



# A Linear Delay Linear Space Algorithm for Enumeration of All Connected Induced Subgraphs\*

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## ABSTRACT

Real biological and social data is increasingly being represented as graphs. Pattern-mining-based graph learning and analysis techniques report meaningful biological biological subnetworks that elucidate important interactions among entities. At the backbone of these algorithms is the enumeration of pattern space. In this work, we propose a linear-space linear-delay reverse search-based algorithm for enumerating all connected induced subgraphs of an undirected graph. Building on this enumeration approach, we propose an algorithm for mining all maximal cohesive subgraphs that integrates vertices' attributes with subgraph enumeration. To efficiently mine all maximal cohesive subgraphs, we propose two pruning techniques that remove futile search nodes in the enumeration tree.

Experiments on synthetic and real graphs show the effectiveness of the proposed algorithm and the pruning techniques. On enumerating all connected induced subgraphs, our algorithm is several times faster than existing approaches. On dense graphs, the proposed approach is at least an order of magnitude faster than the best existing algorithm. Experiments on protein-protein interaction network with cancer gene dysregulation profile show that the reported cohesive subnetworks are biologically interesting.

## CCS CONCEPTS

• **Theory of computation** → **Graph algorithms analysis; Algorithm design techniques;**

## KEYWORDS

Biological Networks, Subgraph Enumeration, Reverse Search

### ACM Reference Format:

Mohammed Alokshiya, Saeed Salem, and Fidaa Abed. 2018. A Linear Delay Linear Space Algorithm for Enumeration of All Connected Induced Subgraphs. In *9th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (ACM-BCB'18), August 29-September 1, 2018, Washington, DC, USA*. ACM, New York, NY, USA, 1 page. <https://doi.org/10.1145/3233547.3233695>

\*This work was supported by National Science Foundation (NSF) grant IIS-1423321.

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ACM-BCB'18, August 29-September 1, 2018, Washington, DC, USA

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ACM ISBN 978-1-4503-5794-4/18/08.

<https://doi.org/10.1145/3233547.3233695>