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Associate Professor of Biological Sciences**

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- Director of Bioinformatics, Center for Translational and Basic Research (CTBR)
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**Lab Web Site:**

- <http://krampis.bioweb.hunter.cuny.edu>

**Research Web Site:**

- <https://agbiotec.github.io/website/>

**Education:**

- Ph. D., 2009, Virginia Polytechnic Institute and State University
- M. Sc., 2003, University of Athens, Greece

**List of Current Manuscripts:**

- <http://tinyurl.com/krampis-publications>

**Academic Appointments:**

- |                    |   |                              |
|--------------------|---|------------------------------|
| - 4/2014 - Present | City University of New York               | Associate Professor          |
| - 4/2014 - Present | Center for Translational & Basic Research | Director of Bioinformatics   |
| - 4/2014 - Present | Weill Cornell Medical College             | Faculty, Computational       |
| Biomedicine        |   |                              |
| - 5/2009 - 4/2014  | J. Craig Venter Institute                 | Assistant Professor          |
| - 8/2003 - 5/2009  | Virginia Bioinformatics Institute         | RA & Bioinformatics Engineer |
| - 8/2000 - 8/2003  | University of Athens, Greece              | Research Assistant (RA)      |

**Research Areas:**

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

computing.

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

1. NGS data pipelines for QC, RNA-seq, Hi-C, metagenomics, variant discovery, genome assembly.

2. Integrative analysis of variation, expression, chromatin and epigenetic data from TCGA, Encode, 4DN.

3. Scalable, accessible pipelines for metagenomics, clinical samples and personal genomics on Galaxy.

4. Interdisciplinary research and novel applications of genomic sequencing and bioinformatics.

1. Portable NGS and bioinformatics with Nanopore Minion and Intel Next Units of Computing (NUC).

2. Touch-enabled, mobile computing interfaces for personal genomics and clinical NGS data visualization.

3. Metabarcoding for conservation and biodiversity monitoring using environmental DNA (eDNA).

4. Algorithmic Information Theory, Computability, and Biologically-Inspired Computing.

1. Emergence, complexity, information content and compressibility of epigenetic networks.

2. Integrating DNA computing with NGS sequencing for reading molecular output with high I/O.

3. Computability and decidability of biologically-inspired and DNA computing models.

## Grants:

1. Principal Investigator.	2017 - 2018	CUNY Advanced Science Research Center
2016 - 2017		CUNY Center for Translational and Basic Research Pilot Award. Project Title: "Expanding Infrastructure and Services for Translational and Basic Research"
2015 - 2016		National Institutes of Health. Project Title: "Expanding Infrastructure and Services for Translational and Basic Research"
2015 - 2017		Weill Cornell Medical College, Clinical and Translational Science Center Pilot Award
2014 - 2016		City University of New York. "Faculty startup award". Amount \$100,000
2014 - 2015		National Institutes of Health. "Development of a Bioinformatics Core and Services"
2011 - 2014		National Institutes of Health. "Large-Scale Prokaryotic and Viral Next-Gen Sequencing"

2. Co-Principal Investigator.	2017 - 2018	National Institutes of Health. Project
2014 - 2015		National Science Foundation. Project Title: "Development of the next-generation

## Honors and Awards:

	2018	Proposal Development / Faculty Research Award
	2017	President's Travel Award, Hunter College, City University of New York
	2014	Entrepreneurship Lab NYC Selected Participant and Mentor
	2011	Bioinformatics Open Source Conference – Best Abstract
	2008	Virginia Tech Graduate Association Executive Board Member
	2008	Virginia Tech Outstanding Interdisciplinary Doctoral Dissertation
	2008	Horace E. Alphin Doctoral Tuition Scholarship
	2007	Virginia Tech Graduate Student Assembly Research Assistant
	2004-2006	James and Ina Mae Doctoral Tuition Scholarship

