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Disassortativity in Biological and Supply Chain Networks

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ABSTRACT:

Network science has allowed researchers to model complex real world systems as networks in order to identify non trivial topological patterns. Degree correlations (or assortativity) is one such non trivial topological property, which indicates the extent to which nodes with similar degrees tend to pair up with each other. Biological networks have long been known to display anti-degree correlations (disassortativity), where highly connected nodes tend to avoid linking with each other. However, the mechanism underlying this structural organisation remain not well understood. Recent work has suggested that in some instances, disassortativity can be observed merely as a model artefact due to simple network representations not allowing multiple link formations between the node pairs. This phenomena is known as structural disassortativity. In this paper, we analyse datasets from two distinct classes of networks, namely; man made supply chain networks and naturally occurring biological networks. We examine whether the observed disassortativity in these networks are structurally induced or owing to some external process. Degree preserving randomisation is used to generate an ensemble of null models for each network. Comparison of the degree correlation profiles of each network, against that of their degree preserving randomised counterparts reveal whether the observed disassortativity in each network is of structural nature or not. We find that in all biological networks, the observed disassortativity is of structural nature, meaning their disassortative nature can be fully explained by their respective degree distributions, without attribution to any underlying mechanism which drives the system towards disassortativity. However, in supply chain networks, we find one case where disassortativity is structurally induced and in other cases where it is mechanistically driven. We conclude by emphasizing on ruling out structural disassortativity in future research, prior to investigating mechanisms underlying disassortativity in networks.

KEY WORDS: ***Supply chain networks, degree disassortativity, biological networks***

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1.0 Introduction

Characterisation and analysis of complex systems as networks can reveal important insights into their various macroscopic structural properties. In recent years, network theory has widely been used to study various natural and man-made complex systems, such as biological and ecological systems, technological networks, social systems, and, transportation and supply chain networks. These studies have revealed various nontrivial topological properties underlying the structure and organisation of the connections (or links) between the individual entities (or nodes) from which each system is made of.

The most well-known feature of most systems is their tendency to display scale free structure, where the degree (the number of connections of a given node) distribution obeys power law. As a result of this heterogeneous distribution of connections among nodes, scale-free networks are characterised by hubs (i.e. the nodes which have relatively higher number of connections compared to others in the system). The mechanism underlying the scale free structure has been explained by the BA model, which suggests that new entrants to a system attach preferentially to the highly connected nodes already present within the system.

In addition to the scale free nature, recent empirical research investigating networked systems have observed mixing patterns of nodes based on various node level properties. A network is said to be assortative if nodes with similar properties tend to connect together, and disassortative otherwise. When the property considered is node degree, one can observe degree correlations in a given network (herein after, this paper considers node degree as the context in which node mixing is discussed).

Data driven studies, to date, have revealed that almost all social networks display assortative mixing, where well connected people tend to know each other. In contrast, disassortativity seems to be a common property of almost all biological (metabolic, protein interaction, predator-prey) and technological networks (WWW, internet) (Pastor et al., 2001; Maslov and Sneppen, 2002; Newman, 2002; Nacher and Akutsu, 2012). Furthermore, recent work undertaken in the area of topological analysis of supply chain networks (SCNs) has also revealed disassortative mixing, where highly connected firms generally tend to avoid each other (Orenstein, 2016; Perera et al., 2016).

While ‘homophily’ (like attracting like) is generally attributed as the mechanism underlying assortative mixing (Barabasi, 2016), disassortative mixing itself and the underlying mechanism remain less well understood. Unlike assortativity, disassortativity can also be induced by the scale-free property of the network. In a simple representation of a network, the nodes are only allowed one link between each other and this creates a conflict between the scale free property and degree correlations of the network – a phenomena referred to as structural disassortativity (Barabasi, 2016).

Structural disassortativity is an artefact of the scale-free model and therefore is not representative of any underlying mechanism which drives the system towards disassortativity. Therefore, it is imperative to rule out structural disassortativity from any disassortativity observed in the data. From contemporary literature, it is evident that various mechanisms have been attributed to observed disassortativity, in biological networks, without first eliminating the possibility of structural disassortativity (Dan et al., 2007; Xu et al., 2010).

In this paper, we investigate the disassortativity of two distinct types of complex network systems, namely; the naturally evolved biological systems and man-made SCNs. Although both these classes of networks have been identified by various studies to be disassortative, no study to date has investigated whether this observed disassortativity is structurally induced or not. Therefore, we examine whether the disassortativity observed in the above two classes of networks are due to an external mechanism or whether they are simply structurally induced as a result of simple network representation.

The remainder of this manuscript is structured as follows. Section two will provide a background to this study and introduce key concepts available in literature relating to degree-correlations. Section three presents the details of the datasets considered and the methodology adopted for analysis. Section four presents the results obtained and section five provides a comprehensive discussion of the results. Section six concludes the paper.

2.0 Literature Review

2.1 Degree Correlated Networks

Degree correlations (also referred to as assortativity) capture the relationship between the degrees of nodes that link to each other. A network is said to display degree correlations if the number of links between the high and low degree nodes are systematically different from what is randomly expected.

A network is said to be assortative when high degree nodes are, on average, connected to other nodes with high degree and low degree nodes are, on average, connected to other nodes with low degree. In contrast, a network is said to be disassortative when, on average, high degree nodes are connected to nodes with low(er) degree and, on average, low degree nodes are connected to nodes with high(er) degree (Noldus and Van Mieghem, 2015).

Assortativity is a key structural property of complex networks, as it can reveal important insights into how various dynamics operate over the network topology. Assortative mixing is found to impact a network's; robustness (to both random failures and intentional attacks), stability, controllability, traffic dynamics, propagation of information or infections and various other dynamic processes (Friedel and Zimmer, 2007; Tanizawa et al., 2012; Perera et al., 2016; Miao et al., 2008; Xue et al., 2010; Chavez et al., 2006; Payne et al., 2009).

