

# Elan Ness-Cohn

🌐 [nesscoder.com](https://nesscoder.com) ✉ [ness.cohn.elan@gmail.com](mailto:ness.cohn.elan@gmail.com) ☎ +1 (847) 420-0296

📄 [github.com/nesscoder](https://github.com/nesscoder) 🔗 [linkedin.com/nesscohn](https://linkedin.com/nesscohn)

## EDUCATION

---

### Ph.D. (Biology)

Northwestern University, Evanston

08/2017–12/2021 (Anticipated)

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

Advisor: Prof. R. Braun, Molecular Biosciences (Comp. Bio and Applied Math Group)

### Graduate Certificate in Teaching

Northwestern Searle Center for Advancing Learning and Teaching

2020–2021

### B.Sc. (Biology), Concentration (Education)

Massachusetts Institute of Technology, Cambridge

2017

Thesis: *Regenerative Medicine and Synthetic Biology: Working Toward the Clinic*

Research Advisor: Prof D. Kim, Biology (Genetics Group)

Research Advisor: Prof R. Jaenisch, Biology (Stem Cell Group)

## EXPERIENCE

---

### Braun Lab

**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.

### Jaenisch Lab

**Undergraduate Research Assistant**, Massachusetts Institute of Technology

2016–2017

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

- ★ Utilized previously acquired laboratory techniques to design/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

### Kim Lab

**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

## COMPUTATIONAL & TECHNICAL SKILLS

---

**Programming:** R • Python • Bash • R Shiny • L<sup>A</sup>T<sub>E</sub>X • git • SQL • HPC (SLURM)

**Data Mining:** statistical analysis • dimensionality reduction • clustering • visualization

**Modeling:** dynamical systems • topological analysis • toy model development

**Machine Learning:** 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

## 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 - 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](https://github.com/nesscoder)

## 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.

## MANUSCRIPTS SUBMITTED / IN PREPARATION

---

- [1] **Ness-Cohn, Elan** and Rosemary Braun. Fasano-Franceschini Test: an Implementation of a 2-Dimensional Kolmogorov-Smirnov test in R. *arXiv*, page 2106.10539, jun 2021 (**in review at JSS**).
- [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.

## PRESENTATIONS

---

- Topological Strategies for the Analysis of Rhythmic Dynamics in Transcriptomic Time-Series Data*  
**Talk**, International Conference on Intelligent Systems for Molecular Biology (ISMB), Virtual 2021
- TimeCycle: Topology Inspired MMethod for the Detection of Cycling Transcripts In Circadian Time-Series Data*  
**Microtalk**, 3rd Annual Conference on Quantitative Approaches in Biology, Northwestern 2020
- TimeCycle: Topology Inspired MMethod for the Detection of Cycling Transcripts In Circadian Time-Series Data (Canceled Covid-19)*  
**Minisymposium**, Conference on the Life Sciences (LS20), California 2020
- TimeCycle: Topology Inspired MMethod for the Detection of Cycling Transcripts In Circadian Time-Series Data*  
**Poster**, 3rd Annual Southeastern Center for Mathematics & Biology Symposium, Georgia Tech 2020
- TimeCycle: Topology Inspired MMethod for the Detection and Direct Comparison of Cycling Transcripts Across Conditions*  
**Poster**, 2nd Annual Conference on Quantitative Approaches in Biology, Northwestern 2019
- TimeTrial: Interactive Application for the Design and Analysis of Transcriptomic Time-Series Data in Circadian Biology Research*  
**Poster**, Chicago Biomedical Informatics Data Jam, Chicago 2019
- TimeCycle: Topology Inspired MMethod for the Detection and Direct Comparison of Cycling Transcripts Across Conditions*  
**Poster**, Chicago Biomedical Informatics Data Jam, Chicago 2019
- TimeCycle: Topology Inspired MMethod for the Detection and Direct Comparison of Cycling Transcripts Across Conditions*  
**Poster**, 1st Annual Conference on Quantitative Approaches in Biology, Northwestern 2018

## TEACHING

---

### Northwestern University – Searle Teaching Certificate Program 2020 – 2021

*A year long sequence of seminars, special-topics workshops, and guidance provided by peer and faculty mentors focused on improving student learning and inclusion in their disciplines.*

★ 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 2020
- IGP 484: Biostatistics, 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

## MENTORSHIP

---

### **Kelly Paquin, Undergraduate Research Assistant**

Quantitative Biology Undergraduate Summer Research Program

Summer 2020

*Automating the Detection of Circadian Genes from Luciferase Reporter Construct in Drosophila*

### **Carolina Clark, Ph.D. Candidate**

DGP Student Assisted Mentoring Program (STAMP)

2020–date

### **Samuel Hamilton, Ph.D. Candidate**

DGP Student Assisted Mentoring Program (STAMP)

2019–date

## AWARDS

---

### **NSF-Simons Center for Quantitative Biology Training Grant**

Northwestern University

2018

### **Boit Prize for Engineering Writing**

Massachusetts Institute of Technology

2017

Senior Thesis - *Regenerative Medicine and Synthetic Biology: Working Toward the Clinic*

## SERVICE

---

### **Professional Memberships and Leadership Roles**

Driskill Graduate Program In the Life Sciences, Student Council Rep

2020–date

NSF-Simons Center for Quantitative Biology Leadership Team, Graduate Student Rep

2019–date