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Data Article

Data on overlapping brain disorders and emerging drug targets in human Dopamine Receptors Interaction Network

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ABSTRACT

Intercommunication of Dopamine Receptors (DRs) with their associate protein partners is crucial to maintain regular brain function in human. Majority of the brain disorders arise due to malfunctioning of such communication process. Hence, contributions of genetic factors, as well as phenotypic indications for various neurological and psychiatric disorders are often attributed as sharing in nature. In our earlier research article entitled "Human Dopamine Receptors Interaction Network (DRIN): a systems biology perspective on topology, stability and functionality of the network" (Podder et al., 2014) [1], we had depicted a holistic interaction map of human Dopamine Receptors. Given emphasis on the topological parameters, we had characterized the functionality along with the vulnerable properties of the network. In support of this, we hereby provide an additional data highlighting the genetic overlapping of various brain disorders in the network. The data indicates the sharing nature of disease genes for various neurological and psychiatric disorders in dopamine receptors connecting protein-protein interactions network. The data also indicates toward an alternative approach to prioritize proteins for overlapping brain disorders as valuable drug targets in the network.

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Specifications Table

Subject area	*Computational Systems Biology*
More specific subject area	*Human Dopamine Receptors Network*
Type of data	*Text files, tables and figures*
How data was acquired	*Systemic database curation and statistical analysis*
Data format	*Analyzed*
Experimental factors	*Common genetic factors responsible for various brain disorders in the network*
Experimental features	*Comprehensive mapping of disease genes and identification of overlapping disease modules in the network*
Data source location	*n/a*
Data accessibility	*Data are within this article*

Value of the data

- The data hints an overlapping disease spectrum of neurological disorders in DRIN.
- The data pinpoint towards common contributing genetic factors of neurological disorders in DRIN.
- The data might encourage researchers to identify additional drug targets in DRIN for future drug discovery endeavors.

1. Data

The data highlighted 25848 associations between 431 proteins and 4312 diseases, disorders and clinical or abnormal human phenotypes in Dopamine Receptors Interactions Network (DRIN) [1]. The associations were refined through stringent statistical analysis to reduce the over representation of

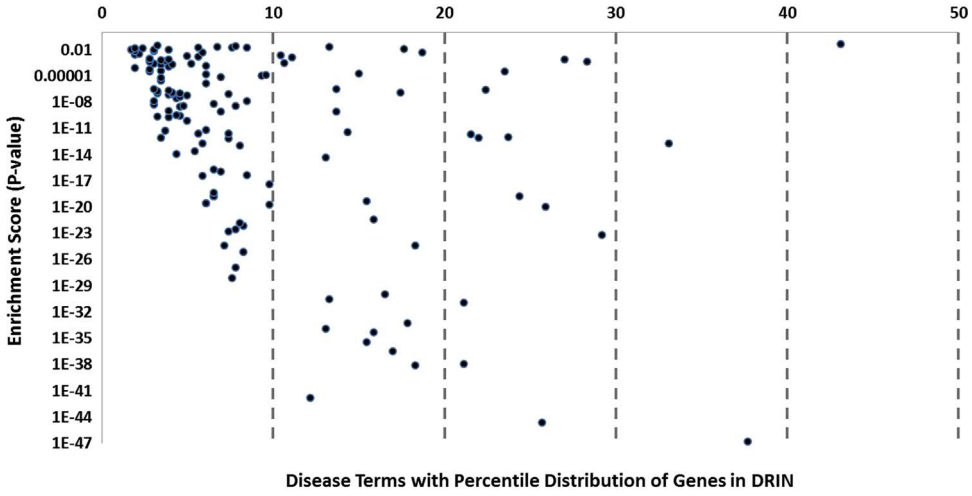

Fig. 1. Gene-disease enrichment analysis in DRIN. In the plot the *X*-axis represents the percentage of genes associated with each disease terms in DRIN and *Y*-axis represents the enrichment statistics (*P*-value cut off < 0.05) of disease terms in DRIN. A total of 143 different disease terms were significantly identified (blue dots) over 4312 disease association in DRIN after bonferroni correction of the *P*-value (two-sided hypergeometric test).