Konstantinos Krampis, Ph.D.

- Associate Professor of Biological Sciences, Hunter College, City University of New York (CUNY)
- PI, Bioinformatics Core Informatics Infrastructures Laboratory (BCIL)
- Director of Bioinformatics, Center for Translational and Basic Research (CTBR)
- Faculty at the Institute for Computational Biomedicine (ICB), Weill Cornell Medical College

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List of current manuscripts: http://tinyurl.com/krampis-publications

Education and Training.

Years	Institution	Degree	Area
8/2003 - 5/2009	Virginia Tech, US	Ph.D.	Bioinformatics
9/1997 - 6/2003	University of Athens, Greece	B.Sc. / M.Sc.	Molecular Biology

Academic Appointments.

Years	Institution	Position
4/2014 - Present	City University of New York, US	Associate Professor
4/2014 - Present	CUNY Center for Translational Research, US	Director of Bioinformatics
4/2014 - Present	Weill Cornell Medical College, US	Faculty, Comput. Biomedicine
5/2009 - 4/2014	J. Craig Venter Institute, US	Assistant Professor
8/2003 - 5/2009	Virginia Bioinformatics Inst., Virginia Tech, US	Bioinformatics Engineer
8/2000 - 8/2003	University of Athens, Greece	Research Assistant

Research Areas.

1. High-throughput bioinformatics infrastructures for cluster and cloud computing platforms.
a. Scalability of data analysis pipelines using distributed computing: Kubernetes, NextFlow, Docker Swarm.
b. Cross-platform bioinformatics through Docker virtualization in clinical and basic research.
c. Visualization of genomic data on cloud databases using HTML5 / D3.js and in-browser computing.

2. Bioinformatics for Next Generation Sequencing (NGS) clinical and personal genomics.
a. NGS pipelines for single-cell RNA-seq, Hi-C, metagenomics, variant discovery, genome assembly.
b. Integrative analysis of variation, expression, chromatin and epigenetic data from TCGA, Encode, 4DN.
c. Scalable, accessible pipelines for metagenomics, clinical samples and personal genomics on Galaxy.

3. Interdisciplinary research and novel applications of genomic sequencing and bioinformatics.
a. Portable NGS and bioinformatics with Nanopore Minion and Intel Next Units of Computing (NUC).
b. Touch-enabled, mobile computing interfaces for personal genomics and clinical NGS data visualization.
c. Metabarcoding for conservation and biodiversity monitoring using environmental DNA (eDNA).

4. Algorithmic Information Theory, Computability, and Biologically-Inspired Computing.
a. Emergence, complexity, information content and compressibility of epigenetic networks.
b. Integrating DNA computing with NGS sequencing for reading molecular output with high I/O.
c. Computability and decidability of biologically-inspired and DNA computing models.

Grants Awarded.

1. Principal Investigator.

2018 - 2023   National Institute of Health, "Biostatistics and Bioinformatics Core for Minority Cancer Health Disparities", Temple University FCCC / Hunter College CUNY Partnership, NIH U54. Amount: $404,635

2018 - 2019   CUNY Advanced Science Research Center (ASRC) Award (bioinformatics sub-contract). "Mechanisms of regulation of progenitor proliferation and transformation" Amount: $10,920

2018 - 2019   CUNY Advanced Science Research Center Award (bioinformatics sub-contract). "Histone Deacetylation in Oligodendrocyte Differentiation" Amount: $14,040

2017 - 2018   CUNY Advanced Science Research Center Award. "NGS for environmental DNA monitoring: understanding global biodiversity through bioinformatics". Amount: $10,000

2016 - 2018   CUNY Center for Translational and Basic Research Award. "Democratizing access to bioinformatics computing for health disparities research". Amount: $78,000

2015 - 2017   National Institutes of Health. "Expanding Infrastructure and Services of CUNY-CTBR Bioinformatics and Genomics Core". Amount: $123,832

2015 - 2017   Weill Cornell Medicine, Clinical Translational Science Center Award. "Cross-platform, scalable Science as a Service (SciaaS) infrastructures for NGS data analysis". Amount: $110,660

