Regular article

Hormones, behavior, and social network analysis: Exploring associations between cortisol, testosterone, and network structure

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Article history:
Received 29 March 2014
Revised 18 July 2014
Accepted 19 July 2014
Available online 27 July 2014

Keywords:
Salivary cortisol
Salivary testosterone
Social network analysis
Exponential random graph modeling

A B S T R A C T

We used a new interdisciplinary paradigm of social network analysis (SNA) to investigate associations between hormones and social network structures. We examine these biobehavioral processes and test hypotheses about how hormones are associated with social network structures using exponential random graph modeling (ERGM) in a cohort of first-year students (n = 74; 93% female; M age = 27 years) from a highly competitive, accelerated nursing program. Participants completed friendship nominations and as a group simultaneously donated saliva (later assayed for cortisol and testosterone). ERGM analyses revealed that salivary cortisol levels were inversely associated with the number of outgoing ties (i.e., network activity). By contrast, testosterone was not related to friendship network structure. Integration of SNA and salivary bioscience creates a novel approach to understanding hormone–behavior relationships within the context of human social ecologies.

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Introduction

Decades of research reveal that hormones increase the probability that behavioral tendencies will be expressed given the appropriate social contextual demands (e.g., Nelson, 2011). A contemporary research focus has been to define sources of individual differences in biological sensitivities and susceptibilities to social contextual forces (e.g., Granger et al., 2012). Broadly considered, the social context in which these biobehavioral processes interrelate is generated by individuals’ social behavior in a group, or manifested as the composition and structure of the group, or nature of interactions (i.e., dynamics) among group members (Roney et al., 2007). Modern social network analysis (SNA) provides a sophisticated multi-dimensional heuristic and set of tactics for analyzing and describing these complex group structures and dynamics (for reviews, see Borgatti et al., 2009; O’Malley and Marsden, 2008; Robins, 2013; Snijders, 2011). The soluble chemical signals of the hypothalamic-pituitary-adrenal (HPA, e.g., cortisol) and hypothalamic-pituitary-gonadal (HPG, e.g., testosterone) axes are associated with various aspects of social context, including social threat and evaluation, social status, dominance and competition (Denson et al., 2009; Dickerson and Kemeny, 2004; Eisenegger et al., 2011).

Surprisingly, empirical attention linking cortisol and testosterone to the structure and dynamics of human social networks has been limited (see Sapolsky, 2005 for research with non-human primate dominance hierarchies). In this paper, we introduce the strategy and tactics of SNA to the field of behavioral biology and consider how SNA could augment understanding of biobehavioral processes in the context of human networks. We illustrate this new paradigm via an example by testing hypotheses related to how cortisol and testosterone are associated with social network structure using exponential random graph modeling (ERGM; Robins et al., 2007).

Social network analysis: basic concepts, assumptions, and tactics

A fundamental assumption of social networks research is that the functioning of a group and this group’s effects on its constituent members depend on the underlying structure of ties within a network (e.g., Valente, 2010). At a broad level, networks emerge as a result of group members’ pursuit of fundamental goals to belong and affiliate (Baumeister and Leary, 1995; Heinrich and Gullone, 2006) and to attain and maintain status (Hawley, 1999). Individual differences in these motivations, behaviors, and hormones lead to different patterns of ties around a focal individual. Not only are individual attributes associated with network tie formation, but connections between individuals also depend on the nature of their ties with other members of a group—a phenomenon known as network self-organization (Robins and Lusher, 2012). For instance, reciprocity is observed in human networks and...
describes the phenomenon ‘if you treat me as a friend, I will treat you the same way,’ whereas transitivity is the propensity to form friendships with friends of friends. Reciprocity and transitivity are referred to as network structural processes because these processes are self-organizing properties of a network itself. Recent research by Fowler et al. (2009) suggests that some tendencies to embed in certain types of network structures may be partially genetically determined. Social network theory assumes that social structures emerge through stochastic and deterministic processes, and that network structural processes and individual attribute-related processes operate simultaneously in networks (Robins and Lusher, 2012). In line with these assumptions, SNA methods involve advanced multivariate modeling techniques designed to examine the multiple processes that contribute to network structure and the effects of network structures on their constituent members (Robins, 2013; Snijders, 2011).

It is noteworthy that descriptive tools of SNA (i.e., quantifying an individual’s position in an overall network structure) have been successfully applied in behavioral biology research with non-human primates (e.g., Croft et al., 2011). For example, high-ranking free-ranging female macaques were shown to have lower glucocorticoid levels when their association networks were smaller and more focused, as indexed by a lower number of outgoing ties (Brent et al., 2011). However, because multiple processes jointly operate in networks, descriptive indices of network position do not disentangle social processes through which networks evolve; these goals are accomplished by statistical modeling of networks (see Robins, 2013; Snijders, 2011 for reviews). There has been a recent push to advance the state of research on social networks in behavioral biology beyond descriptive analyses and to draw on the wealth of statistical modeling of network methods (largely developed in the social sciences) to elucidate how biology, behavior, and network dynamics interrelate (Pinter-Wollman et al., 2014).

