Elan Ness-Cohn, Ph.D.

🌐 nesscoder.com ✉ ness.cohn.elan@gmail.com ☏ +1 (847) 420-0296
 github.com/nesscoder linkedin.com/nesscohn

OVERVIEW

Computational Biologist with software and research publications in top academic journals. Brings a unique blend of math & science literacy, wet & dry lab experience, and educational & business pragmatism, all backed by strong R skills and desire to continue pushing the boundary of the Chicago biotech ecosystem.

EDUCATION

Ph.D. (Biomedical Research)
Northwestern University, Evanston   2022

- Dissertation combined data science and biology to develop new computational methods for understanding the molecular mechanisms and dynamics of circadian rhythms.
- Published in high profile academic journals including Science and Bioinformatics.

Graduate Certificate in Teaching
Northwestern Searle Center for Advancing Learning and Teaching   2021

B.Sc. (Biology), Concentration (Education)
Massachusetts Institute of Technology, Cambridge   2017

COMPUTATIONAL & TECHNICAL SKILLS

Programming: R • Python • Bash • R Shiny • LaTeX • git • SQL • HPC (SLURM)
Machine Leaning: Tidymodels • Keras • Tensorflow
Data Mining: statistical analysis • dimensionality reduction • clustering • visualization
Modeling: dynamical systems • topological analysis • toy model development
Research: algorithm & pipeline development • inter-disciplinary collaboration • software development
Laboratory: CRISPR/Cas-9 genome editing • plasmid design • molecular cloning • qPCR
Languages: English • Hebrew

EXPERIENCE

Entrepreneurial Fellow – Chicago Biomedical Consortium (CBC)   2022–date

- Informed the allocation of $250K grants to accelerate the translation of transformative biomedical technologies across Chicagoland's flagship Universities.
- Developed robust investment theses and project plans defining competitive positionings, timelines, budgets and resource allocations, mitigation plans, competitive landscapes analyses, and clinical/regulatory strategies to accelerate the commercialization of CBC funded projects.

Ph.D. Candidate – Braun Lab, Northwestern University   2017–2022

Topology Inspired Methods for the Design and Analysis of Transcriptomic Time-Series Data in Circadian Biology Research

- Developed a suite of open-source software packages for optimizing the design and analysis of *omic time-series experiments in circadian biology research.
- Lead multiple collaborative projects with peers leveraging inter-disciplinary expertise to investigate hypotheses and problem-solve obstacles.
- Mentored undergraduate and graduate students through various computational research techniques and organizational skills.

Undergraduate Research Assistant – Jaenisch Lab, MIT   2016–2017

Engineering Human Pluripotent Stem Cells With Insulin Reporter to Model Type 1 Diabetes

Undergraduate Research Assistant – Kim Lab, MIT   2015–2016

Regulation of Stress Physiology and Longevity by the EIF3 Translation Inititation Complex in C. Elegans

Software (Highlights)

Fasano-Franceschini Test - R Package
An open-source implementation of the Fasano and Franceschini test – a 2-D Kolmogorov-Smirnov (KS) two-sample test – downloaded by 4100+ in the R community.
    R Package Website: [Link]

TimeCycle - R Package
A non-parametric method that leverages results from dynamical systems theory and topology to test whether a dynamical variable (gene expression) exhibits cycling dynamics.
    R Package Website: [Link] • **Video Tutorial:** [Link]

TimeTrial - R Shiny Web Application
An interactive software suite that enables circadian researchers to perform head-to-head comparisons of four leading cycle detection methods using both synthetic and biological data.
    R Shiny Synthetic Data: [Link] • **R Shiny Biological Data:** [Link] • **Video Tutorial:** [Link]

Additional work can be found on my GitHub profile: ⓘ github/nesscoder

Teaching

Northwestern University – Searle Teaching Certificate Program   2020 – 2021
    • Designed/developed an *Intro to Data Science Lab Course* complete with a course outline, sample lesson plan, sample assessments, grading scheme, evaluation plan, and interpretation of teaching effectiveness.

Northwestern University

What Do Your Data Say? (DataScience Bootcamp), Teaching Assistant	Spring 2020
IGP 486: Advanced Bioinformatics/Genomics, Teaching Assistant	Winter 2020
Collabrative Learning & Intergrated Mentoring in the BioSciences (CLIMB)	
IGP 405: Cell Biology, Teaching Mentor	Winter 2021
IGP 484: Biostatitics, Teaching Mentor	Fall 2019, 2020

Massachusetts Institute of Technology

7.012: Introductory Biology, Teaching Assistant	Spring 2017
18.05: Introduction To Probability and Statistics, Teaching Assistant	Spring 2016
Department of Biology Tutoring Program, Tutor	2016–2017
Intro Biology, Experimental Biology and Communication, Genetics, Biochemistry, Cell Biology	

Publications

[1] **Ness-Cohn, Elan** and Rosemary Braun. TimeCycle: Topology Inspired MEthod for the Detection of Cycling Transcripts in Circadian Time-Series Data. *Bioinformatics*, jun 2021.

[2] **Ness-Cohn, Elan**, Ravi Allada, and Rosemary Braun. Comment on "Circadian rhythms in the absence of the clock gene Bmal1". *Science*, 372(6539), 2021.

[3] **Ness-Cohn, Elan**, Marta Iwanaszko, William L Kath, Ravi Allada, and Rosemary Braun. TimeTrial: An interactive application for optimizing the design and analysis of transcriptomic times-series data in circadian biology research. *J Biol Rhythms*, 35:439–451, 2020.

[4] Douglas J. Cattie, Claire E. Richardson, Kirthi C. Reddy, **Ness-Cohn, Elan**, Rita Droste, Mary K. Thompson, Wendy V. Gilbert, and Dennis H. Kim. Mutations in nonessential eIF3k and eIF3l genes confer lifespan extension and enhanced resistance to ER stress in caenorhabditis elegans. *PLoS Genetics*, 12(9):e1006326, 2016.

[5] **Ness-Cohn, Elan** and Rosemary Braun. Fasano-Franceschini Test: an Implementation of a 2-Dimensional Kolmogorov-Smirnov test in R. *arXiv*, page 2106.10539, sept 2021.

[6] **Ness-Cohn, Elan**, Dae-Sung Hwangbo, Yong-Jae Kwon, Marta Iwanaszko, William L Kath, Ravi Allada, and Rosemary Braun. TimeChange: Topology Inspired MEthod for the detection of differential cycling dynamics in circadian transcriptomic time-series data. *In Preparation*, 2021.