

# Sean, Soonweng, Cho, PhD

Baltimore MD 21202 • sean.cho@jhmi.edu • +1(909)-618-7354

[github.com/sean-cho](https://github.com/sean-cho) • [www.linkedin.com/in/seanswcho](https://www.linkedin.com/in/seanswcho)

## Professional Summary

- Effective bioinformatician with 7 years computational biology and 8 years experimental biology experience.
- Excels in a dynamic, interdisciplinary setting with clinicians, biostatisticians, and experimental scientists.
- Competent in HPC and cloud computing for multi-omic NGS analysis and pipeline development.
- Developed five R packages, Shiny apps, and Python modules for genomics analysis and visualization.
- Well-versed in software version control in a collaborative setting using Git/Github.
- Efficient in data mining of publicly available genomic datasets including TCGA and 1000 Genomes.

## Relevant skills

Research Topics: Cancer genomics, biomarkers, immuno-oncology, mosaicism  
Programming: R & Shiny, Python & conda, Bash, SQL, Git  
Data Analysis: Biostatistics, machine learning, microarray, NGS, pipelines (Snakemake, CWL), genomics, epigenomics, transcriptomics  
Platforms: SGE, Slurm, Amazon Web Services, Seven Bridges Genomics, Docker  
Laboratory: Flow cytometry, qRT-PCR, molecular and cell biology techniques

## Education

Ph.D.	2016	Cellular and Molecular Medicine	Johns Hopkins School of Medicine
B.Sc.	2008	Biotechnology	California State Polytechnic University Pomona

## Professional Experience

### Kennedy Krieger Institute & Johns Hopkins University

Baltimore, MD

*Postdoctoral Fellow, Lab of Dr. Jonathan Pevsner*

*Dec 2016 - Current*

Characterization of somatic mosaicism in neurobehavioral disorders

- Analyzed NGS (genomic, 10x Genomics, and transcriptomic) data to identify variants associated with disease.
- Designed phase-aware computational methods for somatic variant discovery and prioritization that led to increased specificity in variant calling.
- Developed and maintained Dockerfiles and bioinformatics pipelines for high performance cluster or cloud computing to enable efficient genomic analysis and promote reproducibility.
- Generated a 14TB public resource of genomic variant call format (GVCF) files from 1000 Genomes to increase variant calling sensitivity using the Seven Bridges Genomics cloud computing platform.

### Johns Hopkins University School of Medicine

Baltimore, MD

*PhD Candidate, Labs of Drs. Christopher Umbricht and Saraswati Sukumar*

*Sept 2010 – Nov 2016*

*Thesis: Scarcity and sparsity – Genomics studies in a low resource setting*

Multi-omics analysis of archival tissue for biomarker discovery in breast and thyroid cancer

- Designed statistical framework & computational tools for integrative genomic & epigenomic analysis.
- Developed the Epicopy R package for estimating copy number variation from methylation microarrays, effectively increasing the amount and type of data obtained.
- Optimized protocols for DNA/RNA extraction from archival tissue and microarray analysis leading to greater nucleic acid yield and microarray quality.
- Actively collaborated on interdisciplinary teams to make decisions and discoveries for grants and research projects, resulting in thirteen publications.
- Led the development of bioinformatics research strategy, generated pilot data, and successfully co-wrote two competitively funded grants totaling \$300,000.

### Pfizer

La Jolla, CA

*Graduate Intern, Oncology: Computational Biology Group*

*Aug 2015 – Oct 2015*

Multi-omics analysis of breast cancer

- Led the analysis of genomic and transcriptomic data of a unique breast cancer cohort, resulting in a peer-reviewed publication in Nature Communications.

**City of Hope National Cancer Center**

*Research Associate, Lab of Dr. Michael Jensen*

Duarte, CA

*June 2008 – May 2010*

Immuno-oncology research in chimeric antigen receptor (CAR) T-cells

- Designed and constructed lentiviral vectors of CARs for T-cell therapy as a translational research team member.

**California State Polytechnic University, Pomona**

*Undergraduate Research, Lab of Dr. Wei-Jen Lin*

Pomona, CA

*Oct 2007 – June 2008*

Development of a transposon system for gene delivery in Gram-positive bacteria

- Modified and optimized the use of transposon Tn5 for large gene delivery through electroporation.

**Selected Publications** (5 out of 16; complete list at [tinyurl.com/seanswcho](http://tinyurl.com/seanswcho))

Cho S., Kim H., Cope L., Umbricht C. (Accepted, 2019) Measuring DNA copy number variation using high-density methylation microarrays. *Journal of Computational Biology*

Merino V.F. \*, Cho S. \* (equal contribution), Nguyen N., et al. (2018) Induction of cell cycle arrest and inflammatory genes by combined treatment with epigenetic, differentiating, and chemotherapeutic agents in triple-negative breast cancer. *Breast Cancer Research*

Kan Z., Ding Y., Kim J., Jung H.H., Chung W., Lal S., Cho S., et al. (2018) Multi-omics profiling of younger Asian breast cancers reveal distinctive molecular signatures. *Nature Communications*

Kim HS, Umbricht CB, Illei PB, Cimino-Matthews A, Cho S., Chowdhury N., et al. (2016) Optimizing the use of gene expression profiling in early stage breast cancer. *JCO*

Fackler M.J., Bujanda Z.L., Umbricht C., Teo W.W., Cho S., Zhang Z., ..., Sukumar S. (2014) Novel methylated biomarkers and a robust assay to detect circulating tumor DNA in metastatic breast cancer. *Cancer Research*

**Invited Talks**

Cho, S. (2014) "Epicopy: Measuring DNA copy number using Illumina 450K methylation microarrays". Computational Genomics Symposium, Johns Hopkins Hospital

**Posters**

Cho, S., et al. (2016) "Characterization of metastatic follicular thyroid cancer by RNA-seq." 2016 Annual Meeting, American Thyroid Association, Denver CO

Cho, S., et al. (2016) "Characterization of metastatic follicular thyroid cancer by RNA-seq." Surgical Fellows Research Symposium 2016, Johns Hopkins Hospital

Cho, S., et al. (2015) "Epicopy: Measuring DNA copy number variation using Illumina high density methylation microarrays." AACR Annual Meeting 2015, Philadelphia PA

Cho, S., et al. (2015) "Epicopy: Measuring DNA copy number variation using Illumina high density methylation arrays." Safeway Breast Cancer Retreat 2015, Baltimore MD

**Teaching**

Bio-Trac, Bioscience Education Center

Germantown, MD

Guest Lecturer, Advances in Epigenetics: Epigenomics Lecture and Lab

2018

Johns Hopkins University

Baltimore, MD

Teaching Assistant, Practical Genomics Workshop

2018

Tutor (Cellular & Molecular Medicine), Molecular Biology and Genomics

2012