Attributed-based Label Propagation Method for Balanced Modularity and Homogeneity Community Detection

Jenan Moosa[1][a], Wasan Awad[1][b] and Tatiana Kalganova[2][c]
[1]*College of Information Technology, Ahlia University, Manama, Bahrain*
[2]*College of Engineering, Design and Physical Sciences, Brunel University, London, U.K.*

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Abstract: Community Detection is an expanding field of interest in many scopes, e.g., social science, bibliometrics, marketing and recommendations, biology etc. Various community detection tools and methods have been proposed in the last years. This research is to develop an improved Label Propagation algorithm (Attribute-Based Label Propagation ABLP) that considers the nodes' attributes to achieve a fair Homogeneity value, while maintaining high Modularity measure. It also formulates an adaptive Homogeneity measure, with penalty and weight modulation, that can be utilized in consonance with the user's requirements. Based on the literature review, a research gap of employing Homogeneity in Community Detection was identified, and accordingly, Homogeneity as a constraint in Modularity based methods is investigated. In addition, a novel dataset constructed on COVID-19 contact tracing in the Kingdom of Bahrain is proposed, to help identify communities of infected persons and study their attributes' values. The implementation of proposed algorithm performed high Modularity and Homogeneity measures compared with other algorithms.

1 INTRODUCTION

Extensive research was done to detect communities within networks, detected communities are densely connected nodes that are strongly connected to each other in or the subnetwork (community) than to the rest of the network(WU et al., 2020). In social networks, a community can be defined as a group of nodes or persons that are similar to each other and dissimilar from the rest of the group (Raghavan et al., 2007). This indicates that the group of nodes in one community will most likely share the same characteristics or interests. Whereas in attributed networks, the nodes in a community will most likely share the same attributes' values.

To assess the output of generated communities, different number of measures are being used, including Modularity measure which indicates the quality of the generated partitions or communities. However, the integration of different types of constrains or external information on community composition was rarely investigated (Viles & O'Malley, 2017), and Homogeneity as constraint still remains uncharted. In consequence, the detected communities might contain irrelevant nodes in one cluster even-though the communities scored a good fitness score in other measures such as Modularity.

To overcome this, a Homogeneity measure can be integrated with Modularity, to consolidate the evaluation process. So, a method that maximizes both Modularity and Homogeneity is proposed, with Modularity and Homogeneity as objective functions. On the other hand, as constrained community detection shows robust performance on noisy data since it uses background knowledge(Nakata & Murata, 2015) and the restriction of the type considered here has, to our knowledge, remained unstudied, Modularity with Homogeneity as a constraint is also tested to adjust the detection of homogenous communities.

The scientific contributions of this paper are:

1. Develop an Attribute-Based Label Propagation algorithm that considers the nodes' attributes to achieve a fair

[a] https://orcid.org/0000-0002-9081-7748
[b] https://orcid.org/0000-0001-7152-3480
[c] https://orcid.org/0000-0003-4859-7152

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Homogeneity value, while maintaining a high Modularity measure.

2. Formulate an adaptive Homogeneity measure, with penalty and weight modulation, that can be utilized based on the user's requirements.
3. A research gap of employing Homogeneity in Community Detection was identified, and accordingly, Homogeneity as a constraint in Modularity based methods is investigated.
4. Design a novel dataset based on COVID-19 contact tracing in the Kingdom of Bahrain, to help identify communities of infected persons and study their attributes' values.

2 RELATED WORK

Effective community detection is an important tool for analyzing networks; it provides thorough knowledge of the network, in addition to the structure and functional characteristics of the network (WU et al., 2020). Community detection problem is getting more attention, as different algorithms and techniques have been proposed, which includes traditional algorithms (Fortunato, 2010)(Shen et al., 2009), evolutionary algorithms (Karimi et al., 2020)(N. Chen et al., 2020), heuristic (Clauset et al., 2004; Sobolevsky et al., 2014) hierarchical clustering (Lu et al., 2015) , spectral clustering (Luxburg, 2007), label propagation (Raghavan et al., 2007), neural networks (Bruna, 2017), etc.

