

Examining the impact of the COVID-19 pandemic through the lens of the network approach to psychopathology: Analysis of the Brazilian Longitudinal Study of Health (ELSA-Brasil) cohort over a 12-year timespan

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ABSTRACT

Cohort studies have displayed mixed findings on changes in mental symptoms severity in 2020, when the COVID-19 pandemic outbreak started. Network approaches can provide additional insights by analyzing the connectivity of such symptoms. We assessed the network structure of mental symptoms in the Brazilian Longitudinal Study of Health (ELSA-Brasil) in 3 waves: 2008–2010, 2017–2019, and 2020, and hypothesized that the 2020 network would present connectivity changes. We used the Clinical Interview Scheduled-Revised (CIS-R) questionnaire to evaluate the severity of 14 common mental symptoms. Networks were graphed using unregularized Gaussian models and compared using centrality and connectivity measures. The predictive power of centrality measures and individual symptoms were also estimated. Among 2011 participants (mean age: 62.1 years, 58% females), the pandemic symptom 2020 network displayed higher overall connectivity, especially among symptoms that were related to general worries, with increased local connectivity between general worries and worries about health, as well as between anxiety and phobia symptoms. There was no difference between 2008 and 2010 and 2017–2019 networks. According to the network theory of mental disorders, external factors could explain why the network structure became more densely connected in 2020 compared to previous observations. We speculate that the COVID-19 pandemic and its innumerable social, economical, and political consequences were prominent external factors driving such changes; although further assessments are warranted.

1. Introduction

The COVID-19 pandemic has brought unprecedented social, economical, and political changes in societies worldwide. Nonetheless, the impact of the pandemic and its consequences on mental health is

unclear. In a rapid review and meta-analysis that included more than 25 studies and 72,000 people and compared data from before and during the pandemic (up to June 2020), the effects on mental health were highly heterogeneous (Prati & Mancini, 2021), diffculting the interpretation of the findings.

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However, most studies that aimed to evaluate mental health in cohorts in 2020 relied on a unitary approach to mental disorders, by collapsing their different defining symptoms into composite, sum-scores (Kendler, Zachar, & Craver, 2011) and consequently neglecting information that could arise from changes in their organization and interaction. Recently, a network approach to mental disorders that calls for an understanding into the structure of, and associations between, component symptoms has appeared (Contreras, Nieto, Valiente, Espinosa, & Vazquez, 2019). The rationale is that symptoms causally interact through a plethora of processes (e.g., biological, psychological, homeostatic, and societal norms), such that changes in the state of one symptom would affect others over time (Borsboom, 2017). This approach has been further developed into a network theory, which accounts for mental disorders as network states in which groups of mutually reinforcing symptoms actively maintain each other through their causal connections. Factors interacting with the network, but not included in it, form its external field, which when triggered can activate specific symptoms, and eventually spread through the whole network via their connections (Borsboom, 2017). In this framework, more strongly connected networks have a higher chance of maintaining their “active state” and become self-sustaining, thus reflecting pathogenicity (Heeren & McNally, 2018).

This network perspective also allows for an understanding of how other psychological factors, such as coping responses, avoidance behaviors, and the different types of worries, played a role in early 2020, during the COVID-19 outbreak. For instance, one study (Taylor, Landry, Paluszczek, Rachor, & Asmundson, 2020) found that worries about the dangerousness of the disease, and of its socioeconomic impacts, were central nodes of the network, and strongly related to symptoms of fear, compulsion, avoidance and stress.

Therefore, the psychopathological network structure and its changes over time, in a well-defined cohort, can provide new interpretations of how these factors are associated and how they organize into different syndromes or disorders (Borsboom & Cramer, 2013). Here, we investigated the changes of this network in the Brazilian Longitudinal Study of Health (ELSA-Brasil) cohort, using data from its inception (2008) to 2020. We hypothesized that the mid-2020 network would be more connected than the previous networks owing to the influence of collective external stressors (that occurred in 2020) activating it. We also explored whether changes in the network between 2008 and 10 and 2017–19 occurred. Considering that the external factors that took place in 2020 were absent between these two previous observations, we hypothesized that the pre-2020 networks would be similar. Our aims were twofold:

- (1) to estimate and analyze psychopathology network models at each timepoint to investigate whether external factors affected the relationships between symptoms;
- (2) to assess whether centrality measures could be used to identify influential symptoms in the network. We explored both the predictive power of centrality measures and of other non-causal symptom properties in identifying symptoms whose change caused greater impact to the network between two time points.