2014 - 2017   National Institutes of Health. "Development of a Bioinformatics Core and Sequencing Facility for Minority Health Disparities Research". Amount: $485,000

2011 - 2014   National Institutes of Health. "Large-Scale Prokaryotic and Viral Next-Gen Sequencing Data Pipelines Using Cloud Computing". Amount: $661,217

2. Co-Principal Investigator.

2018 - 2023   National Institutes of Health. "TUFCCC/HC Regional Comprehensive Cancer Health Disparity Partnership". Amount: $392,180

2014 - 2015   National Science Foundation. "Development of the Next-Generation Arabidopsis Informatics Portal". Amount: $2,434,910

Grants Submitted.

Jan. 2019   National Institutes of Health. SCORE Program "A Scalable, Accessible Bioinformatics Platform for Democratizing Genomic Data Analysis". Amount: $ 468,000

Dec. 2018   Sloan Foundation, Google Research Awards, Ford Foundation "Integrating bioinformatics software with distributed visualizations on cloud genomic databases". Amount: $100,000

Dec. 2018   National Institutes of Health. "BiomedicaL EducatioN in Data Science (BLENDS)" Initiative to Maximize Research Education in Genomics: Diversity Action Plan: Amount $2,317,425

Sept. 2018   PhRMA Foundation "Development of a scalable bioinformatics platform, democratizing genomics for health disparities research" Amount: $100,000

Honors and Awards.

2018	Honors Proposal Development Program, Weill Cornell Medical College
2018	Proposal Travel Development Award, City University of New York
2017	President's Travel Award, Hunter College, City University of New York
2014	Entrepreneurship Lab NYC Selected Participant and Top 20 (300+ entries) Business Plan
2011	Bioinformatics Open Source Conference – Best Audience Voted Presentation Award
2008	Virginia Tech Graduate Association Executive Board Elected Member
2007	Virginia Tech Outstanding Interdisciplinary Doctoral Student Award
2006	Horace E. Alphin Doctoral Tuition Scholarship
2005	Virginia Tech Graduate Student Assembly Research Award
2004-2006	James and Ina Mae Doctoral Tuition Scholarship

Extramural Invited Presentations.

2019	Next Generation Sequencing and Clinical Diagnostics Conference, Boston, Massachusetts
2019	Bio-Compute Objects Workshop, Federal Drug Administration, Washington, DC
2019	Genomics Sequencing Research Laboratory, American University of Sharjah, United Arab Emirates
2019	Center for Biologics Evaluation and Research, Federal Drug Administration, Washington, DC
2018	Genome Institute Singapore, Agency for Science, Technology and Research (A-Star), Singapore
2018	Department of Mathematics & Computer Science, Southern Denmark University, Odense, Denmark
2018	High-Throughput Sequencing Computational Standards for Regulatory Sciences, Washington, DC
2018	Plant and Animal Genome Conference, San Diego, CA
2017	Dept. of Public Health Sciences, Penn State College of Medicine, Hershey, PA
2017	Dept. of Human Genetics, University of Pittsburgh, Pittsburgh, PA
2017	Intelligent Systems for Molecular Biology (ISMB), Prague, Czech Republic
2017	High-Throughput Sequencing Computational Standards for Regulatory Sciences, Washington, DC
2017	Dept. of Computational Medicine, University of Michigan, Ann Arbor, MI
2016	Bioinformatics Ph.D. Program Guest Lecture, NYU Langonne Medical Center, New York, NY
2015	Global Health Informatics Conference, University of South Florida, Tampa, FL
2015	Biological Sciences Research Seminar, Lehman College, New York, NY
2015	Illumina Basespace Conference, Broad Institute, Cambridge, MA
2014	Galaxy Developer's Conference, John Hopkins University, Baltimore, MD
2014	CTBR 27th Symposium: Bioinformatics & Medical Applications, New York, NY
2012	Cloud Computing Bioinformatics Symposium, Center Genomic Regulation, Spain
2012	Translational Bioinformatics On The Cloud, J&J Inc., New Brunswick, NJ
2012	NIH-NIAID Bioinformatics Symposium, Bethesda, MD
2011	Genomics Standards Consortium, European Bioinformatics Institute, Hinxton, UK

Memberships in Professional Societies.

