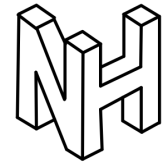


# Niels Hanson

4557 West 14<sup>th</sup> Ave., Vancouver BC V6R 2Y5, +1 (778) 385-4465

[nielshanson@gmail.com](mailto:nielshanson@gmail.com) | [nielshanson.com](http://nielshanson.com) | GitHub: [nielshanson](https://github.com/nielshanson)



## Profile

- Recent Ph.D. graduate looking for a career in Quantitative Analytics, Data Science, or Software Development

## Education

### Ph.D. Bioinformatics

University of British Columbia 2011–2015

### B.Sc. Computer Science (Minor Statistics)

University of British Columbia 2006–2011

## Coursework

- Machine Learning, Data Visualization, Numerical Methods, Algorithms, and Software Development

## Technical Skills

- Proficient in Java, C++, R, Python, JavaScript, PHP, Go, and SQL
- Object-oriented software design
- Large-scale data processing using Hadoop, Apache Spark, and AWS
- HPC programming with Intel Phi-cards
- Data Analysis with ggplot2, dplyr, RMarkdown, NumPy, pandas, scikit-learn, and D3.js

## Projects

- D3.js Visualizations.** Variety of visualizations in the d3.framework for analysis of genomic data (<http://goo.gl/fLntUc>)
- R-Package: fastLSA.** Implementation of the fastLSA correlation method in C and Open-MP (<http://goo.gl/5QPM82>)
- De-Confusion Tables.** An interactive R shiny app. Final project. Developing Data Products. John Hopkins University Coursera Class. July 2014 (<http://goo.gl/Fl78Qh>)

## Selected Publications

- Kim, Konwar, **Hanson**, et al. Koonkie: An Automated Software Tool for Processing Environmental Sequence Information using Hadoop. ASE BigData. Harvard (2014)
- Hanson** et al. Metabolic pathways for the whole community. BMC Genomics (2014)
- Hanson**, et al. MetaPathways v2.0: A master-worker model for environmental PGDB construction on grids and clouds. IEEE CIBCB, Hawaii (2014)
- Konwar, **Hanson**, et al. MetaPathways: a modular pipeline for constructing pathway/genome databases from environmental sequence information. BMC Bioinf. (2013)

## Experience

**Bioinformatics Ph.D. Candidate** 2011–2015  
*Hallam Lab, University of British Columbia*

- Developed MetaPathways, a Python and C++ pipeline for biological sequencing data
- Implemented a Master-worker distributed algorithm to manage a large collection of HPC worker grids
- Enabled sequence-homology search in Hadoop through critical improvements to the YARN scheduler
- Analytically involved in all areas research; author on 10+ peer-reviewed publications

**Teaching Assistant** 2014  
*Marine Biological Laboratory, Woods Hole, MA*

- Conducted tutorials on biological sequence analysis for 60+ post-docs, graduate students, and professors
- Statistical topics: Predictive Models, SVMs, Hierarchical Clustering, Dimensionality Reduction
- General data-literacy topics: data preparation, analysis, visualization, and report generation using R, ggplot2, dplyr, and RMarkdown

**Software Developer** 2011  
*Microbiology and Immunology, UBC*

- Developed a LAMP stack and JavaScript based web application cataloging thousands of bacterial strains
- Ensured accurate requirements via user observation and interviews
- Enhanced the user experience by implementing advanced Boolean search, user histories, and search autocomplete

**Bioinformatics Intern** 2010  
*Eichler Lab, University of Washington*

- Developed a genome visualization and analysis software platform for autistic human genomes
- MySQL back-end database and object-oriented Java MVC-based GUI enabled the visualization of millions of genetic variants predicted via a Hidden Markov Model
- Efficient visualization layout algorithms enabled the rapid analysis of thousands of important genomic alterations

## Interests

- Data Analysis, Information Visualization, Machine Learning, Statistics, Software Design
- Photography, Cooking, Badminton, Triathlons