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Research paper

Temporal stability of depression symptom networks across cultures: Longitudinal analysis of MIDUS and MIDJA

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ABSTRACT

Background: The network approach to psychopathology conceptualizes mental disorders as systems with causally interacting symptoms. While the temporal stability of symptom networks has been examined in single-culture samples, no research has compared stability patterns across cultural contexts.
Methods: Using longitudinal data from the Midlife in the United States (MIDUS; $N = 673$) and Midlife in Japan (MIDJA; $N = 197$), we estimated depression networks using four CES-D subscales (Depressed Affect, Positive Affect, Somatic Symptoms, Interpersonal Problems) at two time points (T1 and T2). Temporal stability was assessed using the Network Comparison Test and correlations between edge weights and centrality indices.
Results: Depression networks demonstrated high temporal stability in both samples, with edge weight correlations of $r = 0.945$ (MIDUS) and $r = 0.902$ (MIDJA) and centrality correlations of $r = 0.957$ (MIDUS) and $r = 0.864$ (MIDJA). Positive Affect showed moderate negative connections to other subscales in the American sample but was functionally independent in the Japanese sample across both time points. The Depressed Affect–Somatic connection was the strongest edge in both cultures but notably stronger in Japan.
Limitations: The MIDJA sample was relatively small, measurement intervals differed between samples, and findings may not generalize beyond these specific midlife populations.
Conclusions: Depression symptom networks show high temporal stability within cultures while exhibiting stable cross-cultural differences in specific-symptom connections. The functional independence of positive affect in Japanese samples has implications for cross-cultural assessments and culturally adapted interventions.

1. Introduction

The network approach to psychopathology proposes that mental disorders arise from direct causal interactions between symptoms (Borsboom, 2017). Symptoms such as insomnia, fatigue, and sad mood mutually influence one another, creating self-sustaining feedback loops (Cramer et al., 2010). In network models, symptoms are represented as nodes, and the unique statistical associations between symptom pairs (after controlling for all other symptoms) are represented as edges. The choice of estimation algorithm depends on the data and research question (e.g., regularized partial correlation models for continuous data, Ising models for binary data), much as one chooses between ordinary least squares and logistic regression.

A critical question in network psychometrics is the temporal stability of network structures. If symptom networks represent stable population characteristics, structures should remain consistent across measurement occasions. Existing evidence from single-culture samples suggests moderate temporal stability, with cross-occasion correlations varying across studies (e.g., $r = 0.62$–0.74 for network structure across PTSD samples, Fried et al., 2018; rs = 0.78 between admission and discharge edge weights in a depression/anxiety partial hospital program sample, Beard et al., 2016).

1.1. Cross-cultural considerations in depression symptom networks

Despite growing interest in the network approach, little research has examined whether depression symptom networks differ across cultures. Cross-cultural differences in depressive symptom expression between Japanese and American populations are well documented: Japanese primary-care patients endorse somatic symptoms more frequently than

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American patients (Waza et al., 1999), and studies of the CES-D show that positively worded items function differently from negatively worded items in Japanese respondents. Iwata et al. (1994) reported that Japanese adolescents' responses to positive affect items diverged markedly from those of American adolescents while negative-item responses were comparable; Iwata and Roberts (1996) extended this finding to Japanese adults, showing that positive affect items did not function as inverse indicators of depressive symptomatology. Cross-national epidemiological surveys document major depressive disorder as a substantial public health concern in both countries, with the National Comorbidity Survey Replication estimating a 12-month prevalence of approximately 6.6% in the United States (Kessler et al., 2003) and the International Consortium of Psychiatric Epidemiology (ICPE) Surveys reporting cross-national variability including a Japanese estimate (Andrade et al., 2003). The qualitative differences in symptom expression noted above raise the possibility that the relationships among depression symptoms — not just their overall levels — may differ across cultures, a question network analysis is well suited to address. These differences may reflect East Asian cultural patterns of somatic communication of psychological distress (Zhou et al., 2016).

From a network perspective, such cultural differences in symptom expression may manifest as differences in the patterns of symptom connections — for example, stronger somatic–affective connections in the Japanese sample, and a different role for positive affect.

A small but growing body of cross-sectional literature has compared network structures across national samples, finding both similarities and differences in how depressive symptoms correlate (Mihić et al., 2024). However, these studies have been exclusively cross-sectional, leaving unanswered whether temporal stability patterns differ across cultural contexts.

1.2. The present study

The present study addresses this gap by examining the temporal stability of depression symptom networks in American and Japanese midlife adults using longitudinal data from the Midlife in the United States (MIDUS) and Midlife in Japan (MIDJA) studies. These studies provide a unique cross-cultural opportunity because they employ a harmonized measure of depression — the Center for Epidemiologic Studies Depression Scale (CES-D) — with longitudinal follow-up in both cultural contexts.