Since 2017	NCI Containers and Workflows Interest Group - NIH Data Science
Since 2016	High-performance Integrated Virtual Environment (HIVE) Consortium, FDA-GWU
Since 2015	IEEE Biological Compute Objects (BCO) Working Group
Since 2013	Illumina Basespace Developers Community
Since 2009	Open Bioinformatics Foundation
Since 2009	Galaxy Developers Community
Since 2006	Bioinformatics IT World
Since 2003	International Society for Computational Biology

Editorial Positions, Boards and Peer-Review Service.

Oxford Bioinformatics; BMC Bioinformatics; BMC Research Notes; Nature Methods; Nature Scientific Reports; PLoS ONE; In Silico Biology; Future Generation Computer Systems; BioMed Research International; British Journal of Mathematics and Computer Science; Journal of Bioinformatics & Computational Biology; Genome Technology; GigaScience; F1000 Research.

Bibliography - Published Manuscripts.

High-throughput bioinformatics infrastructures and cloud computing.

2. Lijeron C, Dang T, Kim B, Ali T, Dong C, Wultsch C and Krampis K. *(2019)* "New Paradigms of Bioinformatics Infrastructure, Data Operations and Cloud Services". *(submitted to J. of Genomics and Data Mining)*

2. Kim B., Ali T., Dong C., Laungani B., Wultsch C., Lijeron C. and Krampis K. *(2019). J of Comput Biol. Mar;26(3):280-284* "miCloud: a plug and play, on-premises bioinformatics cloud, providing seamless integration with Illumina genome sequencers".

3. Ali T, Kim B, Lijeron C, Dong C, Wultsch C and Krampis K *(2018)* "Implementation of a Reproducible, Accessible and Transparent RNA-seq Bioinformatics Pipeline within the Galaxy Platform". *J Comput Sci Syst Biol* 11: 195-199. doi:10.4172/jcsb.1000272

4. Dong C, Lee R, Sayad J and Krampis K *(2018)* "Bioinformatics Programming for Bioavailability Analysis of Sequence Patterns in Public Genomic Databases". *Advancements Bioequiv Availab.* 1(2). ABB.000508.2018.

5. Alterovitz G., Dean D.A., Carole Goble C, Crusoe MR. … Krampis K., et al. *(2017). PLoS Biol. 2018 Dec 31;16(12).* "Enabling Precision Medicine via standard communication of NGS provenance, analysis, and results".

6. Ali T., Kim B., Lijeron C., Ogunwobi O.O., Mazumder R. and Krampis K. *(2017). PeerJ*, 5, p.e3385v1. "TED toolkit: a comprehensive approach for convenient transcriptomic profiling as a clinically oriented application".

7. Kim B., Ali T., Lijeron C. and Krampis K. *(2017). Gigascience.* 6(8), 1–7. "Bio-Docklets: Virtualization Containers for Portable, Scalable NGS Data Analysis".

8. Jensen T.L., Frasketi M., Conway K., Villarroel L., Hill H., Krampis K. and Goll J.B. *(2017). F1000Research*, 6, 2162. "RSEQREP: RNA-Seq Reports, an open-source cloud-enabled framework for reproducible RNA-Seq data processing, analysis, and result reporting".

9. Kim B., Ali T., Hosmer S. and Krampis K. *(2016). Bioinformatics*, 10, 1093. "Visual Omics Explorer (VOE): a Cross-Platform Portal for Interactive Data Visualization".

10. Afgan E., Krampis K., Goonasekera N., Skala K. and Taylor J. *(2015). IEEE-MIPRO*, 38, 223-228. "Building and provisioning bioinformatics environments on public and private clouds".

11. Krampis K. and Wultsch C. *(2015). Methods in Next Generation Sequencing*, 2(1). "A Review of Cloud Computing Bioinformatics Solutions for Next-Gen Sequencing Data Analysis and Research".

12. Kumari P., Mazumder R., Simonyan V. and Krampis K. *(2015). F1000 Research*, 4, 20. "Advantages of distributed and parallel algorithms that leverage Cloud Computing platforms for large-scale genome assembly".

