Analysis of psychostimulant-induced group behaviours using network based framework in *Drosophila melanogaster*

Milan Petrović
Department of Informatics,
University of Rijeka,
Radmile Matejčić 2, 51000 Rijeka, Croatia
Email: milan.petrovic@uniri.hr

Abstract—This paper presents an overview of the field related to tracking, quantification and analysis of animal behavior, with attention to *Drosophila melanogaster* and their application to the analysis of social behavior in terms of social networks analysis.

Examples of using the method of complex networks analysis over social interaction networks of animals and application of the analysis of network measures to changes within the group and the behavior of individuals within the group are presented.

The method of analysis of complex networks at the global, middle and local level is described with reference to measures and their role in the analysis of social networks.

In preliminary work we tested method of complex network analysis over *Drosophila melanogaster* groups, one group was controle and one was psichostymulant induced and tracked changes in their networks.

Keywords - Social networks analysis, Social interaction networks, *Drosophila melanogaster*, psychostimulant-induced behaviours

I. INTRODUCTION

Complex networks analysis is relatively new area that is being actively researched. They have their application in various domains such as distribution networks [1], biological networks [2], , wang2014identification, information networks [3], social networks [4], etc.

Complex networks have also found their application in the field of studying behavior within a group. They enabled the quantification and dynamic display of group behavior using social interaction networks. Many papers use the method of analyzing complex networks in researching animal behavior [?, 5, 27]. Network analysis can be performed at multiple levels. We can approach networks to analyze their basic component which is the node, by exploring measures concerning the local level of the network. Then at the middle level we can observe the relationships between the nodes that occur within the network and the sub-graphs that these nodes form. And finally, we observe the properties of the complete network on a global scale, where we observe measures relating to the whole network. As the mutual relationship of individuals itself does not consist of only one form of behavior but is much more complex. Multilayer networks [6]–[8] and multiplex networks [9, 10] can also be used to display and analyze such complex systems and compelx behaviors.

In this research we are focused on analysis of psychostimulant-induced group behaviours u in *Drosophila melanogaster*.Addiction is a complex disease that in the laboratory environment is reduced to the study of easily measurable addiction-related endophenotypes [11]. Social interaction and drug addiction booth share common neuromodulatory neurons in the brain. *Drosophila melanogaster* has been successfully used as a model organism for the study of behaviours related to addiction: alcohol, nicotine and cocaine [12]–[14].

Decades of basic research on neurobiological mechanisms of drug addiction uncover main protein targets and neuroplastic changes induced by drug addiction. But despite huge success in biological research we are still missing effective method of treating addiction in humans. A potential reason for this is that mechanistic studies using animal models do not incorporate a critical trait of human addiction, volitional choices between drug use and social interaction. Recent studies on rats suggests that social interaction can change the activity of specific neuronal circuits that control drug craving and relapse [15, 16]. To address influence of psychostimulant on social interaction networks before and after the administration of psychostimulants *Drosophila melanogaster* is used.

The rest of the paper is organised as follows. In the second Section overview of related work is given. In the third Section overview of complex network measures is presented. Fourth Section presents experiment and preliminary results. In the fifth Section give future work and last Section concludes the paper.

II. RELATED WORK

A. Animal social networks

Complex networks have proven to as a good tool in for the analysis of complex data and systems [17, 18].

Application of complex networks in the analysis of living beings are social networks or social interaction networks. Social networks are networks in which, a node represents an individual and the link between two nodes represent relationship between these two individuals [19, 20]. Depending of the

domain and task these networks can be constructed as directed or undirected and weighted or unweighted.

Makagon et al. describe standardized mathematical methods for calculating metrics of socialization in interaction networks of animals [21]. They propose a set of standard network measures that can been used for analysis of the social behavior of animals in general. In the proposed (Section IV) approach, we use some of these measures, but we cover the wider set of measures. We include some other network measures that have been usually applied in the domain of collaboration network analysis [22] such as: average strength, shortest path length, global efficiency, transitivity,number of components, modularity, local network measures, etc.

Application of network measures can be used as a tool to find patterns of behavior within groups of animals in different species and thus it can help us observed changes in relationships within the group that occur under a particular external or internal influence and understand behavior on wider scale [23]–[25].

Drewe et al. analyzed interactions of wild merkat population and found significant differences in structure over shorter timescales, they pointed that strongest predictors of network structure were spatial factors and pointed that social network analysis must take spatial factors into account [26].

Further, in [27] authors provided theoretical analysis of macaques networks and concluded that networks of intolerant and tolerant societies appeared to be robust to the loss of individuals.

