Bobby Ranjan

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RESEARCH EXPERIENCE

2021 - present	**Predoctoral fellow** **EMBL Rome, Epigenetics & Neurobiology Unit, Italy** Supervisor: Jamie Hackett Research topic: Intergenerational effects of gut-germline communication
2018 - 2021	**Bioinformatics Specialist** **Genome Institute of Singapore, Spatial & single-cell systems, Singapore** Supervisor: Shyam Prabhakar Research topic: Methods development for scRNA-seq data analysis
2015 - 2016	**Undergraduate Research Experience on Campus (URECA)** **Nanyang Technological University, Singapore** Supervisor: Zheng Jie Research topic: Mathematical modelling of neuronal calcium signalling

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EDUCATION

2021 - present (exp. grad. 2025)	**Doctor of Philosophy	Molecular and Systems Biology** European Molecular Biology Laboratory & Heidelberg University, Germany
2014 - 2018	**Bachelor of Engineering**	**Computer Engineering	GPA: 4.60/5.00** Nanyang Technological University, Singapore Minor in Entrepreneurship Minor in Life Sciences

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FELLOWSHIPS, HONORS AND AWARDS

- **Small Scale Human Ecosystems Funding Award** | EMBL | 2024
- **ISMB Fellowship Award** | International Society for Computational Biology | 2020 & 2021
- **President's Research Scholar** | Nanyang Technological University | 2015

SCIENTIFIC PRESENTATIONS

- **Selected speaker** for **Workshop: From DNA to Phenotype: Epigenetic Mechanisms in Resilience and Adaptation,** "Why your father's microbes matter: Intergenerational effects of gut-germline communication", October 2024, Baeza, Spain.
- **Invited speaker** at **Indian Institute for Science, Education and Research (IISER) Pune**, "The mammalian gut-germline axis and its impact on offspring outcome", December 2023, Pune, India.

- **Selected speaker** for **Human Cell Atlas Asia**, "DUBStepR is a scalable correlation-based feature selection method for accurately clustering single-cell data", October 2020 [Virtual].
- **Selected speaker** for **Single Cell Analyses Meeting**, "scConsensus: combining supervised and unsupervised clustering for cell type identification in single-cell RNA sequencing data", November 2019, Cold Spring Harbor Laboratory, New York, USA.
- **Selected speaker** for **Asia-Pacific Bioinformatics Conference**, "Composite mathematical modelling of calcium signalling behind neuronal cell death in Alzheimer's disease", April 2018, Yokohama, Japan.

TEACHING AND SUPERVISION

- **Invited Lecturer** at the **Sapienza University of Rome,** "Computational Methods in Biology", December 2024, Rome, Italy.
- **Instructor** of **EMBL Rome Bioinformatics Community**, "Lineage algebra for high-dimensional omics data analysis", February-July 2024, Rome, Italy.
- **Mentor and supervisor** for two master students (Kunal Mishra and Jinyu Park) during my appointment at Genome Institute of Singapore. Both master students are co-authors on my publications and are currently enrolled in PhD programmes at National University of Singapore and Columbia University respectively.

TECHNICAL SKILLS

- Computational skills: Fluent in programming (R, Python, Bash), Git administration, server administration, software development, reproducible coding practices.
- Multi-omics data analysis: bulk RNA-seq analysis, metabolomics analysis, single-cell RNA-seq and ATAC-seq analysis and methods development.
- Mouse handling (including in germ-free and BSL2 conditions): Administering oral gavage, IP injections, collecting various tissue samples including blood, testis & epididymis.
- Molecular lab techniques: 10x Genomics single-cell multiome, Flash-frozen tissue transcriptomics & metabolomics, FACS sorting cells from fresh tissue, basic microscopy.
- Scientific writing: Led/co-led writing of grants that brought in over 40.000 € in research funding for my PhD project, highlighted preprints as part of preLights.

SCIENTIFIC SERVICE

- **EMBL Predoc representative** of the Rome Unit, 2022-2024.
- **Lead organizer** of the **EMBL Rome Fellows' Visit to the Human Technopole**, September 2024, Milan, Italy (35 participants).
- **Contributor** for **preLights: The Company of Biologist's preprint highlighting service**, 2020-2021.
- **Member** of the **International Society for Computational Biology** (2020-2022).

PROFESSIONAL DEVELOPMENT

- Three-days **SymbNET Metabolomics Workshop**, June 2023, Lausanne, Switzerland.
- Five-days **EMBO Epigenome inheritance and reprogramming workshop**, September 2022, Split, Croatia.
- Two-weeks **Training course in Laboratory Animal Science**, November 2023, Virtual.
- Nine-weeks **EMBL Predoc Course**, October-December 2021, Heidelberg, Germany.

LANGUAGE SKILLS

English: Native speaker   **Hindi:** Fluent   **Italian:** Novice   **Tamil:** Fluent (spoken)

REFERENCES

Dr. Jamie Hackett | PhD supervisor
EMBL Rome
E-mail: jamie.hackett@embl.it

Dr. Ayele Argaw-Denboba | PhD mentor
Max Planck Institute of Immunobiology and Epigenetics
E-mail: denboba@ie-freiburg.mpg.de

Dr. Shyam Prabhakar | Former supervisor
Genome Institute of Singapore
E-mail: prabhakars@gis.a-star.edu.sg

SELECTED RESEARCH OUTPUTS

*shared first-author

Topic 1: Intergenerational effects of gut-germline communication

Dura* M, **Ranjan* B**, Paribeni R, Paribeni V, Villacorta L, Benes V, Boruc O, Boskovic A and Hackett JA. Embryonic signatures of intergenerational inheritance across paternal environments and genetic backgrounds. *Manuscript in preparation*.

Argaw-Denboba A, Schmidt TSB, Di Giacomo M, **Ranjan B**, Devendran S, Mastrorilli E, Lloyd CT, Pugliese D, …, and Hackett JA. Paternal microbiome perturbations impact offspring fitness. *Nature* 2024, DOI: https://doi.org/10.1038/s41586-024-07336-w.

Topic 2: Methods for single-cell transcriptomics data analysis

Ranjan B, Sun W, Park J, Mishra K, Schmidt F, Xie R, Alipour F, Singhal V, Joanito I, and Prabhakar S. DUBStepR is a scalable correlation-based feature selection method for accurately clustering single-cell data. *Nature Communications* 2021, DOI: https://doi.org/10.1038/s41467-021-26085-2.

Schmidt* F, **Ranjan* B**, Lin QXX, Krishnan V, Joanito I, Honardoost MA, Nawaz Z, and Prabhakar S. RCA2: a scalable supervised clustering algorithm that reduces batch effects in scRNA-seq data. *Nucleic Acids Research* 2021, DOI: https://doi.org/10.1093/nar/gkab632.

Ranjan* B, Schmidt* F, Sun W, Park J, Honardoost MA, Tan J, Arul Rayan N, Prabhakar S. scConsensus: combining supervised and unsupervised clustering for cell type identification in single-cell RNA sequencing data. *BMC Bioinformatics* 2021, DOI: https://doi.org/10.1186/s12859-021-04028-4.