2. Material and methods

2.1. Overview

ELSA-Brasil is a prospective, longitudinal cohort from six universities in major Brazilian cities (São Paulo, Rio de Janeiro, Salvador, Belo Horizonte, Vitória, and Porto Alegre), which began in August 2008 and enrolled active or retired employees of these universities, between 35 and 74 years old, and free of major neurocognitive disorders (Aquino et al., 2012; Schmidt et al., 2015). Baseline, second, and third assessments of the cohort occurred in 2008–10, 2012–14, and 2017–19, respectively, with no new recruitment of participants after its inception.

In 2020, a new wave of assessments were carried out only by the São Paulo research center. Participants were contacted via their personal or work emails using the RedCap platform (one weekly message for three weeks) (Harris et al., 2009), or through text messages and telephone calls if they failed to answer the emails. For the present study, we included all timepoints in which complete CIS-R data were available - i. e. - 2008–10, 2017–19 and the mid-2020 assessments. This study was approved by the Local Ethics Committee at the University Hospital, University of São Paulo and is reported according to the STROBE guidelines (von Elm et al., 2007). All patients provided electronic informed consent for participation in the study.

2.2. Participants

The 2008–10 assessment enrolled 5061 participants from the São Paulo research center. From these, 4191 completed the 2017–19 assessments. Out of these eligible participants, data of 2011 subjects (47.9%) could be included. Reasons for non-inclusion were impossibility of making contact, unwillingness to participate, not completing the questionnaire, or deaths (Fig. S1). In 2020, the mean age of included participants was 62.1 years old ($SD=8.32$, range=47–86). Most were female (58.2%), had a college degree (59.2%), and were of white ethnicity (66.3%) (Table S1).

All analyses included the same 2011 participants that presented completed CIS-R information at each timepoint. Therefore, groups were the same size.

2.3. CIS-R

The CIS-R is the instrument used in ELSA-Brasil to assess mental disorders (Nunes et al., 2016). The complete CIS-R was applied by trained interviewers onsite during the 2008–10 and 2017–19 assessments. In 2020, due to the quarantine measures, we used an electronic, self-reported CIS-R format, that was identical to the one used in clinical interviews. The CIS-R assesses 14 symptoms or “domains”, which are: somatic complaints, fatigue, concentration and forgetfulness, sleep disturbance, irritability, worry about physical health, depression, depression ideas, general worry, anxiety, phobias, panic attacks, compulsions, and obsessions. Scores for each section range from 0 to 4 (except the score for depressive ideas that range from 0 to 5). Therefore the total score ranges from 0 to 57. A symptom is present if the corresponding section score is ≥ 2 (Lewis, Pelosi, Araya, & Dunn, 1992). Additionally, based on the presence or absence of the symptoms, it is possible to establish ICD-10 diagnoses, such as anxiety disorders and depressive disorders, as discussed elsewhere (Brunoni et al., 2021).

2.4. Analyses

All statistical analyses were performed in R version 4.0.5, and the corresponding code is available in the Supplementary materials. A significance level of 0.05 was used. Participants with missing data were excluded from the analysis.

Networks were estimated with *ggmModSelect* using Spearman correlations and plotted with *qgraph* packages (Epskamp et al., 2012; Epskamp, Borsboom, & Fried, 2018). This algorithm searches for an optimal unregularized Gaussian graphical model (GGM) by iteratively changing the initially estimated edges until the Bayesian Information Criterion (BIC) can no longer be improved. We opted for an unregularized model since our dataset contained 14 variables and thousands of observations (Isvoranu & Epskamp, 2021), and used the full symptom score range (from 0 to 4 or 5) in this estimation. Unregularized models are capable of selecting the true model, with increasing probability as sample size increases (Williams & Rast, 2020). Additionally, these models do not rely on the assumption that the true model is sparse, which might not be the case of our data (Epskamp, Kruis, & Marsman, 2017). Networks were estimated for each assessment, with nodes

representing symptoms and edges the partial correlations between them. To compare with the more usual methodology used in network analysis studies, we also conducted analyses using a regularized approach with graphical LASSO regularization (Friedman, Hastie, & Tibshirani, 2008), and the corresponding tuning parameter selected by minimizing the Extended Bayesian Information Criterion (EBIC), which yielded similar results as the ones presented by the unregularized approach, and are presented in the [Supplementary materials](#).

