

Rohit Farmer

rohit.farmer@gmail.com, <https://rohitfarmer.com>, +1(314)-255-6763, Bethesda, MD, USA

Research Summary

I have eight years of post-Ph.D. interdisciplinary research experience, applying computational methods at the intersection of biology, chemistry, and medicine. In my current position at CHI, NIH, I am building tools for high-dimensional analysis of flow/mass cytometry and somascan data and establishing an analysis pipeline for spatial transcriptomics. In the past, I have worked on applying deep learning to large-scale molecular data to understand drug bioactivation and toxicity. I have also worked with protein structure/complex prediction, modeling protein-protein interactions, molecular dynamics simulations, virtual screening, and sequence analysis.

Research & Teaching Experience

2019-now	Computational Biologist	Medical Science & Computing, USA On site at the National Institutes of Health (NIH) NIH Center for Human Immunology, Inflammation, and Autoimmunity (CHI)
2018-2019	Postdoctoral Research Associate	Washington University in St. Louis, USA Department of Pathology and Immunology
2016-2018	Associate Editor	The Allahabad Journal of Science and Technology (Formerly The Allahabad Farmer)
2015-2018	Assistant Professor	Sam Higginbottom University of Agri., Tech. and Sci. (SHUATS), India Department of Computational Biology and Bioinformatics (CBBI)
2008-2011	Assistant Professor	Sam Higginbottom Institute of Agri., Tech. and Sci. (SHIATS), India Department of Computational Biology and Bioinformatics (CBBI)

Administrative Experience

2015-2016	International Training Associate	SHUATS, India Directorate of International Education and Training
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Teaching Assignments

2008	Molecular Genetics (UG, MBGE-441)	SHUATS, India
2009-2011	Biomolecular Modelling (UG, BI-605)	SHUATS, India
2012-2014	<i>Assisted in teaching</i> Physical Biochemistry (UG, Bio143)	University of Birmingham, UK
2015-2017	Concepts of Bioinformatics (UG, CBBI-502)	SHUATS, India
2015-2017	Structural Bioinformatics (UG, CBBI-601)	SHUATS, India
2015-2017	Fundamentals of Bioinformatics and Information Technology (PG, CBBI-701)	SHUATS, India
2015-2017	Computer Aided Drug Designing (PG, CBBI-803)	SHUATS, India

Education

2011-2015	Doctor of Philosophy (Ph.D.) Biosciences	University of Birmingham, UK
2008-2010	Master of Technology (M.Tech.) Bioinformatics <i>CGPA 9.35/10; Silver Medal</i>	Sam Higginbottom Institute of Agri., Tech. and Sci. (SHIATS), India
2004-2008	Bachelor of Technology (B.Tech.) Biotechnology <i>CGPA 8.41/10</i>	Allahabad Agricultural Institute, India

Certifications & Licenses

2021	Amateur Radio Technician Class - KC3SNU	Federal Communications Commission, USA
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2019	Deep Learning with Python and Keras	Udemy
2019	Python for Data Science and Machine Learning Bootcamp	Udemy
2017	Algorithms for DNA Sequencing	Johns Hopkins University, Coursera
2017	Python for Genomic Data Science	Johns Hopkins University, Coursera

Awards & Achievements

2014	Travel grant, 28 th Annual Symposium of The Protein Society, USA	Biochemical Society
2013	Travel grant, 15 th EMBL PhD Symposium, Germany	EMBL
2013	Travel grant, ISMB/ECCB'13, Germany	National Science Foundation
2013	George Parks travel grant, Molecular Perspectives On Protein-Protein Interactions, Poland	University of Birmingham
2012	Travel grant, ECCB'12, Switzerland	Swiss Foundation for Excellence and Talent in Biomedical Research
2011-2014	PhD scholarship	The Darwin Trust of Edinburgh
2010	Silver medal in M.Tech. Bioinformatics	SHIATS

Scientific Skills

Computational Biology: Single cell cytometry data analysis, molecular structure prediction, molecular docking, molecular dynamics simulation, bioinformatics

Experimental Biology: PCR, Gibson assembly, restriction digestion, plasmid transformation, microbiology techniques, HPLC

Data Science & Machine Learning: Data wrangling & visualization, feature engineering, dimensionality reduction, supervised & unsupervised learning, linear & mixed-effects modeling, deep-learning ~ Tidyverse, Lme4, NumPy, Pandas, SciPy, Matplotlib, Seaborn, Plotly, Scikit Learn, Keras, TensorFlow

