MetaRE: search for cis-regulatory elements via meta-analysis of transcriptomic data

D.D. Novikova[1, 2, 3]*, P.A. Cherenkov[1], K.U. Tkachev[2], V.G. Levitsky[1, 2], V.V. Mironova[1, 2]

[1] *Novosibirsk State University, Novosibirsk, Russia*

[2] *Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia*

[3] *Department of Agrotechnology and Food Sciences, Subdivision Biochemistry, Wageningen University and Research Center, Wageningen, Netherlands*

* *e-mail: novikovadd@bionet.nsc.ru*

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Meta-analysis of biological data is becoming more and more popular. This tendency is due to accumulation of the big data in omics, like transcriptome, metabolome and proteome profiles, etc. More than two decades passed from uprise of whole-genome expression profiling methods. Nowadays thousands of transcriptomes are publicly available. Moreover, in many cases several experiments on the same phenomena could be found, providing plenty of material for the meta-analysis. One of the tasks is identification of cis-regulatory elements associated with expression changes in response to a stimulus, which allows to study complicated processes controlled by a set of transcription factors (TFs). We developed an R package MetaRE which provides search for the cis-regulatory elements enriched in the promoters of differentially expressed genes (DEGs) in response to a stimulus [1]. Via meta-analysis of multiple expression profiles, cis-regulatory elements are identified as associated with gene up- or down-regulation in response to a stimulus. Limma, edgeR and GEOquery are built-in in the package to search for DEGs in the transcriptome experiments from GEO database. C++ used to fasten slow components with the built-in Rcpp package to integrate the C++ code into R.

MetaRE package could be applied to any organism with sequenced genome, for which a number transcriptome experiments on a particular topic are available. The package was tested on Arabidopsis and Zebrafish to identify the cis-elements associated with response to auxin [1] and cold stress, correspondingly.

References

1. Cherenkov P. et al. (2017) Diversity of cis-regulatory elements associated with auxin response in Arabidopsis thaliana. Journal Experimental Botany. 69(2):329-339.