

GraphBreak: Network Community detection and annotation in biomedical regulatory informatics context

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Manuscript Source: <https://www.biorxiv.org/content/10.1101/2021.03.07.434249v1>

Manuscript Authors: Abhishek Narain Sing & Abhishek; Narain Singh

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- Depending on the source of the input text, the Sentence Audit may contain occasional html artefacts that are parsed as sentences (E.g. "Download figure. Open in new tab").
- Always consult the original research paper as the true reference source for the text.

Contact Information:

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All queries, feedback or suggestions are also very welcome.

Research Paper Sections:

The sections of the research paper input text parsed in this audit.

[illegible]

Title **GraphBreak: Network Community detection and annotation in biomedical regulatory informatics context**

S1 [001] Abstract

S1 [002] Graph network science is becoming increasingly popular, notably in big-data perspective where understanding individual entities for individual functional roles is complex and time consuming.

Graph network science is becoming increasingly popular, ...
... notably ...
... in big-data perspective ...
... where understanding individual entities ...
... for individual functional roles is complex ...
... and time consuming.

S1 [003] It is likely when a set of genes are regulated by a set of genetic variants, the genes set is recruited for a common or related functional purpose.

It is likely ...
... when a set ...
... of genes are regulated ...
... by a set ...
... of genetic variants, ...
... the genes set is recruited ...
... for a common ...
... or related functional purpose.

S1 [004] Grouping and extracting communities from network of associations becomes critical to understand system complexity, thus prioritizing genes for disease and functional associations.

Grouping ...
... and extracting communities ...
... from network ...
... of associations becomes critical ...
... to understand system complexity, ...
... thus prioritizing genes ...
... for disease ...
... and functional associations.

S1 [005] Workload is reduced when studying entities one at a time.

Workload is reduced ...
... when studying entities one ...
... at a time.

S1 [006] For this, we present GraphBreak, a suite of tools for community detection application, such as for gene co-expression, protein interaction, regulation network, etc.

For this, ...
... we present GraphBreak, ...
... a suite ...
... of tools ...
... for community detection application, ...
... such as for gene co-expression, ...
... protein interaction, ...
... regulation network, ...
... etc.

S1 [007] Although developed for use case of eQTLs regulatory genomic network community study- results shown with our analysis with sample eQTL data-Graphbreak can be deployed for other studies if input data has been fed in requisite format, including but not limited to gene co-expression networks, protein-protein interaction network, signaling pathway and metabolic network.

Although developed ...
... for use case ...
... of eQTLs regulatory genomic network community study- results shown ...
... with our analysis ...
... with sample eQTL data-Graphbreak can be deployed ...
... for other studies ...
... if input data has been fed ...
... in requisite format, ...
... including ...
... but not limited ...
... to gene co-expression networks, ...
... protein-protein interaction network, ...
... signaling pathway ...
... and metabolic network.

S1 [008] GraphBreak showed critical use case value in its downstream analysis for disease association of communities detected.

GraphBreak showed critical use case value ...
... in its downstream analysis ...
... for disease association ...
... of communities detected.

S1 [009] If all independent steps of community detection and analysis are a step-by-step sub-part of the algorithm, GraphBreak can be considered a new algorithm for community based functional characterization.

If all independent steps ...
... of community detection ...
... and analysis are a step-by-step sub-part ...
... of the algorithm, ...
... GraphBreak can be considered a new algorithm ...
... for community based functional characterization.

S1 [010] Combination of various algorithmic implementation modules into a single script for this purpose illustrates GraphBreak's novelty.

Combination ...
... of various algorithmic implementation modules ...
... into a single script ...
... for this purpose illustrates GraphBreak's novelty.

S1 [011] Compared to other similar tools, with GraphBreak we can better detect communities with overrepresentation of its member genes for statistical association with diseases, therefore target genes which can be prioritized for drug-positioning or drug-repositioning as the case be.

Compared ...
... to other similar tools, ...
... with GraphBreak we can better detect communities ...
... with overrepresentation ...
... of its member genes ...
... for statistical association ...
... with diseases, ...
... therefore target genes ...
... which can be prioritized ...
... for drug-positioning ...
... or drug-repositioning ...
... as the case be.

S2 [012] Introduction

S2 [013] By signaling pathway networks, bio-based chemical molecular networks- such as protein-protein interaction networks, gene co-expression networks, gene regulatory networks, metabolic networks-provide a graphical representation of cellular and tissue systems.

By signaling pathway networks, ...
... bio-based chemical molecular networks- ...
... such as protein-protein interaction networks, ...
... gene co-expression networks, ...
... gene regulatory networks, ...
... metabolic networks-provide a graphical representation ...
... of cellular ...
... and tissue systems.

S2 [014] To guide biological experiments, networks must be analyzed by means of community detections, if every gene transcript, gene product, protein, genotypic variants, such as SNPs, were to be characterized individually they could be very difficult to perform.

To guide biological experiments, ...
... networks must be analyzed ...
... by means ...
... of community detections, ...
... if every gene transcript, ...

... gene product, ...
... protein, ...
... genotypic variants, ...
... such as SNPs, ...
... were ...
... to be characterized individually they could be very difficult ...
... to perform.

S2 [015] To increase understanding of network phenomena, network scientists deploy models.

To increase understanding ...
... of network phenomena, ...
... network scientists deploy models.

S2 [016] For this, we introduce GraphBreak, a network analysis tool to understand variant based regulation of expression of genes as a community.

For this, ...
... we introduce GraphBreak, ...
... a network analysis tool ...
... to understand variant based regulation ...
... of expression ...
... of genes ...
... as a community.

S2 [017] It conducts community analysis of overrepresentation association with disease and other function phenotypes, along with linkage association of SNP variants for causative prioritization.

It conducts community analysis ...
... of overrepresentation association ...
... with disease ...
... and other function phenotypes, ...
... along with linkage association ...
... of SNP variants ...
... for causative prioritization.

S2 [018] This network-based community detection has been examined in detail from genomic variants, such as SNPs with expression of genes, but GraphBreak can be used for any network analysis, such as those discussed above. For example, WGCNA [Langfelder, P., et.

This network-based community detection has been examined ...
... in detail ...
... from genomic variants, ...
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... P., ...
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