Given the sample-size constraints in the MIDJA longitudinal sample ($N = 197$), we employed a subscale-level network approach using the four CES-D factors identified by Radloff (1977): Depressed Affect, Positive Affect, Somatic and Retarded Activity (hereafter Somatic Symptoms), and Interpersonal (hereafter Interpersonal Problems). This approach yields stable network estimation while preserving theoretically meaningful symptom clusters across cultures. Supplementary 20-item networks were conducted with the larger MIDUS sample to examine generalization across levels of network granularity.

We addressed three research questions: (1) Are depression symptom networks temporally stable within each cultural sample? (2) Do stability patterns differ between American and Japanese populations? (3) Are there consistent cross-cultural differences in specific network connections across time? Based on prior evidence of moderate-to-high temporal stability of internalizing symptom networks (Beard et al., 2016; Fried et al., 2018; Funkhouser et al., 2020), we hypothesized high temporal stability in both samples (edge correlations >0.70), with the role of Positive Affect differing across cultures — weaker connections to other subscales in the Japanese sample — consistent with prior CES-D measurement studies (Iwata et al., 1994; Iwata and Roberts, 1996).

2. Methods

2.1. Participants and procedure

Data were obtained from the Midlife in the United States (MIDUS) and Midlife in Japan (MIDJA) longitudinal studies, which were designed to enable cross-cultural comparisons using harmonized assessment protocols (Ryff et al., 2015).

2.1.1. MIDUS sample

The MIDUS Biomarker Project recruited participants from the broader MIDUS survey for biomedical assessment. T1 data came from the MIDUS 2 Biomarker Project (linked to MIDUS Wave 2; 2004–2009, three General Clinical Research Centers); T2 from the MIDUS 3 Biomarker Project (linked to MIDUS Wave 3; 2017–2022). Participants who completed the CES-D at both assessments were included ($N = 673$; measurement interval 8–18 years). Demographic characteristics are presented in Table 1.

2.1.2. MIDJA sample

MIDJA recruited a probability sample of adults from the Tokyo Metropolitan Area as the Japanese counterpart to MIDUS. T1 data came from the MIDJA 1 Biomarker Project (2009–2010); T2 from the MIDJA 2 Biomarker Project (2013–2014). Participants who completed the CES-D at both assessments were included ($N = 197$; measurement interval 4–5 years). Demographic characteristics are presented in Table 1.

2.2. Measures

2.2.1. Center for epidemiologic studies depression scale (CES-D)

Depressive symptoms were assessed using the 20-item CES-D (Radloff, 1977). Participants rated how often they experienced each symptom during the past week on a 4-point scale (1 = rarely or none of the time to 4 = most or all of the time). The Japanese version has been validated and demonstrates adequate psychometric properties (Shima et al., 1985; Wada et al., 2007).

Following Radloff's (1977) original factor structure, the 20 items were aggregated into four subscales: Depressed Affect (seven items: could not shake blues, felt depressed, life was failure, felt fearful, felt lonely, crying spells, felt sad), Positive Affect (four items: as good as others, hopeful about future, was happy, enjoyed life), Somatic Symptoms (seven items: bothered by things, poor appetite, trouble concentrating, everything was effort, sleep restless, talked less, could not get going), and Interpersonal Problems (two items: people unfriendly, people dislike me). Subscale scores were computed as the mean of the component items. The four Positive Affect items were retained in their original direction, so that higher Positive Affect scores indicate greater positive affect; the negative correlations between Positive Affect and the three depression-direction subscales reported below therefore reflect the expected inverse association rather than an artifact of differential reverse-scoring.

2.3. Network estimation

Networks were estimated using the EBICglasso algorithm (Friedman et al., 2008; Epskamp and Fried, 2018), the standard method for regularized partial correlation networks with continuous data. The algorithm applies L1-regularization (i.e., lasso regression) to shrink small edge weights to zero, retaining only the strongest unique associations between nodes. Following standard practice (Epskamp and Fried, 2018), we used the Extended Bayesian Information Criterion (EBIC) with the conventional default hyperparameter of $\gamma = 0.5$ to select the regularization parameter, a conservative tradeoff that favors specificity over sensitivity.

Four networks were estimated (MIDUS T1, MIDUS T2, MIDJA T1, MIDJA T2), each containing four nodes representing the CES-D

Table 1
Sample demographics, CES-D subscale descriptive statistics, and cross-cultural comparisons.

