

STACY HUNG

BIOINFORMATICIAN AND FRONT-END DEVELOPER

CONTACT



sshung@gmail.com



[linkedin.com/in/stacyshung/](https://www.linkedin.com/in/stacyshung/)



github.com/stacyhung

LANGUAGES

- R
- Perl
- Java
- SQL
- Bash
- Git
- HTML
- CSS
- Javascript
- Python
- Snakemake

SUMMARY OF QUALIFICATIONS

- Excellent experience in tool development and bioinformatics methods
- Proven analytical, problem-solving and time management skills
- Solid expertise in data mining and data management and analysis
- Exceptional organizational, written and oral communication skills
- Attentive to detail, superior work ethic, independent and team player

RELEVANT EXPERIENCE

SENIOR BIOINFORMATICS SCIENTIST

BC Cancer | Vancouver, BC | May 2017 - present

- Oversee the bioinformatics group (4-6 members) for the Steidl Lab
- Supervise co-op students on MySQL database and R Shiny app development
- Manage space requirements and organization of computational infrastructure
- Provide bioinformatics support for in-house scientists related to NGS analysis, bioinformatics tool development and scientific research questions

BIOINFORMATICS SCIENTIST

BC Cancer | Vancouver, BC | Aug. 2013 - May 2017

- Implemented workflow for the generation of personalized onco-genomics reports leveraging molecular, high-throughput genomics and clinical data to inform on custom treatment options for 300+ lymphoma patients
- Developed Snakemake and R workflows for the analysis of whole-exome and RNAseq datasets across lymphoma patient cohorts and cell lines
- Validated targeted sequencing pipeline using orthogonal approach resulting in a 98.5% accuracy rate for somatic calling
- Employed Bayesian models for integrative analysis of genome-wide microarray and siRNA data to uncover gene target candidates for lung cancer therapies

PHD STUDENT

Department of Molecular Genetics | University of Toronto | Sept. 2007 - Aug. 2013


- Dissertation: *Metabolic Network Analysis of Apicomplexan Parasites to Identify Novel Drug Targets*
- Designed innovative computational methods for more accurate enzyme classification
- Built robust pipeline for metabolic network reconstruction that has been applied to 18+ parasite genomes, and contributed to top-tier science journals including *Nature*
- Analyzed genome-scale microarray and RNA-seq datasets using comparative transcriptomics approaches
- Performed qPCR, functional complementation, spectrophotometric assays, and gene knockouts in *Toxoplasma gondii* to characterize enzymes of therapeutic interest

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EDUCATION

Ph.D. | Molecular Genetics

Collaborative Program in
Genome Biology and
Bioinformatics | University of
Toronto | Toronto, ON
2007 - 2013

**B.Sc. | Honours Biology &
Bioinformatics** | University of
Waterloo | Waterloo, ON
2002-2007

RELEVANT EXPERIENCE (CONT'D)

BIOINFORMATICS RESEARCHER

University of Toronto | Toronto, ON | Apr. - Aug. 2007

- Benchmarked predictive capacity of protein-protein interaction prediction tool
- Refactored Java plug-ins for network visualization software Cytoscape

BIOINFORMATICS SOFTWARE DEVELOPER

Sanofi Pasteur | Toronto, ON | May - Aug. 2004 and May - Aug. 2006

- Developed visualization tools in Java for genome, protein and sequence analysis
- Designed and implemented Java user interface for standardized report generation
- Constructed MySQL database to house antigen-specific information

BIOINFORMATICS RESEARCHER

Michigan State University | East Lansing, MI USA | Jan. - Apr. 2005 and Sept. - Dec. 2005

- Developed novel visualization tools, including custom k-means algorithm, in Java for analyzing and interpreting gene expression data
- Implemented comparative approaches in Java, R and SQL to identify response elements in human and mouse

SELECTED PUBLICATIONS

Hung, S.S.* and Mottok, A.*, et al. Integrative genomic analysis elucidates key oncogenic pathways in primary mediastinal B-cell lymphoma. **Blood**, 134(10):802-813 (2019).

Hung, S.S., Meissner, B., et al. Assessment of Capture and Amplicon-Based Approaches for the Development of a Targeted Next-Generation Sequencing Pipeline to Personalize Lymphoma Management. **Journal of Molecular Diagnostics**, 20(2):203-214 (2018).

Hung, S.S. and Parkinson, J. Post-genomics Resources and Tools for Studying Apicomplexan Metabolism. **Trends In Parasitology**, 27(3):131-140 (2011).

Hung, S.S., Wasmuth, J., et al. DETECT—a Density Estimation Tool for Enzyme Classification and its application to Plasmodium falciparum. **Bioinformatics**, 26, 1690-1698 (2010).

EXTRACURRICULAR ACTIVITIES

- Team Captain, Ride to Conquer Cancer: Team Blood, Sweat and Cures (2018, 2019)
- Team Captain, Cycle for Survival: Team Palo Alto (2016)
- Rider, Ride to Conquer Cancer (2014, 2015, 2018, 2019) - raised a cumulative \$16,250
- Rider, Cypress Challenge (2015 - 2020) - raised a cumulative \$3,855