

Bobby Ranjan

European Molecular Biology Laboratory (EMBL), Rome, Italy

bbbranjan@gmail.com | +39 351 948 1408

[ORCID](#) | [GitHub](#) | [Personal webpage](#) | [Twitter](#) & [Bluesky](#)

NARRATIVE

Computational biologist with 7+ years of experience developing and applying single-cell multi-omics methods, combined with 4 years of hands-on expertise in mouse and molecular biology. Passionate about leveraging gene-environment interactions to uncover mechanisms driving disease risk.

RESEARCH EXPERIENCE

| | |
|--|---|
| 2021 - present (defence Oct 2025) | Predoctoral Fellow European Molecular Biology Laboratory (EMBL), Rome, Italy Supervisor: Jamie Hackett Research topic: Microbiome-mediated epigenetic inheritance of disease risk |
| 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 |

EDUCATION

| | |
|--|--|
| 2021 - present (defence Oct 2025) | Doctor of Philosophy Computational 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 <i>Minor in Life Sciences & Minor in Entrepreneurship</i> |

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

TECHNICAL SKILLS

- **Computational skills:** Fluent in programming (R, Python, Bash), Git administration, server administration, software development, reproducible coding practices (for >10 years).
- **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, dissecting various tissue samples including blood, liver, heart, testis, & sperm.
- **Molecular lab techniques:** 10x Genomics single-cell multiome, sample prep for transcriptomics & metabolomics, FACS sorting cells from fresh tissue, basic microscopy.
- **Scientific writing:** brought in over 40.000 € in research funding for my PhD project, highlighted preprints as part of preLights.

SCIENTIFIC PRESENTATIONS

- **Selected speaker** at **Gordon Research Seminar**, "Mechanisms of Epigenetic Inheritance", August 2025, Barcelona, Spain.
- **Invited speaker** at **University of Cambridge**, "Modelling microbiome-mediated epigenetic inheritance of disease risk", March 2025, Cambridge, United Kingdom.
- **Invited speaker** at **Indian Institute of Science**, "Embryonic signatures of intergenerational inheritance across paternal environments and genetic backgrounds", January 2025, Bengaluru, India.
- **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 of Science, Education and Research (IISER) Pune**, "The mammalian gut-germline axis and its impact on offspring outcome", December 2023, 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**, as part of the Master's course titled "Computational Methods in Biology", December 2024, Rome, Italy.
- **Instructor** at **EMBL Rome Bioinformatics Community**, "The mathematics behind high-dimensional omics data analysis", February-July 2024 & April-July 2025, 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.

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

- Five-days **Gene-environment interactions in human health & disease**, March 2025, Hinxton, United Kingdom.
- 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.

LANGUAGES

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

REFERENCES

Dr. Jamie Hackett

PhD supervisor
EMBL Rome

jamie.hackett@embl.it

Dr. Ayele Argaw-Denboba

PhD mentor and collaborator
Max Planck Institute of
Immunobiology and Epigenetics

denboba@ie-freiburg.mpg.de

Dr. Shyam Prabhakar

Former supervisor
Genome Institute of Singapore

prabhakars@gis.a-star.edu.sg

RESEARCH PUBLICATIONS

8 peer-reviewed publications, 5 as first-author. (* = shared first-author)

Topic 1: Mechanisms of epigenetic inheritance of disease risk

Dura* M, **Ranjan* B**, Serrano JB, ..., Boskovic A and Hackett JA. Embryonic signatures of intergenerational epigenetic inheritance across paternal environments and genetic backgrounds. **EMBO Journal**, 2025. [DOI](#).

[This study captures molecular signatures of how paternal diet, microbiome perturbations, age and genetic background affect the earliest stages of embryonic development, and proposes a novel variability analysis approach ([GenEVA](#)) to capture embryonic responses to paternal conditioning.]

Argaw-Denboba A, Schmidt TSB, Di Giacomo M, **Ranjan B**, Devendran S, Mastroilli E, ..., and Hackett JA. Paternal microbiome perturbations impact offspring fitness. **Nature**, 2024. [DOI](#).

[This study provides the first evidence that disruption of the gut microbiome in male mice directly alters survival and disease risk in offspring, thus discovering the mammalian 'gut-germline axis'.]

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](#).

[DUBStepR is based on the observation in scRNA-seq data that cell-type-specific genes are highly correlated in expression with one another. DUBStepR significantly outperformed existing methods and proposed a new metric for scoring feature selection algorithms.]

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](#).

[RCA2 (Reference Component Analysis 2) projects input scRNA-seq data onto validated reference transcriptomes and clusters cells in supervised space, making it robust and scalable to large datasets.]

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](#).

[scConsensus generates a consensus clustering by combining supervised and unsupervised clustering approaches, and improves the homogeneity of cell types by refining clusters using DE genes.]

Other research contributions

Honardoost MA, Adinatha A, Schmidt F, **Ranjan B**, ..., and Prabhakar S. Systematic immune cell dysregulation and molecular subtypes revealed by single-cell RNA-seq of subjects with type 1 diabetes. **Genome Medicine**, 2024. [DOI](#).

Lee HO, Hong Y, Etioglu HE, ..., **Ranjan B**, ..., and Park WY. Lineage-dependent gene expression programs influence the immune landscape of colorectal cancer. **Nature Genetics**, 2020. [DOI](#).

Ranjan B, Chong KH, and Zheng J. Composite mathematical modelling of calcium signaling behind neuronal cell death in Alzheimer's disease. **BMC Systems Biology**, 2018. [DOI](#).