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A network perspective on animal welfare

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Abstract

The scientific study of animal welfare involves measuring physiological, behavioural, and/or cognitive variables to infer the welfare state of animals. Such an approach implies these measures are indicators, or reflect, an unmeasured latent variable of welfare state. Drawing inspiration from recent developments in human psychology and psychiatry, in this paper we propose an alternative perspective in the form of a network theory of animal welfare. This theory posits that there is no latent variable; rather, welfare is a network system of causal interactions between and within behavioural, physiological, and cognitive components. We then describe a statistical network modelling approach motivated by network theory, in which welfare-related response variables are associated with each other after controlling for all other variables measured. In three examples using simulated data, we demonstrate how this approach can be used, and the sort of novel insights it can bring. These examples cover a range of species and research questions, which network analysis is well suited to address. We believe a network approach to animal welfare science holds promise for developing our understanding of the concept of animal welfare, as well as producing practical and meaningful information to improve the welfare of animals.

Keywords: *affect, animal welfare, complexity, dynamics, networks, statistics*

Introduction

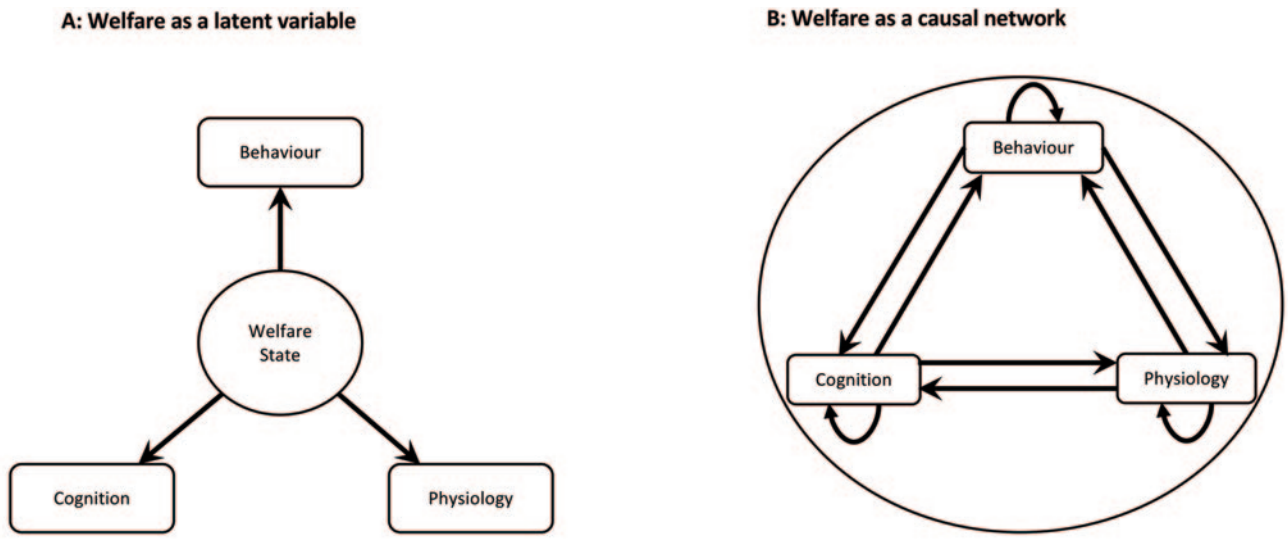
The scientific study of animal welfare is traditionally approached from a 'triangulation' perspective, in which physiological, behavioural, and (more recently) cognitive measures are recorded and used to make inferences about the welfare of an animal or group of animals (Webster 1998). Such an approach implies that these measures all reflect an unobserved variable of welfare state. Despite this triangulation approach, it is a well-recognised problem that welfare is hard to measure, and many measures do not 'agree' or turn out not to be in the direction predicted (Mason & Mendl 1993). There is thus a lack of knowledge about how various welfare measures relate to each other, which may impede our understanding of, and inferences about, animal welfare. In this paper, we propose a network approach to tackle this problem. This perspective carries with it a novel conceptualisation of animal welfare; that is, one that is not based on measures reflecting an unobserved latent variable but, rather, a construct that emerges from mutual interactions in a network system. Drawing inspiration from recent developments in human psychology and psychiatry, we begin by proposing the basis of a network theory of animal welfare. We then move on to discuss how novel insights can be gained by statistically modelling animal welfare measures ('indicators') as networks of interactions.

A network theory of animal welfare

In the human psychology and psychiatry literature, it has been argued that the traditional approach to conceptualising and measuring psychological constructs has been a latent variable perspective, in which the co-variation between measures (eg items on a questionnaire, components of emotion, symptoms of mental illness, and so on) occurs due to an underlying unobservable common cause (van der Maas *et al* 2006; Cramer *et al* 2010; Borsboom & Cramer 2013; Schmittmann *et al* 2013; Fried & Cramer 2017). This implies, for example, that symptoms group together due to a latent variable of the underlying illness which causes all psychiatric symptoms of a disorder. More recently, the network theory approach to psychological phenomena has been proposed (initially by Cramer *et al* 2010, but also see van der Maas *et al* 2006) which essentially posits that components group together because they causally influence each other, *not* because they share a common cause; as such, there are no latent variables and components are not interchangeable (for detailed discussions, see Cramer *et al* 2010; Borsboom & Cramer 2013; Schmittmann *et al* 2013; Borsboom 2017; Fried & Cramer 2017; Dalege *et al* 2018). This suggests that the disorder *is* the causal interactions among symptoms (Borsboom 2017). This powerful idea has been proposed as an alternative conceptualisation of various psychological phenomena, ranging from psychopathology

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Figure 1



Different conceptualisations of animal welfare showing (A) welfare as a latent variable: welfare state of an animal (central circle) is an unmeasured latent variable that gives rise to (directed arrows) measurable indicators at the levels of behaviour, cognition, and physiology that directly reflect the latent variable and (B) network theory: in this conceptualisation there is no latent variable and as such 'welfare state' is not directly labelled. Rather, welfare state is represented by a large circle, within which there is a network system of causal interactions. These interactions occur between (longer directed arrows), and within (curved self-directed arrows) behavioural, cognitive, and physiological levels/measures.

(Cramer *et al* 2016; Borsboom 2017) to personality (Cramer *et al* 2012), attitudes (Dalege *et al* 2016, 2018), intelligence (van der Maas *et al* 2006), and emotions (Lange *et al* 2020), and has been applied to behavioural phenotypes in dogs (Goold *et al* 2016). We believe that this network approach also has considerable potential to transform how we conceptualise animal welfare and opens up new ways of modelling and interpreting welfare data.