2.1 Evaluation Measures

The detected communities are evaluated using a number of evaluation measures such as **Modularity** (M. E. J. Newman & Girvan, 2004), which measures the fraction of the edges in the network that connect vertices of the same type (i.e., within-community edges) minus the expected value of the same quantity in a network with the same community divisions but random connections between the vertices. Modularity has been used to compare the quality of the partitions obtained by different methods, but also as an objective function to optimize (M. Newman, 2003).

Homogeneity was also used as an objective function (Wu & Pan, 2016), a measure was proposed based on Shannon information entropy theory in which the entropy of a set, measures the average Shannon information content of the set. Unfortunately, the modularity values produced in this research were significantly lower than others.

Moayedikiaa (Moayedikia, 2018) used the proposed Homogeneity in (Wu & Pan, 2016) as an objective function by developing an attributed community detection algorithm wrapped by Harmony Search that relies on nodes' importance to form communities. Yet this algorithm performed a long execution time, and it also suffered from entrapment in local optima. Another research proposed a method for community detection based on a higher-order feature termed Attribute Homogenous Motif (P. Li et al., 2018), which integrates both node attributes and higher-order structure of the network. However, the modularity was neglected in this research.

The evaluation measures used can assess one criterion only, so different measures are used to evaluate different aspects of the result. As one method might generate results that perform well in one evaluation measure while fail to achieve a fair result in another one. Thus, an evaluation technique that takes this issue into account needs to be studied.

2.2 Community Detection with Constraints

Constrained community detection approaches are used to take advantage of the existing side information of the network (Ganj et al., 2018). This aids in generating more efficient and actionable results, and help develop data mining techniques that can handle complex and domain-specified constraints (Ganji et al., 2017). Table 1 presents several constrained community detection methods, along with the evaluation measure used to evaluate the results.

Table 1: Community detection with constraints.

Paper	Method	Constraints	Objective function
(Ganj, Bailey and Stuckey, 2018)	Lagrangian Constrained	Must-Link, Cannot-Link	Normalized Mutual Information, Noise Sensitivity
(Ganji, Bailey and Stuckey, 2017)	Programming modelling technology	Global, Community and Instance level	Normalized Mutual Information, Modularity, Run-Time
(Chin and Ratnavelu, 2017)	Label propagation algorithm with constraints	Propagating labels, Communities' Exemption	Normalized Mutual Information, Modularity
(Chin and Ratnavelu, 2016)	Constrained Label Propagation	Number of links of a node to the nodes in a community	Normalized Mutual Information, Normalized Variation Information, Modularity, Modularity density

Most of the current community detection methods consider the structural information of networks, but disregard the fruitful information of the nodes, and this results in the failure of detecting semantically meaningful communities (P. Li et al., 2018). However, Homogeneity was never studied as a constraint, and was always treated as an objective function.

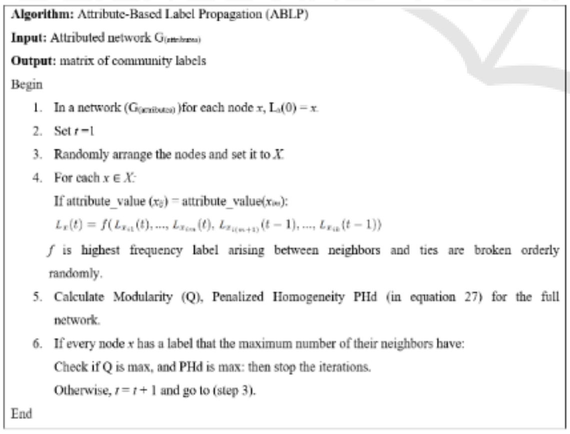
The two objective functions (Modularity and Homogeneity) are conflicting, which means that improving one of them leads to degradation of another (Moayedikia, 2018). Modularity has proven its effectiveness in evaluating community detection problem, many algorithms are based on modularity maximization (Tsung et al., 2020). Hence comes the idea of testing the Homogeneity as a constraint, in addition to testing it as an objective function. As constrained algorithms are effective in dealing with combined optimization problems, due to its wide representation scope and generally applicable solving methods(Y. C. Chen et al., 2010).

3 PROPOSED METHODS

In this section, new Attribute-Based Label Propagation (ABLP) algorithms based on attributes' regulation are proposed.

