Doubly Stochastic Scaling Unifies Community Detection

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Abstract

Graph partitioning, or community detection, has been widely investigated in network science. Yet, the correct community structure on a given network is essentially data-driven. Thus, instead of a formal definition, diverse measures have been conceived to capture intuitive desirable properties shared by most of the community structures. In this work, we propose a preprocessing based on a doubly-stochastic scaling of network adjacency matrices, to highlight these desirable properties. By investigating a range of community detection measures, and carefully generalising them to doubly-stochastic graphs, we show that such a scaling unifies a whole category of these measures—namely, the so-called linear criteria—onto two unique measures to set up. Finally, to help practitioners setting up these measures, we provide an extensive numerical comparison of the capacity of these measures to uncover community structures within block stochastic models, using the Louvain algorithm.

Keywords: Network Analysis, Community Detection, Graph Partitioning Measures, Doubly-Stochastic Scaling.

1. Introduction

By mapping local-level elementary interactions between data, networks provide a powerful template that enables one to analyse emergent behaviours in complex systems, such as biological systems, social networks, etc. [1, Chap.5]. Hence, these last decades, analysis of complex networks has been at the core of several research works [2]. One aspect has gained a lot of attention: the problem of graph partitioning, also called community detection [3, 4, 1, Chap.21]. Defining a network as a set of entities (called nodes or vertices) connected by interactions (called links or edges), the aim of community detection is to partition the set of the nodes into groups of nodes that are similar or strongly related.

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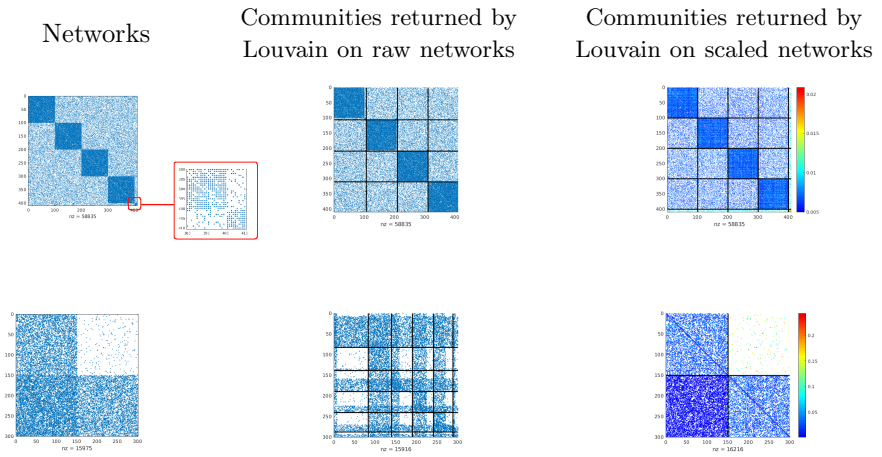


Figure 1: **Left:** Adjacency matrices of networks with community structures. **Middle:** The Louvain algorithm cannot detect the smallest community (top matrix, the smallest community highlighted in the red square); and it is unable to detect the two communities connected in an imbalanced fashion (bottom). **Right:** After scaling, Louvain can detect small communities in presence of larger ones (top); and it can detect the community structure when there is an imbalance in the flows of edges (bottom).

In real-world applications, the rightful community structure depends on the network. For this reason, there exists no formal definition of a community structure since it is always possible to find a community structure that contradicts the definition. However, it is generally admitted that community structures share similar properties: a community should be a group of nodes densely connected, and sparsely connected to the rest of the graph—see Table 1.1 from [5]. Thus, a number of measures that capture these properties have been designed to assess the quality of a community structure proposed on a network, e.g. [6, 7, 8]. Optimising such measures is generally a NP-complete problem [9, 3, 5], thus approximation algorithms have been proposed that perform community detection by approximating the "best" community structure. The most famous is probably the Louvain algorithm [10], that aims to maximise the so-called Newman-Girvan modularity [6]. Because of its simplicity, its accuracy in detecting communities, and its efficiency in terms of computational cost [11], it has been one of the most widely-used community detection algorithms for more than 10 years. But there are communities, very intuitive and yet poorly detected by algorithms in general, that even Louvain is unable to resolve: 1) Small communities in large networks are generally missed—this is typically the so-called resolution limit [12]. 2) In directed networks, flow-based communities are usually not detected in presence of an imbalance of the edges leaving and entering these communities. Points 1) and 2) are illustrated in the middle panels of fig. 1, where the results of Louvain algorithm applied on two toy networks exhibiting such community structures are displayed.

The aim of this study is to investigate the potential of matrix balancing as

a preprocessing for community detection. Our contributions are three-folds:

- We propose a preprocessing based on the so-called doubly-stochastic scaling, to increase the detectability of communities, in particular those usually hardly detectable as illustrated in fig. 1.
- By extending several graph partitioning measures to weighted graphs, in particular doubly-stochastic graphs, we show that our proprecessing unifies these measures onto two unique measures to set up.
- We conduct extensive comparisons of the capacity of these measures to uncover community structures within stochastic block models, which provides guidance for customising them.

The paper is organised as follows: Section 2 lists the definitions and notations to be used through the paper. Section 3 gives an overview of related work. Section 4 presents our method: we introduce the doubly-stochastic scaling (section 4.1) and detail our preprocessing (section 4.2), showing its potential on toy examples and a real-world network (section 4.3). In section 5, we discuss the generalisation of six graph partitioning measures to weighted graphs, in particular doubly-stochastic ones. Section 6 compares these measures, first theoretically in section 6.1, then experimentally in section 6.2. We finally discuss our conclusions and future work in section 7.

2. Definitions and Notations

In this section, we present some definitions and notations to be used through the paper. Basic mathematical objects are listed in table 1.

Object	Typoface	Examples
Unweighted graph	2-element Tuple	$G = (V, E)$
Weighted graph	3-element Tuple	$G = (V, E, \Omega)$
Edge in a directed graph	Tuple of nodes	(u, v)
Edge in a undirected graph	Curly brackets of nodes	$\{u, v\}$
Matrix	Bold capital letter	$\mathbf{A}$, $\mathbf{S}$
Matrix entry	Letter with subscripts	$a_{i,j}$
Matrix of 1s	$\mathbf{J}$	$\mathbf{J}$
Identity matrix	$\mathbf{I}$	$\mathbf{I}$
Transpose of a matrix	$.^T$	$\mathbf{A}^T$
Vector	Bold minuscule letter	$\mathbf{u}$, $\mathbf{x}$
Vector entry	Parentheses on a vector	$\mathbf{u}(i)$
Vector of 1s	$\mathbf{e}$	$\mathbf{e}$
Diagonal matrix from a vector	$\mathcal{D}(.)$	$\mathcal{D}(\mathbf{u})$, $\mathcal{D}(\mathbf{e}) = \mathbf{I}$
Cardinal function	$\|.\|$	$\|S\|$

Table 1: Typography of mathematical objects.

Graphs. In this study, we investigate networks (that we also call graphs) that can be weighted or not. Except when stated otherwise, networks are undirected. For a network $G = (V, E, \Omega)$, V is the set of nodes, $E \subset V \times V$ the set of edges, and the function

$$\begin{array}{rccc} \Omega: & E & \to & \mathbb{R}_+ \\ & \{u,v\} & \mapsto & \omega(\{u,v\}) \end{array}$$

provides the weights of edges. To simplify notations, we will assume that graphs have integer nodes, that is $V = \{1, ..., n\}$.

When there is no possible confusion about the network, letters n and m denote the number of nodes and the total weight of edges respectively, that is $n = |V|$ and $m = \sum_{\{u,v\}\in E} \omega(\{u,v\})$. The degree of a node u is defined as $d_u = \sum_{v:\{u,v\}\in E} \omega(\{u,v\})$. If $\exists \delta \in \mathbb{R} : \forall u \in V, d_u = \delta$, the graph is said to be δ-regular. We will denote by simple graphs the unweighted undirected networks without self-loop—i.e. $\forall u \in V, \{u,u\} \notin E$.

Adjacency Matrices. A (directed) graph $G = (V, E, \Omega)$ can be represented by its adjacency matrix, that is a matrix $\mathbf{A} \in \mathbb{R}^{n\times n}$ where

$$a_{i,j} = \begin{cases} \omega((i,j)) & \text{if } (i,j) \in E \\ 0 & \text{otherwise} \end{cases}.$$

Conversely, given a matrix $\mathbf{A} \in \mathbb{R}^{n\times n}$, we will call the adjacency graph of $\mathbf{A}$ the graph whose $\mathbf{A}$ is the adjacency matrix.

For undirected graphs, when the adjacency graph of $\mathbf{A}$ has no self-loop, then $2m = \sum_{i=1}^{n}\sum_{j=1}^{n} a_{i,j} = \mathbf{e}^T\mathbf{A}\mathbf{e}$. When the adjacency graph of $\mathbf{A}$ is unweighted, we define the complementary of $\mathbf{A}$ (and we denote $\overline{\mathbf{A}}$) the matrix in $\mathbb{R}^{n\times n}$ such that

$$\overline{a}_{i,j} = \begin{cases} 1 & \text{if } \{i,j\} \notin E \\ 0 & \text{otherwise} \end{cases}, \tag{1}$$

that is $\overline{\mathbf{A}} = \mathbf{J} - \mathbf{A}$.

Community Structures. Given a graph $G = (V, E)$, a community structure is a partitioning of the set of nodes V, that is a set of subsets of V: $\mathcal{C} = \{C_t\}_{t=1..k}$ such that $\bigcup_{t=1}^{k} C_t = V$ and $\forall t \neq s, C_t \cap C_s = \emptyset$. This community structure can be represented as an equivalence relation $\mathcal{X}$ on $V \times V$ such that

$$u\mathcal{X}v \iff \exists t \in \{1, .., k\} : u, v \in C_t.$$

It can also be represented as a matrix $\mathbf{X} \in \mathbb{R}^{n\times n}$ such that

$$x_{i,j} = \begin{cases} 1 & \text{if } i\mathcal{X}j \\ 0 & \text{otherwise.} \end{cases}$$

A matrix $\mathbf{X} \in \{0,1\}^{n\times n}$ represents an equivalence relation $\mathcal{X}$ (and hence a community structure) if and only if:

$$\begin{array}{lll} \forall i \in \{1,..,.n\}, & x_{i,i} = 1 & (a) \\ \forall i,j \in \{1,...,n\}, & x_{i,j} = x_{j,i} & (b) \\ \forall i,j,k \in \{1,...,n\}, & x_{i,k} + x_{j,k} - x_{i,j} \leq 1 & (c) \end{array}$$

where $(a),(b),(c)$ indicate respectively the reflexivity, the symmetry and the transitivity of the equivalence relation represented by $\mathbf{X}$ [13]. We will denote by $Eq(n)$ the set of the equivalence relations on a set V such that $|V| = n$. That is, we will write $\mathbf{X} \in Eq(n)$ when a matrix $\mathbf{X} \in \{0,1\}^{n\times n}$ verifies $(a),(b),(c)$, and $\mathcal{X} \in Eq(n)$ for an equivalence relation defined on the set V. For any $\mathbf{X} \in Eq(n)$, its complementary is defined by $\overline{\mathbf{X}} = \mathbf{J} - \mathbf{X}$.

Double Stochasticity. In the following, we specifically focus on networks that have the property of being doubly-stochastic, that is such that their adjacency matrices have their row and column sums equal to 1. Formally, a (directed) network $G = (V, E, \Omega)$ is said to be doubly-stochastic if its adjacency matrix $\mathbf{S} \in \mathbb{R}_+^{n\times n}$ is doubly-stochastic, that is

$$\begin{cases} \mathbf{S}\mathbf{e} = \mathbf{e} \\ \mathbf{S}^T\mathbf{e} = \mathbf{e}. \end{cases} \tag{2}$$

We remark that doubly-stochastic graphs are 1-regular graphs.

In this study, we will preprocess graphs so that they (or equivalently their adjacency matrices) are doubly-stochastic. Transforming a matrix $\mathbf{A} \in \mathbb{R}^{n\times n}$ onto a doubly-stochastic matrix is an operation called "scaling $\mathbf{A}$ onto its doubly-stochastic form". One achieves this by finding two vectors $\mathbf{r}, \mathbf{c} \in {\mathbb{R}_+^*}^n$ such that

$$\begin{cases} \mathcal{D}(\mathbf{r})\mathbf{A}\mathcal{D}(\mathbf{c})\mathbf{e} & = \mathbf{e} \\ \mathcal{D}(\mathbf{c})\mathbf{A}^T\mathcal{D}(\mathbf{r})\mathbf{e} & = \mathbf{e}. \end{cases} \tag{3}$$

The matrix $\mathbf{S} = \mathcal{D}(\mathbf{r})\mathbf{A}\mathcal{D}(\mathbf{c})$ is called the doubly-stochastic scaling of $\mathbf{A}$, and vectors $\mathbf{r}$ and $\mathbf{c}$ are called the scaling factors. The existence of a doubly-stochastic scaling is non-straightforward and will be detailed in section 4.1.

3. Related Work

Doubly-stochastic scaling for community detection. In this study, we design a preprocessing for community detection, based on a doubly-stochastic scaling of adjacency matrices. Doubly-stochastic scaling has already been used in the context of community detection, and more globally of matrix partitioning. It is the first stage of the two-stage algorithm used in [14] to partition migration networks. However, the rationales for scaling in [14] (invariance of relative odds and approximation of maximum entropy) differ from ours; authors even propose solutions to avoid the vanishing effect that we find desirable. Also, in [15], we

proposed to scale a matrix onto its doubly-stochastic form as a preprocessing step for a spectral algorithm, to get singular vectors whose piecewise constant patterns highlight the matrix block structure. Furthermore, in [16], authors also aim to partition a dataset by finding the doubly-stochastic matrix that best approximates the dataset similarity matrix. Finally, in [17], authors propose to use doubly-stochastic scaling to perform co-clustering, by exploiting the piecewise constant shapes of the scaling factors that are expected to approximate the joint densities between the random variables inferring the data, and random variables inferring the partitions.

We remark that all these studies use the doubly-stochastic scaling as a step of a whole pipeline and for a very specific purpose: achieving uniform marginals in the flow table [14], obtaining staircase-like singular vectors [15] or scaling factors [17], or approximating a similarity matrix [16]. On the other hand, our present method is a wider-purpose preprocessing that can be used prior to any community detection method.

Community detection measures. This paper investigates, generalises and unifies a bunch of measures designed to assess the quality of a community structure on a network. As stated in section 1, in a community structure, nodes within a community are densely connected, while being loosely connected to nodes outside their community. Several measures have thus been proposed, that rely on different ways to define "densely" and/or "loosely" connected. We propose to roughly divide them onto two categories: those totally unsupervised, and those partially supervised.

The totally unsupervised measures do not make any *a priori* assumption about the community structure, and are only based on the network structural properties. They can be subdivided onto three families. Measures based on density, such as Newman-Girvan modularity [6] or coverage [18], define a community as a group of nodes with a high density of edges. On the other hand, measures based on sparsity also exist, that consider that the amount of edges between two communities must be low. Among others one can cite conductance, expansion [19], or normalised cut [7]. Some measures are a mixture of density and sparsity, such as LambdaCC [5] or Balanced modularity [13]. Given a dynamic process defined on the graph edges (e.g. a random walk), unsupervised measures from the third kind consider that a community is a group of nodes from which the process will struggle to escape. These are for instance the Map equation [8], Markov stability [20], or the community distance from [21].

Partially supervised measures are derived from some maximum likelihood, and thus require *a priori* hypotheses, or ground truth knowledge, about the network community structure. They are of two kinds: Stochastic Block Model (SBM) based, and node-embedding based. SBM-based measures assume that a modular network is a realisation of some SBM, whose parameters are unknown. Discovering these parameters elucidates the community structure inferred by the SBM. This is done via likelihood maximisation [22]. Finally, node-embedding-based methods aim to find a low-dimensional feature representation of vertices, consistent with the network community structure. They

generally require to know the assignation to a community of a subset of nodes. For instance *node2vec* [23] that aims to maximise the likelihood of preserving node neighbourhoods, needs to know the label of some nodes to learn some hyper-parameters, in order to get a definition of neighbourhood consistent with the network community structure. On the other hand, Graph Convolutional Networks [24] aim to learn node embeddings that minimise the cross-entropy error—that counts the number of falsely labelled nodes—over all nodes whose label is known.

In this study, we focus on a range of unsupervised measures. Most of them were listed in [25], where it was shown that they can be used in the Louvain algorithm instead of the Newman-Girvan modularity. This required the measures to be defined for graphs whose edge weights are integers, and the measures have thus been extended to such graphs when needed. Since generalisation was not the purpose of [25], this was done straightforwardly and did not always fit the philosophy of the initial measures, as shown in section 5.