When considering animal welfare from the animals' perspective, welfare is essentially an internal subjective psychological state (Sandøe & Simonsen 1992; Duncan 2002; Mason & Mendl 1993; Mellor 2012, 2016; Browning 2019), and can be considered somewhat analogous to mental health in humans. We therefore propose that the network conceptualisations developed in human psychology and psychiatry are also valid to animal welfare when viewed from the animals' perspective. That is, if the response variables used in animal welfare research can be justified to be relevant to the welfare of animals, then the network theory position is that these animal welfare measures can be considered components in a network system of causal interactions (Figure 1B). This means that behavioural, physiological, and cognitive components are not necessarily reflective of an unobservable latent variable (Figure 1A), rather, their interactions are what constitute the welfare of an animal (Figure 1B).

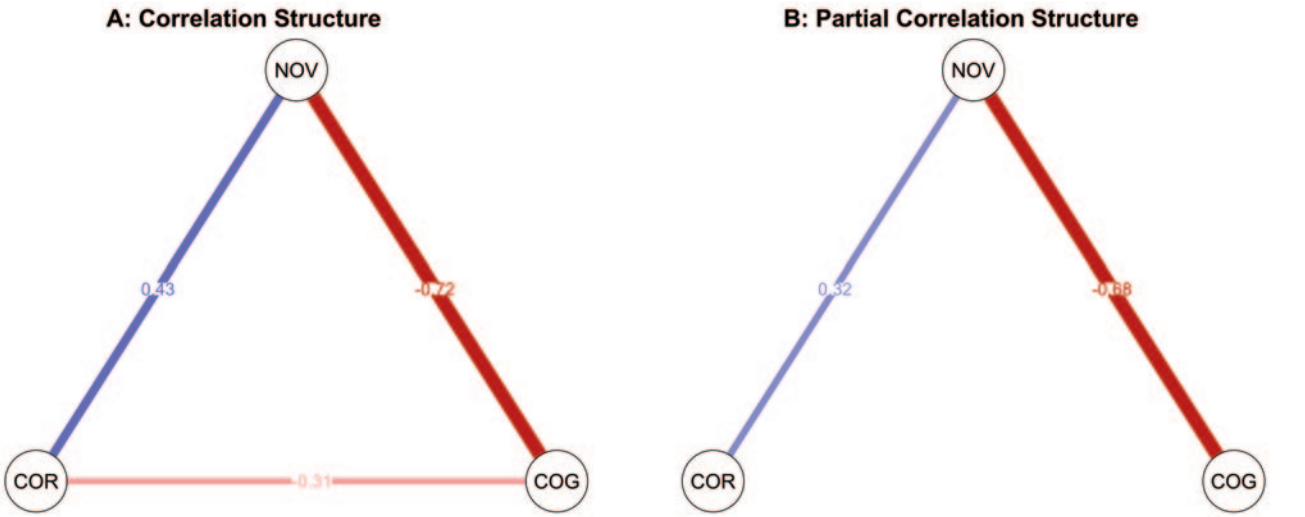
As a simple example, consider the following three welfare measures: fearful posturing (behavioural), low appetite (behavioural), and low body condition score (physical/physiological). These measures do not necessarily independently reflect a single underlying latent construct of welfare. Instead, they may be causally related because they directly influence each other: fearful posturing→low appetite→low body condition score. If an animal is fearful of people and finds itself in an environment regularly exposed to people, this may directly cause a reduction in appetite, which if persistent over time directly influences and causes a low body condition score. This makes intuitive sense. Resource acquisition and consumption is not a priority in the presence of threat, and the lower number of calories consumed due to reduced nutrient intake/poor appetite, will eventually result in weight loss and a low body condition score.

Network theory has important implications for how we think about improving animal welfare. Consider the three welfare measures we have just mentioned. If a latent variable model is the 'true' data-generating mechanism, then to improve scores on these three measures we would have to directly intervene at the level of the unobservable latent variable. If we manipulated a single measure, only that measure would change, and there would be no effect on the other two. However, if the 'true' mechanism is a network model of the form: fearful posturing→low appetite→low body condition score, then in order to improve scores on all three measures one needs to directly target fearful posturing. It can be seen that the two models make very different predictions, and this may be one useful way that the theoretical ideas of network versus latent theories can be empirically tested (for more details, see Marsman *et al* 2018). Additionally, methodologists are beginning to work on formal ways of testing whether a given multivariate dataset is likely to have been generated

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Figure 2



Network representations of the three simulated welfare measures. Response variables are represented as nodes (circles) in the network graphs. Edges (represented by lines) between the nodes represent Pearson's correlations in A, and partial correlations in B, the values of which are also numbered in the middle of each edge. The blue edges represent positive relationships, while the red represent negative relationships. The thickness of each edge represents the absolute magnitude of the parameter, which is why the red negative edges appear thicker. The partial correlation between COR and COG is 0.00, and as such, there is no edge between these two nodes in B. COR, Hair Cortisol; NOV, Fear of Novelty (time spent in proximity to novel object); and COG, Cognitive Bias Test (latency to approach ambiguous probe).

by an underlying latent variable system or a network system (van Bork *et al* 2019).

With this theoretical concept of causal interactions between components of welfare in mind, in the following sections we explain how this idea relates to statistical network models of animal welfare data. We begin by explaining what the networks we are proposing actually represent and proceed to show a series of practical applications using simulated data. All simulations were conducted using R 3.6.1 (R Core Team 2019). The code to reproduce all simulations reported here can be found on the open science framework (Rowland *et al* 2020).

Statistical animal welfare networks

There is already a small body of literature on social network analysis as it relates to animal welfare (for reviews, see Asher *et al* 2009; Kleinhappel *et al* 2016). In such networks, nodes (or vertices) represent individuals, and connections between nodes, called edges, represent the presence and/or strength of physical or social interactions between individuals (Wasserman & Faust 1994; Krause *et al* 2009). However, the approach we describe here differs from these 'traditional' networks in that nodes represent animal welfare-related response variables, rather than individuals, and edges represent statistical (rather than physical or social) associations between them (for explanations and tutorials from the human psychology literature, see Costantini *et al* 2015; Dalege *et al* 2017; Epskamp *et al* 2018a; Epskamp & Fried 2018). Typically, these statistical associations represent partial correlations (see Epskamp *et al* 2018a,b; Epskamp & Fried 2018; Williams & Rast 2020) or regression coefficients (see van Borkulo *et al* 2014; Haslbeck & Waldorp 2020). These parameters represent conditional dependence relations, which describe the association between two variables after taking into account all other nodes in the network, regardless of the network size (Epskamp *et al* 2018a; Altenbuchinger *et al* 2020). Essentially, this allows us to model direct relationships between the various measures, in order to better understand how they interact.

To demonstrate this property of conditional dependence, we simulate and discuss a three-node network with a structure similar to that discussed in previous reviews (Epskamp *et al* 2018a; Altenbuchinger *et al* 2020). We do so, however, within the context of three commonly used animal welfare measures. The purpose of this simulation is not to demonstrate a realistic application to animal welfare, rather, the aim is to provide a simple example that explains the basic building block of the network approach we are proposing. The three measures we chose to simulate are hair cortisol levels (COR), fear of novelty (NOV: measured as time spent in proximity to novel object), and cognitive bias (COG: latency to approach ambiguous probe). We therefore have elements of a behavioural component (time spent in proximity) of an acute affective response (novel object test), as well as a physiological component (hair cortisol) and a cognitive/appraisal component (cognitive bias) of longer-term mood state.