3.1 ABLP Algorithm

The proposed method is an Attribute-Based Label Propagation Algorithm is a Modularity maximization based on Label Propagation algorithm with regards to homogeneity. As Label Propagation is considered as one the effective algorithms amongst the existing algorithms used for community detection because of its time efficiency (Chin & Ratnavelu, 2017).



```
Algorithm: Attribute-Based Label Propagation (ABLP)
Input: Attributed network G_(attributes)
Output: matrix of community labels
Begin
    1. In a network (G_(attributes) )for each node x, L_x(0) = x
    2. Set t =1
    3. Randomly arrange the nodes and set it to X
    4. For each x ∈ X:
       If attribute_value (x_ij) = attribute_value(x_im):
       $L_x(t) = f(L_{x_{i1}}(t), ..., L_{x_{im}}(t), L_{x_{i(m+1)}}(t-1), ..., L_{x_{ik}}(t-1))$
      f is highest frequency label arising between neighbors and ties are broken orderly
      randomly.
    5. Calculate Modularity (Q), Penalized Homogeneity PHd (in equation 27) for the full
       network.
    6. If every node x has a label that the maximum number of their neighbors have:
       Check if Q is max, and PHd is max: then stop the iterations.
       Otherwise, t = t + 1 and go to (step 3).
End
```

Algorithm 1: ABLP.

The concept of the algorithm is based on examining the neighbors of the node in the network. Each node (x) will be labeled with a number that indicates its community. First each node will have a unique label, and then the labels will propagate throughout the process. The label of x will be changed based on its neighbors' labels. Node x will also check the attribute of its neighbor, nodes with similar attributes will most likely have the same label. This step will be iterated, and each node will update its label at every step, the node will get the label that the maximum number of neighbors carry. Finally, *x* will join the community that contains most of his homogeneous neighbors. In this way, ABLP algorithm tries to maximize Modularity and Homogeneity at the same time.

3.2 Constrained ABLP Algorithm

The same concept of the proposed ABLP is followed, with regards of homogeneity as a constraint, which penalizes the Modularity measure by minimizing it based on the achievement of the homogeneity value. So ideally, if the homogeneity degree is high, the modularity measure should remain at its best. However, if the homogeneity degree is low, the Modularity value should be punished and reduced.

```
Algorithm: Constrained Attribute-Based Label Propagation (ABLP)
Input: Attributed network G_(attributes)
Output: matrix of community labels
Constraint: Homogeneity
Begin
    1. In a network (G_(attributes)) for each node x, L_x(0) = x.
    2. Set t =1
    3. Randomly arrange the nodes and set it to X.
    4. For each x ∈ X:
       If attribute_value (x_ij) = attribute_value(x_im):
       $L_x(t) = f(L_{x_{i1}}(t), ..., L_{x_{im}}(t), L_{x_{i(m+1)}}(t-1), ..., L_{x_{ik}}(t-1))$
      f is highest frequency label arising between neighbors and ties are broken orderly
      randomly.
    5. Calculate Modularity (Q), Q(C: H) in equation 29 for the full network.
    6. If every node x has a label that the maximum number of their neighbors have:
       Check if Q is max, then stop the iterations.
       Otherwise, t = t + 1 and go to (step 3).
End
```

Algorithm 2: Constrained ABLP.

The Constrained Attribute-Based Label Propagation algorithm is a highest-modularity, homogeneity constraint-satisfying solution for the community detection problem in attributed networks. The algorithm considers the run that generates the maximum constrained Modularity and proposed measure of Penalized Homogeneity degrees.

4 PROPOSED EVALUATION MEASURE

In this section, Homogeneity Degree that considers the networks' structure, in addition to a Penalized Homogeneity measure are proposed. These measures will later be used to evaluate a number of social networks in the community detection problem.

4.1 Evaluation Measures

Homogeneity in community detection was first proposed by (Wu & Pan, 2016), it was defined based on Shannon information entropy theory, the entropy of a set measures the average Shannon information content of it. This homogeneity measure considers the proportion of the number of nodes with a certain attribute in a community to the total number of nodes in a community. The measure does not consider the network structure, as real-world datasets might have some aspects that need to be considered.

As homogeneity was used as an objective function to measure the homogeneity of the detected communities in the network as one unit, here is the proposal of a new of homogeneity measure that evaluates the homogeneity degree in each community, based on specified attribute values.