Authors in [5] examined prairie dog social groups and found well connected individuals acting as hubs or bridges inside network and pointed that social network analysis is a robust and efficient tool for examining social dynamics.

B. Social networks of Drosophila melanogaster

There are only few studies of the social interaction networks of the *Drosophila melanogaster*. The main reason is that it is hard to collect individual tracking data of large groups of flies.

Schneider et al. authors studied formation of nonrandom social interaction networks of *Drosophila melanogaster* [28]. They set a method of constructing social interaction networks, where mutual interactions are determined according to three criteria: angle, mutual distance of individuals and duration of interaction between individuals.

It is pointed out that social networks formation depends on chemo-sensory cues and that measures in formed networks differ by different wild-type strains. Specific behaviour types and their quantitative values between flies are displayed in [29] and structure stability over time in social interaction networks is shown in [30].

Pasquaretta et al. tested information spreading in social network between 'informed' and 'uninformed' flies, and using social network analysis, showed that selective information use seems to be based on the level of homogeneity of the social network [31].

In [32] authors show that with usage of combined quantitative and genetic tools to is possible to display social network formation and collective behavior in *Drosophila melanogaster* group behaviour.

In [33] authors introduced a computer vision pipeline for tracking and analysis large groups of flies and tracking results were used to track changes in social interaction networks. They compared social interactions of fruit flies that have been isolated with social interactions of the controlled population.

Quantitative behaviour measures differences among individuals differ within population but have positive correlation and permanency of particular behaviour through time of experiment in [34] and measures of position and mutual distance between individual flies can differ, and they depend on sex, genotype and social environment [34, 35].

C. Tracking and annotation software

With the development of artificial intelligence and video tracking techniques, software for tracking animals and their behavior has been developed and improved [36]. There is several programs that that allow tracking *Drosophila melanogaster* on individual level within the group. They differ in the number of individuals, they can track other animals [37]–[40] and some of them are primary developed for flies tracking [34, 41].

The most widespread and most commonly used is Ctrax which enables tracking up to 50 flies [35] . although quite often present Ctrax has been shown to create errors when tracking individuals (loss of tracking, change of identity, etc.) so new software is being developed that solves this problem [42], proved to be more accurate in one-hour videos, where no identity swaps were achieved within groups of up to 50 individuals. With development of this methods and software it is possible to track individuals within a group and then identify the types of their behavior with manual or automatic annotation [33, 43].

D. Complex network analysis software

A library written in the Python programming language, called NetworkX, is used to analyze network data [44]. Gephi an open source software was used to visualize and edit the visual appearance of a given network [45].

III. METHODOLOGY

Network is represented as a graph $G = (V, E)$ which is a pair of two sets, the first set V consisting of vertices and the second set E consisting of edges. In the domain of network analysis, the vertices are referred as nodes and the edges are called links. In weighted networks every link connecting two nodes i and j has an associated weight w_{ij} [46].

The total number of vertices is denoted as N and the total number of edges is denoted as K. On the global level we analyse standard network measures in order to describe network characteristics.

A. Analysis on the global level

At the global level, we observe measures that are related to the entire network. Their values help us to identify the network itself with networks that are similar to it or to give us some properties that a given network possesses.

We will first show the measures that are related to the properties of clustering. In general, the **clustering coefficient** is a measure which defines the presence of loops of order three. The clustering coefficient of a node i is defined as:

$$C_i = \frac{e_{ij}}{k_i(k_i - 1)}$$

where e_{ij} represents the number of pairs of neighbors of a node i that are connected. Then average clustering coefficient is defined as: $\langle c \rangle = \frac{1}{N} \sum_i c_i$. There is another variant of the clustering coefficient which takes into account weights in the network defined for weighted networks denoted as $\langle c_w \rangle$. **Network transitivity** is another measure of clustering, where possible triangles are identified by the number of triads (two links with a shared node):

$$T = 3 \frac{\#triangles}{\#triads}$$

Further, node **asortativity** is a measure of a preference for attaching to other nodes that are similar. There are various possibilities to define similarity. Network is said to show assortative mixing by degree if nodes tend to be connected to other nodes with similar degree. If opposite is true than we say that network show disassortative mixing by degree. It is calculated as Pearson correlation:

$$r = \frac{\sum_{jk} jk(e_{jk} - q_j q_k)}{\sigma_q^2}$$

where e_{jk} is the joint probability distribution of the excess degrees of the two nodes at either end of a randomly chosen link. Here $q_j q_k$ and σ_q^2 are the expected value or mean, and standard deviation, of the excess degree distribution.

