A Call for Complexity in the Study of Social Anxiety Disorder.
Commentary: The aetiology and maintenance of social anxiety disorder: A synthesis of complementary theoretical models and formulation of a new integrated model

Alexandre Heeren1,2* and Richard J. McNally1

1 Department of Psychology, Harvard University, Cambridge, MA, USA, 2 Psychological Science Research Institute, Université Catholique de Louvain, Louvain-la-Neuve, Belgium

Keywords: social anxiety disorder, computational social science, network analysis, complexity, graph theory, etiological factors, maintenance factors, experimental psychopathology

A commentary on

The aetiology and maintenance of social anxiety disorder: A synthesis of complimentary theoretical models and formulation of a new integrated model

Wong and Rapee (2016) conducted a much-needed comprehensive review of etiological and maintenance models of social anxiety disorder (SAD) to formulate a cutting-edge integrative model. We agree that the threat value assigned to social-evaluative stimuli may act as core process bridging etiological (e.g., peer rejection) and maintenance (e.g., attentional bias for threat) factors of SAD that eliminate (e.g., avoidance) potential threat. Their model persuasively postulates multiple causal pathways and loops whereby variables increasingly reinforce the threat-value of social-evaluative stimuli so that they foster the development of secondary processes to further detect and reduce potential threat, culminating in full-blown SAD. We believe that the computational and conceptual tools of network analysis (Borsboom and Cramer, 2013) can render testable the complex dynamic features of their model.

During the last decade, network science has transformed disciplines such as ecology, physics, and sociology (Barabási, 2012). With the recent advances of Borsboom and his colleagues at both the theoretical (Borsboom and Cramer, 2013) and computational levels (Epskamp et al., 2012), we are entering the period when this "network takeover" (Barabási, 2012, p. 14) is opening up new vistas for understanding psychopathology (McNally, 2016; Borsboom, in press). At the simplest level, a network consists of nodes and edges that connect them. In psychopathology, nodes represent symptoms and edges represent association between symptoms. The network approach conceptualizes an episode of disorder as emerging from the dynamic interplay of symptoms. Symptoms possess independent causal powers that influence other symptoms; they are not merely
variables over time, recently developed computational methods allow exploring the within- and between-person temporal dynamics of networks (Epskamp et al., 2016a). In this way, such an approach may provide tools capable of testing whether the network trajectory vary across individuals with SAD so that the temporal dynamic interplay among the etiological factors conspire to transform the threat-value that is assigned to social-evaluative stimuli into a central hub among the network of maintenance factors. Moreover, as some etiological factors are stable (e.g., culture), techniques from network comparison (e.g., van Borkulo et al., 2015) may also help to identify the impact of a given etiological factor on the network dynamics. For instance, as the model assume that aspects of an individual’s culture influence the interactions among the maintenance factors by foster the “centrality” of threat-value assigned to social-evaluative stimuli, comparing the network dynamics of individuals from Western countries to Asian countries would allow directly testing this assumption.

In many applications of network analysis, one need not estimate parameters. For example, to compute a network illustrating collaboration among scientists, one can directly ascertain whether two scientists have co-written one or more articles; one need not “estimate” whether they have published together. This does not hold for networks illustrating symptom-symptom connections; one must estimate these parameters (Epskamp et al., 2016b). To do so reliably requires many subjects when the number of parameter estimates is large (e.g., 362 subjects relative to 17 symptoms; McNally et al., 2015). Unfortunately, to integrate laboratory measures into network analysis can prove challenging as few experimental psychopathology studies have more than 30 subjects per group. Fortunately, statisticians have devised procedures that render tractable such high-dimensionality problems (Friedman et al., 2008). Yet uncertainty remains about the optimal way to estimate networks comprising cognitive, behavioral, and biological processes other than assessment of self-reported symptoms. Indeed, such studies are rare (Heeren and McNally, 2016; Hoorelbeke et al., 2016).

**AUTHOR CONTRIBUTIONS**

AH had the initial ideas and wrote the first draft of the manuscript. All authors then revised the manuscript critically and contributed to and have approved the final manuscript.

**ACKNOWLEDGMENTS**

This work was supported by a postdoctoral fellowship from the Helaers Foundation for Medical Research; the Belgian Foundation for Vocation (≪ Vocatio≫); and the WBI World Excellence Grant—BioWin: The Competitive Cluster in Health and Life Sciences of Wallonia [grant number: sub/2015/226106243177], all awarded to AH. These foundations did not exert any editorial influence over this article.
REFERENCES


Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Copyright © 2016 Heeren and McNally. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) or licensor are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.