Development of a highly sensitive method to detect small RNAs in big data sets using high-performance Computing

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Abstract

Biology became a data-driven science due to the technological advancements in the last decade. To address the challenge of analyzing big datasets produced by high-throughput applications, NSF funded iPlant Collaborative (rebranded to CyVerse), an ongoing project that brings together Biologists, Bioinformaticians and Computer Scientists. As a Bioinformatician by training, my input in the development of the iPlant infrastructure was to: 1) capture metadata from the data generated from collaborators and help with their integration to iPlant resources, 2) design methodologies and pipelines for big-data analysis on molecular markers detection and gene expression variation, and 3) provide feedback to Computer Engineers on generating a user-friendly interface targeted to biologists. With the resources to analyze the data available, the challenge now is to retrieve meaningful biological information. My talk will center on using custom cloud services to analyze 25Gb of maize data, aiming to develop a methodology for novel small RNAs discovery and to study their expression in different developmental stages. The methodology offers a rapid and versatile analysis method, by which the existing small RNA datasets are enriched multifold.

Bio

Christos Noutsos currently holds a computational biology postdoctoral position at Cold Spring Harbor Laboratory. His research focus has been on analysis of big data generated by -o-mics applications. He has been a contributor in iPlant Collaborative, renamed to CyVerse. Currently Christos is working on developing a computational method to discover novel maize small RNAs and study their expression across development. The methodology will be integrated in CyVerse infrastructure for open access by the scientific community. In parallel, Christos is an Adjunct Professor at the School of Professional Studies at NYU, where he teaches Human Genetics. Moreover,
Christos has been involved in publications as an Associate Editor at Current Plant Biology journal, and lately as a Series Editor for a Book on Protocols in Plant Comparative Genomics, Springer. Dr. Noutsos performed his PhD studies at Max Planck Institute for Plant Breeding in Cologne, Germany in the lab of Dr. Dario Leister, studying DNA transfer from the organelles to the nucleus. He received his MSc degree from Wageningen University, The Netherlands in the field of Bioinformatics, where he worked in the in-silico optimization of cDNA-AFLP technique. He obtained his BSc degree from the Technological Educational Institute of Thessaloniki, Greece.

Faculty Host: Konstantinos Michmizos