Overview of Exponential Random Graph Modeling (ERGM) Approach

Here, we focus on one particular approach to statistical modeling of networks—ERGM (Robins et al., 2007), which assumes that patterning of ties is evidence of various network processes, and that each of these processes has a local signature that is represented in a count of certain network structural configurations (i.e., local parameters). In ERGM, the researcher specifies a model with hypothesized local parameters, and the resultant model is used to simulate multiple networks to evaluate whether the hypothesized local network parameters adequately represent the observed network structure. For example, consider a local parameter of reciprocity that models an effect of a fundamental network structural process on tie formation (Rivera et al., 2010): if reciprocated ties in dyads (i.e., local configurations) are observed in a network structure at a greater than chance level, then we can conclude that network process of reciprocity contributed to formation of this structure. As another example to illustrate how individual differences in hormones may be associated with network structure, consider how the local parameter of network activity (i.e., number of outgoing ties that an individual sends) may be associated with hormones. If differences in hormone levels are related to the number of outgoing ties that each individual has in a network at greater than chance levels, this provides evidence that hormone levels are associated with network activity (Goodreau et al., 2009). To further illustrate the association between local processes and global network structures, the local process of network activity is manifested in the number of outgoing ties that an individual has, and when such tendency is aggregated across individuals in the entire group, we get degree distribution, which is a global network property. As previously noted, network structural processes of reciprocity, transitivity, and others also contribute to network formation processes and, therefore, to degree distribution. Degree distribution, in turn, has implications for efficiency and resiliency of the overall network, as well as speed with which information is transmitted in the system (Newman, 2008).

The key advantage of ERGM for the study of behavioral biology is that it can combine data on individual attributes and network structural processes to examine the effect of behavioral data, biological data, and local network configurations on global network structure (Robins et al., 2007). Consider an example of how several processes are implicated in the way that testosterone, aggressive behavior, and sex affect social network structure. If an individual prefers to affiliate with others who are of the same sex (i.e., sex homophily), it is likely that those friends also exhibit similar levels of testosterone and aggressive behavior (characteristics that co-vary with sex). Additionally, these initial similarities (sex, testosterone, and behavior) would be further amplified through transitivity when a friend of a friend becomes a friend. Thus, several distinct social processes occur in this scenario: transitivity, sex homophily, and homophily on individual-level attributes (testosterone and aggressive behavior) that co-vary with sex. If we were to examine the role of aggressive behaviors for social tie formation in a statistical model without controlling for transitivity and homophily on sex and testosterone, we would overestimate contributions of aggressive behaviors to network structure. In summary, the ERGM approach allows us to model how both network structural processes and individual network members’ attributes jointly predict a network structure, which is not feasible in traditional statistical models (OLS regression).

Hormones, behavior, and social network structure

An overarching aim of our research program is to evaluate the effects of social context on hormone-behavior relationships that occur in naturalistic human social ecologies. This aim is consistent with ethological perspective and complements laboratory-based research (e.g., Sapolsky et al., 2000). To understand the role of networks for the study of hormones and behavior, we draw on SNA and examine three main processes: (1) activity or gregariousness, which is the tendency to send out affiliation or friendship ties, (2) popularity, or tendency to receive affiliation or friendship ties, and (3) homophily, or the propensity to affiliate with others who have similar characteristics. We focus on two hormones—cortisol and testosterone—that have been consistently linked with social behavior at an individual level of analysis.

The primary end-product of activity of the hypothalamic-pituitary-adrenal (HPA) axis in humans is cortisol (Chrousos and Gold, 1992), one of the main secretory products involved in regulation of stress and the stress response. Studies show that higher cortisol levels and cortisol reactivity are associated with distress and negative affect, social inhibition–withdrawal, and social anxiety (e.g., Weiner, 1992). Cortisol levels trend higher when individuals (a) appraise a task to be challenging, novel, and/or intense, and (b) experience ruminative thoughts and/or fear of losing social status (Denson et al., 2009). Cortisol is associated with perceived threat to social self as suggested by social self-preservation theory (Dickerson, 2008). HPA axis activity appears to be coordinated among individuals who share common social experience. In the earliest work on this topic (Granger et al., 1998), reported positive associations between maternal and child cortisol levels in a high-risk sample of families. Another study revealed a positive association between mothers’ and adolescents’ cortisol levels, especially when youth engaged in more activities with their mothers and were subject to greater parental supervision (Papp et al., 2009). This pattern suggests that, in some circumstances, the strongest predictor of an individual’s HPA axis activity may be the cortisol level of those sharing that person’s immediate social context (see also Sethre-Hofstad et al., 2002; van Bakel and Riksen-Walraven, 2008; Saxbe and Repetti, 2010). Research has also shown that such family similarity or attenuation in afternoon cortisol levels is associated with shared environment and not underlying genetics (Scheer et al., 2006).