4. Doubly-Stochastic Scaling Preprocessing

In this section we describe and discuss the preprocessing we propose for community detection, that relies on a doubly-stochastic scaling of the graph adjacency matrix. Not every square matrix is amenable to a doubly-stochastic matrix. We thus first provide the conditions for such a scaling to exist, and discuss the relations with graph connectivity. We will then present our preprocessing, and discuss its impact on some community structures.

4.1. Doubly-Stochastic Scaling and Graph Connectivity

The Sinkhorn-Knopp Theorem. Given a square matrix $\mathbf{A} \in \mathbb{R}_+^{n\times n}$, it is not always possible to find two vectors $\mathbf{r}, \mathbf{c} \in \mathbb{R}_+^n$ such that eq. (3) is verified. In order for such a scaling to exist, the pattern of $\mathbf{A}$—i.e. the positions of its nonzero entries—must respect certain conditions, which are provided by the so-called Sinkhorn-Knopp theorem [26]. In order to introduce this theorem, we first provide two definitions about the pattern of a matrix on which it relies. These definitions can be found in [27].

Definition 1. ***Bi-Irreducibility*** *A matrix $\mathbf{A} \in \mathbb{R}^{n\times n}$ is called bi-irreducible if there is no pair of permutation matrices $\mathbf{R}, \mathbf{Q}$ such that:*

$$\mathbf{RAQ} = \begin{bmatrix} \mathbf{A}_1 & \mathbf{A}_{1,2} \\ 0 & \mathbf{A}_2 \end{bmatrix}$$

with $\mathbf{A}_1, \mathbf{A}_2$ two square and non empty matrices.

This definition implies that $\mathbf{A}$ is not amenable to a block triangular matrix by independent permutations of its rows and its columns.

Definition 2. ***Total Support*** *A matrix* $\mathbf{A} \in \mathbb{R}^{n \times n}$ *is said to have a total support if every nonzero entry lies on a strictly positive diagonal. One characterisation of this definition proposed in [27] is that there are two permutation matrices* $\mathbf{R}, \mathbf{Q}$ *such that:*

$$\mathbf{RAQ} = \begin{bmatrix} \mathbf{A}_1 & & \\ & \ddots & \\ & & \mathbf{A}_k \end{bmatrix}$$

with $\mathbf{A}_1, ..., \mathbf{A}_k$ *bi-irreducible matrices.*

We can now enunciate the Sinkhorn-Knopp theorem [26].

Theorem 1. ***Sinkhorn-Knopp*** *Given a matrix* $\mathbf{A} \in {\mathbb{R}_+}^{n \times n}$*, a necessary and sufficient condition that there exists a doubly-stochastic matrix* $\mathbf{S} = \mathcal{D}(\mathbf{r})\mathbf{A}\mathcal{D}(\mathbf{c})$ *with* $\mathbf{r}, \mathbf{c} \in {\mathbb{R}_+^*}^n$*, is that* $\mathbf{A}$ *has a total support. If* $\mathbf{S}$ *exists then it is unique. Vectors* $\mathbf{r}$ *and* $\mathbf{c}$ *are also unique up to a scalar multiple if and only if* $\mathbf{A}$ *is bi-irreducible.*

Relations with the Connectivity of the Adjacency Graph. We now introduce the definition of irreducibility, that draws a link between the connectivity of a network and the pattern of its adjacency matrix.

Definition 3. ***Irreducibility:*** *A matrix* $\mathbf{A} \in \mathbb{R}^{n \times n}$ *is called irreducible if there is no permutation matrix* $\mathbf{Q}$ *such that:*

$$\mathbf{QAQ}^T = \begin{bmatrix} \mathbf{A}_1 & \mathbf{A}_{1,2} \\ 0 & \mathbf{A}_2 \end{bmatrix}$$

with $\mathbf{A}_1, \mathbf{A}_2$ *square and non empty. A characterisation of irreducible matrices from [28] is that they are the adjacency matrices of strongly connected graph.*

Every bi-irreducible matrix is also irreducible. Reciprocally, if a matrix is irreducible with a zero-free main diagonal—$a_{i,i} \neq 0, \forall i \in \{1, ..., n\}$—, then this matrix is bi-irreducible (easily proved by applying the algorithm from [29] to such a matrix). Since definition 3 states that irreducible matrices are adjacency matrices of strongly connected graphs, then the adjacency matrix of every strongly connected graph can be made bi-irreducible (thus scalable) by ensuring that its diagonal is strictly positive (e.g. by adding a positive diagonal matrix to the adjacency matrix, which is equivalent to adding self-loop to the graph).

Remark 1. *For an undirected graph, adding a diagonal matrix to its adjacency matrix is sufficient to make it scalable onto a doubly-stochastic graph, whatever its connectivity. Indeed, every symmetric matrix with a zero-free main diagonal has a total support (Lemma 3.3 from [30]).*

For a directed graph, each strongly connected component must be scaled and partitioned apart[1]*. These components can be found by applying the Dulmage-*

[1]This means that nodes from different strongly connected components cannot end within a same community.

Algorithm 1: Preprocessing Undirected Graphs

Data: A symmetric matrix $\mathbf{A} \in \mathbb{R}_+^{n \times n}$.
Result: A doubly-stochastic matrix $\mathbf{S} \in \mathbb{R}_+^{n \times n}$.
$\varepsilon \leftarrow 10^{-8} \times \min_{i,j:a_{i,j} \neq 0}(a_{i,j})$;
$\mathbf{S} = symscalone(\mathbf{A} + \varepsilon \mathbf{I})$;

Algorithm 2: Preprocessing Directed Graphs

Data: A non-symmetric matrix $\mathbf{A} \in \mathbb{R}_+^{n \times n}$.
Result: A doubly-stochastic matrix $\mathbf{S} \in \mathbb{R}_+^{p \times p}$, with $p \leq n$.
$\mathbf{B} \leftarrow$largest block returned by $dmperm(\mathbf{A} + \mathbf{I})$;
$\varepsilon \leftarrow 10^{-8} \times \min_{i,j:b_{i,j} \neq 0}(b_{i,j})$;
$\mathbf{S} = RAS(\mathbf{B} + \varepsilon \mathbf{I})$;

Mendelsohn decomposition on the graph adjacency matrix whose diagonal has been made zero-free [29].

4.2. The Preprocessing

We propose to apply a doubly-stochastic scaling on networks as a preprocessing for community detection. As discussed in section 4.1, some requirements have to be fulfilled to ensure that the network can be scaled, which depend on whether the graph is directed. The steps to follow to scale a matrix $\mathbf{A} \in \mathbb{R}_+^{n \times n}$ are described in algo. 1 if $\mathbf{A}$ is the adjacency matrix of an undirected graph, respectively in algo. 2 if the adjacency graph of $\mathbf{A}$ is directed.

In algo. 1, *symscalone* is the method from [31] that can compute a doubly-stochastic scaling of a general square matrix with total support. It is particularly well designed for symmetric matrices, in particular, as it preserves the matrix symmetry. In algo. 2, *dmperm* is the Dulmage-Mendelsohn decomposition, evoked in remark 1. When applied to $\mathbf{A} + \mathbf{I}$, it returns the strongly connected components of the adjacency graph of $\mathbf{A}$. The largest component is then scaled using the so-called *RAS* or Sinkhorn-Knopp Algorithm [26, 30]. For both directed and undirected networks, the adjacency graph of the doubly-stochastic matrix $\mathbf{S}$ returned by the algorithm is the one on which communities will be further detected. We remark that for directed network, it means that only the largest strongly connected component will be partitioned. However, this is straightforward to extend to the whole graph, by scaling and partitioning each component in turn.

For both algorithms, it is necessary to add entries in the diagonal of the matrix to scale, to ensure that conditions from theorem 1 are verified. We remark that the addition of diagonal elements leaves the community structure intact, as the community structure of a graph is linked to the diagonal block structure of its adjacency matrix, which is not impacted by its diagonal entries.

In our methods, we choose to add very small entries (10^{-8} times the matrix minimum entry) to impact as little as possible the numerical values in the final scaling. This is an empirical choice which is not theoretically justified, and it would be interesting to analyse how these diagonal entries impact the final scaling. We leave this analysis to further work.

4.3. Impact of our Preprocessing

Rationales on Toy Examples. Our intuition that the doubly-stochastic scaling may improve community detection comes from the two toy examples in fig. 1, that we used in section 1 to illustrate the difficulty of detecting some community structures.

Firstly, doubly-stochastic scaling leverages the weight of the edges in small and large communities. One may think at a trivial example, where a simple graph is composed of two disjoint communities of different size $n_1 > n_2$, such that the probability for two nodes in a same community to be linked is equal to p_{in}, for both communities. Then, in average, a node in the large community shares more links with nodes from its community than a node in the small community ($p_{in} \times n_1 > p_{in} \times n_2$). This is not true anymore if we look at the doubly-stochastic scaling of the adjacency matrix. In this case, every node in both communities shares strictly the same amount of edges with nodes from its community, that is 1 by definition of the doubly-stochastic scaling.

Secondly, the doubly-stochastic scaling can rationally be expected to mitigate against an existing imbalance in the direction of edges, because of its so-called vanishing effect. To understand it, we explain the behaviour of doubly-stochastic scaling on $\mathbf{A} = \begin{bmatrix} 1 & 1 \\ 0 & 1 \end{bmatrix}$. This matrix has no total support. Thus, according to theorem 1, it is not amenable to a doubly-stochastic form. Nevertheless, doubly-stochastic scaling algorithms provide scaling factors $\mathbf{r}$ and $\mathbf{c}$ that tend towards $(0, +\infty)^T$ and $(+\infty, 0)^T$ respectively, such that the doubly-stochastic scaling of $\mathbf{A}$ tends towards $\mathbf{S} = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}$, in which the off-diagonal element had vanished [30, 26].

As a matter of fact, our preprocessing indeed improves the detectability of community structures of the toy examples from fig. 1: Louvain algorithm applied directly on the graphs fails to detect their structures; on the other hand, when applied on the preprocessed graphs, it returns their groundtruth community structures, as shown in the right panels of fig. 1.

Food Web of Florida Bay. Here we observe the impact of our preprocessing on the network of trophic dynamics within Florida Bay. In this directed network, a node is a compartment and an edge indicates carbon exchanges—roughly, an edge from node a to node b means that species in compartment a are eaten by species in compartment b. The network contains 128 compartments, that can be divided onto 9 types according to [32], namely Phytoplankton producers, Seagrass and seagrass roots, Microfauna, Macroinvertebrates, Fishes, Birds, Reptiles, Mammals, and Detritus. This type partitioning corresponds

to the network underlying community structure, according to [33]. The largest strongly connected component contains 103 compartments: 11 are Microfauna, 22 Macroinvertebrates, 47 Fishes, 16 Birds, 3 Reptiles, 2 Mammals, and 2 are Detritus.

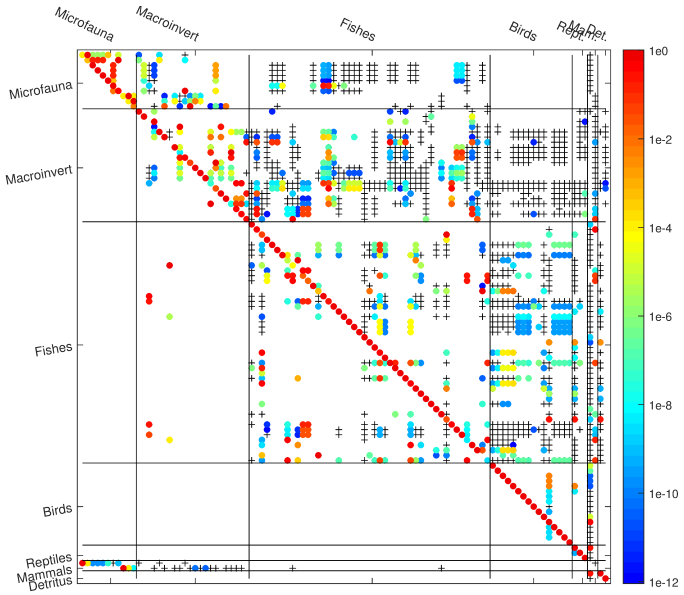


Figure 2: Output of algo. 2 on the Florida Bay network and the groundtruth partitioning.

The matrix $\mathbf{S} \in \mathbb{R}_+^{p\times p}$ returned by algo. 2 is illustrated in fig. 2. The groundtruth community structure is indicated by the black lines. Because numerical values range from 1 to 10^{-82}, only entries higher than 10^{-12} are plotted. Nonzero entries below this threshold are shown by black '+'s. From fig. 2 we observe that the preprocessing clearly tends to make vanish the edges between communities. This is highlighted by the high density of black '+'s in the off-diagonal blocks, meaning that numerous entries in $\mathbf{S}$ off-diagonal blocks have a value that falls below 10^{-12}.

To assess the extent to which the preprocessing indeed sharpens the network community structure, we compare the consistency of these communities on both the raw and the scaled networks, by computing the average strength of node's community membership, for each community. Assuming a matrix $\mathbf{M} \in \mathbb{R}_+^{p\times p}$ and $\mathcal{C}$ its groundtruth community structure. The level to which a node $u \in \{1, ..., p\}$ belongs to a community $C \in \mathcal{C}$ is assessed[2] by $\varphi(u, C) = \dfrac{\sum_{i\in C} m(u,i)}{\sum_{j=1}^{p} m(u,j)}$,

[2] φ is actually the opposite of the so-called mixing parameter introduced in section 6.2.

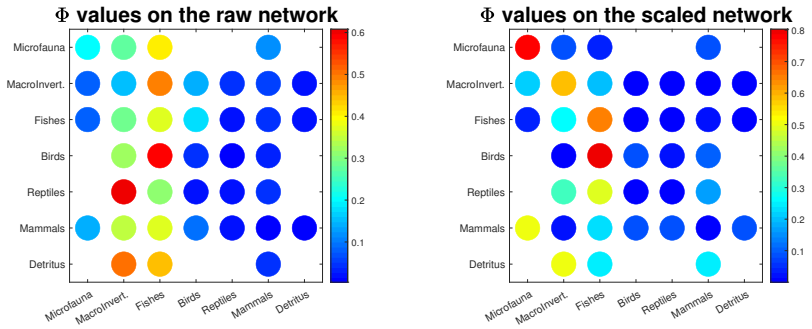


Figure 3: Φ values for the raw network (left) and the scaled network without self-loop (right).

that is the ratio between the amount of edges that node u shares with nodes in C and the degree of u. Thus, the average level to which nodes from community $C \in \mathcal{C}$ belong to community $K \in \mathcal{C}$ is $\Phi(C,K) = \frac{1}{|C|}\sum_{u\in C}\varphi(u,K)$. The higher the reflexive values of Φ, the more consistent the community structure.

We have computed the values of Φ for two matrices that are symmetrisations of the raw and preprocessed directed networks, namely $\mathbf{B}+\mathbf{B}^T$, where $\mathbf{B}$ is the adjacency matrix of the raw network largest strongly connected component; and $\widetilde{\mathbf{S}}+\widetilde{\mathbf{S}}^T$, where $\widetilde{\mathbf{S}}$ is the matrix $\mathbf{S}$ with a zero main diagonal. We remove the diagonal because most of $\mathbf{S}$ diagonal entries are scaled close to 1 (whereas they were initially very small). Thus, keeping the diagonal provides spuriously high values for $\Phi(C,C), \forall C \in \mathcal{C}$, whatever the community structure $\mathcal{C}$.

These values of Φ are displayed in fig. 3. The three last communities that contain no more than 3 nodes are missed by both the raw and the preprocessed matrices. And looking at the structure of these communities restricted to the analysed component in fig. 2, it is indeed not possible to consider them as standalone communities, without having been told so. The community corresponding to the Birds tends to be merged with Fishes by both raw and preprocessed networks. This is also in line with what can be observed from fig. 2. Finally, the three non trivial communities corresponding to Microfauna, Macroinvertebrates and Fishes, are assessed as fairly consistent by the preprocessed network (lowest reflexive value of Φ is 0.58, highest non reflexive value is 0.26). On the other hand, in the raw component, Microfauna and Macroinvertebrates are missed and merged with Fishes. We also remark that the preprocessing has more impact on the consistency of smaller communities—reflexive Φ values are 3.74 times higher in the preprocessed network than in the raw one for Microfauna and Macroinvertebrates, 1.73 for Fishes. These observations illustrate the potential of our preprocessing to increase the detectability of community structures within networks with an imbalance in edge direction between communities, as well as small-scale communities.

