Symptom centrality and infrequency of endorsement identify adolescent depression symptoms
more strongly associated with life satisfaction

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Abstract

Although depression symptoms are often treated as interchangeable, some symptoms may relate to adolescent life satisfaction more strongly than others. To assess this premise, we first conducted a network analysis on the Mood and Feelings Questionnaire (MFQ) in a large ($N = 1,059$), cross-sectional sample of community adolescents (age $M = 14.72 \pm 1.79$). The most central symptoms of adolescent depression, as indexed by strength, were self-hatred, loneliness, sadness, and worthlessness while the least frequently endorsed symptoms were self-hatred, anhedonia, feeling like a bad person, and feeling unloved. Moreover, the more central a depression symptom was in the network (i.e., higher strength), the more variance it shared with life satisfaction ($r = 0.59$, 95% CI: 0.27, 0.76). How frequently a symptom was endorsed was negatively associated with the variance symptoms shared with life satisfaction ($r = -0.48$, 95% CI: -0.63, -0.21). Cross-validated, prediction focused models found central symptoms were expected to predict more out of fold variance in life satisfaction than peripheral symptoms and frequently endorsed symptoms, but not the least frequently endorsed symptoms. These findings show certain depression symptoms may be more strongly associated with life satisfaction in adolescence and these symptoms can be identified by multiple symptom-level metrics. Limitations include use of cross-sectional data and utilizing a community sample. Better understanding which symptoms of depression share more variance with important outcomes like life satisfaction could help us develop a more fine-grained understanding of adolescent depression.

Keywords: adolescent depression, symptom-level, network analysis, life satisfaction

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Depression symptoms are common in adolescents—approximately 18.6% experience clinical levels (Lu, 2019) and more than 20% may experience subclinical levels of depression (Bertha & Balázs, 2013). However, depression is far from a homogenous syndrome (Fried, 2017). For example, 48.6% of 3,703 adults enrolled in a depression treatment trial had a unique pattern of symptoms that no one else endorsed (Fried & Nesse, 2015).

This heterogeneity would not be consequential if all symptoms were equally important, but depressive symptoms are differentially linked to cognitive risk factors, cognitive biases, and psychosocial functioning in adults (Beevers et al., 2018; Fried & Nesse, 2014; Marchetti et al., 2016, 2018). For instance, some symptoms (*sadness*) shared as much as 20.7% of the variance with functioning outcomes, while others (*hypersomnia*) shared as little as 0.7%. This pattern of findings appears to extend to adolescents, as anhedonia is associated with suicidal ideation in adolescents while irritability is not (Gabbay et al., 2015). Ignoring the intrinsic heterogeneity of depression may mask important associations between individual depression symptoms and non-symptom outcomes in adolescents, such as life satisfaction (Fried, 2015; Zadow et al., 2017).

The network theory of psychopathology provides one framework for identifying symptoms that might be important for a variety of outcomes. In this model, symptoms are not outcomes of an underlying disease. Instead, symptoms and the associations between them *are* the disease (McNally, 2016), in that symptoms (i.e., *nodes*) may have reciprocal links (i.e., *edges*) with one another. Some edges may be stronger than others, and this may lead to a network structure where some symptoms are more central, or important, to the network than others. Testing whether these more central symptoms are actually more important to depression

relevant outcomes is crucial; assuming importance based on centrality in a network model alone is a problematic inference (Fried et al., 2018).

A previous network analysis in a large, diverse sample of adolescents has identified *self-hatred*, *loneliness*, *sadness*, and *pessimism* as the most central symptoms of adolescent depression (Mullarkey et al., 2018). However, that study did not link central symptoms to other depression-relevant outcomes. Further, it is essential to assess whether initial findings converge with results in different samples using other measures (Vazire, 2018). None of the indices for the replicability of central symptoms can be applied when utilizing a different measure (Borsboom et al., 2017), but we can descriptively assess whether the symptoms identified as most central in previous analyses are found to be more central in this new sample. We can also utilize newly developed Bayesian methods to directly assess the replicability of the estimated network within this sample (Jones et al., 2020). Other domains of psychopathology in adolescence have similar central symptoms when networks are estimated on different measures (McCuish et al., 2019), but whether this is the case in adolescent depression remains an open, empirical question. Among all the important outcomes associated with adolescent depression, life satisfaction plays a major role (Proctor et al., 2009). For instance, a representative, population based study of adolescents shows life satisfaction is related to positive social and health outcomes (Gadermann et al., 2016). Moreover, life satisfaction is related to but distinct from the absence of depression or other psychopathology (McKnight & Kashdan, 2009) and experiencing symptoms such as sadness are often orthogonal to perceiving one's life as positive (Crowe et al., 2018) and satisfying (Schimmack, 2008).

Still, most prior work linking life satisfaction and depression is based on sum scores of symptoms, while some symptoms of adolescent depression may be more strongly associated with life satisfaction than others. Importantly, network centrality is not the only symptom-level metric that could identify potentially more relevant symptoms. For example, changes in symptoms that were less frequently endorsed were more predictive of overall treatment

response to social anxiety disorder than changes in symptoms identified as more central (Rodebaugh et al., 2018). Thus, although network analysis is a promising approach for identifying key symptoms, other approaches should also be investigated to obtain a more complete picture of symptom importance for depression-related outcomes.

Therefore, in the current study, we first identify symptoms that are most central in the depression symptom network and determine how well the central symptoms converge with previous work while using a different measure of depression in a different sample as has been done with other domains of psychopathology in adolescence (McCuish et al., 2019). We expect that *self-hatred*, *loneliness*, and *sadness* (*pessimism* was not measured in the current study) will be identified as the most central symptoms. Then, we will investigate whether the most central symptoms in the network (i.e., network-centrality approach), as compared to the most peripheral symptoms (i.e., the least central symptoms in the network-centrality approach) and the most/least often endorsed symptoms (symptom endorsement approach), are more strongly associated with life satisfaction in adolescence. The goal of these analyses is to identify which depression symptoms are most strongly associated with life satisfaction in adolescents.

