

Upendra R. Bhattarai, PhD

Curriculum Vitae

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Professional Summary

Molecular biologist and bioinformatician with expertise in multi-omics data generation, analysis, genome assembly, transcriptomics, and high-throughput sequencing. Skilled in applying statistical and computational approaches to complex biological datasets. In addition to bioinformatics, I have extensive molecular wet lab experience, including various sequencing library preparation. I have worked with diverse model organisms, including human, mouse, many different insects, and pathogen, analyzing sequencing data for studies in cancer genetics, Alzheimer's disease, Huntington's disease, developmental biology, and host-parasite interactions. My expertise spans bulk RNA-seq, single-cell RNA-seq, ChIP-seq, CUT&RUN, and Iso-Seq, as well as long-read sequencing using PacBio and Nanopore for genome assembly and annotation. Additionally, I have a strong background in bioinformatics training and international research collaboration.

Current Position

Research Associate

Harvard Chan Bioinformatics Core, Department of Biostatistics, Harvard T.H. Chan School of Public Health, Boston, MA

March 2024 – Present

- Provide bioinformatics consultation and technical support to researchers across Harvard.
- Develop and deliver training workshops on bioinformatics tools, data analysis, and best practices.
- Collaborate with interdisciplinary teams to analyse and interpret high-throughput sequencing and omics data.
- Assist in optimizing computational workflows for large-scale biological datasets.
- Experienced in working with Human, Mouse, and diverse organism models.

Research and Bioinformatics Experience

Postdoctoral Fellow

Extavour lab, Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA

May 2022 – March 2024

- Worked on developing five different hemimetabolous insects as the genetic model species.
- Assembled chromosome level genome assemblies, annotated and carried out comparative genomic analysis.
- Conducted RNA-seq analysis to profile gene expression in temporal and spatial scale.
- Carried out comparative genomics and transcriptomics, identifying evolutionary patterns in gene regulation.

Research Technician

Norwegian Institute for Agricultural and Environmental Research (Bioforsk), Ås, Norway.
2012 – 2013

- Performed several laboratory experiments involving three trophic levels (fungus, mites, and plants).
- Maintain laboratory cultures of Acaro-pathogenic fungi, mites, flies, and plants.
- Carried out different lab experiments on host-pathogen interactions.

Education

PhD in Genetics

University of Otago, New Zealand (2019 – 2023)

- Investigated host-parasite molecular interactions using genomics, transcriptomics, and epigenetics.
- Applied RNA-seq, Nanopore sequencing, Bisulfite sequencing, and network analysis.

PhD in Agricultural Entomology and Pest Control

Northwest A&F University, China (2014 – 2018)

- Studied the mechanism of host manipulation in viral-infected lepidopterans.
- Used genome-wide transcriptomics and functional genomics to study Circadian rhythms and Phototransduction mechanisms.

MSc in Plant Science

Norwegian University of Life Science, Norway (2010 – 2012)

- Focused on interactions between fungal pathogen and their host mites for host behavioral manipulation.

BSc in Agriculture

Tribhuvan University, Nepal (2005 – 2009)

Teaching and Mentorship Experience

- 2024 – Present: Conducting bioinformatics training at Harvard Medical School, School of Public Health, and throughout the Harvard and affiliated Hospitals.
- 2021: Instructor for Genomics Data Carpentry, Genomics Aotearoa.
- 2021: Instructor and organizer, Research Bazaar 2021, Dunedin.
- 2021: Instructor for RNA-seq Analysis Workshop, Genomics Aotearoa, Dunedin.
- 2019: Tutor for Cell Biology (ANAT332), Disability Information & Support, University of Otago.

Selected Publications:

(Full list available upon request)

- Yang, Z., Mogre, S., Jun, H., He, R., Chaudhary, S G., **Bhattarai, U R.**, et al. (2025) Functional profiling of p53 and RB cell cycle regulatory proficiency suggests mechanism-

driven molecular stratification in endometrial carcinoma. *Cancer Research Communication*, PMID: 39932274. DOI: 10.1158/2767-9764.CRC-24-0028.

- Doherty, J.-F. §, **Bhattacharai, U R.** §, Ferreira, S., Poulin, R., Gemmell, N J., & Dowle, E J. (2023). The proof is in the poo: Non-invasive method to detect endoparasitic infection. *Molecular Ecology Resources*, 00, 1– 12. DOI: 10.1111/1755-0998.13763.
- **Bhattacharai UR**, Katuwal M, Poulin R, Gemmell N.J, Dowle E. (2022). Genome assembly and annotation of the European earwig *Forficula auricularia* (subspecies B). *G3 Genes | Genomes | Genetics*. 12 (10). Jkac199. DOI: 10.1093/g3journal/jkac199
- **Bhattacharai U.R**, Li F, Katuwal M, Masoudi A, Wang D. (2018). Phototransduction and circadian entrainment are the key pathways in signalling mechanism for the baculovirus induced tree-top disease in lepidopteran larvae. *Scientific reports*. 8 (1). DOI:10.1038/s41598-018-35885-4

Awards and Certifications

- 2021: Travel grant, University of Otago, for attending Hi-C workshop.
- 2020: Certified Carpentries Instructor (International bioinformatics and data science training).
- 2019: Departmental PhD Scholarship, University of Otago, NZ.
- 2014: Distinguished International Student PhD Scholarship, Northwest A&F University, China.

Selected Conference Presentations

(Full list available upon request)

- 2023: Developing Multi-Species Hemimetabolous Insect Tools (MUSH-IT). Enabling Discovery through GENomics (EDGE) program, annual meeting, NSF & NIH, Alexandria, VA
- 2023: Decoding the molecular mechanisms of host manipulation by parasites. The 98th Annual Meeting of the American Society of Parasitologists. Kansas City, USA.
- 2022: A high-quality genome assembly, annotation, and analysis of the European earwig (*Forficula auricularia*) with a low coverage long-read sequencing. Entomological society of America, Annual meeting, Vancouver, Canada
- 2021: Insights into host manipulation by mind altering parasites through the whole genome, transcriptome, and bisulfite sequencing. Genetics Society of AustralAsia (GSA) conference.