Levin John

Bioinformatician | Data Scientist | Yenepoya University
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I'm a bioinformatician with over three years of experience using machine learning, deep learning, and graph neural networks to make sense of complex biological data. Most of my work focuses on high-throughput proteomics and clinical datasets, where I specialize in building bioinformatics pipelines and statistical analysis for identifying biomarkers. In addition, I have worked with clinicians to establish a risk assessment system for IPF patients in survival analysis with clinical variables. I have collaborated on numerous projects and co-authored in 14 international (journal) publications. My aim is to focus strongly on the translational of data-driven insights into real-world clinical applications.

Key Skills

Machine & Deep Learning: GNN, Transformers, XGBoost, CNN, ANN, Random Forrest

Shrinkage Models: Lasso, Ridge, Elastic Net, Dropout

Bioinformatics: Structural biology (Docking, MDS, Homology Modelling, Pharmacophore screening). Gene set enrichment analysis, Kinase-Interactome, Pathway analysis and development, Large-scale data analysis, Omics – Pipeline development

Programming & Tools: Python, R, Linux, Seaborn, Pytorch, Keras, Tensorflow, Scikit-learn. Seaborn, Matplotlib, Pandas.

Statistical Modeling: Cox/Linear regression, Survival analysis.

Tools & Packages: Schrodinger-Suite, Visual-studio, Anaconda, Autodock, MODELLER, Proteome Discoverer, Adobe Creative Cloud

Research Interest: Phosphoproteomics, Proteomics, Transcriptomics, Metabolomics, Precision Medicine, Structural Biology.

EXPERIENCE

Institute of Regeneration & Repair   *Edinburgh, Scotland*
***Visiting Research Fellow**; Principal Investigator: Dr Nik Hirani*   *April (2025) to Present*
University of Edinburgh
- Developing machine learning models to identify biomarkers in patients with Idiopathic Pulmonary Fibrosis
- Developing a tool for the risk stratification of IPF patients.

Centre for Integrative Omics Data Science (CIODS)   *Mangalore, India*
***Data Scientist/Bioinformatician**; Principal Investigator:* Dr Rajesh Raju   *March (2022) to March 2025*
Yenepoya (Deemed to be University)
- Specialization in Computational and Structural Biology.
- Managing extensive biological data set analysis and developing software solutions and tools to enhance our understanding of biological systems.
- Expertise in applying deep-learning models and bioinformatics techniques to large-scale proteomics, Phosphoproteomics datasets.
- Skilled in deriving structural insights through molecular docking, simulations and other insilico techniques.
- Collaborating with various teams to automate data handling, normalization, and visualization.

Collaborator
- Institute for Regeneration and Repair, Dr Nik Hirani   *January (2024) to present*
  University of Edinburg, Scotland

EDUCATION
- *Master of Science;* ***Bioinformatics (Grade B)***   *August 2019 – July 2021*
  Mahatma Gandhi University
  Kottayam, Kerala, India

- *Bachelor of Science; **Biotechnology*** *June 2016 – March 2019*
  Mahatma Gandhi University
  Kottayam, Kerala, India

PUBLICATIONS

1. **John, L.,** Dcunha, L., Ahmed, M. *et al.* A deep learning and molecular modeling approach to repurposing Cangrelor as a potential inhibitor of Nipah virus. *Scientific Reports* 15, 16440 (2025) *www.nature.com/articles/s41598-025-00024-3*

2. Thaikkad, A., Henna, F., Thomas, S.D., **John, L**. *et al.* Cangrelor and AVN-944 as repurposable candidate drugs for hMPV: analysis entailed by AI-driven in silico approach. *Mol Divers* (2025). https://doi.org/10.1007/s11030-025-11206-6

3. Raghu DH, Dcunha L, Ahmed M, Fahma A, Mahin A, Gopalakrishnan AP, **John L**, Subair S, Shivamurthy PB, Varghese S, Ummar S, Nisar M, Ramesh P, Madar IH, Raju R. Unravelling the phosphoregulatory network of protein kinase C-delta (PKC-δ). Biochim Biophys Acta Proteins Proteom. 2025 Jun 2;1873(5):141080. https://doi.org/10.1016/j.bbapap.2025.141080

4. Lubaba, F., George, M., Ahmed, M., **John, L.**, Goplakrishnan, A. P., Shivamurthy, P. B., Varghese, S., Pahal, P., Nisar, M., Ramesh, P., Madar, I. H., & Raju, R. (2025). Theranostic Target NSUN2, a C(5)-Methyltransferase, Phospho-Regulatory Network Uncovered with Systematic Assembly of 805 Datasets. *Omics: a journal of integrative biology*, *29*(4), 164–177. https://doi.org/10.1089/omi.2025.0025

5. Mahin, A., Gopalakrishnan, A. P., Ahmed, M., Nisar, M., **John, L.,** Shivamurthy, P. B., Ummar, S., Varghese, S., Modi, P. K., Pai, V. R., Prasad, T. S. K., & Raju, R. (2025). Orchestrating Intracellular Calcium Signaling Cascades by Phosphosite-Centric Regulatory Network: A Comprehensive Analysis on Kinases CAMKK1 and CAMKK2. *Omics : a journal of integrative biology*, *29*(4), 139–153. https://doi.org/10.1089/omi.2024.0196

6. Chakraborty S, Mahin A, Shivamurthy P.B, Ahmed M, Gopalakrishnan A.P., **John L**, Varghese S, Ramesh P, Raju. R., 2025. Phosphoproteomic insights into GFPT2-Associated cellular phospho-signaling networks., Biochemistry and Biophysics Reports (2025), 102196 Volume 43, https://doi.org/10.1016/j.bbrep.2025.102196

