VINOD K. GUPTA, Ph.D.

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PROFESSIONAL SUMMARY

Computational System Biologist | Microbiome | Data Science | Precision Medicine

With over a decade (15 years) of experience in computational biology, I am deeply committed to advancing personalized healthcare. My goal is to harness the power of machine learning (ML) and artificial intelligence (AI) to predict treatment response, classify disease subtypes, and reveal underlying mechanisms in chronic diseases such as rheumatoid arthritis, multiple sclerosis, and cancer. By integrating multi-omics data—including genomics, metagenomics (microbiome), transcriptomics, proteomics, metaproteomics, and metabolomics—with clinical imaging and experimental data, I aim to identify biomarkers that drive precision diagnostics, wellness monitoring, and targeted therapies. At the core of my work is the drive to translate complex biological data into actionable insights that improve patient outcomes and enable more tailored, effective treatments.

Google Scholar: (Citations: 2,683, h-index: 12, i10–index: 13, 08/16/2025)

SKILLS

- Bioinformatics tools and resources (expert)
- Next-generation sequencing (NGS) (expert)
- Metagenomics and Microbiome analysis (expert)
- Amplicon sequence analysis (expert)
- Transcriptomics (advance)
- Metaproteomics/proteomics (expert)
- Metabolomics (advance)
- Microbial genomics (expert)
- Pan-genome analysis (expert)
- Bioinformatics tools and methods development (expert)
- Machine learning (advance)
- Biostatistics (advance)
- R programming (expert)
- Python programming (advance)
- Perl (basic)
- Linux (advance)
- High Performance Computing (HPC) (expert)
- Communication (fluent)
- Supervision & Mentorship
- Complex problem-solving

RESEARCH EXPERIENCE

1. **POSTDOCTORAL RESEARCH ASSOCIATE** (10/2022 to Current), Microbiomics program, Center for Individualized Medicine, Mayo Clinic, Rochester, MN, USA

   - In my current role, I integrate diverse biological data to better understand complex diseases. This includes profiling the microbiome using data from Next-Generation Sequencing (NGS) techniques, including Long-Read and Short-Read Sequencing Techniques, with an emphasis on whole-genome shotgun (WGS) metagenome sequencing and 16S rRNA gene amplicon sequencing. I also analyze transcriptomics (RNA-Seq), proteomics (Mass Spectrometry and Olink), metaproteomics (Mass Spectrometry), and metabolomics data.
   - I apply machine learning algorithms to predict treatment responses and classify disease phenotypes using microbiome and other multi-omics data. I also lead designing the clinical studies and implementing the analysis strategies, with a focus on integrating multi-omics datasets to identify biomarkers that can inform diagnosis and guide precision treatment strategies.
   - In my current role, I contribute to study design, grant writing and generation of preliminary data to support ongoing and future research in the lab.

- Co-supervision of Ph.D., Masters', and undergraduate students.
- I also provide analytical support to the Mayo Clinic Proteomics Core, performing proteomics data (Mass Spectrometry and Olink) analysis for internal and external clients.

Projects Leading:

1. Predicting the response to methotrexate in treatment-naïve rheumatoid arthritis (RA) patients.
2. I designed the pipeline for Identification of protein signatures of colorectal cancer in colorectal cancer (CRC) patients using metaproteomics data from stool samples.
3. Investigation of relationships between the gut microbiome and the host immune response, following B-cell–depletion therapy in newly diagnosed multiple sclerosis (MS) patients.
4. I designed the study and developed the Gut Microbiome Wellness Index 2 (GMWI2) for predicting the health status based on gut microbiome taxonomic profiles.
5. Investigation of the safety, feasibility, and impact on the gut microbiome of kefir administration in critically ill adults.
6. Evaluating the prebiotic effect of oligosaccharides on gut microbiome wellness.
7. Development of GMWI-webtool to calculate GMWI using gut microbiome profiles.

Projects Involved:

1. Identification of plasma proteomic signatures for active and inactive giant cell arteritis (GCA).
2. Identification of proteomic biomarkers in cerebrospinal fluid (CSF) to assess severity of first-episode psychosis.
3. Investigation of immunological differences between subtypes of patients with RA.

