JOY NYAANGA

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Ph.D. Candidate

Contact
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Programming
R
Python
Bash
SQL

Tools
RStudio
Jupyter
git/GitHub
AWS
HPC (SLURM)

Data Science
Data visualization
Markdown reports
Machine Learning
Advanced statistical analysis

Research
Experimental design
Package development
Pipeline development
Interdisciplinary collaboration

EDUCATION

Ph.D., Quantitative Biology   **Expected May 2022**
Northwestern University
GPA: 3.9/4.0

M.A., Molecular Biology   **2017 - 2018**
Princeton University
GPA: 3.6/4.0

B.S., Chemistry: Biochemistry   **2013 - 2017**
B.S., Cell & Molecular Biology
John Carroll University
GPA: 3.64/4.0

EXPERIENCE

Ph.D. Candidate   **2018 - Present**
Northwestern University

- Conduct extensive analysis of large experimental data sets in R
- Implement advanced analytical and statistical methods including linear mixed effect models, ANOVA/regression models, model selection, clustering, and maximum likelihood classification in R
- Execute bash scripts for data analysis on HPC with SLURM
- Design and develop an R package hosted on GitHub to facilitate handling and visualization of image-based data
- Present published work at regional and international conferences
- Communicate advanced concepts and articulate key results to interdisciplinary collaborators
- Mentored and managed a team of 6 research assistants in data collection and coding

Data Science Intern   **May 2021 – Sept 2021**
Celsius Therapeutics

- Coded extensively in Python and R to analyze single-cell RNAseq data using supervised and unsupervised machine learning tools
- Analyzed clinical-stage sequencing data to uncover new insights into disease progression using trajectory inference algorithms
- Generated comprehensive reports using Rmarkdown and Jupyter to deliver findings with team leads
- Maintained a reproducible coding environment on AWS EC2 instance

Graduate Researcher   **2017 – 2018**
Princeton University

- Built computational ODE models in Python to study the dynamics of protein networks
- Probed RNA-protein interactions to uncover cellular changes caused by oxidative stress

PUBLICATIONS

Nyaanga, J. Crombie, T. A., Widmayer, S. J. & Andersen, E. C. easyXpress: An R package to analyze and visualize high-throughput *C. elegans* microscopy data generated using CellProfiler. PLoS One (2021)

[Preprint] Nyaanga, J. *et al.,* Highly scaled measurements of *C. elegans* development suggest that physical constraints guide growth trajectories and animal shape. bioRxiv (2021)