To quantify each node's importance in the GGM, we computed two centrality measures: *expected influence*, obtained by summing the weights of all the edges attached to a node (Robinaugh, Millner, & McNally, 2016); and *predictability*, which corresponds to the proportion of explained variance of a node by all the others nodes of the network (Haslbeck & Waldorp, 2018), computed using the *mgm* package. Expected influence quantifies how connected a node is within a network by summing the edge weights while accounting for their sign (positive or negative). We opted for this metric, instead of the strength centrality, which is the sum of the absolute value of the edge weights, since expected influence was shown to be a better predictor of influential nodes in previous studies (Robinaugh et al., 2016; Spiller et al., 2020), specifically in networks with negative edge weights. It therefore provides insight into how much influence this node may have over adjacent nodes in the network. Predictability can be interpreted as a dimensional measure of the network related to the external field which influences it. A higher overall predictability means that nodes are more self-determined, with variances that can better explain each other. In contrast, a lower predictability means that the variance introduced by a node cannot be fully explained by other nodes, therefore showing a larger influence from dimensions that are external to the model. Following recent network analysis guidelines (Epskamp, Borsboom, & Fried, 2018), stability and accuracy of both edge-weight and centrality (expected influence) estimates were assessed through 1000-iterations bootstrap methods using the *bootnet* package. We also computed the correlation between each node's expected influence and its standard deviation to ensure that feature importance measured by the centrality metric was not an artifact of differential variability (Terluin, de Boer, & de Vet, 2016).

To test for differences in overall network connectivity between the three networks, we implemented the *NetworkComparisonTest* (NCT) (Van Borkulo, Epskamp, & Millner, 2016). Global network strength, defined as the weighted sum of the absolute connection values within a network (Barrat, Barthelemy, Pastor-Satorras, & Vespignani, 2004), was used as an overall network connectivity index. Higher values reflect greater interconnectivity among nodes. The NCT is a two-tailed permutation test in which the pairwise difference between groups was calculated repeatedly (1000 times) for randomly regrouped individuals. This approach produces a distribution of values under the null hypothesis (i.e., assuming equality between the groups) that tests whether the observed difference in global network strength differs significantly ($p < .05$; Bonferroni-corrected for multiple edge comparison) between groups. Here, because the same participants were assessed three times, we implemented the paired version of the NCT.

Finally, we investigated the impact of individual symptom activation on the network at subsequent time points, and the predictive power of centrality measures. We employed the methodology described by Robinaugh et al. (Robinaugh et al., 2016), wherein the change in a symptom from Time 1 to Time 2 was correlated to change in the summed score of the remaining symptoms ($\Delta\text{node}-\Delta\text{network}$ association). This measure portrays the extent to which a node could be seen as a driving force of change in the network through changes in its own degree of activation: if a node was activated (Δnode : symptom severity increased), correlated nodes would be triggered and the degree of activation of the whole network would change ($\Delta\text{network}$: other symptoms would also increase). The centrality estimates of each symptom at Time 1 were then correlated to the $\Delta\text{node}-\Delta\text{network}$ association to assess their predictive power. Following recent investigations regarding the centrality

hypothesis (Rodebaugh et al., 2018; Spiller et al., 2020), we also tested *mean symptom severity* and *infrequency of symptom endorsement* (proportion of subjects without the symptom) as predictors of change, to disentangle possible predictive effects of centrality indices from non-causal properties of item scores; and we z-standardized all the included metrics prior to the correlation analysis.