5. Generalisation of some Graph Partitioning Measures to Weighted Networks

In this section, we investigate six measures—or criteria—that assess the quality of a community structure on a graph, namely: the Newman-Girvan modularity [6], Balanced modularity [13], the Deviation to Uniformity criterion [34, Chap.5.2.6], the Deviation to Indetermination criterion [13], the Zahn criterion [35] and the Correlation Clustering criterion [36].

This list of graph partitioning measures is not exhaustive. These measures are actually the linear criteria from [34]. Formally, denoting by F a criterion that assesses the quality of a community structure on a graph represented by its adjacency matrix, F is a linear criterion [25] if it can be written as:

$$\begin{array}{rccc} F: & \mathbb{R}^{n\times n} \times Eq(n) & \longrightarrow & \mathbb{R} \\ & (\mathbf{A}, \mathbf{X}) & \mapsto & \sum_{i=1}^{n}\sum_{j=1}^{n} \varphi(a_{i,j})x_{i,j} + K \end{array}, \tag{4}$$

where $\mathbf{A}$ and $\mathbf{X}$ are respectively a graph adjacency matrix and a community structure, $\varphi : \mathbb{R} \to \mathbb{R}$ is a function and K is some constant scalar.

For each criterion, we address three points:

- First we explain quickly the measure background, that is how it works and why it assesses community structures, as well as its formulation.
- Most of these measures were initially designed for unweighted networks, and some have been generalised to weighted graphs afterward. When such a generalisation exists, we may either use it or derive another one that we find more suitable for the community structure detection on doubly-stochastic graphs. We hence discuss the measure generalisation to weighted graphs and especially to doubly-stochastic ones.
- We provide a reduced form for the problem of finding the best community structure on a graph represented by its adjacency matrix $\mathbf{A}$ using a criterion F. Namely, we express the measure as

$$\mathbf{X}^* = \underset{\mathbf{X}\in Eq(n)}{argmax} \left(F(\mathbf{A}, \mathbf{X}) = \sum_{i,j} \left(\phi(a_{i,j}) - \overline{\phi}(a_{i,j})\right) x_{i,j} \right), \tag{5}$$

  where ϕ and $\overline{\phi}$ are two functions in $\mathbb{R}_+$ respectively called the positive and negative agreements, as in [34]. This reduced form allows us to compare the criteria in section 6.

5.1. Newman-Girvan modularity

Principle. The Newman-Girvan modularity introduced in [6] is the most famous graph partitioning measure. The idea behind this criterion is that a community structure in a network actually characterises the property of assortative mixing in this network [37]. The assortative mixing is the tendancy of similar nodes

to draw connection amongst themselves instead than with dissimilar nodes: as an example, in a social network, people who speak the same language or have similar sociological background have more chance to be friends. Hence, given an assortative network, a good community structure is one such that the fraction of edges that connect nodes in a same community is high.

However, this notion cannot be used as a standalone. Indeed, the trivial structure that brings all the nodes in a same community always maximises this fraction of edges. Thus, to derive the modularity, Newman and Girvan also assume that random graphs do not exhibit a community structure [6]. The modularity is hence designed to compare the fraction of intra-community edges in a network with the expected fraction of intra-community edges in random graphs, with the same degree sequence than the initial graph, that is, random graphs generated using the configuration model. In the configuration model of degree sequence $\{d_1, ..., d_n\}$, the probability of an edge between two nodes i and j is approximated by $d_i d_j / 2m$. The modularity is thus defined as:

$$F_{NG}(\mathbf{A}, \mathcal{C}) = \sum_{C \in \mathcal{C}} \sum_{i \in C} \sum_{j \in C} \left(\frac{a_{i,j}}{2m} - \frac{d_i d_j / 2m}{2m} \right),$$

with $\mathbf{A}$ the adjacency matrix of the network, and $\mathcal{C}$ a community structure. In turn, this can be re-written (as in [38]):

$$F_{NG}(\mathbf{A}, \mathbf{X}) = \frac{1}{2m} \sum_{i,j} (a_{i,j} - \frac{d_i d_j}{2m}) x_{i,j}, \tag{6}$$

with $\mathbf{X} \in Eq(n)$ the matrix representation of community structure $\mathcal{C}$.

Generalisation. The modularity measure from [6] was initially designed for unweighted graphs only. Later in [38], Newman proposed two steps to generalise modularity to weighted graphs. First, he investigates multi-graphs, that are simple networks in which two vertices can share more than one simple edge, as in fig. 4. Newman generalises some basics from simple networks to multi-graphs to derive an adapted modularity. Namely, let $\mathbf{A} \in \mathbb{N}^{n \times n}$ be a multi-graph adjacency matrix: 1) The degree d_i of a vertex i in the multi-graph is the number of simple edges adjacent to i: $d_i = \sum_k a_{i,k}$. 2) The constant $2m$ becomes the

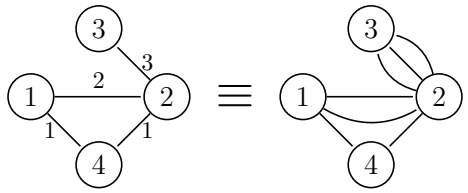


Figure 4: A weighted graph with non-negative integer edges and the corresponding mutligraph.

sum over the degrees, that is $2m = \sum_i d_i$. With these simple adaptations of degrees and edge number, Newman generalises the modularity by simply applying eq. (6) to multi-graphs, with $a_{i,j}$, d_i and $2m$ as defined above.

Secondly, modularity is extended from multi-graphs to non-negative weighted graphs with the following idea: Given a graph whose adjacency matrix can be written as $\mathbf{A} = \alpha\mathbf{N}$, with $\alpha \in \mathbb{R}_+$ and $\mathbf{N} \in \mathbb{N}^{n\times n}$, and considering $d_i = \sum_k a_{i,k}$ and $2m = \sum_i d_i$, then for any $\mathbf{X} \in Eq(n)$, the results of the formula from eq. (6) applied to $\mathbf{A}$ and to $\mathbf{N}$ are equal. Hence, the modularity as defined in eq. (6) can be extended to graphs for which we can find a unit flow—i.e. an α—allowing to consider them as multi-graphs.

We showed in [39, Property 1] that for every square matrix whose entries are rational, a unit flow can be found, but that this is not true for any weighted matrix. However, we also provide [39, Property 2] a proof that eq. (6) can be extended more generally for any undirected weighted graph with positive weights[3]. We will thus directly apply eq. (6) to doubly-stochastic matrices in the following.

Reduced Form. Given an adjacency matrix $\mathbf{A}$, finding the best community structure in the sense of the Newman-Girvan modularity provided in eq. (6) is equivalent to maximising the function

$$\mathbf{X} \mapsto F_{NG}(\mathbf{A}, \mathbf{X}) = \sum_{i,j}(a_{i,j} - \frac{d_i d_j}{2m})x_{i,j}. \tag{7}$$

This provides the reduced form of eq. (5), with positive and negative agreements equal to respectively $\phi(a_{i,j}) = a_{i,j}$ and $\overline{\phi}(a_{i,j}) = d_i d_j/2m$.

Moreover, for a doubly-stochastic graph, we have $\forall i, d_i = 1$ and $2m = n$. Thus, for a doubly-stochastic matrix $\mathbf{S}$, we can simplify the Newman-Girvan modularity as

$$\mathbf{X} \mapsto F_{NG}(\mathbf{S}, \mathbf{X}) = \sum_{i,j}(s_{i,j} - \frac{1}{n})x_{i,j}, \tag{8}$$

and the negative agreement $\overline{\phi}(s_{i,j}) = 1/n$ does not depends on i, j.

5.2. Balanced Modularity

Principle. This criterion has been proposed in [13] to complete the Newman-Girvan modularity. Recall from section 5.1 that, given a simple graph $G = (V, E)$ and a community structure, the Newman-Girvan modularity compares the ratio of edges within communities—i.e. intra-community edges—with the expected ratio of intra-community edges within a random graph that has the same degree sequence than G. Then, the idea behind the Balanced modularity is

[3]Since Newman proposed this extension of modularity to weighted graphs in [38], this measure has been widely applied to any positively valued graph. However, as far as we know, [39] is the first proof that eq. (6) can be consistently applied to such general graphs.

to also take into account the ratio of inter-community edges. In other words, the Newman-Girvan modularity considers that a good community structure on G should have a ratio of intra-community edges "higher than by chance", whereas the Balanced modularity considers that a good community structure should have a ratio of inter-community edges lower than by chance as well.

To take into account the ratio of inter-community edges, the Balanced modularity focuses on the complementaries of the graph and the community structure. We can state its concept as follows:

Let us denote by $\Phi : \mathbb{R}^{n\times n} \times \mathbb{R}^{n\times n} \to \mathbb{R}$ the function such that:

$$\Phi(\mathbf{A}, \mathbf{B}) = \sum_{i,j} \left(a_{i,j} - \frac{\left(\sum_{k=1}^{n} a_{i,k}\right)\left(\sum_{l=1}^{n} a_{j,l}\right)}{\sum_{k=1}^{n}\sum_{l=1}^{n} a_{k,l}} \right) b_{i,j},$$

which is equivalent to the Newman-Girvan modularity from eq. (7) when $\mathbf{A}$ is an adjacency matrix and $\mathbf{B} \in Eq(n)$. Thus, given $\mathbf{A}$ the adjacency matrix of a simple graph and $\mathbf{X}$ a community structure, the Balanced modularity is defined as:

$$F_{BM}(\mathbf{A}, \mathbf{X}) = \Phi(\mathbf{A}, \mathbf{X}) + \Phi(\overline{\mathbf{A}}, \overline{\mathbf{X}}). \tag{9}$$

A simple explicit formula can be derived from eq. (9) by expressing the degrees and number of edges in the complementary of graph, using those of the graph. As it can be indeed observed from fig. 5, we have

$$\begin{cases} \forall i \in \{1, ..., n\}, \overline{d}_i = \sum_{k=1}^{n} \overline{a}_{i,k} = n - d_i \\ \sum_{k=1}^{n} \overline{d}_k = n^2 - \sum_{k=1}^{n} d_i = n^2 - 2m \end{cases}$$

Hence, we can write

$$\begin{aligned} F_{BM}(\mathbf{A}, \mathbf{X}) = & \sum_{i,j} \left(a_{i,j} - \frac{d_i d_j}{2m} \right) x_{i,j} \\ & + \sum_{i,j} \left(\overline{a}_{i,j} - \frac{(n - d_i)(n - d_j)}{n^2 - 2m} \right) \overline{x}_{i,j}, \end{aligned} \tag{10}$$

which is the formula of the Balanced modularity provided in [13].

Generalisation. The Balanced modularity is built on the complementary of the graph, which stands for simple graphs only. However, a generalisation of this criterion to weighted graphs has already been proposed in [25]. It consists in stating that $\overline{a}_{i,j} = \max_{k,l}(a_{k,l}) - a_{i,j} = a_{max} - a_{i,j}$ in eq. (10). But this generalisation does not fit with the spirit of this criterion as stated in eq. (9), because it does not update $\overline{d}_i$ and $\sum_k \overline{d}_k$ according to the new definition of $\overline{\mathbf{A}} = a_{max}\mathbf{J} - \mathbf{A}$ in the second sum in eq. (10). That is, it does not inject the weighted generalisation of $\overline{\mathbf{A}}$ in eq. (9).

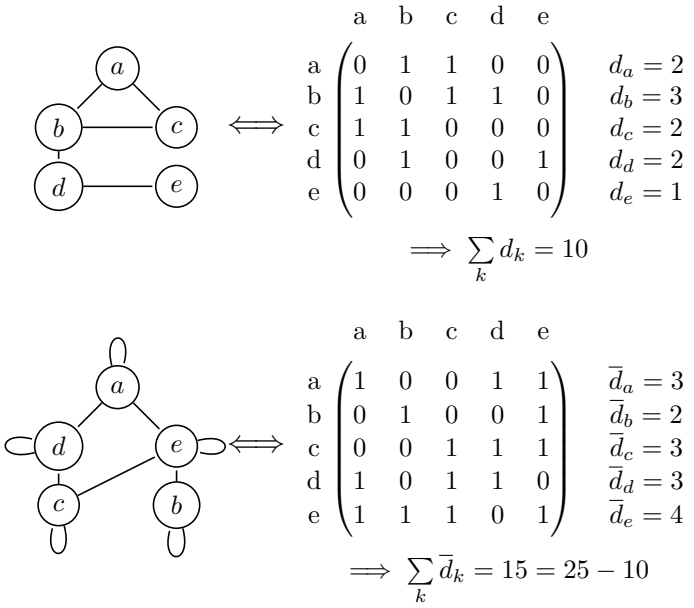


Figure 5: Top: A simple graph and its adjacency matrix. Bottom: the corresponding complementary graph and its adjacency matrix. Degree of each node is given next to the corresponding row, the sum of degrees lies below the matrices.

Hence, we propose another generalisation. Let us consider that, for a weighted graph defined by its adjacency matrix $\mathbf{A}$, the complementary of $\mathbf{A}$ can be expressed as $\overline{\mathbf{A}} = \alpha \times \mathbf{J} - \mathbf{A}$, with α a scalar (that may depends on $\mathbf{A}$). Thus, the degrees of nodes in the complementary graph are:

$$\begin{cases} \forall i \in \{1, ..., n\}, \overline{d}_i = \sum_{k=1}^{n} \overline{a}_{i,k} = \alpha \times n - d_i \\ \sum_{k=1}^{n} \overline{d}_k = \alpha \times n^2 - \sum_{k=1}^{n} d_i = \alpha \times n^2 - 2m, \end{cases}$$

and by injecting $\overline{\mathbf{A}}$ in eq. (9), the Balanced modularity becomes:

$$\begin{aligned} F_{BM}(\mathbf{A}, \mathbf{X}) = & \sum_{i,j} \left(a_{i,j} - \frac{d_i d_j}{2m} \right) x_{i,j} \\ & + \sum_{i,j} \left((\alpha - a_{i,j}) - \frac{(\alpha \times n - d_i)(\alpha \times n - d_j)}{\alpha \times n^2 - 2m} \right) \overline{x}_{i,j}. \end{aligned} \tag{11}$$

It remains to discuss the value of α. First, we remark that, for $\mathbf{A}$ the adjacency matrix of any simple graph, the graph associated with $\mathbf{A} + \overline{\mathbf{A}}$ is the complete graph with self-loop: it is not possible to add any edge in this graph, that is, all edges are saturated. In a general case, given $\mathbf{A} \in \mathbb{R}_+^{n \times n}$ the adjacency matrix of some positively weighted graph, without any other knowledge on the

graph, we can assume that an edge is saturated if its value is a_{max}, with a_{max} as defined above. In this case, we have $\overline{\mathbf{A}} = a_{max}\mathbf{J} - \mathbf{A}$ as in [25]. This generalised Balanced modularity is provided by setting $\alpha = a_{max}$ in eq. (11), which is slightly different than changing $\overline{a}_{i,j}$ for $a_{max} - a_{i,j}$ in eq (10), as proposed in [25].

For doubly-stochastic graphs, we have an upper-bound for the weight of an edge, which is 1. Indeed, as a doubly-stochastic graph is a 1-regular, positively weighted graph, no edge can have a weight above 1. Hence, 1 is the value that saturates an edge, and we can state $\alpha = 1$ in eq. (11) if the matrix is doubly-stochastic.

Reduced Form. We derive the reduced form for the formula given in eq. (11), as this formula can be used for weighted and simple graphs as well (by setting $\alpha = 1$, it becomes equal to eq. (10) when $\mathbf{A}$ represents a simple graph). Recalling that $\overline{\mathbf{X}} = \mathbf{J} - \mathbf{X}$—or equivalently, $\forall i, j, \overline{x}_{i,j} = 1 - x_{i,j}$—, maximising eq. (11) is equivalent to maximising:

$$F_{BM}(\mathbf{A}, \mathbf{X}) = \sum_{i,j} \left(a_{i,j} + \frac{(\alpha n - d_i)(\alpha n - d_j)}{2\alpha n^2 - 4m} - \frac{\alpha 2m + d_i d_j}{4m} \right) x_{i,j} \ , \tag{12}$$

and the positive and negative agreements for the Balanced modularity in the general case can be stated as respectively $\phi(a_{i,j}) = a_{i,j} + \dfrac{(\alpha n - d_i)(\alpha n - d_j)}{2\alpha n^2 - 4m}$ and $\overline{\phi}(a_{i,j}) = \dfrac{\alpha 2m + d_i d_j}{4m}$.

