

# Daniel C. Morgan

SYSTEMS BIOLOGY & BIOINFORMATICS · PH.D.

11 Peabody Terrace | 02138 Cambridge, MA

☎ 617-331-6223 | ✉ Daniel.Morgan@Channing.Harvard.edu | 🌐 www.DanielCMorgan.com | 📷 dcolinmorgan | 🐦 @dcolinmorgan

## Education

### Stockholm University, Sonnhammer Lab

SciLifeLab Stockholm, SE

DOCTORATE OF COMPUTATIONAL SYSTEMS BIOLOGY

April 2019

- Co-Lead collaborative project with Nelander lab @ Uppsala University
- Posters at ICSB 2018 in Lyon and ISMB 2017 in Prague
- Accepted into and completed ISYCB summer program 2015

### The Ohio State University, Chen & Huang Labs

Columbus, OH

MASTER OF BIOINFORMATICS

Dec 2014

- Thesis – A Gene Co-expression Network Mining Approach for Differential Expression Analysis
- OSU Hayes Graduate Research Forum – Genomic Algorithm Identifies Herbs as Potential treatment in Bladder Cancer

### Miami University, Fisk & Letterio Labs

Oxford, OH

BACHELOR OF MICROBIOLOGY | CONCENTRATION: BIOCHEMISTRY & MOLECULAR BIOLOGY

May 2011

- MU Spring Research Forum – The Real Threat of Invasive Species to Southern Ohio Forest Health
- CWRU Research Conference – The Role of Cdk5 in the Survival, Proliferation, and Migration of the Medulloblastoma

## Experience

### Channing Division of Network Medicine, Brigham and Women's Hospital and Harvard Medical School

Boston, MA

POSTDOCTORAL RESEARCH FELLOW

2019-current

- Integrating multi-tissue, multi-omics across subject time points to detail lung disease as process of premature aging
- Investigating methylation potential to describe TF binding affinity for use in multi-omic GRN inference
- Sex-specific drug repositioning for COPD

### Nordling Lab

ME@NCKU, Taiwan

VISITING SCHOLAR

Feb 2017- May 2017

- Designing novel systems approach to balancing & minimizing input and output noise in linear models.

### Elevada

San Diego, CA

BIOINFORMATICS DATA ANALYST

June 2014- Dec 2015

- Remote testing and data analysis and extraction using novel web app & R back-end.
- Expanding Myelodysplastic Syndrome/ Acute Myeloid Leukemia project project to allow customers to compare disparate studies, as well as to primary data through incorporation of ontologies.

## Publications

- |      |  |                                |
|------|--|--------------------------------|
| 2020 | <b>Leveraging methylation information to predict TF binding: a benchmark study</b> , Morgan D, Glass K, DeMeo D  | (drafted)                      |
| 2020 | <b>gpuPANDA: Efficient estimation of gene regulatory networks using the Graphical Processing Unit</b> , Guebila M, Morgan D, Quackenbush J   | (drafted)                      |
| 2020 | <b>Perturbation-based gene regulatory network inference to unravel oncogenic mechanisms</b> , Morgan D, Studham M, Tjärnberg A, Nordling T.E.M., Sonnhammer E.L.L.                                     | (accepted)                     |
| 2018 | <b>A Generalized Framework for Controlling FDR in Gene Regulatory Network Inference</b> , Morgan D, Tjärnberg A, Nordling T.E.M., Sonnhammer E.L.L.  | Bioinformatics, PMID:30169550  |
| 2017 | <b>GeneSPIDER - Gene regulatory network inference benchmarking with controlled network and data properties</b> , Tjärnberg A <sup>†</sup> , Morgan D <sup>†</sup> , Nordling T.E.M., Sonnhammer E.L.L. | Mol. BioSystems, PMID:28485748 |
| 2015 | <b>A Gene Co-Expression Network Mining Approach for Differential Expression Analysis</b> , Morgan D, Huang K   | OSU library, osu1416989632     |