

# A MULTI-SCALE APPROACH FOR BIOLOGICAL GRAPH VISUALIZATION: LOCAL ANALYSIS IN GLOBAL CONTEXT

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## INTRODUCTION

Biologists grapple with large multi-scale graphs to find relevant subgraphs for answering a range of biological questions

Existing biological visualization approaches are broadly of two types:

- Static overviews of the entire graph
- Interactive small-scale views of subgraphs

## DESIGN PROCESS

**USER-CENTERED DESIGN:** meetings with domain experts in systems biology, bioinformatics, and causal reasoning

### THREE MAIN DESIGN GOALS:

- 1 Provide scalable, interactive, and performant visualizations of biological graphs
- 2 Provide iterative local analysis coordinated with global context
- 3 Promote scientific synthesis and discovery

## DATA PROCESSING

Causal assertions are extracted by EMMAA [1], resulting in a set of normalized, qualitative causal statements

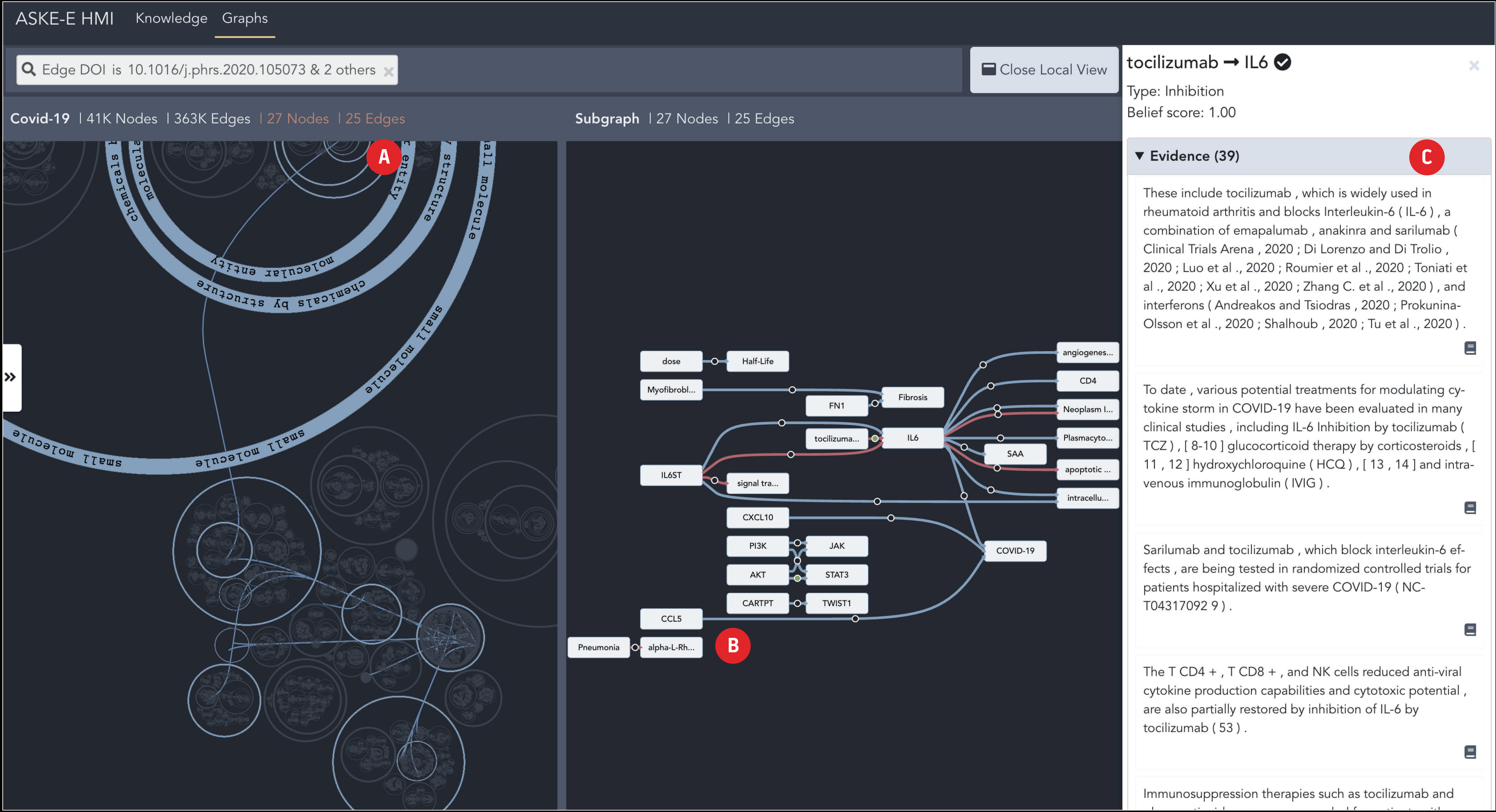
Statements are presented as a multidigraph optimized for real-time browser rendering

## RESULTS

Computational biologists see promise in our approach for various use cases such as **drug interactions** and **disease propagation**