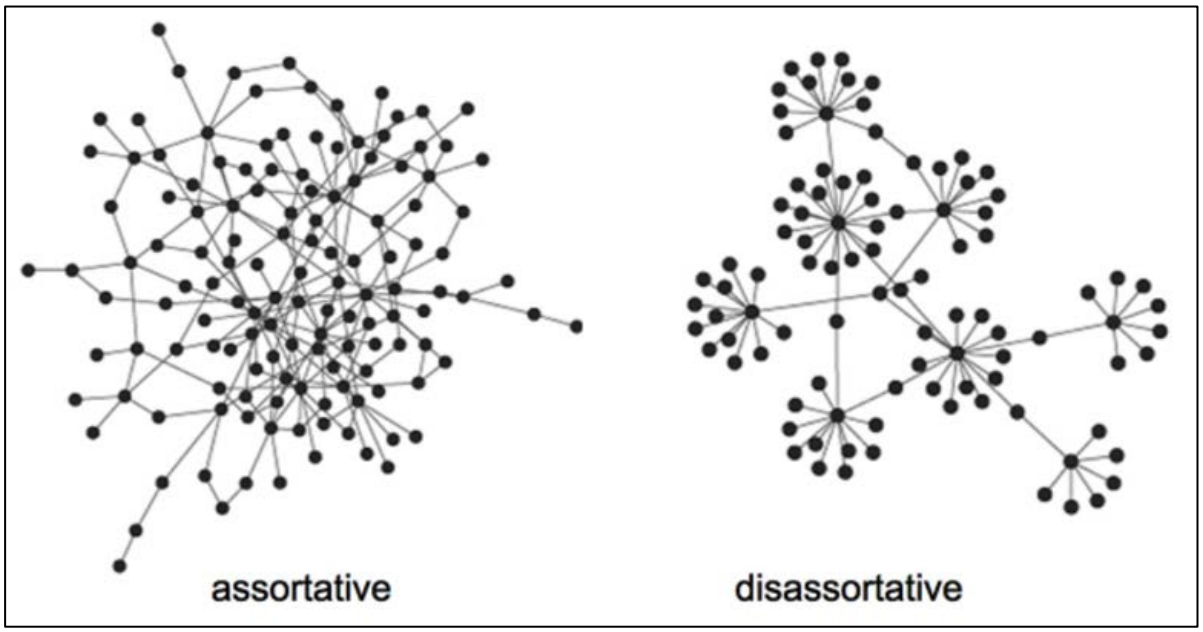

Figure 1: Structure of assortative and disassortative networks (Adapted from Hao et al., 2011)

Figure 1 visually illustrates the structural differences between assortative and disassortative network topologies. In disassortative systems, hubs (the highly connected nodes) tend to avoid each other, instead linking to lower-degree nodes. As a result, the network structure tends to display hub and spoke character (as opposed to core periphery structure observed in assortative networks).

2.2 Degree correlations and the scale free property in networks

Intuitively, scale free networks arising through BA mechanism would have a natural predisposition to be disassortative. The reasoning behind this lies at the fundamental proposition of the BA model, the preferential attachment; which suggests that every time a new node is added to the system, a link is placed between the newly added node *n*, which has degree 0<= dn <=m (where m is the number of links that are added to the system with every new node) and a node that is already present within the system, which is likely a node with a relatively high degree. Thus, iterative placement of links between a low-degree node (i.e. the new nodes that enter the system) and high-degree nodes, will ultimately make the resulting network disassortative, as a whole (Noldus and Van, 2015). However, it has been shown analytically (by Nikoloski et al) and through simulations (by Newman, 2003), network generation using BA model, asymptotically for large N, does not generate any degree correlations (i.e. the resulting network is neutral).

2.2.1 Expected number of links between two nodes in a neutral network

Consider an undirected network of N nodes and M links, with degree distribution p_k, where p_k is the probability that a randomly chosen node on the network will have degree k. Assume that we reach a node by following a randomly chosen link on the network. The degree of this node is not distributed according to p_k, rather it is biased towards nodes of higher degrees (since more links are incident on high degree nodes than on low degree nodes). Therefore, the

degree distribution for the node at the end of a randomly chosen link is proportional to kp_k as opposed to p_k (Newman, 2002).

Let q_k be the probability of having a degree k node at the end of a link. We can write q_k as;

$$q_k = \frac{kp_k}{\langle k \rangle} \quad \textbf{(Eq. 1)}$$

Since the sum of q_k for a given network equals 1, division by the average degree $\langle k \rangle$ is used for normalisation of the probability q_k across the network.

As presented in Callaway et al (2001), we can define the quantity e_{jk} to be the joint probability distribution of finding a node with degree j and a node with degree k, at the two ends of a randomly selected link. Since in an undirected network, this quantity is symmetric on its indices, i.e. $e_{jk} = e_{kj}$, we can invoke sum rules as follows;

$$\sum_{jk} e_{jk} = 1$$

$$\sum_{j} e_{jk} = q_k$$

Accordingly, in a network which has no degree correlations (i.e. a neutral network), we expect that;

$$e_{jk} = q_j q_k \quad \textbf{(Eq. 2)}$$

Replacing q_j and q_k with Eq. 1, we obtain;

$$e_{jk} = \frac{kp_k jp_j}{\langle k \rangle^2} \quad \textbf{(Eq. 3)}$$

Therefore, deviations from the above condition are considered as characteristic of degree correlations in a network.

In a network with degree correlations e_{jk}, the expected number of links between node j and node k can be found as follows;

$$E_{jk} = e_{jk} \langle k \rangle N$$

For a neutral network (with no degree correlations), we can replace e_{jk} with **Eq. 3**, to obtain (Maslov et al., 2004; Boguná et al., 2004);

$$E_{jk} = \frac{kp_k jp_j}{\langle k \rangle} N \quad \textbf{(Eq. 4)}$$

The quantity E_{jk} derived above can be used to estimate the expected number of links between two nodes, when the overall network is neutral.

2.3 Quantifying degree correlations

It is important to be able to quantify the degree correlations of a given network using a single metric. In this regard, we can utilise the average degree of the neighbours, for each node i, as follows;

$$k_{\mathrm{nn}}(k_i) = \frac{1}{k_i}\sum_{n=1}^{N} A_{ij}k_j \quad \textbf{(Eq. 5)}$$

The degree correlation function should consider the above calculation for all nodes with degree k (Pastor-Satorras et al., 2001; Vázquez et al., 2002);

$$k_{\mathrm{nn}}(k) = \sum_j jP(j \mid k) \quad \textbf{(Eq. 6)}$$

In the above function, $P(j \mid k)$ is the conditional probability of reaching a degree j node at the opposite end of a degree k node. In essence, the above function provides the average degree of neighbours for each node of degree k. In order to identify the degree correlations of a given network, the dependence of $k_{\mathrm{nn}}(k)$ on degree k should be investigated.

2.3.1 Neutral networks

Note that in a neutral network, the quantity $P(j \mid k)$ is in fact the same as the quantity q_j, as below (Barabasi, 2016);

$$P(j \mid k) = \frac{e_{jk}}{\sum_j e_{jk}} = \frac{q_j q_k}{q_k} = q_j \quad \textbf{(Eq. 7)}$$

Accordingly, replacing $P(j \mid k)$ with q_j, we obtain;

$$k_{\mathrm{nn}}(k) = \sum_j jq_j \quad \textbf{(Eq. 8)}$$

From Eq1., it is known that $q_j = \frac{jp_j}{\langle k \rangle}$

Therefore, replacing q_j in **Eq. 8** with the above, we obtain the following;

$$k_{\mathrm{nn}}(k) = \sum_j jq_j = \sum_j j\frac{jp_j}{\langle k \rangle} = \frac{\langle k^2 \rangle}{\langle k \rangle} \quad \textbf{(Eq. 9)}$$

As can be seen above, in a neutral network, the average degree of a given node's neighbours, does not depend on the degree of that node (i.e. $k_{\mathrm{nn}}(k)$ is independent of k).