Method

Participants

The adolescent (age $M = 14.72 \pm 1.79$ years old; range: 11 – 19 years; 12-17 years old = 94.28% of sample) sample ($n = 1,059$) was racially diverse (68.08% White/Caucasian, 16.24% Black/African-American, 3.49% Hispanic, 4.34% Asian/Pacific Islander, 1.04% Native American, 5.85% Other, 0.94% missing) and predominantly female (64.97% female, 32.39% male, 1.60% transgender/gender-unsure, 1.04% missing). Socioeconomic status of the sample as indexed by maternal education was also diverse (5.85% did not finish high school, 17.37% high school or

equivalent, 14.54% some college courses but no college degree, 32.96% bachelor's degree, 19.64% master's degree, 7.65% lawyer, doctor, or PhD, 8.58% don't know, 1.98% missing).

Adolescents were universally invited to participate in this study at one public middle school, one public high school, and one private middle/high school; all samples were located in the Southeastern United States. Dates of recruitment and data collection were October to December of 2015. Our sample size was determined by our consent rate at these schools. More detailed recruitment details can be found in two previous studies evaluating different outcomes with the middle and high school participants (Bluth et al., 2017, 2018).

A total of 1,059 participants opted in to the study (informed consent was obtained from all individual participants included in the study, 58 participants opted out), correctly answered two out of three attention probe questions during the survey (244 participants excluded), and had no missing item-level data on the depression symptom inventory (6 participants excluded). These exclusions were performed to reduce bias due to inattention (Hauser & Schwarz, 2016) and distorted correlations in the network (Borsboom, 2017). All participants completed the survey during their school day and provided online assent. The study was approved by the IRBs of all relevant institutions.

Measures

Additional measures, unrelated to the current study's goal, were also administered. For the current analyses, the following two measures were utilized:

Mood and Feelings Questionnaire-Short Form

Depressive symptoms were evaluated with the Mood and Feelings Questionnaire-Short Form (MFQ; Thapar & McGuffin, 1998). The MFQ is a 13-item self-report questionnaire, and all items are measured on a 3-point Likert scale, 0 (*"Not True"*), 1 (*"Sometimes"*), and 2 (*"True"*) in response to statements about symptoms in the past two weeks (e.g., *"I hated myself"*). The

MFQ is used in research and clinical practice with children and adolescents in a variety of settings (Kuo et al., 2005; McKenzie et al., 2011).

Student's Life Satisfaction Scale

Life satisfaction was evaluated with the Student's Life Satisfaction Scale (Huebner, 1991). The SLSS is a 7-item self-report questionnaire and all items are measured on a 4-point Likert scale ranging from 0 ("*Never*") to 3 ("*Almost always*") in response to general statements about one's life satisfaction (e.g., "*I have a good life*"). The scale has adequate test-retest reliability across one year ($r = 0.53$) and has a moderate negative correlation with depression ($r = -0.39$) (Huebner et al., 2000). Importantly, the scale has only one latent factor, making it psychometrically appropriate to sum score (Huebner, 1991). The internal consistency in this sample was $\alpha = 0.85$.

Statistical Analysis

Descriptive Statistics

We first inspected mean, standard deviation, kurtosis, and skewness of all the MFQ items. In line with previous studies (Mullarkey et al., 2018; Rhemtulla et al., 2016), we dichotomized the single, item-level values to signify the absence (i.e., "0" at the MFQ item) or presence (i.e., "1" or "2" at the MFQ item) of depressive symptoms. We applied such an approach, because the optimal way to model networks with trichotomous items is still under debate (Fried et al., 2015).

Network Estimation

Using binary symptoms, it was possible to estimate network models with the eLasso Ising model (van Borkulo et al., 2014). An Ising model can be conceived as a series of pairwise associations among binary variables, after controlling for all the other associations, while shrinking potentially spurious relationships to 0 by means of eLasso regularization (for a more technical description see van Borkulo et al., 2014). This type of network estimation results in a

sparser, easier to interpret network. The binary network was fitted using the *R*-package *IsingFit* 0.3.1 (van Borkulo et al., 2014) and was visualized using *R*-package *qgraph* 1.4.3 (Epskamp et al., 2012). In this visualization blue edges denote positive associations, with thicker edges representing stronger associations.

Symptom centrality was operationalized as *strength centrality* – the sum of the absolute weights of the edge connecting the node to all the other nodes (Valente, 2012). Strength centrality is consistently, statistically more robust than other indices of centrality, and there is evidence that other indices of centrality may be less valid metrics in psychopathology networks (Bringmann et al., 2018).

We tested the stability and accuracy of our network via both a case-dropping bootstrap test for centrality stability and bootstrap confidence intervals for the accuracy of network edges (Epskamp et al., 2017). Centrality and edge-weight stability was operationalized with the correlation stability coefficient (i.e., *CS-coefficient*). CS-coefficient represents the maximum proportion of cases that can be dropped to still obtain a 95% probability that the correlation of the ranking between the centrality indicator/edge-weight in the original network and the case-subset network will amount to 0.7, with CS-coefficients being required to match at least 0.25, but preferentially above 0.5 (Epskamp et al., 2017). In addition, internode centrality difference test was computed with 95% non-parametric bootstrap confidence intervals (CIs; 1,000 bootstrap samples). If zero is included in CI, the two nodes do not differ with respect to that centrality index. All stability and accuracy analyses described above were performed using the *R*-package *bootnet* 1.0 (Epskamp et al., 2017).

Then, we calculated bootstrapped correlations between strength and both endorsement and standard deviation of symptoms in the full sample network. This test allows us to determine whether symptom centrality indexes are substantially influenced by symptoms' differential variability or mean values (Terluin et al., 2016), and treats centrality as the interdependent statistic it is (i.e., if one symptom becomes more central numerically at least one other symptom

will have to become less central numerically) rather than as the independent observations they would be assumed to be using a Pearson or Spearman correlation (Mullarkey et al., 2019).

