# JOY NYAANGA, PHD

# **Bioinformatician**

# 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

Genetics & Genomics R package development Interdisciplinary collaboration

### **EDUCATION**

Ph.D., Quantitative Biology
Northwestern University
GPA: 3.9/4.0

M.A., Molecular Biology
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**

#### Bioinformatician 2022 - Present

Northwestern University

- Manage, organize, and analyze whole-genome sequence data
- Develop and maintain bioinformatics pipelines for variant calling, population genomics, and genome-wide association mappings

#### Ph.D. Candidate 2018 - 2022

Northwestern University

- Conduct extensive analysis of large experimental data sets in R to investigate organismal growth and development
- Implement advanced analytical and statistical methods including linear mixed effect models, ANOVA/regression models, model selection, and clustering in R

#### **Data Science Intern**

May 2021 – Sept 2021

Celsius Therapeutics – a therapeutics company leveraging single-cell RNAseq data to develop and deliver precision medicines.

- Coded extensively in Python and R to analyze single-cell RNAseq 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)

**Nyaanga**, **J.** et al. Changes in body shape implicate cuticle stretch in *C.* elegans growth control. *Cells & Development* (2022)

**[preprint] Nyaanga**, J. & Andersen E.C. Linkage mapping reveals loci that underlie differences in C. *elegans* growth. *bioRxiv* (2022)