The formula will calculate the number of nodes with the specified attribute divided by the total number of nodes in the cluster. It reflects the standard deviation; however, standard deviation finds how concentrated the data is around the mean, in our case, the mean will be ignored, $\mu=0$;

The closer the value is to 1, the more homogeneous the cluster is. This can be calculated in Hc_k which is the Homogeneity of community *k*.

$$\mathrm{Hd} = \sum_{i=1}^{att} \left(\frac{n_{att}}{n}\right)^2 \qquad (1)$$

Where Hd is the average Homogeneity degree in the Communities: *att* is the number of attributes in the network, n_{att} is the number of nodes with each attribute in a community, and *N* is the total number of nodes in the community. The square value is calculated as it adds more weighting to the differences which makes the value more significant.

4.2 Penalized Homogeneity Degree

It should be noted that the Homogeneity degree (Hd) measure proposed in section 4.1 does not consider the number of communities and number of nodes in each community compared to the total number of nodes in the network. To add more flexibility and user-preference to the proposed measure, a penalty will be given, to ensure that nodes among all detected communities are homogeneous, and that distribution is fair.

To add more restrictions to the homogeneity degree, we consider (P), a penalty that takes the number of nodes for each attribute in the community compared to the total number of nodes with this attribute in the network.

$$\mathrm{P} = 1 - \left(\frac{n_{att(\max)}}{\mathrm{N}_{att(\max)}}\right) \qquad (2)$$

Where n_{att} is the number of nodes with each attribute in a community, and $\mathrm{N}_{\mathrm{att}}$ is the number of nodes with this attribute in the network, for the attribute that owns the maximum number of nodes in each community.

$$\mathrm{PHd} = \mathrm{Hd} - \mathrm{P} \qquad (3)$$

Where PHd measures the Penalized Homogeneity Degree. This allows the user to apply an impartial penalty for algorithms that detect a large number of communities that contain a small number of nodes with a certain attribute. It is also possible to set a weight for the penalty, and consider more attribute, based on the user's requirement of how important each attribute is.

$$\mathrm{MAWPHd} = \mathrm{Hd} - \mathrm{P} * w \sum_{i=1}^{z} \mathrm{Hd} - (\mathrm{P}_i * w_i) \qquad (4)$$

Multi-Attribute Weighted Penalized Homogeneity degree can be calculated using the MAWPHd measure. Where *z* is the number of attributes to be considered, and *w* is the weight of penalty to be applied.

On the other hand, to calculate Modularity constrained by Homogeneity, the Penalized Homogeneity Degree will be subtracted from 1 to minimize the penalty of constraint. Because the higher the Homogeneity value, the less punishment is applied on the Modularity.

$$\mathrm{Q(C{:}\ H)} = |\mathrm{Q} - 1 - \text{Penalized Homogeneity Degree}\,| \qquad (5)$$

Where Q(C: PHd) calculates the Modularity with Penalized Homogeneity as Constraint, Q represents Modularity, H is the Homogeneity (can be Hd or PHd, based on the experiment, dataset or research requirements).

The proposed measures of (PHd) and (MAWPHd) allow a more flexible mensuration of Homogeneity on different types of attributed networks, based on the user-defined requirements.

5 RESULTS AND DISCUSSION

In this section, the algorithm will be implemented on two datasets in addition to a proposed dataset of COVID-19 contact tracing. The results will be compared to several existing algorithms. And then will be compared in term of Modularity, and the proposed measures of Homogeneity.

5.1 Datasets

The datasets used for the experiments are attributed social networks from the literature, in addition to a proposed real-world dataset based on the contact tracing of COVID-19 infected persons in the Kingdom of Bahrain.

1 **Political Books (PolBooks)** a social network consists of nodes representing books about US politics. Edges represent frequent co-purchasing of books by the same buyers. Books were labelled by Newman (M. E. J. Newman, 2006) with an attribute describing their political alignments. It consists of 105 nodes, and 441 edges (Figure 1).

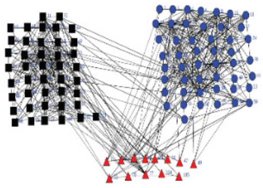


Figure 1: US Political books network (Triangles: neutral, dots: conservative, and squares: liberal) (Q. Wu et al., 2013).