Bayesian Test of Network Replicability

We also wanted to directly test how well we would expect this network to replicate in new, similar samples. We first created random split-halves of the data (a random 529 participants in one split-half, a random 530 participants in the other split-half), and then computed Bayes Factors for the strength of evidence that the strength of each network edge was the same across split-halves (H_0) or different across split-halves (H_1). Direct evidence for H_0 allows us to be more confident the network edges would replicate in new, similar samples while accounting for sampling variability (Jones et al., 2020; Williams et al., 2020). The prior for our analysis was an unrestricted model, or a model agnostic to the size of the partial correlations (Marsman & Wagenmakers, 2017). We considered Bayes Factors >3 to be evidence for the null hypothesis, Bayes Factors $<1/3$ to be evidence for the alternative hypothesis, and Bayes Factors <3 but $>1/3$ to be insufficient information to determine whether either hypothesis is more plausible (Jones et al., 2020). We then repeated this split-half process 10 times to ensure that the results were not unduly influenced by idiosyncracies associated with any given split in the sample and reported the average percentage of edges with evidence for replication (H_0), against replication (H_1), and insufficient evidence for either model across these 10 iterations.

Relative Importance of Depression Symptoms for Life Satisfaction

We then examined whether a symptom's network centrality relates to how much variance that symptom shares with life satisfaction. We first estimated the amount of variance each symptom shared with life satisfaction, as indexed by the Students' Life Satisfaction Scale, using relative importance analysis while controlling for age and gender. To perform the relative importance analysis, we used the *R*-package *relaimpo* 2.2-2 (Grömping, 2006) and specifically utilized the *lmg* metric. This metric calculates the contribution that each variable makes in accounting for the criterion by itself and in combination with the other predictors. In our study,

the relative importance partitions were computed in such a way that they summed to 100% (Grömping, 2007). Each individual predictor's relative importance was also bootstrapped 1,000 times to determine, in an exploratory sense, which predictors shared more variance with life satisfaction and the precision of the estimates (Fried & Nesse, 2014).

Previous analyses have also correlated centrality with different outcomes like treatment response (e.g., Boschloo et al., 2016), but have reported only point estimates and have not reported estimates of uncertainty for these point estimates. This is because the strength centrality statistics for a network are not independent observations, so confidence intervals or p-values based on the assumption of independent and identically distributed observations (e.g., from running a standard correlation test) would not be valid. In other words, a correlation between *calculated* values from two *fixed* samples does not have the same sampling distribution as a correlation between *measured* values from two *random* samples. Moreover, the sampling distribution for centrality measures is non-parametric and typically estimated by bootstrap (Epskamp et al., 2017; Epskamp & Fried, 2016). Thus, correlating centrality metrics with other outcomes, using standard methods, may not be appropriate.

Therefore, to properly take into account the sampling error in the estimation of the correlation between centrality measures and other outcomes, we generated 1,000 bootstrap replicates of the correlation between strength centrality and variance shared with life satisfaction by sampling from the dataset 1,000 times with replacement. This simulates the distribution of results we would obtain if we collected 1,000 new samples of the same size as our current sample. This approach allows us to more appropriately estimate the uncertainty around how well the centrality of a depression symptom is associated with the amount of variance each depression symptom shares with life satisfaction. We then repeated this bootstrapping procedure with frequency of symptom endorsement. This test allows us to determine whether how often a symptom is endorsed is associated with how much variance that symptom shares

with life satisfaction. This bootstrapping style of analysis has been used previously to identify correlations between centrality across data sets (Mullarkey et al., 2019).

While this bootstrapping analysis is robust it does not make full use of the sample size of participants, as the correlation being bootstrapped has an N equal to the number of nodes in the network (13) rather than the sample size (1,059). To test for converging evidence while utilizing the full sample, we also assessed the relative ability for central, peripheral, commonly endorsed, and infrequently endorsed symptoms to predict life satisfaction by comparing cross-validated linear models. We used strength centrality to identify the symptoms that were significantly stronger than 50% or more of other symptoms in the network, as has been done in previous research (Mullarkey et al., 2018). We then created models with an equivalent number of symptoms scoring highest on the other symptom-level metrics – least central/peripheral, commonly endorsed, and infrequently endorsed.

We first fit separate linear regressions with central (*worthlessness, self-hatred, sadness, and loneliness*), peripheral (*fatigue, crying, restless, concentration*), commonly endorsed (*fatigue, restless, concentration, and sadness*), and infrequently endorsed (*anhedonia, self-hatred, bad person, unloved*) symptoms predicting life satisfaction. We then calculated the out of fold variance (R^2_{pred}) by cross-validating each linear model. This type of model prioritizes variance we would expect the models to predict in new samples (See section S1 for further explanation of cross-validation). All data and code used for all analyses can be found on the Open Science Framework (<https://osf.io/pf7qu/>).

Results

Descriptive statistics

Mean, standard deviation, skewness, kurtosis, and frequency of the MFQ symptoms are reported in Table 1. The overall mean and standard deviation (at the item level) of all symptoms,

or a traditional mean score, is $M = 0.58$, $SD = 0.51$ (or $M_{\text{sum score}} = 7.50$, $SD_{\text{sum score}} = 6.57$). The symptoms of *fatigue*, *restless*, *concentration*, and *sadness* were the most commonly endorsed (i.e., third tertile), whereas the symptoms of *anhedonia*, *self-hatred*, *bad person*, and *unloved* were the least commonly endorsed (i.e., first tertile).

