VICTOR YUAN

Vancouver, BC, Canada · 236-998-9998 victor.2wy@gmail.com · Github @wvictor14 · victor.rbind.io

Genomics scientist with 5 years of experience leading and collaborating on multidisciplinary projects in prenatal health and biology, with a specific focus on epigenomics, transcriptomics, and genomics. Expert at analyzing and interpreting genomics data. Strong communicator with experience presenting at many conferences, authoring 10 publications, and publishing bioinformatic tools.

SKILLS

- Genomic analysis for single cell RNAseq, DNA methylation, genetics/genomics
- R, Bioconductor, Shiny, R package development, Python, Linux/Bash, high performance computing

EXPERIENCE

(2019 – present) University of British Columbia Bioinformatics R package developer, planet

- Developed analysis and processing tools in a pipeline for placental epigenetic analysis, implemented in an R package called planet. Wrote well-documented code resulting in a publication on Bioconductor with 800 downloads.
- Development of a processing pipeline and analysis platform to investigate high throughput DNA methylation and genetic data, which is regularly used internally to process 100s of microarray samples.
- In <u>Yuan 2019</u>, I used machine learning to develop a predictor of ethnicity and genetic ancestry based on DNA methylation and genotyping microarray data.
- In <u>Lee 2019</u>, I advised on study design to develop a machine learning model to predict epigenetic age from DNA methylation data, which resulted in a publication in *Aging*.

(2016 – 2022) University of British Columbia

Doctoral Researcher

- In <u>Yuan 2021</u>, I analyzed cell-specific epigenomics in placental samples. Aided study design, generated data, conducted analysis, and authored manuscript, resulting in a publication in *BMC Genomics*.
- Used single cell RNA seq data to identify gene targets to help wet lab scientists create a robust sample collection protocol, which we used to collect over 200 samples.
- Communicated findings through regular monthly internal reports, several annual local conferences, and 2 international conferences.
- Developed an interactive genome browser in Rshiny to visualize high dimensional genomic data, and integrated with UCSC gene information to provide genomic context. This app is used regularly internally and publicly to identify cell-specific genes.

(2018 – 2019) University of British Columbia

Bioinformatics support for single cell RNAseq analysis

• In <u>Treissman, Yuan, ... (2020)</u>, I analyzed single cell RNAseq datasets to validate *in vivo* cell-based developmental models for placenta diseases, resulting in a second author publication, and a pipeline for single cell RNAseq analysis, which is used internally.

- Identifying gene targets and characterizing biological mechanisms of action using omics
- Computational biology, genetics, statistics, applied machine learning, data visualization

• In <u>Wilson, Yuan, ... (2022)</u>, I used public single cell RNAseq datasets to identify commonly expressed genes between heart and placenta, as potential targets for treatment and improving our understanding of congenital heart disease.

(2017 – 2019) University of British Columbia

Bioinformatics support, Doctoral Researcher

• Processed and analyzed TCGA cancer samples for two projects to identify sub-types.

(2014 – 2016) Concordia University

Cell and Molecular Biology Undergraduate Researcher

• For my honours thesis, I optimized a CRISPR protocol for the yeast *c. albicans.*

LEADERSHIP

(2019 – 2020) University of British Columbia

Teaching Assistant for STAT545

• Taught 2 lectures, updated course materials on rmarkdown-based github-hosted class website, and marked deliverables, resulting in improved student learning and satisfaction as determined by end of positive term course and student evaluations.

(2017 - 2022) University of British Columbia

Student mentor for Robinson Lab trainees

• Mentored 6 undergraduate, masters, and PhD students, on genomics study design, and teaching advanced scientific, computational, and communication skill. Wrote analysis pipelines in R and linux for various genomic studies, which resulted in successful thesis projects and follow-up experiments.

(2017 – 2022) University of British Columbia

Workshop content developer and host

• Designed, developed, and hosted 7 workshops on topics including lay scientific communication, and various topics in R programming. Received positive feedback on content and workshop logistics, and increased demand for future workshops.

EDUCATION

2022 (Spring), University of British Columbia, Vancouver, BC, Canada PhD in Genome Sciences and Technology

- (\$1000) Data Science Award, Department of Statistics
- (\$105,000 CAD / 4 years) Frederick Banting and Charles Best Canada Graduate Scholarships Doctoral

2016 Concordia University, Montréal, QC, Canada Bachelor of Science in Cell and Molecular Biology

SELECTED PUBLICATIONS

- 1. Yuan V, Hui D, Yin Y, Peñaherrera MS, Beristain AG, Robinson WP. BMC Genomics. 2021.
- 2. Yuan V, Price EM, Del Gobbo G, Mostafavi S, Cox B, Binder AM, et al. *Epigenetics & Chromatin*. 2019.
- 3. Wilson RL, **Yuan V**, Courtney JA, Tipler A, Cnota JF, Jones HN. *Nature Sci Rep*. 2022.