The maximum number of edges in network if we exclude self-edges and multiedges is $\frac{1}{2}n(n-1)$ where n stands for the number of nodes. If we count all network connections made as m we can easily present network **density** as:

$$\rho = \frac{2m}{n(n-1)}$$

In the following, we continue with the measures related to the length of the path in the network. **Average path length** where d_{ij} denotes the number of links lying on the shortest path between nodes n $i, j \in V$:

$$L = \sum_{i,j} \frac{d_{ij}}{N(N-1)}$$

And the **network diameter** is the longest of all the calculated shortest paths in a network $D = \max(d_{ij})$.

Based on distances between nodes in the network, **global efficiency** is defined as a property which can show how efficiently information is exchanging over the network:

$$E_{glob}(G) = \frac{1}{N(N-1)} \sum_{i \neq j \in G} \frac{1}{d_{ij}}$$

.

Number of components in network shows how well is network connected and enables identification the size of the giant (largest) connected component.

B. Analysis on the middle level

At the middle level of network analysis, the relationships between nodes within given group or set is observed. We call this set or group a sub-graph of the network. Number of nodes in sub-graph is smaller than the total number of nodes in the network and sub-graph size is most often predefined by certain rules or algorithms.

The most important measure at the central level by which communities within a network are identified is **modularity**. It is a measure of the strength of division of a network into communities, and maximum value of the modularity is 1. Community detection is usually performed with the use of the Louvain algorithm [47].

In addition to sub-graph that do not have a predefined number of nodes, we can also observe sets that have a predefined number of nodes. In this way we can observe motifs and graphlets in the network.

Motifs are patterns of directed sub-graphs in the directed networks. The aim of motif-based network characterisation is to detect significantly over-represented and underrepresented patterns of motifs in the network [48], [49]. Motifs in the network defines: their pattern, occurrence and significance in the network. Motifs contribute to a better understanding of the network and its structure, and help predict network behavior. It should be noted that the motifs are consisted of directed edges, where on the other side grapleths don't.

Graphlets are non-isomorphic sub-graphs of a larger network [50]. As noted before, their difference from motifs is that graphlets are sub-grahs of undirected networks. From the node perspective, nodes position within the graphlet and in which graphlets it participates is taken into account.

Graphlets of 2 to 5 nodes and motifs consisting of 3 to 8 nodes are most often searched for in the network, these figures are relevant in terms of computational power, but they are also most often used in research. Sub-graph counting can be performed using Exact Sub-graph Enumeration algorithm [51] and Sub-graph sampling [52].

C. Analysis on the local level

At the local level we observe measures that relate directly to the node itself. These measures are based on the number of node edges and its position within the network itself and the relationship with other nodes.

The number of edges directly connected to node is nodes **degree**. If edges are weighted then the weight degree of the node is considered and in directed network we distinguish *in-degree* and *out-degree* which are based on inbound and outbound node edges. In multigraph two nodes can share multiple edges between them, and therefore node degree does not reflect the number of neighbors of that node [17]. In the context of social networks the degree of node can be interpreted as the amount of interaction of an individual (degree) with other individuals (nodes) in the network [53].

With the help of nodes degree, centrality measures can be derrivered. Centrality measures play important role in social network analysis and their application helps to find most

important nodes (persons/animals) in the network. They can be also used as a specific measure of an individual's behavior within a group (network).

Degree centrality is the most basic measure we can calculate after determining the degree of nodes and it is the fraction of nodes for which is node connected, shares edge. In social networks, the degree centrality can tell us about the connection of the node itself with other nodes in the network and thus about the nodes ability to exchange and receive information from other nodes or to influence their behavior.

While degree centrality can be useful to detect most connected nodes in network, we can't say nothing about 'quality' of neighbours the node is connected with. With **Eigenvector centrality** the node 'importance' in network is measured, and it is measure of how good are adjacent nodes of node connected. It can be interpreted as node centrality based on centrality of nodes neighbors.

The nodes position in the network according to the mean distance to all other nodes is expressed with **closeness centrality** and its application in social networks analysis, for example, may be that a node that has a small distance to all other nodes in the network may indicate that information from that node can spread faster and easier in the network.

While in closeness centrality we look at the length of the path, with the analysis of the path itself, we can make a different approach to interpretation and we can measure fraction of all shortest paths in network that passes through given node defining **betweenness centrality**. This measure can be useful in social networks to find individuals who act as bridges between groups within the network or to determine role in network that node has.

IV. PRELIMINARY RESULTS

This section describes preliminary results for analysis of psychostimulant-induced group behaviours using network based framework in *Drospophila melanogaster*.