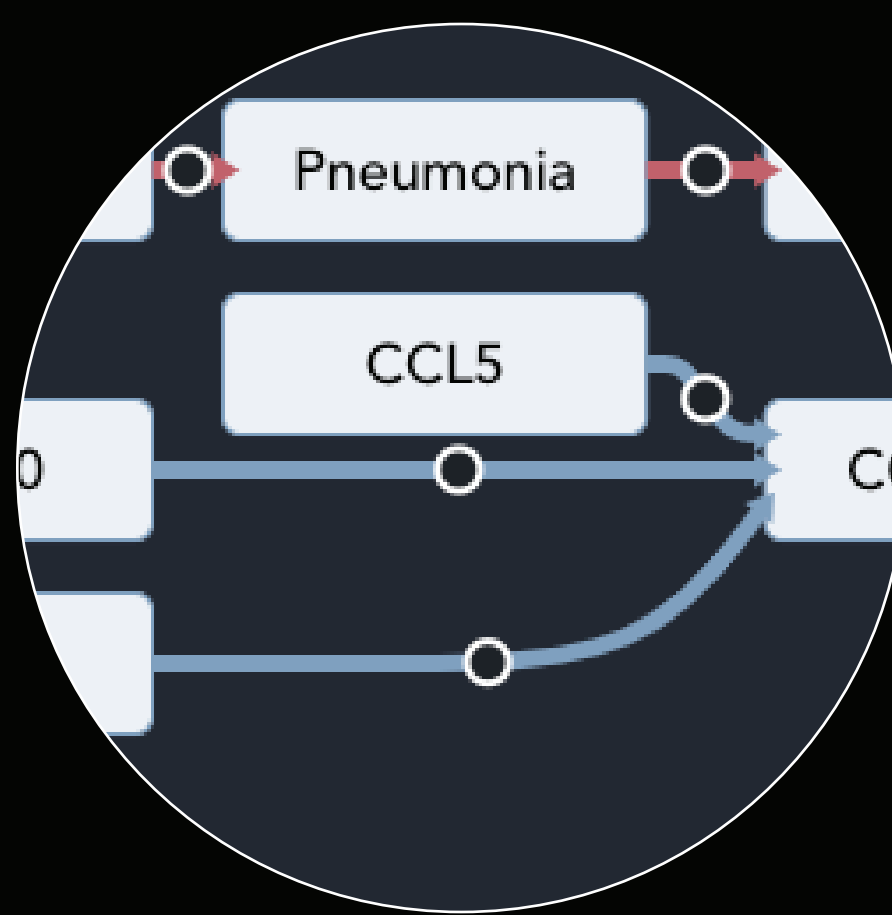
Interactions with biological graphs with **41,000 nodes** and **363,000 edges** were smooth

# Our approach for **scalable graph analysis** enables biologists to interactively **explore, query, and analyze** biological graphs at different scales.



**A GLOBAL VIEW**

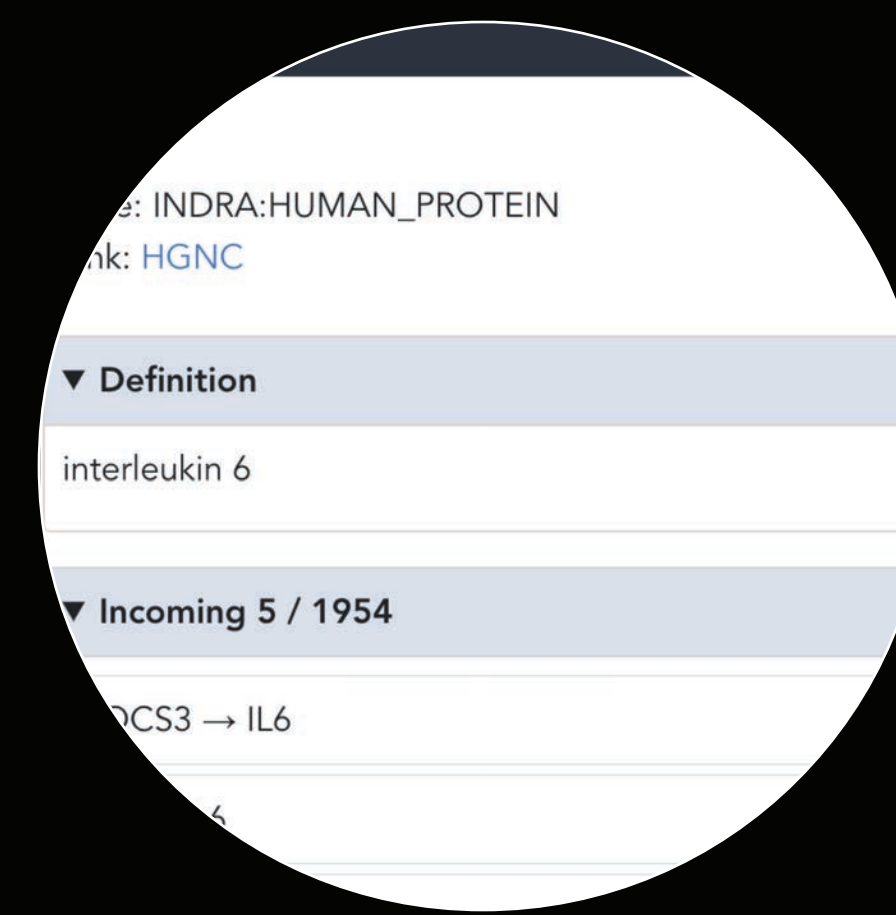
Nodes are organized hierarchically in a biological ontology [2] using a circle-packing layout. Hyperedges are bundled.



**B LOCAL VIEW**

Subgraphs of interest can be extracted with a flow-layout or further examination

Can be interactively expanded via machine-assisted suggestions



**C DRILL-DOWN PANEL**

Nodes and edges in the Local View can be interrogated for evidence from source literature.

Also available are incoming and outgoing edges for subgraph expansion.

### REFERENCES:

[1] B. M. Gyori and J. A. Bachman. EMMAA: Ecosystem of Machine-maintained models with Automated Analysis, 2020

[2] B. M. Gyori and J. A. Bachman. INDRA: BioOntology, 2020