Operating Systems: Linux, Mac OS X, MS Windows

Computer Languages (Proficient): R, Python, Perl

Computer Languages (Familiar): C++, \LaTeX , HTML, CSS, Java Script

Database: SQLite, Neo4J

HPC: SLURM, PBS

Containers & VMs: Docker, Singularity, Oracle Virtual Box

VCS: Git, Mercurial

Transferable Skills Training

2018	Mentorship Training Program	Washington University in Saint Louis, USA
2018	Mentoring Undergraduate Research	Washington University in Saint Louis, USA
2012	Leading Academics, Leadership development program	University of Birmingham, UK
2012	One day course on Poster Presentations: Planning the Content	University of Birmingham, UK
2012	Talent Pool, Training program on entrepreneurship	University of Birmingham, UK
2012	One day course on Speed Reading	University of Birmingham, UK
2011	One day course on Time Management	University of Birmingham, UK

Conferences Attended & Organised

2022	CSHL Biological Data Science, Virtual	Poster Presentation
2021	CSHL Systems Immunology, Virtual	Poster Presentation
2020	CSHL Biological Data Science, Virtual	Poster Presentation
2019	Symposium on Personal Control of Genomic Data for Research, USA	Participant
2019	FOCIS 2019, USA	Participant
2015	National Conference on Bioinformatics Panorama in Agriculture and Health, India	Sponsor Liaison
2014	1 st RSG-UK Student Symposium on Computational Biology and Life Sciences, UK	Secretary
2014	Synthetic Biology of Antibiotic Production II, Spain	Short Talk
2014	The 28 th Annual Symposium of the Protein Society, USA,	Poster Presentation
2013	15 th EMBL PhD Symposium, Germany	Short Talk
2013	ISMB/ECCB'13, Germany	Poster Presentation
2013	Molecular Perspectives On Protein-Protein Interactions, Poland	Poster Presentation
2012	11 th European Conference on Computational Biology, Switzerland	Poster Presentation
2012	3 rd BEAR Postgraduate Conference on Research Computing, UK	Secretary and Sponsor Liaison
2010	The Eighth Asia Pacific Bioinformatics Conference, India	Poster Presentation
2009	National Workshop on Functional Genomics and Proteomics, India	Participant
2009	International Conference on Open Source for Computer Aided Drug Discovery, India	Poster Presentation

Professional Memberships

2013-2014	The Protein Society
2012-2015	International Society for Computational Biology (ISCB)
2012-2015	Biochemical Society

Extra Curricular Positions Held

2013-2014	Co-Founder and Secretary, Regional Student Group, UK	Student Council, ISCB
2011-2012	Secretary, Bharat Parivar, Guild of Students	University of Birmingham
2009-2010	Vice president for Society of Biotechnology	SHIATS

Community Involvement

2019	Reviewed 1 research article for MEEGID - Infection, Genetics and Evolution.
2020	Reviewed 1 research article for Biophysical Journal.
2020-2023	Reviewed 8 research articles for the Journal of Biomolecular Structure & Dynamics.
2021-2022	Reviewed 7 research articles for ACS Omega.
2021	Reviewed 1 research article for Textile Research Journal.
2022	Contributed curated datasets for data science education and advancement at https://www.kaggle.com/rohitfarmer .
2022-now	Built and maintained https://www.dataalltheway.com , a tutorial website with concepts, methods, and example code on data science, statistics, and machine learning.

Software Developed

HDStIM: High Dimensional Stimulation Immune Mapping <https://niaid.github.io/HDStIM/>

Publications

Rohit Farmer. Modelling polyketide synthases and related macromolecular complexes. *PhD Thesis. University of Birmingham*, 2015. <https://etheses.bham.ac.uk/id/eprint/5909/>

Book Chapter

Farmer R.*, Thomas C. M., and Winn P. J. Modelling Polyketide Synthases and Similar Macromolecular Complexes. In: Wadhwa G., Shanmughavel P., Singh A., Bellare J. (eds) *Current trends in Bioinformatics: An Insight*. Springer, Singapore, 2018, 121-144. https://doi.org/10.1007/978-981-10-7483-7_7

Submitted Peer Reviewed Article(s)

2022 - **Farmer R.**, Apps R., and Tsang J. S. Multiparameter stimulation mapping of signaling states in single pediatric immune cells reveals heightened tonic activation during puberty.