One traditional approach to investigate how the measures relate to each other would be, for example, to calculate Pearson's correlation coefficients between each pair of variables (Figure 2A). In our simulated data set, hair

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cortisol positively correlates with fear of novelty, fear of novelty negatively correlates with cognitive bias, and hair cortisol also negatively correlates with cognitive bias, and so the three measures are linearly associated. However, such correlations are a poor estimate of direct relationships/dependencies, primarily because there is a large degree of uncertainty as to whether the correlation is mediated by a third (or more) variable(s) (Costantini *et al* 2015; Altenbuchinger *et al* 2020). An alternative approach that does take into account the effects of other variables when estimating associations, and which is closer to the causal interaction conceptualisation of welfare, is estimation of conditional dependencies. In this example, we can estimate conditional dependence by calculating partial correlation coefficients (Epskamp *et al* 2018a,b; Epskamp & Fried 2018; Williams & Rast 2020) and representing these as a graphical network (Figure 2B). Therefore, in the three-node network we estimate here, in Figure 2B, an edge between two nodes represents a correlation after controlling for the effects of the third node. If that relationship is 0 (rare in empirical data), not statistically significantly different from 0, or does not survive other methods of model selection, then we infer that those two measures are conditionally independent, meaning there is no evidence of a causal relationship (Epskamp & Fried 2018; Altenbuchinger *et al* 2020).

In Figure 2B, because the edges represent partial correlations, the network model shows that hair cortisol and cognitive bias do not directly interact when fear of novelty is controlled for. That is, hair cortisol and cognitive bias are conditionally independent and therefore *not* causally related. However, hair cortisol and fear of novelty do predict each other after controlling for cognitive bias. As such, in this simulation if an animal is measured to have a 'pessimistic' cognitive bias (high latency to approach ambiguous probe), it is more likely to have high hair cortisol levels if they also present with fear of novelty (latency to approach novel object). Likewise, fear of novelty and cognitive bias predict each other after controlling for the effect of hair cortisol. That is, if an animal has high hair cortisol levels, it is also likely to have a 'pessimistic' cognitive bias if they also have a fear of novelty. By conditioning on all variables, we see that although hair cortisol and cognitive bias initially correlated (Figure 2A), once fear of novelty is taken into account, they have no predictive relationship (Figure 2B). Therefore, if this example were real data from a study that we had carried out, we could conclude that knowing the concentration of cortisol on its own would not necessarily provide us with any useful information to make a welfare inference.

Conditional dependence between variables is an important statistical property of this approach because such relationships are more likely to indicate possible causal pathways (Epskamp *et al* 2018a,b; Epskamp & Fried 2018). Therefore, exploratory estimation of networks containing many more than three variables can be used to generate causal hypotheses. While conditional dependence relations estimated from cross-sectional data is a better estimation of causality than non-conditional associations, it is still only considered an estimate. This is, in part, because such models assume that all relevant measures have been included in the model (Epskamp & Fried 2018), and the direction of the effect is unknown (Epskamp *et al* 2018a,b). Using the simulated example, we have just worked through, imagine if we had only measured hair cortisol and cognitive bias. We would not have known that the correlation between them is conditional on fear of novelty had we not also measured fear of novelty. Missing important variables in the system may also affect our estimates of network metrics derived from network models and can induce edges in networks that would not be present had the relevant variable(s) been included (Epskamp & Fried 2018). This is an important limitation of undirected network models that prevents strong causal interpretations being made. However, all statistical models have limitations which are important to bear in mind when making statistical and theoretical inferences, and network models are not immune to this. Nonetheless, the network in Figure 1B provides an example of the conceptual basis of the network approach we are proposing, and the building blocks of larger network models.

In the following sections, we provide three different examples of applications of statistical network modelling to animal welfare science using simulated data, introduce some of the metrics used to summarise network structures and their characteristics, and discuss the novel application of these metrics to animal welfare data.

Network models as a tool to identify intervention targets

Network theory proposes that welfare can be conceptualised as a network system of mutual interactions (Figure 1B). In a statistical network model, edge weights in conditional networks denote the strength of *potential* causal relationships (Epskamp & Fried 2018). As such, network models can be viewed as exploratory statistical models that can be used to generate causal hypotheses. From a network theory perspective, these causal hypotheses are substantively different to hypotheses that would be derived from a latent variable theory (Marsman *et al* 2018; van Bork *et al* 2019). That is, if we intervened at the level of an individual variable, network theory posits that the probability distribution of the other variables will subsequently change (due to the connections in the system), a prediction that would not be made if the causal model is assumed to be a latent variable that gives rise to the indicators and in which the indicators are independent of each other (Marsman *et al* 2018). We discuss this idea here as an example within the context of shelter dog welfare.

We start by simulating some cross-sectional data, which allows the estimation of an undirected network that encapsulates our uncertainty regarding the direction of the associations. Suppose you are interested in identifying (i) estimates of causal relationships in welfare measures, and (ii) using this

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information to identify potentially important variables for targeted intervention. You conduct a cross-sectional study measuring fourteen binary variables on the 7th day, post-shelter intake. Such binary data have been collected and reported before in the shelter dog welfare literature (for example, see the Quality of Life Assessment Tool in Kiddie & Collins 2014). We simulate data for this hypothetical study following Dalege *et al* (2017), using parameter estimates of a previously reported human major depression network (Cramer *et al* 2016) as inputs. However, we consider the results within the context of the variables representing welfare measures rather than human depressive symptoms. That is, we arbitrarily renamed the variables such that the network resembles a logically feasible shelter welfare network.

We then use the simulated binary data to estimate a network of conditional dependencies between variables (Epskamp 2015). In the case of binary variables, the edge weights represent logistic regression coefficients (van Borkulo *et al* 2014) that can still be interpreted as conditional dependencies as described in the previous section. We identify potentially important measures/nodes by calculating the network metric of strength centrality (Epskamp *et al* 2018a). This is a useful metric here because strength centrality tries to capture the relative importance of each individual node within the network by representing the magnitude and number of connections of each node (for detailed discussions, see Bringmann *et al* 2019 and cf Hallquist *et al* 2019). In the psychopathology network literature, the centrality hypothesis suggests central symptoms are important because they are more likely to activate a larger range of other symptoms (Cramer *et al* 2010; Robinaugh *et al* 2020). Based on this, if targeted node level intervention is feasible, then it may be that nodes with the highest strength centrality make good intervention targets (Cramer *et al* 2010; Fried *et al* 2017; Robinaugh *et al* 2020). Such a concept may also apply to animal welfare.

