Elan Ness-Cohn

🌐 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 pragmatism, all backed by strong R skills and desire to continue pushing the boundary of human knowledge.

EDUCATION

Ph.D. (Biology)
Northwestern University, Evanston   08/2017–10/2021 (Anticipated)
- 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   2020–2021

B.Sc. (Biology), Concentration (Education)
Massachusetts Institute of Technology, Cambridge   2013–2017

COMPUTATIONAL & TECHNICAL SKILLS

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

EXPERIENCE

Ph.D. Candidate, Northwestern University   08/2017–date
Topology Inspired Methods for the Design and Analysis of Transcriptomic Time-Series Data in Circadian Biology Research
- Created a user-friendly, web-based platform for circadian researchers to optimize the design and analysis of *omic time-series experiments.
- Developed a novel reference-free, non-parametric method using principles from dynamical system theory and topological analysis to identify cycling genes in circadian transcriptomic time-series data.
- Formulated a novel reference-free, non-parametric method using principles from dynamical system theory and inferential statistics to identify differentially cycling genes across experimental conditions in circadian transcriptomic time-series data.

Undergraduate Research Assistant, Massachusetts Institute of Technology   2016–2017
Engineering Human Pluripotent Stem Cells With Insulin Reporter to Model Type 1 Diabetes
- Designed/cloned fusion gene plasmid and accompanying CRISPR/Cas9 guide RNAs for targeted tagging of gene of interest.
- Supported in the *in vitro* differentiation of pluripotent stem cells to insulin producing beta-like cells.

Undergraduate Research Assistant, Massachusetts Institute of Technology   2015–2016
Regulation of Stress Physiology and Longevity by the EIF3 Translation Inititation Complex in C. Elegans
- Designed/cloned fusion gene plasmid and accompanying CRISPR/Cas9 guide RNAs for targeted tagging of gene of interest.
- Generated CRISPR/Cas9 transgenic lines of *C. Elegans* through Microinjection.

Software (Highlights)

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 - Rshiny 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 2020
IGP 484: Biostatitics, Teaching Mentor	Fall 2019

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

Introductory Biology, Introductory Experimental Biology and Communication, Genetics, Biochemistry, Cell Biology

Publications

[1] **Ness-Cohn, Elan**, Ravi Allada, and Rosemary Braun. Comment on "circadian rhythms in the absence of the clock gene bmal1". *Science*, 372(6539), 2021.

[2] **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.

[3] 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.

Manuscripts submitted / in preparation

[1] **Ness-Cohn, Elan** and Rosemary Braun. TimeCycle: Topology Inspired MEthod for the detection of cycling transcripts in circadian time-series data. *bioRxiv*, page 2020.11.19.389981, 2020 (**in Review at Bioinformatics**).

[2] **Ness-Cohn, Elan** and Rosemary Braun. TimeChange: Topology Inspired MEthod for the detection of differential cycling dynamics in circadian transcriptomic time-series data. *In Preparation*, 2021.

[3] **Ness-Cohn, Elan** and Rosemary Braun. Fasano–franceschini test: an implementation of a 2-dimensional kolmogorov–smirnov in r. *In Preparation*, 2021.