3. Results

3.1. Aim 1: psychopathological networks and their changes over time

The estimated GGM networks are shown in Fig. 1, and their corresponding stability analyses are available in the [Supplementary materials](#) (Figs. S3 to S8). All the estimated GGMs show highly stable centrality estimates (all CS-coefficients = 0.75). There were no significant correlations between node's expected influence and standard deviation for any of the networks (2008–10, 2017–19, and mid-2020 with correlation values of 0.44, 0.39, and 0.48, all p s $> .05$, respectively).

The NCT revealed no significant differences between the structures of 2008–10 and 2017–19 networks (Fig. 1). Conversely, the mid-2020 network was significantly more connected than previous ones (Fig. 1; 2008–10, 2017–19, and mid-2020 global strength scores of 5.45, 5.32, and 5.80, respectively, with $p_{2008-10 \text{ vs. } 2017-19} = 0.43$, and $p_{2017-19 \text{ vs. } \text{mid-2020}} < 0.001$). Comparing individual edges between these two networks, the edge between general worries and worries about physical health ($p < 0.001$) and the one between anxiety and phobia symptoms ($p < 0.001$) were significantly stronger in the mid-2020 network. Centrality analysis (and the NCT's features for comparing nodes' expected influence between networks) indicated a significant increase, from previous networks to the mid-2020 network, of general worries' expected influence (after bonferroni correction for multiple comparisons; difference = 0.26, $p = 0.05$), with this node becoming the third most central node in the network (Fig. S2).

There was an overall increase in the predictability of symptoms from the 2017–19 to the mid-2020 network (mean predictability of 0.24 and 0.33, respectively) (Table S2). Interestingly, the predictability measures of depression symptoms and depressive ideas were virtually the same in this time period, such that this increase is attributed to the remaining symptoms.

3.2. Aim 2: symptom activation and centrality prediction

Changes in all symptoms were correlated to changes in networks for both 2008–10–2017–19, and 2017–19 to mid-2020 comparisons (Tables S3 and S4). Centrality metrics of expected influence and predictability were significantly correlated with the $\Delta\text{node}-\Delta\text{network}$ association for both comparisons (Fig. 2). No significant findings emerged for *mean symptom severity* and *infrequency of endorsement* metrics.

4. Discussion

4.1. Main findings

In 2011 participants from the ELSA-Brasil cohort over a 12-year timespan that includes three assessments performed in 2008–10, 2017–19, and mid-2020, we evaluated changes in the psychopathological network over time. Regarding the first aim, we found an increase in the overall network connectivity of the mid-2020 symptom network compared to previous ones. Moreover, following our second aim, we showed the predictive power of centrality metrics on changes in the network, markedly reinforced by the lack of predictive power of non-causal metrics such as mean symptom severity or how frequent the symptom is in the sample. Several stressful events occurred globally in 2020 which could have contributed to these network changes, including not only the COVID-19 pandemic and its far-reaching consequences, with its wide scope and capacity for changing people's everyday lives,