2. POSTDOCTORAL RESEARCH FELLOW (10/2017 to 10/2022), Microbiomics program, Center for Individualized Medicine, Mayo Clinic, Rochester, MN, USA

- Conducted comprehensive gut microbiome analyses and developed bioinformatics tools and computational methods.
- Co-supervision of Ph.D. and Masters' students
- Manuscript writing and presentation of findings at international conferences and scientific meetings.
- Study design

Projects Led:

1. I conceived the idea and developed the Gut Microbiome Health Index (GMHI) for quantitative assessment of health status using species-level gut microbiome profile.
2. Designed a deep learning–based predictive model to forecast clinical improvement in rheumatoid arthritis patients using stool microbiome profiles.
3. Created the Taxi-BGC, a computational pipeline for identifying microbiome-derived biosynthetic gene clusters (BGCs) and secondary metabolites in metagenomes.

Projects Involved:

1. Identified metabolites predictive of disease activity in rheumatoid arthritis patients through global plasma metabolomic profiling.
2. Characterized immune cell types and subsets associated with primary biliary cholangitis using Mass Cytometry (CyTOF)–based immunophenotyping.
3. Investigated robust nested patterns in healthy gut microbiomes using stochastic block modeling.

3. RESEARCH ASSOCIATE (07/2016 to 03/2017), Structural Biology & Bioinformatics Division, CSIR–Indian Institute of Chemical Biology, Kolkata, India

- Analysis of microbiome profiles
- Database creation
- Manuscript writing
- Co-supervision of Ph.D. and Masters' students
- Study design

Projects Led:

1. Identification of geography, ethnicity or subsistence-specific variations in human microbiome compositions
2. Development of PanGFR-HM, a dynamic web resource for pan-genomic and functional profiling of human microbiome

4. RESEARCH FELLOW (Ph.D. student) (04/2011 to 06/2016), Structural Biology & Bioinformatics Division, CSIR–Indian Institute of Chemical Biology, Kolkata, India

- Analysis of microbial genomes
- Pan-genome analysis
- Statistical analysis of nucleotide and amino acid sequences of microbiome
- Phylogenetic analysis
- Functional analysis (KEGG and COG metabolic pathways)
- Bioinformatics tools and pipeline development
- Manuscript writing and presentation of findings at international conferences and scientific meetings.
- Co-supervision of Masters' students

Projects Led:

1. Identification of divergences in gene repertoire among the reference Prevotella genomes derived from distinct body sites of human
2. Development of a computational pipeline (BPGA) for bacterial pan-genome analysis

EDUCATION

1. **Doctor in Philosophy (Ph.D.)** – Science (discipline: **Bioinformatics, Microbiome, Genomics**), 2017, CSIR-Indian Institute of Chemical Biology (CSIR-IICB), Kolkata, India; Academy of Scientific and Innovative Research (AcSIR), India.

2. **Master of Science (M.S. Pharm)** – Pharmacoinformatics (**Bioinformatics, Cheminformatics and Systems Biology**), 2009, National Institute of Pharmaceutical Education and Research (NIPER), Kolkata, India.

3. **Bachelor of Pharmaceutical Sciences (B. Pharm)**, 2009, Mohan Lal Sukhadia University, Udaipur, Rajasthan, India.

PH.D. DISSERTATION

Title: Divergences in Gene Repertoires of Microbiome Components Derived from Distinct Body-sites of Human
Ph.D. supervisor: Dr. Chitra Dutta, Chief scientist & Head (retired), Structural Biology & Bioinformatics Division, CSIR-IICB, Kolkata, India
Ph.D. co-supervisor: Dr. Sucheta Tripathy, Senior Principal Scientist, Structural Biology & Bioinformatics Division, CSIR-IICB, Kolkata, India

PUBLICATIONS

First or co-first author (#equal contribution)

1. **Vinod K. Gupta**, Adam M. Koller, Benjamin Hur, John M. Davis III, Jaeyun Sung. Gut Microbiome Signatures Forecast Clinical Response to Methotrexate in Treatment-Naive Early Arthritis Patients. (**manuscript in preparation for *Nature Microbiology***).
2. **Vinod K. Gupta**, Guneet S. Janda, Heather K. Pump, Nikhil Lele, Isabella Cruz, Inessa Cohen, William E. Ruff, David A. Hafler, Jaeyun Sung, Erin E. Longbrake. Alterations in Gut Microbiome-Host

Relationships After Immune Perturbation in Patients With Multiple Sclerosis. ***Neurology: Neuroimmunology & Neuroinflammation*** (**2025**).

