

Furthering data analysis of next-generation sequencing to facilitate research

August 11 2015

Researchers at Cincinnati Children's Hospital Medical Center have developed a user-friendly, integrated platform for analyzing the transcriptomic and epigenomic "big data."

Reporting their platform in *Genome Biology*, scientists say that the new platform—called BioWardrobe—could help <u>biomedical researchers</u> answer questions about both basic biology and disease.

The recent proliferation of <u>next-generation sequencing</u> (NGS)-based methods for analysis of <u>gene expression</u>, <u>chromatin structure</u> and protein-DNA interactions have opened new horizons for molecular biology. These methods include RNA sequencing (RNA-Seq), chromatin immunoprecipitation sequencing (ChIP-Seq), DNase I sequencing (DNase-Seq), micrococcal nuclease sequencing (MNase-Seq), assay for transposase-accessible chromatin sequencing (ATAC-Seq) and others.

The sheer volume of the data obtained from sequencing requires computational data analysis. However, the bioinformatics and programming expertise required for this analysis is usually absent in typical biomedical laboratories, according to the authors. This results in data inaccessibility or delays in applying modern sequencing-based technologies to pressing questions in basic and health-related research.

"Although biologists can perform experiments and obtain the data, they often lack the programming expertise required to perform computational data analysis," says Artem Barski, PhD, senior author and assistant



professor in the Divisions of Allergy and Immunology and Human Genetics at Cincinnati Children's. "BioWardrobe aims to empower researchers by bridging this gap between data and knowledge."

Andrey Kartashov, MS and Barski collaboratively developed BioWardrobe to facilitate the analysis and utilization of both newly generated and publically available datasets.

"Huge amounts of published data have been deposited in public databases, such as Gene Expression Omnibus or Short Read Archive, but remain inaccessible to majority of researchers due to lack of bioinformatics expertise," Kartashov said. "BioWardrobe allows biologists to analyze the data without having to learn how to program."

More information: BioWardrobe *Genome Biology* Publication - www.genomebiology.com/2015/16/1/158

Provided by Cincinnati Children's Hospital Medical Center

Citation: Furthering data analysis of next-generation sequencing to facilitate research (2015, August 11) retrieved 27 April 2024 from https://phys.org/news/2015-08-furthering-analysis-next-generation-sequencing.html

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.