

Biplabendu Das

Department of Biology, Stanford University, California, USA 94305
Email: biplabendu.das@gmail.com | Website: <https://github.com/biplabendu>

Summary

As an integrative biologist and data scientist, I have over six years of experience in molecular biology techniques and utilizing bioinformatics, statistical modeling, and network analyses of time-series data to study the interplay between circadian rhythms, behavioral plasticity, and infectious disease outcomes. Currently, I am a postdoctoral researcher at Stanford University, where I focus on studying the ecological role of circadian clocks through genomics and behavioral analyses. I am seeking a computational-oriented position where I can fully utilize my biological expertise and skill set in statistical programming and bioinformatics, including developing software packages, Shiny applications, and websites using R, Markdown, and Git.

Education

2017-22 **Doctor of Philosophy**, Biology, University of Central Florida (UCF), USA
2016-17 **Master of Science**, Biology, Indian Institute of Science (IISc), India
2012-16 **Bachelor of Science-Research**, Biology major and Earth Sciences minor, IISc, India

Awards and Honors

2022 **Best dissertation award**, Department of Biology, UCF
2022 **Emmett Chappell Award**, Society for Research on Biological Rhythms
2019 **Best poster award**, 2nd Indo-Swiss Meeting on Evolutionary Biology
2019 **Best manuscript of 2018**, Journal - Myrmecological News

Computational Expertise

Programming Languages: R, Python, UNIX, Markdown, MATLAB | **App Development:** Shiny | **Database management:** MySQL | **Data-wrangling:** tidyverse, dplyr, lubridate, stringr, janitor, dbplyr | **Visualization:** plot, ggplot2, igraph, heatmap2, UpsetPlot | **Clustering:** dendextend, WGCNA | **Statistical packages:** lme4, stats, limma, mgcv, LimoRhyde, eJTK-Cycle, WaveletComp, timecourseRnaseq | **Reproducibility:** Git, Conda, GitHub Pages | **Bioinformatics:** proteinortho, interproscan, BMAP, HISAT2, Samtools, CuffLinks

Software and Website Development

Develop and deploy websites for sharing data analyses. Reproducible, transparent data analyses pipelines using R, that are hosted on a website using Markdown and GitHub Pages. (example: [link to website](#))

Shiny app for comparative genomics and transcriptomics. Open-source R software to compile and visualize data from multiple genomics datasets. (Main developer, [link to app](#))

timecourseRnaseq: R package to analyze time-course RNAseq data. Provides functions to run GO/PFAM enrichment analyses and plot results. (Main developer, [link to package](#))

Recent Publications

(2023) **Das, B.**, and Gordon, D.M. Biological rhythms and task allocation in ant colonies. *Current Opinion in Insect Science* (*in review*)

(2023) **Das, B.**, Brouns, R., Will, I., Brachmann, A., de Bekker, C. Using RNASeq to investigate the involvement of the *Ophiocordyceps* clock in ant host infection and behavioral manipulation. *bioRxiv*

(2023) **Das, B.**, Brachmann, A., de Bekker, C. Both behavior-manipulating and non-manipulating entomopathogenic fungi affect rhythmic gene expression in carpenter ant foragers upon infection. *bioRxiv*

(2022) de Bekker, C. and **Das, B.** Hijacking time: How *Ophiocordyceps* fungi could be using ant host clocks to manipulate behavior. *Parasite Immunology*

(2021) **Das, B.** and de Bekker, C. Time-course RNASeq of *Camponotus floridanus* forager and nurse ant brains suggests links between plasticity in the biological clock and behavioral division of labor. *BMC Genomics*

Research and Mentoring Experiences

2022-Present | Postdoctoral researcher, Biology, Stanford University, USA

Mentor: Prof. Deborah Gordon

- Working on projects that use newly generated and previously published RNA sequencing data from ant brains, and long-term field behavioral data to characterize an ecological role of circadian rhythms.
- Have built a SQL database of more than 50 behavioral datasets from field studies of ants, collected over a decade, transforming each into a standardized format.
- Developed an analytical pipeline to collect 20 years of legacy weather data via web scraping HTML tables from weather station websites in Arizona to test the effect of the environment on ant behavior
- Ongoing research has resulted in one review paper, and two manuscripts are in preparation.

2017-2022 | Doctoral research, Genomics and Bioinformatics Cluster, Biology, UCF, USA

Mentor: Asst. Prof. Charissa de Bekker

- Worked on seven projects to explore how circadian rhythms and collective behavior of ants change during the progression of infectious diseases, especially ones that change host behavior.
- Developed a statistical framework to model time-series RNASeq data as gene expression networks and used it to examine how parasites impact the circadian rhythms in the host's brain ([de Bekker and Das, 2022](#)), which leads to a time-of-day specific death of the host.
- Worked extensively with experimental techniques – fungal culturing, controlled infections, extracting and sequencing mRNA from ant brains – as well as designing apriori statistical approaches to test hypotheses.
- Trained four undergraduate students and one master's student in techniques related to bioinformatics, automated behavioral tracking, data engineering, visualization, and statistical modeling.
- My PhD research has resulted in six publications, seven talks and five poster presentations.

2015-2016 | Bachelor thesis, Institute of Science and Technology, Austria and IISc, India

Mentors: Prof. Sylvia Cremer, Prof. Raghavendra Gadagkar

- Conducted controlled viral infections in ants and designed assays to quantify the behavioral responses of ants to viral infections and to determine if ants have the ability to detect viral infections in their nest members.
- Obtained an ISTernship Fellowship (Austrian government) and a Grant-in-Aid of Research (Sigma Xi)

Voluntary and Teaching Experience

2017-2021 | Graduate Teaching Associate, Biology, UCF, USA

- Served as the instructor-of-record for an upper-level field ecology course, for two years, that required students to independently collect and analyze data to test their hypotheses
- Developed coursework by incorporating R-programming for exploratory data analyses and null hypothesis testing into the curriculum of the aforementioned field ecology course. ([link to tutorial](#))
- Taught Introductory Biology laboratory to first- and second-year undergraduate students for two years

2021-Present | DEIJ Committee Member, International Union for the Study of Social Insects

- Serving as a member of the Diversity, Equity, Inclusion, and Justice committee for the International Union for the Study of Social Insects (IUSSI), a global society for social insect researchers.
- Led a data-driven approach to identify sources of inequity among society members by collecting and analyzing demography data through a global survey.
- Created a website to host the results of the aforementioned demography analyses ([link to website](#)).

Recent Presentations

(2022) Seminar Talk Essig Museum Brunch, UC Berkeley, USA; **Invited Talk** Think and Drink seminar, Stanford University, USA; **Symposium Talk** 19th IUSSI International Congress, USA; **Guest Lecture**, Animal Behavior course, University of North British Columbia; **Invited Talk**, Global Talk Series, Society for Research on Biological Rhythms **(2021) Talk** Allee Competition, Animal Behavior Society meeting; **Poster** Cold Spring Harbor Symposium on Biological Timekeeping

Academic Services

Editor of Myrmecological News Blog (present); **Reviewer** for Royal Society Proceedings B, Insectes Sociaux, Myrmecological News, Annals of Entomological Society of America