Niels Hanson

4557 West 14th Ave., Vancouver BC V6R 2Y5, +1 (778) 385-4465
nielshanson@gmail.com | nielshanson.com | GitHub: nielshanson

Profile

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

Education

B.Sc. Computer Science (Minor Statistics)
University of British Columbia *2006–2011*
Ph.D. Bioinformatics
University of British Columbia *2011–2015*

Coursework

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

Technical Skills

- Proficient in Java, C++, R, Python, JavaScript, and PHP
- Object-oriented software design
- Cloud data processing experience using AWS and Hadoop
- HPC programming using Intel Phi-cards
- Data Analysis using the ggplot2, RMarkdown, and d3.js

Experience

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

- Developed MetaPathways, a Python and C++ pipeline for next-generation sequencing data
- Implemented a Master-worker distributed algorithm for managing a collection of non-cooperative HPC worker grids.
- Processed next-generation sequencing information in Hadoop via 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 sequence analysis for 60+ post-docs, graduate students, and professors
- Statistical topics: Linear Models, SVMs, Hierarchical Clustering, PCA, NMDS
- Data Visualization in R: lattice, ggplot2, and RMarkdown

Software Developer *2011*
Microbiology and Immunology, UBC

- Developed a database-driven web-application for bacterial strains
- Utilized the LAMP stack, JavaScript, and PHP to create an easy-to-use web interface
- Implemented usability improvements via an advanced search form, user search histories, and intelligent autocomplete

Projects

- **De-Confusion Tables**. An interactive R shiny app. Final project. Developing Data Products. John Hopkins University Coursera Class. July 2014 (http://goo.gl/FI78Qh).
- **D3.js Visualizations**. Variety of visualizations in the d3.framework for analysis of genomic data (http://goo.gl/fLntUc).
- **R-Package: fastLCA**. Implementation of correlation method fastLCA in C and Open-MP (http://goo.gl/5QPM82).

Selected Publications

For full references see Google Scholar (http://goo.gl/aYo3Wa).

- Kim, Konwar, **Hanson**, *et al.* Koonkie: An Automated Software Tool for Processing Environmental Sequence Information using Hadoop. ASE BigData. Harvard. (2014)
- **Hanson**, *et al.* MetaPathways v2.0: A master-worker model for environmental Pathway/Genome Database 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 Bioinformatics (2013)

Journal & Conference Reviewing

- IEEE Conferences CIBCB 2014 and 2015
- Symposium on Bioinformatics Research and Applications ISBRA 2015

Interests

Data Analysis, Information Visualization, Machine Learning, Statistics, High-performance Computing, Web-app Creation, Software Design

References

Provided upon request.