016 (**talk**)

5. *An analysis of splicing variation across the Sequence Read Archive with Rail-RNA*. Genome Informatics, Cold Spring Harbor Lab, October 2015 (**talk**)

6. *Rail-RNA: analyzing many RNA sequencing samples with Elastic MapReduce*. Amazon Web Services Public Sector Symposium, Washington, DC, June 2015 (**talk**)

7. *Scalable and integrative analysis of many RNA sequencing samples with Rail-RNA*. Center for Computational Genomics, Johns Hopkins University, April 2015 (**talk**)

8. *Rail-RNA–-a scalable MapReduce pipeline for analyzing many RNA-seq samples*. Biological Data Science, Cold Spring Harbor Lab, November 2014 (**poster**)

9. *Scalable software for analyzing many RNA sequencing samples*. Young Investigators Symposium, Johns Hopkins University, October 2014 (**talk**)

Below, my name is highlighted in fields where authorship order is relevant.

Preprints

1. C Wilks, P Gaddipati, **A Nellore**, B Langmead. "Snaptron: querying and visualizing splicing across tens of thousands of RNA-seq samples," bioRxiv; https://doi.org/10.1101/097881 (**computational biology**)

2. L Collado-Torres*, **A Nellore***, K Kammers, S Ellis, M Taub, K D Hansen, A E Jaffe, B Langmead, J T Leek. "recount: A large-scale resource of analysis-ready RNA-seq expression data," bioRxiv; https://doi.org/10.1101/068478 (**computational biology**; *equal contribution)

Publications

3. **A Nellore**, A E Jaffe, J P Fortin, J Alquicira-Hernández, L Collado-Torres, S Wang, R A Phillips III, N Karbhari, K D Hansen, B Langmead, J T Leek. "Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive," *Genome Biology*, vol. 17, 30 December 2016, pages 266 (**computational biology**)

4. L Collado-Torres, **A Nellore**, A C Frazee, C Wilks, M I Love, B Langmead, R A Irizarry, J T Leek, A E Jaffe. "Flexible expressed region analysis for RNA-seq with derfinder." *Nucleic Acids Research,* vol. 45, issue 2, 29 September 2016, pages e9 (**computational biology**)

5. **A Nellore**, L Collado-Torres, A E Jaffe, J Alquicira-Hernández, C Wilks, J Pritt, J Morton, J T Leek, B Langmead. "Rail-RNA: Scalable analysis of RNA-seq splicing and coverage," *Bioinformatics*, advance access: https://doi.org/10.1093/bioinformatics/btw575 (**computational biology**)

6. **A Nellore**, C Wilks, K D Hansen, J T Leek, B Langmead. "Rail-dbGaP: analyzing dbGaP-protected data in the cloud with Amazon Elastic MapReduce," *Bioinformatics,* advance access: http://dx.doi.org/10.1093/bioinformatics/btw177 (**computational biology**)

7. **A Nellore** and R Ward. "Recovery guarantees for exemplar-based clustering," *Information and Computation*, vol. 245, October 2015, pages 165-180 (**machine learning**)

8. A Ramos, A Diaz*, **A Nellore***, R Delgado, K-Y Park, G Gozales-Roybal, M Oldham, J S Song, and D Lim. "Integration of genome-wide approaches identifies lncRNAs of adult neural stem cells and their progeny in vivo," *Cell Stem Cell*, vol. 12, issue 5, 2 May 2013, pages 616-628 (**computational biology**; *equal contribution)

9. R Haq, J Shoag, P Andreu-Perez, S Yokoyama, H Edelman, G Row, D Frederick, A Hurley, **A Nellore**, A Kung, J Wargo, J S Song, D Fisher, Z Arany, and H Widlund. "Oncogenic BRAF regulates oxidative metabolism via PGC1a and MITF," *Cancer Cell*, vol. 23, issue 3, 18 March 2013, pages 302-315 (**computational biology**)

10. **A Nellore**, K Bobkov, E Howe, A Pankov, A Diaz, and J S Song. "NSeq: a multithreaded Java application for finding positioned nucleosomes from sequencing data," *Frontiers in Genetics*, vol. 3, 11 January 2013 (**computational biology**)

11. A Diaz, **A Nellore**, and J S Song. "CHANCE: comprehensive software for quality control and validation of ChIP-seq data," *Genome Biology*, vol. 13, 15 October 2013, pages R98 (**computational biology**)

12. A Nellore. "Applications of the gauge/gravity duality," thesis at Princeton University, September 2010 (**string theory**)

13. S S Gubser and A Nellore. "Ground states of holographic superconductors," *Physical Review D*, vol. 80, issue 10, 11 November 2009 (**string theory**)

14. A Cherman and A Nellore. "Universal relations of transport coefficients from holography," *Physical Review D*, vol. 80, issue 6, 9 September 2009 (**string theory**)

15. A Cherman, T Cohen, and A Nellore. "Bound on the speed of sound from holography," *Physical Review D*, vol. 80, issue 6, 3 September 2009 (**string theory**)

16. S S Gubser and A Nellore. "Low-temperature behavior of the Abelian Higgs model in anti-de Sitter space," *Journal of High Energy Physics*, vol. 2009, page 8, 1 April 2009 (**string theory**)

17. S S Gubser and A Nellore. "Mimicking the QCD equation of state with a dual black hole," *Physical Review D*, vol. 78, issue 8, 29 October 2008 (**string theory**)

18. S S Gubser, A Nellore, S S Pufu, and F D Rocha. "Thermodynamics and bulk viscosity of approximate black-hole duals to finite-temperature quantum chromodynamics," *Physical Review Letters*, vol. 101, issue 13, 23 September 2008 (**string theory**)

19. A Cherman, T D Cohen, and A Nellore. "Quantization of exotic states in SU(3) soliton models: a solvable quantum mechanical analog," *Physical Review D*, vol. 70, issue 5, 11 November 2004 (**nuclear theory**)

20. T D Cohen, D C Dakin, R F Lebed, and A Nellore. "Pion-nucleon scattering relations at next-to-leading order in 1/N," *Physical Review D*, vol. 69, issue 5, 16 September 2004 (**nuclear theory**)

21. T D Cohen, D C Dakin, A Nellore, and R F Lebed. "Excited baryon decay widths in large N QCD," *Physical Review D*, vol. 69, issue 5, 1 March 2004 (**nuclear theory**)

22. G Oskam, **A Nellore**, R L Penn, and P C Searson. "The growth kinetics of TiO2 nanoparticles from titanium (IV) alkoxide at high water/titanium ratio, *The Journal of Physical Chemistry B*, vol. 107, issue 8, pages 1734-1738 (**materials science**)