# BEIJING WU

beijing0128@gmail.com

+1.408.221.2544

Pleasanton, CA 94566

## ABOUT

I am an experienced researcher in the biomedical field. My career goal is to maximize the synergy between genomic medicine and biomedical informatics to provide patients with precisely targeted treatment recommendations. I aim to develop tools and quantitative methods needed to discern signals and elucidate patterns in large biological data sets to inform product strategies and guide assay and bioinformatic pipeline development.

## EDUCATION

**Bachelor of Science**
*magna cum laude*
**Pharmacological Chemistry**

UC San Diego • La Jolla, CA
December 2009
GPA: 3.845

## RELEVANT SKILLS

**Programming Languages:**
C++, Python, R, Bash (Unix Shell)

**Data Analyses:**
Data Query, Data Cleaning and Preparation, Exploratory Analysis, Statistical Modeling, Machine Learning

**Data Visualization:**
ggplot2, shiny, matplotlib, PowerBI

**Soft Skills:**
Problem-Solving, Attention to Detail, Research, Communication (Written, Verbal, and Visual), Convert Data-Based Insights into Decisions, Teamwork

## PROFESSIONAL EXPERIENCE

**Principal Scientist**                    August 2018 – Present

Reagent and Assay Development, Roche Sequencing Solutions, Pleasanton, CA

- ❖ Focused on the development of the KAPA Target Enrichment products from business development activities to product launch and post-launch product care.
- ❖ Worked closely with software engineers and bioinformatics teams to develop customer-facing data analysis pipeline.

**Senior Research Associate**              July 2017 – August 2018

Research and Development, GRAIL Inc., Menlo Park, CA

- ❖ Developed GRAIL's targeted methylation assay to target key informative genomic regions, which allowed targeted methylation analysis of cell-free DNA to detect multiple cancer types, at early stages, at >99% specificity for population screening.

**Life Science Research Professional**     January 2010 – July 2017

Department of Genetics, Stanford University School of Medicine, Stanford, CA

- ❖ Invented Single Cell ATAC-seq (Assay for Transposase Accessible Chromatin) on a programmable microfluidics platform, which analyzes chromatin accessibility at single-cell level, enabling the construction of an epigenomic landscape of human hematopoiesis to characterize differentiation trajectories, and providing insights into gene regulatory mechanisms. This work was featured in *Nature Biotech* and *Genome Biology.*
- ❖ Eleven (11) relevant peer-reviewed publications, including second author papers in *Nature* and *Nature Genetics*.

**Undergraduate Researcher**              January 2009 – December 2009

Department of Chemistry and Biochemistry, UC San Diego, La Jolla, CA

- ❖ Worked on a biophysical research project on the thermodynamics and kinetics of *E. coli* outer membrane protein folding. Contributed to a publication in *Biophysical Journal*.

## RELEVANT COURSES & CERTIFICATION

**Linear Algebra for Machine Learning** • UCSD Extension
Winter 2019

**Data Abstract & Structures** • De Anza College
Spring 2020

**Data Visualization Method and Tools** • De Anza College
December 2020

**Applied Data Science Specialization by IBM** • Coursera

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|---|---|
| Python for Data Science and AI | November 2020 |
| Data Analysis with Python | Credential ID: |
| Data Visualization with Python | WMZV82JT53HZ |
| Applied Data Science Capstone | |

**Machine Learning by Stanford University** • Coursera
Expected Completion February 2021