However, for a doubly-stochastic matrix $\mathbf{S}$, a certain number of simplifications can be done that allow to reduce the formula of eq. (12): with $\alpha = 1$, by remarking that $\forall i, d_i = 1$ and $2m = n$:

$$\begin{aligned} F_{BM}(\mathbf{S}, \mathbf{X}) &= \sum_{i,j} \left(s_{i,j} + \frac{(n - d_i)(n - d_j)}{2n^2 - 4m} - \frac{2m + d_i d_j}{4m} \right) x_{i,j} \\ &= \sum_{i,j} \left(s_{i,j} + \frac{(n-1)^2}{2n^2 - 2n} - \frac{n+1}{2n} \right) x_{i,j} \\ &= \sum_{i,j} \left(s_{i,j} + \frac{n-1}{2n} - \frac{n+1}{2n} \right) x_{i,j} \\ &= \sum_{i,j} \left(s_{i,j} - \frac{1}{n} \right) x_{i,j}, \end{aligned}$$

which allows us to simplify the positive and negative agreements as $\phi(s_{i,j}) = s_{i,j}$ and $\overline{\phi}(s_{i,j}) = \dfrac{1}{n}$, with the latter one that does not depends on i, j.

5.3. Deviation to Uniformity

Principle. This criterion, proposed in [34, Chap.2.5.6], is based on a principle very similar to Newman-Girvan's one. The main conceptual difference between

these two criteria is that, given a graph and a community structure, the Deviation to Uniformity criterion compares the ratio of intra-community edges within the graph with the expected ratio of intra-community edges within δ-regular random graphs, by stating δ as the average degree in the initial graph—whereas the random model in Newman-Girvan modularity has the same degree sequence than the initial graph.

Such a random model corresponds to graphs where edges are uniformly distributed among nodes, and thus the probability that there is an edge between two nodes i and j is equal to $\frac{\sum_k d_k}{n^2}$, where d_ks are the degrees of the nodes in the initial graph. Hence, given $\mathbf{A} \in \mathbb{R}_+^{n \times n}$ the adjacency matrix of some positively weighted graph, and $\mathbf{X} \in Eq(n)$ a community structure, the Deviation to Uniformity can be written as:

$$F_{DU}(\mathbf{A}, \mathbf{X}) = \sum_{i,j} \left(a_{i,j} - \frac{\sum_k d_k}{n^2} \right) x_{i,j} \tag{13}$$

This criterion has been defined for weighted graphs such that those that fall into the scope of this study, so we do not discuss its generalisation.

Reduced Form. The reduced form

$$F_{DU}(\mathbf{A}, \mathbf{X}) = \sum_{i,j} \left(\phi(a_{i,j}) - \overline{\phi}(a_{i,j}) \right) x_{i,j}$$

is directly derived from eq. (13) by stating the positive and negative agreements as respectively $\phi(a_{i,j}) = a_{i,j}$ and $\overline{\phi}(a_{i,j}) = \frac{\sum_k d_k}{n^2}$.

Furthermore, for a doubly-stochastic matrix $\mathbf{S}$, we have $\sum_k d_k = n$ and we can simplify the criterion from eq. (13) as:

$$F_{DU}(\mathbf{S}, \mathbf{X}) = \sum_{i,j} \left(s_{i,j} - \frac{1}{n} \right) x_{i,j}, \tag{14}$$

in which case, the negative agreement becomes $\overline{\phi}(s_{i,j}) = \frac{1}{n}$.

5.4. Deviation to Indetermination

Principle. This criterion, introduced in [13], is based on the principle of indetermination between two categorical variables, that we briefly explain below. Given a set $\mathcal{S}$ of M objects, and P, Q two categorical variables on $\mathcal{S}$. Roughly, a categorical variable indicates the category taken by an object of the set. For instance, the objects can be human beings, and the categories are mother tongues,

or first names, as far as we can consider that each human being has only one mother tongue and only one first name. Formally, we can state:

$$P: \begin{array}{ccc} \mathcal{S} & \to & \{p_1, ..., p_\pi\} \\ u & \mapsto & P(u) \end{array} \quad \text{and} \quad Q: \begin{array}{ccc} \mathcal{S} & \to & \{q_1, ..., q_\sigma\} \\ u & \mapsto & Q(u) \end{array}$$

where $\{p_1, ..., p_\pi\}$ are the categories of variable P—e.g., languages if $P(u)$ is the mother tongue of individual u—, respectively $\{q_1, ..., q_\sigma\}$ the categories of variable Q. We remark that, as a unique category is attributed to each object by a variable, P and Q also represent equivalence relations—e.g., two individuals named *Morgan* are in relation according to Q if the variable Q represents first names. We remark that P and Q can be represented by two matrices $\mathbf{P} \in \{0,1\}^{M \times \pi}$, respectively $\mathbf{Q} \in \{0,1\}^{M \times \sigma}$, such that:

$$\mathbf{P}(u,i) = \begin{cases} 1 & \text{if } P(u) = p_i \\ 0 & \text{otherwise} \end{cases}, \ \mathbf{Q}(u,i) = \begin{cases} 1 & \text{if } Q(u) = q_i \\ 0 & \text{otherwise} \end{cases},$$

which allows us to write the equivalence relations defined by the variables P and Q as $\mathbf{C}^{(p)} = \mathbf{P}\mathbf{P}^T \in Eq(M)$, respectively $\mathbf{C}^{(q)} = \mathbf{Q}\mathbf{Q}^T \in Eq(M)$. We can also derive their contingency table $\mathbf{N} = \mathbf{P}^T\mathbf{Q}$, with

$$n_{i,j} = |\{u \in \mathcal{S} : P(u) = p_i \text{ and } Q(u) = q_j\}|$$

the number of objects with both category p_i from P and category q_j from Q.

Given these matrix notations, we explain below the indetermination between categorical variables. Considering two categorical variables as two equivalence relations—or partitionings—, an interesting problem is to measure their association [40], which is done by comparing the agreements and disagreements between the two variables—these notions are illustrated in table 2.

$P \setminus Q$	$Q(u) = Q(v)$	$Q(u) \neq Q(v)$
$P(u) = P(v)$	agreement	disagreement
$P(u) \neq P(v)$	disagreement	agreement

Table 2: All possible agreement/disagreement relations between two objects u and v according to two categorical variables P and Q.

Indetermination is a special case of association: strictly speaking, one says two variables are indetermined if their number of agreements is equal to the their number of disagreements, that is:

$$\sum_{u,v \in \mathcal{S}} \left(c_{u,v}^{(p)} \times c_{u,v}^{(q)} + \overline{c_{u,v}^{(p)}} \times \overline{c_{u,v}^{(q)}} \right) = \sum_{u,v \in \mathcal{S}} \left(c_{u,v}^{(p)} \times \overline{c_{u,v}^{(q)}} + \overline{c_{u,v}^{(p)}} \times c_{u,v}^{(q)} \right)$$

The notion of indetermination can be generalised to allow one to weight positive and negative cases differently: it might worth to give more weight to objects that are related than to those that are not [41]. Recall that π (respectively σ) is the number of categories for variable P (respectively Q), an interesting

generalisation of indetermination is to weight positive cases with $\pi - 1$ and negative cases with 1 in P, respectively $\sigma - 1$ for positive and 1 for negative cases in Q. This provides the following equality for indetermination:

$$\begin{aligned}(\pi-1)(\sigma-1)\sum_{u,v\in\mathcal{S}} c^{(p)}_{u,v}\times c^{(q)}_{u,v} + \sum_{u,v\in\mathcal{S}} \overline{c^{(p)}_{u,v}}\times\overline{c^{(q)}_{u,v}} = \\ (\pi-1)\sum_{u,v\in\mathcal{S}} c^{(p)}_{u,v}\times\overline{c^{(q)}_{u,v}} + (\sigma-1)\sum_{u,v\in\mathcal{S}}\overline{c^{(p)}_{u,v}}\times c^{(q)}_{u,v}\end{aligned} \tag{15}$$

This choice of weights is special because two categorical variables that verify eq. (15) verify also other properties, e.g. they make vanish the so-called Jansen-Vegelius criterion, one of the most famous association criteria. Besides, eq. (15) is strongly related to another special case of association, called the geometrical independence—see [41] for comparisons and discussions about the different notions of independence and indetermination. From here, we use the term indetermination to speak about the generalised indetermination weighted as in eq. (15).

It has be shown in [41] that eq. (15) can be rewritten using the contingency table $\mathbf{N}$ as

$$\forall i,j : n_{i,j} - \left(\frac{\sum_t n_{i,t}}{\sigma} + \frac{\sum_s n_{s,j}}{\pi} - \frac{M}{\pi\times\sigma}\right) = 0.$$

Thus, for any contingency table $\mathbf{N}\in\mathbb{N}^{p\times q}$, the deviation to indetermination is measured by

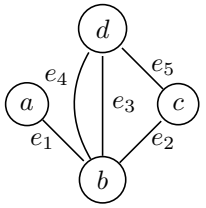
$$\sum_{i,j}\left(n_{i,j} - \frac{\sum_t n_{i,t}}{q} - \frac{\sum_s n_{s,j}}{p} + \frac{\sum_{t,s} n_{t,s}}{p\times q}\right). \tag{16}$$

The Deviation to Indetermination criterion is based on eq. (16), and can be understood as follows: Let $\mathbf{N}\in\mathbb{N}^{p\times p}$ be a contingency table built on two variables with the same categories $\mathbf{P},\mathbf{Q}\in\{0,1\}^{M\times p}$, thus, an equivalence relation $\mathbf{X}\in Eq(p)$ that maximises

$$\sum_{i,j}\left(n_{i,j} - \frac{\sum_t n_{i,t}}{p} - \frac{\sum_s n_{s,j}}{p} + \frac{\sum_{t,s} n_{t,s}}{p^2}\right) x_{i,j} \tag{17}$$

groups together categories such that $\mathbf{P}$ and $\mathbf{Q}$ are highly determined (or far from the indetermination) when restricted to categories from a same group.

The parallel with community structures is done by remarking that a simple or multi-graph can be seen as the contingency table of two categorical variables, whose categories are nodes and which are defined on a set $\mathcal{S}$ consisting in the end nodes of edges. An example is provided in fig. 6. In this figure, the edges of a multi-graph have been named $e_1,...,e_5$, and we define two categorical variables on their end nodes: each edge can be written $e=(u,v)$, where u and v are the end nodes of e, with u the source node ($e(s)$) and v the target node ($e(t)$). As the direction of an edge is immaterial in a undirected graph, the two categorical



$$\iff \quad \mathbf{N} = \left(\begin{array}{c|cccc} & a & b & c & d \\ \hline a & 0 & 1 & 0 & 0 \\ b & 1 & 0 & 1 & 2 \\ c & 0 & 1 & 0 & 1 \\ d & 0 & 2 & 1 & 0 \end{array}\right)$$

$$\mathbf{P} = \left(\begin{array}{c|cccc} & a & b & c & d \\ \hline e_1(s) & 1 & 0 & 0 & 0 \\ e_1(t) & 0 & 1 & 0 & 0 \\ e_2(s) & 0 & 1 & 0 & 0 \\ e_2(t) & 0 & 0 & 1 & 0 \\ e_3(s) & 0 & 1 & 0 & 0 \\ e_3(t) & 0 & 0 & 0 & 1 \\ e_4(s) & 0 & 1 & 0 & 0 \\ e_4(t) & 0 & 0 & 0 & 1 \\ e_5(s) & 0 & 0 & 1 & 0 \\ e_5(t) & 0 & 0 & 0 & 1 \end{array}\right) \quad \text{and} \quad \mathbf{Q} = \left(\begin{array}{c|cccc} & a & b & c & d \\ \hline e_1(s) & 0 & 1 & 0 & 0 \\ e_1(t) & 1 & 0 & 0 & 0 \\ e_2(s) & 0 & 0 & 1 & 0 \\ e_2(t) & 0 & 1 & 0 & 0 \\ e_3(s) & 0 & 0 & 0 & 1 \\ e_3(t) & 0 & 1 & 0 & 0 \\ e_4(s) & 0 & 0 & 0 & 1 \\ e_4(t) & 0 & 1 & 0 & 0 \\ e_5(s) & 0 & 0 & 0 & 1 \\ e_5(t) & 0 & 0 & 1 & 0 \end{array}\right)$$

Figure 6: A multi-graph is the contingency table of two categorical variables defined on the end nodes of edges.

variables are created by swapping the role of end nodes—e.g. in fig. 6, $\mathbf{P}$ sees e_1 as (a, b), whereas $\mathbf{Q}$ states $e_1 = (b, a)$.

Thus, considering $\mathbf{A} \in \mathbb{N}^{n \times n}$ the adjacency matrix of some multi-graph as the contingency table of two such variables, one can look for the community structure that groups together the nodes such that these two categorical variables are highly determined on these nodes. Roughly, given such a group of nodes, it means most of the edges have either both or none of their end nodes in this group. By adapting eq. (17) to the specific case of multi-graphs, we remark that finding such a community structure is equivalent to finding $\mathbf{X} \in Eq(n)$ that maximises:

$$F_{DI}(\mathbf{A}, \mathbf{X}) = \sum_{i,j} \left(a_{i,j} - \frac{d_i}{n} - \frac{d_j}{n} + \frac{\sum\limits_k d_k}{n^2} \right) x_{i,j}. \tag{18}$$

Generalisation. This criterion is naturally defined on mutli-graphs, since we can write them as contingency tables. Using the same trick than for Newman-Girvan modularity, this criterion can be extended to undirected graphs with positive weights, that is, to symmetric matrices in $\mathbb{R}_+^{n \times n}$ by applying eq. (18) by stating that $\forall i \in \{1, ..., n\}, d_i = \sum\limits_k a_{i,k}$.

Reduced Form. To get the reduced form of the Deviation to Indetermination criterion, the formula of eq. (18) can be rewritten as in eq.(5) by choosing the

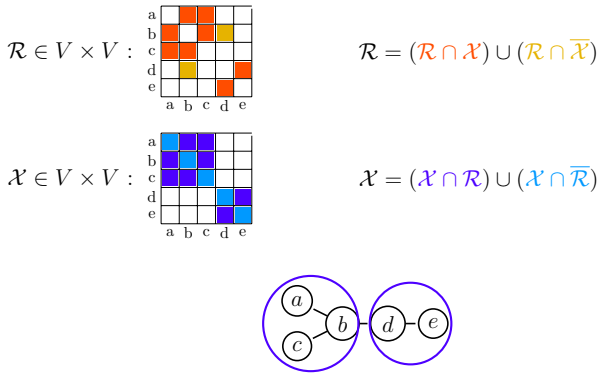


Figure 7: Top: The Zahn 's distance defined between two relations is based on the set representation of these relations. Bottom: A symmetric relation can be seen as a simple graph. An equivalence relation corresponds to a community structure.

positive and negative agreements as respectively

$$\phi(a_{i,j}) = a_{i,j} + \frac{\sum_k d_k}{n^2} \quad \text{and} \quad \overline{\phi}(a_{i,j}) = \frac{d_i + d_j}{n}.$$

Besides, for a doubly-stochastic matrix $\mathbf{S}$, simplifications can be done. Indeed, by remarking that, in this case, $\forall i, d_i = 1$ and $\sum_k d_k = n$, we can rewrite eq. (18) as:

$$F_{DI}(\mathbf{S}, \mathbf{X}) = \sum_{i,j} \left(s_{i,j} - \frac{1}{n} \right) x_{i,j}, \tag{19}$$

and the positive and negative agreements become respectively $\phi(s_{i,j}) = s_{i,j}$ and $\overline{\phi}(s_{i,j}) = 1/n$, the latter not depending on i, j.

5.5. Zahn Criterion

Principle. Strictly speaking, the Zahn criterion does not assess the consistency of a community structure on a given network. However, it can be straightforwardly extended to such a purpose, as we will see.

The Zahn criterion has been designed to compare two relations over a set of objects [35]. More precisely, given a finite set V and a symmetric relation $\mathcal{R}$ over this set (that is $\forall (u, v) \in V \times V$, $\mathcal{R}$ verifies $u\mathcal{R}v \iff v\mathcal{R}u$), Zahn aims to find the equivalence relation $\mathcal{X}$ which is the closest to $\mathcal{R}$. To this aim, Zahn designs a distance between two relations by considering both relations as subsets of the cardinal set $V \times V$, and counting the number of pairs that belong to only one subset. An example is provided in the top panel of fig. 7, where the symmetric relation $\mathcal{R}$ and the equivalence relation $\mathcal{X}$ are defined on a set $V = \{a, b, c, d, e\}$. They are represented as subsets of $V \times V$ by grids, where a coloured case means that the two corresponding objects are related. For instance, by looking at the row of object a in the grids, we see that $a\mathcal{R}b$

and $a\mathcal{R}c$ for $\mathcal{R}$, and $a\mathcal{X}a$, $a\mathcal{X}b$, and $a\mathcal{X}c$ for relation $\mathcal{X}$. This can be rewritten $(a,b),(a,c) \in \mathcal{R}$ and $(a,a),(a,b),(a,c) \in \mathcal{X}$. In both grids, the dark coloured cells correspond to pairs of objects that belong to both relations and the light ones are pairs that lie in only one subset.

