Daniel C. Morgan

SYSTEMS BIOLOGY & BIOINFORMATICS · PH.D.

Hong Kong, Hong Kong

📱 +852-7075-2663 | ✉ dcolinmorgan@gmail.com | 🏠 https://dcolinmorgan.github.io | dcolinmorgan | 🐦 @dcolinmorgan

Skills

PROGRAMMING LANGUAGES

- Python, Bash Shell, R, MATLAB, Latex

CONCEPTS

- Network Science, Deep Learning / Machine Learning/ Statistics, Control Systems Theory,

DATA SCIENCE TOOLS

- RAPIDS/ CUDA, Pandas/ cudf, Numpy/ cupy, Pytorch, TensorFlow 2.0, SciPy/ cuml, Seaborn, Conda, d3.js

TOOLS/SOFTWARE

- Git/ Github, Jira, AWS, Docker/ Singularity, Linux

Experience

Graphistry.com — *San Francisco, CA*

(REMOTE) GRAPH, DATA, ML SCIENTIST/DEV — *2022-current*

- develop GPU-accelerated network analysis toolkit and libraries
- build graph-based analysis and machine learning pipelines
- serve biotech clients (metagenomics/-omics) to better understand and act on their data

University of Hong Kong, School of Biomedical Sciences — *Hong Kong*

POSTDOCTORAL RESEARCH FELLOW — *2021-2022*

- Profiling metagenomic bipartite species-protein networks in colorectal carcinoma and hypertension
- Time course investigation of response to antibiotic treatment
- Mentoring PhD and MSc students

Harvard Medical School, Channing Division of Network Medicine — *Boston, MA, USA*

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

National Cheng Kung University, Department of Mechanical Engineering — *Tainan, Taiwan*

VISITING SCHOLAR IN NORDLING LAB — *Feb 2017- June 2017*

- Designing novel systems approach to balancing, minimizing and optimize input and output noise in dynamical biological systems using differentiable regulatory models.

Genomenon.com (previously Elevada) — *San Diego, CA, USA*

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.

Ohio State University, Comprehensive Cancer Center — *Columbus, OH, USA*

GRADUATE RESEARCH ASSISTANT — *2013-2014*

- Developed optimization methods for correlating therapy responsiveness, resulting in novel gene module identification in lung cancer patients.
- Utilized network analysis methods for modeling disease, isolating pathways of perturbation, and relating to effects of drug interaction in restoring wild type gene expression.

Miami University, Department of Molecular Biology — *Oxford, OH, USA*

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.

Case Western Reserve University, Pharmacology Department *Cleveland, OH, USA*

Research Intern *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.

Publications

2023	**Altered human gut virome in patients undergoing antibiotics therapy for Helicobacter pylori**, Wang L, Yao H, **Morgan D**, et.al.	*(Nature Commun, PMID:37069161)*
2022	**Leveraging methylation to predict TF binding**, **Morgan D**, DeMeo D, Glass K	*bioRxiv, bioRxivID:491666*
2021	**gpuZoo: Cost-effective estimation of gene regulatory networks using the Graphics Processing Unit**, Guebila, Marouen Ben and **Morgan, Daniel C** and Quackenbush, John	*NARGAB, PMID:35156023*
2020	**Uncovering cancer gene regulation by accurate regulatory network inference**, Seçilmiş D, Hillerton T, **Morgan D**, Tjärnberg A, Nelander S, Nordling T.E.M. , Sonnhammer E.L.L	*NPJ Syst Biol Appl., PMID: 33168813*
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.	*Scientific Reports, PMID: 32843692*
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*

Education

Stockholm University, SciLifeLab & Sonnhammer Lab *Stockholm, SE*

Doctorate of Computational Systems Biology *April 2019*

- Thesis – Towards Reliable Gene Regulatory Network Inference
- 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, USA*

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, USA*

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

Projects / Open Source

Graphistry

3 merged PR, 20225+, 2983- *2022-current*

- graphistry
- cu-cat

NetZoo

5 merged PR, 22837+, 7729- *2019-2019*

- gpuZoo publication
- 20 PR

GeneSPIDER

co-creator of project *2015-2019*