Testosterone is a product of the hypothalamic-pituitary-gonadal (HPG) axis (Nelson, 2011). In post-pubertal males, testosterone is very efficiently produced in the Leydig cells of the testes, but in females the majority of testosterone is derived from the less efficient peripheral metabolism of the HPA product dehydroepiandrosterone, DHEA (Nelson, 2011). Individual differences in testosterone levels have been associated
with risk-taking, aggressive and antisocial behavior, dominance, winning/losing, and contests for social rank and status (see Booth et al., 1999; Eisenegger et al., 2011; Mazur and Booth, 1998 for reviews). Testosterone levels in males rise in anticipation of competitive events; after the event, levels generally continue to rise (or stay elevated) for the winners but often decline for the losers (for review, see Mazur and Booth, 1998). The few studies that have included females suggest the changes in testosterone in response to competition are similar, although less pronounced, than for males (e.g., Kivlighan et al., 2005). Testosterone is linked to higher levels of prosocial and fairness-oriented behaviors suggesting involvement in status-related behaviors driven by prosocial tendencies (Eisenegger et al., 2010; van Honk et al., 2012). Testosterone has also been found to increase reward sensitivity (Hermans et al., 2010) and reduce fear (van Honk et al., 2005). Relationships between testosterone and social behavior in human networks may manifest not only through the agonistic strategies as suggested by past research on dominance hierarchies, but also through prosocial behavior and approach motivation systems (Eisenegger et al., 2011). This possibility is consistent with the notion that humans tend to succeed in resource control and status acquisition by employing both prosocial and aggressive strategies (Hawley, 1999). Only one study has indirectly suggested homophily on testosterone: (Bernhardt et al., 1998) reported that testosterone levels increased among fans of winning sports teams and decreased among fans of losing sports teams.

Present study

We evaluate how cortisol and testosterone are associated with the processes of network activity, popularity, and homophily in a circumscribed social network of nursing students from an accelerated professional program at Johns Hopkins University. This professional program is consistently ranked among the highest in the United States, and graduates are placed in higher-paying and more socially desirable jobs depending on their class ranking and performance. In our past research with this sample (Kornienko et al., 2013), we used individual-level analyses (ANOVA) to document that social status indicators based on popularity and gregariousness in the network were associated with salivary cortisol levels. This study extends prior findings in two ways: (1) we use ERGM to estimate the associations between hormones and network ties while controlling for additional network structural effects (reciprocity, transitivity) as well as confounding homophily on age, sex, and race, and (2) we consider effects of testosterone, which has been linked to social behavior, competition, and dominance hierarchies (e.g., Mazur and Booth, 1998; Sapolsky, 2005). We hypothesized that cortisol would be negatively associated with network activity because prior research has linked increased cortisol with social withdrawal, anxiety, and inhibition (Granger et al., 1994, 1996). Regarding the associations between cortisol and network popularity processes, the current thinking about the resources and provisions, which are linked to network popularity, suggests that it may be associated either positively or negatively with cortisol levels. On one hand, popular individuals may have higher levels of social capital (e.g., Brent et al., 2011), which may buffer them against challenging situations, leading to a negative association with cortisol levels. On the other hand, cortisol may be positively associated with network popularity because such social position implies increased visibility among friends, which is likely to be associated with mobilization of resources to “remain on top of the game,” so to speak (Del Giudice et al., 2011). Testosterone has been linked with pursuit of status, dominance (Eisenegger et al., 2011), fear reduction (van Honk et al., 2005), and increased reward motivations (Hermans et al., 2010), we predicted that testosterone would be positively associated with both network activity and popularity. Past research has demonstrated homophily for cortisol levels in family groups (Granger et al., 1998; Papp et al., 2009) and for testosterone levels in peer groups in the context of sports (Bernhardt et al., 1998), we hypothesized that similarity on levels of cortisol and testosterone would be associated with increased odds of friendship tie formation, leading to positive homophily effects for both hormones.

Material and methods

Participants

The participants were nursing students enrolled in the accelerated class of the School of Nursing, Johns Hopkins University (Baltimore, MD, USA). Students from the accelerated class were invited to participate in this study and gave their consent. The study was approved by the Institutional Review Board at the Johns Hopkins University School of Medicine and informed consent was obtained from all participants.

