KONSTANTINOS KRAMPIS, Ph.D.

Associate Professor, Biological Sciences
Hunter College, City University of New York (CUNY)

Director of Bioinformatics
Center for Translational and Basic Research (CTBR-CUNY)

Adjunct Faculty, Institute of Computational Biomedicine
Weill Cornell Medical College

Next Generation Computational Infrastructures for Accessible, Standardized, Scalable Bioinformatics.

Next Generation Sequencing (NGS) technology has become fully integrated in every aspect of medical and biological research, and we can now affordably capture all genomic and transcriptomic features of cellular function with unprecedented scale and detail. In this seminar, I will discuss what I believe are key elements for the next generation of bioinformatics infrastructures towards achieving scalability and accessibility, and how to streamline genomic data analysis similarly to the way pre-packaged laboratory reagent kits have done for biological sample processing. The ideas will be presented within the context of genomic data science, which is defined by large-scale sequencing projects involving integrative analysis of differential gene expression, mapping and annotation of genomic variation. The presentation will also focus on metagenomics analysis, which allows us to study the impact that thousands of microbial species have on the metabolic activities, disease resistance and even mental health of a host organism, and further for environmental and ecological niches. I will present examples of software applications we have developed by leveraging the latest web and mobile computing technologies, enabling researchers to easily interpret complex genomic and metagenomic datasets through rapid analysis and intuitive visualizations. I will also demonstrate our standardized and computationally scalable tools, using the Galaxy platform that runs within cloud computing (Docker) containers, allowing for seamless bioinformatics analysis pipeline composition, execution, and data management. With the cost of NGS at a point where it has become affordable for every independent research lab, it is key that we remove all bioinformatics data analysis barriers, in order to democratize genomic sequencing applications in all aspects of biological and environmental research.

CITATIONS:

Brown SM, Chen H, Hao Y, Laungani BP, Ali TA, Dong C, Lijeron C, Kim B, Wultsch C, Pei Z, Krampis K. (*2019*). *GigaScience*. Apr 3;8(4). “MGS-Fast: Metagenomic shotgun data fast annotation using microbial gene catalogs”.

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”.

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”.

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”.

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”.

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”.

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”.