We experimented with a network based approach for analysis of the group behaviours of adult *Drosophila melanogaster* males. We performed a quantitative analysis of social interaction networks structure and topology on the local, middle and global network level. The main goal of this experiment was is to identify which network properties capture the psychostimulant-induced behaviour in the social interaction networks of fruit flies. More precisely, the aim of this experiment is to explore which network measures can differentiate between psychostimulant-induced behaviours and usual group behaviours.

We used circular arena reduced to two dimensional motion and video recording of flies' interactions. Next, by using open source software Flytracker [29] we identified touch events of flies and based on these data, we construct a set of weighted social interaction networks [**?**]. In social interaction networks, nodes represent flies, edges denote interactions between two flies and weights count frequencies of interactions between two flies. We compare social interaction networks of two different groups of flies: (i) CTRL networks based on the

social interactions of the group of flies raised on the regular food (ii) COC networks based on the social interaction of flies that was administrated orally trough food to 0.5 mg/mL of cocaine for 24 hours before tracking.

We observe the behaviour of the individual within the network on the local level and the global measures of the network. By distributing a local network measure, we can see the differences in the behaviour of the individual. Preliminary results confirm our assumption that there are certain measures that may differentiate between CTRL and COC networks.

A. Data acquisition

Male flies are selected for the experiment the and processed day before with the cold anesthesia, after which they stay together in a bottle for next 24 hours. In the first bottle, males are placed on a normal nutrient medium. In the second, they are on a substrate that contains drugs.

The arena is made of plexiglass, the lower part is made of blurred white plexiglass for lighted background. The upper part is transparent so the movement can be observed. The arena was made with the help of Faculty of Engineering, Department of Mechanical Engineering [1].

For video tracking we use Flytracker program, which extracts the position of all individual flies and some other measures. The output of the program in tables that have all individual units recorded for each frame.

Time duration of observation is 10 min. Flies are placed in the arena, filming process start after first 15 min used for for environment adaptation.

B. Network construction

Network is represented as a graph $G = (V, E)$ which is a pair of two sets, the first set V consisting of vertices and the second set E consisting of edges.

Based on the data extracted using Flytracker, we constructed weighted networks of interactions between flies. The network is constructed in such a way that each fly is a node and the link is established if two flies have interaction within two body distances (4mm) longer than 0.5 seconds. The weights in the graph are determined as total time spent in contact (within 4mm) and count of how many times flies made contact during one observation.

We separate networks into two different groups: CTRL networks and COC networks based group of flies raised on the regular food and group of flies that was administrated with cocaine.

C. Network based analysis of SIN

In this Section we present the preliminary results of the comparison of five CTRL networks and five COC networks. Additionally, we calculated average values of all global measures for both network classes. All values of global network measures are reported in Table I.

It is possible to identify set of measures that exhibit certain differences between CTRL networks and COC networks. It

measure	average CTRL	average COC
N	30.40	27.40
K	43	72.20 5
$<k>$	2.82	5.19
$<s>$	4.25	7.83
d	0.10	0.19
L	2.63	2.09
D	6.00	4.20
E_{glob}	0.27	0.47
c	0.21	0.30
T	0.26	0.41
d_{het}	0.85	0.72
r	-0.12	-0.01
N_C	8.40	3.40
GCC	22.6	25
Q	0.31	0.20

TABLE I: Global measures in social interaction networks for COC and CTRL populations: number of nodes N, number of links K, avg degree $<k>$, avg. strength $<s>$, density d, avg. path length L, diameter D, global efficiency E_{glob}, clustering coeff. c, transitivity T, heterogeneity d_{het}, asortativity r, number of components N_C, size of giant component GCC and modularity Q.

is shown that there is a significant difference for values of average degree and strength. Values of average degree are twice as high in the COC networks than in the CTRL networks. Consequently, values of network density are also twice as high in COC networks. Transitivity is higher in COC networks as well. For average clustering coefficient there are higher values in COC networks for weighted and unweighted measures of clustering, while average weighted clustering coefficient measure have small difference between networks. Average betweenness centrality does not differ significantly between networks for unweighted values, while for weighted values we have slightly higher measures for COC networks.

For range measures there are slightly higher values in diameter and shortest path length in CTRL networks. Values of degree heterogeneity and assortativity do not show any differences between networks.

On the middle level, there are differences in number of communities. On average, CTRL networks have twice more communities than COC networks, this fact is due to the large number of individuals that are not connected to the rest of the network in CTRL networks. As well, values of the modularity measure differ in terms that these values are higher in CTRL networks than in COC networks. Size of communities is on average slightly larger in COC networks, including an average value of the biggest community in networks (see table II).

Measure	Ave CTRL	Ave COC
Number of communities	11.6	6.8
Number of single element communities	7	2.4
Number of communities without single	4.6	4.4
Biggest community size	7.8	8.4
Size of the second biggest community	5.8	6.6
modularity (Q)	0.307	0.1964

TABLE II: Measures of the middle layer for COC and CTRL networks.

