

Graphery: a Biological Network Algorithm Tutorial Webservice

Heyuan Zeng
Computer Science Department
Reed College
zengl@reed.edu

Anna Ritz
Biology Department
Reed College
aritz@reed.edu

CCS CONCEPTS

• Applied computing → Interactive learning environments;
Biological networks.

KEYWORDS

Biological networks, web-based visualization, graph algorithms

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1 INTRODUCTION

Network visualization is crucial for integrating and interpreting experimental and annotated evidence across different biological scales. Web-based platforms have emerged to enable collaboration among biological and computational researchers [1, 3]. As network-based visualization becomes popular in the scientific community, developing materials to train biologists to understand the outputs of network-based approaches are essential. We present Graphery, a web-based graph algorithm tutorial that is designed for biological researchers. A test deployment is available for reviewers at

<https://graphery.reedcompbio.org>

2 FEATURES AND IMPLEMENTATION

Graphery is organized around the concept of a *tutorial*, which describes and provides code for a classic graph algorithm (Figure 1). A tutorial contains three parts: Markdown-style content, interactive graphs, and a code editor. The editor enables users to step forward and back in the code and see changes applied to the corresponding graph. The editor also allows more programming-savvy users to edit the existing code and see their modifications applied on the graphs. Users can run code in the editor locally or in the cloud. Together, these three panels allow users to gain a deeper understanding of the algorithm described.

For each tutorial, users may select one of multiple *real-world biological networks* to better understand the implications of the algorithm described. These small graphs will come from biological applications such as animal social networks, ecology food webs, molecular interaction networks, and phylogenetic trees.

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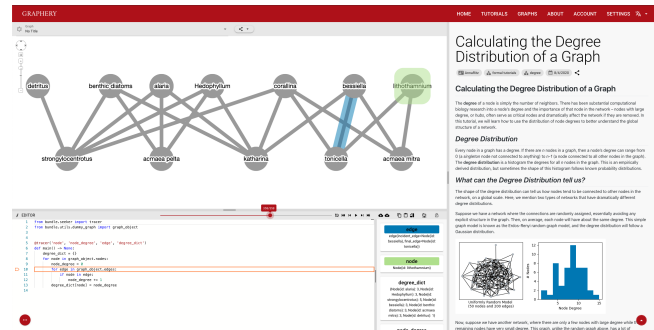


Figure 1: A Graphery tutorial with a food web network [2].

The frontend skeleton is powered by Quasar, a Vue framework. Inside of the skeleton, we use Cytoscape.js to visualize graphs specified by cyjs, the Monaco Editor to display and format code, and Axios to handle API calls. We use PostgreSQL for the backend database, which is accessed via a GraphQL API on a Django backend manager.

3 DISCUSSION

Graphery is a biology-focused tutorial for researchers to understand graph algorithms within a context of biological networks that are relevant to their work. Discipline-focused tutorials will be essential for researchers to interpret their biological data. Graphery also has promise in educating undergraduate science majors about computational approaches to biological questions, and we are planning a beta test to improve the existing functionality and user interactions in the fall in an undergraduate computational systems biology course at Reed College. Additionally, we plan to support Graphery tutorials in English, Chinese, and Spanish. Through Graphery, we hope to engage with the biological community looking to understand network analysis, which serves as a start to a community-contributed learning platform.

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