

Dr. Ravi Prabhakar More

Address: 1 Chatsworth Avenue, Cambridge CB4 3LT, United Kingdom (UK)

Email: ravipmore7@gmail.com, Mobile: +44 7721143680

Web Profiles: [ravimore](#), [Google Scholar](#), [GitHub](#), [Linkedin](#)

SUMMARY

Ph.D. Bioinformatics with 7 years of post-doctoral research work experience in rare disorders genomics mainly Autism, BPAD, SCZ, SeSAME, and Stem Cell lines assessment. WGS/WES/scRNA-Seq analysis workflow development on HPC and DNAexus cloud platforms. Proficiency in Perl/Python/bash shell scripting, GitHub, and Conda/Docker containers. Contributed as first and corresponding author to the Autism families (WGS) study and research paper is under revision in the Nature- Molecular Psychiatry journal.

RESEARCH EXPERIENCE

August 2019 to Present Research Associate – Bioinformatics, University of Cambridge, United Kingdom

- Department of Paediatrics (July 2021 to present)
 - Supervisors: Prof. David Rowitch and Dr. Joo Wook Ahn (EGLH, NHS)
 1. The NeuralNET project: Development of WGS-based clinical diagnosis pipeline for rare disorders families on cloud computing platform.
- Autism Research Centre ([ARC](#)), Department of Psychiatry (August 2019 to July 2021)
 - Supervisors: Prof. Sir Simon Baron-Cohen, Dr. Varurn Warrier, Dr. Charles Bradshaw
 1. The identification of rare genetic variants in the highly multiplex families of Autism (n=112 WGS, n=323 WES) and extremely talented mathematicians cohort (n=61 WGS; n=774 WES)
 2. Development of VarFilter-PD (Variant Filtering at Phenotype and Diagnosis level in the pedigree) tool using WGS/WES data by implementing Perl/bash shell scripts on HPC clusters.

[GitHub: <https://github.com/ravimore8386/VarFilter-PD>.](https://github.com/ravimore8386/VarFilter-PD)

July 2016 - July 2019 Bioinformatician,

National Centre for Biological Sciences ([TIFR-NCBS](#)), Bengaluru, India

1. The identification of rare genetic variants in families of Bipolar disorder, Schizophrenia, and SeSAME syndrome (n=71 WES)
2. Development of WGS-based GenomicQC tool for stem cell line assessment (n=14) [dx.doi.org/10.17504/protocols.io.vuae6se](https://doi.org/10.17504/protocols.io.vuae6se)

April 2015 - July 2016 Research Associate - Bioinformatics

National Bureau of Agricultural Insect Resources ([ICAR-NBAIR](#)), Bengaluru, India

1. Transcriptome (RNA-Seq) and DNA Barcoding of Insects.

April 2010 - March 2015 Project Assistant - Bioinformatics

National Environmental Engineering Research Institute ([CSIR-NEERI](#)), Nagpur, Maharashtra, India

1. Metagenome analysis and Bacteria/Plant DNA Barcoding

July 2009 - April 2010 Senior Lecturer, Shivchhatrapati College, Aurangabad, MH, India

RESEARCH INTERNSHIP

Research Trainee on project ‘Study of Horizontal Gene Transfer events in the microbes’, Prof. Ikuo Uchiyama Lab, National Institute for Basic Biology (NIBB), Okazaki, Japan (September-November 2011).

EDUCATION

- **Ph.D. Bioinformatics** (Faculty of Science) Awarded: 17th April 2015
Swami Ramanand Teerth Marathwada University ([SRTMU](#)), Nanded, Maharashtra, India
(Registration: 10th May 2011, Thesis Submission: 26th June 2014)
Topic: DNA Barcoding: Pattern-Based Approach for Creating a Gene Specific Signature
Supervisor: Dr. Hemant Purohit, National Environmental Engineering Research Institute (CSIR-[NEERI](#)), Nagpur, India
- **M.Sc. Bioinformatics** (73.45 %) (13th July 2009)
Swami Ramanand Teerth Marathwada University (SRTMU), Nanded, Maharashtra, India
- **B.Sc. Microbiology, Chemistry, Botany** (67.76 %) (22nd December 2006)
Dr. Babasaheb Ambedkar Marathwada University ([BAMU](#)), Aurangabad, Maharashtra, India