13. Krishnakumar V., Hanlon M.R., Contrino S., Ferlanti E.S., Krampis K…and Town C.D. *(2014). Nucleic Acids Research*, 28(43), 1003-1009. "Araport: the Arabidopsis Information Portal".

14. Krampis K., Booth T., Chapman B., Tiwari B., Field D. and Nelson K.E. *(2012). BMC Bioinformatics*, 13, 42. "Cloud Biolinux: pre-configured and on-demand computing for the genomics community"

Bibliography - Published Manuscripts (continued).

Bioinformatics for Next Generation Sequencing (NGS) clinical and personal genomics.

1. King CH, Desai H, Sylvetsky A, LoTempio J ... Krampis K, et al. *(2019).* "A new standard for defining a baseline of healthy human gut microbiomes" (in preparation for *PLoS One*).

2. Deutsch DR, Euler CW, Utter B, Schuch R, Verratti K, Krampis K, Beyer W and Fischetti VA. *(2019).* Alteration of Canonical B. anthracis Phenotypes After Exposure to a B. cereus Bacteriophage" (in preparation for *Nature Sci. Reports*).

3. Brown S.M., Hao Y., Chen H., Laungani B.P., Ali T.A., Dong C., Lijeron C., Kim B., Krampis K. and Pei Z. *(2019). Gigascience*. Accepted for publication – in print. "Fast functional annotation of metagenomic shotgun data by DNA alignment to a microbial gene catalog".

4. Di L., Wan Z., Akther S., Ying C., Larracuente A., Li L., Di C., Nunez R., Cucura D.M., Goddard N., Krampis K. and Qiu W. (*2018*). *J. of Clinical Microbiology J Clin Microbiol. 2018 Oct 25;56(11)*. "Genotyping and quantification of Lyme pathogen strains by deep sequencing of outer surface protein C (ospC) amplicons"

5. Das D.K., Ali T., Krampis K. and Ogunwobi O. *(2017). Data in Brief,* 11, 131-35. "Fibronectin and androgen receptor expression data in prostate cancer obtained from a RNA-sequencing bioinformatics analysis"

6. Das D.K., Naidoo M., Ilboudo A., Park J.Y., Ali T., Krampis K., Robinson B.D., Osborne J.R. and Ogunwobi O. (*2016*). *Experimental Cell Research*, 348(2), 190-200. "miR-1207-3p regulates the androgen receptor in prostate cancer via FNDC1/fibronectin".

7. Bubnell J., Jamet S., Tomoiaga D., D'Hulst C., Krampis K. and Feinstein P. *(2015). PloS ONE*, 10(10), p.e0141712. *"*In Vitro Mutational and Bioinformatics Analysis of the M71 Odorant Receptor and Its Superfamily".

8. Cole C., Krampis K., Karagiannis K., Almeida J.S., Faison W.J., Motwani M., Wan Q., Golikov A., Pan Y., Simonyan V. and Mazumder R. *(2014). BMC Bioinformatics*, 15, 28. " Non-synonymous variations in cancer and their effects on the human proteome: workflow for NGS data biocuration and proteome-wide analysis of TCGA data."

9. Shamsaddini A., Yang P., Johnson E., Krampis K., Simonyan V. and Mazumder M. *(2014). BMC Genomics*, 15, 918. "Census-based rapid and accurate metagenome taxonomic profiling".

Interdisciplinary research and novel applications of genomic sequencing and bioinformatics.

1. Wultsch C, Perkins S, Kelly MJ, Waits LP, Amato G, Quigley H and Krampis K. *(2019)* "A new perspective in carnivore ecology and conservation: comparative gut microbiome composition, diversity, and functionality in sympatric Neotropical jaguars and pumas". (in preparation for *Nature Ecol. and Evolution*).

2. Wultsch C, Benton A, Sosa Medina G, McNitt D, Alonso R, Kelly MJ and Krampis K. *(2019)* "Bacterial gut, skin and oral microbiomes of free-ranging bobcats (*Lynx rufus*)" (in preparation for *Microbiome*).

