OMB No. 0925-0001 and 0925-0002 (Rev. 10/2021 Approved Through 01/31/2026)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.  
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Nicholas Giangreco

eRA COMMONS USER NAME (credential, e.g., agency login): 14654270

POSITION TITLE: Quantitative Translational Scientist

EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)

| INSTITUTION AND LOCATION | DEGREE  (if applicable) | Completion Date  MM/YYYY | FIELD OF STUDY |
| --- | --- | --- | --- |
| University of Rochester | B.S. | 05/2014 | Biochemistry |
| Columbia University | M.A. | 01/2018 | Systems Biology |
| Columbia University | M.Phil | 01/2019 | Systems Biology |
| Columbia University | Ph.D. | 10/2021 | Cellular, Molecular, and Biomedical Studies, Focus in Systems Biology |
|  |  |  |  |

**A. Personal Statement**

**My research and professional work focus within computational biology and precision medicine to generate data driven hypotheses, novel analytics, and reproducible research tools. My academic background in systems biology and bioinformatics laid the foundation for my expertise in integrating multi-omics data with real-world clinical evidence. During my Ph.D., I developed computational analyses in pediatric drug safety, biomarker discovery, autoimmune and obesity research, and electronic health record (EHR) standardization, leading to multiple peer-reviewed publications and open-source tools.**

**Currently, as a senior data scientist in precision medicine at Regeneron Pharmaceuticals, I manage the execution of data architecture and software development projects that drive innovation in biomarker discovery and translational research. I lead the development and maintenance of nearly a dozen software packages and applications that empower clinical biomarker data monitoring and analysis. I develop automated project management and portfolio reporting tools that provide senior leadership with real-time insights into project progress and resource allocation. Additionally, I mentor interns and junior data scientists in best practices for reproducible data science, web application development, and machine learning for clinical research.**

**My previous and current work spans development of computational methods, data pipelines, and data driven research to better understand disease and optimize patient treatment strategies. With my experience in both academia and industry, I am well-positioned to lead research efforts that translate cutting-edge computational methods into clinically impactful innovations.**

**Completed projects that I would like to highlight include:**

**NIH R01GM107145**

**Tatonetti (PI)**

**2016-2021**

**Drug Effect Discovery Through Data Mining and Integrative Chemical Biology**

**UL1 TR001873**

**Reilly (PI)**

**2016-2021**

**Clinical and Translational Science Award**

**Citations:**

1. **Biswas, S., Shahriar, S., Giangreco, N. P., Arvanitis, P., Winkler, M., Tatonetti, N. P., Brunken, W. J., Cutforth, T., & Agalliu, D. (2022). Mural Wnt/β-catenin signaling regulates Lama2 expression to promote neurovascular unit maturation. Development (Cambridge, England), 149(17), dev200610.** <https://doi.org/10.1242/dev.200610>
2. **Giangreco, N. P., Lina, S., Qian, J., Kuoame, A., Subbian, V., Boerwinkle, E., Cicek, M., Clark, C. R., Cohen, E., Gebo, K. A., Loperena-Cortes, R., Mayo, K., Mockrin, S., Ohno-Machado, L., Schully, S. D., Tatonetti, N. P., & Ramirez, A. H. (2021). Pediatric data from the All of Us research program: demonstration of pediatric obesity over time. JAMIA open, 4(4), ooab112.** <https://doi.org/10.1093/jamiaopen/ooab112>
3. **Kim-Hellmuth, S., Bechheim, M., Pütz, B., Mohammadi, P., Nédélec, Y., Giangreco, N., Becker, J., Kaiser, V., Fricker, N., Beier, E., Boor, P., Castel, S. E., Nöthen, M. M., Barreiro, L. B., Pickrell, J. K., Müller-Myhsok, B., Lappalainen, T., Schumacher, J., & Hornung, V. (2017). Genetic regulatory effects modified by immune activation contribute to autoimmune disease associations. Nature communications, 8(1), 266.** <https://doi.org/10.1038/s41467-017-00366-1>

**B. Positions, Scientific Appointments, and Honors**

**Positions and Scientific Appointments**

**2021 – Present     Senior Data Scientist, Precision Medicine, Regeneron Pharmaceuticals, Tarrytown, NY**

**2016 – 2021      Graduate Research Assistant, Department of Systems Biology, Columbia University, New York, NY**

**2021        Solution Science Intern, DNAnexus, San Francisco, CA**

**2019         Clinical Informatics Intern, Regeneron Genetics Center, Tarrytown, NY**

**2018         Computational Biology Intern, Genetic Leap Inc., New York, NY**

**2014 – 2016      Post-Baccalaureate Trainee, National Human Genome Research Institute, Bethesda, MD**

**2018 – 2019     Member, Observational Health Data Sciences and Informatics (OHDSI) Consortium**

**2017 – 2023     Co-Founder & Secretary, New York Health Artificial Intelligence Society (501(c)(3))**

**2017 – 2018     Member, American Medical Informatics Association (AMIA)**

**2013 – 2014     Member, International Society for Computational Biology (ISCB)**

**Honors**

**2019       Finalist, Three-Minute Thesis Competition, Columbia University Graduate School of Arts and Sciences**

**2018       Best Contribution in Methodological Research, OHDSI Symposium**

**2018       Travel Award, Columbia Graduate School of Arts and Sciences**

**2017       Columbia Diversity Fellowship**

**2016       Department of Systems Biology Merit Fellowship, Columbia University**

**2014       Donald Charles Award, University of Rochester Department of Biology**

**2013     Fulbright Fellowship Alternate, Sweden (Molecular Modeling)**

**2013       Travel Award, ISMB/ECCB Computational Biology Conference, Berlin, Germany**

**C. Contributions to Science**

### ****AI-Driven Precision Pharmacovigilance for Drug Safety**** My graduate thesis work pioneered data-driven, biologically inspired computational approaches that leverage real-world data (RWD) to identify age- and population-specific adverse drug reactions. My work in pediatric pharmacovigilance has enhanced drug safety monitoring by integrating electronic health records with pharmacogenomic data, reducing the risk of medication-related complications in vulnerable populations.