Table 1. Mean, standard deviation, minimum, maximum, skewness, and kurtosis, and frequency of the MFQ Symptoms (n = 1,059)

Symptoms	MFQ #	Mean	Std Dev	Min	Max	% Absence ("0")	% Presence ("1 or 2")
Sadness	1	0.78	0.69	0	2	37.11	62.89
Anhedonia	2	0.39	0.60	0	2	66.67	33.33
Fatigue	3	0.92	0.78	0	2	35.03	64.97
Restless	4	0.80	0.75	0	2	39.85	60.15
No Good	5	0.47	0.69	0	2	63.74	36.26
Crying	6	0.53	0.75	0	2	62.98	37.02
Concentration	7	0.85	0.75	0	2	36.92	63.08
Self-hatred	8	0.37	0.67	0	2	73.47	26.53
Bad Person	9	0.35	0.62	0	2	72.62	27.38
Loneliness	10	0.63	0.74	0	2	52.97	47.03
Feel Unloved	11	0.35	0.65	0	2	74.69	25.31
Worse Than Others	12	0.56	0.75	0	2	59.77	40.23
Did Wrong	13	0.50	0.69	0	2	61.10	38.90

Network estimation, centrality and edge stability tests, replicability estimate, and intranetwork comparison

The network of depressive symptoms, as estimated with the Ising model, is shown in Figure 1 (See Section S2 for Item Informativeness). *Sadness*, *worthlessness*, *loneliness*, and *self-hatred* are displayed toward the middle of the network, while *feeling restless*, *concentration problems*, and *fatigue* were more peripheral. All edges present in the model indicated positive associations between symptoms. Strength and edge-weights had excellent stability, indicating the order of central symptoms and edge-weights would remain largely consistent across samples (See Section S3 for Stability Tests and Significance Tests for Individual Edge-Weights). Our Bayesian tests with 10 sets of random split-halves of the data indicate on average 91.92% of edges were best explained by the replication model, 7.94% of edges had insufficient information to be classified in the replication or non-replication model, and 0.14% of edges (or less than one edge per test) were best explained by the non-replication model. Therefore, we continued with our assessment of network parameters given converging evidence of stability and replicability across these metrics.

Figure 1 Network of Mood and Feelings Questionnaire depression symptoms in 1,059 adolescents

In terms of strength, *feeling worthless*, *sadness*, *self-hatred*, and *loneliness* were statistically stronger than 50% or more of the other symptoms (Figure 2). Thus, these four symptoms appeared to be particularly central in this sample's depression symptom network. In contrast, some symptoms appeared to be peripheral, such as *fatigue* and *feeling restless*. Strength did not significantly correlate with standard deviation ($r = -0.11$, 95% CI: -0.35 , 0.08) but did have a moderate negative correlation with symptom endorsement ($r = -0.34$, 95% CI: -0.53 , -0.18 , (See Section S4).

Figure 2 Worthlessness, sadness, self-hatred, and loneliness are the strongest symptoms in this sample's symptom network. Note: Black boxes indicate the symptom is stronger than the other symptom ($p < .05$ following Holm-Bonferroni correction). Gray boxes indicate that symptom strength does not differ between those symptoms

External Validity: Life Satisfaction

We then conducted a relative importance analysis to determine how much variance the mean of each depressive symptom shares with life satisfaction as indexed by the SLSS. This analysis helps us understand to what extent endorsing different symptoms is associated with a decrease in reported life satisfaction. A linear model with all MFQ symptoms, gender, and age as predictors explains 44.49% of the variance in life satisfaction. Different symptoms appeared to share widely varying amounts of relative variance with life satisfaction, from as low as 2.9%

(*feeling restless*) to 12.6% (*sadness*, Figure 3). These differentials are highlighted by our exploratory bootstrapping analyses, which indicate that 38 out of 80 possible symptom comparisons (47.5%) differed from one another.

Figure 3 The relative amount of variance individual depressive symptoms share with life satisfaction

Crucially, at a group level across 13 symptoms following bootstrapping, node strength was strongly positively correlated with the amount variance the symptom shares with life satisfaction ($r = 0.59$, 95% CI: 0.27, 0.76), indicating that as a symptom becomes more central it becomes more informative about life satisfaction. Further, how often each symptom was endorsed was significantly and negatively correlated with relative importance of the symptom for

life satisfaction following bootstrapping ($r = -0.48$, 95% CI: -0.63, -0.21), indicating that as a symptom becomes more commonly endorsed it becomes less informative about life satisfaction. After controlling for symptom endorsement, node strength is still significantly, positively related to variance shared with life satisfaction ($r = 0.46$, 95% CI: 0.14, 0.67). When controlling for node strength, infrequency of endorsement was no longer significantly associated with variance associated with life satisfaction ($r = -0.29$, 95% CI: -0.48, 0.00), though the absolute value of its confidence interval still overlapped with node strength's confidence interval.

We then formally compared the cross-validated linear models to utilize the entire sample in assessing whether certain kinds of symptoms better predicted life satisfaction. The central symptoms model predicted 35.55% of the out of fold variance, the peripheral symptoms model predicted 29.22% of the variance, and the commonly endorsed model predicted 26.84% of the variance. The central symptom model had a significantly higher R^2_{pred} than the peripheral symptoms model (95% CI for R^2_{pred} difference between the models: -0.10, -0.02) and the commonly endorsed model (95% CI for R^2_{pred} difference between the models: -0.12, -0.05). However, the least frequently endorsed symptoms predicted 37.30% of the variance, and neither model had a significantly higher R^2_{pred} than the other (95% CI for R^2_{pred} difference between the models: -0.02, 0.05).

These results retained the same pattern when we compared models containing symptoms uniquely identified by centrality (*sadness, loneliness, worthlessness*; 33.84% of the variance) and uniquely identified by infrequency of endorsement (*bad person, unloved, anhedonia*; 36.92% of the variance) as predictors of life satisfaction (95% CI for R^2_{pred} difference between the models: -0.01, 0.07). Therefore, central symptoms predicted significantly more out of fold variance than peripheral symptoms and commonly endorsed symptoms. However, the most central symptoms do not predict more out of fold variance in life satisfaction than the most infrequently endorsed symptoms. This pattern of results holds when using continuous symptom severity as predictors rather than binarized symptom endorsement (See Section S5).

Discussion

In the current study, we found that both strength centrality and infrequency of symptom endorsement could identify symptoms that were more strongly associated with life satisfaction. *Sadness, self-hatred, loneliness, and worthlessness* were the most central symptoms in adolescent depression while *anhedonia, self-hatred, bad person, and unloved* were the least frequently endorsed symptoms. Although assessed with a different questionnaire in a sample of adolescents recruited from a different part of the United States, the central symptoms identified in this study strongly converge with the central symptoms identified in prior work (Mullarkey et al., 2018). Further, Bayesian replicability estimates using split-halves of the current sample indicated we would expect this adolescent depression network to generally replicate in a new, similar sample.