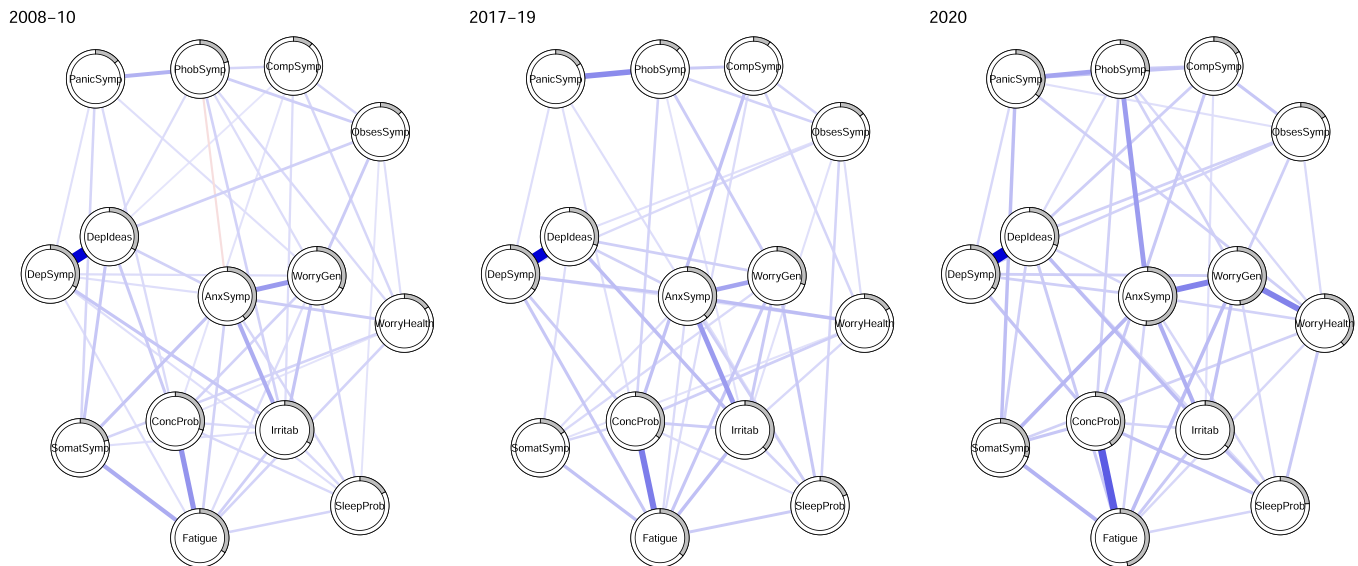


Fig. 1. Symptom networks, (2008–10; 2017–19): Baseline and pre-pandemic networks are more sparsely connected. The connections approximate symptoms with shared psychopathologies, such as fatigue and concentration problems; depression and depressive ideas; anxiety, irritability and worries; and panic and phobia symptoms. (2020): The pandemic network is more densely connected, with symptoms showing stronger interconnections, especially fears and anxiety.

