

Fold-change Specific Enrichment Analysis (FSEA): an approach for functional enrichment analysis of transcriptomic data

Wiebe D.^{1*}, Omelyanchuk N.¹, Zemlyanskaya E.¹, Mironova V.^{1,2}

¹ *Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia*

² *Institute for Water and Wetland Research, Radboud University, Nijmegen, Netherlands*

* wiebe@bionet.nsc.ru

Currently, transcriptomic experiments are the most common approach to studying gene expression dynamics in response to experimental conditions. Previously, we found that gene expression profiling data contains more information than is routinely extracted with standard approaches [1]. In order to fill this gap, we developed a new method for functional annotation of differentially expressed genes from transcriptome data with respect to their fold changes – Fold-change Specific Enrichment Analysis (FSEA). FSEA identifies Gene Ontology (GO) terms, which are annotated to genes with similar changes in the pattern of expression. We named GO terms found by FSEA as fold-change-specific in response to stimulus under investigation. Approbation identified many responses to abiotic factors, treatments, and diseases as regulated in a fold-change-specific manner. One of the most interesting findings offered by FSEA showed that there are two prevailing responses of functionally-related gene groups, either weak or strong. It is noteworthy that some fold-change-specific GO terms are invisible by classical algorithms for functional gene enrichment. Such GO terms were not enriched compared to the genome background, but were regulated by a factor within specific fold-change intervals. Application of FSEA to cancer-related transcriptomes revealed gene groups with a tightly coordinated response that could be potential regulators, markers, and therapeutic targets in oncogenic processes. To make FSEA available to researchers, we implemented it as the FoldGO Bioconductor R package (<https://www.bioconductor.org/packages/release/bioc/html/FoldGO.html>) along with a web-server version (<https://webfsgor.sysbio.cytogen.ru/>).

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References

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