In line with previous work on adult depression (Fried & Nesse, 2014), some depression symptoms share far more variance with life satisfaction than others in adolescents. Nearly half of all possible pairwise comparisons revealed one symptom of depression sharing significantly more variance with life satisfaction than another symptom. Further, the variance depression symptoms shared with life satisfaction ranged from 2.9% (*feeling restless*) to 12.6% (*sadness*). These results provide the first empirical evidence that some symptoms of depression are more closely associated with life satisfaction than others in adolescents. *Sadness* in adults also shares the most variance out of any depression symptom with psychosocial functioning (Fried & Nesse, 2014), so future developmental psychopathology research should examine whether sadness is the strongest predictor of other important outcomes.

Importantly, strength centrality and infrequency of endorsement identified which symptoms were more strongly related to life satisfaction. Applying a bootstrapping method to the estimation of the network and calculating variance each symptom shares with life satisfaction allowed us to calculate more robustly whether strength centrality and infrequency of endorsement are significantly associated with the variance a symptom shares with life

satisfaction. Our second method included out of fold prediction, implying the more central symptoms alone could predict 35.55% of the variance in adolescent life satisfaction in unseen data while infrequently endorsed samples could predict 37.30%. In contrast, the least central, or peripheral symptoms, could only predict 29.22% of the out of fold variance in life satisfaction, while commonly endorsed symptoms could only predict 26.84% – both significantly less than the most central symptoms.

Symptom centrality and symptom endorsement rate were modestly negatively associated in this sample, and thus are likely not redundant. Further, our analyses indicate strength centrality was still positively associated with how much variance a symptom shared with life satisfaction after controlling for endorsement rate. While endorsement rate technically no longer significantly relates to how much variance a symptom shares with life satisfaction after controlling for centrality, the impact of the covariate was relatively small. Symptoms identified uniquely by infrequency of endorsement (*anhedonia, bad person, unloved*) predict a similar amount of out-of-fold variance in life satisfaction as symptoms uniquely identified by centrality (*sadness, loneliness, worthlessness*).

Symptom centrality and infrequency of symptom endorsement may both be viable ways to identify more important symptoms within adolescent depression. Infrequency of endorsement may be an especially useful symptom level metric in samples where identifying central symptoms via network analysis is not appropriate (e.g., the sample size is too small to estimate a network where strength is stable). Empirically testing different methods for identifying more important symptoms of adolescent depression across a variety of outcomes will help us develop a more nuanced picture of which frameworks for identifying important symptoms will be practically useful.

An important limitation of these analyses is the cross-sectional nature of the data. Variance shared is not variance predicted over time, much less a causal relationship, and any interpretations drawn from these data should be tempered by those caveats. Another potential

limitation of these analyses is that they were drawn from community adolescents, rather than a clinical population. Recruiting a clinical sample could change the relationship between individual symptoms and life satisfaction. Although past work demonstrates that network structure does not differ by diagnostic status, it could influence the overall connectivity of the network (Santos et al., 2017). However, there are advantages to using a sample not selected for clinical severity, as none of the statistical procedures can be confounded by Berkson's or collider bias – where selecting on one variable (e.g, clinical severity) distorts the associations between other variables of interest (de Ron et al., 2019). Selecting for clinical severity will also inherently restrict the range of which symptoms are more vs. less frequently endorsed. Future research could examine if infrequency of endorsement still identifies informative symptoms for outcomes despite this range restriction in clinical samples.

Overall, these results indicate that the most central symptoms of adolescent depression include *self-hatred*, *worthlessness*, *loneliness*, and *sadness* while the least frequently endorsed were *self-hatred*, *anhedonia*, *feeling like a bad person*, and *feeling unloved*. Importantly, the central symptoms were consistent with prior work even though they were identified with a different measure of depression. Further, depression symptom centrality and infrequency of endorsement were strongly associated with life satisfaction across methods whereas a higher endorsement rate was not. This finding further supports the informativeness of the network approach (i.e., external validity) for identifying central symptoms of adolescent depression, though in this case infrequency of symptom endorsement was just as informative. Longitudinal studies are needed to ascertain if individual depression symptoms differentially predict life satisfaction over time, and also whether life satisfaction reciprocally predicts change in specific symptoms. Intervention studies that target central and infrequently endorsed depression symptoms could also help disentangle whether the relationships between individual depression symptoms and life satisfaction are causal in nature. Nevertheless, findings from the current study suggest that self-hatred, worthlessness, loneliness, sadness, feeling unloved, and feeling

like a bad person may be particularly pertinent to the experience of depression in adolescence – especially in how adolescent depression relates to concurrent life satisfaction. Applying symptom level approaches to adolescent depression may provide new theoretical and clinical insights that further our understanding of this heterogeneous disorder.

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Supplementary Material for Symptom centrality and infrequency of endorsement identify adolescent depression symptoms more strongly associated with life satisfaction

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Section S1: A Brief Explainer of Cross Validation

K-fold cross-validation is a procedure similar to creating testing and training datasets in machine learning. Sample sizes typical in psychology, however, do not easily allow for holding out a portion of the data to be “tested” after a predictive model has been “trained” on an initial part of the data. Without cross-validation, however, we tend to overestimate how much our models will apply to out of sample data.

One way to solve this predicament is K-Fold cross-validation. If we have (for example) 10 folds, we divide the data into 10 random sections and train the model on the first 9. We then see how much variance that model predicts in the 10th section (test set). We then repeat this process 10 times and average how much variance the model predicts across the 10 test sets.

We can then use the “compare” function from the beset package in R to determine which models (e.g., a model with central symptoms vs. a model with peripheral symptoms) predict the most cross-validated variance in an outcome (e.g., well-being).

In other words, these analyses give us a way to directly compare the predictive ability of symptoms expected to be important under network, severity, and endorsement models head to head.

Using these analyses also allows us to use all of our substantial sample size (1,055) rather than relying on correlations between statistics like mean and symptom strength ($n = 13$, or number of symptoms).

