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| **Upendra R. Bhattarai, PhD**  *Curriculum Vitae* | 51 Hill Rd #309  Belmont, MA 02478  +1 617 230 7583 (Cell)  [ubhattarai@hsph.harvard.edu](mailto:ubhattarai@hsph.harvard.edu)  <https://github.com/upendrabhattarai> |

**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. **§**, **Bhattarai, 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.
* **Bhattarai 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
* **Bhattarai 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.