2 **American College Football** network, represents the games between Division IA colleges during regular season fall in 2000 (Girvan & Newman, 2002). It consists of 115 teams and 613 games, divided into 12 conferences (Figure 2).

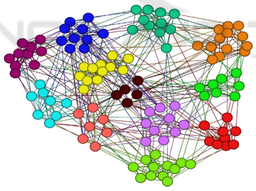


Figure 2: American College football network (each team is represented by a different color) (Binesh & Rezghi, 2018).

3 **Proposed Dataset: COVID-19 Contact Tracing:** The COVID-19 pandemic has been termed as the most consequential global crisis since the World Wars. Because of the rapid prevalence of this virus, health organizations all over the world tend to track and store all data related to this pandemic. This includes the contact tracing, number of cases, number of deaths, etc. The availability of rich textual data from various online sources can be used to understand the growth, nature and spread of COVID-19(Usman et al., 2020). According to World Health Organization (World Health Organization, 2021), contact tracing is the process of identifying, assessing, and managing people who have been exposed to a disease to prevent onward transmission. When systematically applied, contact tracing will break the chains of transmission of an infectious disease and is thus an essential public health tool for controlling infectious disease outbreaks. When contact tracing data is compiled it can be represented by a network, and hence structured into a graph, which can be analysed using graph mining techniques.

As any network can be outlined in a graph, and the graph is composed of a set of nodes which can be individuals or entities, and edges that represent the connections and interactions between the nodes(Bedi & Sharma, 2016).

A dataset was proposed in (Moosa et al., 2021), it is based on the spread of virus between countries. An open-source contact tracing data was used to follow the spread of virus from January to March 2020, between the countries worldwide, which started in China and expanded to other countries. Each country is represented by a node, and an edge is used when a country has a contact infected person from another country. Unfortunately, this dataset cannot be used in this research as it is not attributed network.

The data used to form this dataset was available on Bahrain’s Ministry of Health website, and was publicly available, it contained the contact tracing of citizens who were infected by the COVID-19 virus, the details include the case number, age, nationality, gender, travel history (if any), and the other case number contacted which caused the infection. Since the data was publicly available on the website and it does not contain any personal information which makes it impossible to recognize any of the cases, it did not require any ethical approval. The cases cover the period 01/April/2020 to 10/May/2020.

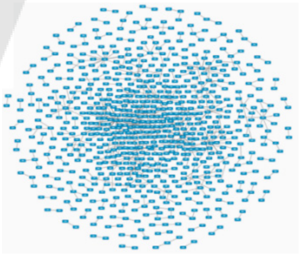


Figure 3: Proposed Dataset: COVID-19 contact tracing in the Kingdom of Bahrain.

The dataset consists of 750 cases represented by nodes and 589 relationships between the cases (contacted persons) represented by edges. Other cases were ignored as the source of getting the virus was unknown as they were tested as part of a campaign to obtain random samples from the community or tested positive after developing symptoms without clear idea of the contacted persons.

5.2 Experiments of Work

The proposed ABLP algorithm, along with several existing algorithms will be implemented. The algorithms used for comparison are:

- Asynchronous Label Propagation (LPA) (Raghavan et al., 2007)
- Graph Embedding with Self Clustering (GEMSEC) (Rozemberczki et al., 2019)
- An Edge Enhancement Approach for Motif-aware (EdMot) (P.-Z. Li et al., 2019)
- Deep Autoencoder-like Nonnegative Matrix Factorization (DANMF) (Ye et al., 2018)

5.3 Results

The main purpose of proposing the algorithm is to maximize homogeneity, while maintaining a high Modularity value. So, the Homogeneity degree will be calculated and compared as an objective function. And then the results will be tested again with consideration of Homogeneity as a constraint.

5.3.1 Homogeneity as an Objective Function

It is observed that considering the nodes' attributes values will result in more homogeneous communities. Nodes with similar attributes are beyond any doubt share the same value, however, they may not necessarily be neighbours or share direct ties. So, paying more attention to the node's values helps detect denser communities in terms of interests or preferences.

The results are shown in Tables 1,2,3 and 4. Where Hd states the proposed Homogeneity measure in detected communities (equation 1), P is the proposed penalty measure (equation 2) and PHd is the proposed Penalized Homogeneity degree values (equation 3).