7. M Nisar, S P Soman, S Sreelan, **L John**, S M Pinto, R K Kandasamy, Y Subbannayya, T S K Prasad, S Kanekar, R Raju, Rex D A B., ProteoArk: A one-pot proteomics data analysis and visualization tool for biologists. *Journal of Proteome research (*2025*). https://pubs.acs.org/doi/10.1021/acs.jproteome.4c00556*

8. Cartlidge, MK., Brown, K., Chaudhuri, N., Corte, TJ., Dieude, P., **John, L,** et al, 2024. A modified Delphi exercise in physician-perceived risk factors for drug-induced pneumotoxicity in patients with rheumatological disease. *BMC Pulmonary Medicine (2024).* https://doi.org/10.1186/s12890-024-03287-0

9. Sanjeev, D., Mendon, S., George, M., **John, L**., Perunelly Gopalakrishnan, A., Nisar, M., Rafi, A., Priyanka, P., Yandigeri, T., Raju, R. and Kanekar, S., 2024. Exploring the phospho-landscape of NEK6 kinase: systematic annotation of phosphosites and their implications as biomarkers in carcinogenesis. *JPP (2024)*https://doi.org/10.1007/s42485-024-00146-8

10. **John, L.,** George, M., Dcunha, L. et al. Elucidating the phosphoregulatory network of predominant phosphosite in AXL kinase: an integrative bioinformatic approach. *J Proteins Proteom (2024).* https://doi.org/10.1007/s42485-024-00147-7

11. Daniel Thomas, S., Vijayakumar, K., **John, L**., Krishnan, D., Rehman, N., Revikumar, A., Kandel Codi, J.A., Prasad, T.S.K., SS, V. and Raju, R., 2024. Machine learning strategies in microRNA research: bridging genome to phenome. *OMICS: A Journal of Integrative Biology (2024)*, 28(5), pp.213-233. https://doi.org/10.1089/omi.2024.0047

12. Priyanka, P., Gopalakrishnan, A.P., Nisar, M., Shivamurthy, P.B., George, M., **John, L.,** Sanjeev, D., Yandigeri, T., Thomas, S.D., Rafi, A. and Dagamajalu, S., 2024. A global phosphosite-correlated network map of Thousand And One Kinase 1 (TAOK1). *The International Journal of Biochemistry & Cell Biology (2024),* 170, p.106558. https://doi.org/10.1016/j.biocel.2024.106558

13. Banjan, B., Koshy, A.J., Kalath, H., **John, L**., Soman, S., Raju, R. and Revikumar, A., 2024. Potential protein kinase inhibitors that target G-quadruplex DNA structures in the human telomeric regions. *Molecular Diversity (2024),* pp.1-15. http://doi.org/10.1007/s11030-023-10768-7

14. Sanjeev, D., George, M., **John, L**., Gopalakrishnan, A.P., Priyanka, P., Mendon, S., Yandigeri, T., Nisar, M., Nisar, M., Kanekar, S. and Balaya, R.D.A., 2024. Tyr352 as a predominant phosphosite in the understudied kinase and molecular target, HIPK1: implications for cancer therapy. *OMICS: A Journal of Integrative Biology (2024)*, 28(3), pp.111-124. https://doi.org/10.1089/omi.2023.0244

15. Thatai, A.K.S., Ammankallu, S., Balaya, R.D.A., Soman, S.P., Nisar, M., Babu, S., John, L., George, A., Anto, C.K., Sanjeev, D. and Kandiyil, M.K., 2023. VirhostlncR: A comprehensive database to explore lncRNAs and their targets in viral infections. Computers in Biology and Medicine (2023), https://doi.org/10.1016/j.compbiomed.2023.107279

TEACHING AND MENTORSHIP

Training and leading the data visualization team at CIODS   *September 2022 – March 2025*
- Teaching and Instructing intern's bio-curation, data handling, interpretation & visualization, programming, and structural biology techniques.
- Collaborating and working with interdisciplinary teams in developing data visualization and generating video tutorials for in-house tools and scientific illustration for publications.
- Member of International Society for Computational Biology (ISCB)

Journal Reviewer   *August 2024 - present*
- *Computers in Biology and Medicine (Impact factor: 7.0)*
- *NeuroMolecular Medicine (Impact factor: 3.3)*
- *Scientific Reports (Impact factor: 4.3)*

Participation, Courses and Other Certificates (Selected)

- Fundamentals of Data Science in Precision Medicine and Cloud Computing – By Department of Genetics, Standford Medicine   *August 2025*
- Resource Person – Workshop on Molecular Docking organized by Yenepoya Homoeopathic College and CIODS at Ayush Campus, Yenepoya University   *March 2025*
- Invigilator – Yentech Mania   *April 2024*
  Organized by Yenepoya Institute of Technology (YIT).
- Presented a poster Titled "*Cardioprotective and antioxidant potential of Hybanthus Enneaspermus (l.) F. Muell. in isoproterenol induced myocardial rats*" in an international symposium ON "*Cardiovascular metabolomics*" Organized by Centre for Systems Biology and Molecular Medicine in collaboration with the London School of Hygiene and Tropical Medicine.   *May 2023*
- Courses completed in Coursera includes "*AI For Everyone*"authorized by DeepLearning, "*Overview of Data Visualization*" authorized by Coursera Project Network, "*The R Programming Environment*" authorized by Johns Hopkins University, "*Antimicrobial resistance - theory and methods*" authorized by the Technical University of Denmark (DTU)
- Participated in the International lecture workshop on "*Cell Cycle and Cell Death*" supported by EMBO, Chaired by Sir. Tim Hunt (2001 Nobel laureate).
- Symposium on "*International symposium on Bioinformatica Indica 2020*" Organized by the Department of Computational Biology and Bioinformatics, University of Kerala Thiruvananthapuram.

REFERENCES

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