

NETLAS:



TOWARD AN INTEGRATED ATLAS FOR EXPLORATION AND **ANALYSIS OF NETWORK MEDICINE DATA**

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PROBLEM STATEMENT

- Different sources
- Heterogeneous data
- Varying degrees of confidence for the interactions
- Analysis influenced by multiple aspects

We have integrated datasets covering three main topics of network medicine:

- Genes (IntAct, Biogrid, Mint, Innate, Dip, Matrixdb)
- Diseases (DisGeNET, Biosnap)
 - Drugs

We introduced a scoring system for link reliability that considers three factors:

- Detection method (Sm)
- Interaction type (St)
- Number of publications (Sp)

$$S_{MI} = \frac{K_p \times S_p(n) + K_m \times S_m(cv) + K_t \times S_t(cv)}{K_p + K_m + K_t}$$

VISUAL EXPLORATION

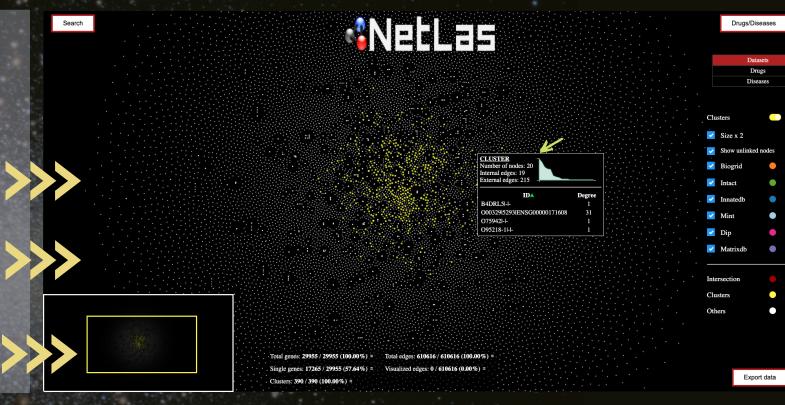
(DGI, Biogrid)

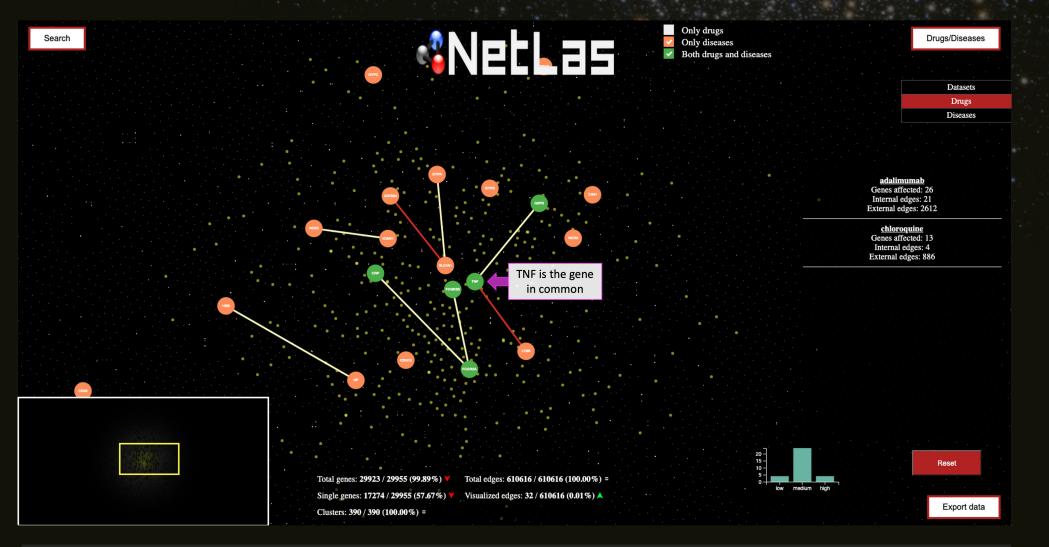
Focusing on data exploration and using the visualization of multilayer network as the first attempt to allow exploration and analysis capabilities, we are developing NetLas (NETwork medicine atLAS)

The visual overview of NetLas represents the gene layer coming from our integrated dataset as the base block.

Due to potential visual clutter we have defined clusters of genes based on their centrality score. The clusters are visualized as yellow dots that can be expanded.

On this visualization, the user can investigate the interaction between genes or explore the genes that compose a cluster.





The genes of Malaria in orange, while in green, the genes that have in common the disease and drugs. Adalimumab acts on four genes; while inspecting Chloroquine, which operates on two genes, it is possible to see that they have in common one single gene TNF, the most important one. This is a starting point for the investigation of a drug combination strategy.



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For more information visit

https://aware-diag-sapienza.github.io/NetLas-prototype/

One prominent use is support to drug repurposing.

The analyst can find a disease and study the affected genes, through the superimposition of layers and coordinated views that help to investigate the associations.

Then she can go into details and compare the drugs that involve part of those genes.

ON-GOING

We are improving the analysis capabilities and the multilayer visual representation.

We are focusing on exploring the links' reliability information to support a quality-driven analysis