Variable	MIDUS T1	MIDUS T2	MIDJA T1	MIDJA T2	Cross-cultural test
Sample Demographics					
N	673	673	197	197	–
Age, M (SD)	54.38 (9.67)	65.98 (9.76)	54.56 (13.17)	58.89 (13.19)	T1: $t(260.9) = -0.18$, $p = 0.856$ T2: $t(261.9) = 7.00$, $p < 0.001$
Female, n (%)	369 (54.8%)	369 (54.8%)	109 (55.3%)	109 (55.3%)	$\chi^2(1) = 0.00$, $p = 0.966$
CES-D Subscale Scores, M (SD)					
Depressed Affect	1.262 (0.436)	1.264 (0.422)	1.294 (0.476)	1.297 (0.479)	T1: $t(298.9) = -0.84$, $p = 0.402$, $d = -0.07$ T2: $t(290.9) = -0.86$, $p = 0.390$, $d = -0.08$
Positive Affect	3.385 (0.657)	3.282 (0.701)	2.080 (0.705)	2.148 (0.744)	T1: $t(302.9) = 23.21$, $p < 0.001$, $d = 1.95$ T2: $t(305.0) = 19.06$, $p < 0.001$, $d = 1.60$
Somatic Symptoms	1.471 (0.444)	1.540 (0.457)	1.389 (0.453)	1.363 (0.414)	T1: $t(314.5) = 2.26$, $p = 0.025$, $d = 0.19$ T2: $t(347.9) = 5.17$, $p < 0.001$, $d = 0.40$
Interpersonal Problems	1.207 (0.431)	1.237 (0.465)	1.206 (0.487)	1.195 (0.450)	T1: $t(291.8) = 0.04$, $p = 0.965$, $d = 0.00$ T2: $t(328.3) = 1.13$, $p = 0.259$, $d = 0.09$

Note. T1 and T2 = first and second longitudinal measurement occasions (MIDUS 2 / MIDJA 1 Biomarker Projects and MIDUS 3 / MIDJA 2 Biomarker Projects, respectively). CES-D subscales scored on a 1–4 scale, with Positive Affect retained in its original direction (higher scores indicate greater positive affect). Cross-cultural mean comparisons are independent-samples Welch's *t*-tests; effect sizes are Cohen's *d* (pooled SD). Sex distribution comparison uses Pearson's chi-square test with Yates' continuity correction. Values for the female-percentage row are identical at T1 and T2 because the same longitudinal participants were assessed at both time points. The MIDUS T2 versus MIDJA T2 age difference reflects the longer measurement interval in MIDUS (8–18 years) compared with MIDJA (4–5 years).

subscales. Networks were visualized using the qgraph package (Epskamp et al., 2012), with blue and red edges indicating positive and negative partial correlations, respectively, and edge thickness scaled to magnitude.

2.4. Network comparison test

Temporal stability was assessed using the Network Comparison Test (NCT; van Borkulo et al., 2023), which evaluates differences between networks in (a) network structure (the largest single edge-weight difference), (b) global strength (sum of absolute edge weights), and (c) specific edge weights through permutation testing. For each comparison, 1000 permutations were performed.

Within-culture temporal stability was examined by comparing T1 and T2 networks within each sample, and we computed Pearson correlations between T1 and T2 edge weights and between T1 and T2 strength centrality values to quantify the similarity of network structure over time.

2.5. Bootstrap stability analysis

Centrality stability was assessed using the case-dropping bootstrap (Epskamp et al., 2018). The correlation stability coefficient (CS coefficient) indicates the maximum proportion of cases that can be dropped while maintaining a correlation ≥0.70 with the original centrality estimates; values ≥0.50 indicate good stability.

Bootstrap confidence intervals for edge weights were estimated using 1000 nonparametric samples to assess edge precision (see Supplementary Fig. S1).

2.6. Supplementary analysis: 20-item networks

To examine whether temporal stability findings generalized to more granular representations, supplementary analyses used 20-node networks with individual CES-D items as nodes. Because reliable estimation of larger networks requires substantially larger samples (Epskamp et al., 2018), these analyses were limited to MIDUS ($N = 673$). The same procedures (EBICglasso, NCT, and bootstrap stability) were applied.

2.7. Data analysis

All analyses were conducted in R (version 4.5.2) using the qgraph (Epskamp et al., 2012), bootnet (Epskamp et al., 2018), NetworkComparisonTest (van Borkulo et al., 2023), and missRanger (Mayer, 2019) packages. Following reporting recommendations for cross-sectional psychological network analyses (Burger et al., 2023), adapted to the present longitudinal data, we report network structures, centrality indices, stability coefficients, and network comparison results.

Missing data were handled using pairwise deletion, the default approach for EBICglasso estimation in qgraph. We inspected missingness at the item and case level for the 20 CES-D items at each assessment. Item-level missingness was negligible in MIDUS (mean: 0.49% at T1, 0.19% at T2; maximum: 0.72% at T1, 0.40% at T2) and modest in MIDJA (mean: 5.71% at T1, 4.47% at T2; maximum: 8.64% at T1, 5.18% at T2). Case-level (multivariate) missingness — the percentage of participants with at least one missing CES-D item — was 1.75% in MIDUS T1 (22 of 1255), 1.20% in MIDUS T2 (9 of 747), 12.04% in MIDJA T1 (46 of 382), and 9.45% in MIDJA T2 (31 of 328). Subscale composites were computed as means of available items, and participants with any missing item at either time point were excluded from longitudinal analyses. The majority of MIDJA missing cases reflected participants who skipped the CES-D entirely (10 of 46 at T1; 9 of 31 at T2), with the remainder missing only one or two items.