Section S2: Item Informativeness

```
##Checking whether there is any poorly informative item  
des<-describe(dataset[,c(2:14)])
```

```

table(dataset$mfq2)/10.59 # as for the item with the lowest variance, only 66
% report no symptom, whereas 34% report the presence of the symptom

##
##      0      1      2
## 66.66667 27.47875  5.85458

describe(des$sd) #average informativeness is 0.701284

##   vars  n mean   sd median trimmed  mad min  max range  skew kurtosis   s
e
## X1    1 13  0.7 0.06  0.69      0.7 0.08 0.6 0.78  0.18 -0.37   -1.28 0.0
2

des$sd[2] #informativeness for mfq2 = 0.5964481

## [1] 0.5964372

mean(des$sd)-2.5*sd(des$sd) #informativeness for mfq2 is comprised in the +-
2.5 SD

## [1] 0.5567384

#Hence, I recommend that no item should be excluded

```

Section S3: Stability Tests and Significance Tests for Individual Edge-Weights

```

## Re-estimate to have proper labels for the figures

names(networkdata)<-c("Sadness","Anhedonia","Fatigue","Restless","Worthless",
                     "Crying","Concentration", "SelfHatred","BadPerson",
                     "Lonely","Unloved","WorseOthers","DidWrong")

network<-estimateNetwork(networkdata, default="IsingFit")

## |
|                                     | 0%
|
|=====| 8%
|
|=====| 15%
|
|=====| 23%
|
|=====| 31%
|
|=====| 38%
|
|=====| 46%

```

```
|=====| 54%
|=====| 62%
|=====| 69%
|=====| 77%
|=====| 85%
|=====| 92%
|=====| 100%
```

Then accuracy test

```
set.seed(33)
tic()
boot1 <- bootnet(network, nBoots = 1000, type="nonparametric", progressBar = F
, verbose = F)
toc()
```

735.639 sec elapsed

```
plot1<-plot(boot1, order="sample", labels=F) #Figure 3
plot2<-plot(boot1, "edge", plot="difference", onlyNonZero = TRUE, order="sample", labels=F) #Figure 4
plot3<-plot(boot1, "strength", order="sample", labels=T) #Figure 5
```

Then stability test

```
tic()
boot2<-bootnet(network, type="case", caseN=50, verbose = F)
toc()
```

461.282 sec elapsed

```
plot4<-plot(boot2)
```

```
corStability(boot2) #CS-stability indices
```

```
## === Correlation Stability Analysis ===
```

```
##
```

```
## Sampling levels tested:
```

```
##   nPerson Drop%  n
## 1      265  75.0 23
## 2      280  73.6 22
## 3      295  72.1 22
## 4      310  70.7 19
## 5      325  69.3 20
## 6      340  67.9 21
## 7      356  66.4 15
```

```

## 8      371  65.0 20
## 9      386  63.6 21
## 10     401  62.1 12
## 11     416  60.7 13
## 12     431  59.3 22
## 13     446  57.9 20
## 14     461  56.5 18
## 15     477  55.0 20
## 16     492  53.5 16
## 17     507  52.1 18
## 18     522  50.7 13
## 19     537  49.3 27
## 20     552  47.9 25
## 21     567  46.5 24
## 22     582  45.0 24
## 23     598  43.5 17
## 24     613  42.1 12
## 25     628  40.7 26
## 26     643  39.3 25
## 27     658  37.9 17
## 28     673  36.4 18
## 29     688  35.0 23
## 30     703  33.6 20
## 31     719  32.1 21
## 32     734  30.7 16
## 33     749  29.3 18
## 34     764  27.9 13
## 35     779  26.4 21
## 36     794  25.0 19
## 37     809  23.6 13
## 38     825  22.1 20
## 39     840  20.7 35
## 40     855  19.3 28
## 41     870  17.8 25
## 42     885  16.4 18
## 43     900  15.0 26
## 44     915  13.6 14
## 45     930  12.2 17
## 46     946  10.7 14
## 47     961   9.3 21
## 48     976   7.8 24
## 49     991   6.4 21
## 50    1006   5.0 23
##
## Maximum drop proportions to retain correlation of 0.7 in at least 95% of the
## samples:
##
## edge: 0.707
## - For more accuracy, run bootnet(..., caseMin = 0.693, caseMax = 0.721)
##

```

```
## intercept: 0.75 (CS-coefficient is highest level tested)
##   - For more accuracy, run bootnet(..., caseMin = 0.736, caseMax = 1)
##
## strength: 0.75 (CS-coefficient is highest level tested)
##   - For more accuracy, run bootnet(..., caseMin = 0.736, caseMax = 1)
##
## Accuracy can also be increased by increasing both 'nBoots' and 'caseN'.
plot2 # Significance tests for individual edge-weights
```

Section S4: Associations Between Strength Centrality, Endorsement Frequency, and Standard Deviation of Symptoms

Bootstrapped Correlation Between Centrality and SD of Items

```
## One-time correlation:  $r = -0.11$  95% CI(-0.35, 0.08)

ad_dep_well_being_centrality_sd_binarized<-cor(psych::describe(dataset_binari
zed[,2:14])$sd,CentrIndex_Study_2$node.centrality$Strength)
ad_dep_well_being_centrality_sd_binarized
```



```
## [1] -0.1074427

## Now bootstrapping

boots <- 1000
set.seed(33)
row_ids_study_2_centrality_sd_bin <- purrr::map(1:boots,
  ~ sample.int(nrow(dataset_binarized), replace = TRUE)
)

get_cor_sd_centrality_bin <- function(i, df){
  df_boot_study_2_centrality_sd_bin <- df[i,]
  sd_rank_study_2_bin <- psych::describe(df_boot_study_2_centrality_sd_bin[,2:14])$sd
  results_study_2_centrality_sd_bin <- estimateNetwork(df_boot_study_2_centrality_sd_bin[,2:14], default = "IsingFit", verbose = FALSE)
  cent_rank_study_2_sd_bin <- centrality_auto(results_study_2_centrality_sd_bin)$node centrality$Strength
  cor(sd_rank_study_2_bin, cent_rank_study_2_sd_bin)
}

tic()
sd_centrality_bin_cor <- mclapply(row_ids_study_2_centrality_sd_bin, get_cor_sd_centrality_bin, df = dataset_binarized, mc.cores = detectCores(logical = FALSE) - 1L)
toc()

## 746.527 sec elapsed

#create dataframe of bootstrapped correlations
boot.cor_sd_centrality_bin_cor <- as.data.frame(do.call(rbind, sd_centrality_bin_cor))
names(boot.cor_sd_centrality_bin_cor) <- "r"

round(quantile(boot.cor_sd_centrality_bin_cor$r, c(.025)), 2)

## 2.5%
## -0.35

round(quantile(boot.cor_sd_centrality_bin_cor$r, c(.975)), 2)

## 97.5%
## 0.08

## This takes forever so I should save the data

# Save an object to a file
saveRDS(boot.cor_sd_centrality_bin_cor, file = "sd_centrality_bin_cor.rds")
# Restore the object
# readRDS(file = "endorse_centrality_cor.rds")
```

