Network modularity is widely misused in ecological analyses

Abstract

Stop using modularity maximization.

## Introduction

Ecosystems are composed of interactions between species and their environment. These interactions form networks that enable the persistence of species, ecosystems, and the services ecosystems provide people. In the last few decades, *network science* has developed to understand networks across a variety of domains. This field has developed numerous quantitative tools for describing network structure, which have seen increasing adoption in ecosystem science in the burgeoning subfield of network ecology (Delmas et al. 2019). One such property is *modularity* (denoted ), which is a metric that describes “how well” nodes of a network can be grouped into *modules*, first introduced in Newman and Girvan (2004). Modularity has been widely adopted as a metric of interest in ecological networks, and in principle the grouping of species into modules could contain biologically meaningful information.

Unfortunately, the most popular method identifying modules in ecological networks is Modularity Maximization (MM), which has many well documented flaws for robustly identifying modules in networks (Good, de Montjoye, and Clauset 2010; Fortunato and Barthélemy 2007; Lancichinetti and Fortunato 2011; Peixoto 2021). Still, MM is widely used in network ecology. In a brief literature survey, we found MM methods overwhelmingly prevelent in the analysis of ecological networks. Here we cover what modularity maximization is, and why it doesn’t work for identifying modules/groups in networks. We suggest methods for community detection based on Stochastic Block Models (Karrer and Newman 2011; Peixoto 2014; Yen and Larremore 2020) for identifying modules in ecological networks.

## What is modularity?

Consider a directed network defined by an adjacency matrix , where if nodes and share an edge, and otherwise. Let denote the total number of edges in the network, and be the degree (the number of edges) associated with node . Let denote the *group* (or module) that node belongs to. Modularity () is then defined as

where is a function that equals if , and equals otherwise. It is essential to emphasize that **modularity is not a property of a network *alone***. It is only defined for a network *and a set of group assignments for each node*, .

This value can be interpreted intuitively as how many more edges exist between members of the same group than would be expected if edges were distributed “at random”. As pointed out by Peixoto (2021), there is an implicit null model in what “at random” means in this definition, namely the Chung-Lu configuration model (Chung and Lu 2002), where the probability of an edge existing between nodes and is .

## What is modularity maximization?

Modularity maximization (MM) is one of many potential methods for the problem of taking an observed network and infering which group each node belongs to. In network science literature, this problem is called *community detection*. This method originated during the mid-2000s (Newman and Girvan 2004) and was popularized through the efficeincy of the Clauset-Newman-Moore (CNM) algorithm (Clauset, Newman, and Moore 2004) and the Louvain algorithm (Blondel et al. 2008), both of which made implementation of MM feasible for very large networks (hundreds or thousands of nodes). Six years later after its proposal, Good, de Montjoye, and Clauset (2010) (with Clauset, architect of CNM, as senior author) showed that in practical contexts modularity maximization is flawed for all but idealized networks. More recently, Peixoto (2021) more thoroughly explores this issue, showing how MM can massively overfit and find highly modular partitions () in networks with no modular structure.

## Why doesn’t modularity maximization work?

As pointed out by Peixoto (2021), modularity maximization fails on two fronts: it simultaneously *overfits* (by finding clusters that have high modularity but are entirely sporatic and unrelated to the mechanisms by which the network was generated) and *underfits* (by having a limit on the size of what communities are recoverable relative to the size of the whole network, called the *resolution limit* (Fortunato and Barthélemy 2007)).

### Overfitting via a poor choice of objective function

Degeneracy of the modularity function, lots of very similar local optima across widely different group partitions.

“The magnitude of the degeneracy problem, and the dependence of on the size and number of modules in the network, suggests that modules identified through modularity maximization should be treated with caution in all but the most straightforward cases.” Good, de Montjoye, and Clauset (2010).

