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Using gene expression and systems biology to interrogate auditory hallucinations in schizophrenic patients

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Schizophrenia is a severe mental disorder affecting around 1% of the population. This disease presents a complex aetiology that has not been completely unveiled yet. Auditory hallucinations are a very significant and disruptive symptom of schizophrenia affecting between 60% and 80% of schizophrenic patients.

In this paper we have used a network-based transcriptomic analysis aiming to identify differences in gene expression between schizophrenic patients with and without auditory hallucinations.

Gene expression data from blood samples drained from 30 schizophrenia patients were generated using Affymetrix Human Gene 2.0 ST Genechips. Affymetrix Expression console was used for normalization and quality control purposes. The RMA normalization method was applied for gene summarization and then a filter applied to keep only the most variably expressed probesets (4,508). These dataset was analysed using the weighted gene co-expression network analysis (WGCNA) package in R.

The gene co-expression network analyses allowed us to identify eleven different gene modules based on their topological overlap. These modules were related to the relevant phenotypic information and allowing us to identify modules related with different phenotypic traits of interest.

Gene co-expression network analysis is a useful tool for the analysis of gene expression analysis. Its application in the analysis of schizophrenia gene expression provides an insight on the molecular mechanisms related with this disease and the differences at the molecular level between patients presenting auditory hallucinations and those that do not.

In our analysis we have been able to identify different gene modules containing genes expression profiles that can be related with clinically relevant phenotypes. These gene modules could be functionally annotated and related with different pathways and gene ontology terms that are relevant in the context of this analysis.

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