Following the centrality hypothesis, the shelter dog network in Figure 3 and its centrality characteristics may give us useful information to design interventions aiming to improve the welfare state of dogs in a shelter. It would be challenging to implement a targeted intervention on every single node. Therefore, practically speaking, the most time and cost-effective interventions would be those that are simple to deliver, and which target nodes that have the largest effect on the overall network. Based on the centrality hypothesis, in our example we could hypothesise that intervening specifically on response to novelty (NOV), which has the highest strength centrality, would be more efficacious than intervening on kennel activity (ACT), which has the lowest strength centrality. A targeted NOV intervention could be implemented with desensitisation and classical counterconditioning to a variety of novel stimuli (Zulch & Mills 2012). ACT could be intervened on via remote operant counter conditioning with reward contingent on stationary, calm behaviour.

To simulate the two interventions described above, we implemented an intra-individual dynamic model previously reported in Cramer *et al* (2016), which was initially developed to model major depression in humans. In short, this models the time course of symptom activation within an individual where nodes are either active or inactive. At each time step, node activity is determined by a probability influenced by (i) the state of the system at the previous time-point, and (ii) parameters from the network structure we have estimated (for more details on the model, see Cramer *et al* 2016).

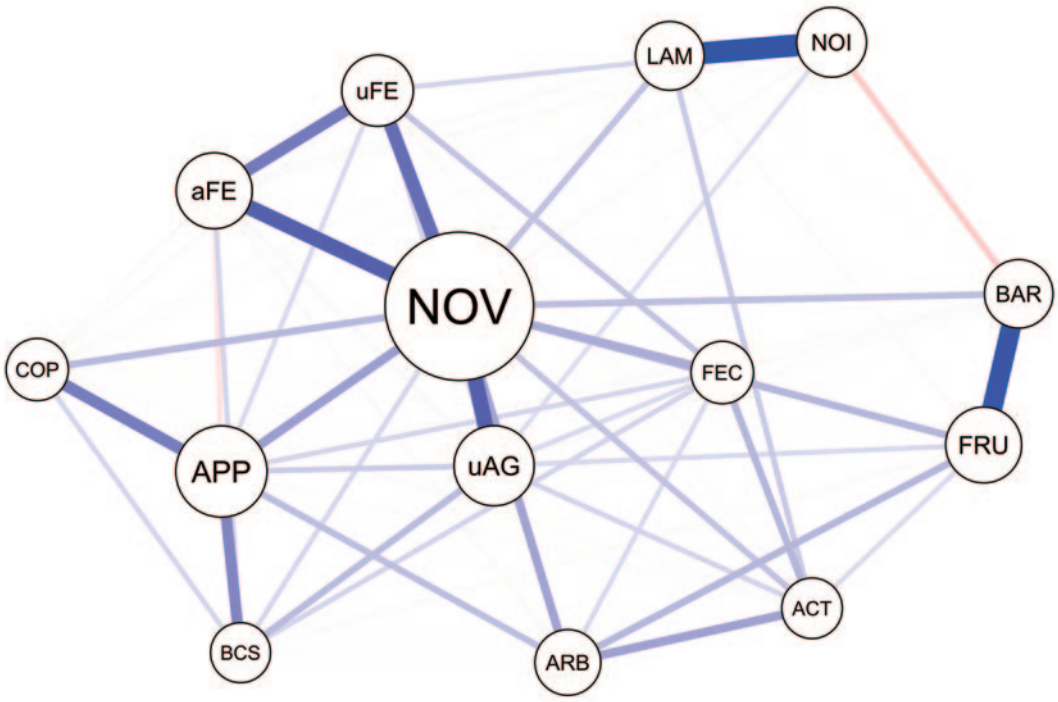
We applied this model in two simulations. In both, we start with all nodes being inactive (they are assigned 0) and halfway through the simulation we intervene on the system. The high centrality intervention involves setting the NOV node to always be 0, and the low centrality intervention involves setting the ACT node to always be 0. That is, the dog no longer avoids approaching novel objects, and in the other, the dog no longer remains active for over half the sampling period. We then calculate the probability of each node being active as the number of time-points after intervention that the node is active/total number of time-points after the intervention.

This simulation demonstrates that intervention on the high centrality node has a much greater effect on the network than intervention on the low centrality node (Figure 4). It is readily apparent that the high centrality intervention results in a marked decrease in all nodes activation probability (Figure 4B compared to A), whereas the low centrality intervention either has almost no effect on node activation probability or a very small effect on a small subset of nodes (4C compared to A). Further, we can also calculate the median number of nodes active across all time-points after intervention. In the high centrality intervention, the median number of nodes active is 1, compared to 12 in the low centrality intervention.

We believe that estimating network structures and using node-level metrics such as centrality is a promising approach for identifying intervention targets for experimental manipulation. However, there are limitations of this approach. In undirected networks, the direction of association (and causality) is unknown. Thus, a node in an undirected network may have a high centrality score either because it has lots of outgoing edges or because it has lots of incoming edges. This limitation may be somewhat overcome using directed networks (a form of network model which we consider in more detail in the *Discussion*). Additionally, causal effects could be identified in an empirical study testing an undirected centrality intervention (Marsman *et al* 2018). That is, if a node is at the end of many causal pathways, and thus was highly central in an undirected network, then an intervention experiment on it would not result in improvements to the rest of the multivariate system. Unfortunately, there are very few reports in the human psychology literature empirically testing the causality of these ideas, although some non-causal designs exist providing some support (Zwicker *et al* 2020). Nonetheless, we believe the centrality hypothesis is useful to pursue in animal welfare science. In the following section, we discuss how statistical network models and their comparisons may be useful for making welfare inferences in experimental work.

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Figure 3



Undirected network of 14 simulated binary shelter dog welfare variables. This network shows several characteristics embedded within the layout which facilitates visual inspection (for more details on network visualisations, see Epskamp *et al* 2012). The network is constructed from logistic regression coefficients where each regression contains all other nodes as a predictor. Blue edges represent positive regression coefficients ≥ 0.5, and red edges represent negative regression coefficients ≤ –0.5. Grey edges denote coefficients < –0.5 and < 0.5. Edge thickness represents size of the regression coefficient, which here range between –0.82 and 3.28. The layout is based on the Fruchterman and Reingold algorithm (Fruchterman & Reingold 1991) which places nodes that are more strongly connected closer together (Epskamp *et al* 2012), and node size is proportional to strength centrality such that nodes with greater strength centrality appear larger (Cramer *et al* 2010). NOV, does not approach novel object; uAG, aggressive behaviour present on approach of unknown person; BAR, vocalises for more than half of sampling time; NOI, displays fearful posturing upon sudden white noise; FRU, Persistent attempts for entire period of acute insolvable task; LAM, dog is lame; ARB, repetitive behaviour present; COP, coprophagia present during sampling; ACT, active for more than half of sampling period; BCS, scores low or high on body condition score; APP, left more than half of breakfast meal; uFE, fearful posture on approach of unknown person; FEC, faecal inconsistency present; aFE, fearful posturing present during sampling in absence of people.

Comparing networks to aid welfare inference

Networks can be compared qualitatively via visual inspection, but statistical inferences cannot be made without formal testing (Fried *et al* 2020). In this example, we demonstrate how network comparisons and formal testing of network characteristics can be used to aid inferences about welfare.

