CURRICULUM VITÆ

updated December 24, 2019

1. Biographical Information

Joseph Daniel Romano, PhD

Born October 25, 1990 in Raleigh, North Carolina

Married to Sarah Prehn Romano, DDS (m. August 10, 2019)

2. Professional Information

Current Position: Postdoctoral Researcher

Institution: University of Pennsylvania

Email Address: joseph.romano [*at*] pennmedicine.upenn.edu

Institutional Affiliations:

Department of Biostatistics, Epidemiology, & Informatics;
Institute for Biomedical Informatics;
Center of Excellence in Environmental Toxicology.

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3700 Hamilton Walk
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Philadelphia, PA 19104–6116

3. Academic History

University of Vermont, January 2010–May 2014:

B.S. in Molecular Genetics , Honors Scholar, May 2015.
Research Advisor: Neil Sarkar, PhD, MLIS, FACMI

Columbia University, September 2014–May 2019:

M.A. in Biomedical Informatics, December 2016
MPhil in Biomedical Informatics, May 2018
PhD (Biomedical Informatics), May 2019
Dissertation: "Computational Toxinology"
Doctoral Advisor: Nicholas Tatonetti, PhD

4. Employment Record

Graduate Research Assistant, Columbia University, New York, New York, 2014–2019.
Postdoctoral Researcher, University of Pennsylvania, Philadelphia, Pennsylvania, 2019–.

5. Publications

5.1. Papers (peer-reviewed)

P1. **Romano, J.D.**, Tharp W.G., & Sarkar, I.N. Exploring Complex Disease Gene Relationships Using Simultaneous Analysis. *UVM Honors College Theses* **35** (2014).

P2. **Romano, J.D.**, Tharp W.G., & Sarkar, I.N. Adapting Simultaneous Analysis Phylogenomic Techniques to Study Complex Disease Gene Relationships. *Journal of Biomedical Informatics* **54** (2014), 10–38.

P3. **Romano, J.D.**, & Tatonetti, N.P. VenomKB, a new knowledge base for facilitating the validation of putative venom therapies. *Scientific Data* **2** (2015), 150065.

P4. Boland, M.R., Jacunski, A., Lorberbaum, T., **Romano, J.D.**, Moskovitch, R., & Tatonetti, N.P. (2016). Systems biology approaches for identifying adverse drug reactions and elucidating their underlying biological mechanisms. *Wiley Interdisciplinary Reviews: Systems Biology and Medicine,* **8**,2 (2016), 1040–122.

P5. **Romano, J.D.**, & Tatonetti, N.P. Using a Novel Ontology to Inform the Discovery of Therapeutic Peptides from Animal Venoms. *AMIA Summits on Translational Science Proceedings* (2016), 209–218. Awarded second place, TBI Student Paper Competition.

P6. **Romano, J.D.**, Bernauer M., McGrath S., Nagar S.D., & Freimuth R. A Decade of Translational Bioinformatics: A Retrospective Analysis of "Year-in-Review" Presentations. *AMIA Informatics Summit Proceedings* (2019).

P7. **Romano, J.D.**, & Tatonetti N.P. Informatics and computational methods in natural product drug discovery: A review and perspectives. *Frontiers in Genetics,* **30** (2019), 368.

5.2. Other Publications (preprints and other non-refereed contributions)

R1. **Romano, J.D.**, Nwankwo V., & Tatonetti N.P. VenomKB v2.0: A knowledge repository for computational toxinology. *bioRxiv* (2018), 295204.

R2. **Romano, J.D.**, Li H., Realubit R., Douglass E., Califano A., Karan C., & Tatonetti N.P. Discovering therapeutic activities from venoms using differential gene expression. *bioRxiv* (2019), 699280.

6. Conference Presentations

C1. Observational Health Data Sciences and Informatics (OHDSI). *Innovation and Application @ Columbia* (2015), New York, NY.

C2. Data-Driven Clinical Research Generalizability Assessment and Improvement. *8^{th} Annual Mid-Atlantic Healthcare Informatics Symposium* (2015), Philadelphia, PA.

C3. Venom Peptides as Therapeutic Agents: Can we use Phylogenetics to Inform Drug Discovery? *13^{th} Annual Rocky Mountain Bioinformatics Conference* (2016), Aspen, CO.

C4. Building a Centralized Resource for Computational Venom Research. *National Library of Medicine Informatics Training Conference* (2016), Columbus, OH.