Procedure

Participating students were invited to an in-person data collection session, which took place on a Monday between 12 pm and 1 pm. At the in-person session, the participants were asked to donate a saliva sample. After the saliva collection, participants completed a friendship nomination inventory and a short questionnaire on demographics, health and medication use. They received a free lunch and a coffee card to thank them for their participation. As part of the larger data collection project, participants completed additional measures in an online survey on personality, empathy, social support, coping strategies, and perceived stress.

Salivary biomarkers

Following (Granger et al., 2012), whole saliva samples were collected by passive drool into a 2 mL cryogenic vial. Samples were collected from every participant simultaneously and then immediately placed on ice and transferred to the laboratory where they were stored frozen at −80 °C until assay. Samples were assayed for salivary cortisol and testosterone using commercially available enzyme immunoassays without modification to the manufacturers’ recommended protocols (Salimetrics, Carlsbad, CA). For cortisol, the test used 25 μL of sample, had a lower limit of sensitivity of 0.007 μg/dL, range of sensitivity from 0.007 to 3.0 μg/dL. For testosterone, the test used 50 μL of sample and the sensitivity of the protocol ranged from 1.0 to 600 pg/mL. Inter-assay and intra-assay precision (coefficient of variation) were both assayed, on average, less than 15% and 10% respectively. Raw hormone levels were transformed using square-root transformation due to positive skew in the raw data for both testosterone and cortisol and then centered within each sex given that sex differences exist in salivary testosterone levels (Nelson, 2011).

Behavioral assessments

For the friendship nomination inventory, an alphabetized list was constructed which contained the ID codes and names of all students who agreed to participate in the study. Participants wrote their own ID on the first page of the questionnaire booklet. They were then asked to list the IDs of their classmates that were their closest friends; they could name as many classmates as they wanted. At the end of the session, students returned the alphabetized list with the ID codes and names of all participants to the study team. This list was subsequently destroyed, so that the questionnaires only contained ID numbers and no names. Based on friendship nominations data, a matrix of unilateral or asymmetrical and binary-coded friendship ties was created in which a cell value of 1 for the intersection of row A and column B
denoted that B was nominated as a friend by A, and a cell value of 0 denoted that no friendship nomination of B was made by A. To control for confounding network activity processes (i.e., homophily on sociodemographic variables), we included the following control variables in our estimation of network structure: sex, race/ethnicity, and age. Sex was coded as 0 = male and 1 = female, and race/ethnicity was coded as Asian, African-American/Black, Hispanic, and White.

Analytical strategy and tactics

ERGM tests whether local processes affecting ties between pairs of individuals explain a global or group-level network structure (Robins et al., 2007). Thus, the structure of network ties is the dependent variable that is modeled as a function of local processes describing (a) network structural processes (e.g., reciprocity and transitivity) and (b) social processes that are associated with individual’s attributes (i.e., activity, popularity, and homophily). ERGM follows a maximum likelihood approach to select a model of local processes that maximizes the probability of reproducing the observed global network. The analyses use the Markov Chain Monte Carlo (MCMC) estimation method of simulating a distribution of random networks using a set of starting parameter values that were generated by pseudo-likelihood. Over several iterations, this method optimizes the parameter values by comparing the distributions of simulated networks to the observed data. ERGM analyses calculate the log-odds (logit) probability that a friendship tie exists, conditional on the rest of the network. To ease interpretation of results, the model produces parameter estimates for each of the network structural and social processes describing the increase in the log-odds that a specified tie is formed, if adding this tie would increase the network statistic for the particular process by one (Goodreau et al., 2009). For example, consider a structural process of transitivity, which is modeled by counting the number of triangle configurations (i.e., groups of three friends). A positive parameter coefficient for transitivity suggests that the observed network contains a greater number of triangles than expected by chance, and a negative coefficient indicates that the network has a lower number of triangles than expected by chance. In other words, the sign of the coefficient in the model tells us whether two friends of a single individual are more (positive) or less (negative) likely to be friends with each other.