To do this, we simulated cross-sectional multivariate normally distributed data for two groups. Suppose these data reflect the results of an experiment that housed laboratory mice in one of two conditions, solitary or in groups of four (group), and that after a one-month period, a cross-sectional battery of animal welfare measures was collected for each mouse (the simulated data). The variables simulated include a mixture of cognitive, behavioural, and physiological variables, as well as a mixture of acute emotional 'anxiety' tests and longer-term mood state measures (see Figure 5). A number of papers have been published investigating group housing of mice (Whittaker *et al* 2012; Bailoo *et al* 2018). This example is not a simulated replication of these studies, but rather a simplified example inspired by them to reflect a realistic experimental animal welfare study.

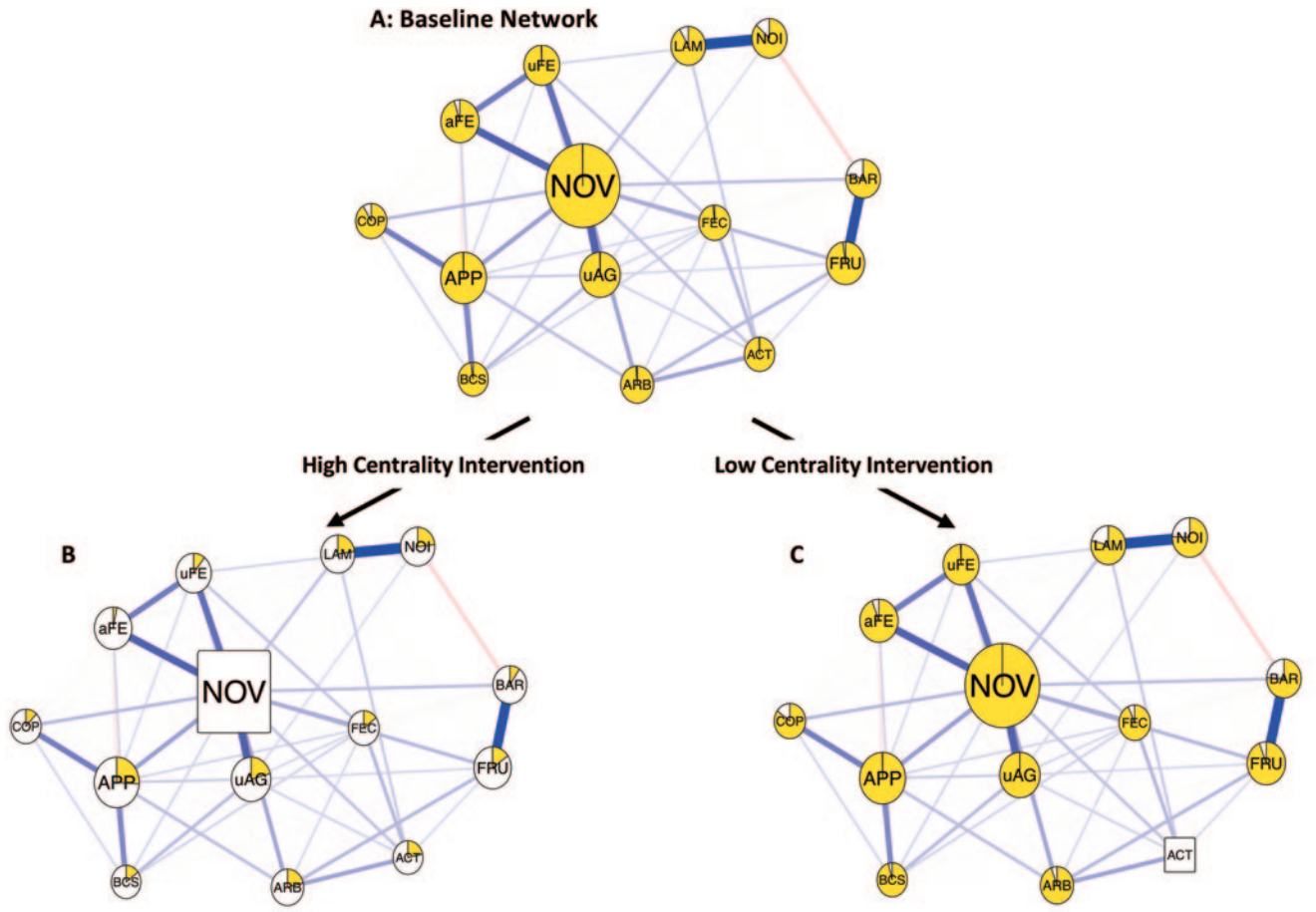
We are primarily interested in whether the means are different between the two groups. In this simulated example, independent *t*-tests indicate that there are no mean differences between groups on any measure (all $P > 0.05$, following Bonferroni correction; see supplementary Figure 1 in the supplementary material to papers published in *Animal Welfare*: https://www.ufaw.org.uk/the-ufaw-journal/supplementary-material).

In addition to looking at mean differences, network analysis provides us with a complementary approach focusing on relations (Wasserman & Faust 1994). In a setting such as this example, one useful metric is network connectivity. Connectivity is a network level metric that summarises the strength of connections in a network (Cramer *et al* 2016). High connectivity networks have more and/or stronger connections between their nodes compared to low connectivity networks. In the psychopathology literature, this has led to proposal of the connectivity hypothesis, which states

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Figure 4



Undirected binary variable networks of (A) baseline network prior to intervention, this is the same for the two simulations, (B) network after high centrality intervention on the NOV node, and (C) network after low centrality intervention on the ACT node. The nodes intervened on (NOV and ACT) in the two simulations are square-shaped. The edge weights remain constant in this simulation and are thus the same across all three networks. However, the probability of each node being active after intervention (number of time-points node active/total number of time-points) is represented by a yellow pie chart filling each node. A completely yellow-filled node represents that the node is always active (probability equals 1), and a completely white node represents that the node is always inactive (probability equals 0; seen in NOV and ACT which are constrained to being inactivated in the two respective intervention simulations).