On local network level we analysed individual flies as nodes in terms of four centrality measures: closeness centrality and degree centrality. The results are shown as box plots diagrams in Fig. 1 and in Fig. 2. There are differences in values in these centrality measures distributions for which COC networks tend to have higher values than CTRL networks.
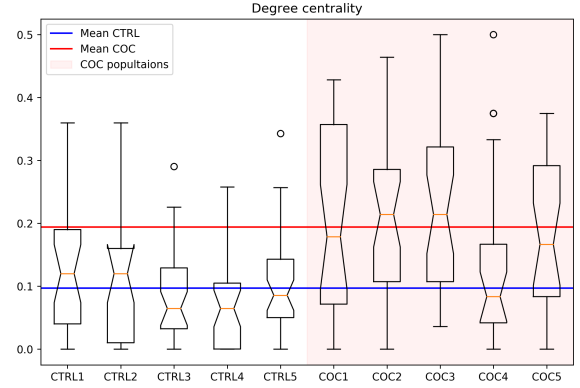

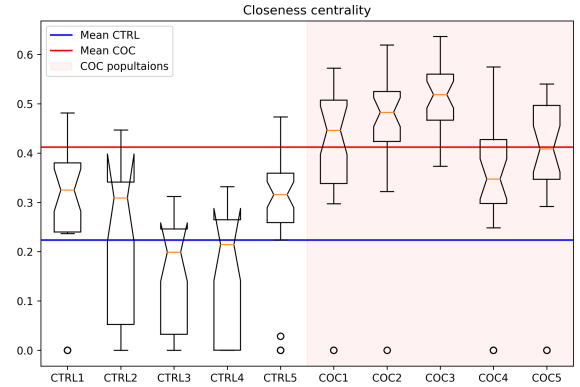Fig. 1: Degree centrality measures distributions across CTRL and COC social interaction networks.

Fig. 2: Closeness centrality measures distributions across CTRL and COC social interaction networks.

V. FUTURE WORK

With this approach of analysis, a universal tool can be created to monitor changes in the system that occur during external influence on system participants, in our case nodes in the network. And thus one can observe the changes that occur over individuals after a certain influence of the mentioned external force occurs on them.

The approach to behavior analysis using the method of complex networks has already proven to be a good and useful tool. Thus, it can be used to investigate in detail the values that the behavior of a particular group or individual creates.

This approach facilitates and simplifies the quantification of behavior and can be used as assistant tool in the research of the genetic background responsible for behavior.

For the further work we plan to extend this preliminary experiment in few directions: (i) investigate which network measures are important for the study of social interactions of *Drosophila melanogaster* in different conditions. Different conditions refer to different amounts of psychostimulants that would be given to the group before the experiment itself, and also changes in the group that would first be observed without the influence of psychostimulants and after the influence of the same. Experiments with specific strains of *Drosophila melanogaster* would then be performed, and their network properties would also be examined and compared with networks created with populations that were on psychostimulant.

(ii) Develop a network-based methodology for the analysis of *Drosophila melanogaster* SIN-s that can be applied to various situations in terms of quantitative analysis and comparison of drugged / non-drugged, mutants / non-mutants groups of flies.

(ii) Another idea is to expand the proposed methodology to analysis of complex networks in such a way that a multilayer or multiplex network is created from the monitoring data by interpretation. Here it is necessary to explore the application of multiplex and multilayer networks. And it should be added that in addition to data analysis, the interpretation itself with complex networks.

(iii) It is also possible to perform an analysis of the trajectory of individuals using machine learning and deep learning methods. Preliminary results showed that it is possible to perform precise classification with deep learning in distinguishing behaviors and trajectory segments between individuals of the control group and the group under psychostimulant.

VI. CONCLUSION AND DISCUSSION

This paper provides an overview of existing research and methods for network-based analysis of SIN of the *Drosophila melanogaster*. Further examples are presented by analyzing social interaction networks on animal networks and overview of the measures of complex networks is then given. Preliminary results of the research focused on the comparison of behaviours between two populations of *Drosophila melanogaster*: usual group behaviours vs. psychostimulant-induced behaviour in terms of social interaction networks is presented. The comparison is performed on the global, middle and local network level.

On the local level we can see that the average values of degree and closeness centrality are almost twice as high for COC networks, while the measures of eigenvector centrality and betweenness across COC and CTRL networks are on average equal, while. Thus, it could be concluded that psychostimulant treatment increased the activity of nodes in the networks.