2.3.2 Correlated networks

In correlated networks, $k_{nn}(k)$ depends on k. In assortative networks, where hubs tend to connect with each other, this relationship is expected to be positive (and vice versa for disassortative networks).

2.3.2.1 Correlation exponent

The correlation exponent characterises the relationship between $k_{nn}(k)$ and k, as follows (Pastor-Satorras et al., 2001);

$$k_{nn}(k) = ck^{\mu} \quad \textbf{(Eq. 10)}$$

Where c is th1e constant of proportionality.

As per the above, the correlation exponent can be used to quantify the level of degree correlations in a given network. For neutral networks, one would expect μ to be zero. For assortative and disassortative networks, μ would be >0 and <0, respectively.

It is noted that some studies use the degree correlation coefficient, *r, proposed by Newman (2002)* to characterise the level of degree correlations that exists in a network. However, in this study, we use μ (as per Eq. 10) to characterise the degree correlations of networks analysed.

Structural Cutoff: From Eq. 4, it is clear that only when the degrees of node k and node j, are above a certain threshold, the expected number of links E_{jk} is >1 (i.e. prediction of multiple links), which gives rise to degree correlations. This threshold is termed structural cut-off, k_s and it scales as (Boguná et al., 2004);

$$k_s(N) \sim (\langle k \rangle N)^{1/2}$$

Natural Cutoff: The degree distribution P_k of a scale free network is approximated with power law as follows;

$$P_k \sim k^{-\gamma}$$

where k is the degree of the node and γ is the degree exponent (also known as the power law or the scale free exponent). The popular BA model generates networks with γ = 3. For a scale-free network, the expected maximum degree k_{max} (also known as the natural cut-off) which represents the expected size of the largest hub is estimated as follows (Barabasi, 2016);

$$k_{max} \sim k_{min} N^{\frac{1}{\gamma - 1}} \quad \textbf{(Eq. 11)}$$

where k_{max} and k_{min} are the expected maximum and minimum degree of a node, respectively. N is the system size, in terms of the number of nodes.

2.3.3 Origin of Structural Disassortativity

Comparing k_{max} to k_s reveals two distinct regimes (Barabasi, 2016);

When γ >3: $k_{max} \sim N^{<0.5}$. Therefore k_{max} is always less than k_s. This means that the degree required by the largest hub to trigger the structural cut-off is higher than the degree of the largest hub in the network. Therefore, when γ **>3**, there will be no nodes for which E_{jk} is >1 – thus no conflict between degree correlations and the simple network requirement is observed.

When γ <3: $k_{max} \sim N^{>0.5}$, thus exceeding k_s (which scales at 0.5). Consequently, the nodes with degrees $> k_s$ can violate $E_{jk} > 1$ condition. Such networks will have fewer links between its hubs than predicted by Eq. 4 (due to simple network representation, the two largest hubs cannot have multiple links between them to maintain the neutral status of the network). Such networks will inevitably become disassortative. This is known as structural disassortativity. Such disassortativity may not be a result of any microscopic property of the network, rather it is purely due to the structural limitations of the simple network representation.

2.4 Deciphering Observed Degree Correlations in Real World Networks

An important question is whether the degree distribution on its own is sufficient to describe the structure of a network, i.e. whether the degree correlations observed in the network is explained by the ensembles of networks generated by its degree distribution while preserving the degree vector.

In the case of assortative networks, the observed degree correlations cannot be due to the structural cut-off since the effect of hubs is opposite. As such, the degree distribution cannot explain the observed degree correlations in assortative networks. Therefore, there is some unknown mechanism during the evolution of the network which drives it into an assortative state. Some researchers (McPherson et al., 2001; Aral et al., 2009; Rivera et al., 2010) have attributed this to homophily (i.e. like attracting like).

In the case of disassortative networks, the absence of structural cut-off can be partially responsible for disassortativity. However, deeper analysis is required to determine whether the observed degree anti-correlations in a given network is due to structural disassortativity or some unknown mechanism. In this regard, degree preserving randomisation plays an important role, as discussed below.

2.4.1 Degree Preserving Randomisation (DPR)

DPR can help establish whether or not the degree-correlations observed in a network is simply an artefact of the network's inherent structural properties or a property unique to the nodes.

DPR involves rewiring the original network, to generate an ensemble of null models, while preserving the degree vector (Noldus and Van, 2015). At each time step, the DRP process randomly picks two connected node pairs and switch their link targets. This switching is repeatedly applied to the entire network. The resulting network represents a null model where each node still has the same degree, yet the paths through the network have been randomised.

Comparison of trend lines between the original/observed degree correlation function $k_{nn}(k)$ and the randomised degree correlation function $k_{nn}^{R}(k)$ (obtained as an average through a number of DPR trials) can reveal if the degree correlations observed in the original network are structural or not. If the original $k_{nn}(k)$ and the randomised $k_{nn}^{R}(k)$ trends are identical, then the degree correlations observed in the original network are purely structural, i.e. the degree correlations can entirely be explained by the degree distribution without attribution to any other external mechanism. However, if the original $k_{nn}(k)$ indicates degree correlations which diverge from the randomised $k_{nn}^{R}(k)$ trend, there is an underlying mechanism which induces the degree correlations in the original network (Barabasi, 2016).

3.0 Methods

Two distinct classes of networks were considered in this study, namely; the man-made SCNs and natural biological networks. Four network datasets from each network class was considered for analysis. Table 1 provides the description of each network along with the data source.

Table 1: Description of the network datasets considered

	Network Description	Data Source
SCNs		
Industrial Organic Chemicals	SCN firms are represented as nodes and contractual relationships as links.	Willems (2008).
Farm Machinery and Equipment		
Primary Batteries, Dry and Wet		
Aircraft Engines and Engine Parts		
Biological Networks		
Metabolic (C.Elegans)	Nodes are substrates and links are metabolic reactions.	Duch and Arenas (2005). Data obtained from networkrepository.com (Rossi and Ahmed, 2015).
Mouse Brain Visual Cortex	Nodes represent neurones and links represent neural connections.	Data obtained from networkrepository.com (Rossi and Ahmed, 2015).
Food Web	Nodes are predators and prey, links are predator-prey relationships.	Ulanowicz et al., 1998. Data obtained from networkrepository.com (Rossi and Ahmed, 2015).
Protein Protein Interactions (Yeast)	Nodes represent various proteins and links represent interactions between them.	Ito et al., 2001.