2022 - Apps R., Biancotto A., Candia J., Kotliarov Y., Perl S., Cheung F., **Farmer R.**, Mule M. P., Chen J., Martins A. J., Shi R., Zhou H., Bansal N., Schum P., Olnes M. J., Milanez-Almeida P., Han K. L., Sellers B. A., Cortese M., Hagan T., Roupahel N., Pulendran B., King L., Manischewitz J., Khurana S., Golding H., Most R. G. van der, Dickler H. B., Germain R. N., Schwartzberg P. L., and Tsang J. S. High dimensional dynamic response pattern discovery reveals acute and persistent impacts of H5N1 vaccination with and without adjuvant.

Published Peer Reviewed Articles

Google Scholar: *h-index 11, i10-index 12*, http://bit.ly/rf_cite

22. Flynn N. R., Ward M. D., Schleiff M. A., Laurin C. M. C., **Farmer R.**, Conway S. J., Boysen G., Swamidass S. J., and Miller G. P. Bioactivation of isoxazole-containing bromodomain and extra-terminal domain (bet) inhibitors. *Metabolites*, 11(6), 2021.
21. **Farmer R.**, Thomas C. M., and Winn P. J. Structure, function and dynamics in acyl carrier proteins. *PLOS ONE*, 14(7):1–17, 2019.
20. Konda A. K., **Farmer R.**, Soren K. R., P. S. S., and Setti A. Structural modelling and molecular dynamics of a multi-stress responsive WRKY TF-DNA complex towards elucidating its role in stress signalling mechanisms in chickpea. *Journal of Biomolecular Structure and Dynamics*, 36(9):2279–2291, 2018.
19. Dhusia K., Yadav P. K., **Farmer R.**, and Ramteke P. W. Inhibition of polyamine biosynthesis for toxicity control in *Serratia marcescens* strain WW4 by targeting ornithine decarboxylase: A structure-based virtual screening study. *International Journal of Computational Biology and Drug Design*, 11(1-2):114–134, 2018.
18. Lodhi S. S., **Farmer R.**, Jaiswal Y. K., and Wadhwa G. In Silico Structural, Virtual Screening and Docking Studies of Human Cytochrome P450 2A7 Protein. *Interdisciplinary Sciences: Computational Life Sciences*, 7(2):129, 2015.
17. Lodhi S. S., **Farmer R.**, Singh A. K., Jaiswal Y. K., and Wadhwa G. 3D structure generation, virtual screening and docking of human Ras-associated binding (Rab3A) protein involved in tumourigenesis. *Molecular Biology Reports*, 41(6):3951, 2014.
16. Khanim F., Davies N., Veliça P., Hayden R., Ride J., Pararasa C., Chong M. G., Gunther U., Veerapen N., Winn P. J., **Farmer R.**, Trivier E., Rigoreau L., Drayson M., and Bunce C. Selective AKR1C3 inhibitors do not recapitulate the anti-leukaemic activities of the pan-AKR1C inhibitor medroxyprogesterone acetate. *British Journal of Cancer*, 110(6):1506–1516, 2014.
15. Kumar S., **Farmer R.**, Turnbull A. P., Tripathy N. K., and Manjasetty B. A. Structural and functional conservation profiles of novel cathepsin L-like proteins identified in the *Drosophila melanogaster* genome. *Journal of Biomolecular Structure and Dynamics*, 31(12):1481–1489, 2013.
14. Haines A. S., Dong X., Song Z., **Farmer R.**, Williams C., Hothersall J., Płoskoń E., Wattana-Amorn P., Stephens E.R., Yamada E., Gurney R., Takebayashi Y., Masschelein J., Cox R. J., Lavigne R., Willis C. L., Simpson T. J., Crosby J., Winn P. J., Thomas C. M., and Crump M. P. A conserved motif flags acyl carrier proteins for β -branching in polyketide synthesis. *Nature Chemical Biology*, 9(11):685–692, 2013.
13. Singh S., Sablok G., **Farmer R.**, Singh A. K., Gautam B., and Kumar S. Molecular dynamic simulation and inhibitor prediction of cysteine synthase structured model as a potential drug target for trichomoniasis. *BioMed Research International*, 2013(390920), 2013.