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| Figure 1: The issue with modularity maxmimization: there are many local optima with similar values that correspond to qualitatively very different group partitions. |

### Underfitting via the resolution limit

The second issue with modularity maximization is that is cannot identify communities that at smaller than a certain size. The threshold for smallest community identifiable via MM is a function of the total size over the network, and called the “resolution limit” in the network science literature (Fortunato and Barthélemy 2007; Lancichinetti and Fortunato 2011).

## Modularity maximization is rampant in ecological network studies

We found in a survey of 50+ papers on ecological networks, modularity maximization is extremely common as the method for finding communities. The goal of this paper is not to shame or call-out specific papers, but to highlight that a widely adopted practice has fundemental flaws, and to advocate a principle alternative for community detection.

We suspect MM is so prolific because it is widely available in many packages for network analysis, including bipartite, which uses a method for modularity maximization for bipartite networks proposed by Dormann and Strauss (2014), and the very popular libraries igraph and networkx. Another widely applied method is from Guimerà and Nunes Amaral (2005), which uses simulated annealing for MM. The prolific availability of software to run MM-based community detection leads researchers down the “path of least resistance”.

## What instead of modularity maximization?

The state-of-the-art for community detection in networks are using a family of models called Stochastic Block Models (SBMs). Although the initial idea dates back several decades (Holland, Laskey, and Leinhardt 1983), modern research into using SBMs for community detection was spurred by regonition of the flaws with modularity maxmization (Good, de Montjoye, and Clauset 2010). SBMs have several advantages over modularity maximization. SBM inference is naturally posed as a Bayesian inference problem (Hofman and Wiggins 2008), which allows us to explicitly account for uncertainty in our estimate of the best node partition . Further, hierarchical SBMs (Peixoto 2014), where each block is itself an SBM, enables multi-scale community detection.

### What is a stochastic block model?

SBMs are a *probabilistic generative model*. This means for a fixed set of input parameters, SBMs can be sampled to produce different possible realizations of networks from the *distribution* of possible networks given the input parameters. In their simplest form, SBMs take a partition of the nodes into a groups , and a mixing or block matrix , where is the probablity of an edge existing between nodes in groups and respectively.

This enables much more flexability in the types of community structure exist in networks. Modularity maximization can only capture *one type* of community structure—*assortative* communities, where links within communities are more common that those between communities. In contrast, community structure in networks can take on a variety of different forms: assortative, disassortative (where *between group* edges are more likely than *within group*), core-periphery (where a set of densely connected nodes form a ‘core’, and other ‘periphery’ nodes that have few edges and tend to be attached to core nodes ), and ordered (like trophic levels in a food-web).

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| Adapted from Clauset (2022). Shows how SBMs can account for community structure beyond simple assortativity. |

### How do we infer community structure from stochastic block models?

We can use Markov Chain Monte Carlo (MCMC) sampler to take an observed matrix and obtain an estimate of the posterior distribution of the mixing matrix and group assignments, . To do this, we need to define the likelihood of observing some network from a given community partition , and mixing matrix . There are differences in the best way to define both likelihood and priors depending on underlying assumptions about network structure.

For unipartite networks, a common version is the Degree-Corrected SBM (DC-SBM, Karrer and Newman 2011), which explicitly accounts for the degree distribution by including the empirical degree sequence in the likelihood of observing each graph. Yen and Larremore (2020) develops a model specifically for bipartite networks, where the bipartite structure is directly incorporated into the generative model, improving performance for detecting communities in bipartite networks. Another promising line of research is hierarchical/nested SBMs (NSBMs), first proposed by Peixoto (2014). In NSBMs, each “block” is *itself* another SBM. This enables multi-scale community detection that can circumvent the issue of resolution limits from modularity maximization.

## Conclusion

In summary, community detection is great, but modularity maximization is useless. There are times when modularity, as a method of quantifying the assortativity of edges in a graph given a set of group assignments , could correspond to an interesting ecological question. However, using modularity *as the criteria* to select the group assignments is too unreliable to be the basis ecological conclusions. As an alterative, we should use *stochastic block models* to infer the structure of modules within ecological networks.

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