In this study, all the above networks were considered as undirected/unweighted networks. Initially, for each network, the degree correlation was established from the degree distribution. Then, 50 independent runs of DPR was conducted for each network dataset. During DPR no self-loops and multi-links between nodes were allowed.

In addition, for each network, the number of hub nodes with degrees $> k_s$ which can violate $E_{jk} > 1$ condition was calculated. For the two largest hubs, in each network, the number of links

required between them to maintain the neutral status (i.e. no degree correlation) was also calculated. These results are presented in Section 4.

4.0 Results

The following table outlines basic properties of the networks considered.

Table 2: Basic properties of the networks considered

	Nodes	**Links**	γ **(correlation)**	μ	$\langle k \rangle$	$\langle k^2 \rangle$	$\frac{\langle k^2 \rangle}{\langle k \rangle}$
SCNs							
Industrial Organic Chemicals	1479	2069	1.503 (0.891)	-0.136	2.798	27.190	9.718
Farm Machinery and Equipment	706	908	0.925 (0.85)	-0.273	2.572	27.630	10.743
Primary Batteries, Dry and Wet	617	753	1.555 (0.967)	-0.685	2.441	19.460	7.972
Aircraft Engines and Engine Parts	2025	16225	0.846 (0.869)	-0.366	16.025	1802.060	112.453
Biological Networks							
Metabolic (C.Elegans)	453	2025	0.956 (0.358)	-0.258	8.940	358.490	40.098
Mouse Brain Visual Cortex	193	214	1.092 (0.913)	-1.014	2.218	28.746	12.963
Food Web	54	353	0.537 (0.329)	-0.298	13.074	233.296	17.844
Protein Protein Interactions (Yeast)	790	761	1.806 (0.999)	-0.421	1.927	12.268	6.368

As shown in the table above, the degree distributions of all the networks considered can be reasonably approximated as scale free. The scale free exponent of all these networks are below 2. The degree correlations of these networks were established using Eq.10. As indicated by negative μ, all the networks indicate disassortative mixing. Also, the average degree of a given node's neighbours, for a neutral scenario of each network (without degree correlations), is provided in the right most column, as approximated using Eq. 9.

Table 3: Hub characteristics of the networks considered

	Degree of the largest hub	Degree of the second largest hub	Neutral network prediction, E_{jk} (between two largest hubs)	Structural cut-off, k_s	% of nodes with degree > k_s
SCNs					
Industrial Organic Chemicals	48	26	0.302	64.329	0
Farm Machinery and Equipment	30	20	0.330	42.613	0
Primary Batteries, Dry and Wet	25	23	0.382	38.808	0
Aircraft Engines and Engine Parts	241	233	1.730	180.141	1.90%
Biological Networks					
Metabolic (C.Elegans)	237	123	7.198	63.640	1.77%
Mouse Brain Visual Cortex	31	30	2.173	20.688	3.63%
Food Web	48	40	2.720	26.571	5.56%
Protein Protein Interactions (Yeast)	56	33	1.214	39.013	0.13%

Table 3 provides insights onto the hub structure of the networks considered. The neutral network prediction, E_{jk} provides the number of links required between the two largest hubs, for each network to maintain the neutral nature. For example, consider the Metabolic (C.Elegans) network, which has two largest hubs with degrees 237 and 123, respectively. Using Eq. 4, we establish that these two largest hubs should be connected by 7-8 links, in order for the network to be neutral. However, due to the simple network representation, two nodes can be connected, at most, by one link. Therefore, when E_{jk} is greater than 1, this induces structural disassortativity in networks. Also, the networks which include E_{jk} >1, include nodes with degrees which are above the structural cut-off, k_s.

The following plots illustrate the degree correlation function, $k_{nn}(k)$ for each network considered. The Red circles indicate degree correlations observed from each network with the line of best fit shown in light Red.

The Blue squares indicate average $k_{nn}^{R}(k)$, obtained from 50 independent trials of DPR (the error bars show the range of $k_{nn}^{R}(k)$ obtained). The line of best fit for average $k_{nn}^{R}(k)$ is presented in light Blue colour.

The horizontal Black dashed line indicates the degree correlations prediction, using Eq. 9, for a neutral network, with the same degree distribution as the considered network.