C5. High-sensitivity Stroke Phenotyping using Recurrent Neural Networks. *AMIA Joint Summits on Translational Science* (2017), San Francisco, CA.

C6. Deep recurrent neural networks identify transgender patients. *AMIA Annual Symposium* (2017), Washington, DC.

C7. Computational Resources for Personalized Genomics: High Performance Clusters and Bioinformatics Resources for Analysis and Functional Interpretation of Next-Generation Sequencing Data. *AMIA Informatics Summit* (2018), San Francisco, CA. Tutorial session available to conference attendees.

C8. `VenomSeq`—A platform for drug discovery from animal venoms using differential gene expression. *AMIA Informatics Summit* (2018), San Francisco, CA.

C9. Engineering Innovative Informatics Solutions to Support Venom-Based Drug Discovery. *Gordon Research Conference on Venom Evolution, Function, and Biomedical Applications* (2018), West Dover, VT.

C10. Analyzing Whole Exome Sequencing: Unstructured Data to Variant Interpretation. *AMIA Informatics Summit* (2019), San Francisco, CA.

7. Teaching Experience

7.1. Coursework Taught

English Language Teaching Assistant (Fall 2011). Nihon University College of International Relations, Mishima, Japan.

MMG 104—Introduction to Recombinant DNA Technology, Teaching Assistant (Spring 2012). University of Vermont, Burlington, VT.

BINF G4000—Acculturation to Programming and Statistics, Teaching Assistant (Fall 2016). Columbia University, New York, NY.

BINF G4006—Translational Bioinformatics, Guest Lecturer—2 lectures (Fall 2016). Columbia University, New York, NY.

BINF G4003—Symbolic Methods in Biomedical Informatics, Teaching Assistant (Spring 2017). Columbia University, New York, NY.

BINF G4003—Symbolic Methods in Biomedical Informatics, Guest Lecturer (Spring 2018). Columbia University, New York, NY.

World Scholars SAT+ Summer Program, Guest Lecturer (Summer 2018). Yale Divinity School, New Haven, CT.

BMIN 525—Introduction to Python Programming, Teaching Assistant (Fall 2019). University of Pennsylvania, Philadelphia, PA.

7.2. Formally Mentored Trainees

Marine Saint-Mézard (MS; ENSTA-ParisTech)—Summer research intern, Columbia University; Summer 2018.

Soline Boussard (BS; University of Pennsylvania)—Undergraduate researcher, University of Pennsylvania; Fall 2019–present.

8. Professional Society Memberships and Elected Positions

American Association for the Advancement of Science, 2014–.
American Medical Informatics Association, 2012–.
Communications director, Genomics and Translational Bioinformatics Working Group, 2015–.
Chair, Student Working Group, 2018–
American Society of Clinical Pharmacology and Therapeutics, 2017–.
International Society for Computational Biology, 2014–.
International Society on Toxinology, 2016–.
New York Academy of Sciences, 2014–2019.

9. Awards, Fellowships, and Honors

AP Scholar with Honors, College Board, 2009.
Eagle Scout, Boy Scouts of America, 2009.
National Merit Scholar, National Merit Scholarship Corporation, 2009.
Vermont Scholar, University of Vermont, 2010–2014.
Honors Scholar, University of Vermont, 2014.
Graduate Research Fellow in Biomedical Informatics, Columbia University, 2015–2017.
Parent grant: `T15-LM007079` (PI: Hripcsak).
Funding institution: US National Library of Medicine
Postdoctoral Research Fellow in Environmental Health Sciences, University of Pennsylvania, 2019–.
Parent grant: `T32-ES019851` (PI: Penning).
Funding institution: National Institute of Environmental Health Sciences.

10. Review Activities

10.1. Journals

BioData Mining.
Nature Communications.
Nature Scientific Reports.
Scientific Data.

10.2. Conferences and Symposia

AMIA Annual Symposium.
AMIA Joint Summits on Translational Science.
Scientific Program Committee Member, Translational Bioinformatics, 2019.
Translational Bioinformatics "Year-in-Review" Committee Member, 2016–2018.
IEEE International Conference on Healthcare Informatics.
Pacific Symposium on Biocomputing.
Symposium on Artificial Intelligence for Learning Health Systems (SAIL)
Organizing Committee Member, 2020.
World Congress on Health and Biomedical Informatics (MEDINFO).
Assistant Editor, 2015–2017.