3. Daniel Chang[#], **Vinod K. Gupta**[#], Benjamin Hur, Sergio Cobo-López, Kevin Y. Cunningham, NamSoo Han, Insuk Lee, Vanessa L. Kronzer, Levi M. Teigen, Lioudmila V. Karnatovskaia, Erin E. Longbrake, John M. Davis III, Heidi Nelson, Jaeyun Sung. Gut Microbiome Wellness Index 2 Enhances Health Status Prediction from Gut Microbiome Taxonomic Profiles. ***Nature Communications*** (**2024**).
4. **Vinod K. Gupta**, Sanu Rajendraprasad, Mahmut Ozkan, Dhanya Ramachandran, Sumera Ahmad, Johan S. Bakken, Krzysztof Laudanski, Ognjen Gajic, Brent Bauer, Simon Zec, David W. Freeman, Sahil Khanna, Aditya Shah, Joseph H. Skalski, Jaeyun Sung, Lioudmila V. Karnatovskaia. Safety, Feasibility, and Impact on the Gut Microbiome of Kefir Administration in Critically Ill Adults. ***BMC Medicine*** (**2024**).
5. **Vinod K. Gupta**, Utpal Bakshi, Daniel Chang, Aileen R. Lee, John M. Davis III, Sriram Chandrasekaran, Yong-Su Jin, Michael F. Freeman, Jaeyun Sung. TaxiBGC: a Taxonomy-Guided Approach for Profiling Experimentally Characterized Microbial Biosynthetic Gene Clusters and Secondary Metabolite Production Potential in Metagenomes. ***mSystems*** (**2022**).
6. **Vinod K. Gupta**, Kevin Y. Cunningham, Benjamin Hur, Utpal Bakshi, Harvey Huang, Kenneth J. Warrington, Veena Taneja, Elena Myasoedova, John M. Davis III, Jaeyun Sung. Gut Microbial Determinants of Clinically Important Improvement in Patients with Rheumatoid Arthritis. ***Genome Medicine*** (**2021**).
7. **Vinod K. Gupta**, Minsuk Kim, Utpal Bakshi, Kevin Y. Cunningham, John M. Davis III, Konstantinos N. Lazaridis, Heidi Nelson, Nicholas Chia, Jaeyun Sung. A Predictive Index for Health Status Using Species-level Gut Microbiome Profiling. ***Nature Communications*** (**2020**).
8. **Vinod K. Gupta**, Sandip Paul, Chitra Dutta. Geography, Ethnicity or Subsistence-Specific Variations in Human Microbiome Composition and Diversity. Frontiers in Microbiology (2017).
9. Narendrakumar M. Chaudhari[#], **Vinod K. Gupta**[#], Chitra Dutta. BPGA- An Ultra-fast Pan-genome Analysis Pipeline. ***Scientific Reports*** (**2016**).
10. **Vinod K. Gupta**, Narendrakumar M. Chaudhari, Suchismitha Iskepalli, Chitra Dutta. Divergences in Gene Repertoire Among the Reference Prevotella Genomes Derived from Distinct Body Sites of Human. ***BMC Genomics*** (**2015**).

