Biconnectivity in directed graphs

Minsoo Yang[1] *and Byungjun Min*[1,2,*]
[1] *Department of Physics, Chungbuk National University, Cheongju, Chungbuk 28644, Korea*
[2] *Advanced-Basic-Convergence Research Institute, Chungbuk National University, Cheongju, Chungbuk 28644, Korea*

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Extended Abstract

Motivation. Strongly Connected Components (SCCs) are sets of mutually reachable nodes in directed networks: nodes within an SCC have paths that allow them to reach one another[1]. While SCCs provide fundamental information regarding the topology of a directed network, they cannot guarantee structural resilience because they are vulnerable to the removal of a single node. To capture this, we study Strongly Biconnected Components (SBCs). SBCs are sets of nodes where at least two independent, mutually reachable paths exist. This problem involves identifying regions of the network topology that satisfy stricter connectivity requirements. Through this, we can obtain information regarding the more robust substructure of the network[2].

Approach and Methodology. We investigate the size of the largest SBC of directed random graphs. We develop an analytical methodology for estimating the size of SBCs using the generating function formalism.

SBCs are subsets of SCCs. A node in an SBC remains part of the SCC even if any single node is removed. This is because even if one of the two mutually reaching paths is lost, another path remains to reach other nodes in the SCC. (Fig. 1a) In our simulations, we exploit this characteristic to explore SBCs in directed graphs. Within an SCC consisting of M nodes, we remove one node and then re-identify the SCC. After that, we restore the removed node. By repeating this process for all M nodes, we can find the SBCs.

Results. We generated directed random graphs using the configuration model, identified the nodes forming the Giant Strongly Biconnected Component in the graph, and its size. we derived the generating functions from the degree distributions of the graph and developed an analytical framework to calculate the size of the giant SBC. Our analysis reveals that while SBCs emerge at the same percolation threshold as SCCs, their growth is slower due to the stricter connectivity requirements. (Fig. 1b) The degree distribution of random networks follows a poisson distribution. By applying the generating function calculated from this distribution to our theoretical framework, we can determine the size of the largest SBC (Red line). Although the simulation approach presented above may not be the optimal method, it allows for the precise identification of which nodes belong to the SBC by exploiting its unique properties (Red symbols).

Conclusions and Outlook. Identifying SCCs in directed graphs is a crucial topic because they often represent functional modules. To identify the core connections that maintain these

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[*] bmin@cbnu.ac.kr

modules and their functions, we introduced SBCs, which satisfy stricter connectivity requirements than SCCs. SBCs capture robust module that maintain connectivity even when nodes are removed. The framework developed in this study can serve as a tool for analyzing the stability of modules in robust infrastructure design and biological regulatory networks. A representative example is the connectome of the Drosophila larval brain[3]. Fortunately, in such cases, one can represent the network using only high-priority links by applying a link weight cut-off. In future research, we may investigate SBCs in the Drosophila larval brain connectome and the specific roles these constituent neurons play in brain signal transmission.

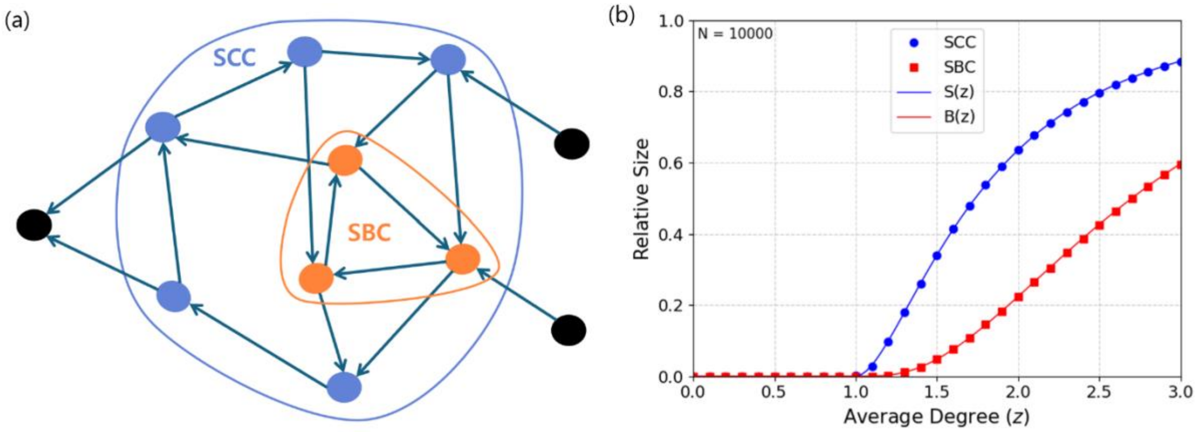

Figure 1. **(a)** SBCs are sets of the nodes that are connected each other by at least two independent paths. **(b) The relative size of the giant SCC and SBC in random graphs.** The relative sizes were obtained by averaging over 100 realizations for each average degree in directed random graphs with 10,000 nodes.

References

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