

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 Herbals 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

Hong Kong University, Lab of Data Discovery for Health

Hong Kong

RESEARCH FELLOW

2021-current

- Investigating primary metagenomic profiles across age
- Integrating and predicting single-cell across -omic

Harvard Medical School, Channing Division of Network Medicine

Boston, MA

POSTDOCTORAL RESEARCH FELLOW

2019-2021

- 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

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

2021	Sex-Specific Network-based Drug Repositioning in COPD , Morgan D , Lopes-Ramos C, Glass K, Quackenbush J, DeMeo D	<i>in-progress</i>
2021	Leveraging methylation information to predict TF binding: a benchmark study , Morgan D, DeMeo D, Glass K	<i>(pre-print)</i>
2021	gpuPANDA: Efficient estimation of gene regulatory networks using the Graphical Processing Unit , Guebila M, Morgan D, Glass K, Kuijjer M, DeMeo D, Quackenbush J	<i>(pre-print)</i>
2020	Uncovering cancer gene regulation by accurate regulatory network inference from uninformative data , Seçilmiş D, Hillerton T, Morgan D, Tjärnberg A, Nelander S, Nordling T.E.M. , Sonnhammer E.L.L	<i>NPJ Syst Biol Appl., PMID: 33168813</i>
2019	Perturbation-based gene regulatory network inference to unravel oncogenic mechanisms , Morgan D , Studham M, Tjärnberg A , Nordling T.E.M. , Sonnhammer E.L.L.	<i>Scientific Reports, PMID: 32843692</i>
2018	A Generalized Framework for Controlling FDR in Gene Regulatory Network Inference , Morgan D, Tjärnberg A , Nordling T.E.M. , Sonnhammer E.L.L.	<i>Bioinformatics PMID:30169550</i>