

# Jin Kweon, MSc

437-240-1343 | Montreal, Canada | [yjkweon24@berkeley.edu](mailto:yjkweon24@berkeley.edu) | <https://www.linkedin.com/in/jin-kweon/>

## SUMMARY

Analytical and results-driven data scientist with a strong foundation in data analysis and computational biology gained through a Master's in Experimental Medicine at McGill University and hands-on research experience. Skilled in developing scalable algorithms and statistical models to uncover biological insights. Seeking opportunities in data analytics, computational biology, or bioinformatics to apply expertise in Python, R, and machine learning to solve complex problems.

## EDUCATION

### McGill University

MSc, Experimental Medicine – GPA: 4.00

Thesis: "DTractor: Advancing cell type deconvolution of spatial transcriptomics with deep neural network, transfer learning and matrix factorization"

Montreal, QC

Jan 2023 – Dec 2024

### McGill University (Military service: 2019 – 2021)

PhD Candidate, Quantitative Life Science Withdrawn

Montreal, QC

Aug 2018 – Dec 2021

### University of California, Berkeley

Bachelor of Arts, Statistics (Focus: Mathematics / Economics) – Major GPA: 4.00

Berkeley, CA

Aug 2016 – May 2018

- **Relevant Coursework:** Applied Machine Learning, Structure and Interpretation of Computer Programs, Multivariate Statistics, Linear Algebra, Linear Modeling, Statistical Bioinformatics, Genomics for drug discovery and development

## WORK & LEADERSHIP EXPERIENCE

### Copoly.ai and Genentech

Computational Biologist

Toronto, ON

May 2025 – Present

- Developed novel statistical framework to detect disease-associated cell-cell interactions through differential correlation analysis of cell abundance, extending beyond methods like CNA and Milo to capture complex disease mechanisms.
- Designed systematic pairwise interaction testing framework across cellular neighborhoods using interaction terms, enabling detection of coordinated disease responses in ophthalmology, immunology, and IBD with genetics and spatial integration.
- Accelerated therapeutic target discovery by modeling synergistic interactions between cellular neighborhoods in disease pathology using single-cell atlas data as key contributor within gCS CBT-OMNI department.

### Montreal General Hospital

Data Analyst

Montreal, QC

Feb 2025 – Present

- Pioneered ESDE 2025 award-winning methodology merging multiple clinical databases (REDCap, TSQIC, ACCESS) that revealed preoperative emotional distress significantly extends hospital stays in esophageal cancer patients.
- Generated key findings on quality-of-life improvements 1-year post-esophagectomy: neoadjuvant treatment type has no effect on outcomes and severe preoperative symptoms predict greater surgical benefits.
- Led analysis team linking textbook outcome achievement (2021 consensus definition) with statistically significant improvements in recurrence and survival, establishing foundation for perioperative care optimization research.
- Developed web-based scoring tools for FACT assessments to serve the broader surgical oncology community, and benchmarked seven imputation techniques-including VAE, DAE, and Bayesian PCA-for clinical database optimization.

### Douglas Research Center

Computational Biologist

Montreal, QC

Mar 2025 – May 2025

- Boosted predictive accuracy from 55% to 95% by developing upgraded Python algorithms for meffil and ewaff R packages to detect differentially methylated positions by better leveraging non-linear relationships in the model between CpG methylation sites and phenotype variables.
- Engineered novel spline model methodology improving upon Enmix combp and bumhunter packages, successfully identifying previously undetectable sex-specific methylation regions and site changes across tissues and age.
- Created comprehensive model framework to analyze both sex-dependent and sex-independent methylation effects while ensuring robust evaluation of tissue-specific or tissue-consistent proliferation patterns over age.

### Research on developing cell type deconvolution algorithms

Montreal, QC

- Implemented the *DTractor* software that demonstrated higher accuracy, resolution, robustness, efficacy, and scalability on two simulated datasets and three real datasets, outperforming eight other popular and commonly used deconvolution methods.
- Developed a method that uses deep neural network training on sc/snRNA-seq and spatial transcriptomics (ST) data, incorporating transfer learning from scRNA-seq reference data to ST data, and conducting iterative matrix factorizations.
- Decomposed ST at cell-type resolutions to gain insights into spatial organization in pancreatic adenocarcinoma, uncovering tumor microenvironment interactions and offering rare capability to estimate cell counts per location.

