

# Michael Son

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Meticulous and analytical researcher with expertise in molecular biology techniques and data analysis. Detail-oriented and methodical professional proficient in conducting rigorous experimental research utilizing state-of-the-art equipment. Familiar with gathering, cleaning, and organizing data for use by technical and non-technical personnel. Advanced understanding of statistical, algebraic, and other analytical techniques.

## SKILLS

- Programming Languages: Python | SQL  
Libraries: NumPy | pandas | Matplotlib | Seaborn | Plotly | Scikit-Learn | Imbalanced-Learn | XGBoost | Keras | Scikit-Image
- Data Science: Data Cleaning | Data Analysis | Data Visualization | Feature Engineering | Machine Learning | Neural Networks | Deep Learning
- Molecular Biology Techniques: Cell Culture | Western Blot | Immunocytochemistry | DNA/RNA Isolation | Molecular Cloning | PCR
- Analytical Techniques: UV-VIS Spectroscopy | Dynamic Light Scattering | Zeta Potential | Analytical Ultracentrifugation | SEDFIT | SEDANAL | Oligonucleotide Quantification | Capillary Electrophoresis | qPCR | Fragment Analysis | EvaEZ Fluorometric Polymerase Assay | Qubit dsDNA HS Assay
- Equipment Used: Analytikjena Specord 210 Plus | Malvern Instruments Zetasizer Nanoseries | Veriti Dx Thermal Cycler | Beckman Coulter Optima L-90K Ultracentrifuge | 7900HT Fast RT-PCR System | Agilent Fragment Analyzer System | Applied Biosystems 3500 Series Genetic Analyzer | Applied Biosystems SeqStudio Flex Series Genetic Analyzer

## PROJECTS

### Lending Club Loan Approval Optimization

- Constructed a binary classifier to differentiate unprofitable loans from the rest.
- Tools Used: NumPy | pandas | Matplotlib | Seaborn | Scikit-Learn | Imbalanced-Learn | XGBoost
- Best Model: eXtreme Gradient Boosting
- Best Model Performance: Minority F1 = 0.56 | Majority F1 = 0.89 | ROC AUC = 0.80  
Accuracy = 83%

### Melanoma Tumor Size Prediction

- Developed a regressor to predict melanoma tumor sizes.
- Tools Used: NumPy | pandas | Matplotlib | Seaborn | Scikit-Learn | Keras
- Best Model: Random Forest
- Best Model Performance: MSE = 8.25 | R2 = 0.23

## WORK EXPERIENCE

### Associate Scientist II – R&D

01/2022 – Present

*Tecan Genomics, Inc. | Redwood City, CA*

- Design and conduct experimental studies to develop enzymes used in NGS library preparation.
- Develop and perform various molecular assays for QA/QC of enzymes.

### System Verification & Validation Engineer, Scientist

08/2021 – 01/2022

*Thermo Fisher Scientific | South San Francisco, CA*

- Performed various verification tests on the Applied Biosystems SeqStudio Flex Series Genetic Analyzer, as a member of the Verification & Validation team.
- Filed and reported deviations observed during the verification tests of the Applied Biosystems SeqStudio Flex Series Genetic Analyzer.
- Identified and corrected errors in test protocols and associated documentation, contributing to quality assurance.

### Engineering Intern

05/2017 – 08/2017

*IMS & Nano Tech Co., Ltd. | Seoul, South Korea*

- Evaluated potential algorithms for the signal processing of 3D imaging sensors based on white light scanning interferometry (WSI), as a member of the Research & Development team.
- Recommended and implemented the SEST algorithm in the imaging sensor in development, witnessed significant improvement in the scanning speed while retaining the accuracy.
- Inspected technical translation of imaging device configuration and notification settings for quality assurance.
- Identified and fixed technical translation errors in configuration and notification settings of the imaging device, enabling the product shipping without any delays or losses.

### Student Research Assistant

05/2013 – 08/2013

*Korea Institute of Science and Technology | Seoul, South Korea*

- Performed cell culture, western blot, immunocytochemistry, DNA/RNA isolation, PCR, and molecular cloning for the in vitro loss-of-function studies on PAR 3/6 proteins.
- Verified the extent of PAR 3/6 proteins' influence on the axon regeneration of adult mice dorsal root ganglion.
- Planned and executed chronic stress model study entailing axon regeneration in adult mice neurons.

## EDUCATION

### Data Science Career Track

05/2021

*Springboard | San Francisco, CA, US*

- Hands-on curriculum with 1:1 industry expert mentor oversight, and completion of 2 in-depth capstone projects.
- Mastered skills in Python, SQL, data analysis, data visualization, hypothesis testing, and machine learning.

### Master of Science | Chemical and Bioengineering

09/2019

*Friedrich-Alexander-Universität Erlangen-Nürnberg | Erlangen, Bavaria, Germany*

Master's Thesis: Protein Aggregation Studies of the Model System Beta-Lactoglobulin via Multiwavelength Analytical Ultracentrifugation

- Conducted a comprehensive investigation into protein aggregation, utilizing nanoscale analytical equipment such as Zetasizer and Optima L-90K Ultracentrifuge equipped with multiwavelength (MWL) absorbance optics to perform several advanced analytical techniques including dynamic light scattering (DLS) and analytical ultracentrifugation (AUC).
- Analyzed the concentration and pH-dependence of protein-protein interaction (PPI) via SEDFIT and SEDANAL.
- Successfully quantified the monomer-dimer self-association kinetics of PPI using equilibrium coefficient and solution non-ideality parameters (Gralen coefficient, diffusion interaction parameter, osmotic second virial coefficient).
- Endorsed AUC as a profound quantitative method for analyzing protein solution behavior.

**Honours Bachelor of Science | Neuroscience/Cell Molecular Biology Double Major**

06/2014

*University of Toronto – St. George | Toronto, ON, Canada*

- HBS. in Neuroscience and Cell Molecular Biology with an emphasis on human biology, cell biology, and associated pathologies.