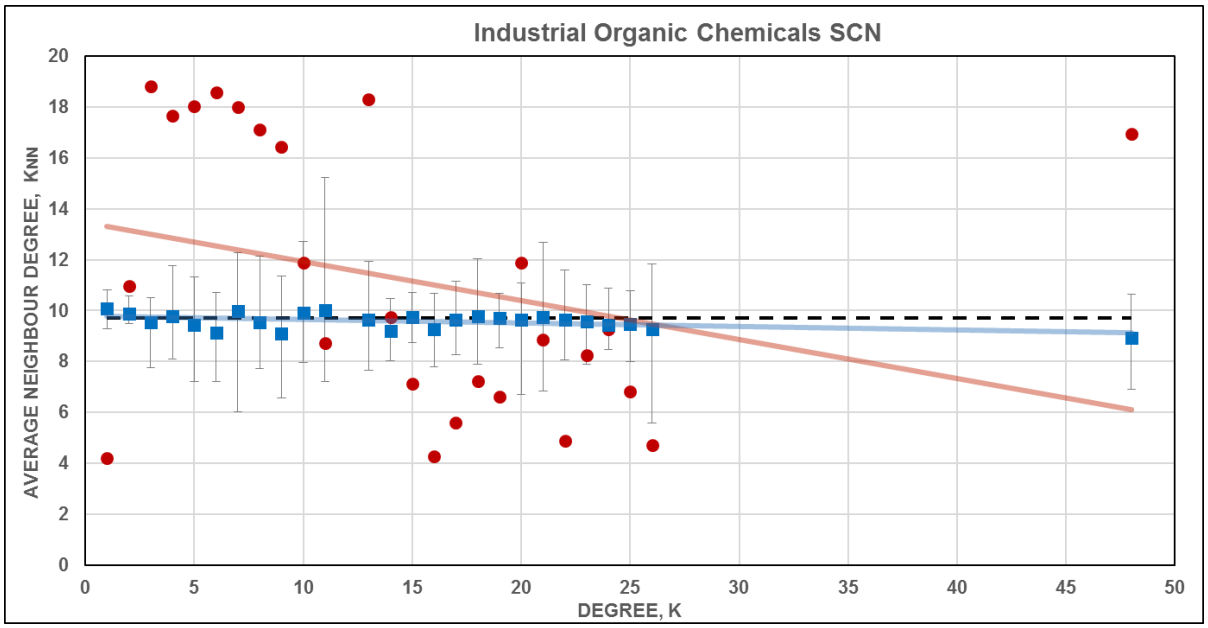

Figure 2a: Industrial organic SCN

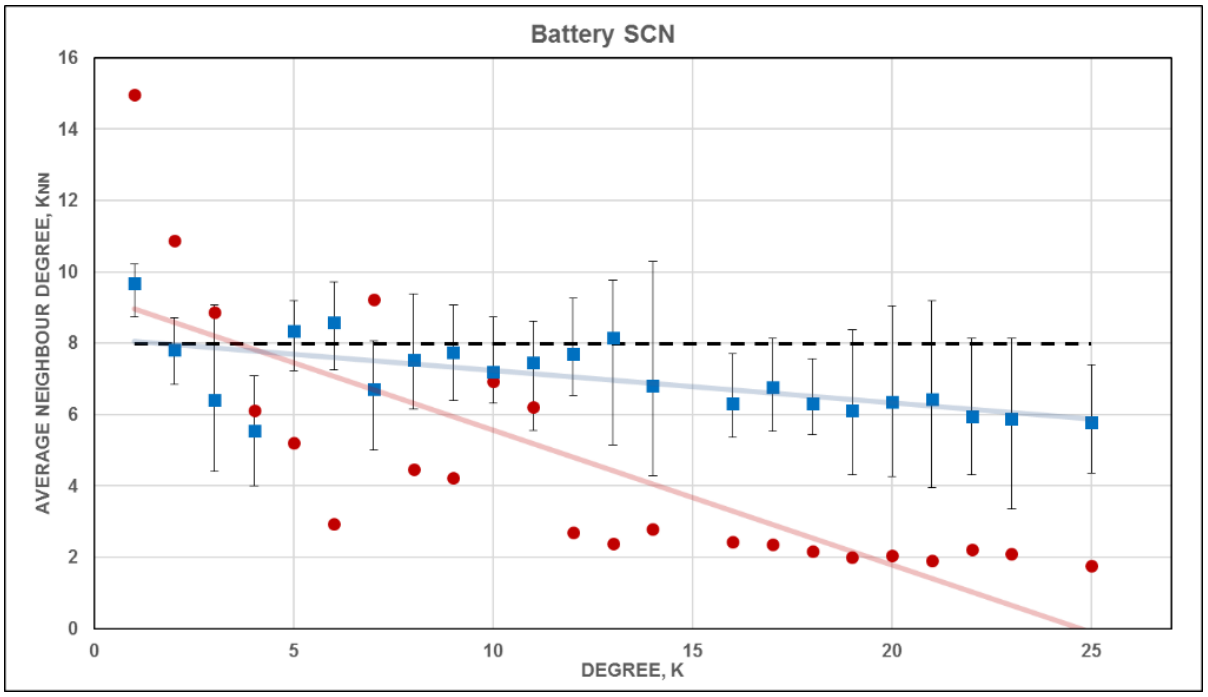

Figure 2b: Battery SCN

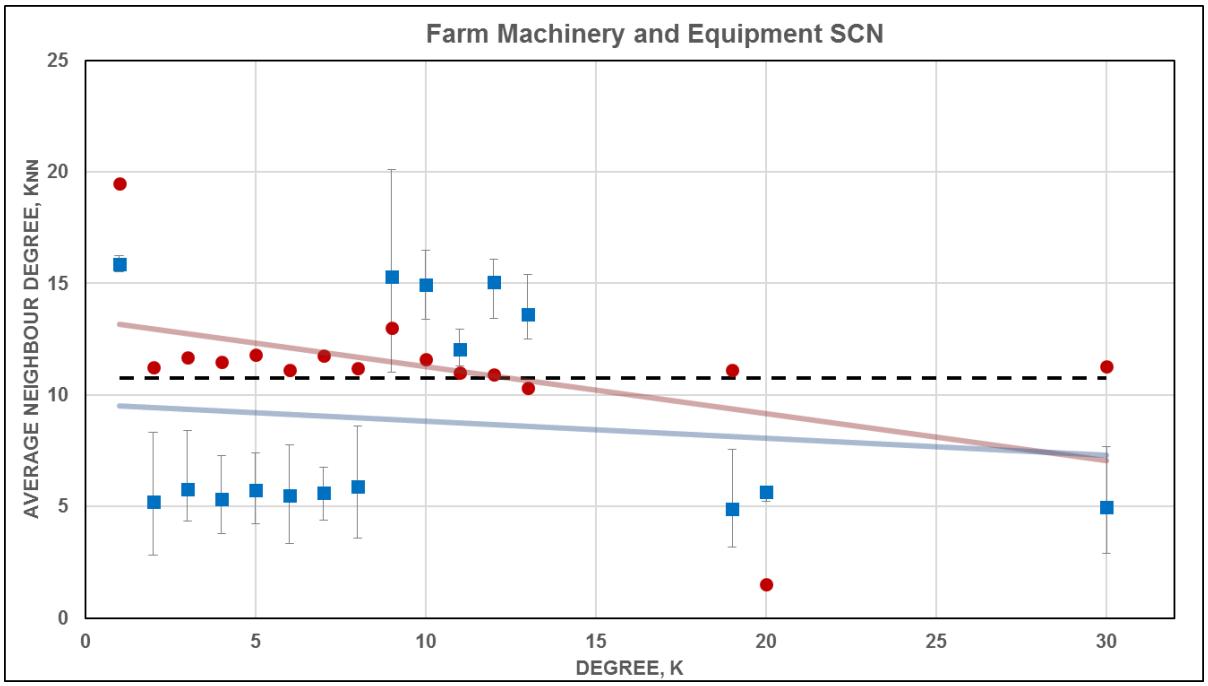

Figure 2c: Farm machinery and equipment SCN