With this matching between the relations defined on a set V and the subsets of $V \times V$, we can write the distance defined by Zahn:

$$d_Z(\mathcal{R},\mathcal{X}) = |\overline{\mathcal{X}} \cap \mathcal{R}| + |\overline{\mathcal{R}} \cap \mathcal{X}|, \tag{20}$$

with $\mathcal{R}$ a symmetric relation, and $\mathcal{X}$ an equivalence relation.

In [34], it is proposed to use this criterion to assess community structures on simple graphs, by remarking that a simple graph can be characterised by a symmetric relation over the finite set of its nodes, and a community structure on this graph is an equivalence relation over the graph nodes as well. The bottom panel of fig. 7 illustrates the relations $\mathcal{R}$ and $\mathcal{X}$ as respectively a graph and a community structure. Zahn's distance is also rewritten in [34] to get a matrix-oriented formulation of this criterion: by denoting $\mathbf{A}$ the adjacency matrix of the simple graph associated with the symmetric relation $\mathcal{R}$, respectively $\mathbf{X}$ the matrix representation of the equivalence relation $\mathcal{X}$, we remark:

$$\begin{aligned}\mathcal{R} \cap \overline{\mathcal{X}} &= \{(i,j) \in V \times V : a_{i,j}(1-x_{i,j}) \neq 0\} \\ \mathcal{X} \cap \overline{\mathcal{R}} &= \{(i,j) \in V \times V : x_{i,j}(1-a_{i,j}) \neq 0\}\end{aligned}$$

Hence we can rewrite the Zahn's distance with the formula

$$d_Z(\mathbf{A},\mathbf{X}) = \frac{1}{2}\sum_{i,j}(a_{i,j}\overline{x}_{i,j} + x_{i,j}\overline{a}_{i,j}). \tag{21}$$

When used for community detection, the Zahn criterion is often stated as equivalent to the so-called Condorcet criterion [34]. However, in [39, Chap.1.1.3], we found that the Condorcet criterion cannot be extended to the problem of finding the best community structure given a graph.

Finally, we observe that the criterion of eq. (21) defines a distance in the formal mathematical sense (i.e., it is positive, symmetric, separable and verifies the triangle inequality). We note that this does not hold anymore for any generalisation we present below.

Generalisation. As we have seen, Zahn's distance, which is originally designed for comparing relations over a finite set, is straightforward to extend to simple graphs and their community structures. On the other hand, its generalisation to weighted graphs is not as straightforward since there is no trivial matching between a weighted graph and a symmetric relation.

However, a generalisation of Zahn's criterion to weighted graphs has already been proposed in [25]. It is directly derived from eq. (21) by defining the complementary of the real-valued matrix $\mathbf{A}$ as $\overline{\mathbf{A}} = a_{max}\mathbf{J} - \mathbf{A}$, with $a_{max} = \max_{i,j}(a_{i,j})$. This leads to the criteria

$$d^{\omega}_{Z,1}(\mathbf{A},\mathbf{X}) = \frac{1}{2}\sum_{i,j}\big(a_{i,j}(1-x_{i,j}) + x_{i,j}(a_{max}-a_{i,j})\big). \tag{22}$$

Nevertheless, we propose other generalisations, as this one does not always seem suitable. Indeed, our initial rationale for generalising criteria to weighted graphs is to enable the application of these criteria on doubly-stochastic scalings of graphs. Assume our initial graph is a simple graph, associated with a symmetric relation $\mathcal{R}$ over the set of nodes, and let us call $\mathbf{A}$ the adjacency matrix of the doubly-stochastic scaling of this graph, and $\mathbf{X}$ some community structure. Then, given Zahn's criterion as defined in eq. (22):

- There is an imbalance between the impact on the criterion of pairs in $\mathcal{R} \cap \overline{\mathcal{X}}$ and in $\mathcal{X} \cap \overline{\mathcal{R}}$: a pair in $\overline{\mathcal{R}} \cap \mathcal{X}$ always results in a penalisation of the criterion equal to a_{max}, whereas a pair in $\mathcal{R} \cap \overline{\mathcal{X}}$ results in a penalisation equal to $a_{i,j} \leq a_{max}$. Hence, each pair in $\overline{\mathcal{R}} \cap \mathcal{X}$ penalises the criterion equally to the highest penalisation that can be reached by a pair in $\mathcal{R} \cap \overline{\mathcal{X}}$.
- Except for pairs (i, j) such that $a_{i,j} = a_{max}$, every pair that lies in $\mathcal{X} \cap \mathcal{R}$ penalises the criterion.

We believe that these two bullet points are non desirable aspects of the previous generalisation of Zahn criterion. For this reason, we propose other generalisations. As authors of [25], we choose generalisations that simply redefine the complementary of $\mathbf{A}$ in eq. (21). That is, we define the generalised criterion as

$$d_Z^{\omega}(\mathbf{A}, \mathbf{X}) = \sum_{i,j} \left(a_{i,j}(1 - x_{i,j}) + x_{i,j}(\alpha - a_{i,j}) \right), \tag{23}$$

with α some constant to set up. We have found that choosing α as the mean element of the matrix $\mathbf{A}$, that is, $\alpha = a_{mean}$, was a good trade-off to mitigate against the two drawbacks listed above, indeed:

- Each element in $\overline{\mathcal{R}} \cap \mathcal{X}$ penalises the criterion with the value a_{mean}.
- An element in $\mathcal{X} \cap \mathcal{R}$ penalises the criterion only if its value is below a_{mean}. Otherwise it even favours the criterion.

We consider two possible definitions of $\alpha = a_{mean}$, namely:

$$a_{mean} = \frac{1}{n^2} \sum_{i,j} a_{i,j}, \quad \text{and} \tag{24}$$

$$a_{mean} = \frac{1}{nnz} \sum_{i,j} a_{i,j}. \tag{25}$$

We denote by $d_{Z,2}^{\omega}$ the criterion from eq. (23) obtained with $\alpha = a_{mean}$ from eq. (24), respectively $d_{Z,3}^{\omega}$ the one obtained using $\alpha = a_{mean}$ from eq. (25).

A toy example of the different behaviours of $d_{Z,1}^{\omega}$, $d_{Z,2}^{\omega}$ and $d_{Z,3}^{\omega}$ is illustrated fig. 8. This figure shows a weighted graph with two disjoint components, where each component is a clique with its unique own edge value. In red and in blue, two community structures are proposed, that we denote respectively $\mathbf{X}_r$

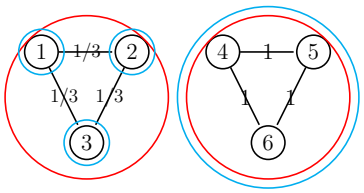


Figure 8: A weighted graph and two community structures.

and $\mathbf{X}_b$. The criterion from eq (22) has a smaller value for $\mathbf{X}_b$ than for $\mathbf{X}_r$ ($d^{\omega}_{Z,1}(\mathbf{A}, \mathbf{X}_r) = 5$; $d^{\omega}_{Z,1}(\mathbf{A}, \mathbf{X}_b) = 4$). This means that $\mathbf{X}_b$ is a community structure that better approximates the groundtruth structure of the graph than $\mathbf{X}_r$ according to this criterion. On the other hand, the criterion $d^{\omega}_{Z,2}$ states that $\mathbf{X}_r$ is better than $\mathbf{X}_b$ ($d^{\omega}_{Z,2}(\mathbf{A}, \mathbf{X}_r) = -2$; $d^{\omega}_{Z,2}(\mathbf{A}, \mathbf{X}_b) \sim -0.7$), which may be a more desirable situation. Finally, $d^{\omega}_{Z,3}$ considers the two structures as equivalent ($d^{\omega}_{Z,3}(\mathbf{A}, \mathbf{X}_r) = d^{\omega}_{Z,3}(\mathbf{A}, \mathbf{X}_b) = 2$).

Remark 2. *With both generalisations from eq (23) using $\alpha = a_{mean}$, negative values are possible, and the symmetry is not preserved ($d_Z(\mathbf{A}, \mathbf{X}) \neq d_Z(\mathbf{X}, \mathbf{A})$), whereas eq (22) ensures the positivity of the results and preserves the symmetry, since $\forall \mathbf{X} \in Eq(n), x_{max} = 1$.*

Reduced form. We now aim to find formulations of eqs. (21), (22) and (23) that fit with the reduced form from eq. (5). We first remark that, given $\mathbf{A}$ the adjacency matrix of some graph, the Zahn criterion $d_Z(\mathbf{A}, .)$ is an objective function that one aims to minimise, whereas in eq. (5), the criterion must be a function to maximise. Hence, we express the opposite of d_Z and remark that minimising the function given in eq (21) is equivalent to maximising:

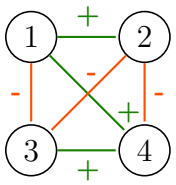
$$\mathbf{X} \mapsto F_Z(\mathbf{A}, \mathbf{X}) = \sum_{i,j} \left(a_{i,j} - \frac{1}{2} \right) x_{i,j}. \tag{26}$$

For unweighted graphs, the positive and negative agreements of the Zahn's criterion are thus respectively $\phi(a_{i,j}) = a_{i,j}$ and $\overline{\phi}(a_{i,j}) = 1/2$.

For weighted graphs, keeping the general formulation of eq. (23), the opposite of d^{ω}_Z produces the following reduced form for Zahn's criterion:

$$F^{\omega}_Z(\mathbf{A}, \mathbf{X}) = \sum_{i,j} \left(a_{i,j} - \frac{\alpha}{2} \right) x_{i,j}. \tag{27}$$

with $\alpha = \underset{i,j}{max}(a_{i,j})$ for the generalisation of eq. (22) and $\alpha = a_{mean}$ for our proposed generalisation. Moreover, our generalisation on a doubly-stochastic $\mathbf{S}$ implies that $\alpha = 1/n$ when the mean of $\mathbf{S}$ is chosen as defined in eq. (24), respectively $\alpha = n/nnz$ for the mean as in eq. (25). Both negative agreements $\overline{\phi}(s_{i,j}) = 1/2n$ and $\overline{\phi}(s_{i,j}) = n/2nnz$ do not depend on i, j.



$$
\begin{aligned}
E^+ &= \{\{1,2\},\{1,4\},\{3,4\}\} \\
&= \{\{i,j\} : \ell(\{i,j\}) = +\} \\
E^- &= \{\{1,3\},\{2,3\},\{2,4\}\} \\
&= \{\{i,j\} : \ell(\{i,j\}) = -\}
\end{aligned}
$$

Figure 9: In the graph to the left, the green edges are similarities between the nodes they link. The set of these edges is denoted by E^+. The orange edges link nodes that are dissimilar. The set of these edges is E^-.

5.6. Correlation Clustering Criterion

Principle. The Correlation Clustering has been first introduced by Bansal et al. in [36]. Their problem can be stated as follows: given a set of objects such that, for each pair of objects, one knows if the objects are similar or dissimilar, the aim is to find a clustering that "maximises agreements", or equivalently "minimises disagreements". They model the set of objects as a complete graph such that each pair of nodes (objects)—or equivalently, each edge—has a label "+" if objects are similar, and a label "-" if objects are dissimilar (see fig. 9), and give a formal definition of maximising agreements/minimising disagreements:

- Maximising agreements means finding a clustering with both as many edges labelled "+" having end nodes in a same cluster as possible, and as many edges labelled "-" with end nodes in different clusters as possible. With notations from fig. 9, it means solving:

$$
\underset{\mathbf{X} \in Eq(n)}{argmax} \left(\sum_{\{i,j\} \in E^+} x_{i,j} + \sum_{\{i,j\} \in E^-} \overline{x}_{i,j} \right).
$$

- Minimising disagreements means finding a clustering with both as few edges labelled "+" with end nodes in different clusters as possible, and as few edges labelled "-" having end nodes in a same cluster as possible. With notations from fig. 9, it means solving:

$$
\underset{\mathbf{X} \in Eq(n)}{argmin} \left(\sum_{\{i,j\} \in E^+} \overline{x}_{i,j} + \sum_{\{i,j\} \in E^-} x_{i,j} \right).
$$

One of the authors' rationales for formalising a clustering problem as a correlation clustering problem was that, on the contrary of other clustering methods that used to exist, the correlation clustering problem can be solved without setting the number of clusters in advance. This makes this technique very suitable for community detection, where the number of communities is generally not known [36].

A few years later, Demaine et al. [42] extended the correlation clustering problem to general weighted graphs[4]. Given a weighted, labelled graph $G = (V, E, \Omega, \ell)$ where:

- $\Omega : \begin{array}{ccc} E & \longrightarrow & \mathbb{R}_+ \\ \{i,j\} & \mapsto & \omega(\{i,j\}) \end{array}$ indicates edge weights,
- $\ell : \begin{array}{ccc} E & \longrightarrow & \{+,-\} \\ \{i,j\} & \mapsto & \ell(\{i,j\}) \end{array}$ indicates edge labels,

they focus on a generalised formulation of the "minimising disagreements" problem by looking for

$$\underset{\mathbf{X}\in Eq(n)}{argmin} \left(\sum_{\substack{\{i,j\}\in E \\ \ell(\{i,j\})=-}} \omega(\{i,j\}) x_{i,j} + \sum_{\substack{\{i,j\}\in E \\ \ell(\{i,j\})=+}} \omega(\{i,j\}) \overline{x}_{i,j} \right) \tag{28}$$

In [34], it is proposed to separate positive and negative labels in the weight indicator Ω, that we can formulate as creating two functions Ω^+ and Ω^- such that:

$$\begin{array}{ccccc} \Omega^+ : & E & \longrightarrow & & \mathbb{R}_+ \\ & \{i,j\} & \mapsto & \omega^+(\{i,j\}) = \begin{cases} \omega(\{i,j\}) & \text{if } \ell(\{i,j\}) = +, \\ 0 & \text{otherwise.} \end{cases} \end{array}$$

and

$$\begin{array}{ccccc} \Omega^- : & E & \longrightarrow & & \mathbb{R}_+ \\ & \{i,j\} & \mapsto & \omega^-(\{i,j\}) = \begin{cases} \omega(\{i,j\}) & \text{if } \ell(\{i,j\}) = -, \\ 0 & \text{otherwise.} \end{cases} \end{array}$$

which allows to simplify eq. (28) as:

$$\underset{\mathbf{X}\in Eq(n)}{argmin} \sum_{i,j} \left(\omega^+(\{i,j\}) \overline{x}_{i,j} + \omega^-(\{i,j\}) x_{i,j} \right). \tag{29}$$

By denoting

$$g_{CC}(G, \mathbf{X}) = \sum_{i,j} \left(\omega^+(\{i,j\}) \overline{x}_{i,j} + \omega^-(\{i,j\}) x_{i,j} \right),$$

we remark that minimising $\mathbf{X} \mapsto g_{CC}(G, .)$ is equivalent to minimising a function d_{CC} defined by:

$$\mathbf{X} \mapsto d_{CC}(G, \mathbf{X}) = \sum_{i,j} \left(\omega^-(\{i,j\}) - \omega^+(\{i,j\}) \right) x_{i,j}. \tag{30}$$

[4] Bansal et al. already gave a generalisation for complete weighted graphs whose weights lie in $[-1, 1]$ in [36].

Generalisation. The case of graphs with positive and negative edges is beyond the scope of this study, since we only investigate positively weighted networks. However, in such networks, one can assume that the existence of an edge indicates that its two end nodes are similar. In turn, one can assume that dissimilarities between nodes are indicated by the absence of edges. Hence, we propose to generalise the correlation clustering to positively weighted graphs, by considering that dissimilarity between two nodes is characterised by an absence of edge. For this purpose, we define the pattern of a matrix as the following function:

$$\begin{array}{rccc} \mathcal{P}: & \mathbb{R}^{n\times n} & \longrightarrow & \{0,1\}^{n\times n} \\ & \mathbf{M} & \mapsto & \mathcal{P}(\mathbf{M}) = \mathbf{P}^{\mathbf{M}} \end{array}$$

such that $p_{i,j}^{\mathbf{M}} = \begin{cases} 1 & \text{if } m_{i,j} \neq 0 \\ 0 & \text{otherwise.} \end{cases}$. Hence, given $G = (V, E, \Omega)$ some positively weighted graph and $\mathbf{A} \in \mathbb{R}^{n\times n}$ its adjacency matrix, the absence of edge in G can be characterised by $\mathbf{J} - \mathbf{P}^{\mathbf{A}}$. Thus, denoting by $\lambda > 0$ the penalisation for clustering together nodes that are dissimilar, the correlation clustering from eq. (30) becomes:

$$d_{CC}^{\lambda}(\mathbf{A}, \mathbf{X}) = \sum_{i,j} \left(\lambda \times (1 - p_{i,j}^{\mathbf{A}}) - a_{i,j}\right) x_{i,j}, \tag{31}$$

where $\mathbf{A}$ is the adjacency matrix of some positively weighted graph, and $\mathbf{X}$ a community structure on this graph. Our generalisation of the correlation clustering hence depends on some parameter $\lambda > 0$ to set up.