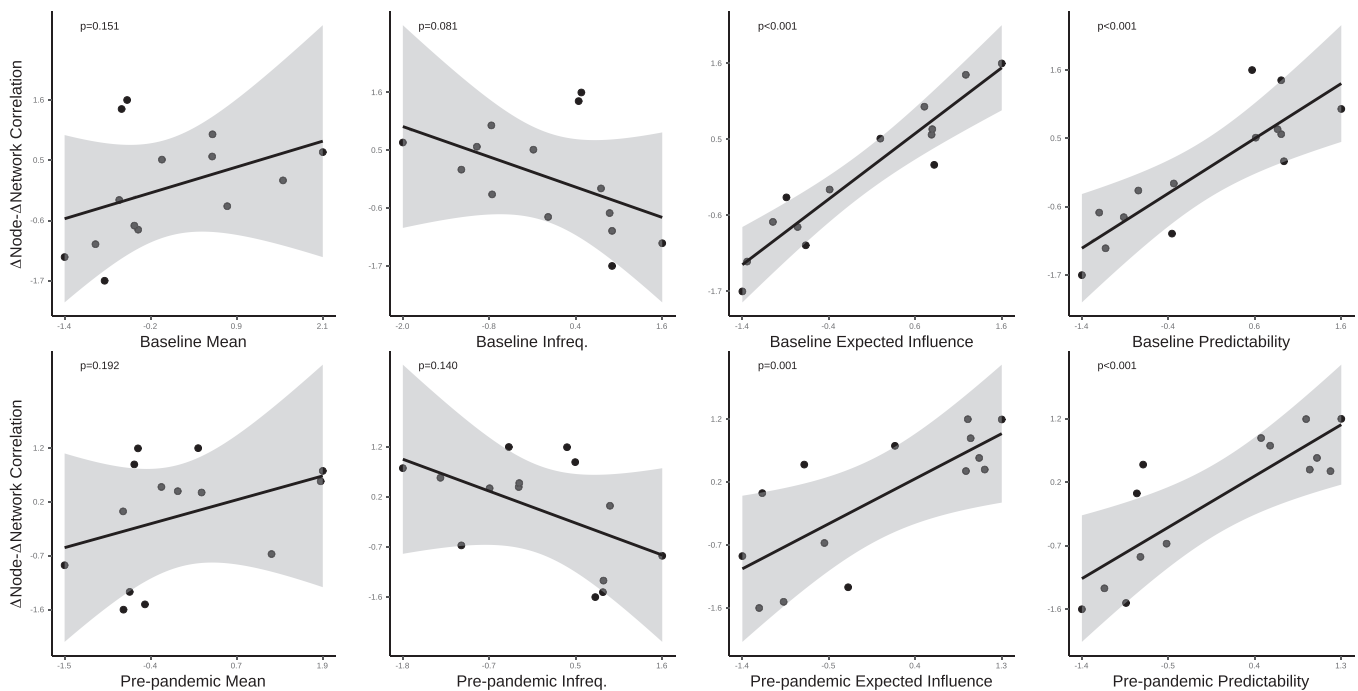


Fig. 2. Node metrics' correlations with Δ node- Δ network association, Correlations between non-centrality metrics of mean symptom severity (Mean) and infrequency of symptom endorsement (Infreq.), and centrality metrics of expected influence and predictability, with the Δ node- Δ network association. This association is obtained by correlating the degree of change in a symptom with the change in the remaining symptoms of the network excluding the analyzed symptom, and portrays how much an individual symptom drives changes in the network. The graphed correlations between symptom metrics and the Δ node- Δ network association thus display whether these metrics point out important symptoms in the networks.

but also political and ethnic tensions, geopolitical conflicts, and a growing awareness of the impending threats of climate change. Additionally, in the local context, the belligerent and denialist positioning of the Brazilian president, who further radicalized his positions after the pandemic outbreak (Anonymous, 2021), could have also played a role as an external field stressor activating the mid-2020 network and increasing its overall connectivity (Ponce, 2020).

The increase in the overall connectivity of the mid-2020 network was accompanied by a significant increase in the expected influence of

general worries, which became a central node in this network, especially related to increased associations with worries about health. There was also an increased connection between anxiety and phobia symptoms, suggesting that fear and worry were key factors in the environment of uncertainty produced by the pandemic (Asmundson & Taylor, 2020). Indeed, the COVID stress syndrome is characterized by fears (of the disease itself and of foreigners spreading the virus) and worries (of the dangerousness of COVID-19 and its socioeconomic costs (Taylor, Landry, Paluszek, Fergus et al., 2020)). Moreover, our observations

dovetail with previous network studies of mental health data during the beginning of the pandemic (Wang, Hu, Feng, Wilson, & Chen, 2020; Zavlis et al., 2021), which reported a coalescence of anxiety and depression symptoms around symptoms of worry in a sample of the UK adult population, and a change in the influence of irritability, loss of energy and psychomotor symptoms in a sample of the Chinese population. Our findings expand on these studies that did not include pre-2020 data, compared assessments within a short timeframe, and used scales assessing item-level symptoms of anxiety and depression, rather than a comprehensive psychiatric assessment approach such as the CIS-R.

Regarding predictability, we found an increase of this centrality metric for almost all symptoms from earlier to mid-2020 assessments. Predictability shows how well a symptom can be modeled by the other symptoms in the network, and is expected to decrease - and not increase - when external factors increase their influence upon the nodes (Hartung, Fried, Mehnert, Hinz, & Vehling, 2019). Our apparent contradictory finding could be explained by considering that a large circumscribed external factor (such as the pandemic) impacted multiple symptoms in the network, increasing shared variance among symptoms, and thus predictability. Possibly, the data became more uni-dimensional during the pandemic, perhaps indicating a stronger influence of potential underlying mechanisms.

Further, the investigation into the predictive power of centrality measures has shown expected influence and predictability to be more precise metrics of symptom importance within the estimated networks than mean symptom severity or infrequency of symptom endorsement. Although we did not test the generalizability of these findings to other datasets and scales, we contribute to the centrality hypothesis discussion with robust results on the largest dataset yet on which this methodology was tested (Bringmann et al., 2019; Papini, Rubin, Telch, Smits, & Hien, 2020; Rodebaugh et al., 2018; Spiller et al., 2020). It should be noted that this procedure assumes the constructs obtained at different assessments to be invariant, while, in fact, the network structure increased in connectivity during the pandemic, and therefore changed. However, the true model that the network models attempt to portray is determined by the causal relationship between symptoms (Haslbeck, Ryan, Robinaugh, Waldorp, & Borsboom, 2019), and as such, should itself be invariant.

