MEGHNA VERMA, Ph.D.

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SUMMARY OF QUALIFICATIONS & SKILLS

- PhD with 5+ years of industry experience at AstraZeneca supporting regulatory and clinical development strategy through model-informed drug development (MIDD)
- Quantitative Systems Pharmacologist data modeler with fluency in MATLAB/Simbiology, R, & knowledge of MONOLIX, data wrangling, and data visualization using Python
- Proven track record in building PK/PD, viral dynamics, QSP trimer-based model of TCE used in DLBCL and autoimmune diseases, cytokine release models.
- Recognized contributor to Emergency Use Authorization (EUA) for EVUSHELD, with experience authoring ICH-compliant reports.
- Adept in cross-functional collaboration, scientific communication, and publication. Actively expanding capabilities in AI-driven modeling and tool integration.
- Collaborated cross-functionally with pharmacometricians, clinical pharmacologists, bioscience, translational medicine, and regulatory teams' departments (safety sciences, biosciences, translational sciences, oncology and autoimmune TAs)
- Created modeling templates to promote reproducibility and reporting consistency across programs.
- Presented findings at ACoP, ASCPT, ISCB and internal scientific forums; mentored team members and contributed to modeling strategy

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SKILLS

Modeling: Experienced in PK/PD Modeling, QSP, Viral Dynamics, Disease Progression Modeling (autoimmune and oncology TA)
Programming skills: Bash, R, MATLAB, Python, basic knowledge of C/C++ and data structures/algorithms, MATLAB/SimBiology, R, MONOLIX, Python, Git, Bash; Currently learning: NONMEM
- AI Tools: ChatGPT (prompt-based prototyping and literature synthesis), Google Gemini (search and summarization), Claude (document reasoning), GitHub Copilot (code generation for modeling scripts)
- Scientific Writing: IND & EUA reports (provided comments for ICH M15), internal modeling templates, peer-reviewed publications
Project-related: Experience with collaboration on multiple projects involving teams from multidisciplinary backgrounds: oncology, inflammation and immunology. Strong oral/written communication, data visualization, and scientific reporting skills. Managed and led independent as well as collaborative team projects. Member of the Inflammation and Immunology ISoP working group

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RESEARCH INTERESTS, AND LEADERSHIP SKILLS

Oncology (DLBCL), immunology (RA, Lupus), and infectious diseases (COVID-19, HIV-HPV, H.pylori, C.difficile) modeling applied to mAbs and TCEs programs, scientific communication, regulatory filling experience with ICH M15 based EUA report and IND supporting work. Demonstrated leadership skills by holding conference chair and coordinator (for the SysMod community), mentoring, and cross-functional collaboration. AI tool adoption (ChatGPT, Gemini, Claude) to streamline literature synthesis, coding template and ways of working efforts at AstraZeneca.

EDUCATION

Ph.D., Translational Biology, Medicine & Health (Computational immunology), Virginia Tech, VA, USA **Dec '19**
Advisor: Josep Bassaganya-Riera, Stanca M. Ciupe
Dissertation: Systems modeling and simulation of immune responses against infectious diseases
M.S., Biomedical Engineering, (Adv. Certificate in Bioinformatics), Drexel University, PA, USA **July '14**
B.E., Biomedical Engineering, Mumbai University, MH, India **May '11**

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WORK EXPERIENCE

Associate Director, Systems Medicine, Clinical Pharm & Quantitative Pharm **Jan '20- Present**
Clin Pharm and Safety Sciences, BioPharm R&D, AstraZeneca, Gaithersburg, MD, USA

