

CYDNEY NIELSEN

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RESEARCH INTERESTS

High-throughput technologies have changed the scale and resolution at which we can investigate cellular states. We require improved computational methods to increase our analysis throughput and make the most of the vast data we produce. I develop techniques for performing automated analyses and interactive data explorations, exploiting synergies between the two to answer pressing questions in genomics.

EDUCATION

Massachusetts Institute of Technology, Cambridge, MA, USA

Ph.D., Biology (specialty: Computational Biology) — June 2008

Dissertation Title: Mammalian Gene Regulation through the 3' UTR

University of British Columbia, Vancouver, BC, Canada

B.Sc., Microbiology and Immunology — May 2001

Honours Thesis Title: Phylogenetic analysis of baculoviruses using DNA polymerase gene fragments

AWARDS

2011 — Michael Smith Foundation for Health Research (MSFHR)
Provincial Postdoctoral Fellowship (British Columbia)

2010 — Canadian Institutes for Health Research (CIHR)
National Postdoctoral Fellowship, Canada

2009 — US National Science Foundation International Science and
Engineering Visualization Challenge, Finalist

2009 — IEEE InfoVis Best Paper Award, Atlantic City, NJ, USA

2006 — Natural Sciences and Engineering Research Council (NSERC)
National Postgraduate Scholarship, Canada (*for study abroad*)

2005 — Biology Retreat Poster Prize, MIT, Cambridge, MA, USA

2004 — Herman Eisen Fellowship, MIT, Cambridge, MA, USA

2003 — Presidential Fellowship, MIT, Cambridge, MA, USA

2001 — Dolman Prize, UBC, Vancouver, Canada
(*awarded to the top undergraduate in Microbiology*)

2001 — Wesbrook Scholar, UBC, Vancouver, Canada

RESEARCH

Research Associate, Department of Pathology, UBC and the BC Cancer Agency, Department of Molecular Oncology

Vancouver, BC, Canada

June 2013 - present

Goal: To develop visualizations for discovery in cancer genomics

- Currently leading a team to design and implement a flexible web-based visualization platform for cancer genomics data.
- Advisor: Sohrab Shah, Assistant Professor, Pathology, UBC

Postdoctoral Fellowship, Michael Smith Genome Sciences Centre

Vancouver, BC, Canada

Sept. 2008 - May 2013

Goal: To develop computational techniques and interactive visual representations for understanding genomic data

- Developed a clustering and visualization approach, Spark, to investigate epigenetic signatures in diverse human and mouse tissues: <http://www.sparkinsight.org>
- Designed an interactive visualization tool for genome assembly analysis, ABySS-Explorer (Best Paper Award InfoVis '09): <http://www.bcgsc.ca/platform/bioinfo/software/abyss-explorer>
- Advisor: Steven Jones, Professor, Medical Genetics, UBC

PhD, Department of Biology, MIT

Cambridge, MA, USA

June 2004 - June 2008

Goal: To improve our understanding of mammalian post-transcriptional gene regulation

- Investigated nucleosome distributions across mammalian polyadenylation sites and uncovered evidence that nucleosome positioning is predictive of polyadenylation site usage
- Uncovered novel microRNA targeting determinants and integrated these features into a scoring scheme, TargetRank, available at <http://genes.mit.edu/targetrank/>

Thesis Committee:

- Advisor: Chris Burge, Professor of Biology, MIT
- Phillip Sharp, Institute Professor of Biology, MIT
- Richard Young, Professor of Biology, MIT

**INDUSTRY
EXPERIENCE**

- 2001-03 **Whitehead Institute Center for Genome Research**
(now Broad Institute)
Cambridge, MA, USA
Genomics Data Analyst
- Coordinated a team to improve genome quality of the *Neurospora crassa* shotgun sequencing genome assembly
 - Collaborated with the Fungal Genomics team and Chris Burge (Department of Biology, MIT) to examine intron evolution among fungal species
- 2000 **Bioinformatics Core Facility**
CMMT, Vancouver, BC, Canada
Co-op student
- Developed a hand-curated database of fish promoter sequences based on literature searches and sequence analysis, employing computational biology tools under the supervision of Francis Ouellette
- 1999 **TerraGen Diversity Inc.**
Vancouver, BC, Canada
Co-op student
- Constructed a large insert cloning vector to be used in the company's efforts to clone high molecular weight DNA from environmental samples (such as soil) containing uncultivable microbial populations. This vector was designed for expression in a surrogate host, generating libraries of small molecules for subsequent screening and potential drug discovery.

**TEACHING
EXPERIENCE**

- 2007 **Teaching Assistant**
7.91, Computational and Systems Biology, MIT
- Taught weekly tutorials
 - Prepared and graded problem sets and exams
 - Designed and assisted students with Python programming problems
- 2004 **Teaching Assistant**
7.102, Introductory Biology, MIT
- Taught tutorials twice a week
 - Collaborated with other TAs to prepare and grade problem sets and exams

PUBLICATIONS

PEER-REVIEWED

Ferstay JA, **Nielsen CB**, Munzner T. Variant View: Visualizing Sequence Variants in their Gene Context. *IEEE Transactions on Visualization and Computer Graphics* (Proceedings Information Visualization). 2013 19(12):2546-55.