Following guidelines for ERGM model specification for directed networks (Robins and Draganova, 2012), we included effects of cortisol and testosterone on three network processes: (1) activity, which is estimated based on the sum of hormone levels for all individuals’ outgoing ties in the network, (2) popularity, which is estimated based on the sum of hormone levels for all individuals’ incoming ties, and (3) homophily, which estimates the effect of absolute difference between salivary hormones for each two connected individuals on the likelihood of tie formation between them (i.e., for continuous variables, the absolute differences between attributes of actors are used; a positive parameter estimate denotes heterophily (i.e., larger difference in scores contributes to tie formation) and a negative estimate indicates homophily (i.e., small differences in scores contributes to tie formation)). To control for the homophily on confounding individual-level characteristics, we included three effects to describe uniform homophily on sex and race/ethnicity and absolute difference homophily on age. We also included the key network structural effects [see Table 2 for graphical representation of all effects]: edges, or ties (this structural effect describes conditional log-odds of forming a tie between two individuals if none of the network and social processes that we hypothesize to affect network selection were included in the model), reciprocity (this effect describes a tendency for reciprocated nominations), geometrically weighted popularity (this effect describes the tendency for individuals with higher in-degrees to form partnerships with others), geometrically weighted activity (this effect describes a tendency for individuals with higher out-degrees to form partnerships with others), geometrically weighted edge-wise shared partners (i.e., closed triads describing a tendency for two individuals who have ties to each other to also have multiple shared friends), and geometrically weighted dyad-wise shared partners (i.e., open triads describing a tendency for any two network partners (linked or not) to have shared ties). In addition to this main model used to test our hypotheses about associations between hormones and network structure (i.e., associations between cortisol and testosterone and network activity, popularity, and homophily), we estimated a baseline model, in which the six hormone-related effects were omitted. Thus, the baseline model included network structural effects (i.e., edges, reciprocity, geometrically weighted popularity, geometrically weighted activity, geometrically weighted edge-wise shared partners, geometrically weighted dyad-wise shared partners) and controls for confounding individual-level characteristics (i.e., homophily on sex, race, and age).

We used curbed exponential family models in which the corresponding parameters for geometrically weighted effects were estimated from the data in order to improve the performance of the maximum likelihood estimation algorithm and avoid model degeneracy (Hunter, 2007; Hunter et al., 2008a). After the final models were identified and estimated, we conducted a graphical assessment of goodness of model fit in which we used MCMC simulations to examine how well the observed network matched a large number of simulated networks based on the estimated model (Hunter et al., 2008b). Given that ERGM is an autoregressive, generative model, a traditional approach to model selection and evaluation of goodness of fit, such as AIC or BIC, are not applicable to ERGM because such indices assume independence of observations and their identical distribution in the sample, which do not apply to social network models (Goodreau, 2007; Hunter et al., 2008b). Thus, network scientists have recommended graphical assessment of model fit instead, in which one examines whether repeated simulations based on the modeled parameters are able to reproduce key features of the observed data which themselves were not included in the model (Goodreau, 2007; Hunter et al., 2008b).

We conducted ERGM analyses using two specifications of the friendship network: the first full-sample network consisted of 74 individuals (69 females and 5 males) who sent 388 friendship ties to each other and the second female-only network consisted of 69 females who sent 335 friendship ties to each other. This choice was driven by the concern that, given sex differences exist in testosterone levels, 7% of males in the sample increased variance on testosterone but precluded examination of sex differences. Removal of 7% of the sample resulted in a 14% reduction in the number of ties; same-sex and cross-sex ties exist in this network and network analyses rely on the interdependence of ties, these results should be interpreted with caution.

In addition to basic descriptive statistics at the individual level, we calculated network-level descriptive statistics for the full friendship network (i.e., number of ties, and density; Table 1 and Preliminary Analyses below) and used network visualization to depict the associations between hormone levels and friendship network structure in our sample (Figs. 1–2). Network descriptive statistics and visualizations were conducted using sna package (Butts, 2008) and ERGM analyses were conducted using statnet package version 3.1-0 (Handcock et al., 2008) in R version 3.0.0 (R-Project; http://www.r-project.org).

Results

Preliminary analyses

Our descriptive analyses focus on two levels of analysis: (1) the individual and (2) the full friendship network. Table 1 presents a summary of the sociodemographic composition of our full sample and cortisol and testosterone levels. Network-level descriptive statistics indicated that our network of 74 nursing students (males and females) had 388 directed ties; each individual had an average of 5.24 outgoing ties (SD = 3.05, range 0–15) and 5.24 incoming ties (SD = 2.77, range 0–12). We observed that the network had a density (i.e., proportion of existing ties relative to the total possible ties) of .07, suggesting that most of the total possible ties in the network do not exist. This level of density is consistent
with other research on human social networks (Wasserman and Faust, 1994). We present a visualization of the friendship network in Figs. 1 and 2, where each node represents an individual, circles are females and squares are males, the size of node corresponds to untransformed cortisol (Fig. 1) and testosterone (Fig. 2), and paths connecting nodes reflect directed (single head) or reciprocal (double head) friendship ties.

Contributions of cortisol and testosterone to network structure

We next examined the multiple network and biobehavioral processes that are associated with friendship network structure. Before discussing the contributions of cortisol and testosterone to network processes, we describe network structural effects and confounding homophily on sex, age, and race/ethnicity. Table 2 presents the results of ERGM of friendship network structure as a function of social and network structural processes, with graphical illustrations to aid the interpretation of these processes. Model 1 presents the results obtained from the full network comprised of males and females, whereas results for Model 2 were obtained by considering the friendship network of females only. Homophily on sex was omitted from Model 2.

