

# STACY HUNG

BIOINFORMATICIAN AND ASPIRING FRONT-END DEVELOPER

## CONTACT



sshung@gmail.com



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



[github.com/stacyhung](https://github.com/stacyhung)

## LANGUAGES

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

### ASPIRING FRONT-END DEVELOPER

Feb 2020 - present

- Building personal website: <https://github.com/stacyhung/stacyhung.github.io>

### 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
- 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 Apicomplexans 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*
- 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