



**Konstantinos Krampis,  
Associate Professor of Biological Sciences**

- 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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**Lab Web Site:**

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

**Research Web Site:**

- <http://www.bioitx.com>

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

2. Co-Principal Investigator.

2017 - 2018

National Institutes of Health

2014 - 2015

National Science Foundation. Project Title: "Development of the m

**Honors and Awards:**

2018

Proposal Development / Faculty

2017

President's Travel Award, Hunter College

2014

Entrepreneurship Lab NYC Selected Partner

2011

Bioinformatics Open Source Conference

2008

Virginia Tech Graduate Association Executive

2008

Virginia Tech Outstanding Interdisciplinary

2008

Horace E. Alphin Doctoral Tuition Scholarship

2007

Virginia Tech Graduate Student Assembly

2004-2006

James and Ina Mae Doctoral Tuition Scholarship

**Teaching and Mentoring:**

1. Courses Developed and Taught.

2014 - 2016

"Programming

2015 - Present

"Computational Molecular Biology" pattern matching, alignment,

2015 - Present

"Next-Generation Sequencing Data Analysis" sequencing technology, data

2. Workshops Developed and Taught.

2018

"A Plug and

2017

"Deploying Large-Scale Bioinformatics Open Source with Kubernetes"

2016

"NGS Sample Processing and Data Analysis with COBALT"

2015

"Scalable, Intuitive Genomic Data Analysis with Galaxy"

2014

"Cloud BioLinux: Pre-Configured Bioinformatics and Data Management"

2013

"Genomic Sequencing Data Analysis using Cloud Computing and Hadoop"

2012

"South Africa National Research Network Workshop: Cloud Bioinformatics"

2012

"Empowering Genomics, in Support of Agricultural Research, Food Security and

2011

"Cloud BioLinux for Bioinformatics Open Society for Agricultural Research"

2011

"Biologically Inspired Approaches to Resilient Machine Cognition"

2010

"From monolithic to distributed bioinformatics services, Seattle, WA."

3. Graduate Students Mentored. 2015 - Present Jason Mighty,
- 2015 - Present Allen Pan, Ph.D. Candidate, *Teaching Biological Sciences Department*
  - 2014 - Present Juliette Gorson, Ph.D. Candidate, *Chemistry Dept*
  - 2014 - 2017 Samuel Hosmer, Ph.D. Candidate, *Mathematics Dept*
  - 2010 - 2012 Priti Kumari, M.Sc. *Parallel Bioinformatics Dept*
  - 2010 - 2012 Vivek Sarangi, M.Sc. *Biodevelopmental Biology Dept*

4. Undergraduate Students and Interns Mentored. 2014 - Present
- 2016 Science Research Mentor at Urban Barcoding Project (UBRP) by
  - 2015 Mentor, Science Research Mentoring Program (SRMP), American
  - 2014 Summer Bioinformatics Workshop organized by Hunter Science I

**Institutional Committee and Scientific Service:**

1. Graduate and undergraduate education committees. 2016 - Present
- 2015 - Present Bioinformatics M.Sc. Program at CUNY. Designed and wrote the
  - 2015 - 2016 CUNY Data Science Committee. Contributed towards designing I
  - 2014 - 2015 CUNY Quantitative Biology Program Faculty. Worked towards pla

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

3. Memberships in Professional Societies. Since 2013 Illum
- 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
	2017
	2017
	2017
	2017
	2017
	2016
	2015
	2015
	2015
	2014
	2014
	2012
	2012
	2012
	2011

**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. Wulsch 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., Wulsch 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:**

2014 - Present

Video tutorials on published

<http://tinyurl.com/BCIL-channel>

2014 - Present

Bioinformatics Core Infra<https://>res Labor

[github.com/BCIL](https://github.com/BCIL)

2014 - Present

Docker containers with <https://>figured bi

[hub.docker.com/u/bcil](https://hub.docker.com/u/bcil)

2012 - Present

Cloud BioLinux Project <http://>the first Bioin

[loudbiolinux.org](http://loudbiolinux.org)

<https://en.wikipedia.org/wiki/CloudBioLinux>