In our Model 1, using full friendship network, we did not document significant homophily on sex, age, and race. The lack of sex homophily was not surprising given that our network contained 69 females but only 5 males. It also appeared that friendship networks in this cohort are not driven by homophily on race and age that are frequently observed in adolescent networks (Goodreau et al., 2009). Presence of large portion of a sample that was homogeneous in these attributes may have lowered our power to detect the typically reported assortative mixing patterns (McPherson et al., 2001).

Considering structural effects, we found a negative effect of edges (coefficient = $-2.44, p < .001$), which describes the conditional log-odds of forming a tie between two individuals if none of the network and social processes that we hypothesized to be associated with network structure were included in the model. This negative effect suggests that friendship formation was unlikely outside of the hypothesized network and social processes (Goodreau et al., 2009). The positive reciprocity effect (coefficient = $3.41, p < .001$) indicated that individuals were likely to reciprocate friendship ties. Taken together these results show that uni-directed edges are relatively unlikely to form outside of reciprocated edges; thus, unrequited friendships are less likely in the network. The positive closed triads effect (coefficient = $.65, p < .001$) indicated that two individuals who have ties to each other also have multiple

Table 1

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Fig. 1. Cortisol levels and friendship network in nursing students. Note: Visual representation of friendship network and individuals’ cortisol levels. Nodes are individuals, and links between nodes represent friendship ties. Square nodes are males, circle nodes are females. Node size corresponds to the individual’s cortisol levels multiplied by a constant of 15 to improve readability (larger nodes reflect higher levels of cortisol).
shared friends (i.e., transitivity). The negative open triads effect (coefficient = −.22, p < .10) indicated that there was a trend that any two network partners were not likely to have shared ties.

Results for contributions of hormones to the propensity to make friends are presented in Table 2. Activity, popularity, and homophily coefficients are reported as conditional log-odds. Consistent with our hypothesis, we documented that cortisol had a negative effect on the tendency to send out ties in the network, which describes overall network activity (coefficient = −2.72, p < .01). Contrary to our hypotheses, however, salivary cortisol did not have significant effects on popularity and homophily processes, and testosterone was not significantly associated with any of the three network structure processes in this friendship group.

In Model 2, using female-only network, we replicated the patterns of results from the full network. Considering the contributions of salivary hormones to network structure, we observed that cortisol continued to have a negative effect on the propensity to send out friendship ties; however, the magnitude of the coefficient decreased (coefficient = −1.74, p < .05). We did not document significant effects of testosterone on network selection processes in either model. Given that the two models produced virtually identical results, we focus on discussing the findings from Model 1 in the remainder of this section.

**Assessment of model fit**

Following established guidelines (Goodreau, 2007; Hunter et al., 2008b), we evaluated the robustness of Model 1 through Monte Carlo Markov Chain simulations to examine how well the observed network matched a large number of simulated networks, which were based on the estimated Model 1. We examined the five key characteristics of network structure for simulated and observed networks (i.e., geodesic distance, edge-wise shared partners, indegree, outdegree, and triad census). Fig. 3 contains the visual representation of the match between the simulations based on the model and the observed data. In this figure, the thick black line represents the observed network properties, and gray lines represent 95% confidence intervals for the simulated networks that were based on the model. The placement of the line within the 95% confidence interval boundaries indicated that our model produced good to excellent goodness-of-fit statistics. These plots suggested that Model 1, which was based on local network, hormone, and individual-attribute related processes, was able to account for substantial variance in the observed global network data. As a contrast, Fig. 4 provides a graphical model fit assessment for a baseline model in which all associations between hormones and network structure were omitted; this model only included network structural processes and controls for homophily on confounding individual attributes (i.e., sex, race, and age). As this figure shows, the goodness of fit for the baseline model declined, especially in regards to representing the distributions of incoming and outgoing ties observed at the network level. This suggests that the inclusion of hormone effects increased our ability to explain the network structure of this sample.

**Discussion**

In this social ecology, variation in cortisol levels was related to activity processes in the social network. Specifically, higher levels of cortisol were associated with a lower propensity to send out friendship nominations to peers. Importantly, the application of advanced SNA tactics (i.e., ERGM) reveal that the association between cortisol levels and structure of social ties explains variation above and beyond potentially confounding network structural processes (e.g., reciprocity) and homophily on age, race, and sex. After taking structural processes and similarity between individuals on sociodemographic characteristics into account, cortisol activity was not related to popularity or homophily, nor was there any evidence that variation in testosterone was related to friendship network structure. The findings have several noteworthy implications and are discussed in relation to prevailing theoretical
assumptions about the bi-directional nature of the relationships between hormones, behavior, and social context.