Younesy H, **Nielsen CB**, Möller T, Alder O, Cullum R, Lorincz MC, Karimi MM, Jones SJM. An Interactive Analysis and Exploration Tool for Epigenomic Data. *Computer Graphics Forum* (Proceedings EuroVis 2013) 32(3pt1), 91–100.

Nielsen CB, Younesy H, O'Geen H, Xu X, Jackson AR, Milosavljevic A, Wang T, Costello JF, Hirst M, Farnham PJ, Jones SJM. Spark: A navigational paradigm for genomic data exploration. *Genome Research*. 2012 22(11):2262-9.

Leung AK, Young AG, Bhutkar A, Zheng GX, Bosson AD, **Nielsen CB**, Sharp PA. Genome-wide identification of Ago2 binding sites from mouse embryonic stem cells with and without mature microRNAs. *Nature Structural and Molecular Biology*. 2011 18(2):237-44.

Zhou X, Maricque B, Xie M, Li D, Sundaram V, Martin EA, Koebbe BC, **Nielsen C**, Hirst M, Farnham P, Kuhn RM, Zhu J, Smirnov I, Kent WJ, Haussler D, Madden PA, Costello JF, Wang T. The Human Epigenome Browser at Washington University. *Nature Methods*. 2011 29;8(12):989-90.

Maunakea AK, Nagarajan RP, Bilenky M, Ballinger TJ, D'Souza C, Fouse SD, Johnson BE, Hong C, **Nielsen C**, Zhao Y, Turecki G, Delaney A, Varhol R, Thiessen N, Shchors K, Heine VM, Rowitch DH, Xing X, Fiore C, Schillebeeckx M, Jones SJ, Haussler D, Marra MA, Hirst M, Wang T, Costello JF. Conserved role of intragenic DNA methylation in regulating alternative promoters. *Nature*. 2010 466(7303):253-7.

Nielsen CB, Cantor M, Dubchak I, Gordon D, Wang T. Visualizing genomes: techniques and challenges. *Nature Methods*. 2010 7(3 Suppl):S5-S15.

Nielsen CB, Jackman SD, Birol I, Jones SJ. ABySS-Explorer: Visualizing genome sequence assemblies. *IEEE Transactions on Visualization and Computer Graphics* (Proceedings Information Visualization). 2009 15(6):881-8. **InfoVis09 Best Paper Award**

Spies N*, **Nielsen CB***, Padgett RA, Burge CB. Biased chromatin signatures around polyadenylation sites and exons. *Molecular Cell*. 2009 36(2):245-54.

Birol I, Jackman SD, **Nielsen CB**, Qian JQ, Varhol R, Stazyk G, Morin RD, Zhao Y, Hirst M, Schein JE, Horsman DE, Connors JM, Gascoyne RD, Marra MA, Jones SJ. De novo transcriptome assembly with ABySS. *Bioinformatics*. 2009 25(21):2872-7.

Nielsen CB*, Shomron N*, Sandberg R, Hornstein E, Kitzman J, Burge CB. Determinants of targeting by endogenous and exogenous microRNAs and siRNAs. *RNA*. 2007 13(11):1894-1910.

Nielsen CB*, Friedman B*, Birren B, Burge CB, Galagan JE. Patterns of intron gain and loss in fungi. *PLoS Biology*. 2004 2(12):e422.

Galagan JE *et al.*, incl. **Nielsen CB**. The genome sequence of the filamentous fungus *Neurospora crassa*. *Nature*. 2003 422(6934):859-868.

Nielsen CB, Cooper D, Short SM, Myers JH, Suttle CA. DNA polymerase gene sequences indicate western and forest tent caterpillar viruses form a new taxonomic group within the baculoviruses. *Journal of Invertebrate Pathology*. 2002 81(3):131-147.

* authors contributed equally

INVITED COMMENTARIES

Nielsen C, Wong B.
Points of view: Representing genomic structural variation. *Nature Methods*. 2012 7(7):631.

Nielsen C, Wong B.
Points of view: Managing deep data in genome browsers. *Nature Methods*. 2012 9(6):521.

Nielsen C, Wong B.
Points of view: Representing the genome. *Nature Methods*. 2012 9(5):423.

O'Donoghue SI, Gavin AC, Gehlenborg N, Goodsell DS, Hériché JK, **Nielsen CB**, North C, Olson AJ, Procter JB, Shattuck DW, Walter T, Wong B.
Visualizing biological data-now and in the future. *Nature Methods*. 2010 7(3 Suppl):S2-4.

