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1 Introduction

2 Network Structure

In this article, we will analyse a metabolic network of the Chinese hamster ovary (CHO) cell. The CHO cell is frequently used in biological and medical research and in the production of biopharmaceuticals[1].

We have used a whole-cell metabolic network of the Chinese hamster ovary (CHO) cell that was taken from the BiGG database[2, 1]. The original network contains 4,456 metabolites that take part in 6,663 reactions. The reactions and metabolites are annotated with additional metadata, such as name, BiGG ID, subsystem etc.

We have simplified the network to a simple directed graph, where reactions are represented with nodes. If one reaction produces a metabolite that is used by another reaction, they are connected by an arc. This network has 6,663 nodes and 656,609 arcs.

The network has a very large connected component of 6,036 nodes, while the other components are very small, as they are composed of at most 4 nodes. The largest connected component contains a strongly connected component of 5,307 nodes, while the other nodes are isolated. These probably represent parts of the metabolism where metabolites enter or leave the cell.

The network has scale-free structure. Its in-degree, out-degree and degree distributions are plotted in figure 1. The estimated scale factors for the network are $\gamma_{in} = 2.5$, $\gamma_{out} = 2.3$ and $\gamma = 2.0$.

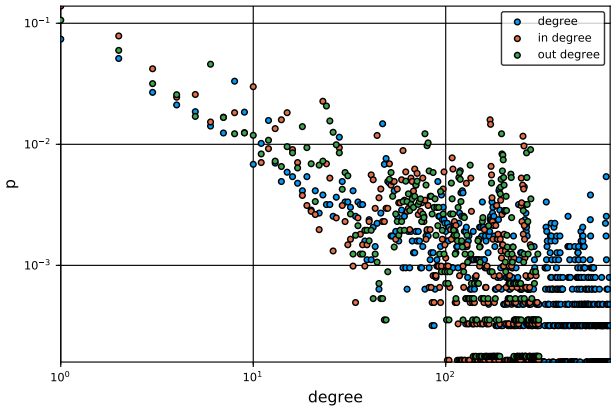

Fig. 1. The in-degree, out-degree and degree distributions of the network.

3 Authors contributions

All the authors were involved in the preparation of the manuscript. All the authors have read and approved the final manuscript.

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