

# NATHANIEL HAWKINS

I am currently pursuing my PhD in computational biology at Michigan State University. My research is on applying methods from the field of natural language processing to analyzing biomedical text. Included in this work are aspects of machine learning, data science, algorithm design/development, and high-performance computing.


I am broadly interested in the field of computational science and using computers to advance our understanding of complex problems. My general areas of interest include machine learning, scientific software development, algorithms and data structures, parallel programming and multiprocessing, high-performance computing, and the application of these concepts to solving domain-specific problems.



## EDUCATION

2019

### **PhD. Student, Computational Biology**

Department of Computational Mathematics, Science, and Engineering  
 Michigan State University

- Applying natural language processing methods for analyzing biomedical text
- Engineering Distinguished Scholar
- Rasmussen Fellow

2014  
|  
2018

### **B.S., Physics (Minor Computational Science)**


Department of Physics And Astronomy  
 Michigan State University

- Board of Trustee's Scholar

## SELECTED POSITIONS

2018  
|  
2019

### **Curriculum Developer and Educational Researcher**

Department of Computational Mathematics, Science, and Engineering  
 Michigan State University

- Conducted research interviews with experts in the field of computational science to understand practices and key concepts to broadly inform the development of future curricula.
- Performed comprehensive review of department's existing undergraduate computational modeling and data science curricula.
- Created course materials on introductory python programming (e.g. numpy arrays, version control in git, agent-based modeling using python class, etc.).

2017  
|  
2018

### **Undergraduate Researcher**

Piermarocchi Group  
 Michigan State University

- Developed algorithm to determine "best" number of clusters in single-cell RNA sequencing data by calculating adjusted rand index of repeated trials as a measure of internal consistency.
- Applied algorithms and methods from statistical physics (e.g., the Hopfield model) to gene expression data to model the cell cycle and other attractor-based systems.
- Used virtual image creation software (Docker) to build and execute models on high performance cloud computing platforms.

## SELECTED PUBLICATIONS, POSTERS, AND TALKS

2019

### **Polled Digital Cell Sorter (p-DCS): Automatic identification of hematological cell types from single cell RNA-sequencing clusters**

BMC Bioinformatics

- Third author.

## CONTACT

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-  [github.com/nathawkins](https://github.com/nathawkins)
-  [nathawkins.info](http://nathawkins.info)
-  (269) 823-2741

## SKILLS

Highly experienced in

Python  
Bash  
C/C++

Experience with

OpenMPI  
CUDA  
R  
SQLite  
Ruby

## MORE INFO

See full CV at [nathawkins.info](http://nathawkins.info) for more complete list of positions, publications, and awards.

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