RESEARCH PUBLICATIONS

Top key publications:

1. Identifying rare genetic variants in 21 highly multiplex autism families: the role of diagnosis and autistic traits.
More Ravi*, Warrier Varun*, Brunel Helena, Buckingham Clara, Smith Paula, Allison Carrie, Holt Rosemary, Bradshaw Charles +, and Baron-Cohen Simon** [* + Equal contribution, # Corresponding]
Nature Molecular Psychiatry, 2022 (**Manuscript under revision**) (IF 15.992)
2. Genomic-QC: Large-scale genomic data mining to assess the quality of HiPSC lines.
More Ravi, Rao M, Mukherjee O#.
Cell and Gene Therapy Insights, 5(2), 203–219, 2019. [[JOURNAL](#)]
3. Exome sequencing in families with severe mental illness identifies novel and rare variants in genes implicated in Mendelian neuropsychiatric syndromes.
Ganesh S., Ahmed P H., Nadella R. K., **More Ravi**, Seshadri M., Viswanath B., ... & Rao M.
Psychiatry and clinical neurosciences, 73(1), 11-19, 2019. (IF 3.489) [[PUBMED](#)]
4. Identification and functional characterization of two novel mutations in KCNJ10 and PI4KB in SeSAME syndrome without electrolyte imbalance.
Nadella R. K., Chellappa A., Subramaniam A. G., **More Ravi**, ... & Kannan R.
Human genomics, 13(1), 1-13, 2019. (IF 3.351) [[PUBMED](#)]
5. INDEX-db: the Indian exome reference database (Phase I).
Ahmed P H., **More Ravi**, Viswanath B., Jain S., Rao M. S., Mukherjee O., & ADBS Consortium.
Journal of Computational Biology, 26(3), 225-234, 2019. (IF 0.879) [[PUBMED](#)]
6. Mining and assessment of catabolic pathways in the metagenome of a common effluent treatment plant to induce the degradative capacity of biomass.
More Ravi, Mitra S., Raju S. C., Kapley A., & Purohit H. J.
Bioresource Technology, 153, 137-146, 2014. (IF 7.539) [[PUBMED](#)]
7. The identification of discriminating patterns from 16S rRNA gene to generate signature for bacillus **More Ravi** & Purohit H. J.
Journal of Computational Biology, 23(8), 651-661, 2016. (IF 0.879) [[PUBMED](#)]
8. matK-QR classifier: a patterns based approach for plant species identification.
More Ravi, Mane R. C., & Purohit H. J.
BioData mining, 9(1), 1-15, 2016. (IF 2.672) [[PUBMED](#)]

Other publications:

9. Metagenomic analysis of oxygenases from activated sludge.
Jadeja N. B., **More Ravi**, Purohit H. J., & Kapley A.
Bioresource Technology, 165, 250-256, 2014. (IF 7.539) [[PUBMED](#)]