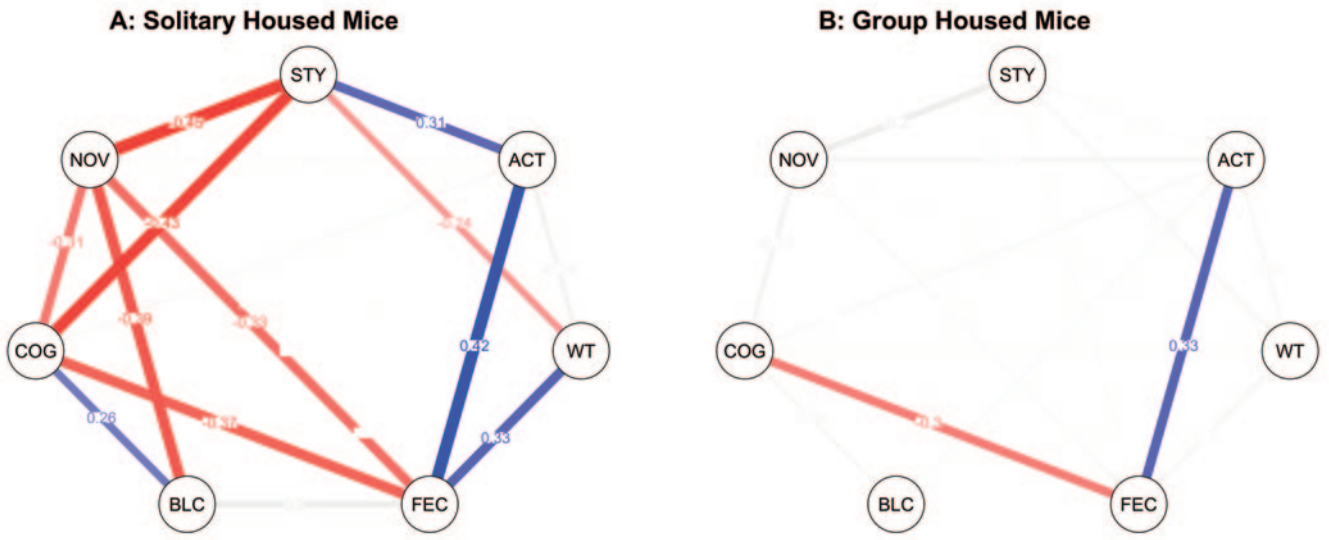
that highly connected networks are vulnerable to symptom spread and thus activation of a large range of symptoms, whereas low connectivity networks are more resilient (Cramer *et al* 2016; Borsboom 2017). This hypothesis has some support from group-level studies (for an overview, see Robinaugh *et al* 2020), computational models (Cramer *et al* 2016), and individual temporal network models (Wichers *et al* 2016, 2020). This quantitative concept of resilience and vulnerability based on network connectivity has also been proposed more generally for a variety of complex adaptive networks (Scheffer *et al* 2018). Based on the variables included in the current example, and the way they are measured (see the legend to Figure 5), strong absolute connections between variables would be indicative of a compromised welfare compared to a lesser connected network. For the benefit of this example, we are therefore interested in testing the hypothesis that network connectivity is different between the solitary condition compared to the group condition.

We estimate the partial correlation network (Epskamp *et al* 2018a), identifying edges that are statistically significantly different from 0 using Fisher *Z* transformations (Williams *et al* 2019; Williams & Rast 2020). The resulting network for both groups is shown in Figure 5.

When inspecting the partial correlation networks generated from our simulated data, notable differences between the two groups are immediately visually apparent. The first striking difference is that the group-housed condition network (Figure 5B) contains only two statistically significant partial correlations (ACT–FEC and FEC–COG), and is comprised of smaller edge weights in general, and such a finding would suggest lower connectivity. Network comparison procedures are an active area of network methodology research and a number of approaches have now been developed (van Borkulo *et al* 2016; Haslbeck *et al* 2019a; Williams *et al* 2020). Here, we demonstrate one such method, which is the permutation-based network comparison test developed by

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Figure 5



Showing partial correlation networks for mice in two conditions from simulated data for (A) solitary-housed condition network and (B) group-housed condition network. Blue edges represent statistically significant positive partial correlations, and red edges represent statistically significant negative partial correlations. Grey edges represent partial correlations that are not statistically significantly different from 0 after Fisher *Z* transformation ($P \geq 0.05$). The magnitude of the partial correlation is shown numerically on each edge weight, as well as coded by the thickness of the edge. The edge thickness indicates higher absolute partial correlations, and the thickness is comparable between the two networks to aid visual comparison, that is, 0.33 in A is the same thickness as 0.33 in B (Epskamp *et al* 2012). Nodes are placed in a circle in the same order in each network to aid visual comparison, and therefore node position does not represent any particular property of the network structure. STY, overall stereotypy level; ACT, time spent active in home cage; WT, weight; FEC, faecal cortisol; BLC, blood cortisol sampled immediately after response to novel object test; COG, cognitive bias (time spent in ambiguous arms in radial maze task); NOV, novel object test (time spent in close proximity to novel object).

van Borkulo *et al* (2016), implemented in the NetworkComparisonTest R package. In short, this method resamples from the data and randomly assigns group membership, re-estimates the network, calculates the network metrics of interest, and then repeats this process for a defined number of iterations — here we used 1,000. The network metric of interest obtained in the original sample can then be compared to the null distribution obtained by the permutations to obtain a *P*-value. We used this procedure on our simulated dataset to test the null hypothesis that there is no difference in global connectivity between the two groups' networks. Second, one can also test whether there are differences in specific individual edge weights. Here, we tested only the edges that were identified as statistically significant in the original network estimation. This is an example of an exploratory analysis of edge weight differences. However, if a researcher specified expected differences *a priori*, then such hypotheses could be tested in a confirmatory manner using the network comparison test.

This analysis indicates that the global network connectivity between the two groups is statistically significant with connectivity being greater in the solitary-housed condition (Solitary: 4.35, Group: 1.93, difference = 2.43; $P < 0.001$). We therefore reject the null hypothesis that the groups have the same network connectivity. The results of the individual edge weight comparisons are shown as a network in Figure 6.

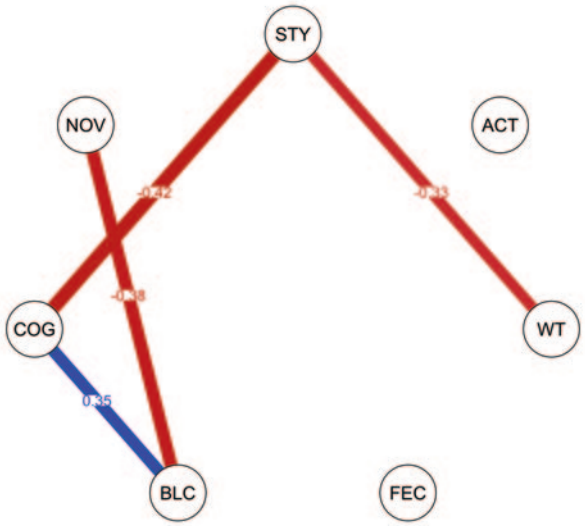
In our simulated experiment, based on the differences in network connectivity without differences in group means, we would infer that the solitary-housed mice have a more vulnerable welfare network system. Mice that present with compromised welfare on any one measure would be more likely to have a compromised score on another. For example, in this simulation, mice with high stereotypy levels in solitary, when compared with group, are more likely to spend less time in ambiguous arms, spend less time in proximity to novel objects and have a larger cortisol response to this novelty exposure, be generally more active in their cage, and have higher faecal cortisol levels. Such a cascade of events would be less pronounced in the group-housed mice because the connectivity of the network is weaker. Further, consider the statistically significant edge weight difference between NOV-BLC. This edge weight is –0.39 in solitary mice, and –0.01 in group mice. Mechanistically, this edge would represent an acute cortisol stress response to novelty exposure. As such, in this simulation, mice in the solitary condition which did not spend much time near the novel object, had a larger cortisol response to this test, compared to mice that spent little time near the object in the group condition. Given these differences, should one really conclude that there is no difference in welfare between the two groups?

