A revisit to evaluating accuracy of community detection using the normalized mutual information

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Normalized Mutual Information (NMI) has been widely used to evaluate accuracy of community detection algorithms. In this notes we show that NMI is seriously affected by systematic error due to finite size of networks, and may give wrong estimate of performance of algorithms in some cases.

A simple expression for the estimate of this error is derived and tested numerically. We suggest to use a new measure to the accuracy of community detection, namely relative Normalized Mutual Information (rNMI), which is NMI minus the expected NMI of random partitions. This measure is very close to zero for two random partitions even with a short length, so it can overcome the problem of NMI.

Detection of community structure, which asks to group nodes in a network into assortative groups, is a key problem in network science, computer science, sociology and biology. Many algorithms have been proposed for this problem, see ref. [1] for a review. However on a given network, different algorithms usually give different results. So evaluating performance of these algorithms and finding the best ones are important tasks.

Usually the evaluations are performed on benchmark networks each of which has a reference partition. These benchmarks include networks generated by generative models, like Stochastic Block Model [2] and LFR model [3], with a planted partition as the reference partition; and some real-world networks, like famous Karate Club network [4] and Political Blog network [5], with a partition annotated by domain experts as the reference partition. The accuracy benchmarks include networks generated by generative models, like Stochastic Block Model [2] and LFR model [3], with a planted partition as the reference partition; and some real-world networks, like famous Karate Club network [4] and Political Blog network [5], with a partition annotated by domain experts as the reference partition. The accuracy of a community detection algorithm is defined as similarity between the reference partition and partition found by the algorithm, and evaluation can be done by comparing this similarity: the larger similarity, the better performance of the algorithm has on the given network.

Without the generality, in this notes we call the reference partition $A$ and the detected partition $B$, and our task is to study the measure to the similarity between partition $A$ and partition $B$.

When the number of groups are identical, saying that $q_A = q_B = q$, the similarity can be easily defined by overlap, the number of equal group labels in $A$ and $B$, maximized over all possible permutations:

$$O(A, B) = \max_{\pi} \left( \frac{1}{n} \sum_{i=n}^n \delta_{A_i, \pi(B_i)} - \frac{1}{q} \right),$$

where $n$ is number of nodes, and $\pi$ ranges over all permutations of $q$ groups.

However we can see that the overlap is non-zero even if partition $B$ is a random partition: there are roughly $\frac{n}{q}$ identical labels in two partitions if labels are distributed uniformly. One way to refine it is to normalize the overlap in such a way that it scales from 0 to 1 [6, 7]:

$$O(A, B) = \max_{\pi} \left( \frac{1}{n} \sum_{i=n}^n \delta_{A_i, \pi(B_i)} - \frac{1}{q} \right) / \left(1 - \frac{1}{q}\right).$$

However using overlap as the similarity has two problems: first, when number of groups $q$ is large, maximizing modularity over $q!$ permutations is difficult; second, when number of partitions, $q_A$ and $q_B$, are not identical, the overlap is ill-defined.

Another well-accepted measure of similarity is the Normalized Mutual Information (NMI) [8, 9], which is well-defined even when $q_A \neq q_B$. Many studies use NMI to evaluate their algorithms or to compare different algorithms [10]. To define NMI we needs to approximate the marginal probability of a randomly selected node being in group $a$ and $b$ by $P_A(a) = \frac{n_a}{n}$ and $P_B(b) = \frac{n_b}{n}$ respectively, and $n_a$ and $n_b$ denote group size of $A$ and $B$ respectively.

The spirit of Mutual Information is to compute the dependence of these two distributions, by computing Kullback Leibler (KL) distance between joint distribution $P_{AB}(a, b)$ and the product of two marginal distributions $P_A(a)P_B(b)$:

$$I_{AB}(P_A, P_B) = \sum_{a=1}^{q_A} \sum_{b=1}^{q_B} P_{AB}(a, b) \log \frac{P_{AB}(a, b)}{P_A(a)P_B(b)}.$$

$$\text{rNMI} = \frac{I_{AB}(P_A, P_B) - I_{AB}(P_A^{\text{rand}}, P_B^{\text{rand}})}{I_{AB}(P_A^{\text{rand}}, P_B^{\text{rand}})} - 1,$$

where $P_A^{\text{rand}}$ and $P_B^{\text{rand}}$ are random partitions.