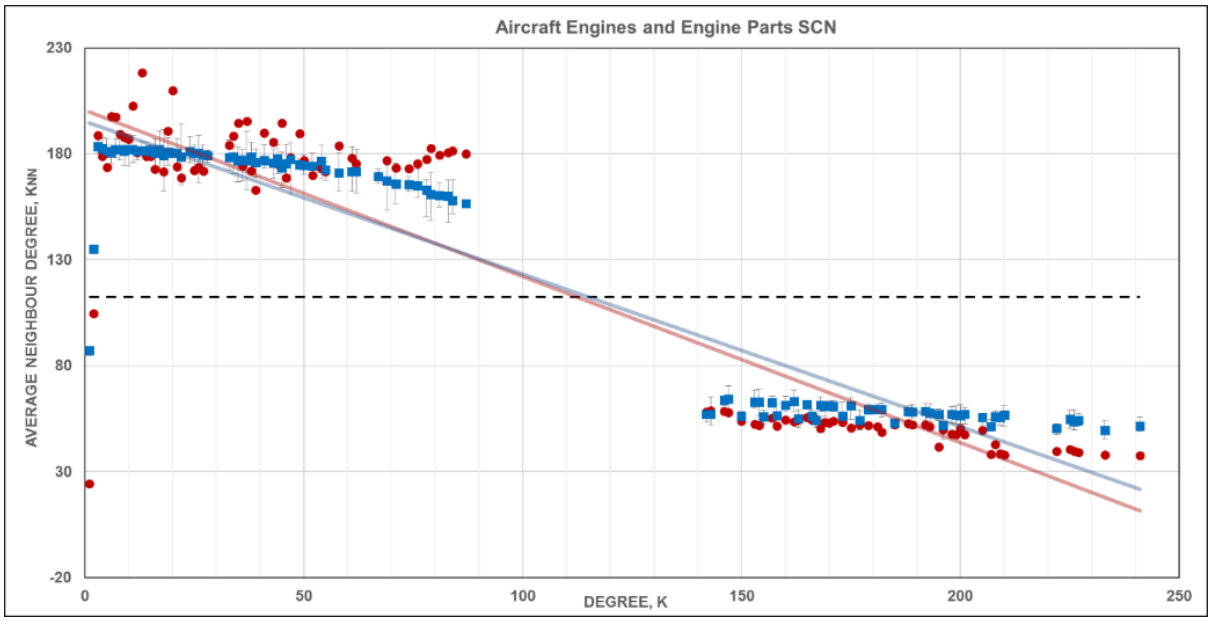

Figure 2d: Aircraft engines and engine parts SCN

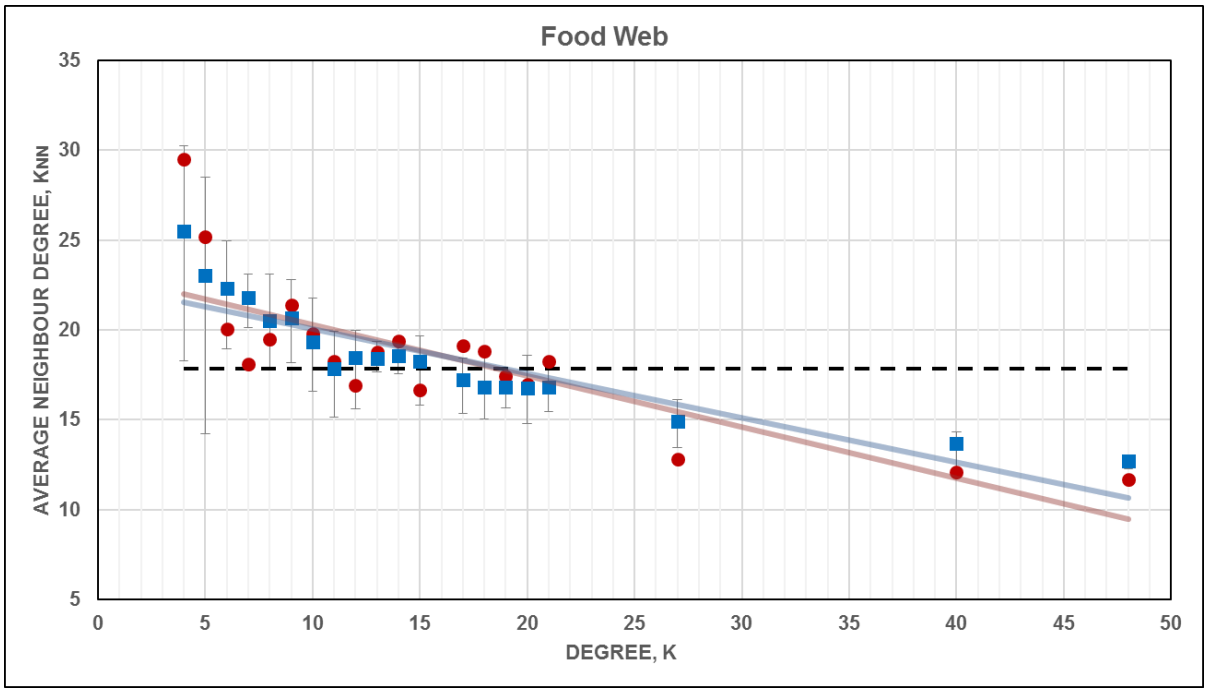

Figure 3a: Food web

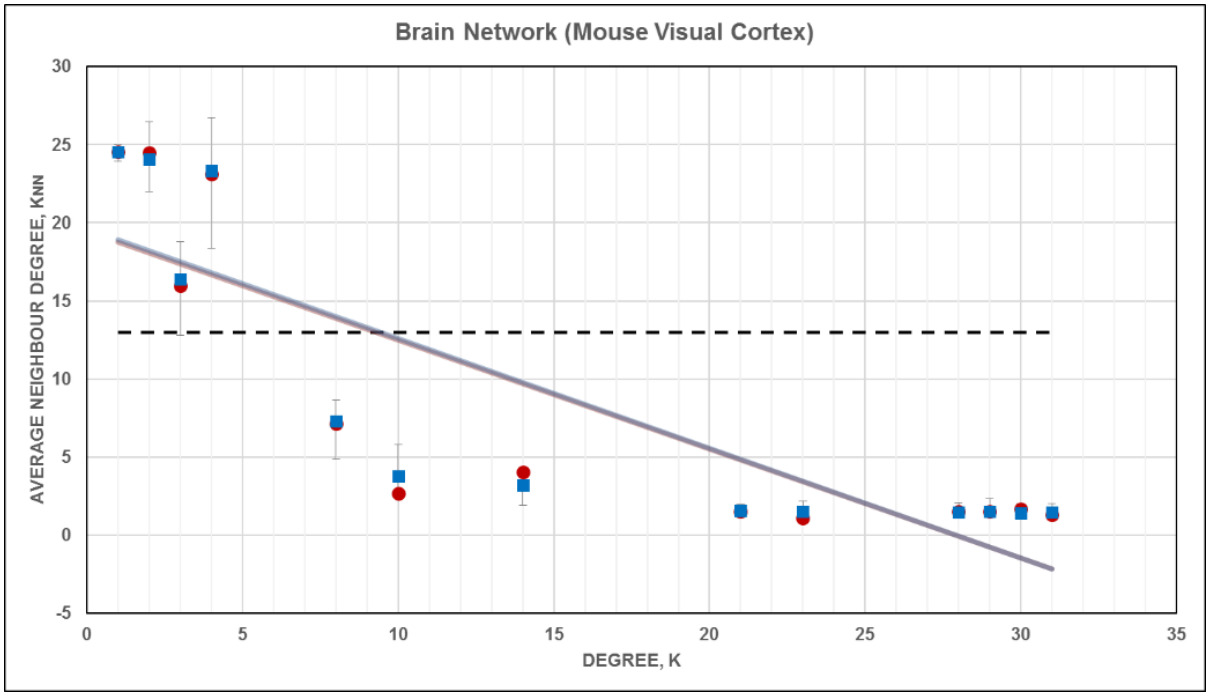

Figure 3b: Brain network (mouse visual cortex)