This simulated example demonstrates the additional insights that network analysis can bring to animal welfare inferences

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Figure 6



Network representation of individual edge weight differences between groups. In this network, an edge is present if the network comparison test identified a statistically significant ($P \leq 0.05$) difference in the partial correlation between the solitary- and group-housed conditions. The number in the middle of each edge is the difference between the solitary-group partial correlation minus the corresponding group-housed condition partial correlation. The thickness of the edge is proportional to the size of the difference.

in experimental studies. That is, it shows how network analysis of relations can identify potentially important welfare differences between groups in spite of no mean differences. Network comparisons can, however, be used to answer all sorts of different questions relevant to animal welfare. We next turn to an example of how statistical network modelling can be useful for identifying differential and specific effects of stressors on components of welfare.

Network models as a tool to identify specific direct associations between stressors and components of welfare

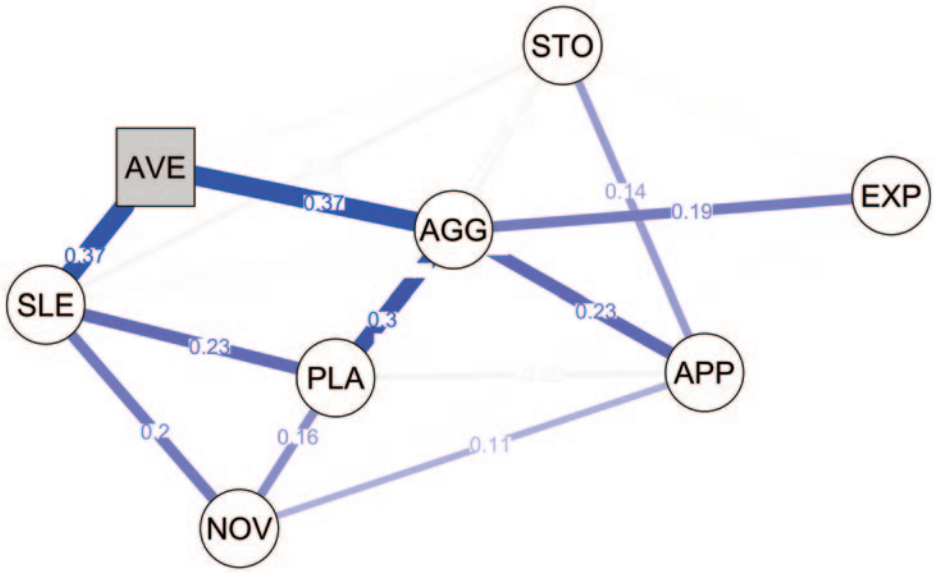
In the human clinical psychology and psychiatry literature, network analysis has been used to explore how stressors are associated with particular symptoms. For example, spousal loss in the form of bereavement or marital breakdown, is primarily associated with the symptom of loneliness which, in turn, is associated with other depressive symptoms (Fried *et al* 2015; Burger *et al* 2020). Animal welfare science is often concerned with the effects of stressors on measures of welfare. Therefore, the approach just described lends itself quite intuitively to animal welfare applications. That is, it is logical that not all stressors have exactly the same effect, and that different measures (or components) of welfare are differentially affected depending on the particular type of stressor. To our knowledge, this has never been systematically investigated, and statistical network models that include the stressor(s) as a node(s) in the network are well suited to explore such differential effects.

Consider the following simplified simulation representing a hypothetical study where a five-point Likert scale questionnaire is delivered to pet dog owners asking about seven components of welfare (where higher scores indicate increased severity of the welfare component). Suppose we combine this with a question about a particular stressor, in this case, how strongly participants agree or disagree that they use aversive methods to train or manage their dog's behaviour. An undirected network model can be estimated from such data in which the edges represent partial correlation coefficients. This example highlights how specific welfare effects can be visualised. In our simulation, the aversive techniques node is strongly conditionally associated specifically with aggressive behaviour toward owners and owner-perceived sleep disturbances, which are in turn associated with measures of other components of welfare. Networks such as these may reveal important information for managing welfare in the presence of a given stressor. In this example, if the data were real, one could hypothesise that minimising use of aversive techniques, and implementing interventions to improve sleep quality and to reduce aggressive behaviour toward owners, would be preferable over alternatives that are more specific to other nodes. If this approach was extended to study a variety of different stressors, then we would better understand the differential effects on components of welfare that different stressors exert.

In conclusion, the approach described above would not only aid in our understanding and conceptualisation of the specific welfare consequences of various stressors but may also help us to tailor interventions specific to the relevant stressor(s) present.

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Figure 7



Partial correlation network from simulated pet dog questionnaire data. Blue edges represent statistically significant positive partial correlations, and grey edges represent partial correlations not significantly different from 0 using *Z* tests. The magnitude of the partial correlation appears as a number in the middle of the corresponding edge and determines the thickness of each edge. The square node with grey filling represents the stressor of interest, and the circle white-filled nodes represent different components of welfare. As these are simulated data no questions were actually administered to generate these data but the following is an example of the sorts of questions that the nodes could represent: AVE, 'I use verbal and/or physical punishment to train my dog or manage their behaviour'; SLE, 'My dog does not sleep well overnight nor for periods during the day'; AGG, 'My dog can be aggressive towards me and other household members'; PLA, 'My dog is not very playful'; NOV, 'My dog can be worried by new objects, sounds, or places'; APP, 'My dog has a poor appetite'; STO, 'My dog regularly has loose stools'; EXP, 'My dog does little exploring and sniffing on walks.'

Discussion

In this paper we have drawn inspiration from human psychiatry and psychology to introduce a network perspective on animal welfare. Specifically, we have (i) introduced the basis of a network theory of animal welfare, and (ii) presented examples of how statistical network modelling can be readily applied to animal welfare science.

The network theory we have introduced proposes that welfare can be conceptualised as a network of mutual interactions between cognitive, behavioural, and physiological components (Figure 1B). This is in contrast to a latent theory, in which indicator variables are caused by a latent variable of welfare state (Figure 1A). The network conceptualisation can be approximated using statistical network models of conditional dependencies among welfare-related response variables. At this point, however, it is useful to further clarify this difference between network theory, and network analysis (statistical network models). Network theory is a theoretical model that the 'true' data-generating mechanism involves mutual interactions within a network system, and network analysis is a statistical model describing the covariance structure of a given dataset (Epskamp *et al* 2018b; Haslbeck *et al* 2019b; Fried 2020). While the use of network modelling in human psychology and psychiatry proceeded, and was therefore largely motivated by, the development of network theory (Cramer *et al* 2010), fitting a statistical network model does not necessarily provide support for a given network theory (Haslbeck *et al* 2019b; van Bork *et al* 2019; Fried 2020). The practical applications of network analysis that we presented in this paper with simulated data are similarly motivated by the development of a network theory of animal welfare, but these statistical models can be estimated and analysed whether one subscribed to network theory or not. For example, network analysis is a useful tool if one is simply interested in predictive relationships between variables (Epskamp *et al* 2018b; Epskamp & Fried 2018). However, we envisage that as the network perspective develops there will be a strong relationship between network theory and network analysis. That is, network theoretical models of animal welfare problems can be developed, and the predictions from these models can be specifically tested with statistical network models estimated on empirical data (Haslbeck *et al* 2019b). While these distinctions are important topics that will be required to be fleshed out in detail as the network theory of animal welfare is developed, a complete treatment of these distinctions is beyond the scope of the current paper. We direct readers to recent papers in the human psychology literature for more detailed discussions (Haslbeck *et al* 2019b; Fried 2020).