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Due to the property of KL distance, this quantity is non-negative. \( I_{AB}(P_A, P_B) = 0 \) means \( P_A \) and \( P_B \) are independent, that detected partition has nothing to do with the ground-true partition. On the other hand, if \( I_{AB}(P_A, P_B) \) is much larger than 0, the detected partition and the ground true partition are similar. In practice the joint distribution can also be approximated by frequencies

\[
P_{AB}(a, b) = \frac{n_{ab}}{n},
\]

where \( n_{ab} \) is number of nodes that both in group \( a \) of partition \( A \) and in group \( b \) of partition \( B \). Eq.\((3)\) can be written as

\[
I(P_A, P_B) = H(P_A) + H(P_B) - H(P_{AB}),
\]

where

\[
H(P_A) = - \sum_a P_A(a) \log P_A(a)
\]

is the Shannon entropy of distribution \( P_A \), and \( H(P_{AB}) \) is the entropy of the joint distribution \( P_{AB} \). Note that using conditional distribution \( P_{AB}(a|b) = P_{AB}(a, b)/P_B(b) \), one can rewrite Eq.\((3)\) as

\[
I(P_A, P_B) = H(P_A) - H(P_{A|B}).
\]

which has a interpretation that amount of information (surprise) gained on distribution \( P_A \) after known \( B \). If this information gain is 0, it means knowledge of \( B \) does not give any information about \( A \), so two partitions has nothing to do with each other. Obviously the larger \( I_{AB}(P_A, P_B) \), the more similar two partitions are. But this is still not a idea metric for evaluating community detection algorithms since it is not normalized. One way to normalize it is to choose normalization as \( H(P_A) + H(P_B) \), and Normalized Mutual Information is written as

\[
\text{NMI}(P_A, P_B) = \frac{2I(P_A, P_B)}{H(P_A) + H(P_B)},
\]

Since \( H(P_{AB}) \leq H(P_A) + H(P_B) \), \( \text{NMI}(P_A, P_B) \) is bounded below by 0. Also note that \( H(P_{AB}) = H(P_A) = H(P_B) \) when \( A \) and \( B \) are identical, which means in this case \( \text{NMI}(P_A, P_B) = 1 \). After NMI was introduced as a measure for comparing community detection algorithm, it becomes very popular in community detection. However in some cases we find this measure gives un-consistent result, one example is shown in Fig.\(1\) left. In the figure we computed NMI of partitions obtained by four algorithms and the planted partition in the stochastic block model with \( \epsilon = 1 \). The stochastic block model (SBM) is also called the planted partition model. It has a planted, or true, partition with \( \epsilon \).

The commonly studied case where the \( q \) groups have equal size and where \( p \) has only two distinct entries, \( p_{rs} = c_{in}/n \) if \( r = s \) and \( c_{out}/n \) if \( r \neq s \). We use \( \epsilon = c_{out}/c_{in} \) to denote the ratio between these two entries. So in Fig.\(1\) left, where \( \epsilon = 1 \), the networks are deep in the un-detectable phase \( [6] \), and are essentially random graphs. Though in each network there is a planted partition, but no algorithm could be able to find it or find a partition that is correlated with it. However from the figure only Modularity BP gives zero NMI on all networks, other three algorithms give positive NMI, and Infomap gives quite large NMI on all networks. Does it mean Infomao could find the planted configuration in the non-detectable phase of SBM? We think it is not the case, the problem comes from NMI. In Fig.\(1\) right we plot the number of groups found by different algorithms then we found that only Modularity BP gives one group while other algorithms report increasing number of groups with system size increases. Thus from this result we can guess that large NMI may come from large number of groups.

Recall that in computing the NMI of two partitions, we use \( n_{ab} \) to approximate \( p_{ab} \), which is fine with \( n \rightarrow \infty \) but will lead to finite size effects with a finite \( n \). Since NMI can be seen as a function of entropies, we can express the finite size effect of NMI as finite size effect of entropy. It is known \([15] \) that if entropy \( H \) is estimated using finite samples with \( q \) states, the simply correction can be written as

\[
H_n = H - \langle H_n \rangle = \frac{q - 1}{n},
\]

where \( \langle H_n \rangle \) is the expected entropy with \( n \) samples and \( H_n \) is the entropy with \( \infty \) samples. In our system, if we use number of nodes in the network as sample size, then the difference between NMI estimated using \([10] \) in our network and in the network with infinite number of nodes can be expressed as

\[
\text{NMI}_n(P_A, P_B) - \text{NMI}_\infty(P_A, P_B) \approx \frac{1}{2n} \frac{q_a q_b - q_a - q_b + 1}{H(P_A) + H(P_B)},
\]
One thing we can infer from last equation is that in finite-size networks, two random partitions $A$ and $B$ have positive NMI which is a function of system size and number of groups in two partitions.

$$\text{NMI}^\text{random}_{n}(q_A, q_B) \approx \frac{1}{2n} q_a q_b - q_a - q_b + 1.$$

To test our estimate, in Fig. 2 we compared NMI of two random partitions $A$ and $B$ with $q_A = 10$ groups in partition $A$ and different number of groups in partition $B$. We can see that equation (9) gives a good estimate of NMI between two random partitions. Moreover, from the figure we see that with larger system size, NMI is smaller and our estimate is more accurate. This is because Eq. (7) is only a first order approximation. We note that in similar finite-size effect for Mutual Information has been studied, though in a different context.