INVITED TALKS

- University of Victoria - Computer Science, Victoria, BC, Canada
Nov 2014. "Interactive Data Visualization in the Wild: Challenges of Big Data in Cancer Genomics"
- Beyond the Genome 2014: Cancer Genomics, Boston, MA, USA
Oct 2014. "Re-inserting Human Interaction into Cancer Genome Interpretation"
- Simons Foundation Biotech Symposium, Complex Data Visualization: Approach and Application, New York, NY, USA
Sept 2014. "Visualizing Cancer Genomes: Techniques and Challenges"
- IEEE Symposium on Biological Data Visualization, Atlanta, GA, USA
Oct 2013. "Sequence and Omics Data"
- University of Calgary, Bioinformatics Program, Calgary, AB, Canada
March 2013. "From Data to Insight"
- University of Toronto, The Donnelly Centre for Cellular & Biomolecular Research and Department of Computer Science, Toronto, ON, Canada
March 2013. "From Data to Insight"
- Ontario Cancer Institute, Toronto, ON, Canada
Feb 2013. "Coupling Computation and Visualization to Extract Insight from Genomic Data"

- Ontario Institute for Cancer Research, Toronto, ON, Canada
Feb. 2013. "Coupling Computation and Visualization to Extract Insight from Genomic Data"
- University of Ontario Institute of Technology, Oshawa, ON, Canada
Feb 2013. "Leveraging Domain Knowledge to Advance Visual Analytics"
- University of Calgary, Dept. of Computer Science, Calgary, AB, Canada
Feb 2013. "Leveraging Domain Knowledge to Advance Visual Analytics"
- Worcester Polytechnic Institute, Bioinformatics, Worcester, MA, USA
Jan 2013. "Computational Approaches and Challenges in Genomics"
- IEEE Symposium on Biological Data Visualization, Seattle, WA, USA
Oct 2012. "Systems Biology and Omics Data"
- The Canadian Visual Analytics School 2012 - Summer Edition, Simon Fraser University, Burnaby, Canada
Jul 2012. "Visual Analytics for Genomics"
- Visualizing Biological Data (VIZBI) conference, Heidelberg, Germany
Mar 2012. "Visualizing Assemblies for NGS"
- Visualizing Biological Data (VIZBI) tutorial, Heidelberg, Germany
Mar 2012. "Visualization Principles" (in collaboration with Jessie Kennedy and Martin Krzywinski)
- IEEE Symposium on Biological Data Visualization, Providence, RI, USA
Oct 2011. "Current Challenges in Genomic Data Visualization"
- Vancouver Institute for Visual Analytics, Vancouver, Canada
Oct 2011. "Complementing Computation with Visualization in Genomics"
- University of California, San Francisco, Reference Epigenome Mapping Center Workshop, San Francisco, CA, USA
Jul 2010. "Interactive Visualization for Epigenomics"
- European Bioinformatics Institute, Interfaces Forum, Hinxton, UK
Mar 2010. "Complementing Computation with Visualization in Genomics"
- Simon Fraser University, School of Computing Science, Burnaby, BC
Dec 2009. "Visualizing Genomic Data"
- University of British Columbia, Science One Program, Vancouver, BC
Mar 2009. "Interdisciplinary Science"
- Vancouver Bioinformatics User Group (VanBUG), Vancouver, BC
Dec 2008. "Genomic Data Visualization: Making Sense of Large-Scale Data Sets"
- MIT, Biology Department Retreat, Hyannis, MA, USA
May 2008. "Nucleosome Positioning at Gene 3' Ends"

PROFESSIONAL ACTIVITIES

Community

- Organizing Committee Member, Symposium on Biological Data Visualization (BioVis), 2011- present - www.biovis.net
- Program Committee Member, IEEE Information Visualization, 2013
- Workshop Session Chair, EMBO Workshop on Visualizing Biological Data (VIZBI), 2010 - www.vizbi.org
- MIT Chipperfield Memorial Lectureship Committee Member. 2004-2005.

Supervision

- UBC Master's Student (Computer Science) Co-Supervisor together with Tamara Munzner, Vancouver, Canada, 2012-2013.
- UBC Co-op Students (Computer Science) Supervisor Vancouver, Canada, 2009-present.
- MIT Undergraduate Research Opportunities Program Supervisor Cambridge, MA, USA, 2008.

Reviewer

- Journals: Bioinformatics, BMC Bioinformatics, Genome Research, Nature, Nature Methods, PLoS Computational Biology, PLoS One, RNA. 2004-present.
- Conferences: ACM SIGCHI Conference on Human Factors in Computing Systems (CHI), Eurographics Conference on Visualization (EuroVis), IEEE Symposium on Biological Data Visualization (BioVis), IEEE Information Visualization. 2010-present.

GRANTS

- "Building a Bridge from the Cancer Genome to the Cancer Clinic with Visual Analytics". Canadian Cancer Society Research Institute. Awarded 2013. Principle Investigator: Sohrab Shah. Co-applicants/Participants: Samuel Aparicio, David Huntsman, Janessa Laskin, Marco Marra, **Cydney Nielsen**
- "An Epigenomic Data Coordination Centre for Canada". CIHR. Awarded 2012. Principle Investigator: Steven Jones. Co-applicants: Inanc Birol, **Cydney Nielsen**, Matt Lorincz, Mohammad Karimi

REFERENCES

Available upon request.