Because MIDJA T1 multivariate missingness exceeded the conventional 10% threshold above which analyses may be biased (Bennett, 2001), and following the principled approach of Schafer and Graham (2002), we conducted a sensitivity analysis using random forest imputation via the missRanger package (Mayer, 2019), specifying predictive mean matching with k = 5 nearest donors and 100 trees per variable (seed = 2026; both values are explicit user-specified parameters rather than missRanger defaults). Imputation was applied at the item level to the MIDJA T1 and T2 biomarker samples prior to subscale calculation. After imputation and longitudinal merge by participant ID, the imputed analytic sample comprised $N = 243$ (vs. $N = 197$ under listwise deletion). Imputed networks used the same EBICglasso settings ($\gamma = 0.5$) and were compared with the listwise networks using Pearson and Spearman edge-weight correlations, edge-by-edge difference inspection, bootstrapped 95% edge-weight confidence intervals (1000 nonparametric samples), and case-dropping CS coefficients (1000 samples). Results are reported in Supplementary Table S1 and summarized in the Results.

2.8. *Transparency and openness*

This study used secondary data from MIDUS and MIDJA, publicly available through the Inter-university Consortium for Political and Social Research (ICPSR). The analysis plan was preregistered on the Open Science Framework (https://osf.io/dnb6u/?view_only=a64eacb12e014cabb0aaca249ee95514). We report all measures and exclusions; analysis code is available from the corresponding author on reasonable request.

3. Results

3.1. *Participants*

The longitudinal analytic samples comprised 673 MIDUS participants (United States) and 197 MIDJA participants (Japan), all of whom completed the CES-D at both T1 and T2 biomarker assessments. Detailed sample characteristics, including measurement intervals, are reported in the Methods.