10. In depth analysis of rumen microbial and carbohydrate-active enzymes in Indian crossbred cattle.
 Jose V. L., **More Ravi**, Appoothy T., & Arun A. S.
Systematic and applied microbiology, 40(3), 160-170, 2017. (IF:3.224) [[PUBMED](#)]
11. Exploring the metabolically active rumen microbiota and its fibrolytic potential in crossbred cattle fed on fibrous diet through metatranscriptomics.
 Jose L, **More Ravi**, ... & Bhatta, R.
Journal of microbiology, biotechnology and food sciences 10 (2), 182-189, 2020. [[JOURNAL](#)]
12. Morphological and molecular characterization of reared parasitoid wasps of the genus Glyptapanteles Ashmead 1904 associated with Lepidoptera in India.
 Gupta A., Venkatesan T. & **More Ravi**.
PloS one, 11(3), e0150765, 2016. (IF 2.740) [[PUBMED](#)]
13. Metagenomic insights into the rumen microbial fibrolytic enzymes in Indian crossbred cattle fed finger millet straw.
 Jose V. L., Appoothy T., **More Ravi** & Arun A. S.
AMB Express, 7(1), 1-11, 2017. (IF 2.499) [[PUBMED](#)]
14. Gut Bacterial Diversity of Insecticide-Susceptible and -Resistant Nymphs of the Brown Planthopper Nilaparvata lugens Stål (Hemiptera: Delphacidae) and Elucidation of Their Putative Functional Roles, Malathi M., **More Ravi**, ... & Tongmin S.
Microbiol. Biotechnol. 28(6): 976-986, 2018. (IF 3.530) [[PUBMED](#)]
15. Metagenomic approach to characterize soil microbial diversity of Phumdi at Loktak Lake.
 Puranik S., Pal R. R., **More Ravi** & Purohit H. J.
Water Science and Technology, 74(9), 2075-2086, 2016. (IF: 1.638) [[PUBMED](#)]
16. Diversity of the cultivable gut bacterial communities associated with the fruit flies Bactrocera dorsalis and Bactrocera cucurbitae (Diptera: Tephritidae).
 Gujjar N. R., Govindan S., Verghese A., Subramaniam S., & **More Ravi**.
Phytoparasitica, 45(4), 453-460, 2017. (IF 1.13) [[JOURNAL](#)]
17. Associated bacterial diversity of insecticide-susceptible and -resistant brown planthopper, Nilaparvata lugens (Homoptera: Delphacidae) analyzed by culture-dependent and independent methods.
 Malathi V, Jalali S, Lyju V, Gracy R, **More Ravi**,...& Venkatesan T.
Phytoparasitica, 1-11, 2017. (IF 1.13) [[JOURNAL](#)]
18. Morphological and molecular characterization of Microplitis maculipennis Szépligeti (Hymenoptera: Braconidae) from India with notes on its generic placement.
 Venkatesan T., Gupta, A., **More Ravi**, Raguraman P., & Baskhar R.
Journal of Biological Control, 32(4), 215-223, 2018. [[JOURNAL](#)]
19. Host-insect and host-plant associated diversity in microbiota isolated from most important Oriental-Australian region egg parasitoid.
 Jalali S. K., Sriram S., Venkatesan T., **More Ravi**, ... & Ojha R.
Journal of Biological Control 31(4), 229-239, 2017. [[JOURNAL](#)]
20. Genome sequence of *M. tuberculosis* C2, a cerebrospinal fluid clinical isolate from central India.
 Kashyap R. S., Bhullar S. S., **More Ravi**, ...& Dagnawala, H. F.
Genome announcements, 2(4), 2014. [[PUBMED](#)]
21. RNAi: Gene Silencing Approach in *C. elegans* and *H. sapiens*.
 Gomase V. S. & **More Ravi**.
International Journal of Molecular Biology, 1(1), 9-14, 2010. [[JOURNAL](#)]

NGS ANALYSIS PIPELINES DEVELOPMENT

1. VarFilter-PD tool: VARiant FILTERing at Phenotype and Diagnosis level in pedigree using

- WGS/WES data [Github: https://github.com/ravimore8386/VarFilter-PD](https://github.com/ravimore8386/VarFilter-PD)
2. GenomicQC tool: WGS-based iPSC lines assessment [dx.doi.org/10.17504/protocols.io.vuae6se](https://doi.org/10.17504/protocols.io.vuae6se)
 3. Whole Exome Sequencing (WES) analysis pipeline [dx.doi.org/10.17504/protocols.io.vrhe536](https://doi.org/10.17504/protocols.io.vrhe536)
 4. Analysis for the INDEX (INDian Exome) database <http://indexdb.ncbs.res.in/>
 5. *matK*-QR Classifier: Plant species identification [Github:https://github.com/ravimore8386/matK-QR-classifier](https://github.com/ravimore8386/matK-QR-classifier)
 6. DNABari-ID: Bacteria species identification [Github: https://github.com/ravimore8386/DNA_BarID](https://github.com/ravimore8386/DNA_BarID)
 7. ADBS-BioinfoTools (Dendrogram/Venn) [Github: https://github.com/husaynahmed/ADBS-BioinfoTools](https://github.com/husaynahmed/ADBS-BioinfoTools)