- Development of TCE model platform with trimer dynamics to justify the dose in autoimmune to decide human efficacious dose in autoimmune disease (Rheumatoid Arthritis, Lupus, Myositis) indication for a TCE asset acquired in oncology. The work contributed to support the internal decision making for IND filling of AZD0486.
- Built a cytokine release model utilizing cytokine release assay data from safety sciences for the autoimmune disease indication.
- Development of viral dynamic model for SARs-CoV-2 and its variants to justify the prophylactic and treatment dose of EVUSHELD (long-acting mAb approved for use in immunocompromised individuals), supporting the PROVENT and TACKLE programs.
- Drafted and submitted the modeling reports and contributed towards the success, filling and approval of the EVUSHELD. The contributions led to EVUSHELD achieving the emergency use approval (EUA) from the Food Drug Administration (FDA).
- Experienced in drafting responses to various regulatory agencies including EMA, Canada HA, FDA and Swiss regulatory agencies. Collaborated and worked closely with the Clinical Pharmacologist for the approval of EVUSHELD.
- Contributed towards writing the modeling report and analysis plan (per ICH M15 standards). Worked closely with Bioscience, Translational and Precision medicine, Clinical Pharmacologist. Pharmacometricians towards the success of the modeling efforts.
- Assessed and compared the immune response dynamics with other influenza viral dynamic models to derive insights regarding immune responses in SARs-CoV-2
- Conducted competitive landscape analyses comparing doses provided by competitor mAbs and justified the dose for the emerging variants of concerns SARs (delta, omicron)
- Contributed towards the ways of working initiative at AstraZeneca by creating modeling report templates (promoting reproducibility of work to be submitted at the regulatory agencies)

Graduate Research Assistant **Aug '15-Dec'19**
Nutritional Immunology & Molecular Medicine Lab, Biocomplexity Institute, Virginia Tech
<u>PI and Co-PI:</u> Josep Bassaganya-Riera, Stanca M. Ciupe, Stefan Hoops.

- Investigated and utilized an integrated agent-based and differential equations based mechanistic models of host immune responses against infectious diseases such as Clostridium difficile and Helicobacter pylori (GitHub: https://github.com/NIMML/ENISI-MSM).
- Developed a mechanistic ordinary differential-equation (ODE) simulation model of HIV/HPV coinfection in MATLAB and COPASI.
- Performed MATLAB and COPASI simulations to demonstrate the effectiveness of antiretroviral treatments in HIV/HPV co-infected in-silico patients.
- Utilized R and machine learning methods to design in silico clinical trials and studied the effect of various treatment paradigms in Crohn's disease virtual patients
- Built surrogate models using AI that can be used to speed virtual population generation in QSP model building.

WORK EXPERIENCE (CONTD.)

Graduate Research Assistant
Network Dynamic and Simulation Science Lab, University at Virginia **Feb '15-June '15**

- Utilized an epidemiological software web tool SIBEL and evaluated the effectiveness of influenza vaccine on in silico populations in the U.S rural and urban population (comparison case study).
- Performed simulations to study the sensitivity of influenza vaccine compliance and efficacy during a flu outbreak in both urban vs. rural setting. Performed comparative analysis in the percentage drop-in attack rates between these areas post intervention (including vaccine and social distancing).

AWARDS & FELLOWSHIPS

AZ awards	Cytokine Release Syndrome model for CAR-T and TCE therapies (Nick Brown, Global Head AI)
AZ CEO award	COVID-19 project: played significant role in fight against COVID-19 (Pascal Soriot, CEO)
	COVID-19 project: scientific excellence within tight timelines (Stefan Platz, SVP)
	COVID-19 project: for the modeling work in support of AZD7442 (Mark Esser, VP)
	COVID-19 project: Tremendous contribution to help AstraZeneca's strategic decisions, prophylaxis dose recommendations for immunocompromised patients, fight against Omicron variant and Emergency use authorization filing.
	COVID-19 project: for modeling the response to SARs-CoV-2, Omicron variant of concern and treatment and prophylaxis study
Biopharmaceutical R&D Award in AstraZeneca	COVID-19 project: played a critical role fir the success use if EVUSHELD Tremendous support for the success and approval of EVUSHELD, only pre-exposure prophylaxis approved monoclonal antibody.
ISCB Community (Coordinator, SysMod)	SysMod Lead Co-ordinator for the ISCB's computation modeling of systems modeling
Travel Awards	11th International Conference on Systems Biology of Human Diseases UCLA, June '18
	3rd Annual SysMod Intelligent Systems in Molecular Biology Conference Chicago, July '18
	Opening workshop at the Statistical and Applied Mathematical Sciences Institute, Aug '18
	Graduate Student Assembly at Virginia Tech, June '18
Winner, Poster Presentation	Biocomplexity Institute Research Symposium '16
Dean's Fellowship for Academic Excellence	Drexel University for years '12- '13 and '13- '14
Sir Ratan Tata Trust Scholarship	Awarded by Indian government for academic excellence, '09- '10