Finally, all our findings are strengthened as we showed that the 2008–10 and 2017–19 network structures were virtually unchanged. This is important because, due to the worldwide impact of the COVID-19 pandemic, it was not possible to concurrently compare a sample in 2020 that did not suffer its influence. Nonetheless, we could show that, within the same sample, no changes in the network structure have been observed before 2020.

4.2. Research implications

According to the network approach to psychopathology, the external field of a network plays an important role driving the network structure by triggering symptoms (Borsboom, 2017), and can be composed of myriad types of stressors such as adverse life events, or harmful behaviors. The results from our analyses suggest the presence of such stressors reorganizing the relationship between symptoms and activating the pandemic symptom network, although only causing slight changes to their prevalence rates. Moreover, the increase in the centrality of “worry” hints at a main pathway through which these stressors could act, and is consistent with previous research about the COVID stress syndrome and its network structure, in which “worries” also occupy central positions. Note that the observation of “worry” as a central feature of the network structure of the stress-response to COVID-19 dovetails with prior research conducted elsewhere (e.g., (Hoffart, Johnson, & Ebrahimi, 2021; Taylor, Landry, Paluszek, Rachor, et al., 2020; Wang et al., 2020)). Considering these findings, along with the questioned feasibility of interventions targeting single nodes, and the questioned utility of centrality measures for signaling node importance (Bringmann et al., 2019), national-level interventions which focus

on external stressors, as opposed to specific nodes (e.g., financial aids to vulnerable groups, vaccination efforts, and others), may be better suited to defuse the activated network. Note that the World Health Organization has provided useful tools and guidelines for mass communication in the context of previous major public health crises (e.g., (WHO, n.d.)).

Also, our findings highlight the necessity of mapping out the societal-level causal mechanisms that influence specific symptoms, thus extending our understanding into the nature of mental disorders, specifically how they arise and are maintained (Fried, Nesse, Guille, & Sen, 2015; Stein, Lund, & Nesse, 2013). Network models are powerful tools that allow a visualization of how factors are related in a population, but are limited by the boundaries of the network itself. Therefore, an effort should be made by researchers to incorporate these external factors into the networks, in order to define more complex system networks that include how different adverse life events give rise to different symptoms (Keller, Neale, & Kendler, 2007).

Notwithstanding the limitations of not directly including these external variables in the network models, our study provides a remarkable example of the dynamics of symptom networks: external stressors are triggering symptoms, which through their causal connections mutually influence one another, activating the psychopathological network. Whether or not this activation persists over time will depend on the resilience of the network: weakly connected networks may not have strong enough interactions to sustain symptom activity. On the other hand, more densely connected networks can be more self-sustaining, and ultimately lead to a disorder state even after the removal of the external stimulus (a property known as hysteresis) (Cramer et al., 2016). In fact, such networks have been related to worsened psychopathology (Heeren & McNally, 2018; van Borkulo et al., 2015). Thus, our findings can provide insights to other working groups longitudinally investigating the mental health of populations before, during and after the pandemic. In fact, as a divide between the pandemic duration between rich and poor countries is likely due to vaccination availability and scalability (Dyer, 2020), psychopathology networks might change differently among populations.

Moreover, pandemics are dynamic events (Cacciapaglia, Cot, & Sannino, 2021), and psychopathology likely changed following community-wide levels of distress, which depends on various factors such as prevalence of infection in one's community, adequate government planning to deal with the virus, and stressful restrictions such as lockdowns (Taylor, 2019). Therefore, results of this psychopathology study could have been different depending on when symptoms were assessed during the pandemic. Nonetheless, although we did not carry out intensive longitudinal measurements of symptoms throughout the pandemic, our assessment occurred in a critical period of time, at the beginning of the pandemic in Brazil, in which severe lockdown measures had been enforced. It should be underscored that we performed our assessment approximately 8 weeks after the first COVID-19 death in Brazil, which strictly aligns with similar research conducted elsewhere (e.g., (Pierce et al., 2020)).