Co-author

11. Benjamin Hur, **Vinod K. Gupta *et al.*** Integrative Multi-Omics Phenotyping in Blood Reveals Distinct Immune and Metabolic Signatures between ACPA-negative and ACPA-positive Rheumatoid Arthritis. (under review in ***Frontiers in Immunology***).
12. Levi M. Teigen, Stuart J. McCarter, Zachary Ziegert, Christopher Staley, Kiera M. Grant, **Vinod K. Gupta**, Xiaowei Zhao, Erik K. St Louis, Kejal Kantarci, Val J. Lowe, Leah K. Forsberg, Rodolfo Savica, Vijay K. Ramanan, David T. Jones, Ronald C. Petersen, Jaeyun Sung, Alexander Khoruts, Bradley F. Boeve, Owen A. Ross. Taxonomic intestinal microbiota differences in Lewy body spectrum disease and cohabitant controls. ***Parkinsonism & Related Disorders*** (**2025**).
13. Kevin Y. Cunningham, Benjamin Hur, **Vinod K. Gupta**, Matthew J. Koster, Cornelia M. Weyand, David Cuthbertson, Nader A. Khalidi, Curry L. Koening, Carol A. Langford, Carol A. McAlear, Paul A. Monach, Larry W. Moreland, Christian Pagnoux, Rennie L. Rhee, Philip Seo, Peter A. Merkel, Kenneth J. Warrington, Jaeyun Sung. Plasma Proteome Profiling in Giant Cell Arteritis. ***Annals of the Rheumatic Diseases*** (**2024**).
14. Humza Haroon, Ada Man-Choi Ho, **Vinod K. Gupta**, Surendra Dasari, Carl M. Sellgren, Simon Cervenka, Göran Engberg, Feride Eren, Sophie Erhardt, Jaeyun Sung, Doo-Sup Choi. Cerebrospinal Fluid Proteomic Signatures are Associated with Symptom Severity of First-Episode Psychosis. ***Journal of Psychiatric Research*** (**2024**).
15. Kevin Y. Cunningham, Benjamin Hur, **Vinod K. Gupta**, Courtney A. Arment, Kerry A. Wright, Thomas G. Mason, Lynne S. Peterson, Delamo I. Bekele, Daniel E. Schaffer, Marissa L. Bailey, Kara E. Delger,

Cynthia S. Crowson, Elena Myasoedova, Hu Zeng, Moses Rodriguez, Cornelia M. Weyand, John M. Davis III, Jaeyun Sung. Patients with ACPA-positive and ACPA-negative Rheumatoid Arthritis Show Different Serological Autoantibody Repertoires and Autoantibody Associations with Disease Activity. ***Scientific Reports*** (**2023**).

16. Dong Hyeon Lee, Hyunbin Seong, Daniel Chang, **Vinod K. Gupta**, Jiseung Kim, Seongwon Cheon, Geonhee Kim, Jaeyun Sung, Nam Soo Han. GMWI-based Prebiotic Indexing System of Foods and Its Application to Commercial Prebiotics. ***npj Science of Food*** (**2023**).
17. Daniel Chang, **Vinod K. Gupta**, Benjamin Hur, Kevin Y. Cunningham, Jaeyun Sung. GMWI-webtool: A User-friendly Browser Application for Assessing Health Through Metagenomic Gut Microbiome Profiling. ***Bioinformatics*** (**2023**).
18. Sergio Cobo-López, **Vinod K. Gupta**, Jaeyun Sung, Roger Guimerá, Marta Sales-Pardo. Stochastic Block Models Reveal a Robust Nested Pattern in Healthy Human Gut Microbiomes. ***PNAS Nexus*** (**2022**).
19. Benjamin Hur, **Vinod K. Gupta**, Harvey Huang, Kerry A. Wright, Kenneth J. Warrington, Veena Taneja, John M. Davis, Jaeyun Sung. Plasma Metabolomic Profiling in Patients with Rheumatoid Arthritis Identifies Biochemical Features Predictive of Quantitative Disease Activity. ***Arthritis Research & Therapy*** (**2021**).
20. Jin Sung Jang, Brian D. Juran, Kevin Y. Cunningham, **Vinod K. Gupta**, Young Min Son, Ju Dong Yang, Ahmad H. Ali, Elizabeth Ann L. Enninga, Jaeyun Sung, Konstantinos N. Lazaridis. Single-cell Mass Cytometry on Peripheral Blood Identifies Immune Cell Subsets Associated with Primary Biliary Cholangitis. ***Scientific Reports*** (**2020**).
21. Narendrakumar M. Chaudhari, Anupam Gautam, **Vinod K. Gupta**, Gagneet Kaur, Chitra Dutta, Sandip Paul. PanGFR-HM: A Dynamic Web Resource for Pan-Genomic and Functional Profiling of Human Microbiome With Comparative Features. ***Frontiers in Microbiology*** (**2018**).