Measure of modularity which is on average higher for CTRL networks shows that CTRL networks have higher tendency to form communities that COC networks. This property may indicate that increased activity in COC networks did not increased interactions within the communities (groups of flies) in population, but on the contrary, the communication is spreading outside the communities. On the global level, measures related to the number of links in the network are significantly higher in COC networks, and thus the measures that include the shortest path have resulted in increased values in COC networks. Consequently, this resulted in increased global efficiency in COC networks.

Overall, we can conclude that there are differences between in values of certain measures of COC and CTRL networks. To confirm these preliminary findings for interaction networks of *Drosophila melanogaster* we will perform similar experiments in much larger sets of networks.

REFERENCES

[1] A. Yazdani and P. Jeffrey, "Robustness and vulnerability analysis of water distribution networks using graph theoretic and complex network principles," in *Water Distribution Systems Analysis 2010*, 2010, pp. 933–945.

[2] B. H. Junker and F. Schreiber, *Analysis of biological networks*. John Wiley & Sons, 2011, vol. 2.

[3] J. Leskovec, K. J. Lang, A. Dasgupta, and M. W. Mahoney, "Statistical properties of community structure in large social and information networks," in *Proceedings of the 17th international conference on World Wide Web*, 2008, pp. 695–704.

[4] P. J. Carrington, J. Scott, and S. Wasserman, *Models and methods in social network analysis*. Cambridge university press, 2005, vol. 28.

[5] J. L. Verdolin, A. L. Traud, and R. R. Dunn, "Key players and hierarchical organization of prairie dog social networks," vol. 19, pp. 140–147. [Online]. Available: https://linkinghub.elsevier.com/retrieve/pii/S1476945X14000683

[6] S. Boccaletti, G. Bianconi, R. Criado, C. I. Del Genio, J. Gómez-Gardenes, M. Romance, I. Sendina-Nadal, Z. Wang, and M. Zanin, "The structure and dynamics of multilayer networks," *Physics Reports*, vol. 544, no. 1, pp. 1–122, 2014.

[7] S. Martinčić-Ipšić, D. Margan, and A. Meštrović, "Multilayer network of language: A unified framework for structural analysis of linguistic subsystems," *Physica A: Statistical Mechanics and its Applications*, vol. 457, pp. 117–128, 2016.

[8] . Vukić, S. Martinčić-Ipšić, and A. Meštrović, "Structural analysis of factual, conceptual, procedural, and metacognitive knowledge in a multidimensional knowledge network," *Complexity*, vol. 2020, 2020.

[9] P. J. Mucha, T. Richardson, K. Macon, M. A. Porter, and J.-P. Onnela, "Community structure in time-dependent, multiscale, and multiplex networks," *science*, vol. 328, no. 5980, pp. 876–878, 2010.

[10] G. Menichetti, D. Remondini, P. Panzarasa, R. J. Mondragón, and G. Bianconi, "Weighted multiplex networks," *PloS one*, vol. 9, no. 6, p. e97857, 2014.

[11] K. Kaun, A. Devineni, and U. Heberlein, "Drosophila melanogaster as a model to study drug addiction," *Human genetics*, vol. 131, pp. 959–75, 02 2012.

[12] J. L. Catalano, N. Mei, R. Azanchi, S. Song, T. Blackwater, U. Heberlein, and K. R. Kaun, "Behavioral features of motivated response to alcohol in drosophila," *bioRxiv*, 2020.

[13] R. Bainton, L. Tsai, C. Singh, M. Moore, W. Neckameyer, and U. Heberlein, "Dopamine modulates acute responses to cocaine, nicotine and ethanol in drosophila," *Current biology : CB*, vol. 10, pp. 187–94, 03 2000.

[14] A. Filošević, S. Al-samarai, and R. Andretic, "High throughput measurement of locomotor sensitization to volatilized cocaine in drosophila melanogaster," *Frontiers in Molecular Neuroscience*, vol. 11, p. 25, 02 2018.

[15] M. Venniro, M. Zhang, D. Caprioli, J. Hoots, S. Golden, C. Heins, M. Morales, D. Epstein, and Y. Shaham, "Volitional social interaction prevents drug addiction in rat models," *Nature Neuroscience*, vol. 21, no. 11, pp. 1520–1529, 2018.

[16] M. Venniro and Y. Shaham, "An operant social self-administration and choice model in rats," *Nature Protocols*, vol. 15, 03 2020.

[17] M. Newman, *Networks: An Introduction.* USA: Oxford University Press, Inc., 2010.