Remark 3. *When focusing on simple networks, this generalisation of the Correlation Clustering criterion is close to the* LambdaCC *function proposed in [43].*

Remark 4. *Another way to generalise the Correlation Clustering criterion may be to consider that a positively weighted graph is actually a complete graph, where an edge whose weight is equal to 0 is the strongest case of dissimilarity. In this case, one can shift the weights so that the graph has positive and negative values. Given* $\mathbf{A}$ *the adjacency matrix, the most straightforward way to do so is to consider that an edge is a dissimilarity if it is below the mean value of* $\mathbf{A}$*, that is* $\frac{\sum_k d_k}{n^2}$*. In this case, the criterion from eq. (30) becomes:*

$$d_{CC}^{\omega}(\mathbf{A}, \mathbf{X}) = -\sum_{i,j} \left(a_{i,j} - \frac{\sum_k d_k}{n^2} \right) x_{i,j},$$

which is equivalent to the formula of the Deviation to Uniformity criterion developed in Section section 5.3.

Reduced Form. We aim to reduce the formula from eq. (31) to make it fit with eq. (5). As the Correlation Clustering criterion defined at eq. (31) is a criterion

to minimise to obtain the best community structure, we look at its opposite for finding its reduced form, and we observe that minimising d^{λ}_{CC} is equivalent to maximising

$$F^{\lambda}_{CC}(\mathbf{A}, \mathbf{X}) = \sum_{i,j} \left(a_{i,j} - \lambda \times (1 - p^{\mathbf{A}}_{i,j}) \right) x_{i,j}. \tag{32}$$

The positive and negative agreements for this generalised criterion are respectively $\phi(a_{i,j}) = a_{i,j}$ and $\overline{\phi}(a_{i,j}) = \lambda \times (1 - p^{\mathbf{A}}_{i,j})$.

6. Comparison of the Criteria

In this section, we compare the criteria from section 5. In table 3, we recall the reduced formulations of these criteria when applied on simple or doubly-stochastic graphs.

6.1. Homogenisation on doubly-stochastic graphs

The first key result which is directly observed from the table is that, with the doubly-stochastic generalisation, many criteria become equivalent, as stated in theorem 2.

Theorem 2. *Given $\mathbf{S} \in \mathbb{R}^{n \times n}$ the adjacency matrix of some doubly-stochastic graph, and $\mathbf{X} \in Eq(n)$ a community structure, thus*

$$F^{\omega}_{NG}(\mathbf{S}, \mathbf{X}) = F^{\omega}_{BM}(\mathbf{S}, \mathbf{X}) = F^{\omega}_{DU}(\mathbf{S}, \mathbf{X}) = F^{\omega}_{DI}(\mathbf{S}, \mathbf{X})$$

Theorem 2 extends theorem 6.1 from [34], which states that these criteria are equivalent in the case of k-regular simple graphs. Besides, the doubly-stochastic Zahn modularities, while not strictly equivalent to these four criteria, have very similar formulations. Actually, one can draw a parallel between Zahn formulations and the so-called generalised Newman-Girvan modularity, that can be used to mitigate against the so-called resolution limit of the Newman-Girvan modularity—that is, its unability to highlight "small" communities [12]. This function is defined in [44] as the parametrised function:

$$F^{\gamma}_{NG}(\mathbf{A}, \mathbf{X}) = \sum_{i,j} \left(a_{i,j} - \gamma \frac{d_i d_j}{2m} \right) x_{i,j},$$

with $\mathbf{A}$ the adjacency matrix of some simple graph, $\mathbf{X} \in Eq(n)$, and $\gamma > 0$ the parameter. Indeed, in definition 4, we also define a parametrised criterion for the doubly-stochastic version of Newman-Girvan modularity.

Definition 4. *Given $\mathbf{S} \in \mathbb{R}^{n \times n}$ the adjacency matrix of some doubly-stochastic graph, $\mathbf{X} \in Eq(n)$, and $\gamma > 0$ a scalar, the parametrised doubly-stochastic Newman-Girvan modularity is defined as*

$$F^{\omega,\gamma}_{NG}(\mathbf{S}, \mathbf{X}) = \sum_{i,j} \left(s_{i,j} - \frac{\gamma}{n} \right) x_{i,j}.$$

Criteria	If $\mathbf{A}$ represents a Simple Graph	If $\mathbf{S}$ is Doubly-Stochasic
Newman-Girvan Modularity	$F_{NG}(\mathbf{A},\mathbf{X}) = \sum_{i,j}\left(a_{i,j} - \frac{d_i d_j}{2m}\right) x_{i,j}$	$F^{\omega}_{NG}(\mathbf{S},\mathbf{X}) = \sum_{i,j}\left(s_{i,j} - \frac{1}{n}\right) x_{i,j}$
Balanced Modularity	$F_{BM}(\mathbf{A},\mathbf{X}) = \sum_{i,j}\left(a_{i,j} + \frac{(n-d_i)(n-d_j)}{2n^2-4m} - \frac{2m+d_i d_j}{4m}\right) x_{i,j}$	$F^{\omega}_{BM}(\mathbf{S},\mathbf{X}) = \sum_{i,j}\left(s_{i,j} - \frac{1}{n}\right) x_{i,j}$
Deviation to Uniformity	$F_{DU}(\mathbf{A},\mathbf{X}) = \sum_{i,j}\left(a_{i,j} - \frac{2m}{n^2}\right) x_{i,j}$	$F^{\omega}_{DU}(\mathbf{S},\mathbf{X}) = \sum_{i,j}\left(s_{i,j} - \frac{1}{n}\right) x_{i,j}$
Deviation to Indetermination	$F_{DI}(\mathbf{A},\mathbf{X}) = \sum_{i,j}\left(a_{i,j} + \frac{2m}{n^2} - \frac{d_i+d_j}{n}\right) x_{i,j}$	$F^{\omega}_{DI}(\mathbf{S},\mathbf{X}) = \sum_{i,j}\left(s_{i,j} - \frac{1}{n}\right) x_{i,j}$
Zahn Modularity	$F_{Z}(\mathbf{A},\mathbf{X}) = \sum_{i,j}\left(a_{i,j} - \frac{1}{2}\right) x_{i,j}$	$F^{\omega}_{Z,1}(\mathbf{S},\mathbf{X}) = \sum_{i,j}\left(s_{i,j} - \frac{s_{max}}{2}\right) x_{i,j}$ $F^{\omega}_{Z,2}(\mathbf{S},\mathbf{X}) = \sum_{i,j}\left(s_{i,j} - \frac{1}{2n}\right) x_{i,j}$ $F^{\omega}_{Z,3}(\mathbf{S},\mathbf{X}) = \sum_{i,j}\left(s_{i,j} - \frac{n}{2nnz}\right) x_{i,j}$
Correlation Clustering	$F^{\lambda}_{CC}(\mathbf{A},\mathbf{X}) = \sum_{i,j}\left(a_{i,j} - \lambda \times (1 - p^{\mathbf{A}}_{i,j})\right) x_{i,j}$	$F^{\omega,\lambda}_{CC}(\mathbf{S},\mathbf{X}) = \sum_{i,j}\left(s_{i,j} - \lambda \times (1 - p^{\mathbf{S}}_{i,j})\right) x_{i,j}$
Parametrised Modularity	$F^{\gamma}_{NG}(\mathbf{A},\mathbf{X}) = \sum_{i,j}\left(a_{i,j} - \gamma\frac{d_i d_j}{2m}\right) x_{i,j}$	$F^{\omega,\gamma}_{NG}(\mathbf{S},\mathbf{X}) = \sum_{i,j}\left(s_{i,j} - \frac{\gamma}{n}\right) x_{i,j}$

Table 3: Reduced formulations of the different criteria when applied on simple (respectively doubly-stochastic) graphs.

These parametrised versions of the Newman-Girvan modularity have been added to our list of criteria, as the last row of table 3, for both simple and doubly-stochastic graphs. The doubly-stochastic versions of the Zahn criterion can be expressed using definition 4, as stated in property 1.

Property 1. *Given $\mathbf{S} \in \mathbb{R}^{n\times n}$ the adjacency matrix of some doubly-stochastic graph and $\mathbf{X} \in Eq(n)$, the doubly-stochastic Zahn criteria can be expressed as parametrised doubly-stochastic Newman-Girvan modularities, using the following values for the γ parameter:*

- $F^{\omega}_{Z,1}(\mathbf{S},\mathbf{X})$ *is obtained with* $\gamma = \dfrac{n \times s_{max}}{2}$,
- $F^{\omega}_{Z,2}(\mathbf{S},\mathbf{X})$ *is obtained with* $\gamma = \dfrac{1}{2}$,
- $F^{\omega}_{Z,3}(\mathbf{S},\mathbf{X})$ *is obtained with* $\gamma = \dfrac{n^2}{2 \times nnz(\mathbf{S})}$.

Thus, the Correlation Clustering criterion is the unique doubly-stochastic criterion from table 3 that cannot be expressed as a parametrised doubly-stochastic Newman-Girvan modularity. We now provide our main result in result 1.

Result 1. *The generalisation to doubly-stochastic graphs unifies the criteria. Namely, we have two families of parametrised criteria:*

1. *The Newman-Girvan-like ones :*

$$F^{\omega,\gamma}_{NG}(\mathbf{S},\mathbf{X}) = \sum_{i,j}\left(s_{i,j} - \frac{\gamma}{n}\right)x_{i,j}$$

2. *The Correlation Clustering-like ones:*

$$F^{\omega,\lambda}_{CC}(\mathbf{S},\mathbf{X}) = \sum_{i,j}\left(s_{i,j} - \lambda \times (1 - p^{\mathbf{S}}_{i,j})\right)x_{i,j}$$

Each criterion is obtained from one of these generalisations, using a specific parameter.

6.2. Numerical Comparisons

In this section we compare the behaviours of the different criteria to uncover community structures, applied on modular simple graphs on one hand, and their doubly-stochastic preprocessing on the other hand. To that purpose, we will optimise those criteria using the optimisation framework proposed by the Louvain algorithm, as it as been proved possible to do in [25].

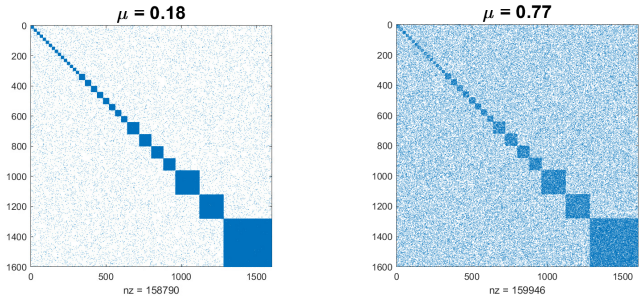


Figure 10: Two instances from the benchmark, built using the pair of probabilities of the first row (left panel) and the last row (right panel) of table 4.

Benchmark. For these numerical experiments, we have built a range of random modular networks, using eight Stochastic Block Models (SBMs). In brief, SBMs are random models for generating networks with some block structure. Generally, the assignations of nodes to blocks and the probabilities of edges within and between blocks are given. Edges are drawn randomly. Models in which intra-block probabilities are higher than inter-block probabilities produce networks with community structures [45]. Each SBM has been used to generate 10 graphs of 1600 nodes, with an average degree equal to 100, and partitioned into 31 blocks: 16 blocks of 20 nodes, 8 blocks of 40 nodes, 4 blocks of 80 nodes, 2 blocks of 160 nodes and one block of 320 nodes. They all have one unique probability of intra-block edge and one unique probability of inter-block edge, denoted respectively by p_{in} and p_{out}. These SBMs differ in the values of parameters p_{in} and p_{out}, which have been chosen so that the community structures of the random graphs become less and less sharp. The sharpness of the community structure has been assessed by the so-called mixing parameter [4]. Initially, the mixing parameter measures the strength of a node's community membership by computing the ratio between its links outside the community and its degree. The greater the mixing parameter for each node, the weaker the community structure. The network mixing parameter μ is the mean value of the nodal mixing parameters [11]. Two instances from our benchmark are illustrated in fig. 10. These are two modular networks generated by the extreme SBMs.

Once that the 80 benchmark graphs had been built using SBMs from the `NetworkX` library[5], we have preprocessed them using algo. 1. The pairs of intra- and inter-edge probabilities p_{in} and p_{out} used in our SBMs are showed in table 4, along with the corresponding theoretical mixing parameters, and the average mixing parameters observed on the simple graphs, and on the doubly-stochastic scaling of these graphs, respectively. All numbers have been multi-

[5] `https://networkx.org/documentation/networkx-2.5/reference/generated/networkx.generators.community.stochastic_block_model.html#networkx.generators.community.stochastic_block_model`

p_{in}	7.32	6.58	5.83	5.09	4.34	3.60	2.86	2.11
p_{out}	0.06	0.13	0.19	0.25	0.31	0.38	0.44	0.5
μ_{theo}	1.79	3.02	3.98	4.81	5.56	6.27	6.97	7.67
$\widetilde{\mu_{bin}}$	1.80	3.04	4.00	4.84	5.58	6.30	6.99	7.69
$\widetilde{\mu_{stoch}}$	1.70	2.91	3.96	4.69	5.43	6.15	6.83	7.53

Table 4: Edge probabilities in each SBMs (p_{in} and p_{out}), theoretical mixing parameters (μ_{theo}), and the observed average mixing parameters on the simple ($\widetilde{\mu_{bin}}$) and preprocessed ($\widetilde{\mu_{stoch}}$) graphs.

plied by 10 to improve readability. We observe that the mixing parameters of doubly-stochastic scalings tend to be slightly below those of the initial simple graphs, and of the theoretical value as well.

Scores. To assess the quality of the community structures returned by Louvain, we compare them to the groundtruth by adapting the definitions of Precision, Recall and F1-score to community detection. Namely, assume we have $\mathbf{X}^* \in Eq(n)$ the groundtruth, and $\widetilde{\mathbf{X}} \in Eq(n)$ a community structure returned by Louvain. We define the number of true positives as the number of pairs of different elements that are put together by both community structures, that is $TP = \sum_{i<j} \widetilde{x}_{i,j} \times x^*_{i,j}$. The number of false positives is the number of pairs that are put together by $\widetilde{\mathbf{X}}$ but not by $\mathbf{X}^*$: $FP = \sum_{i<j} \widetilde{x}_{i,j} \times (1 - x^*_{i,j})$. And the number of false negatives is the number of pairs that are put together by $\mathbf{X}^*$ but not $\widetilde{\mathbf{X}}$, namely $FN = \sum_{i<j} (1 - \widetilde{x}_{i,j}) \times x^*_{i,j}$. Now, we can derive Precision, Recall and F1-score of $\widetilde{\mathbf{X}}$ as usual:

- Precision: $Prec(\widetilde{\mathbf{X}}) = \dfrac{TP}{TP + FP}$
- Recall: $Rec(\widetilde{\mathbf{X}}) = \dfrac{TP}{TP + FN}$
- F1-score: $F1(\widetilde{\mathbf{X}}) = 2 \times \dfrac{Prec(\widetilde{\mathbf{X}}) \times Rec(\widetilde{\mathbf{X}})}{Prec(\widetilde{\mathbf{X}}) + Rec(\widetilde{\mathbf{X}})}$.

Furthermore, since the Louvain algorithm is sensitive to node labelling, we have applied it four times to each network in our benchmark, using a random labelling. Thus, in the following figures, we plot curves whose points are the average score of the 40 returned community structures (10 networks and 4 runs of Louvain). Besides, for each points, these 40 community structures are also summarised by box plots, that indicate the median (white circle with black point), 25th and 75th percentiles (edges of the large box), and extreme values (extrema points of vertical segments).