PUBLICATIONS

- Volkova, Sokolov, Tettamanti F, **Verma M,** et al., 2025. An Integrative Mechanistic Model of Type 1 IFN-Mediated Inflammation in Systemic Lupus Erythematosus. (**CPT:PSP**)
- Beattie KA, **Verma M,** Brennan RJ, Sher A et al., 2024. Quantitative systems toxicology modeling in pharmaceutical research and development: An industry wide survey and selected case study examples. **(CPT:PSP)**
- M Lai C, Pichardo-Almarza C, **Verma M** et al., 2024. T-cell engagers: model interrogation as a tool to quantify the interplay of relative affinity and target expression on trimer formation **(Frontiers in Pharmacology)**
- Puniya BL, **Verma M**, Drager A., 2024. Perspectives on computational modeling of biological systems and the significance of the SysMod community **(Bioinformatics Advances)**

- **Verma M,** Gall L, Biasetti J, Veroli Di G et al., 2023. Quantitative Systems Modeling Approaches Towards Model-Informed Drug Development: Perspective Through Case Studies. **Frontiers in Systems Biology**):
- **Verma M**, Modeling Host Immune Responses in Infectious Diseases, Virginia Tech, 2019
- **Verma M**, Bassaganya-Riera J, Tubau-Juni N, Leber A, Hoops S, et al,. 2019. High-Resolution Computational Modeling of Immune Responses in the Gut. 2019., **(GigaScience, Data-Driven Multicellular Systems Biology),**
- Chen Xi, Wang W, Xie G, Hontecillas R, **Verma M**, Leber A, et al,. 2018. Multi-Resolution Sensitivity Analysis of Model of Immune Response to Helicobacter pylori Infection via Spatio-Temporal Metamodeling. **Frontiers in Applied Mathematics and Statistics**, section Mathematics of Computation and Data Science. doi: 10.3389/fams.2019.00004
- **Verma M**, Hontecillas R, Tubau-Juni N, Abedi V, Bassaganya-Riera J., 2018. Challenges in Personalized Nutrition and Health. Frontiers in nutrition. 2018;5:117.
- Mayorga LS, Cebrian I, **Verma M**, Hoops S, et al., 2018. Reconstruction of endosomal organization and function by a combination of ODE and agent-based modeling strategies. **Biology direct**. 2018 Jan;13(1):25.
- Mayorga LS, **Verma M**, Hontecillas R, Hoops S, Bassaganya-Riera J. Agents and networks to model the dynamic interactions of intracellular transport. **Cellular logistics.** 2017 Oct 2;7(4):e1392401. 10.1080/21592799.2017.1392401 PMID: 29296512.
- **Verma M**, Erwin S, Abedi V, Hontecillas R, Hoops S, et al., 2017. Modeling the mechanisms by which HIV-associated immunosuppression influences HPV persistence at the oral Mucosa. **PloS one**. 2017 Jan 6;12(1): e0168133. 10.1371/journal.pone.0168133 PMID: 28060843.

BOOK CHAPTERS

- Zand R, Abedi V, Hontecillas R, Lu P, Noorbakhsh-Sabet N, **Verma M**, et al., 2016 Development of Synthetic Patient Populations and In Silico Clinical Trials. Accelerated Path to Cures. 2018 Apr 25:57.
- Abedi V, L. P., Hontecillas R, **Verma M**, Vess G.A, et al. ,2016. Phase III Placebo-Controlled, Randomized Clinical Trial with Synthetic Crohn's Disease Patients to Evaluate Treatment Response. In T. Q. e. Arabnia H (Ed.), **Emerging Trends in Applications and Infrastructures for Computational Biology, Bioinformatics, and Systems Biology** (pp. 411-427). Cambridge, Morgan Kaufmann/Elsevier, 2016.