Table 1: Results on Books Dataset.

Algorithm	Number of detected communities	Q	Proposed Hd	Proposed P	Proposed PHd
Proposed ABLP (2021)	**4**	**0.5270**	0.652361	**0.515306**	**0.137055**
LPA (Raghavan et al., 2007)	7	0.4812	**0.683000**	0.736321	-0.05332083
EdMot (P.-Z. Li et al., 2019)	7	0.5092	0.648959	0.747983	-0.099023914
GEMSEC (Rozemberczki et al., 2019)	10	0.3362	0.649814	0.851763	-0.201949147
DANMF (Ye et al., 2018)	8	0.4920	0.604294	0.784587	-0.18029309

As seen in Table1, the highest modularity value was achieved in Books dataset by the proposed Attribute-Based Label Propagation algorithm with a value of 0.527, followed by EdMot algorithm with a value of 0.5092.

As for the Homogeneity degree (before applying the penalty), LPA achieved a high rate, however its penalty was high because it detected two small communities with node sizes 4 and 3, and all nodes in both communities had the same attribute value. This resulted in a high penalty and therefore a very low penalized homogeneity degree. GEMSEC also had an elevated penalty value for the same reason. This gives rise to ABLP algorithm achieving the highest assessment value among all other algorithms.

The Modularity measure values of American College Football dataset were likely close by the experimented algorithm. However, Homogeneity measure was significantly low as the communities detected included nodes from diversified conference values.

Table 2: Results on Football Dataset.

Algorithm	Number of detected communities	Q	Proposed Hd	Proposed P	Proposed PHd
Proposed ABLP (2021)	**9**	**0.66054**	**0.65051592**	**0.107761374**	**0.542754546**
LPA (Raghavan et al., 2007)	9	0.61000	0.546660025	0.181218165	0.365441861
EdMot (P.-Z. Li et al., 2019)	9	0.65130	0.179555235	0.670508936	-0.4909537
GEMSEC (Rozemberczki et al., 2019)	10	0.56151	0.196957798	0.707377622	-0.510419825
DANMF (Ye et al., 2018)	8	0.62101	0.157589739	0.626488442	-0.468898703

For a higher homogeneity value, the community should contain nodes with the least number of attribute values possible. To better understand what happened, the average number of attribute values in a community can be calculated, and obviously, the closer the value to 1, the better.

In American College football dataset, the number of attribute values is 12, which can be considered high to some extent compared to Books dataset which consisted of 3 attribute values. It was observed that when a community consists of nodes with more than 3 different attribute values, the homogeneity value is relatively low. To prove this, a measure of Average Attribute value (AAv) in a community is proposed and calculated, as seen in Table 3. It can be clearly perceived that higher Average Attribute value result in higher penalty and thus a lower PHd value. This draws a conclusion, that having multiple attribute values in one community results in a non-homogeneous environment.

Table 3: The average number of attribute value.

Algorithm	Proposed P	Proposed PHd	AAv
	min	max	min
Proposed ABLP (2021)	**0.107761374**	**0.542754546**	**2.78**
LPA (Raghavan et al., 2007)	0.181218165	0.365441861	5.44
EdMot (P.-Z. Li et al., 2019)	0.670508936	-0.4909537	7.2
GEMSEC (Rozemberczki et al., 2019)	0.707377622	-0.510419825	6.6
DANMF (Ye et al., 2018)	0.626488442	-0.468898703	9.625

As for the proposed dataset, since it is a real-world contact tracing network, and the number of edges is less than the number of nodes, so the penalty will not be considered as the nodes did not have enough connections with one another.

The highest modularity value was again achieved by the ABLP followed by EdMot. As well as the

Table 4: Results on Proposed dataset.

