

# Bobby Ranjan

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<https://www.bobbyranjan.com>

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## RESEARCH EXPERIENCE

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

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## EDUCATION

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

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## FELLOWSHIPS, HONORS AND AWARDS

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- **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

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## SCIENTIFIC PRESENTATIONS

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- **Invited speaker** at **Indian Institute of Science**, "Embryonic signatures of intergenerational inheritance across paternal environments and genetic backgrounds", January 2025, Bangalore, 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 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.

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## TEACHING AND SUPERVISION

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- **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.

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## TECHNICAL SKILLS

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- **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, collecting various tissue samples including blood, testis, epididymis & sperm.
- **Molecular lab techniques:** 10x Genomics single-cell multiome, flash-frozen tissue 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.

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## SCIENTIFIC SERVICE

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- **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).

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## PROFESSIONAL DEVELOPMENT

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- 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.

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## LANGUAGES

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

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## REFERENCES

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### Dr. Jamie Hackett

PhD supervisor  
EMBL Rome

[jamie.hackett@embl.it](mailto:jamie.hackett@embl.it)

### Dr. Ayele Argaw-Denboba

PhD mentor  
Max Planck Institute of  
Immunobiology and Epigenetics

[denboba@ie-freiburg.mpg.de](mailto:denboba@ie-freiburg.mpg.de)

### Dr. Shyam Prabhakar

Former supervisor  
Genome Institute of Singapore

[prabhakars@gis.a-star.edu.sg](mailto:prabhakars@gis.a-star.edu.sg)

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## SELECTED RESEARCH OUTPUTS

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7 peer-reviewed publications, 4 as first-author (+1 pre-print). For full list of publications: [Google Scholar](#)

\* 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. *bioRxiv*, DOI: <https://doi.org/10.1101/2024.11.25.624914>. (also, In Revision)

*The study uncovered novel insights into how paternal conditions - such as diet, microbiome perturbations, and age - affect the earliest stages of embryonic development, while also providing foundational principles for future research into epigenetic inheritance.*

Argaw-Denboba A, Schmidt TSB, Di Giacomo M, **Ranjan B**, Devendran S, Mastroilli 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>.

*The study provided the first evidence that disruption of the gut microbiome in males directly alters disease risk and mortality in offspring with multiple orthologous strategies, including common human antibiotics. This work also uncovered the existence of the mammalian 'gut-germline axis' that signals to the reproductive system via hormonal and metabolite changes.*

### 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>.

*DUBStepR is based on the observation that, in a heterogeneous sample, genes characterising specific cell types/states are highly correlated in expression with one another. DUBStepR significantly outperformed existing methods in identifying disease-associated cell types and subtypes, and proposed a new metric for assessing feature selection called the Density Index (DI).*

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>.

*RCA2 (Reference Component Analysis 2) projects input scRNA-seq data onto validated reference transcriptomes and clusters cells in this supervised space, thus making it robust against technical variations and suitable for 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: [https://doi.org/10.1186/s12859-021-](https://doi.org/10.1186/s12859-021-04028-4)

[04028-4](https://doi.org/10.1186/s12859-021-04028-4).

*scConsensus generates a consensus clustering by combining supervised and unsupervised clustering approaches that improves the separation and homogeneity of cell types by refining clusters using differentially expressed genes, thus leveraging the strengths of both clustering paradigms.*