## Teaching and Mentoring:

1. Courses Developed and Taught.	2014 - 2016	"Programming for Computational Biology"
2015 - Present		"Computational Molecular Biology" pattern matching, alignment, read mapping
2015 - Present		"Next-Generation Sequencing Data Analysis" sequencing technology, data formats
2. Workshops Developed and Taught.	2018	"A Plug and Play, on-Premise Bioinformatics Workflow for Healthcare and Academia"
2017		"Deploying Large-Scale Bioinformatics Workflows with Kubernetes and Docker"
2016		"NGS Sample Processing and Data Analysis with the COBALT Pipeline"
2015		"Scalable, Intuitive Genomic Data Analysis with Galaxy and Nextflow"
2014		"Cloud BioLinux: Pre-Configured Bioinformatics and Data Science Applications"
2013		"Genomic Sequencing Data Analysis using Cloud Computing and Bioinformatics"
2012		"South Africa National Research Network Workshop: Computational Biology in the Cloud"
2012		"Empowering Genomics, in South Africa: Workshop, Policy and Community Solutions"
2011		"Cloud BioLinux for Bioinformatics and Data Science Applications"
2011		"Biologically Inspired Approaches to Resilient Machine Cognition, Ocala, FL"
2010		"From monolithic to distributed bioinformatics services, Seattle, WA."
3. Graduate Students Mentored.	2015 - Present	Jason Mighty, Ph.D. California State University, Fullerton

2015 - Present	Allen Pan, Ph.D. Candidate, <i>Teaching Assistant, Department of Biological Sciences, University of Maryland</i>
2014 - Present	Juliette Gorson, Ph.D. Candidate, <i>Chemistry, Deep Expression, College &amp; Adult Education Center, CUNY</i>
2014 - 2017	Samuel Hosmer, Ph.D. Candidate, <i>Mathematics, Department of Mathematics, College &amp; Adult Education Center, CUNY</i>
2010 - 2012	Priti Kumari, M.Sc. Bionformatics, <i>Parallels, BioChemistry Dept, George Washington University</i>
2010 - 2012	Vivek Sarangi, M.Sc. Bioinformatics, <i>Developmental Biology Dept, George Washington University</i>

4. Undergraduate Students and Interns Mentored. 2014 - Present Bioinformatics

2016	Science Research Mentor at Urban Barcoding Project (UBRP) by Cold Spring Harbor Laboratory
2015	Mentor, Science Research Mentoring Program (SRMP), American Museum of Natural History
2014	Summer Bioinformatics Workshop organized by Hunter Science High-School

## Institutional Committee and Scientific Service:

1. Graduate and undergraduate education committees. 2016 - Present Co-Chair

2015 - Present	Bioinformatics M.Sc. Program at CUNY. Designed and wrote the program proposal
2015 - 2016	CUNY Data Science Committee. Contributed towards designing Data Science program
2014 - 2015	CUNY Quantitative Biology Program Faculty. Worked towards planning new program

2. Editorial Positions, Boards and Peer-Review Service. . *Oxford Bioinformatics; BMC Bioinformatics*

3. Memberships in Professional Societies. . Since 2013 Illumina Basespace

Since 2009	Open Bioinformatics Foundation
Since 2009	Bioinformatics Open Source Conference
Since 2009	Galaxy Developers Community
Since 2006	Bioinformatics IT World
Since 2003	International Society for Computational Biology

## Extramural Invited Presentations:

1. Graduate and undergraduate education committees. 2018 High-Th

2017	Dept. of Public Health Sciences, Penn State College of Medicine, Hershey,
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 Science
2017	Dept. of Computational Medicine, University of Michigan, Ann Arbor, MI
2016	Bioinformatics Ph.D. Program Guest Lecture, NYU Langone Medical Center
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 for 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