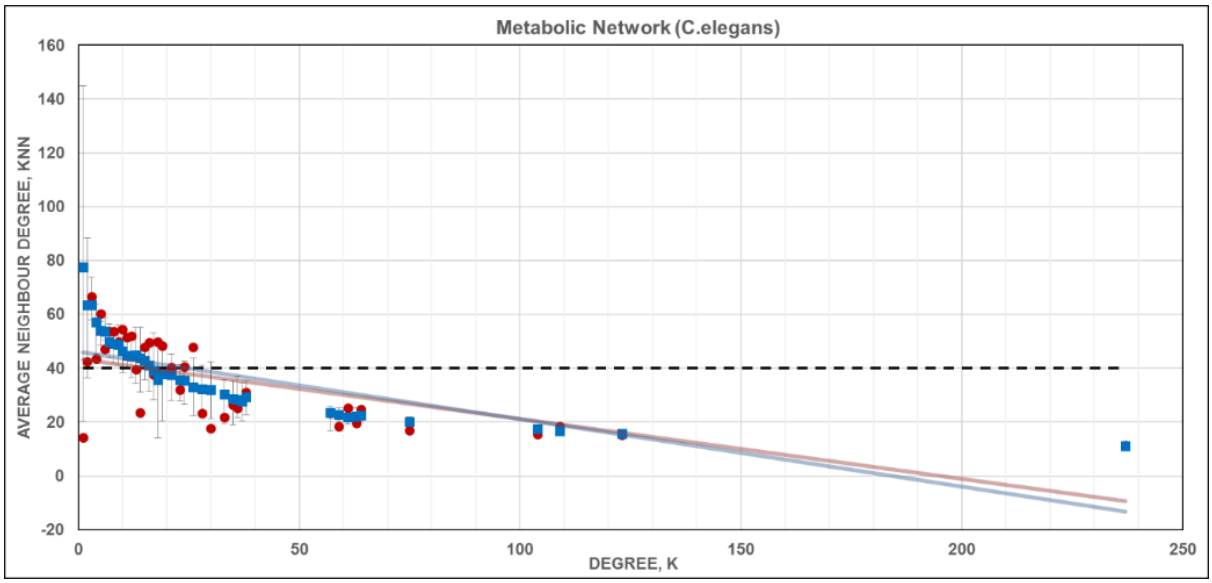

Figure 3c: Metabolic network (C. elegans)

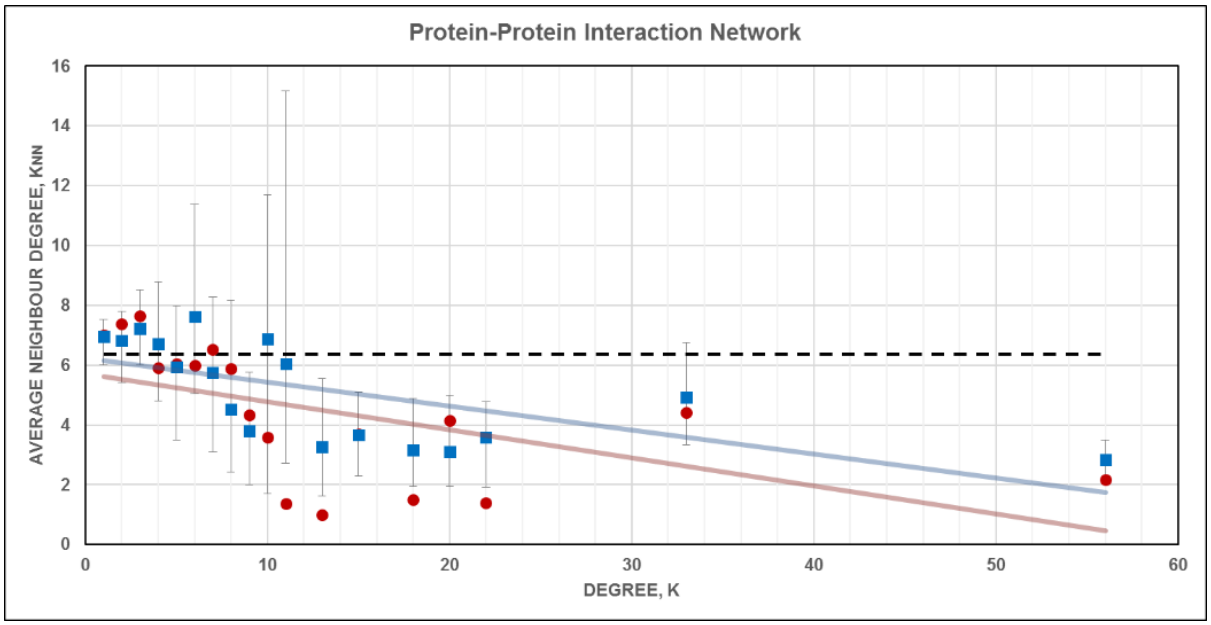

Figure 3d: Protein-Protein interaction network

5.0 Discussion

5.1 General observations from the results

From the results presented in Section 4, it is clear that all networks from both classes, show disassortativity – where average neighbour degree decays for higher degree nodes. Although all considered networks show disassortativity, there is an important distinction. The biological networks consistently show disassortativity which is structurally induced, while the SCNs show both structural and 'physical' disassortativity. Here, the term 'physical' is used to describe disassortativity which is driven by an underlying mechanism.

Consider the biological networks presented in Figures 3a-d. The scaling of $k_{nn}(k)$ for these networks are almost indistinguishable from $k_{nn}^{R}(k)$. This implies that the disassortativity which is materialised and observed in these networks are attributable to their degree distributions (i.e. DRP process can achieve the same level of disassortativity for the same degree distribution). Therefore, these networks are structurally disassortative, meaning their disassortative nature can be fully explained by their respective degree distributions, without attribution to any underlying mechanism which drives the system towards disassortativity.

In contrast, consider the SCNs presented in Figures 2a-c. The $k_{nn}(k)$ of these networks decay more rapidly than $k_{nn}^{R}(k)$. Also, the majority of the observed degree correlation data points for these networks, lie outside the range indicated by DPR. Therefore, the disassortativity of these networks cannot be fully explained by their respective degree distributions. There is an underlying mechanism which drives these systems towards disassortativity. However, the aircraft engines and engine parts SCN, presented in Figure 2d, indicates structural disassortativity as evident by the indistinguishable scaling of $k_{nn}(k)$ and $k_{nn}^{R}(k)$. This observation is further corroborated by E_{jk} being greater than 1 for this network. Therefore, it is evident that while all biological networks considered in this study indicate disassortativity which is of structural origin, the SCNs can include both structural and physical disassortativity.

