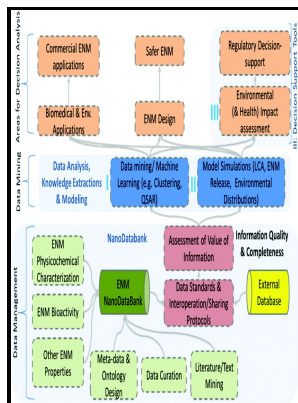# Pathway analysis for drug discovery - computational infrastructure and applications

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ANTON YURYEV, PhD, is the Senior Director of Application Science at Ariadne Genomics Inc. Moreover, the method can be easily applied to other experimental techniques, such as RNA-seq.

Pathway Analysis for Drug Discovery: Computational Infrastructure and Applications by Anton Yuryev

From a methodological point of view, DSEA is able to highlight pathways that are significantly modulated by most of the drugs in the input drug-set relative to the other drugs in the database. This gene-set comprises 38 genes, including CFTR itself. DSEA correctly identifies the golden-standard pathways even when up to three random drugs are added to the drug-set 75% of the drug-set To test the convergence properties of DSEA, we ran the analysis by varying the number of drugs in the drug-sets, in order to understand how many drugs were needed in order for the golden standard pathways to become significant.

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The toy example shows how a set of three drugs is found to consistently downregulate one pathway top arrow , while upregulating another one bottom arrow 3.

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