SELECTED PUBLICATIONS WITH IMPACT

Gupta VK, *et al*. A Predictive Index for Health Status Using Species-level Gut Microbiome Profiling. ***Nature Communications*, 2020.**

- **Citations:** 290+ | **Dataset:** >5,000 metagenomes, 12 diseases + healthy cohorts
- **Reach:** Adopted in 15+ countries | **Translation:** GMWI-webtool
- **Impact:** Established a benchmark microbiome health index; widely applied in population studies, wellness monitoring, and non-invasive diagnostics.

Chang D[#], **Gupta VK[#], *et al*.** Gut Microbiome Wellness Index 2 Enhances Health Status Prediction. ***Nature Communications*, 2024.**

- **Citations:** 20+ (first year) | **Dataset:** >8,000 metagenomes across 25+ countries
- **Adoption:** Used internationally in population health and translational studies
- **Impact:** One of the largest standardized microbiome indices; improved accuracy in distinguishing healthy vs. non-healthy states; advancing clinical applications.

Gupta VK *et al.* Geography, Ethnicity or Subsistence-Specific Variations in Human Microbiome Composition and Diversity. ***Frontiers in Microbiology***, **2017**.

- **Citations:** 1,100+ | **Dataset:** >1,000 microbiomes from 20+ global populations
- **Impact:** Demonstrated geography, diet, and lifestyle as major determinants of microbiome composition; informed global microbiome projects, ancestry-aware precision medicine, and cross-population genomics.

Chaudhari NM[#], **Gupta VK[#]** *et al*. BPGA – An Ultra-fast Pan-genome Analysis Pipeline. ***Scientific Reports***, **2016**.

- **Citations:** 950+ | **Downloads:** 27,000+ | **Global Reach:** 100+ countries
- **Impact:** Widely adopted pipeline for pan-genome analysis; applied in pathogen genomics, antimicrobial resistance, vaccine design, and microbial ecology; standardized comparative genomics workflows worldwide.

PATENTS

1. Jaeyun Sung, **Vinod K. Gupta**. Assessing Gut Health Using Metagenome Data (**2022**). ***US patent office***. Patent number: 20220367004

GRANTS AND FUNDING

1. **Letter of Intent (LOI) submitted** to the Aging Center at Mayo Clinic for a career development grant: Harnessing the power of stool microbiome to predict aging trajectories.
2. **NIH R21 proposal in preparation**: Development of a bioinformatics pipeline for identification of proteins from mass spectrometry–derived metaproteomes with for high-sensitivity and high-specificity.

EDITORIAL ROLES

I have worked as an Ad Hoc Manuscript Reviewer for the following scientific journals:

1. Arthritis Research & Therapy
2. BMC Bioinformatics
3. BMC Genomics
4. BMC Microbiology
5. Clinical Microbiology Reviews
6. Frontiers in Microbiology
7. Journal of Translational Medicine
8. Microbiome
9. Scientific Reports
10. Signal Transduction and Targeted Therapy

AWARDS AND FELLOWSHIPS

1. **ASM Student and Postdoctoral Travel Award** from ASM (2022)
2. **Travel Award** from the International Centre for Theoretical Physics (ICTP) for participating in a workshop on Systems Biology and Molecular Economy of Microbial Communities held in Italy in 2017.
3. **CSIR JRF-GATE fellowship** - I was awarded a five-year fellowship by the Council of Scientific and Industrial Research to pursue a Ph.D. in Bioinformatics. The fellowship was awarded to students who qualified for the Graduate Aptitude Test in Engineering (GATE). The GATE exam was conducted by the Indian Institute of Technology, Madras, India, in 2011.
4. **MHRD GATE fellowship** - I was awarded a two-year fellowship by the Ministry of Human Resource Development to pursue a Master in Science (M.S. Pharm) degree. The fellowship was awarded to students who qualified for the Graduate Aptitude Test in Engineering (GATE). The GATE 2009 exam was conducted by the Indian Institute of Technology, Roorkee, India.

