Dear Editor,

We are submitting our manuscript “Coherence of Molecular Mechanisms In Major Human Disease and Traits” to be considered for publication in *BMC Bioinformatics*. This manuscript will be of interest to the network analysis community.

The main highlights of our work are:

* A novel method for comparing molecular networks. We introduce a metric for measuring the coherence of molecular mechanisms in the networks of phenotype-specific genes. This metric is independent of the size of molecular networks, allowing for comparing coherences across phenotype-specific networks of different sizes. The high coherence of a molecular network may inform about the therapeutically targetable molecular mechanisms.
* Coherence estimation and comparison across 116 phenotype-specific networks from seven disease- and five trait categories, including the estimation of statistical significance of coherence measures.
* Validation of our approach using different protein-protein interaction (PPI) databases.
* Identification of diseases and traits with high or low coherence. E.g., metabolic diseases and traits showed consistently high coherence, while psychiatric disorders and intelligence-related traits were the least coherent.

All data used in the manuscript was sourced from publicly available repositories (GWAScatalog, STRING, and Biogrid PPIs, MSigDb). All code and data needed to reproduce our results are made available on our GitHub repository <https://github.com/dozmorovlab/disease_coherence>. We also want to assure that this manuscript is not being considered for publication elsewhere.

With our best regards,  
On behalf of all authors,

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