[18] M. Kivela, A. Arenas, M. Barthelemy, J. P. Gleeson, Y. Moreno, and M. A. Porter, "Multilayer networks," vol. 2, no. 3, pp. 203–271. [Online]. Available: https://academic.oup.com/comnet/article-lookup/doi/10.1093/comnet/cnu016

[19] T. Wey, D. T. Blumstein, W. Shen, and F. Jordán, "Social network analysis of animal behaviour: a promising tool for the study of sociality," vol. 75, no. 2, pp. 333–344. [Online]. Available: https://linkinghub.elsevier.com/retrieve/pii/S0003347207004393

[20] S. P. Borgatti, M. G. Everett, and J. C. Johnson, *Analyzing social networks.* Sage, 2018.

[21] M. M. Makagon, B. McCowan, and J. A. Mench, "How can social network analysis contribute to social behavior research in applied ethology?" vol. 138, no. 3, pp. 152–161.

[22] A. Meštrović, *Collaboration Networks Analysis: Combining Structural and Keyword-Based Approaches.* Springer, Cham, 02 2018, pp. 111–122.

[23] N. Pinter-Wollman, E. A. Hobson, J. E. Smith, A. J. Edelman, D. Shizuka, S. de Silva, J. S. Waters, S. D. Prager, T. Sasaki, G. Wittemyer, J. Fewell, and D. B. McDonald, "The dynamics of animal social networks: analytical, conceptual, and theoretical advances," vol. 25, no. 2, pp. 242–255. [Online]. Available: https://academic.oup.com/beheco/article-lookup/doi/10.1093/beheco/art047

[24] P. Sah, J. D. Méndez, and S. Bansal, "A multi-species repository of social networks," *Scientific data*, vol. 6, no. 1, pp. 1–6, 2019.

[25] P. Sah, J. Mann, and S. Bansal, "Disease implications of animal social network structure: a synthesis across social systems," *Journal of Animal Ecology*, vol. 87, no. 3, pp. 546–558, 2018.

[26] J. A. Drewe, J. R. Madden, and G. P. Pearce, "The social network structure of a wild meerkat population: 1. inter-group interactions," vol. 63, no. 9, pp. 1295–1306. [Online]. Available: http://link.springer.com/10.1007/s00265-009-0782-x

[27] I. Puga-Gonzalez, S. Sosa, and C. Sueur, "Social style and resilience of macaques' networks, a theoretical investigation," vol. 60, no. 3, pp. 233–246. [Online]. Available: http://link.springer.com/10.1007/s10329-018-0684-5

[28] M. H. D. Jonathan Schneider and J. D. Levine, "Social structures depend on innate determinants and chemosensory processing in drosophila," vol. 109, pp. 17174–17179.

[29] E. Eyjolfsdottir, S. Branson, X. P. Burgos-Artizzu, E. D. Hoopfer, J. Schor, D. J. Anderson, and P. Perona, "Detecting social actions of fruit flies," in *Computer Vision – ECCV 2014*, D. Fleet, T. Pajdla, B. Schiele, and T. Tuytelaars, Eds. Springer International Publishing, vol. 8690, pp. 772–787, series Title: Lecture Notes in Computer Science.

[30] T. Alisch, J. D. Crall, A. B. Kao, D. Zucker, and B. L. de Bivort, "MAPLE (modular automated platform for large-scale experiments), a robot for integrated organism-handling and phenotyping," vol. 7.

[31] C. Pasquaretta, M. Battesti, E. Klenschi, C. A. Bousquet, C. Sueur, and F. Mery, "How social network structure affects decision-making in drosophila melanogaster," *Proceedings of the Royal Society B: Biological Sciences*, vol. 283, no. 1826, p. 20152954, 2016.

[32] P. Ramdya, J. Schneider, and J. D. Levine, "The neurogenetics of group behavior in *Drosophila melanogaster*," vol. 220, no. 1, pp. 35–41. [Online]. Available: http://jeb.biologists.org/lookup/doi/10.1242/jeb.141457

[33] G. Liu, T. Nath, G. A. Linneweber, A. Claeys, Z. Guo, J. Li, M. Bengochea, S. De Backer, B. Weyn, M. Sneyders, H. Nicasy, P. Yu, P. Scheunders, and B. A. Hassan, "A simple computer vision pipeline reveals the effects of isolation on social interaction dynamics in drosophila," vol. 14, no. 8.

[34] A. Iyengar, J. Imoehl, A. Ueda, J. Nirschl, and C.-F. Wu, "Automated quantification of locomotion, social interaction, and mate preference in *Drosophila* mutants," vol. 26, no. 3, pp. 306–316.

[35] K. Branson, A. A. Robie, J. Bender, P. Perona, and M. H. Dickinson, "High-throughput ethomics in large groups of drosophila," vol. 6, no. 6, pp. 451–457.

