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

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.

REFERENCES:


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