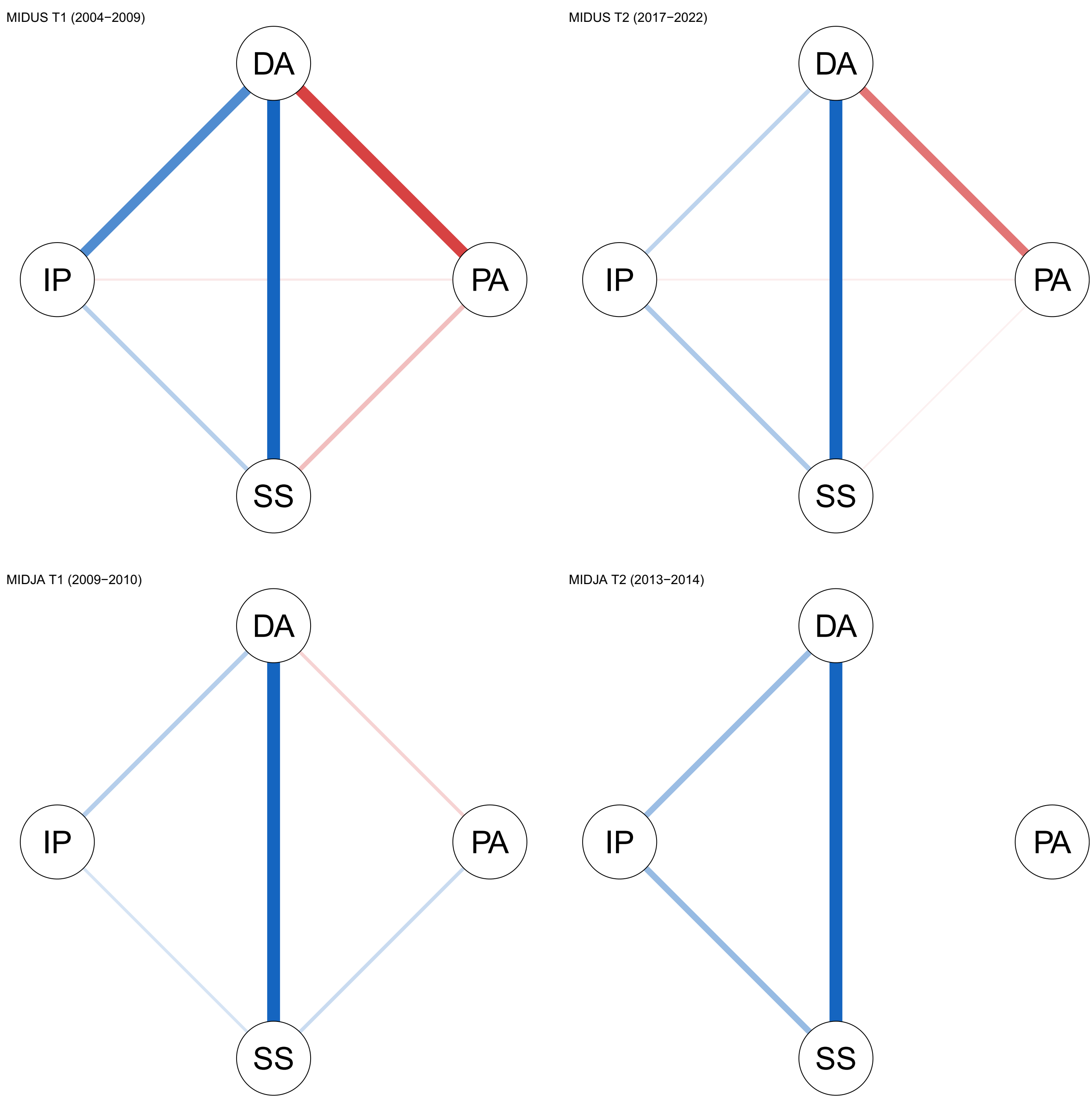

Fig. 1. Depression symptom networks for MIDUS (United States) and MIDJA (Japan) samples at two time points. Nodes represent CES-D subscales: DA = Depressed Affect; PA = Positive Affect; SS = Somatic Symptoms; IP = Interpersonal Problems. Blue edges indicate positive partial correlations; red edges indicate negative partial correlations. Edge thickness represents the magnitude of the regularized partial correlation. Networks were estimated using EBICglasso (γ = 0.5). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

3.2. Descriptive statistics

Table 1 presents descriptive statistics for the four CES-D subscales at both time points and independent-samples Welch's *t*-tests comparing means across cultures. Mean subscale scores (range: 1–4) showed a substantial cross-cultural difference in Positive Affect: MIDUS participants scored higher (T1: M = 3.39, SD = 0.66; T2: M = 3.28, SD = 0.70) than MIDJA participants (T1: M = 2.08, SD = 0.71; T2: M = 2.15, SD = 0.74) at both time points (T1: t(302.9) = 23.21, $p < 0.001$, Cohen's d = 1.95; T2: t(305.0) = 19.06, p < 0.001, d = 1.60). Cross-cultural differences in Depressed Affect and Interpersonal Problems were small and non-significant (all $p > 0.25$, $|d| < 0.10$). For Somatic Symptoms, MIDUS scored slightly higher than MIDJA at both time points (T1: t(314.5) = 2.26, $p = 0.025$, d = 0.19; T2: t(347.9) = 5.17, p < 0.001, d = 0.40), with effect sizes much smaller than those for Positive Affect. Within-sample comparisons across time points showed no clinically meaningful changes in either culture.

3.3. Subscale correlation patterns

Zero-order correlations among subscales revealed a notable cross-cultural difference in the role of Positive Affect. In the MIDUS sample, Positive Affect showed moderate negative correlations with other subscales ($r = -0.37$ to -0.60 across time points), consistent with the theoretical structure of the CES-D. In contrast, Positive Affect in the MIDJA sample was largely uncorrelated with other subscales ($r = -0.07$ to 0.08 across time points), suggesting the functional independence of positive affect items in the Japanese sample. This pattern was consistent across both time points and aligned with the findings from previous cross-cultural studies of CES-D measurement properties (Iwata et al., 1994; Iwata and Roberts, 1996; Iwata et al., 1998), which similarly reported that positive affect items did not function as inverse indicators of depressive symptomatology in Japanese respondents.

3.4. Network estimation and visualization

Depressive symptom networks were estimated using EBICglasso regularization for each sample at each time point. Fig. 1 shows the four estimated networks. Visual inspection revealed consistent structural patterns within each culture over time. The MIDUS networks showed negative edges connecting Positive Affect to Depressed Affect across both time points, whereas these edges were absent or substantially weaker in the MIDJA networks. The strongest edges in both cultures connected Depressed Affect and Somatic Symptoms, reflecting the well-established relationship between affective and somatic manifestations of depression.

3.5. Temporal stability: Network comparison test results

Network Comparison Tests (NCT) were conducted to examine temporal stability within each cultural sample. Table 2 presents the NCT results.

For the MIDUS sample, the NCT revealed a statistically significant difference in the overall pattern of associations between T1 and T2 (M = 0.164, $p = 0.046$), suggesting subtle changes in symptom connections over the 8–18 year interval, although global network strength did not differ significantly (S = 0.108, $p = 0.062$). Despite the significant largest-edge change, edge weights ($r = 0.945$) and strength centrality ($r = 0.957$) were highly correlated across time points, indicating that the rank ordering of edges and node centrality remained largely unchanged.