* 1. **Giangreco, N. P.**, Elias, J. E., & Tatonetti, N. P. (2022). No population left behind: Improving paediatric drug safety using informatics and systems biology. British journal of clinical pharmacology, 88(4), 1464–1470. <https://doi.org/10.1111/bcp.14705>
  2. **Giangreco, N. P.**, & Tatonetti, N. P. (2021). Evaluating risk detection methods to uncover ontogenic-mediated adverse drug effect mechanisms in children. BioData mining, 14(1), 34. <https://doi.org/10.1186/s13040-021-00264-9>
  3. **Giangreco, N. P.**, & Tatonetti, N. P. (2022). A database of pediatric drug effects to evaluate ontogenic mechanisms from child growth and development. Med (New York, N.Y.), 3(8), 579–595.e7. <https://doi.org/10.1016/j.medj.2022.06.001>

### ****Integrating Proteomics and Clinical Data to Predict Heart Disease Progression and Treatment Outcomes**** Alongside the previous research, collaborations with cardiologist Dr. Barry Fine has included integrating proteomics data and RNASeq data with clinical records to develop predictive models for disease progression and treatment response. Through harmonization of exosome proteomics with patient-derived clinical data, we identified robust, novel blood-based biomarkers associated with primary graft dysfunction (PGD) within 24 hours of heart transplant surgery. This work enhanced the ability to identify generalizable biomarkers across geographically diverse patient cohorts, leading to more precise and individualized therapeutic interventions. Importantly, we filed a patent (WO2022060842A1) for quantifying PGD risk on a per subject basis using an adaptive Monte Carlo cross-validation (MCCV) model.

1. Castillero, E., Ali, Z. A., Akashi, H., **Giangreco, N.**, Wang, C., Stöhr, E. J., Ji, R., Zhang, X., Kheysin, N., Park, J. S., Hegde, S., Patel, S., Stein, S., Cuenca, C., Leung, D., Homma, S., Tatonetti, N. P., Topkara, V. K., Takeda, K., Colombo, P. C., … George, I. (2018). Structural and functional cardiac profile after prolonged duration of mechanical unloading: potential implications for myocardial recovery. American journal of physiology. Heart and circulatory physiology, 315(5), H1463–H1476. <https://doi.org/10.1152/ajpheart.00187.2018>
2. **Giangreco, N. P.**, Lebreton, G., Restaino, S., Jane Farr, M., Zorn, E., Colombo, P. C., Patel, J., Levine, R., Truby, L., Soni, R. K., Leprince, P., Kobashigawa, J., Tatonetti, N. P., & Fine, B. M. (2021). Plasma kallikrein predicts primary graft dysfunction after heart transplant. The Journal of heart and lung transplantation : the official publication of the International Society for Heart Transplantation, 40(10), 1199–1211. <https://doi.org/10.1016/j.healun.2021.07.001>
3. **Giangreco, N. P.**, Lebreton, G., Restaino, S., Farr, M., Zorn, E., Colombo, P. C., Patel, J., Soni, R. K., Leprince, P., Kobashigawa, J., Tatonetti, N. P., & Fine, B. M. (2022). Alterations in the kallikrein-kinin system predict death after heart transplant. Scientific reports, 12(1), 14167. <https://doi.org/10.1038/s41598-022-18573-2>
4. **Developing Computational Tools for Reproducible Clinical and Multi-Omics Research To support large-scale, reproducible clinical and multi-omics research, I have developed open-source software tools that facilitate the integration, analysis, and interpretation of biomedical data. One of my key contributions is KIDSIDES, an R data package designed for mining pediatric drug safety signals. KIDSIDES harmonizes safety records from the Food and Drug Administration Adverse Event System (FAERS) to systematically identify age-specific adverse drug reactions. KIDSIDES has improved our ability to assess pediatric drug safety profiles and optimize medication use in children. Additionally, I developed cohorts, a Python package that streamlines the management and analysis of multi-omics clinical data. cohorts enables the integration of genomic, transcriptomic, and proteomic datasets with structured clinical data, allowing for scalable data integration. Together these computational tools enhance data-driven research in translational medicine and clinical informatics.** 
   1. **Nicholas P. Giangreco**, Barry Fine, Nicholas P. Tatonetti. cohorts: A Python package for clinical ’omics data management. bioaRxiv doi: <https://www.biorxiv.org/content/10.1101/626051>
   2. **Giangreco N (2023). kidsides: Download, Cache, and Connect to 'KidSIDES'.** <https://github.com/ngiangre/kidsides>**,** <https://ngiangre.github.io/kidsides/>**,** [https://nsides.io](https://nsides.io/)**.**