

The construction of gene networks for Mycobacterium Tuberculosis by analyzing next-generation sequencing data

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Introduction

Determination of bacterial resistance to antibiotics is an expensive and complicated process. To efficiently create new drugs one needs to understand interactions between different genes and communications within the bacterial regulatory network. To solve this problem methods of identification of expressed genes groups are important.

Methods and Results

We developed an algorithm for assessment of modulons (groups of genes co-expressed in specific conditions) in Mycobacterium Tuberculosis (strain H37Rv). For this purpose we selected a set of expression data obtained with Next-Generation Sequencing from GEO (Gene Expression Omnibus)[1]. To identified clusters for co-expressed genes, we used self-organizing neural networks[2] and analyzed correlation between different groups of experiments. The results of each experiment consisted in the form a vector of expression levels of each gene.

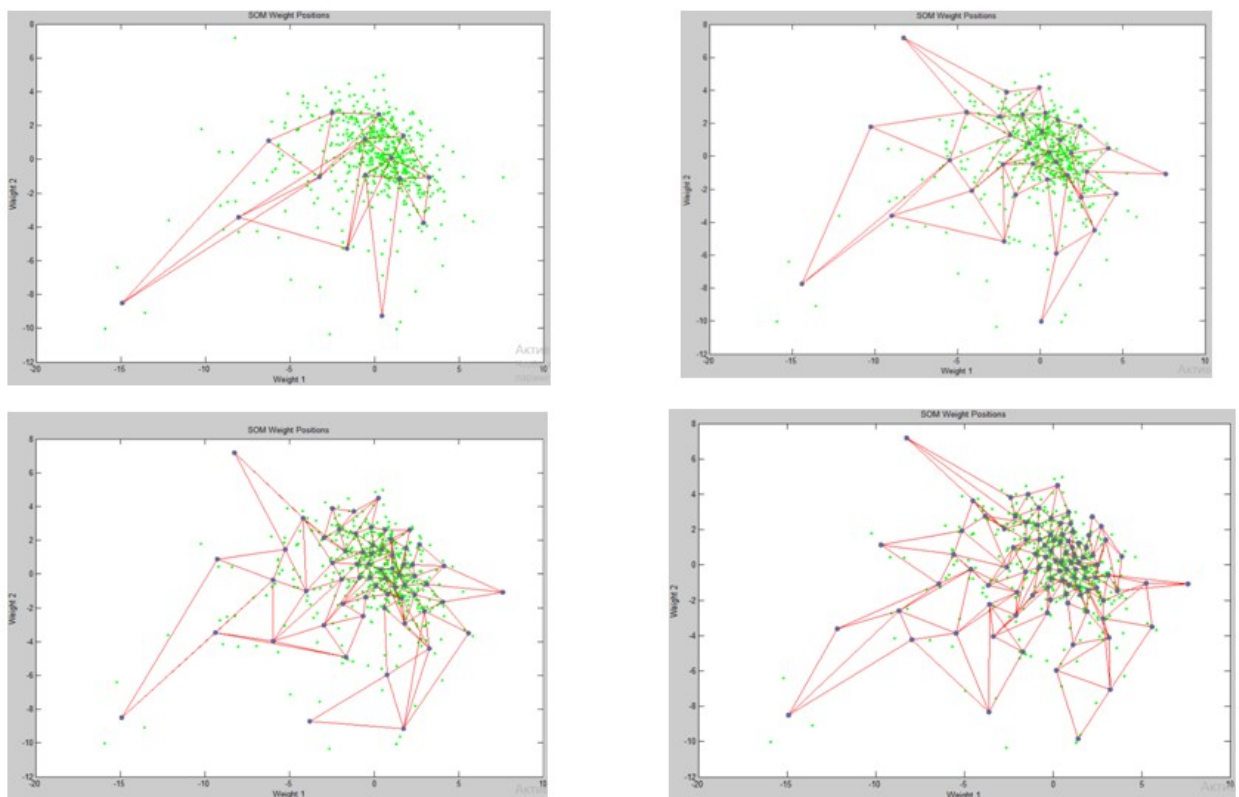


Figure 1. Self organizing maps of gene expression data for different numbers of neurons in the Kohonen network.

We took experiments of cell cultures treated by eicosatetraynoic, linoleic and oleic acid. Number of experimental data for eicosatetraynoic acid was 12, for linoleic acid was 40 and for oleic acid was 54. Experimental data we used for learning the Kohonen neural network.

To test the algorithm, we reproduced relations between genes that are described in paper [3]. There table below contains genes at rows and columns with the cells containing the number of neurons in self organized map. By (*) we mark connections found in [3].

	MT0082	grpE	pks16	fxsA	MT2727	nei1	rpiB	trxB
MT0082	-			5x3				
grpE	*	-	7x5					
pks16	*	*	-					
fxsA	*	*	*	-				
MT2727					-	9x7		
nei1					*	-		
rpiB					*	*	-	5x3
trxB					*	*	*	-

References

1. Edgar, R., Domrachev, M., & Lash, A. E. (2002). Gene Expression Omnibus: NCBI gene expression and hybridization array data repository. *Nucleic acids research*, 30(1), 207-210.
2. Kohonen, T. (1990). The self-organizing map. *Proceedings of the IEEE*, 78(9), 1464-1480.
3. Sherrid, A. M., Rustad, T. R., Cangelosi, G. A., & Sherman, D. R. (2010). Characterization of a Clp protease gene regulator and the reactivation response in *Mycobacterium tuberculosis*. *PLoS One*, 5(7), e11622.