3. Wultsch C, DeBarba M, Kelly MJ, Waits LP and Krampis K. *(2019)* "Resource partitioning and niche overlap in a Neotropical felid community examined by DNA metabarcoding" (in preparation for *Molecular Ecology*).

4. Ingala M., Simmons N.B., Wultsch C., Krampis K., Speer K.A. and Perkins S. *(2018) Front Microbiol. 2018 May 1;9:803* "Comparing Microbiome Sampling Methods in a Wild Mammal" Fecal and Intestinal Samples Record Different Signals of Host Ecology, Evolution".

Bibliography - Interdisciplinary research and novel applications (continued).

5. Prince S.J., Song L., Qiu D., dos Santos J.V.M., Chai C., Joshi T., Patil G., Valliyodan B., Vuong T.D., Murphy M. and Krampis, K. (*2015*). *BMC Genomics*, 16(1), 132. "Genetic variants in root architecture-related genes in a Glycine soja accession, a potential resource to improve cultivated soybean".

6. Wang H., Waller L., Tripathy S., St. Martin S.K., Zhou L., Krampis K. et al. *(2010). The Plant Genome* 3(1), 23-40. "Analysis of genes underlying soybean QTLs conferring partial resistance to *P. sojae*".

7. Zhou L., Mideros S.X., Bao L., Hanlon R., Arredondo F., Tripathy S., Krampis K. et al. *(2009). BMC Genomics*, 26(10), 49. "Infection and genotype remodel the entire Soybean transcriptome".

8. Tyler B.M., Tripathy S., Kale S.D., Zhou L., Ferreira A., Dou D., Arredondo F.D., Mideros S.X., Bao L., Krampis K. and Jerauld, A. *(2010). Phytopathology* 99 (6), S164. "Comparative and functional genomics of oomycete infection".

9. Prasinos C., Haralampidis K., Milioni D., Samakovli D., Krampis K. and Hatzopoulos P. *(2008). Plant Molecular Biology*, 67(4), 323. *"*Complexity of Hsp90 in organelle targeting".

10. Wang H., Berry S., St. Martin S.K., Zhou L., Krampis K. et al. (2008). *Phytopathology* 98 (6), S165. "Allele mining for genes associated with partial resistance to Phytophthora sojae in soybean".

11. Krampis K., Tyler B.M. and Boore J.L. *(2006) Molecular Plant Microbe Interactions,* 19(12), 1329-1336. "Extensive variation in nuclear mitochondrial DNA content between the genomes of *P. sojae* and *P. ramorum*".

12. Tyler B.M., Tripathy S…, Krampis K., et al. *(2006) Science* 313(5791), 1261-1266. "*Phytophthora* genome sequences uncover evolutionary origins and mechanisms of pathogenesis".

13. Prasinos C., Krampis K., Samakovli D. and Hatzopoulos P. (*2005*). *Journal of Experimental Botany*, 56(412), 633-644. "Tight regulation of expression of two Arabidopsis cytosolic Hsp90 genes during embryo development".

Bibliography - Monographs & Book Chapters.

1. Krampis K. "Cloud Computing for Bioinformatics Data Science". Monograph to be published in 2019, contract signed with *Cambridge University Press*, Cambridge, UK.

2. Guest Editor for special issue on "Scalable, Reproducible, Accessible Bioinformatics Computing for Genomic Data Science", *International Journal of Genomics*, scheduled publication in 2019.

3. Krampis K., Efstratios E. and Brown S.T. *(2015, 2017).* "*Cloud-Based Next-Generation Sequencing Informatics*". Book Chapter in *Next-Generation DNA Sequencing Informatics* (pp. 361-370), First & Second Edition. Cold Spring Harbor Press, NY.

4. Rusch D.B., Miller J., Krampis K., Tovchigrechko A., Sutton G., Yooseph S. and Nelson K.E. (*2014*). *"Bioinformatics for Genomes and Metagenomes in Ecology Studies"*. Book Chapter in *Infectious Microecology* (pp. 203-226). Springer GmbH & Co, Berlin, Germany.