[36] S. R. Egnor and K. Branson, "Computational analysis of behavior," vol. 39, no. 1, pp. 217–236. [Online]. Available: http://www.annualreviews.org/doi/10.1146/annurev-neuro-070815-013845

[37] L. P. J. J. Noldus, A. J. Spink, and R. A. J. Tegelenbosch, "EthoVision: A versatile video tracking system for automation of behavioral experiments," vol. 33, no. 3, pp. 398–414. [Online]. Available: http://link.springer.com/10.3758/BF03195394

[38] M. Gershow, M. Berck, D. Mathew, L. Luo, E. A. Kane, J. R. Carlson, and A. D. T. Samuel, "Controlling airborne cues to study small animal navigation," vol. 9, no. 3, pp. 290–296. [Online]. Available: http://www.nature.com/articles/nmeth.1853

[39] S. Ohayon, O. Avni, A. L. Taylor, P. Perona, and S. Roian Egnor, "Automated multi-day tracking of marked mice for the analysis of social behaviour," vol. 219, no. 1, pp. 10–19. [Online]. Available: https://linkinghub.elsevier.com/retrieve/pii/S0165027013002070

[40] A. Pérez-Escudero, J. Vicente-Page, R. C. Hinz, S. Arganda, and G. G. de Polavieja, "idTracker: tracking individuals in a group by automatic identification of unmarked animals," vol. 11, no. 7, pp. 743–748. [Online]. Available: http://www.nature.com/articles/nmeth.2994

[41] N. A. Swierczek, A. C. Giles, C. H. Rankin, and R. A. Kerr, "High-throughput behavioral analysis in c. elegans," vol. 8, no. 7, pp. 592–598. [Online]. Available: http://www.nature.com/articles/nmeth.1625

[42] T. Nath, G. Liu, B. Weyn, B. Hassan, A. Ramaekers, S. De Backer, and P. Scheunders, "Tracking for quantifying social network of drosophila melanogaster," in *Computer Analysis of Images and Patterns*, R. Wilson, E. Hancock, A. Bors, and W. Smith, Eds. Springer Berlin Heidelberg, vol. 8048, pp. 539–545, series Title: Lecture Notes in Computer Science. [Online]. Available: http://link.springer.com/10.1007/978-3-642-40246-3_67

[43] M. Kabra, A. A. Robie, M. Rivera-Alba, S. Branson, and K. Branson, "JAABA: interactive machine learning for automatic annotation of animal behavior," vol. 10, no. 1, pp. 64–67. [Online]. Available: http://www.nature.com/articles/nmeth.2281

[44] A. A. Hagberg, D. A. Schult, and P. J. Swart, "Exploring network structure, dynamics, and function using networkx," in *Proceedings of the 7th Python in Science Conference*, G. Varoquaux, T. Vaught, and J. Millman, Eds., Pasadena, CA USA, 2008, pp. 11 – 15.

[45] M. Bastian, S. Heymann, and M. Jacomy, "Gephi: An open source software for exploring and manipulating networks," 2009.

[46] R. Albert and A.-L. Barabási, "Statistical mechanics of complex networks," *Reviews of modern physics*, vol. 74, no. 1, p. 47, 2002.

[47] V. D. Blondel, J.-L. Guillaume, R. Lambiotte, and E. Lefebvre, "Fast unfolding of communities in large networks," *Journal of Statistical Mechanics: Theory and Experiment*, vol. 2008, no. 10, Oct 2008.

[48] R. Milo, S. Shen-Orr, S. Itzkovitz, N. Kashtan, D. Chklovskii, and U. Alon, "Network motifs: simple building blocks of complex networks," *Science*, vol. 298, no. 5594, pp. 824–827, 2002.

[49] H. Rizvić, S. Martinčić-Ipšić, and A. Meštrović, "Network motifs analysis of croatian literature," *arXiv preprint arXiv:1411.4960*, 2014.

[50] N. Pržulj, D. G. Corneil, and I. Jurisica, "Modeling interactome: scale-free or geometric?" *Bioinformatics*, vol. 20, no. 18, pp. 3508–3515, 2004.

[51] S. Wernicke, "A faster algorithm for detecting network motifs," in *International Workshop on Algorithms in Bioinformatics.* Springer, 2005, pp. 165–177.

[52] N. Kashtan, S. Itzkovitz, R. Milo, and U. Alon, "Efficient sampling algorithm for estimating subgraph concentrations and detecting network motifs," *Bioinformatics*, vol. 20, no. 11, pp. 1746–1758, 2004.

[53] R. Diestel, "Graph theory. 2005," *Grad. Texts in Math*, vol. 101, 2005.