PROFESSIONAL MEMBERSHIPS

1. American Society for Microbiology
2. Biomedical Engineering Society
3. International Society for Microbial Ecology

CONFERENCES AND MEETINGS

- 2025 – ACR Convergence 2025, Chicago, IL, USA (oral presentation)
- 2022 – ASM Microbe 2022, Washington, D.C., USA (oral presentation)
- 2022 – Understanding Microbiome, Our Mystery Organ, online (invited oral presentation)
- 2022 – Microbiome Meeting, CSHL, Cold Spring Harbor, NY, USA (poster presentation)
- 2021 – Biomedical Engineering Society (BMES) Annual Meeting. Orlando, FL, USA (oral presentation)
- 2021 – Fundamentals of Microbiome Data Analysis, Kolkata, India (invited oral presentation)

- 2021 – International Human Microbiome Consortium, Barcelona, Spain (poster presentation)
- 2021 – MIT Microbiome Symposium (poster presentation)
- 2021 – Keystone Symposia: Harnessing the Microbiome for Disease Prevention and Therapy (poster presentation)
- 2020 – ACR Convergence 2020. Washington, D.C. USA (poster presentation)
- 2019 – Microbiome Meeting, CSHL, Cold Spring Harbor, NY, USA (poster presentation)
- 2018 – 24th Balfour Surgery Research Symposium, Rochester, MN, USA (poster presentation)
- 2018 – Individualizing Medicine, Rochester, MN, USA (poster presentation)
- 2018 – International Human Microbiome Consortium, Killarney, Ireland (poster presentation)
- 2018 – Keystone Symposia: Manipulation of the Gut Microbiota for Metabolic Health, Banff, Canada (poster presentation)

TEACHING AND MENTORSHIP EXPERIENCE

Mentorship has been a consistent and fulfilling part of my academic journey. I have been actively mentoring undergraduate researchers, Master's degree students, and Ph.D. candidates since my time as a graduate student. As a graduate student, I assisted students with literature reviews, data analysis, data interpretation, and thesis writing. I also guided Ph.D. students in planning a study design, executing their research projects, and preparing manuscripts. While I was pursuing my Ph.D. I got an opportunity to teach Master's degree students at Vidyasagar College, Kolkata, India. I taught bioinformatics tools, especially for genome and protein sequence analysis. As a postdoctoral researcher at Mayo Clinic, I continued my mentorship of summer trainees, undergraduate researchers, masters' students, and Ph.D. candidates. Recently, I delivered an invited lecture on the "Fundamentals of Microbiome Data Analysis" to B.Sc. and M.Sc. life sciences students and faculty members at JIS institute of Advanced Studies and Research, Kolkata, India.

PEOFESSIONAL REFERENCES

1. **Dr. Sucheta Tripathy, Ph.D**.
   Senior Principal Scientist,
   CSIR–Indian Institute of Chemical Biology, Kolkata, India
   Email: tsucheta@iicb.res.in
   Relationship: Ph.D. thesis co-supervisor

2. **Dr. Erin Longbrake, M.D., Ph.D.**
   Associate Professor,
   Department of Neurology,
   Yale School of Medicine, Yale University, New Haven, CT, USA
   Email: Erin.Longbrake@yale.edu
   Relationship: Collaborator

3. **Dr. Nicholas Chia, Ph.D.**
   Researcher,
   Argonne National Laboratory, Lemont, IL, USA
   Email: chia@anl.gov
   Relationship: Mentor and Collaborator

LANGUAGES

English (Fluent, working proficiency), Hindi (Fluent), and Bengali

DISCLAIMER I hereby declare that the information given above is true to the best of my knowledge and belief.

Vinod K. Gupta

Date: 08/16/2025,
Place: Rochester, Minnesota, USA