The three examples of applications of network modelling we presented in this paper included: (i) identifying poten-

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tially important intervention targets; (ii) comparing networks between experimental groups to aid welfare inferences; and (iii) identifying differential and specific effects of stressors on components of welfare. It should be noted that this is not an exhaustive list of potential applications. We decided to present these three examples for a number of reasons. The first is that they demonstrate novel and diverse applications of network modelling to animal welfare science. That is, they provide examples of applications across types of research and species, and each example demonstrates how different network metrics can be useful for different aspects of animal welfare research. Secondly, we wanted to provide examples of realistic studies that could be conducted and implemented in the current state of progression of the field. In part, we hope that in reading this paper, researchers are inspired to develop their own novel applications to problems within their given specialities or areas of interest that network analysis may be well suited to addressing. For example, an approach similar to the last example on stressors could be adopted to identify measures that are specifically and directly related to choices animals make in preference-testing paradigms. Network analysis may also be well suited to examine the multiple measures that are often taken in single welfare-related tests, for example, open field test and elevated plus maze. More generally, network analysis can be used to study components of emotion (Lange *et al* 2020), to uncover mechanisms of change in interventions (Blanken *et al* 2019), to examine links between welfare and genetics (for example, in human psychosis, see Isvoranu *et al* 2020), to identify early warning signals that may precede and predict a change in welfare state (for human mental health examples, see van de Leemput *et al* 2014; Wichers *et al* 2016, 2020), to develop welfare assessment protocols originating from a network perspective (for the human psychometric perspective, see Christensen *et al* 2020), and to test predictions from formal quantitative models (as described in Haslbeck *et al* 2019b).

It should be noted that in this paper we have focused our examples on undirected networks. This is primarily because we believe that undirected networks estimated from cross-sectional data is, at present, the most realistic application. It is, however, important to note that there are a large variety of different types of network models, which may all have uses in animal welfare science. For example, one can use intensive time-series data (for individuals or groups) to generate directed networks, in which the direction of associations can be identified (Epskamp *et al* 2018b; Haslbeck & Waldorp 2020). This provides additional information on dynamics, that is, the direction of associations, and is thus a closer representation of the causal dynamics that network theory proposes. However, while directed network models provide this additional information, they present practical challenges on how to realistically collect such data. Intensive time-series data of welfare-related response variables would present significant time and financial investment. Even if such practical constraints were overcome, many welfare measures would not be suitable for repeat sampling due to learning effects. In our view, directed network models will be particularly useful and feasible to analyse automated high throughput data collection when this becomes more feasible in animal welfare research. Indeed, there are significant advances being made in technology involving sensors to collect data from animals automatically (Neethirajan 2020), and in the near future, large-scale time series data collection may make directed network models possible.

We have also avoided too many technical details of the statistical procedures underlying network estimation and analysis. That is, we did not directly discuss the multivariate or univariate approaches to estimating network structures, nor did we discuss the large variety of model selection routines that are available. These are complicated topics that are best dealt with separately so as not to detract from the focus of the current piece of work, which is on the theoretical and practical applications of the approach. Generally speaking, there are a large number of undirected network estimation and analysis packages available for the R programming language (Epskamp *et al* 2012, 2018a; van Borkulo *et al* 2014; Epskamp 2015; Williams *et al* 2019; Haslbeck & Waldorp 2020; Williams & Rast 2020), which only require a basic working knowledge of R to utilise. Readers may find the following tutorials in the human psychology literature useful in this regard (Costantini *et al* 2015; Dalege *et al* 2017; Epskamp *et al* 2018a; Epskamp & Fried 2018).

It is also important to note that we focused our discussion primarily on components of welfare that reflect compromised welfare. However, there is a growing recognition that welfare is not just about avoiding negative states but also about promoting positive experiences (Mellor 2012, 2016). While we have not directly discussed this here, it should be noted that the same general principles still apply to the study of components of 'positive' welfare. However, the interpretations of such models, and the network metrics obtained may be different. Consider the network metric of global connectivity. Whereas high connectivity between 'negative' welfare nodes is likely to indicate vulnerability, high connectivity between 'positive' welfare nodes is likely to represent a good thing for welfare. Further, if positive and negative welfare components are included in the same network model, this may identify negative conditional dependence relationships between them. Such information may be important because these relationships could indicate that positive nodes can inhibit the activity of negative welfare components (or *vice versa*). Certainly, moving forward, network analysis will be well suited to study the direct interactions between negative and positive components of welfare.

There are some inherent limitations of the approach we have introduced. From a practical perspective, perhaps the most noteworthy is related to statistical power and sample size.

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Network models involve estimation of a large number of parameters which increases drastically with the size of the network (Epskamp *et al* 2018a). Therefore, the sample sizes typically required to obtain stable and accurate networks, and confidently identify non-zero conditional dependencies, can be large (Epskamp *et al* 2018a). Further, statistically speaking, sample size requirements in network-based studies is reported to not be a trivial problem, and there is therefore a lack of specific recommendations on sample size calculation in the network literature (Fried & Cramer 2017; Epskamp *et al* 2018a; Epskamp & Fried 2018), although work is underway in this area (Epskamp & Fried 2018; Lafit *et al* 2021). Practically speaking, this means that cross-sectional undirected network analysis is not feasible for small sampled studies involving, say, 20 animals. However, while exploratory statistical network modelling is not possible in small studies, this does not necessarily negate a role for network theory in such cases. A researcher may want to test a specific conditional interaction between a small number of variables based on predictions from a theoretical model. In such cases, the network approach has still been useful to derive a prediction (in the form of theory development), and provided that prediction does not involve necessarily having to estimate a large network, but that say, it predicts a conditional independency between two variables when conditioned on a third, then such a test may be feasible in smaller studies.

Animal welfare implications

The work we have presented in this paper has implications for both theoretical developments and applied aspects of animal welfare. That is, a network approach to animal welfare science holds promise for developing our understanding of the concept of animal welfare in the form of network theory. Further, the application of statistical network modelling has potential to test theoretical predictions, as well as produce immediately practical and meaningful information to improve the welfare of animals. This paper has only introduced the basis of the network perspective, and our primary aim is to stimulate discussion as the ideas and approaches are refined.

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