TRAINING

1. Training at School of Biological Sciences, Bioinformatics Training, University of Cambridge, UK
 - Analysis of bulk RNA-seq data (2-4 September 2019)
 - Analysis of single-cell RNA-seq data (16-17 December 2019)
 - ChIP-seq and ATAC-seq analysis (23-24 October 2019)
 - Statistics for Biologists in R (19-20 September 2019)
2. rRNA Sequencing, Phylogeny & Next Generation Genome Sequencing, BIT, Ranchi, India (2010)
3. Bioinformatics Tools and Data Analysis, Barkatullah University, Bhopal, India (2008)

NGS WORKFLOW & PROGRAMMING SKILLS

WGS/WES	Reads pre-processing (FASTQC, AfterQC), Alignment (samtools, BWA, PICARD, IGV), Variant Calling and <i>denovo</i> (VarScan/GATK), Annotation (ANNOVAR/VEP), CNV, SV, STR (GATK4 PreprocessIntervals, GASV, STRScan), Variant analysis (VCFtools, BCFtools), Databases (dbSNP, UCSC/Ensembl, gnomAD/ExAc, Allen, Atlas, Gtex).
scRNA-Seq	Seurat pipeline: QC, NormalizeData, Find Variable Features, ScaleData, RunPCA, RunUMAP, Harmony – Integration, Cluster identification and annotation, DE genes.
RNA-Seq	Alignment (TopHat/Star), Transcript assembly and Abundance estimation (Cufflink/htseq-count, Cuffmerge), Differential expression (Cuffdiff, EdgeR), CLC Genomics Workbench
ChIP/ATAC-seq	Alignment (Bowtie2/BWA) File manipulation and filtering (Samtools, Bedtools), peaks calling (MACS2) Peak annotation (HOMER), QC and downstream analysis of peaks (ChIPseeker), Profile/metaprofile plots, filtering reads/peaks (DeepTools), Motif identification & enrichment (MEME, TOMTOM).
Metagenomics	RAST/MG-RAST, MEGAN, Mauve, Standalone BLAST, MrBayes/RaXML/Phyliip.
Languages	Perl/Python, Bash shell scripts, Unix commands, and R for statistics/rna-seq.
HPC-OS	HPC Slurm Workload Manager, Linux Red Hat, Ubuntu, Macintosh.

BOOK PUBLICATIONS

- Co-editor and author in the book ‘Soft computing in biological sciences’, Springer publication, Editors: Kalia V. C., Purohit H. J., **More Ravi**, ISBN 978-981-10-7455-4 <https://tinyurl.com/23sv8vxm>
- Soft-computing methods and tools for Bacteria DNA Barcoding, **More Ravi**, Purohit H.J.
 - Fish DNA Barcoding: A comprehensive survey of the Bioinformatics tools and databases, Mane R. C., Ganesh H, **More Ravi**, Pal R., Purohit H. J.
 - Bioinformatics tools for shotgun metagenomic data analysis, Pal R., **More Ravi**, Purohit H. J.

AWARDS

1. 'Outstanding Project Personnel' for contribution to R&D activity, CSIR-NEERI, Nagpur, India (2014).
2. 'Second Prize' for Computer aided drug design project at MANIT, Bhopal, India (2008)
3. 'Star of MGM', MGM's College of CS & IT, Nanded, India (2008)

CONFERENCES AND POSTERS

1. The online conference was attended ‘UK Biobank Scientific Conference 2021 (25 February 2021)

2. The online conference was attended 'The BRAIN Conference 2021' (4-5 March 2021)
3. The poster presented at the Annual Review of Research DBT-InStem, ADBS Consortium, Bengaluru, India <https://tinyurl.com/yhn9tn3c> (6-8 March 2017)
 - **More Ravi** et al., Genomic Insights into The Indian Reference Exome.
 - Jagtap S., Bhatia P., **More Ravi** et al., Gene Mutations in Families Neuropsychiatric Illness.



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