

Daniel C. Morgan

SYSTEMS BIOLOGY & BIOINFORMATICS · PH.D.

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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

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|------|--|---------------------------------------|
| 2020 | Leveraging methylation information to predict TF binding: a benchmark study , Morgan D, Glass K, DeMeo D | (under review) |
| 2020 | gpuPANDA: Efficient estimation of gene regulatory networks using the Graphical Processing Unit , Guebila M, Morgan D, Quackenbush J | (drafted) |
| 2020 | Perturbation-based gene regulatory network inference to unravel oncogenic mechanisms , Morgan D, Studham M, Tjärnberg A, Nordling T.E.M., Sonnhammer E.L.L. | Scientific Reports, Article no: 14149 |
| 2018 | A Generalized Framework for Controlling FDR in Gene Regulatory Network Inference , Morgan D, Tjärnberg A, Nordling T.E.M., Sonnhammer E.L.L. | Bioinformatics PMID:30169550 |
| 2017 | GeneSPIDER - Gene regulatory network inference benchmarking with controlled network and data properties , Tjärnberg A [†] , Morgan D [†] , Nordling T.E.M., Sonnhammer E.L.L. | Mol. BioSystems, PMID:28485748 |
| 2015 | A Gene Co-Expression Network Mining Approach for Differential Expression Analysis , Morgan D, Huang K | OSU library, osu1416989632 |