Bootstrapped Correlation Between Centrality and Endorsement Frequency of Items

```
## Endorsement Rate with Centrality
```

```
## One-time correlation:  $r = -0.34$  95% CI(-0.53, -0.18)
```

```
ad_dep_well_being_endorse_centrality <- cor(psych::describe(dataset_binarized[,  
2:14])$mean, CentrIndex_Study_2$node.centrality$Strength)  
ad_dep_well_being_endorse_centrality
```

```
## [1] -0.3369801
```

```
## Now bootstrapping
```

```
boots <- 1000  
set.seed(33)  
row_ids_study_2_centrality_endorse_bin <- purrr::map(1:boots,  
  ~ sample.int(nrow(dataset_binarized), replace = TRUE)  
)
```

```
get_cor_endorse_centrality_bin <- function(i, df){  
  df_boot_study_2_centrality_endorse_bin <- df[i,]  
  endorse_rank_study_2_bin <- psych::describe(df_boot_study_2_centralit  
y_endorse_bin[,2:14])$mean  
  results_study_2_centrality_endorse_bin <- estimateNetwork(df_boot_stu  
dy_2_centrality_endorse_bin[,2:14], default = "IsingFit", verbose = FALSE)  
  cent_rank_study_2_endorse_bin <- centrality_auto(results_study_2_cent  
rality_endorse_bin)$node.centrality$Strength  
  cor(endorse_rank_study_2_bin, cent_rank_study_2_endorse_bin)  
}
```

```
tic()  
endorse_centrality_bin_cor <- mclapply(row_ids_study_2_centrality_endorse_bin  
, get_cor_endorse_centrality_bin, df = dataset_binarized, mc.cores = detectCo  
res(logical = FALSE) - 1L)  
toc()
```

```
## 726.684 sec elapsed
```

```
#create dataframe of bootstrapped correlations
```

```
boot.cor_endorse_centrality_bin_cor <- as.data.frame(do.call(rbind, endorse_c  
entrality_bin_cor))  
names(boot.cor_endorse_centrality_bin_cor) <- "r"
```

```
round(quantile(boot.cor_endorse_centrality_bin_cor$r, c(.025)), 2)
```

```
## 2.5%
```

```
## -0.53
```

```

round(quantile(boot.cor_endorse_centrality_bin_cor$r, c(.975)), 2)

## 97.5%
## -0.18

## This takes forever so I should save the data

# Save an object to a file
saveRDS(boot.cor_endorse_centrality_bin_cor, file = "endorse_centrality_bin_cor.rds")
# Restore the object
# readRDS(file = "endorse_centrality_cor.rds")

```

Section S5: Continuous Symptoms as Predictors of Life Satisfaction in Cross-Validated Linear Regressions

Defining Central, Peripheral, Severe, and Endorsement

We selected the most central symptoms by seeing which symptoms were stronger than 50% or more of the other symptoms in the network (sadness, self-hatred, loneliness, and worthlessness).

For peripheral symptoms, we chose the 4 least central symptoms (to match the number of central symptoms) indexed by strength in this network (fatigue, restless, crying, and anhedonia).

Identifying Most and Least “Severe” Symptoms

For the most severe symptoms, we chose the 4 symptoms with the highest mean ratings on severity from our continuous data (fatigue, restless, concentration, and sadness).

Figuring out the most and least "severe" symptoms

```

networkdata_ordered_by_symp_severity <- dataset %>%
  dplyr::select(contains("mfq"), -mfqmean) %>%
  dplyr::summarise_all(funs(sum)) %>%
  mutate_all(funs(./1059)) %>%
  gather(symptom, average_severity) %>%
  arrange(average_severity) %>%
  print()

```

```

##      symptom average_severity
## 1      mfq9      0.3493862
## 2     mfq11      0.3503305
## 3      mfq8      0.3711048
## 4      mfq2      0.3918791
## 5     mfq5      0.4730878

```

```
## 6      mfq13      0.4995279
## 7      mfq6      0.5297450
## 8      mfq12      0.5580737
## 9      mfq10      0.6270066
## 10     mfq1      0.7837583
## 11     mfq4      0.8016997
## 12     mfq7      0.8470255
## 13     mfq3      0.9159585
```

The Most Central Symptoms Predict More Variance in Well-Being Than the Least Central Symptoms

A model with the most central symptoms predicts 39.02% of the variance in well-being, while a model with the most peripheral symptoms predicts 29.31%. When comparing the models, the 95% CI for the difference between them does not include 0 (-0.14,-0.06).