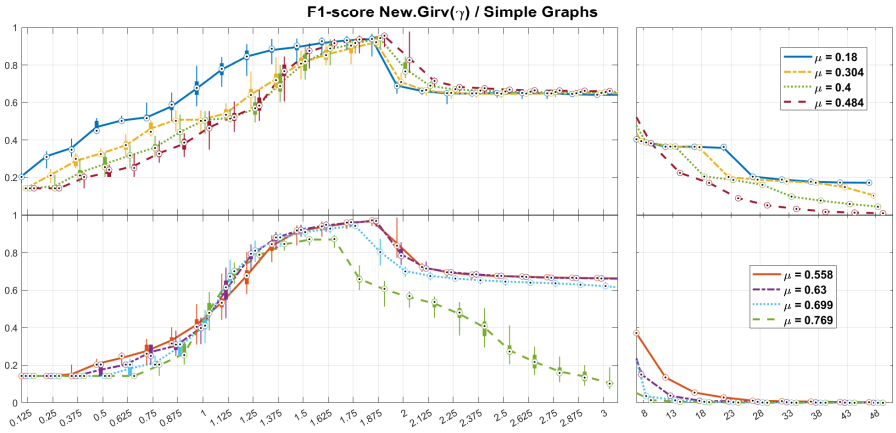


Figure 11: The $F1$-score (y-axis) over γ (x-axis) of the parametrised Newman-Girvan modularity on simple graphs.

Finally, discussions about the number of communities returned by Louvain often help to explain some observations done on the scores. Indeed, as the number of communities is not constrained, Louvain algorithm may find either more or less communities than expected, which will have an impact on Precision and Recall. Thus, we also compare the number of communities returned by Louvain with the expected number (31 in our tests). Formally, given n_c the number of communities in the returned structure $\widetilde{\mathbf{X}}$ we compute:

$$r(\widetilde{\mathbf{X}}) = \begin{cases} n_c/31 & \text{if } n_c \geq 31, \\ 31/n_c & \text{otherwise.} \end{cases}$$

This allows a fairer comparison between the criteria that over- or under-partition the graphs. We indicate that the number of communities is higher (respectively lower) than expected with a "+" (respectively a "-") exponent. When the comparison is done on a bunch of community structures, it may happen that some structures have more communities than expected, while other have less. We indicate such cases with the exponent "*"—see table 5.

Parametrised Newman-Girvan Modularities. We first focus on the behaviours of the parametrised Newman-Girvan modularities, when varying the parameter γ. The $F1$-scores (y-axis) over γ parameters (x-axis) of the Newman-Girvan modularities applied on simple and preprocessed graphs are provided in fig. 11 and 12 respectively. As stated in the legends, each curve corresponds to one mixing parameter value $\widetilde{\mu_{bin}}$ from table 4.

On these figures, we observe that both modularities are able to provide community structures close to the groundtruth for some $\gamma \in [1.25, 2]$. In the right panels, one can also observe that, for very large γ's, $F1$-score tends to 0. This means that, whatever the sharpness of the groundtruth community

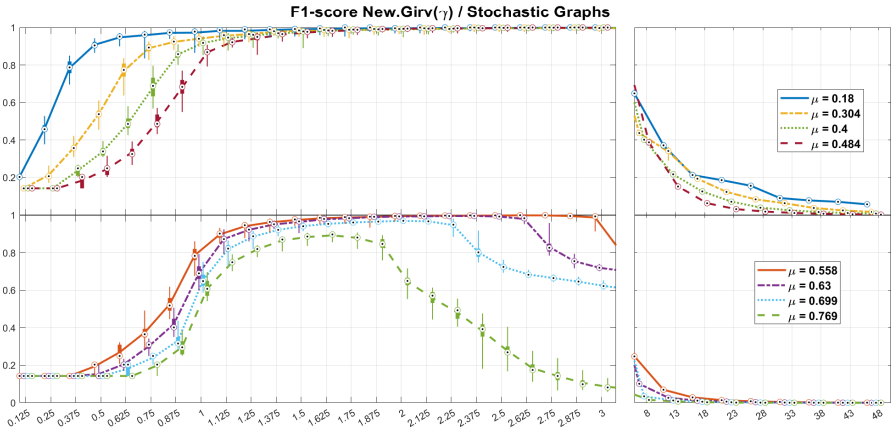


Figure 12: The $F1$-score (y-axis) over γ (x-axis) of the parametrised Newman-Girvan modularity on doubly-stochastic graphs.

structure, it exists some γ beyond which Louvain returns the structure with one community per node. We also observe that the fundamental difference between simple and doubly-stochastic criteria is that the parametrised Newman-Girvan modularity is much more sensitive to γ variations when applied on simple graphs than on doubly-stochastic ones. Indeed, in fig. 11, the $F1$-score curves are quite sharp: for each μ, there is a peak at the γ value that maximises the $F1$-score. Besides, this peak is not located at the same γ across the μ's (1.625 for $\mu = 0.769$, 1.75 for $\mu = 0.699$ and 1.875 for the other values of μ). On the other hand, in fig. 12, the $F1$-score curves are much smoother and the maxima lie along a plateau, whose length depends on the mixing parameter μ. Thus, there is much more chance to pick a γ which will provide a sound community structure for doubly-stochastic scaled graphs than for raw simple ones.

Correlation Clustering Criteria. We now focus on the behaviours of the Correlation Clustering criteria, when varying the parameter λ. As previously, $F1$-scores over λ parameters are provided in fig. 13 and 14, for Louvain algorithm applied on simple and doubly-stochastic graphs, respectively.

This time, criteria on both simple and doubly-stochastic graphs highlight plateaus at their maxima. However, one can observe that these plateaus do not appear for the same parameter values. Indeed, there is a factor 100 between the x-axes of the two figures (on the left panel of fig. 13, x-axis limits are 10/n and 500/n, while these are 1/10n and 50/10n for fig. 14). This observation is consistent with property 2.

Property 2. *Given* $\mathbf{A}$ *the adjacency matrix of a simple graph, and* $\lambda > nnz(\mathbf{A})/2$. *Assume that* $\mathbf{X}^* = \underset{\mathbf{X} \in Eq(n)}{argmax} \; F^{\lambda}_{CC}(\mathbf{A}, \mathbf{X})$. *Thus*

$$\forall i \neq j, a_{i,j} = 0 \implies x^*_{i,j} = 0.$$

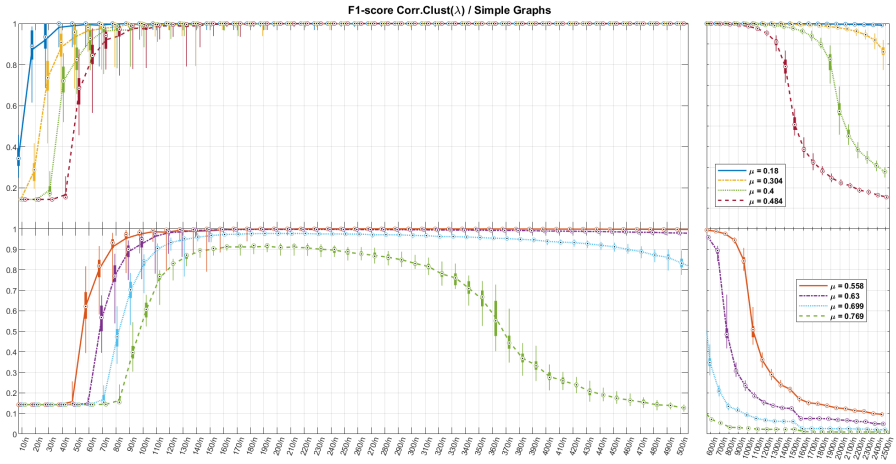


Figure 13: The $F1$-score (y-axis) over λ (x-axis) of the Correlation Clustering criterion on simple graphs.

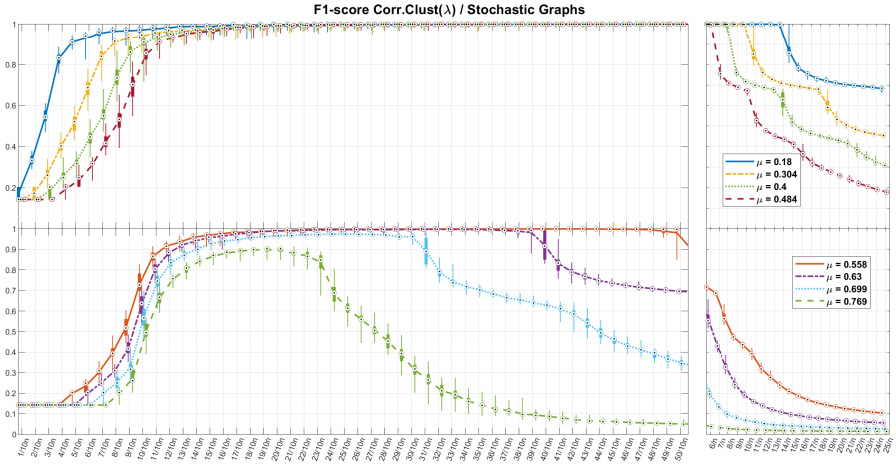


Figure 14: The $F1$-score (y-axis) over λ (x-axis) of the Correlation Clustering criterion on doubly-stochastic graphs.

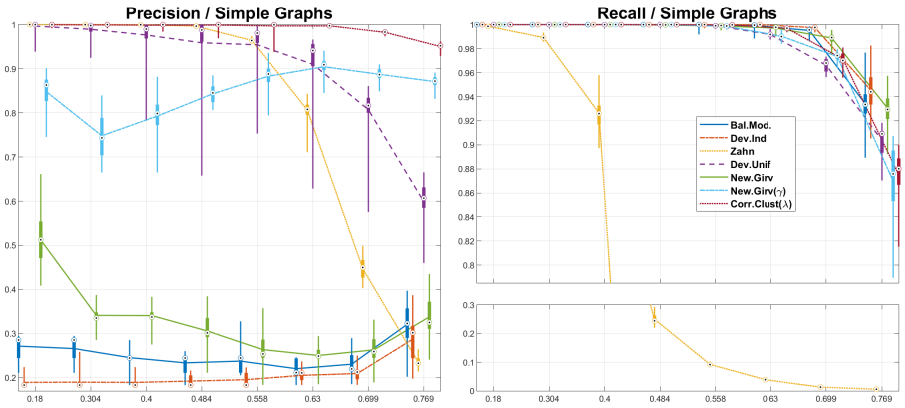


Figure 15: Precision and Recall (y-axes) of all the criteria to be applied on simple graphs, over the mixing parameters (x-axes).

Respectively, if $\mathbf{S} \in \mathbb{R}^{n \times n}$ *is doubly-stochastic, and* $\lambda_\omega > n/2$*, thus* $\mathbf{X}^* \in Eq(n)$ *that maximises* $F_{CC}^{\omega,\lambda_\omega}(\mathbf{S}, .)$ *is such that*

$$\forall i \neq j, s_{i,j} = 0 \implies x^*_{i,j} = 0.$$

690

Proof. Straightforward by adapting the proof from [39, Property 8]. □

This property states that, for large values of the λ parameter, in the community structure that optimises the Correlation Clustering criterion, each community must be a clique of the graph. In our benchmark, this strong constraint
695 implies that, for such λ values, the optimal community structure does not fit the groundtruth one. Thus, in property 2, λ and λ_ω provide an upper bound beyond which the Correlation Clustering criterion is not able to resolve the groundtruth community structure when applied on simple (respectively doubly-stochastic) graphs from our benchmark. As our networks have been built with an average
700 degree equal to 100, we have that $\lambda \approx 100 \times \lambda_\omega$, which is consistent with the differences of x-axes between fig. 13 and 14.

Finally, we remark that, opposite to our observations on Newman-Girvan modularities, maximum plateaus are smoother for simple graphs.

All Criteria on Simple Graphs. In this paragraph, we compare the different
705 behaviours of all the criteria designed for simple graphs. Recall and Precision are displayed in fig. 15. The parameters for the Correlation Clustering and the parametrised Newman-Girvan criteria are $\lambda = 210/n$ and $\gamma = 1.625$, respectively. They have been chosen so that the average $F1$-score is maximised over all the mixing parameters.

710 From the right panel, we observe that, except Zahn criterion, all the measures return high scores of Recall (all above 0.8 even for the largest mixing parameter).

This is consistent with the fact that, except when used with the Zahn criterion, the Louvain algorithm tends to return structures with less communities than expected, when applied on simple graphs, as it can be seen from -highlighted cells in table 5. Thus, some of the groundtruth communities are merged into the returned ones. And a high value of Recall means that the returned communities tend to cover the groundtruth ones. On the other hand, Louvain with Zahn criterion returns almost 5 times more communities than expected when $\mu = 0.484$, and this ratio keeps increasing with μ, which explains the slump of this criterion Recall curve. This was an expected result, since it has been shown in [34] that the community structure which maximises the Zahn criterion is such that subgraphs induced by each community must be 1/2-dense. Looking at the values of p_{in} and p_{out} from table 4, groundtruth communities are expected to respect this property up to $\mu = 0.484$, included. However, Louvain algorithm only finds an approximate of the best community structure for the criterion, which explains why the slump starts at $\mu = 0.484$ in our tests.

When looking at the left panel, we can roughly divide the remaining measures into two categories: the Balanced Modularity, the Deviation to the Indetermination and the Newman-Girvan modularity, that exhibit low Precision scores, and the Deviation to the Uniformity, the Correlation Clustering criterion and the parametrised Newman-Girvan modularity that exhibit much better Precision values. Once again, this is consistent with the ratio of the number of communities returned by Louvain, highlighted in table 5. Indeed, low Precision values are expected when groundtruth communities are merged into the returned ones. And from -highlighted cells in table 5, one can remark that the tendency of Louvain algorithm to provide less communities than expected is emphasised for the criteria with lower Precision scores.

Finally, one can focus on the somehow strange shape of the parametrised Newman-Girvan modularity, that achieves its minimum for the second smallest value of mixing parameter. As we observed in fig. 11, the parameter value γ that maximises the $F1$-score is not consistent over all the mixing parameters. Thus our choice of γ, which is a trade-off between the mixing parameters, clearly disadvantages the first mixing parameters.

All Criteria on Doubly-Stochastic Graphs. Here, we discuss the behaviours of all the criteria for doubly-stochastic graphs. The parameters for the Correlation Clustering criterion is $\lambda = 20/10n$; and $\gamma = 1.75$ for the parametrised Newman-Girvan modularity. As previously, the parameters have been chosen to maximise the average $F1$-score over mixing parameters. Recall and Precision are displayed in fig. 16. From the Recall curves on the right panel, we observe three different behaviours. First, we remark that two of the three versions of the Zahn criteria ($F^{\omega}_{Z,1}$ and $F^{\omega}_{Z,3}$) exhibit very low Recall values, even for the smallest mixing parameter. From -highlighted cells in table 5, it can be seen that, for $\mu = 0.18$, Louvain used with $F^{\omega}_{Z,1}$ returns in average almost 47 times more communities than expected. Recalling that there are 31 groundtruth communities for 1600 nodes in the networks from our benchmark, this means that, in the community structure returned by this version of Louvain, a community

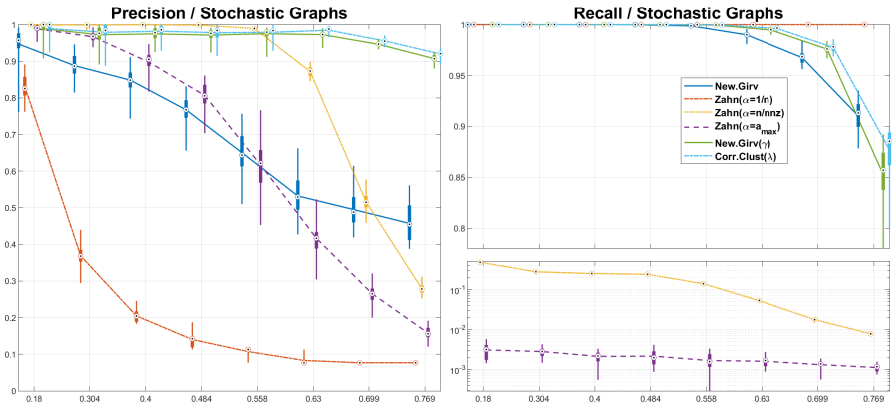


Figure 16: Precision and Recall (y-axes) of all the criteria to be applied on doubly-stochastic graphs, over the mixing parameters (x-axes).

contains in average about 1.1 node. On the other hand, Louvain used with $F^{\omega}_{Z,3}$ returns communities containing 5.35 nodes in average, when $\mu = 0.18$. While larger than for $F^{\omega}_{Z,1}$, this size is yet more than three times smaller than the smallest communities from the groundtruth community structures, which contain 20 nodes. This explains the low Recall scores of $F^{\omega}_{Z,1}$ and $F^{\omega}_{Z,3}$. Opposite to this is the behaviour of Louvain used with the other version of the Zahn criterion, namely $F^{\omega}_{Z,2}$. Its Recall curve is constant, equal to 1, which means that it does not split any of the groundtruth communities. However, when looking at -highlighted cells in table 5, we see that, from $\mu = 0.558$, the number of communities returned by Louvain with $F^{\omega}_{Z,2}$ is less than two, meaning that it has returned some community structures where all the nodes belong to a unique community, and the Recall of this trivial community structure is 1. Thus, Louvain used with $F^{\omega}_{Z,2}$ does not split existing communities, but tends to merge them into one unique community as the mixing parameter increases. Finally, the parametrised and non-parametrised Newman-Girvan modularities, along with the Correlation Clustering criterion, have Recall values that remain equal to 1 for mixing parameters up to $\mu = 0.558$, and then start to decrease. The fact that parametrised Newman-Girvan and Correlation Clustering criteria have a lower Recall value than the Newman-Girvan modularity for $\mu = 0.769$ is explained by the fact that Louvain algorithm used with the two former criteria returns more communities than expected for this mixing parameter—see -highlighted cells in table 5.