For MIDJA, neither the overall pattern of associations (M = 0.172, $p = 0.579$) nor global strength (S = 0.346, $p = 0.358$) differed significantly between time points, indicating a consistent symptom-relationship structure over the 4–5 year interval. Edge weight ($r = 0.902$) and centrality ($r = 0.864$) correlations also demonstrated high temporal stability.

Table 2
Network comparison test results: temporal stability within cultures.

Comparison	*M*	*p*	*S*	*p*	Edge *r*	Centrality *r*
MIDUS T1 vs T2	0.164	0.046*	0.108	0.062	0.945	0.957
MIDJA T1 vs T2	0.172	0.579	0.346	0.358	0.902	0.864

Note. *M* = maximum difference in edge weights (network structure test); *S* = difference in global strength; Edge *r* = Pearson correlation between edge weights across time points; Centrality *r* = Pearson correlation between strength centrality across time points. *$p < 0.05$.

3.6. Edge-level temporal stability

Fig. 2 displays scatter plots of the edge weights at T1 versus T2 for each sample. Table 3 presents the specific edge weight values and their temporal changes in detail.

In the MIDUS sample, the Depressed Affect–Somatic edge remained the strongest positive connection at both time points, increasing slightly from 0.431 to 0.552. The negative edge between Depressed Affect and Positive Affect remained stable (−0.391 to −0.366). In the MIDJA sample, the Depressed Affect–Somatic edge was notably stronger than in MIDUS (0.741 at T1, 0.582 at T2), whereas the Depressed Affect–-Positive Affect connection was substantially weaker and became non-significant at T2 (regularized to zero).

3.7. Bootstrap stability analysis

Centrality stability was assessed using a case-dropping bootstrap procedure. The correlation stability coefficient (CS coefficient) indicates the maximum proportion of cases that can be dropped while maintaining a correlation of at least 0.70 with the original centrality indices. Table 4 presents the CS coefficients for each network.

All networks demonstrated CS coefficients exceeding the recommended threshold of 0.50, with values ranging from 0.695 to 0.751 (see Supplementary Fig. S2). These results indicate that the centrality estimates were stable and interpretable across all networks, supporting the reliability of the cross-temporal comparisons.

3.8. Sensitivity analysis: Listwise deletion vs. random forest imputation

To address the higher multivariate missingness observed in MIDJA, we re-estimated the Japanese networks using imputed data ($N = 243$; see Methods) and compared them with the listwise networks ($N = 197$). The imputed and listwise networks were highly congruent (edge weight correlations $r = 0.938$ at T1 and $r = 0.980$ at T2; 11 of 12 listwise edge values fell within the imputed-network 95% bootstrap confidence intervals). The principal cross-cultural finding — a strong Depressed Affect–Somatic connection in the Japanese sample — was preserved (T1: 0.741 vs. 0.701; T2: 0.582 vs. 0.613) with imputed 95% CIs excluding zero at both time points ([0.595, 0.807] and [0.518, 0.708], respectively). The two weak T1 edges in the listwise network (DA–PA = −0.158; PA–SS = 0.172) were regularized to zero under imputation, leaving Positive Affect completely disconnected at both time points — strengthening rather than weakening the conclusion of functional independence. Centrality stability was good under imputation (CS = 0.749 at both T1 and T2), matching or exceeding the listwise values. The full comparison, bootstrapped 95% CIs, and CS coefficients are presented in Supplementary Table S1.

3.9. Supplementary analysis: 20-item networks

To examine whether temporal stability findings generalized to the item level, supplementary analyses were conducted using 20-node networks with the MIDUS longitudinal sample ($N = 673$). The MIDJA sample was excluded from this analysis because of insufficient sample