Continuous Symptoms Cross Validation

Let's Look at the Linear models

```
slss_central_cont_lm <- lm(mslss~ mfq1 + mfq5 + mfq8 + mfq10,data = dataset)
summary(slss_central_cont_lm)
```

```
##
## Call:
## lm(formula = mslss ~ mfq1 + mfq5 + mfq8 + mfq10, data = dataset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.62843 -0.34271  0.05746  0.37157  1.58510
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.34271    0.02547 131.226 < 2e-16 ***
## mfq1          -0.25731    0.03122  -8.241 5.06e-16 ***
## mfq5          -0.18550    0.03682  -5.038 5.54e-07 ***
## mfq8          -0.09023    0.03792  -2.379  0.0175 *
## mfq10         -0.20238    0.03051  -6.633 5.25e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5346 on 1050 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.3957, Adjusted R-squared:  0.3934
## F-statistic: 171.9 on 4 and 1050 DF, p-value: < 2.2e-16
vif(slss_central_cont_lm)
```

```

##      mfq1      mfq5      mfq8      mfq10
## 1.722106 2.348000 2.354569 1.885725

slss_central_cont_lm_val <- validate(slss_central_cont_lm)

## How well do the most peripheral symptoms do at predicting well-being?

slss_peripheral_cont_lm<-lm(mslss~ mfq3 + mfq4 + mfq6 + mfq2,data = dataset,
                           nest_cv = T, seed = 33)
summary(slss_peripheral_cont_lm)

##
## Call:
## lm(formula = mslss ~ mfq3 + mfq4 + mfq6 + mfq2, data = dataset,
##     nest_cv = T, seed = 33)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.90230 -0.38666  0.03177  0.42697  1.50419
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.28732    0.02937 111.910 < 2e-16 ***
## mfq3          -0.07647    0.02738  -2.792 0.005329 **
## mfq4          -0.09977    0.02812  -3.547 0.000406 ***
## mfq6          -0.19251    0.02666  -7.220 9.98e-13 ***
## mfq2          -0.36238    0.03431 -10.562 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5756 on 1050 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.2993, Adjusted R-squared:  0.2966
## F-statistic: 112.1 on 4 and 1050 DF, p-value: < 2.2e-16

vif(slss_peripheral_cont_lm)

##      mfq3      mfq4      mfq6      mfq2
## 1.452777 1.407531 1.285023 1.326345

slss_peripheral_cont_lm_val <- validate(slss_peripheral_cont_lm)

## Do central symptoms do a better job of predicting than peripheral symptoms ?
## They do!

beset::compare(slss_central_cont_lm_val,slss_peripheral_cont_lm_val)

##              Model1 Model2   Delta 95% CI for Delta
## Mean Absolute Error  0.436  0.468  0.0320 [0.017, 0.047]
## Mean Cross Entropy   0.795  0.869  0.0739 [0.043, 0.1]

```

```
## Mean Squared Error    0.287  0.333  0.0457  [0.026, 0.065]
## Variance Explained    0.390  0.293 -0.0971  [-0.14, -0.055]
```

The Most Central Symptoms Predict More Variance in Well-Being Than the “Most Severe” On Average Symptoms

A model with the most central symptoms predicts 39.02% of the variance in well-being, while a model with the most severe symptoms predicts 32.58%. When comparing the models, the 95% CI for the difference between them does not include 0 (-0.09,-0.03).

Now what about the most severe items?

```
slss_severe_cont_lm<-lm(mslss~ mfq3 + mfq4 + mfq7 + mfq1,data = dataset)
summary(slss_severe_cont_lm)
```

```
##
## Call:
## lm(formula = mslss ~ mfq3 + mfq4 + mfq7 + mfq1, data = dataset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.07930 -0.39893  0.03871  0.42787  1.68038
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.42927    0.03062  112.008 < 2e-16 ***
## mfq3          -0.06355    0.02684   -2.368  0.0181 *
## mfq4          -0.03095    0.02884   -1.073  0.2834
## mfq7          -0.17499    0.02929   -5.974 3.17e-09 ***
## mfq1          -0.38854    0.03088  -12.581 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5623 on 1050 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.3314, Adjusted R-squared:  0.3288
## F-statistic: 130.1 on 4 and 1050 DF, p-value: < 2.2e-16

slss_severe_cont_lm_val <- validate(slss_severe_cont_lm)
```

Do central symptoms do a better job of predicting than the most commonly endorsed symptoms?

They do!

```
beset::compare(slss_central_cont_lm_val,slss_severe_cont_lm_val)

##              Model1 Model2   Delta 95% CI for Delta
## Mean Absolute Error  0.436  0.460  0.0242  [0.012, 0.037]
## Mean Cross Entropy   0.795  0.845  0.0502  [0.025, 0.075]
```

```
## Mean Squared Error    0.287  0.317  0.0303  [0.015, 0.045]
## Variance Explained    0.390  0.326 -0.0644 [-0.096, -0.032]
```

The Most Central Symptoms Do Not Predict More Variance in Well-Being Than the “Least Severe” On Average Symptoms

A model with the most central symptoms predicts 39.02% of the variance in well-being, while a model with the least severe symptoms predicts 35.71%. When comparing the models, the 95% CI for the difference between them does not include 0 (-0.07, 0.02).

Now what about the most severe items?

```
slss_least_severe_cont_lm<-lm(mslss~ mfq9 + mfq11 + mfq8 + mfq2,data = dataset)
summary(slss_least_severe_cont_lm)
```

```
##
## Call:
## lm(formula = mslss ~ mfq9 + mfq11 + mfq8 + mfq2, data = dataset)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.61614 -0.35645  0.02834  0.38386  1.61482
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.18757    0.02101 151.729  < 2e-16 ***
## mfq9          -0.11395    0.03882  -2.936  0.00340 **
## mfq11         -0.29669    0.03539  -8.384  < 2e-16 ***
## mfq8          -0.13206    0.03951  -3.342  0.00086 ***
## mfq2         -0.25969    0.03420  -7.592 6.91e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5486 on 1050 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.3634, Adjusted R-squared:  0.361
## F-statistic: 149.9 on 4 and 1050 DF, p-value: < 2.2e-16
```

```
slss_least_severe_cont_lm_val <- validate(slss_least_severe_cont_lm)
```

Do central symptoms do a better job of predicting than the most commonly endorsed symptoms?

They do!

```
beset::compare(slss_central_cont_lm_val,slss_least_severe_cont_lm_val)
```

```
##              Model1 Model2      Delta 95% CI for Delta
## Mean Absolute Error 0.436  0.446  0.00949 [-0.0043, 0.024]
```

## Mean Cross Entropy	0.795	0.821	0.02637	[-0.0015, 0.056]
## Mean Squared Error	0.287	0.303	0.01554	[-9e-04, 0.033]
## Variance Explained	0.390	0.357	-0.03303	[-0.07, 0.002]