It is easy to see that if we use NMI in evaluating similarity between a detected partition $B$ and ground-true partition $A$, then NMI prefers large number of partitions, which gives systematic bias to evaluation. One way to fix this bias is to consider statistical significance of NMI value, by comparing it to NMI of a null model. In this notes we choose random configuration $C$, which has the same group-size distribution as the detected partition, as null model, and define the \textit{relative Normalized Mutual Information} (rNMI) as

$$\text{rNMI}(A, B) = \text{NMI}(A, B) - \langle \text{NMI}(A, C) \rangle,$$

where $\langle \text{NMI}(A, C) \rangle$ is the expected NMI between the ground-true configuration $A$ and a random partition $C$, averaged over realization of $C$.

So if partition $B$ has a large number of groups, though NMI$(A, B)$ could be large, a random configuration having same distribution as $B$ also has large number of groups and hence a large NMI$(A, C)$. Thus rNMI$(A, B)$ could be very small.

Actually the idea of computing statistical significance by comparing score of a partition to expected score of a null model has been used everywhere in science. For example, well-known score for community structure, Modularity [17], compares the number of internal edges of a partition to the expected number of internal edges in random graphs.

One way to compute $\langle \text{NMI}(A, C) \rangle$ is to generate several random configurations $C$, compute NMI for $A$ and $C$ then take average. In practice we find that usually 10 realization of $C$ is already good enough. If we really care about the computational speed, one can use an less accurate expression

$$\langle \text{NMI}(A, C) \rangle = \frac{1}{2n} q_a q_b - q_a - q_b + 1.$$

In Fig. 3 left we plot the rNMI given by the same four algorithms used in Fig. 1, where we can see that now all algorithms report zero rNMI, telling us correctly that no one has found useful information about planted partition in the SBM networks in un-detectable phase.
FIG. 2: Normalized Mutual Information between two random partitions $A$ and $B$. Partition $A$ always has $q_A = 10$ groups, while $B$ has different ($q_B$) groups. Each group in the partition has the same expected size. In other words group labelling for each node is chosen independently according to $\frac{1}{q_A}$ for partition $A$ and $\frac{1}{q_B}$ for partition $B$. The lines are theoretical estimates and points with error-bars are experimental data, with each point averaged over 10 random instances. From top to bottom, system size are $n = 1000, 2000, 4000$ and $8000$.

To test the accuracy of this measure, in Fig. 3 right we compare the rNMI and overlap for two partitions, the planted partition and the one detected by Belief Propagation, for benchmark networks generated by stochastic block model. In this benchmark the detectability transition happens at $\epsilon^* = 0.2$. With $\epsilon > \epsilon^*$ the planted configuration is un-detectable, which means the detected partition should be not correlated with the planted partition. In this case $q_A = q_B$, so overlap defined in (2) is a good measure. In the figure we see that value of rNMI and overlap are consistent: they both have high values in detectable phase and low values in un-detectable phase. We see that the overlap is not perfectly zero in un-detectable phase, because in maximizing overlap over permutations the effect of noise has been induced. So in this sense our measure which report almost zero values in un-detectable phase, is a better measure for similarity of two partitions in undetectable phase than overlap, even when $q_A = q_B$.

In Fig. 4 we compare NMI and rNMI for three algorithms, Louvain, Informap and Modularity BP, on benchmark networks generated by LFR model [3] with different system size. From left panel of Fig. 4 we see that if we use NMI as the measure to accuracy of these algorithms, we may conclude that Infomap works better than Louvain in this set of benchmarks, however from Fig. 4 right we see that Louvain actually works better than Infomap because it gives larger rNMI than Infomap. And the different of rNMI between Louvain and Infomap are larger when system size increases. So this figure tells us that using NMI may give a wrong estimate of performance of community detection algorithms.

In this notes we showed numerically and analytically that using normalized mutual information as a measure to accuracy of community detection algorithms has a systematic error when number of groups given by algorithms are much different. And we proposed to fix this problem by using the relative normalize mutual information which considers the statistically significance of NMI by comparing the NMI of two partitions to the expected value of random partitions. We note that there are better ways for estimate finite-size effect of entropy, e.g. a Bayesian estimate proposed in [18]. We put it in future work to refine $\langle \text{NMI}(A, C) \rangle$ in expression of rNMI (10) using Bayesian approaches.

Implementation of rNMI and examples of using it can be found at [19].
FIG. 3: (Left) Relative Normalized Mutual Information given by the same four algorithms on the same set of networks used in Fig 1. Each point is averaged over 10 realizations. (Right) Relative Normalized Mutual Information compared with overlap in networks generated by stochastic block model with 10000 nodes, 6 groups, average degree 6 and different $\epsilon = c_{out}/c_{in}$.

FIG. 4: Normalized Mutual Information and Relative Normalized Mutual Information for three algorithms, Infomap [11], Louvain [13] and Modularity BP [14] on LFR benchmarks [3] with different system sizes. The parameters of networks are: average degree $c = 8$, mixing parameter $\mu = 0.45$, maximum degree is 50, community sizes range from 200 to 400, exponent of degree distribution is $-2$. and exponent of community size distribution is $-1$.

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