Algorithm	Number of detected communities	Q	Proposed Hd
Proposed ABLP (2021)	191	0.983010	**0.801190189**
LPA (Raghavan et al., 2007)	204	0.938420	0.7216702
EdMot (P.-Z. Li et al., 2019)	183	**0.986023**	0.481694661
GEMSEC (Rozemberczki et al., 2019)	8	0.327030	0.336852091
DANMF (Ye et al., 2018)	10	0.394328	0.306138357

homogeneity value which was the highest in the proposed measure and the Label Propagation Algorithm. It is also noticeable that while Edmot achieved a high modularity value, it scored a comparatively low homogeneity measure. As for GEMSEC and DANMF, both algorithms detected a low number of communities with high number of nodes in one community, then divided the rest of the nodes on the remaining communities. This manifestly resulted in a low modularity value as well as a low homogeneity measure.

5.3.2 Homogeneity as Constraint

Here the homogeneity is treated as a constraint, which minimizes the Modularity value based on the achievement of the homogeneity value. When the Homogeneity value is high, modularity measure should remain at its best. On the contrary, when the value of Homogeneity is low, the Modularity value should be punished and reduced. This is tested with the same experiments, as seen in Table 5 and 6. Where Q(C: H) is the value of Modularity constrained with Homogeneity (equation 5). For Books and Football datasets, PHd Homogeneity value is considered since a penalty was applied.

Table 5: Homogeneity as constraint in Books dataset.

Algorithm	Q	Proposed PHd	Q(C: H)
Proposed ABLP (2021)	**0.5270**	**0.137055**	**0.610055**
LPA (Raghavan et al., 2007)	0.4800	-0.05332083	0.46667917
EdMot (P.-Z. Li et al., 2019)	0.5092	-0.099023914	0.391776086
GEMSEC (Rozemberczki et al., 2019)	0.3362	-0.209080443	0.454696557
DANMF (Ye et al., 2018)	0.4920	-0.18029309	0.32768291

Table 6: Homogeneity as constraint in Football dataset.

Algorithm	Q	Proposed PHd	Q(C: H)
Proposed ABLP (2021)	**0.66054**	**0.542754546**	**0.882214546**
LPA (Raghavan et al., 2007)	0.61000	0.365441861	0.755441861
EdMot (P.-Z. Li et al., 2019)	0.65130	-0.455997939	0.107297939
GEMSEC (Rozemberczki et al., 2019)	0.56151	-0.510419825	0.071929825
DANMF (Ye et al., 2018)	0.62101	-0.468898703	0.089908703

And as the proposed COVID-19 dataset did not need the penalty measure, the value of constrained Homogeneity will be Hd.

Table 7: Homogeneity as constraint in proposed dataset.

Algorithm	Q	Proposed Hd	Q(C: H)
Proposed ABLP (2021)	0.983010	**0.801190189**	0.788390189
LPA (Raghavan et al., 2007)	0.938420	0.7216702	0.660099987
EdMot (P.-Z. Li et al., 2019)	**0.986023**	0.481694661	0.467717661
GEMSEC (Rozemberczki et al., 2019)	0.327030	0.336852091	0.336117909
DANMF (Ye et al., 2018)	0.394328	0.306138357	0.299533643

Testing the homogeneity as a constraint helps in evaluating the results in terms of Modularity and Homogeneity at the same time. Here is it assumed that both measures have the same importance or weight in the results. However, a weight can be assigned to the measures based on how important each measure is. This will facilitate in the evaluation process based on the defined user requirements, which are aligned with the dataset itself. So, if the user is interested more in the Homogeneity than Modularity, a ratio of 70/30 can be applied, where Homogeneity is responsible for 70% of the measure and the Modularity is for the other 30%. This can be calculated as |1- (0.3 * Q – 0.7 *H). In other words, this way can be personalized according to the nature of the dataset and the expected detected communities.

6 CONCLUSION

Community detection in attributed networks can be evaluated in many aspects. The mostly used evaluation measures such as Modularity, cannot address the evaluation of Homogeneity. Hence, Attribute-Based Label Propagation ABLP algorithm, that considers the attribute values of nodes while maintaining a high Modularity, and Homogeneity and values is proposed. And to support evaluating the proposed algorithm, an adaptable homogeneity measure is also proposed. This measure assesses the homogeneity in an attributed network and can be penalized based on the type of the dataset. Experiments on existing social networks were conducted as well as on the newly proposed COVID-19 dataset which is based on the contact tracing of the virus infected persons in the Kingdom of Bahrain. The algorithm appears to have good results in terms of the discussed evaluation measures. As future work, we tend to study the attribute consideration on the familiar community detection algorithms.

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