## **Bibliography - Published Manuscripts**

### **- High-throughput bioinformatics infrastructures for cluster and cloud computing platforms.**

1. 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".
2. Ali T., Kim B., Lijeron C., Ogunwobi O.O., Mazumder R. and Krampis K. (2017). PeerJ Preprints, 5, p.e3385v1. "TED toolkit: a comprehensive approach for convenient transcriptomic profiling as a clinically oriented application".
3. 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".
4. Alterovitz G., Dean D.A., .... Krampis K., et al. (2017). bioRxiv, p.191783. "Enabling Precision Medicine via standard communication of NGS provenance, analysis, and results".
5. Kim B., Ali T., Dong C., Laungani B., Wultsch C., Lijeron C. and Krampis K. (2017). bioRxiv, p.209734. "miCloud: a plug and play, on-premises bioinformatics cloud, providing seamless integration with Illumina genome sequencers".
6. 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".
7. 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".
8. 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”.

9. 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”.

10. 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”.

11. 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”.

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

1. Brown S.M., Hao Y., Chen H., Laungani B.P., Ali T.A., Dong C., Lijeron C., Kim B., Krampis K. and Pei Z. (2017). bioRxiv, p.120402. “Fast functional annotation of metagenomic shotgun data by DNA alignment to a microbial gene catalog”.

2. 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”

3. 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”.

4. 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”.

5. 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.”

6. 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”.

## **7. Interdisciplinary research and novel applications of genomic sequencing and bioinformatics.**

1. Wultsch C., Perkins S.L., Kelly M.J., Waits L.P., Quigley H., Amato G., and Krampis K. (In Prep). Molecular Ecology. “A new perspective in carnivore ecology and conservation: comparative gut microbiome composition, diversity, and functionality in sympatric Neotropical jaguars and pumas”.

2. Wultsch C., DeBarba M., Schmieder A., Graham T., Wait L.P., Kelly M.J. and Krampis K. (In Prep). Scientific Reports. “Carnivore Feeding Ecology: Advances using a DNA Metabarcoding Approach”.

3. Ingala M.R., Simmons N.B., Wultsch C., Krampis K., Speer K.A., and S.L. Perkins. (In

Prep). Applied and Environmental Microbiology. "Comparing Fecal and Intestinal Sampling Methods in Mammal Microbiome Research".

4. 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".

5. 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*".

6. 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".

7. 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".

8. 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".

9. 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".

10. 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*".

11. 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".

12. 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**

1. .Krampis K. "Cloud Computing for Bioinformatics: Next-Gen Sequencing and Large-Scale Data Analytics" Monograph to be published in 2019, contract signed with Cambridge University Press, Cambridge, UK.



## Bibliography - Book Chapters

1. 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.
2. 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.
3. 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 (Chpt. 7). Caister Academic Press, Norfolk, U.K.
4. 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.
5. 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.
6. 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.
7. Miller J., Rusch D., Krampis K., Tovchigrechko 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.
8. Tyler B.M., Jiang R.H., Zhou L., Tripathy S., Dou D., Torto-Alalibo T., Li H., Mao Y., Liu B., Vega-Sanchez M., Mideros S.X., Hanlon R., Smith B.M., 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 - Other Media:

<a href="http://url.com/BCIL-channel">http://url.com/BCIL-channel</a>	2014 - Present	Video tutorials on public bioinformatics s
<a href="https://github.com/BCIL">https://github.com/BCIL</a>	2014 - Present	Bioinformatics Core Infrastructure Laboratory (BC
<a href="https://hub.docker.com/u/bcil">https://hub.docker.com/u/bcil</a>	2014 - Present	Docker containers with public bioinformati
<a href="http://cloud.bioinformatics">http://cloud.bioinformatics</a>	2012 - Present	Cloud BioLinux Project and the first Bioinformatics

[nux.org](https://nux.org/en.wikipedia.org/wiki/CloudBioLinux)  
[en.wikipedia.org/wiki/CloudBioLinux](https://en.wikipedia.org/wiki/CloudBioLinux)

<https://>