5. Goll J.B, Szpakowski S., Krampis K. and Nelson K.E. (2014). *"Next-generation sequencing, metagenomes, and the human microbiome".* Book chapter in *Bioinformatics and Data Analysis in Microbiology*. Caister Press, U.K.

Bibliography - Monographs & Book Chapters (continued).

6. Nelson K.E., Madupu R., Szpakowski S., Goll J.B., Krampis K. and Methe B.A. *(2014). "Next-generation sequencing, metagenomes, and the human microbiome"*. Book chapter in *Next-generation Sequencing: Current Technologies and Applications* (pp. 141-155). Caister Academic Press, Norfolk, U.K.

7. Quirino B.F., Barreto C.C., Pappas G.J., Zengler K., Krampis K. and Krüger R.H. *(2013).* "Genomes and Post-Genome Technology" Book Chapter in *Prokaryotes* (pp. 329-344). Springer GmbH & Co., Berlin, Germany.

8. Madupu R., Rogers Yu-H., Rusch D., Miller J., Krampis K. and Nelson K.E. *(2012).* "*Microbiomes*". Book Chapter in *Encyclopedia of Molecular Cell Biology and Molecular Medicine.* Wiley-VCH Verlag GmbH & Co., Weinheim, Germany.

9. Miller J., Rusch D., Krampis K., Tovichgrechko A., Sutton G., Yooseph S. and Nelson K.E. (*2012).* "*Bioinformatics for Genomes and Metagenomes in Microbial Ecology Studies*". Book Chapter in *Encyclopedia of Molecular Cell Biology and Molecular Medicine.* Wiley-VCH Verlag GmbH & Co., Weinheim, Germany.

10. Tyler B.M., Jiang R.H., Zhou L., Tripathy S.,.., Krampis K., Ye K., Martin S.S., Dorrance A.E., Hoeschele I. and Sagahi Maroof M.A. (*2008*). "*Functional genomics and bioinformatics of the Phytophthora sojae soybean interaction*". Book Chapter in *Genomics of Disease* (pp. 67-78). Springer GmbH & Co, NY.

Bibliography - Software and Online Media.

1. Video tutorials on published bioinformatics software: http://tinyurl.com/BCIL-channel

2. Bioinformatics Core Infrastructures Laboratory (BCIL), repository for active open source bioinformatics software development projects: https://github.com/BCIL

3. Docker containers with pre-configured bioinformatics data pipelines: https://hub.docker.com/u/bcil

Teaching and Mentoring.

1. University Courses Developed and Taught.

2015 - Present "*Computational Molecular Biology*". Sequence pattern matching, alignment, read mapping, variant calling, genome assembly, and gene prediction algorithms, in addition to data structures for efficient NGS data storage, taught based on the latest literature.

2015 - Present "*Next-Generation Sequencing Data Analysis*". Concepts of sequencing technology, data formats and bioinformatics tools, implementation of data pipelines on the command line or online Galaxy interface for RNA-seq, ChIP-seq, and metagenomics.

2014 - 2016 "*Programming for Computational Biology*". Computer coding for biologists, covering basic data types, program flow control, functions, regular expressions, working with NGS files, and object-oriented programming.

Teaching and Mentoring. (continued)

2. Workshops Developed and Taught.

2018   "A Plug and Play, on-Premises Bioinformatics Cloud, Providing Seamless, Single-Step Execution of NGS Pipelines*"*, Plant and Animal Genome International Conference, San Diego, CA.

2017   "*Deploying Large-Scale Bioinformatics Workflows with Kubernetes on a Google Cloud Computer Cluster"*, Bioinformatics Open Source Conference & Hackathon, Prague, Czech Republic.

2016   "*NGS Sample Processing and Data Analysis through the CTBR Facility and Bioinformatics Computer Cluster"*, workshop for CUNY and Weill Cornell Medical College faculty and students, New York, NY.

2015   "*Scalable, Intuitive Genomic Sequencing Data Analysis with Galaxy and Cloud BioLinux*", New York City College of Technology, New York, NY.

2014   "*Cloud BioLinux: Pre-Configured and On-Demand Virtual Machines for NGS Data Analysis*", 27th CTBR Symposium: Bioinformatics Applications in Health Disparities, New York, NY.