An overarching aim of this research program (Kornienko et al., 2013) is to utilize SNA heuristics and tactics to provide a multidimensional view on complex processes linking naturally occurring ecology of a social network to hormones and behavior. Consistent with recent thinking in behavioral ecology (Pinter-Wollman et al., 2014), we advocate that SNA provides sophisticated means of conceptualizing, describing, and modeling social ecology that would augment the current theoretical perspectives that integrate biological, behavioral, and social perspectives on development, health, and behavior (Belsky, 2005; Booth et al., 2000; Boyce and Ellis, 2005; Ellis et al., 2011). Typically, conceptual models of these processes focus attention on variation in reactivity and regulation of environmentally responsive biological systems such as the HPA axis. The current work adds to this research by suggesting that individual differences in the activity of these biological systems may also be associated with social network structures.

Networks of relationships that emerge in social groups and organizations are unique from other systems of social relationships (i.e., parent–child and family relationships) because individuals within the network play an active role in creating their social context. To understand the role of social networks for the study of hormones and behavior requires an understanding of the processes associated with how individuals form social ties; this is known as network selection processes (for a review see, Veenstra et al., 2013) and business organizations (for a review see, Balkundi and Harrison, 2006). Understanding how these social contexts differ from one another is critical to interpreting cortisol levels, and those with higher popularity status had higher cortisol levels (Kornienko et al., 2013). This past work conceptualized status in a friendship network as an attribute of an individual (although based on individual’s position in a network). Despite the novelty of the approach, that analysis was limited in that it used individual-level analysis (i.e., ANOVA), which treated the network as a given social context with independent observations, and could not simultaneously account for both network-level structural processes and social processes related to individual members’ attributes in the prediction of network structure. In contrast, the advanced SNA modeling approaches applied here employ simulation-based inference to model how multiple and simultaneously-occurring social processes are associated with observed global network structure. Our results extend prior observations by revealing that cortisol levels were uniquely associated with network activity. Researchers seeking to answer questions such as, “Is the structure of friendship ties within a network associated with hormone levels?” and “Are individuals with similar levels of hormones more or less likely to be friends?” are encouraged to utilize the ERGM approach illustrated in this paper.

Social ecologies are landscapes with distinct features and characteristics. The underlying structure of ties and social dynamics has implications for the functioning of a group and this group’s effects on its constituent members (Valente, 2010). In humans, the structure and dynamics of a social network are differentially associated with group- and individual-level outcomes in relationships among peers in school settings (for a review see, Veenstra et al., 2013) and business organizations (for a review see, Balkundi and Harrison, 2006). Understanding how these social contexts differ from one another is critical to interpreting...
the meaning and implications of biology–behavior links observed within them. The proximal features of the professional training environment in which this study’s social network evolved are noteworthy. In the academic nursing program that was sampled, individuals are placed under high performance expectations, there is a high monetary cost to participate, the probability of social evaluative threat is high, there are multiple competing demands, daily decisions have “high stakes,” and students are rewarded based on individual performance. These features are not necessarily unique to nursing school; they may also characterize professional training environments in medical schools, military specializations, finance, and professional sports. Contemporary theory (Belsky, 2005; Booth et al., 2000; Boyce and Ellis, 2005; Ellis, et al., 2011) implies that individuals who are more biologically sensitive to context are likely to express high and variable levels of HPA axis activity in these circumstances. Those who are the most biologically sensitive may have self-selected out of these circumstances or be at the highest risk for burn out or drop out. The majority of those who self-select into these high performance training conditions are likely to represent a unique subgroup with a history of excelling in high-stakes and high-pressure professional situations. In these circumstances, our findings suggest that the individuals who have self-selected into this program and who have higher cortisol levels tend to be less active in the social network. One possibility is that, under these demanding conditions of nursing school training, individuals in this group may have little time and energy to invest in social relationships because they are too busy with their academic work. Another possibility is that having fewer ties may be “protective” in the sense that friends within the program are likely to be experiencing similar challenges and use co-rumination as a coping mechanism, which may amplify stress (Schwartz-Mette and Rose, 2012) rather than buffer against it (Hostinar et al., 2014). Whereas these potential mechanisms need to be explored in the future research, these possibilities tend to be consistent with prior findings at the individual level showing that higher levels of HPA axis activity are associated with social withdrawal, anxiety, and inhibition (Granger et al., 1994, 1996).

Although we did not observe homophily on salivary cortisol levels within this network as we hypothesized, it seems worthwhile for future research to examine how various combinations of cortisol levels between friends may contribute to persistence and turnover of social relationships. We based this hypothesis in prior research suggesting dyadic co-regulation of cortisol between the members of marital (Saxbe and Repetti, 2010) and mother–child (Sethre-Hofstad et al., 2002; Van...
However, it is plausible that the distinct nature of the social relationships that are considered in this study has a different effect on the social co-regulation of HPA axis activity. Friendships among adult peers are distinct from family relationships in that they are horizontal and voluntary (Reis et al., 2000). This difference may imply that individuals tend to synchronize HPA activity in permanent social relationships, but that peers can elect to stop being friends and exit relationships when the experience is incongruent with either member’s social agenda or reactionary style.

