

Daniel C. Morgan

SYSTEMS BIOLOGY · PH.D. STUDENT

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“live in the world you make.”

Education

Stockholm University

Stockholm, SE

DOCTORATE OF COMPUTATIONAL SYSTEMS BIOLOGY

2015-2019

- Accepted to ISYCB summer program

The Ohio State University

Columbus, OH

MASTER OF BIOINFORMATICS 3.3 GPA

2012-2014

- 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

Oxford, OH

BACHELOR OF MICROBIOLOGY | CONCENTRATION: BIOCHEMISTRY & MOLECULAR BIOLOGY

2006-2011

- MUSpring 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

Science for Life Laboratory (SciLifeLab)

Stockholm, SE

RESEARCHER, PH.D. STUDENT

2015-2019

- Use RNAi to knockdown Myc pathway genes (multiple perturbation sets), use RNA-Seq to get expression matrix and earlier time points to get perturbation matrix.
- Produce model inspired by fluid dynamics to represent data properties.

Elevada

Columbus, OH & San Diego, CA

BIOINFORMATICS DATA ANALYST

June 2014-2015

- Myelodysplastic Syndrome/ Acute Myeloid Leukemia project
- Remote testing and data analysis and extraction using novel web application with R back-end.
- Expanding upon the MDS/AML project to allow customers to compute amongst differing studies, as well as to organize their own primary data through incorporation their own ontologies.

The Ohio State University Comprehensive Cancer Center

Columbus, OH

GRADUATE RESEARCH ASSISTANT

2013-2014

- Developed MATLAB matrix optimization methods for correlating therapy responsiveness, resulting in novel gene module identification in lung cancer patients.
- Investigated data from disparate levels of biology to identify novel micro-RNA whose increased expression in ovarian carcinoma is responsible for down regulating the protein expression of the associate gene, which is otherwise similarly expressed between terminal and survivor patient populations.
- Utilized network analysis methods for modeling disease, isolating pathways of perturbation, and relating to effects of drug interaction in restoring wild type gene expression.

Department of Molecular Biology, Miami University

Oxford, OH

ECOSYSTEM RESEARCH ASSISTANT

2010- 2011

- Set up experiments in wooded enclosures, collected field samples and interpreted findings.
- Collaborated with team to analyze and identify broad range microbial nutrient cycling, including community composition and genome mapping identification.
- Sequence microbial population; took soil samples from under indigenous and invasive plant species to determine nutritional relationship. Analyzed nitrogen and phosphorous composition to determine predominant populations.

Pharmacology Dept., Case Western Reserve University

Cleveland, OH

RESEARCH INTERN

Summers 2009&10

- Assayed the Medulloblastoma as an enigmatic adolescent brain tumor: in vivo via three mouse models , in vitro via three tissue cultures from human patients & induced mouse models.
- Investigated the chemical effect on antibody response. Used Diversity Oriented Synthesis to mimic natural structural change to ensure maximal chemical space coverage. Activated mouse macrophage cells with LPS, inoculated with small molecules derived from Lanosterol backbone & isolated protein after lysis.

Skills

LANGUAGES

- Proficient in MATLAB
- Familiar with R, Python, Perl, MySQL, Javascript, Unix systems

TECHNIQUES

- Proficient in PCR, Microarray, Western Blot, Cell Culture, Animal Husbandry
- Familiar with RPPA, RNA-Seq

Honors & Awards

DOMESTIC

2013-2014 **co-winner**, Jane A. Blank Award for outstanding bioinformatics graduate student

Columbus, OH

Presentation

tranSMART Foundation Annual Meeting

University of Michigan

PRESENTER REPRESENTING ELEVADA

Oct. 2014

- Introduced Elevada's ALS platform for comprehensive and aligned i2b2 ontologies, as well as including data from several formats

Publications

GeneSPIDER

A Tjärnberg et al.

JOURNAL OF BIOINFORMATICS

2015

- GeneSPIDER-Generation and Simulation Package for Informative Data ExploRation A Tjärnberg et al., 2015

Masters Thesis

D.Morgan & K.Haung

THE OHIO STATE UNIVERSITY

2014

- A Gene Co-Expression Network Mining Approach for Differential Expression Analysis Daniel C Morgan, 2015

References

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|------|--|-------------------------|
| 2015 | Torbjorn Nordling, Ph.D. , Assistant Professor Department of Mechanical Engineering National Cheng Kung University, tn@kth.se | <i>Ph.D. co-advisor</i> |
| 2014 | Kun Huang, Ph.D. , Associate Professor Senior Advisor, OSU Biomedical Informatics, Kun.Huang@osumc.edu | <i>M.Sc. co-advisor</i> |
| 2014 | Steven K. Clinton M.D., Ph.D. , Professor OSU College of Medicine, Steven.Clinton@osumc.edu | <i>M.Sc. project PI</i> |
| 2014 | James L. Chen, M.D. , Associate Professor OSU College of Medicine, James.Chen@osumc.edu | <i>M.Sc. co-advisor</i> |