2013   "*Genomic Sequencing Data Analysis using Cloud Computing and the Amazon EC2 platform*", NYU Center for Health Informatics and Bioinformatics, New York, NY.

2012   "*South Africa National Research Network Workshop - Cloud BioLinux for High Performance Data Analysis*", Center of High Performance Computing, Johannesburg, South Africa.

2012   "*Empowering Genomics in South Africa Workshop - Cloud Computing Solutions for Genome Sequence Data Analysis*", University of Limpopo, Polokwane, South Africa.

2011   "*Cloud BioLinux for Bioinformatics Open Source Applications*", International Society for Computational Biology Conference, Vienna, Austria.

2011   "*Biologically Inspired Approaches to Resilience*", Institute of Human and Machine Cognition, Ocala, FL.

2010   "*From monolithic to distributed bioinformatics on the cloud*", Amazon Web Services, Seattle, WA.

3. Graduate Students Mentored.

Dennis Huang, Biology Ph.D. Student, CUNY Advance Science Center Graduate Center, Thesis topic "*Single-cell sequencing and epigenetic networks in neuron damage in neurological disorders*" (2019).

Enis Berg Coban, Computer Science Ph.D. Candidate, Hunter College and CUNY Graduate Center, Thesis topic "*Manifold Learning algorithms for Noise Control and Trajectory Inference in Single Cell Sequencing Data*" (2019).

Brian Sulkow, Mathematics Ph.D. Student, CUNY Graduate Center, Thesis topic "*Analysis of large-scale ENCODE and TCGA epigenetic network datasets using Information Theory and Kolmogorov Complexity*" (2018).

Li Li, Biology Ph.D. Candidate, Hunter College and CUNY Graduate Center, Thesis topic, "*Identification of Lyme pathogen strains by Deep Next Generation Sequencing of outer surface proteins*" (2018).

Irene Hoxie, Biology Ph.D. Candidate, Queens College and CUNY Graduate Center, Thesis topic, "*Bacteriophage phi6 and related species genomic segment assembly and annotation*" (2018).

Tangerine Yu, Biology Ph.D. Student, Hunter College and CUNY Graduate Center, Lab rotation – training in next-generation sequencing techniques; development of bioinformatics pipeline for metagenomics analysis (2017).

Teaching and Mentoring. (continued)

Melissa Ingala, Comparative Biology Ph.D. Candidate, Richard Gilder Graduate School, American Museum of Natural History, Thesis topic "*Comparative Metagenomics of Wild Mammals for Identifying Signals of Host Ecology and Evolution*" (2017).

Kelly Speer, Comparative Biology Ph.D. Candidate, Richard Gilder Graduate School, American Museum of Natural History, Thesis topic "*Microbiomes and Feeding Ecology in Neotropical Bats*" (2017).

Carol Henger, Biology Ph.D. Candidate, Fordham University, Thesis topic "*Conservation genetics and feeding ecology of coyotes in New York City*" (2017).

Rachael Joakim, Comparative Biology Ph.D. Student, Richard Gilder Graduate School, American Museum of Natural History and CUNY Graduate Center, Thesis topic "*Tropical vertebrate microbiomes*" (2017).

Allen Pan, Biology Ph.D. Candidate, Hunter College and CUNY Graduate Center, Thesis topic "*Neuroscience of addiction*" (2016).

Hasan Zumrut, Biology Ph.D. Candidate, Lehman College and CUNY Graduate Center, Thesis topic "*Development of novel NGS data analysis methods of SELEX Libraries*" (2016).

Jason Mighty, Biology Ph.D. Candidate, Lehman College and CUNY Graduate Center, Thesis topic "*Ocular degeneration genetics and small RNAs*" (2016).

Juliette Gorson, Chemistry Ph.D. Candidate, Hunter College and CUNY Graduate Center, Thesis topic "*Discovery of cancer inhibiting compounds in venomous marine snail transcriptome*" (2015).

Samuel Hosmer, Mathematics Ph.D. Candidate, CUNY Graduate Center, Spring 2015 internship on "*Implementation of cloud computing based data analysis pipeline for CHIP-seq genomic sequencing data*" (2015).