The lack of findings for testosterone is worthy of comment. It is tempting to speculate that this null result suggests that testosterone is not as relevant for predominantly female and female-only networks as it might be for mixed sex or all-male networks. Numerous studies reveal that the source, levels, and behavioral correlates of testosterone show distinct sex differences (e.g., Eisenegger et al., 2010), and that, in females, changes in testosterone in response to competition are generally the same, although less pronounced and consistent across studies, than for that of males (e.g., Kivlghan et al., 2005; Mazur and Booth, 1998). So it may be the case that, in our predominantly female sample, individual differences in testosterone were less pronounced as related to competition and social dominance. Alternatively, in this particular high-stakes academic training program, individuals may be primed for competing for academic status rather than social status, making variation in testosterone unrelated to social network structure in this unique context. Future studies of the role of testosterone and HPG axis activity in human network structures and dynamics using SNA methodology seem well justified.

Although this study introduced and applied novel methods of SNA, some limitations should be noted. The social circumstances of the nursing students enabled us to study associations between hormone activity and network processes in a stressful and competitive academic environment. The nature of these circumstances, while potentially enhancing our ability to detect effects, also limits our ability to generalize these findings to other networks (e.g., families, communities). Although the analyses utilized a complete network data collection approach in that both individuals and their friends provided information about ties, it should be noted that not all students within the nursing program cohort participated in the study, so our results should be interpreted with some caution.
Future research on hormones, behavior and social network analysis

Modern behavioral endocrinology assumes that biology and behavior are reciprocally linked (e.g., Granger et al., 2012), and that these associations are also dynamically embedded into a particular social context. SNA provides methodological contributions to the field of behavioral biology because it allows us to jointly consider biology, behavior, and social networks. For instance, longitudinal applications of social network modeling (i.e., stochastic actor-based modeling; SABM; Snijders et al., 2010) are especially relevant because these methods allow for an examination of how individuals select their social networks and are influenced by them over time. Specifically, it is important to explore direct and indirect contributions of hormones to network selection and social influence processes. To date, we only have a limited understanding of the role that hormones play in these processes. Previous research has showed that adolescents with greater testosterone have greater levels of delinquency when they were surrounded by delinquent friends, but greater prosociality when they had prosocial friends (Rowe et al., 2004). This evidence suggests that greater testosterone is positively associated with behavioral homophily, but we do not know if this similarity results from initial selection of friends who are prosocial or delinquent, or from social influence that operates in the peer context once a friendship is formed. SABM approach allows examining the role of hormones as moderators of network selection and social influence processes.

Concluding comment

Understanding the dynamics of biobehavioral processes in the context of collaborative team networks within organizations seems like a worthwhile next step. Individuals are selected for collaborative team networks based on complimentary but distinct skills; these networks are also characterized by multiplex relationships including formal professional ties and informal friendship and advice ties (for a review, see Balkundi and Harrison, 2006). The structure of ties within organizations contributes to task performance and team effectiveness to the same extent as the structure of advice ties (Balkundi and Harrison, 2006). Our findings raise the possibility that individual differences in hormone levels may be associated with not only network structures, but also other emergent features such as cohesion and vitality that are important dimensions of team climate. If future longitudinal research discovers that these bi-social dynamics are related to performance, continuity of function in team networks, then findings from hormone-inclusive SNA research may have implications for selecting, training, and maintaining the performance integrity and problem-solving efficiency of professional working groups in complex and chaotic environments. Ultimately, the outcome of such an effort may enable the early detection of individuals or subgroups within larger working teams that disrupt and interfere with larger team goals.

Acknowledgments

OK was supported in part by funds from the T. Denny Sanford School of Social and Family Dynamics at Arizona State University as part of the Lives of Girls and Boys Research Enterprise (http://lives.clas.asu.edu/). KHC was supported in part by a grant from the National Institute of Mental Health (T-32MH018834 to Nicholas S. Ialongo, PI). DO was supported by a Rubicon award (446-10-026) from the Netherlands Organization for Scientific Research. In the interest of full disclosure, DAG is founder and Chief Strategy and Scientific Advisor at Salimetrics LLC (Carlsbad, CA) and the nature of this relationship is managed by the policies of the committees on conflict of interest at Johns Hopkins University School of Medicine and the Office of Research Integrity and Assurance at Arizona State University. We thank Dr. David R. Schaefer, the editor, and two anonymous reviewers for their constructive comments. Special thanks to Tracy Hand and Jessica Bayer for technical support with salivary immunoassays, and Amber Pinkard for assistance with data collection.

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