

# Elan Ness-Cohn

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## OVERVIEW

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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

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### 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

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**Programming:** R • Python • Bash • R Shiny •  $\text{\LaTeX}$  • git • SQL • HPC (SLURM)

**Machine Learning:** 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

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### Ph.D. Candidate, 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, 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 Initiation 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)

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### 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 3100+ 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

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### 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: Biostatistics, 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

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- [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 (**in review at The R Journal**).
- [6] **Ness-Cohn, Elan**, Dae-sung Hwangbo, 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.