Limor Cohen, Biology Ph.D. Student, Hunter College and CUNY Graduate Center, Lab rotation – training in next-generation sequencing techniques and bioinformatics analyses (2014).

Priti Kumari, M.Sc. Bionformatics, Biochemistry Department, George Washington University, Thesis project "*Parallel and Cloud Computing Based Genome Assembly Using Bidirected String Graphs*" (2013).

Vivek Sarangi, M.Sc. Bionformatics, Biochemistry Department, George Washington University, Thesis project "*Development and Evaluation of Cloud Computing Infrastructures for Next-Gen Sequencing Data analysis*" (2012).

4. Undergraduate Students and Interns Mentored.

Tahir Ramzan, Rajveer Singh, Mohammed Rahman, Ariel Avshalumov. Mathematics and Computer Sciences Major, "*Human microbiome and minority health: unravelling variations associated with disease and health disparities*" (research to be presented at the Hunter College Undergraduate Student Research Conference and BioConductor NYC Conference in Spring 2019).

Mohammed Rahman, Ariel Avshalom. Mathematics and Computer Sciences Major, "*MicrobiomeExplorer*: *An interactive and web-based R Shiny analysis platform for microbiome research*" (research to be presented at the Hunter College Undergraduate Student Research Conference and BioConductor NYC Conference in Spring 2019).

Teaching and Mentoring. (continued)

Catherine Ng, Ariel Avshalom, Anna Fernadez and Simran Kaur, Mathematics and Biological Sciences Majors, "*Assessing transcriptome and transcription factor sites in RNA-seq and ChIP-seq NGS through downstream computational analysis in the Galaxy web platform*" (presented at the Hunter College Undergraduate Student Research Conference in Spring 2018).

Philip Ort, Biological Sciences Major (graduation Fall 2018), "*Computational analysis of cancer cell line differential gene expression datasets using the Galaxy web platform*".

Joseph Sayad, Computer Science Major, (graduation Spring 2018), "*Development of Distributed Bioinformatics Algorithms using Intel Next Unit of Computing Systems*".

Trami Dang, Physics Major, (graduation Fall 2016), "*Development of Cloud Computing Pipeline for Methylation Bi-Sulfite Sequencing Data Analysis*".

Bobby Linguani, Biological Sciences Major, (graduation Fall 2016), "*Large-Scale Human Microbiome Bioinformatics Pipelines in Galaxy and Docker Containers*", manuscript submitted with NYU collaborating group.

Kevin Raz, Biological Sciences Major, (graduation Fall 2016), "*Implementation of Portable Metagenomic Data Analysis Pipelines with Pynast and Visualizations*".

Roy Lee, Biological Sciences Major, (graduation Spring 2016), "*Cross-Platform Blast Toolkits using Docker Software Containers*".

Thahmina Ali, Biological Sciences Major, (graduation May 2015), "*Implementation of a comprehensive, standardized, scalable, user-friendly, RNA-seq analysis pipeline*", manuscript currently under peer review. Thamina worked in the Krampis' lab as Bioinformatics Analyst and recently was accepted as Ph.D. student at Columbia University.

Baekdoo Kim, Computer Science Major, (graduation December 2014), "*The Visual Omics Explorer (VOE): Providing a Highly Interactive, Cross-Platform Portal for Omics Data Visualization*", manuscript was published in 2016.

Institutional Committee and Scientific Service.

2016 - Present	Co-Chair, Ethics and Integrity Committee at the City University of New York. Faculty working group to write a report for federal financial assistance accreditation by the Middle States Committee.
2015 - Present	Bioinformatics M.Sc. Program at CUNY. Designed and wrote the program proposal, assembling a group of faculty and curriculum using existing and newly designed courses.
2015 - 2016	CUNY Data Science Committee. Contributed towards designing Data Science courses and developed two training grant proposals (NSF, NIH) to fund a Bioinformatics Data Science Ph.D. program.
2014 - 2015	CUNY Quantitative Biology Program Faculty. New bioinformatics syllabi and course modules, for undergraduate (e.g., biology, computer science) and graduate (e.g., bioinformatics) curricula.