SELECTED TALKS, POSTERS & HACKATHONS

- **Verma M.,** 2024 'Quantitative Systems Pharmacology (QSP) Approach to Understand the Variability of Patient Responses to T-cell Bi specifics in Hematological Malignancies. at ACoP15
- **Verma M.**, 2023 'Quantitative systems toxicology modelling applications in the
- pharmaceutical industry: insights from an EFPIA wide survey examining the current landscape' at ACoP14
- **Verma M.**, 2022 'Perspective: stability analysis of a published viral dynamic model of SARS-CoV-2 infection', at the 5th Annual (Computational Modeling of Biological Systems Community), SysMod meeting at ISMB 2022 Conference, Wisconsin (Virtual Poster)
- Dunyak J**, Verma M.**,2021 'Catching up to the COVID-19 pandemic via PBPK & Viral Dynamic Modeling & Simulations ', at the American Society of Clinical Pharmacology and Therapeutics ASCPT 2021. (Virtual Talk)
- **Verma M.**, 2019 'Computational modeling of the immune response to Clostridium difficile infection', at the 4th Annual, SysMod meeting at ISMB 2019, Basel, Switzerland (Poster)https://www.iscb.org/cms_addon/conferences/ismbeccb2019/posters.php?track=SysMod%20COSI&session=A
- **Verma M.**, 2018 'Advancing systems immunology using hybrid agent-based model of *Helicobacter pylori* infection', at the 3rd Annual (Computational Modeling of Biological Systems Community), SysMod meeting at ISMB 2018 Conference, Chicago. (Talk and Poster): https://www.iscb.org/cms_addon/conferences/ismb2018/posters.php?track=SysMod&session=A
- **Verma M.**, 2018 'A vision for precision medicine and health', at the Biocomplexity Institute's 2017 Research Symposium at Virginia Tech. (Talk)
- **Verma M**, Bassaganya-Riera J, Tubau-Juni N, Leber A, Hoops S, et al., 2018. *Advancing systems immunology using hybrid agent-based model of Helicobacter pylori infection,* Systems Biology of Human Diseases (SBHD), UCLA, U.S.A. June 2018. (Poster)

- **Verma M**, Bassaganya-Riera J, Tubau-Juni N, Leber A, Hoops S, et al., 2018.. *Advancing systems immunology using hybrid agent-based model of Helicobacter pylori infection,* BioIT-World, Boston,USA. May 2018. (Poster)
- NCBI NIH Data Science Hackathon at NIH Bethesda Campus (April 16- April 18, 2018) (project details: CLINT: An electronic medical record pipeline using neurosynth to link clinical data with fMRI research literature - https://github.com/NCBI-Hackathons/clint).
- Virginia Tech organized SheHacksVT Hackathon -2018, built a GUI based application to calculate the number of calories in a meal - https://github.com/meghna-verma/SheHacksVT

PEER REVIEWER AND CONTRIBUTIONS TO THE SYSMOD COMMUNITY

- **Chaired** Computational Modeling of Biological Systems (SysMod), Community of Special Interest (COSI), (chapter of ISCB) and SysMod ISCB Webinar organizer (Served: 2023-Present)
- **Reviewer in Cancer Medicine**: Development of Prediction Model of Low Anterior Resection Syndrome for Colorectal Cancer Patients after Surgery Based on Machine Learning Technique
- **Reviewer in PLOS One**: Cellular genome-scale metabolic modeling identifies new potential drug targets against hepatocellular carcinoma
- **Reviewer in Gigabyte (published review),** DAPT: A package enabling distributed automated parameter testing
- **Reviewer in PLOS Computational Biology:** A computational model of cytokine release syndrome during CAR T-cell therapy
- **Reviewer in PLOS Computational Biology:** Multiscale modeling of collective cell migration elucidates the mechanism underlying tumor-stromal interactions in different spatiotemporal scales
- **Reviewer in Nature Publications Journal, Systems Biology and Applications:** Mapping the dynamics of insulin-responsive pathways in the blood-brain barrier endothelium using time-series transcriptomics data
- **Reviewer in Frontiers in Medicine:** Implications of Using Host Based-Response Diagnostics on Infectious Diseases Management: A Review
- **Reviewer in Journal of Biosciences:** Emergent phenomena in living systems: a statistical mechanical perspective
- **Reviewer in 2021 IEEE 18th India Council International Conference (INDICON):** Diabetes Prediction using Logistic Regression, Decision Tree and Random Forest'