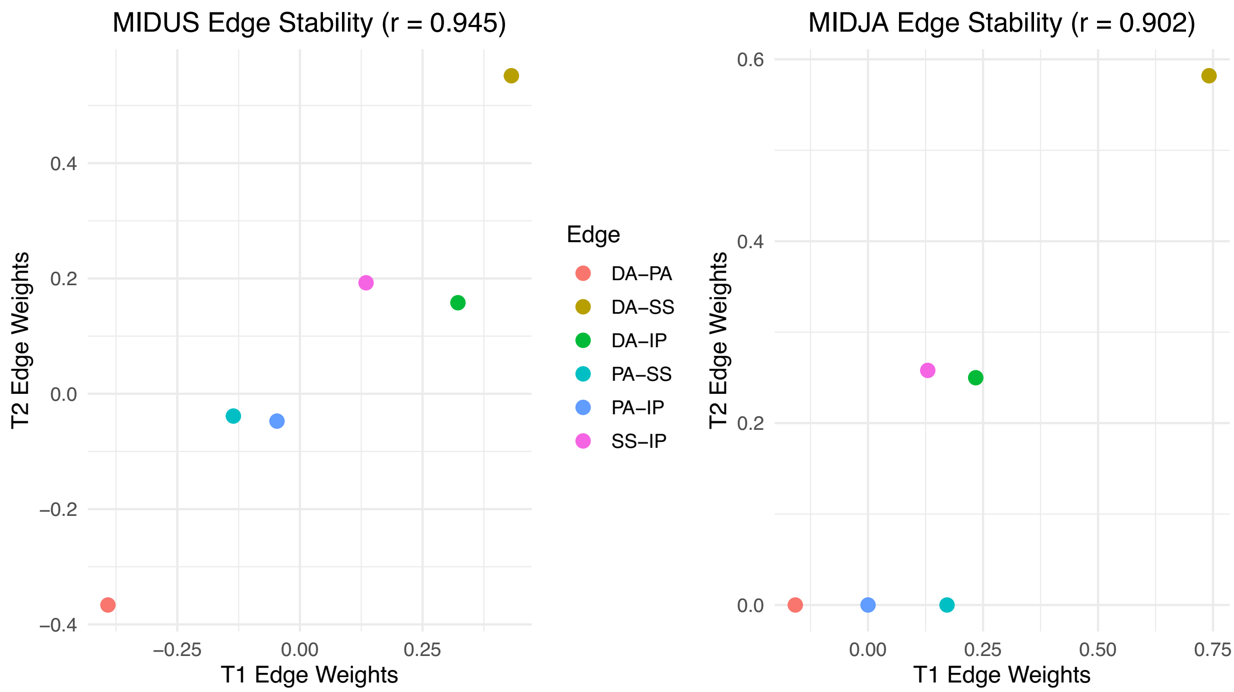

Fig. 2. Temporal stability of edge weights in MIDUS (left) and MIDJA (right) samples. Each point represents one edge, with T1 weight on the x-axis and T2 weight on the y-axis. Pearson correlations between time-specific edge weights were $r = 0.945$ (MIDUS) and $r = 0.902$ (MIDJA), indicating high temporal stability.

Table 3
Edge weights by sample and time point.

Edge	MIDUS T1	MIDUS T2	Δ	MIDJA T1	MIDJA T2	Δ
DA–PA	−0.391	−0.366	0.025	−0.158	0.000	0.158
DA–SS	0.431	0.552	0.121	0.741	0.582	−0.159
DA–IP	0.322	0.158	−0.164	0.234	0.250	0.016
PA–SS	−0.136	−0.039	0.097	0.172	0.000	−0.172
PA–IP	−0.047	−0.047	0.000	0.000	0.000	0.000
SS–IP	0.135	0.193	0.058	0.130	0.258	0.128

Note. DA = Depressed Affect; PA = Positive Affect; SS = Somatic Symptoms; IP = Interpersonal Problems. Δ = T2 − T1. Values represent regularized partial correlations estimated using EBICglasso ($\gamma = 0.5$). Edge values of 0.000 indicate edges regularized to zero.

Table 4
Centrality stability coefficients (CS coefficient).

Network	CS (Strength)	Interpretation
MIDUS T1	0.750	Good
MIDUS T2	0.750	Good
MIDJA T1	0.695	Good
MIDJA T2	0.751	Good

Note. CS = correlation stability coefficient, indicating the maximum proportion of cases that can be dropped while maintaining a correlation of at least 0.70 between the original and resampled centrality indices. CS ≥ 0.50 indicates good stability; CS 0.25–0.50 indicates acceptable stability; CS < 0.25 indicates poor stability (Epskamp et al., 2018).

size for reliable 20-node network estimation. The results demonstrated high temporal stability at the item level: the edge weight correlation between time points was $r = 0.803$, and the strength centrality correlation was $r = 0.930$. The NCT for global strength was not significant ($S = 0.309$, $p = 0.205$), consistent with the subscale-level findings. These supplementary results support the robustness of the temporal stability patterns across different levels of network granularity.

4. Discussion

This study examined the temporal stability of depression symptom networks in American and Japanese midlife adults using longitudinal data from the MIDUS and MIDJA studies. Three key findings were obtained. First, depression symptom networks demonstrated remarkably high temporal stability in both cultural samples, with edge weight correlations exceeding 0.90 in both the United States ($r = 0.945$) and Japan ($r = 0.902$). Second, consistent cross-cultural differences were observed in the role of Positive Affect, which showed moderate negative connections to other subscales in the American sample but weak-to-absent connections in the Japanese sample across both time points. Third, the Depressed Affect–Somatic connection was the strongest edge in both cultures but notably stronger in Japan, a pattern that remained consistent over time.