Another important aspect of all the networks, considered in this study, are their scale free exponent, which always lies below 2. Many properties of a scale-free network depend on the value of the degree exponent, γ. Therefore, it is interesting to establish how the network properties vary with γ. For a scale-free network, the expected maximum degree k_{max} (the natural cut-off) which represents the expected size of the largest hub can be estimated using Eq.11 (Barabasi, 2016). Based on Eq. 11, when $\gamma<2$, the exponent $\frac{1}{\gamma-1}$ is larger than 1. Therefore, the link acquisition rate of the largest hub (i.e. node with k_{max}) is faster than the growth of the network in terms of the number of nodes present. Accordingly, no large networks can exist in this regime, since the largest hub will eventually run out of nodes to connect to. In this scenario, the high-degree nodes are disproportionately attractive. This winner-takes-all dynamic leads to a hub-and-spoke network topology in which all nodes are within a short distance from each other.

From Table 3, it can be seen that in the cases where structural disassortativity is observed, this is due to the relatively minor proportion of the super-rich nodes whose degrees exceed the structural cut-off, k_s. However, as γ continues to increase beyond 2, the networks include smaller and less numerous hubs, which ultimately leads to a topology similar to that of a random network where all nodes have almost the same number of connections.

5.2 Biological networks

It is known that in assortative networks, due to high degree nodes pairing up with each other, percolation and formation of a giant component is facilitated, while the opposite is true for disassortative networks. Also, another unfavourable implication of disassortativity is that since high degree nodes are less connected to one another, many paths between nodes in the network are dependent on high degree nodes. Therefore, failure of a high degree node (under a targeted attack which selectively compromises hubs) in a disassortative network, would have a relatively large impact on the overall connectedness of the network (Noldus and Van, 2015). In particular, since most low degree nodes are connected to hubs in a disassortative network, removal of a hub also removes these low degree nodes. In comparison, in assortative networks, removal of hubs are less damaging due to the presence of multiple/redundant hubs which are connected with each other to form the core of the network.

Sinha (2009) acknowledges that assortative mixing in networks has favourable implications in terms of robustness and questions why natural evolution of biological networks has favoured disassortativity. Justification is then put forth relating the advantages for dynamical stability of networks arising from disassortative structures. It is not difficult to imagine that assortative network structure can lead to cascading disruptions – where a disruption at one leaf node can spread quickly within the network through the connected hubs (Brintrup et al., 2016). On the other hand, disassortative networks are generally resilient against cascading impacts arising node failures – since hubs are not connected with each other, the likelihood of disruption impacts cascading from one hub node to another is minimised (Song et al, 2006).

A number of previous studies have stated that the mechanism underlying the origin of disassortativity in biological/cellular networks remains unexplained (Barabasi and Oltvai, 2004; Atanas, 2007; Barzel et al., 2012; Walhout et al., 2012; Sah et al, 2014). However, some studies have formulated plausible mechanisms which may underlie the observed disassortativity in biological networks (Dan et al., 2007; Xu et al., 2010) while a number of other studies have constructed network growth models which can mimic the observed disassortative mixing of biological networks (Tian and Shi, 2007; Takemoto and Oosawa, 2007; Zhou et al., 2009; Wang et al., 2015). While most of these mechanisms relate to duplication and divergence principles, no attempt has been made to first rule out the structural disassortativity. As shown in the results presented in this study, it is evident that the observed disassortativity in biological networks (those which were investigated in this study) is structurally induced, meaning their disassortative nature can be fully explained by their respective degree distributions, without attribution to any underlying mechanism which drives the system towards disassortativity.

The above result reveals the importance of moving beyond simple network representation (which allows, at most, only one undirected link between any pair of nodes) when studying disassortativity in biological networks. Our findings confirm that the restriction to single links between node pairs, in simple network representations, accounts for all of the anti-degree correlations observed in the biological network cases considered.

In addition, the direction of the links provide important information in relation to the structure of the biological networks. For metabolic networks in particular, a meaningful understanding

requires one to consider the direction and the temporal aspects of the interactions (Almaas, 2007). Piraveenan et al (2012) have shown that although undirected biological networks may appear disassortative, when directedness is considered, they do in fact become assortative. Therefore, future analysis of biological systems should consider representation of networks as directed with multi-link formations allowed between nodes.

5.3 Supply chain networks

As shown in the results, apart from the Aircraft Engines and Engine Parts SCN, the remaining 3 SCNs all indicated disassortativity driven by an underlying mechanism. A reason for this physical disassortativity in SCNs could be due to the heterogeneity in the functions undertaken by the firms which are represented as nodes in the network model. Such disassortative mixing has been observed commonly in economic systems (Barabasi, 2016). For example, in economic settings, trade typically takes place between individuals or organisations of different skills and specialities. The above is certainly true in the SCN – where a supplier is most likely to link with a manufacturer, rather than to another supplier. This inherent functional property, in the SCN context, is likely to be responsible for forcing the SCNs towards disassortative mixing – which leads to hub and spoke network topology.

Nacher and Akutsu (2012), and Molnar et al. (2013) have examined the dynamical control of a network by considering a model of reduced complexity, where a minimum set of possible nodes dominates the whole system, called the Minimum Dominating Set (MDS). An important finding suggests that only a few nodes are needed to control the entire network if $\gamma < 2$, whereas many nodes are required if it is larger than 2. When $\gamma < 2$, the number of connections in the network increases faster than the number of nodes, resulting in highly heterogeneous network connectivity. Such networks tend to be dense and centralised with small average shortest path lengths, and therefore are inherently easy to dominate. Given the vital role of coordination and control in SCNs, particularly due to largely unpredictable market demand conditions, it could be that SCNs self-organise themselves towards hub-and-spoke topologies where $\gamma < 2$, so as to minimize the size of the MDS. Being able to control the overall network through control of a handful of firms can have remarkable advantages in an economic context (Perera et al, 2015).

6.0 Conclusions

In this paper, we have investigated the observed disassortative tendencies in man-made supply chain networks and naturally occurring biological networks. Degree preserving randomisation is used to generate an ensemble of null models for each network. Comparison of the degree correlation profiles of each network, against that of their degree preserving randomised counterparts reveal whether the observed disassortativity in each network is of structural nature or not. We find that in all biological networks, the observed disassortativity is of structural nature, meaning their disassortative nature can be fully explained by their respective degree distributions, without attribution to any underlying mechanism which drives the system towards disassortativity. However, in supply chain networks, we find one case where disassortativity is structurally induced and in other cases where it is mechanistically driven.

Future work should focus on investigating a plausible mechanism underlying the disassortative mixing observed in networks. However, as outlined in this paper, a vital step for any future

research aiming to establish the mechanism underlying disassortativity is to rule out structural disassortativity by thorough analysis. If a network is found to be structurally disassortative, then no specific mechanism is needed to be invoked to account for its disassortativity.

7.0 References

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