# Introduction

"Exploring modularity in biological networks" is a philosophical take on the importance of mathematical models in life science. It stood out from the other papers we looked at because it is more an essay than a paper, regarding the usefulness of network science in the biological field, which we found quite interesting. Often, we are more occupied with how we do science instead of why and to what end we do it, we, therefore, chose this paper as it has a different viewpoint than most papers and further question the usefulness of using mathematical models such as graph theory or network science.

The author of this paper offers philosophical viewpoints on the way science is performed. Notably, she splits science into several subcategories such as explanatory, predictive, integration, and unifying science and states that mathematical models play an especially integral and active role in the fields of exploratory science. This means that mathematical models are used especially to find correlations and other interesting phenomena within biological datasets, rather than to confirm established theses. Initially, these kinds of experiments were opposed to confirmatory experiments (experiment, designed to test and confirm hypotheses), but in recent times it became clear that exploratory experiments are often guided by background science, but lack a firm theoretical framework.

Furthermore, the author heightens the increasing importance of network science through the rise of omics projects, as networks facilitate the processing of a large amount of data acquired by these projects. Network science can be used in a biological context as biological systems provide a high degree of modularity. Modularity is understood as a key feature of biological systems and can be found in many different areas such as protein interaction, signaling pathways neurobiological systems, and ecological systems. Modularity requires parts of the system to be more like one another than the parts are like other clusters. To show modularity graph models are used as they are easy to visualize and represent modular systems quite well. The author defines these models as an instrument which “performs epistemic function in scientific inquiry” meaning that a model is a reduced image of the reality which is still capable of representing relevant features of the original system.

# Methods

The main methodological focus of this paper is to highlight the misconceptions and benefits of exploratorive mathematical models. In order to differentiate and articulate explorative network models the author implies that it is important to understand tools and methods used. Exploration is one of the key elements to discover new phenomena. But other than implied exploration is not free of direction of theories or knowledge. Furthermore the autor focuses on the search for biological modularity models. To clarify the relationships of modular biological systems, the paper refers to a study by Ravasz et al. (Ravasz E et al., doi:10.1126/science.1073374). The modular biological network systems presented there aimed to investigate and model the hierarchical organization of modular metabolic networks. Ravsz et al. showed that the metabolic network of 43 organisms are somewhat organized into small and highly connected topological modules. Those modules can be simulated using a graph-theory approach. The smallest unit or module concists of four densly interconnected nodes. This small unit was connected with three identical units by connecting the external nodes with the central node of the original cluster. This step is repeated iteratively and scales up quit fast and quadruples the number of nodes in each step.The clustering structure of the modules are therefore following a hierarchical power law .

This model is in theory scale free and can be further modified to use different base node configurations, and is therefore not limited in its complexity. Ravasz et al. investigated whether a hierarchical model as described above is able to describe the complex metabolic processes of 43 microorganisms. They measured the clustering coefficient for all investigated microorganisms. The exploratory approach showed that is well approximated and therefore provided evidence for an hierarchical organization of the metabolic system. They concentrated on the metabolic network of *Escherichia coli* to investigate the relationships between topological modularity and the functional classification of metabolites. As a baseline a previously established graph-theretical representation was used. This network then was conducted to a complexity reduction process. Non-branching pathways were replaced with equivalent links. Furthermore they detected topolocial overlaps between substrates as they concluded that the larger a overlap between substrates is, the more likely it is that they belong to the same functional class. Using the same method on an overlap matrix a global topologic representation of the metabolism was provided. Tightly interconnected modules visuialize a group of metabolites and as well smaller nested topological modules could be visualized. They showed that all highly connected metabolites correspond to their respective biochemical reaction within the metabolism.

Therefore the study of Ravasz et al. is a good example how one can use explorative methods to investigate unkown or new phenomena.

# Discussion

All in all, the author tries to extend and continue previous works on the usability of theoretical network approaches and their role in (exploratory) science. This was done by providing examples from different branches of life science and showing that one network can be used for several exploratory functions like exploring the solution space, reveal new research questions, and providing more insight into (the structure of) problems and research questions. Furthermore, this paper stands out of the majority by not arguing if network analysis and/or graph theoretical approaches can be useful in life science or if network approaches in explanatory science conflicts with mechanistic research like, as other work (Green et al. 2018, DOI: 10.1007/s11229-016-1307-6, Levy and Bechtel. 2013 DOI: 10.1086/670300). By making a case and showings that networks are already in use and have shown to be useful. In the end, this paper is a philosophical essay about the potential use and function of graph theory in different subfields of biology and exploratory science in general rather than a paper about the application of graph theory to solve a specific problem or question. Because of this, it was hard to get a grip on the graph-theoretical aspect and methodology of this paper. But it was interesting to see graph theory can be examined from an abstract point of view even though graph theory is in most cases already an abstraction of the biological reality. Which did not occur in the lecture.