Finally, although the study as a whole is longitudinal, the networks themselves are cross-sectional and unevenly spaced, with almost 10 years between the first two assessments, preventing causal interpretations of symptom connections. In order to disentangle these causal relationships, a dataset with more time points, preferably evenly spaced, would be better suited (Bringmann et al., 2013). In fact, the time lag between observations importantly influences the interpretation of an effect (Deboeck & Preacher, 2016; Funkhouser, Chacko, Correa, Kaiser, & Shankman, 2021), since it is possible that relationships between different symptoms occur at shorter or longer time periods. Thus, further investigations into causal effects should consider these factors and employ appropriate models (Jacobson, Chow, & Newman, 2019; Rhemtulla & van Bork, 2021; Voelkle, Oud, Davidov, & Schmidt, 2012).

4.3. Limitations

Some limitations are worthy of notice. First, due to the quarantine measures, it was impossible to collect CIS-R data onsite. Therefore, we used an electronic, self-applied CIS-R format that was identical to the one used in clinical interviews. Notwithstanding, the online version was self-applied, whereas the onsite version was read by trained personnel. Still, previous studies have already validated and compared an electronic, self-applied CIS-R version with its standard format, showing that the electronic version presents valid and reliable performance (Lewis et al., 1988; Lewis, 1994). In fact, a validation study showed that the performance of both versions was similar (Head et al., 2013). In that study, no differences between mean scores in 12 of the 14 symptom scores were observed. Moreover, both versions presented similar accuracy in diagnosing psychiatric disorders. Second, our sample had particular characteristics that limit its generalizability, such as being composed by older, educated participants. Moreover, our sample is occupational and not population-based, being composed of public servants of the University of São Paulo. Their income, which is on average higher than the national income, was essentially unaffected during the pandemic. Thus, our findings should not be considered as nationally representative, but rather interpreted in the context of longitudinal changes within the same sample. Nonetheless, even representing a part of the Brazilian population, our results are interesting for samples in different countries with similar characteristics. Importantly, we used a well-defined cohort, which decreased the risk of selection bias, enhancing the external validity and generalizability of the findings, in contrast to snowball sampling. Finally, attrition rates were relatively high: although the differences between people who did and did not participate in the 2020 assessment were mostly small, a higher educational level was observed in those who participated, which is probably associated with the spectrum of digital literacy within the sample. Although approximately only half of the eligible sample answered our survey, this is in line with studies performed in the UK and the Netherlands during the pandemic that showed participation rates of 25–55% (Evandrou, Falkingham, Qin, & Vlachantoni, 2021; Pan et al., 2021; Pierce et al., 2020). Such low rates observed worldwide are explained by the fast organization for collecting timely data during the pandemic - for instance, pre-pandemic data shows that initial response survey rates are typically around 30% and increase only after many contacts, which usually take several months (Fincham, 2008).

5. Conclusion

To conclude, we used network analysis to provide insights into the relationship between mental symptoms over time and during 2020, when the COVID-19 pandemic began. We showed significant changes in the network structure in mid-2020, compared to earlier assessments, with increased overall connectivity between symptoms, possibly driven by the pandemic stressor (including its far-reaching social, economic, and political consequences) activating the network. Because increased overall network connectivity may signal increased risk of mental disorders, longitudinal studies that employ the network approach are warranted in the present and for other samples.

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CRediT authorship contribution statement

PJCS, ARB and AH designed the study. LR, LAdS, IK contributed in the data collection phase. PJCS, PSB and DF prepared the data. PJCS and AH performed the statistical analyses. PJCS, ARB and AH wrote the first draft of the manuscript. ARB, AH, PSB, PAL, IMB, ICP, JWS, SB, ACG, IdSS, LR, LAdS, IK, and PJCS interpreted the data and contributed to the manuscript with significant intellectual content. All authors have read and approved the final version of the manuscript prior to submission.

Data availability

Data will be made available on request.

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Conflict of Interest Statement

The authors have no conflicts of interest to declare.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at [doi:10.1016/j.janxdis.2021.102512](https://doi.org/10.1016/j.janxdis.2021.102512).

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