* Corresponding Author

12. Paital B., Kumar S., **Farmer R.**, and Chainy G. B. N. In silico prediction of 3D structure of Mn superoxide dismutase of *Scylla serrata* and its binding properties with inhibitors. *Interdisciplinary Sciences: Computational Life Sciences*, 5(1):69, 2013.
11. Kumari S., Shridhar S., Singh D., Priya P., **Farmer R.**, Hundal J., Sharma P., Bavishi K., Schrick K., and Yadav G. The role of lectins and HD-ZIP transcription factors in isoprenoid based plant stress responses. *Proceedings of the Indian National Science Academy*, 78(4):671–691, 2012.
10. Lodhi S. S., **Farmer R.**, Singh A. K., Wadhwa M., Jaiswal Y. K., and Wadhwa G. Statistical analysis of differential gene expression profile for colon cancer. *Indian Journal of Biotechnology*, 11:396–403, 2012.
9. Gautam B., Singh G., Wadhwa G., **Farmer R.**, Singh S., Singh A. K., Jain P. A., and Yadav P. K. Metabolic pathway analysis and molecular docking analysis for identification of putative drug targets in *Toxoplasma gondii*: novel approach. *Bioinformation*, 8(3):134–141, 2012.
8. Fazil M. H. U. T., Kumar S., **Farmer R.**, Pandey H. P., and Singh D. V. Binding efficiencies of carbohydrate ligands with different genotypes of cholera toxin B: Molecular modeling, dynamics and docking simulation studies. *Journal of Molecular Modeling*, 18(1), 2012.
7. Paital B., Kumar S., **Farmer R.**, Tripathy N. K., and Chainy G. B. N. In silico prediction and characterization of 3D structure and binding properties of catalase from the commercially important crab, *Scylla serrata*. *Interdisciplinary Sciences: Computational Life Sciences*, 3(2):110–120, 2011.
6. Singh S., Singh G., Singh A. K., Gautam B., **Farmer R.**, Lodhi S. S., and Wadhwa G. Prediction and analysis of paralogous proteins in *Trichomonas vaginalis* genome. *Bioinformation*, 6(1):31–34, 2011.
5. Jeyakumar E., Lawrence R., **Farmer R.**, and Sahai S. *In vitro* and *In silico* analysis of xylanase produced by *Bacillus licheniformis*. *Applied Biological Research*, 13(1):17–27, 2011.
4. Yadav P. K., Singh R., Jain P. A., Singh S., Gautam B., and **Farmer R.** *In silico* epitope prediction for glycoprotein D in human herpes simplex virus-1. *Int J Pharm Sci Rev Res*, 7(2):148–153, 2011.
3. Yadav P. K., Sachan R., Tandon S., Singh S., Gautam B., **Farmer R.**, and Jain P. A. *In silico* study of heterodimerization of TLR2 and TLR6. *Int J Pharm Sci Rev Res*, 7(1):113–120, 2011.
2. Gautam B., Katara P., Singh S., and **Farmer R.** Drug target identification using gene expression microarray data of *toxoplasma gondii*. *International Journal of Biometrics and Bioinformatics (IJBB)*, 4(3):113, 2010.
1. **Farmer R.**[†], Gautam B., Singh S., Yadav P. K., and Jain P. A. Virtual screening of AmpC/ β -lactamase as target for antimicrobial resistance in *Pseudomonas aeruginosa*. *Bioinformation*, 4(7):290–4, 2010.

Preprints

3. Mulè, M. P., Martins, A. J., Cheung, F., **Farmer, R.**, Sellers, B., Quiel, J. A., Jain, A., Kotliarov, Y., Bansal, N., Chen, J., Schwartzberg, P. L., Tsang, J. S. Multiscale integration of human and single-cell variations reveals unadjuvanted vaccine high responders are naturally adjuvanted. *medRxiv*, 2023.03.20.23287474; doi: <https://doi.org/10.1101/2023.03.20.23287474>
2. **Farmer R.**, Apps R., Quiel J., Sellers B. A., Cheung F., Chen J., Mukherjee A., McGuire P. J., and Tsang J. S. Multiparameter stimulation mapping of signaling states in single pediatric immune cells reveals heightened tonic activation during puberty. *bioRxiv*, 2022.11.14.516371; doi: <https://doi.org/10.1101/2022.11.14.516371>
1. Rahman F., **Farmer, R.**, Das S., Vayani F. and Hassan M. Highlights of the 1st Student Symposium of the ISCB RSG UK. *F1000Research*, 4:154, 2015. <https://doi.org/10.12688/f1000research.6616.1>

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[†] Corresponding Author