Working with text: Read the following abstract of an essay titled "An integrated network visualization framework towards metabolic engineering applications" and then do the exercises below.

(Adapted from: Noronha A, Vilaça P, Rocha M. An integrated network visualization framework towards metabolic engineering applications. http://www.ncbi.nlm.nih.gov/pubmed/25547011).

1) Four sentences are missing in the text. Put them into the correct place in the text.

2) How are the ideas in the abstract linked together? Highlight all words/phrases linking the text together.

3) How does the text progress from sentence to sentence? Try to replace each sentence with a short explanation of the logic of the argument; importantly, do not refer to the text's content, but explain the text's dynamics through a more general explanation (for example, "Sentence X provides an introduction to the concept, sentence X+1 provides an example of the concept's use, …")

Abstract

Background

Over the last years, several methods for the phenotype simulation of microorganisms, under specified genetic and environmental conditions have been proposed, in the context of Metabolic Engineering (ME). **[A]** On the other hand, in the context of Systems Biology research, biological network visualization has reinforced its role as a core tool in understanding biological processes. However, it has been scarcely used to foster ME related methods, in spite of the acknowledged potential.

Results

In this work, an open-source software that aims to fill the gap between ME and metabolic network visualization is proposed, in the form of a plugin to the OptFlux ME platform. The framework is based on an abstract layer, where the network is represented as a bipartite graph containing minimal information about the underlying entities and their desired relative placement. **[B]** A user-interface makes it possible to edit, manipulate and query nodes in the network, providing tools to visualize diverse effects, including visual filters and aspect changing (e.g. colors, shapes and sizes). **[C]**

Conclusions

[D]

1) These tools are particularly interesting for ME, since they allow overlaying phenotype simulation results or elementary flux modes over the networks.
2) The framework and its source code are freely available, together with documentation and other resources, being illustrated with well documented case studies.
3) The framework provides input/output support for networks specified in standard formats, such as XGMML, SBGN or SBML, providing a connection to genome-scale metabolic models.
4) These methods provided insight on the functioning of microbial metabolism and played a key role in the design of genetic modifications that can lead to strains of industrial interest.