Looking at the Precision curves on the left panel of fig. 16, we observe that the non-parametrised version of the Newman-Girvan modularity is not competitive with the parametrised Newman-Girvan and the Correlation Clustering criteria. On the other hand, these two latter ones exhibit an extremely close behaviour. About the two versions of the Zahn criteria with low Recall values, one highlights the highest Precision up to $\mu = 0.558$—namely $F^{\omega}_{Z,3}$—, while

Precision of the other one ($F^{\omega}_{Z,1}$) decreases quickly. This is due to the fact that, as already discussed, the latter one returns essentially one community per node, and such communities are not taken into account in our formulation of the Recall. Finally, the version of the Zahn criterion $F^{\omega}_{Z,2}$ with the best possible Recall score, also exhibit the worst results in terms of Precision, with a slump of its Precision as soon as the second smallest mixing parameter.

Summary. Average F1-scores of all measures are provided in table 6, along with the corresponding standard deviation. To improve readability, F1-scores have been multiplied by 10, and standard deviation by 100. Parameters for the Correlation Clustering criteria and parametrised Newman-Girvan modularities are those that maximise the average F1-score, as explained in the previous paragraphs. We observe that the most accurate criteria are the parametrised ones. Indeed, the criterion which provides the best F1-score overall is the Correlation Clustering criterion on simple graphs (F^{λ}_{CC}), closely followed by the Correlation Clustering and parametrised Newman-Girvan criteria on doubly-stochastic graphs ($F^{\omega,\lambda}_{CC}$ and $F^{\omega,\gamma}_{NG}$). Last from this pool is the parametrised Newman-Girvan modularity on simple graphs (F^{γ}_{NG}). These four criteria exhibit average F1-scores above 0.85 for all the mixing parameters.

We now compare the four criteria unified by theorem 2, namely the Deviation to Indetermination (F_{DI}), Balanced Modularity (F_{BM}), Newman-Girvan modularity (F_{NG}) and Deviation to Uniformity (F_{DU}). First, we observe that the latter provides very high F1-scores compared to the other measures. Except for the largest mixing parameter value, and its high standard deviations, the Deviation to Uniformity is almost competitive with the parametrised criteria. This is an artifact due to the networks in our benchmark, whose community structures are typical deviations to regular graphs. On the other hand, the three others are not competitive with the doubly-stochastic Newman-Girvan modularity (F^{ω}_{NG}) that generalises them all.

Our last observations concern the Zahn criteria. From table 6, it seems that none of the doubly-stochastic versions of the Zahn criterion can compete with the one for simple graphs. However, it can be seen from table 5 that the number of communities returned by the Zahn criteria are quite different, making them hard to compare them based on their F1-score. To highlight this, in fig. 17, we plot the confusion matrices of Louvain used with F_Z (left panel), respectively $F^{\omega}_{Z,3}$ (right panel) for one community structure obtained with $\mu = 0.4$ (for each measure, we choose the community structure that provides the maximum F1-score). We observe that their behaviours are opposite: the community structure returned using Zahn criterion for simple graphs correctly detects the largest communities, but split those of sizes 20 and 40: nodes from the groundtruth 20-node communities have been assigned to 36 communities by Louvain (16 were expected), and nodes from the 40-node communities have been split into 22 communities (8 expected). On the other hand, Louvain used with $F^{\omega}_{Z,3}$ perfectly detects communities of size 20, 40 and 80. However, it splits the two communities of size 160 into 20 communities, and the 320-node community into 225 ones.

	Comparison # Uncovered Blocks VS # Expected Blocks							
μ	0.18	0.304	0.4	0.484	0.558	0.63	0.699	0.769
F_{DI}	$7.56^{-}(0.52)$	$7.6^{-}(0.47)$	$7.52^{-}(0.56)$	$7.48^{-}(0.6)$	$7.17^{-}(0.76)$	$6.78^{-}(0.84)$	$6.77^{-}(0.84)$	$6.43^{-}(0.85)$
F_{BM}	$4.72^{-}(0.48)$	$4.86^{-}(0.53)$	$5.29^{-}(0.5)$	$5.63^{-}(0.69)$	$5.66^{-}(0.69)$	$6.21^{-}(.084)$	$6.05^{-}(0.74)$	$6.05^{-}(0.74)$
F_{NG}	$2.79^{-}(0.2)$	$3.95^{-}(0.27)$	$4.1^{-}(0.45)$	$4.53^{-}(0.58)$	$5.13^{-}(0.71)$	$5.47^{-}(0.68)$	$5.58^{-}(0.78)$	$5.76^{-}(0.78)$
F_{Z}	$1.16^{+}(0.06)$	$1.68^{+}(0.1)$	$2.9^{+}(0.23)$	$4.99^{+}(0.19)$	$7.97^{+}(0.29)$	$11.26^{+}(0.27)$	$13^{+}(0.14)$	$13.38^{+}(0.14)$
F_{DU}	$1.01^{-}(0.01)$	$1.02^{-}(0.03)$	$1.04^{-}(0.03)$	$1.06^{-}(0.05)$	$1.09^{-}(0.05)$	$1.2^{-}(0.07)$	$1.55^{-}(0.1)$	$1.94^{-}0.14$
F_{NG}^{γ}	$1.79^{-}(0.07)$	$2.01^{-}(0.09)$	$2.07^{-}(0.13)$	$1.92^{-}(0.1)$	$1.73^{-}(0.12)$	$1.6^{-}(0.09)$	$1.54^{-}(0.08)$	$1.08^{*}(0.05)$
F_{CC}^{λ}	$1^{-}(0.01)$	$1^{-}(0.01)$	$1.01^{-}(0.01)$	$1^{*}(0.01)$	$1.01^{*}(0.02)$	$1.04^{*}(0.03)$	$1.39^{+}(0.07)$	$1.94^{+}(0.07)$
$F_{Z,1}^{\omega}$	$46.9^{+}(1.39)$	$46.8^{+}(1)$	$47.2^{+}(1.22)$	$46.4^{+}(1.93)$	$45.8^{+}(2.04)$	$43^{+}(1.73)$	$40.5^{+}(2.23)$	$36.3^{+}(2.26)$
$F_{Z,2}^{\omega}$	$1.89^{-}(0.13)$	$3.95^{-}(0.32)$	$7.4^{-}(0.66)$	$11.67^{-}(2.8)$	$17.44^{-}(5.19)$	$28.28^{-}(5.96)$	$31^{-}(0)$	$31^{-}(0)$
$F_{Z,3}^{\omega}$	$9.72^{+}(0.24)$	$9.46^{+}(0.2)$	$8.94^{+}(0.18)$	$8.12^{+}(0.28)$	$7.38^{+}(0.22)$	$8.73^{+}(0.18)$	$10.93^{+}(0.09)$	$12.69^{+}(0.17)$
F_{NG}^{ω}	$1.2^{-}(0.06)$	$1.54^{-}(0.07)$	$1.83^{-}(0.09)$	$2.21^{-}(0.12)$	$2.7^{-}(0.24)$	$3.36^{-}(0.32)$	$3.95^{-}(0.35)$	$4.47^{-}(0.39)$
$F_{NG}^{\omega,\gamma}$	$1.02^{-}(0.03)$	$1.07^{-}(0.05)$	$1.1^{-}(0.05)$	$1.14^{-}(0.06)$	$1.16^{-}(0.05)$	$1.16^{-}(0.05)$	$1.18^{-}(0.05)$	$1.23^{+}(0.08)$
$F_{CC}^{\omega\lambda}$	$1.02^{-}(0.02)$	$1.04^{-}(0.04)$	$1.06^{-}(0.04)$	$1.1^{-}(0.05)$	$1.1^{-}(0.04)$	$1.08^{-}(0.05)$	$1.1^{-}(0.05)$	$1.28^{+}(0.09)$

Table 5: Average ratio scores of the community structures returned by Louvain, with standard deviations between parentheses. Top : : more communities than expected; : number of communities less than half the expected number, in average. Bottom: : less than 2 communities, in average; : less than 6 nodes per community, for $\mu = 0.18$.

	F1-scores							
μ	0.18	0.304	0.4	0.484	0.558	0.63	0.699	0.769
F_{DI}	3.18 (1.7)	3.19 (2)	3.18 (1.6)	3.22 (1.7)	3.27 (2)	3.4 (2)	3.46 (2.5)	4.38 (5.7)
F_{BM}	4.27 (2.7)	4.20 (3.1)	3.94 (2)	3.78 (2.4)	3.83 (3)	3.61 (2.5)	3.74 (3)	4.76 (5.1)
F_{NG}	6.75 (5.4)	5.09 (1.9)	5.08 (2.4)	4.67 (4.3)	4.16 (4)	4 (2.9)	4.14 (4.1)	4.94 (5.2)
F_{Z}	9.99 (0.03)	9.95 (0.1)	9.62 (0.7)	3.99 (2.2)	1.69 (0.6)	0.75 (0.5)	0.25 (0.2)	0.12 (0.07)
F_{DU}	9.98 (0.6)	9.95 (0.8)	9.88 (2.1)	9.78 (4)	9.75 (3.6)	9.47 (4.6)	8.79 (3.2)	7.19 (3.5)
F_{NG}^{γ}	9.17 (2.5)	8.55 (3.3)	8.84 (2.6)	9.15 (1.3)	9.37 (1.6)	9.45 (1.2)	9.28 (0.1)	8.70 (1.7)
F_{CC}^{λ}	10 (0.1)	10 (0.1)	9.99 (0.2)	9.99 (0.3)	9.98 (0.6)	9.97 (0.1)	9.77 (0.4)	9.11 (1.4)
$F_{Z,1}^{\omega}$	0.06 (0.3)	0.06 (0.2)	0.04 (0.1)	0.04 (0.2)	0.03 (0.1)	0.03 (0.1)	0.03 (0.1)	0.02 (0.1)
$F_{Z,2}^{\omega}$	9.08 (2.1)	5.38 (3.2)	3.4 (2.2)	2.46 (3.3)	1.94 (2.1)	1.53 (2.3)	1.43 (0)	1.43 (0)
$F_{Z,3}^{\omega}$	6.47 (0.3)	4.33 (0.5)	4.01 (0.2)	3.86 (0.3)	2.45 (0.7)	1 (0.5)	0.3 (0.3)	0.2 (0.1)
F_{NG}^{ω}	9.72 (2.6)	9.40 (1.8)	9.18 (2.1)	8.68 (2.6)	7.86 (4.7)	6.9 (4.8)	6.54 (4)	6.07 (4.4)
$F_{NG}^{\omega,\gamma}$	9.94 (1)	9.86 (1.3)	9.87 (1)	9.85 (0.8)	9.87 (0.8)	9.84 (0.6)	9.61 (0.5)	8.79 (1.9)
$F_{CC}^{\omega\lambda}$	9.94 (0.9)	9.89 (1.3)	9.91 (0.9)	9.89 (0.9)	9.89 (0.9)	9.9 (0.4)	9.66 (0.6)	8.98 (1.5)

Legend for the F1-scores

0 2.5 5 7.5 10

Table 6: Average F1-scores ($\times 10$) of the community structures returned by Louvain with criteria from table 3. Standard deviations ($\times 10^2$) between parentheses.

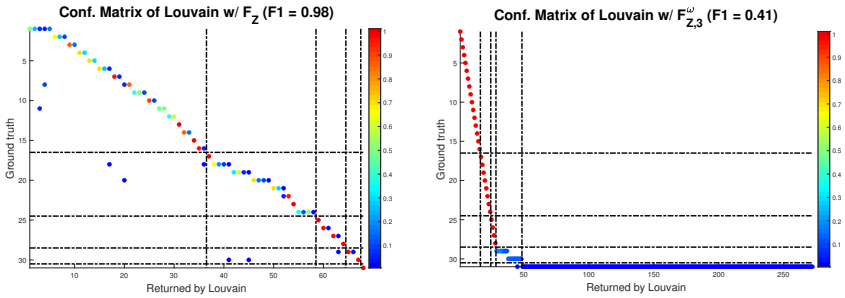


Figure 17: Confusion matrices of one community structure returned by Louvain used with F_Z (left), respectively $F^{\omega}_{Z,3}$ (right).

This illustrates that finding the more desirable partitioning remains application-dependant, and should not be chosen on the basis of maximum $F1$-score only.

7. Conclusion and Future Perspectives

Broadly speaking, the aim of this study was to investigate the utility of doubly-stochastic scaling as a preprocessing for community detection. Our proposed preprocessing was presented in section 4, along with illustrations of its potential to sharpen community structures on toy examples and a real-world network. In section 5, we have generalised a range of graph partitioning measures to weighted networks, with a particular focus on the case of doubly-stochastic ones. Of utmost interest is our result that the doubly-stochastic scaling unifies these measures, as stated in section 6.1. That is, all of the six measures defined for simple graphs can be expressed using only two parametrised measures for doubly-stochastic graphs. Extensive comparisons of these measures have been conducted using SBMs in section 6.2, where we observed that the measures the most able to accurately uncover community structures are the parametrised ones, for both simple and doubly-stochastic graphs, but foremost that a great care should be given to the choice of the measure in Louvain, as different measures behave extremely differently.

In the future, we would like to investigate the impact of the diagonal that we add to ensure the convergence of the scaling in algo. 1 and 2, in terms of numerical values within the resulting preprocessed graph. This would provide us with theoretical basis to help making the right choice. Furthermore, to keep improving community detection methods, we would like to incorporate the knowledge obtained from scaling factors to the process of discovering communities. Indeed, after scaling, all nodes have the same degree. This may be seen as a non desirable feature, as it means that some initial information about node centrality (namely, the degree) is lost. And for real applications, the more central the node, the more harmful an error of assignation on this node. However, as stated in [30], another kind of information about node centrality, similar to hub and authority

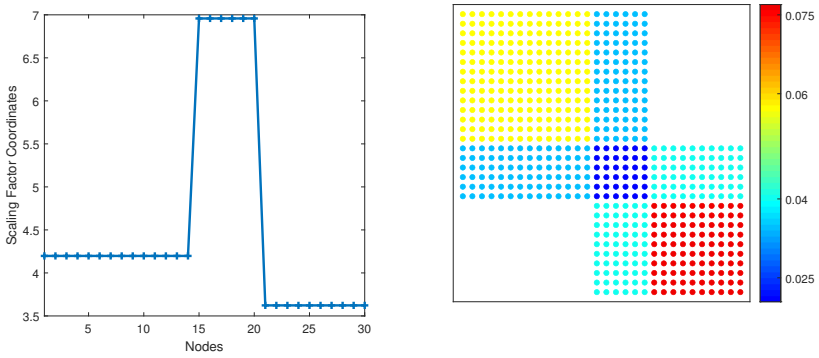


Figure 18: Doubly-stochastic scaling of a toy example of overlapping communities. Left: Values of the scaling factor. Right: The scaling form of a simple graph exhibiting two overlapping communities.

centralities from [46], is conveyed by the scaling factors, and should be exploited to ensure that a greater care is taken to the correct assignation of nodes of high centrality. Finally, we would like to extend our preprocessing to the detection of overlapping communities. Indeed, in many applications, one node can be involved in more than one community [47]. In a doubly-stochastic scaling, a node belonging to many communities should produce high scaling factors (because of its high degree) and thus low numerical values in the doubly-stochastic scaling, as illustrated in fig. 18. This may provide a framework to identify those nodes.

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Conflict of interest

The authors declare that they have no conflict of interest.

Availability of code and data

All the material needed to reproduce the experimental results from Section 6.2 can be found at `github.com/luleg/StochasticMeasuresLouvain`.

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