**Research on developing AI drug design-related algorithms**

Montreal, QC

Research Analyst (single cell project)

Sep 2021 – Nov 2023

- Introduced *scBeacon*, an innovative framework built upon a VQ-VAE framework, deep contrastive siamese network, and a greedy iterative strategy, to effectively pinpoint differential genes and identify the same cell population across different biological conditions forming cluster pairs.
- Advanced biomarker discovery by liberating differential gene analysis from manual annotation constraints, enabling *scBeacon* to identify critical cluster pairs and potential therapeutic targets in COVID-19 datasets.
- Demonstrated therapeutic response by mapping cytarabine-induced cellular adaptations using optimal embedding vector quantization and probabilistic models, revealing elusive drug resistance pathways in treatment populations.

**Adecco and Apple**

Singapore

Apple Map Data Analyst

Jan 2022 – Dec 2022

- Optimized Apple Maps search accuracy in Korea through over 100 systematic evaluations of pedestrian routes, driving directions, search results, and auto-complete functions across iOS and macOS platforms.
- Resolved over 200 critical map bugs by implementing enhanced dataset analysis techniques, directly improving user navigation experience and reducing test-reported errors by 20%.
- Led development of comprehensive quality assurance protocols that measurably increased map data and query accuracy metrics across four key dimensions: location relevance, name verification, address precision, and pin placement.

**Onbi, a smartphone application development company**

Seoul, South Korea

Co-founder & CFO

Nov 2012 – June 2017

- Successfully led the “School Mom” project, an app designed to provide news and services to parents, resulting in our application being adopted by nearly 12,000 schools and attracting 50,000 users in Korea by conducting extensive surveys and researching trends and needs over several years.
- Organized an application that earned 2nd place in a South Korean National Founding Contest, with "School Mom" being recognized as influential in many schools nationwide.
- Managed diplomatic negotiations with major investors, securing a \$100,000 contract through effective cold-calling.
- Achieved a net profit of over \$10,000 within six months through meticulous budget management and consulting.

**SKILLS**

- Proficient in R, Python [pytorch, tensorflow, scanpy]. Basic knowledge of Java, SQL, CSS, HTML, MATLAB, Linux, C++

**PUBLICATIONS & ACKNOWLEDGEMENTS**

- **Yong Jin Kweon**, Chenyu Liu, Gregory Fonseca, Jun Ding (2025). DTractor enhances cell type deconvolution in spatial transcriptomics by integrating deep neural networks, transfer learning, and matrix factorization. <https://www.biorxiv.org/content/10.1101/2025.04.12.648541v1>  
GitHub: <https://github.com/mcgilldinglab/DTractor>
- Chenyu Liu, **Yong Jin Kweon**, Jun Ding (2023). scBeacon: single-cell biomarker extraction via identifying paired cell clusters across biological conditions with contrastive siamese networks. <https://arxiv.org/abs/2311.02594>  
GitHub: <https://github.com/mcgilldinglab/scBeacon>
- Yuying Lu, Camille Morencé, **Yong Jin Kweon**, Archer Yi Yang, Jun Ding (2025). SC2CD Co-optimizes Spatial Clustering and Cell Decomposition through Bidirectional Information Flow in Single-Cell Spatial Transcriptomics.
- Haber, J.R. (2020). Sorting Schools: A Computational Analysis of Charter School Identities and Stratification. Sociology of Education. <https://doi.org/10.1177/0038040720953218>

## PRESENTATIONS

---

- Nisha Suarez, **Jin Kweon**, Mehrnoush Dehghani, Lorenzo Ferri, Sara Najmeh, Carmen Mueller, Jonathan Cools-Latrigue, Jonathan Spicer, Trafford Crump. (2025). Testing the effect of changes in emotional distress on post-esophagectomy outcomes. European Society for Diseases of the Esophagus (ESDE) conference. Amsterdam, Netherlands, May. 12, 2025. DOI: 10.17605/[OSF.IO/UWBN2](https://doi.org/10.17605/OSF.IO/UWBN2)
- Samir Amin, Joshua Cheruvathur, **Jin Kweon**, Mehrnoush Dehghani, Sara Najmeh, Carmen Mueller, Jonathan Cools-Lartigue, Lorenzo Ferri, R. Trafford Crump. (2025). Rethinking Recovery Predictors in Esophageal Cancer Surgery. European Society for Diseases of the Esophagus (ESDE) conference. Amsterdam, Netherlands, May. 12, 2025. DOI: 10.17605/[OSF.IO/QNHSE](https://doi.org/10.17605/OSF.IO/QNHSE).
- Albouy, P., **Kweon, Y.J.**, Whittaker, H., Baillet, S., Zatorre, R.J. (2018). Enhancing learning-related plasticity with information-based neuromodulation. Auditory learning and plasticity symposium. Montreal, Canada, Oct. 23, 2018.