4.1. Temporal stability of depression networks

The high temporal stability observed here has theoretical and methodological significance. The edge weight correlations of $r = 0.945$ (MIDUS) and $r = 0.902$ (MIDJA), and centrality correlations of $r = 0.957$ (MIDUS) and $r = 0.864$ (MIDJA), place these findings at the high end of published network stability estimates. By comparison, Fried et al. (2018) reported network structure correlations of $r = 0.62$–0.74 across four PTSD samples, and Funkhouser et al. (2020) reported edge correlations of rs = 0.53–0.87 across four non-clinical samples (rs = 0.36–0.66 for clinical–non-clinical comparisons). The present results exceed these benchmarks, suggesting that depression-symptom organization remains structurally consistent over multi-year intervals — a pattern compatible with the network theory of psychopathology, which conceptualizes mental disorders as configurations of mutually reinforcing symptom-symptom interactions (Borsboom and Cramer, 2013).

The MIDUS NCT detected a statistically significant change in the strongest single connection between symptoms ($M = 0.164$, $p = 0.046$) that MIDJA did not ($M = 0.172$, $p = 0.579$); however, because NCT tests the maximum edge difference and is sensitive to single large edge changes, the high overall edge-weight correlations in both samples suggest the MIDUS difference is of modest practical significance.

4.2. Cross-cultural differences in positive affect

Perhaps the most striking finding was the consistent cross-cultural difference in how Positive Affect relates to other depression symptoms. In the American sample, Positive Affect showed moderate negative correlations with other subscales ($r = -0.37$ to -0.60 across time points), consistent with Western conceptualizations of depression as the joint presence of negative affect and absence of positive affect. In contrast, Positive Affect in the Japanese sample was largely uncorrelated with other subscales ($r = -0.07$ to 0.08), suggesting functional independence in this cultural context.

Cultural differences in affect valuation provide one explanation: European Americans value high-arousal positive states more than East Asians (Tsai, 2007; Tsai et al., 2006).

CES-D-specific work supports this pattern: Iwata et al. (1994), Iwata and Roberts (1996), and Iwata et al. (1998) showed that Japanese responses to positively worded items diverge from American responses while negatively worded items remain comparable, leading these authors to conclude that positive-affect items in their original wording cannot adequately assess depressive disorders in Japanese populations.

These differences are reinforced by context-dependent constructions of emotional experience in Japanese samples (Uchida and Kitayama, 2009) and dialectical co-occurrence of positive and negative emotions (Miyamoto et al., 2010), which together may render positive and negative symptoms less inversely correlated.

Consistency across time strengthens the interpretation that this reflects stable cultural difference rather than measurement artifact, with implications for cross-cultural depression screening that relies on positive-affect items.

4.3. The depressed affect–somatic connection across cultures

The Depressed Affect–Somatic edge was the strongest connection in both cultures and at both time points, underscoring the fundamental link between affective and somatic manifestations of depression. This connection was notably stronger in the Japanese sample (0.741 at T1) than in the American sample (0.431 at T1), aligning with research on cultural differences in somatic symptom presentation.

East Asian patients more broadly emphasize somatic over psychological symptoms in depression presentation (Kleinman, 1982; Ryder et al., 2008), and in Japanese samples specifically, somatic symptoms have been shown to be tightly linked with depressive symptomatology (Saint Arnault and Kim, 2008). Traditional Japanese medicine (Kampo), described as integral to psychosomatic medical practice in Japan, exemplifies this integrated mind–body framing (Ushiroyama, 2013).

A complementary explanation may lie in cross-cultural differences in physiological pathways linking affective and somatic symptoms. In American samples, body mass index (BMI) and adipose tissue are associated with elevated systemic inflammation, which in turn shows robust associations with several somatic and motivational depressive symptoms — loss of energy, feeling that everything was an effort, changes in appetite, sleep problems, and little interest in doing things — but not with purely affective symptoms such as feeling sad, hopeless, or fearful (Frank et al., 2021; Lee and Giuliani, 2019). Mean BMI is substantially lower in Japan than in the United States, and obesity prevalence is correspondingly far lower (approximately 3.5% in Japan vs. 35% in the United States; Borovoy and Roberto, 2015). Somatic depressive symptoms in American samples may therefore reflect a heterogeneous mixture of inflammation-driven and affect-driven pathways, whereas Japanese somatic symptoms may be driven proportionally more by affective processes — potentially yielding the tighter Depressed Affect–Somatic coupling observed in the present MIDJA networks. We offer this as a hypothesis rather than a tested mechanism, as our analyses did not include inflammatory biomarkers or BMI; future cross-cultural network studies that model BMI, inflammation (e.g., CRP, IL-6), and metabolic indices as covariates or additional nodes would help disentangle physiological from cultural-psychological contributions.

4.4. Clinical implications

The network approach has generated interest in identifying central symptoms as intervention targets, including highly influential nodes identified through expected influence (Robinaugh et al., 2016) and bridge symptoms that connect symptom clusters across disorders (Jones et al., 2021). However, the clinical translation of centrality has methodological limits (Bringmann et al., 2019; Rodebaugh et al., 2018), and our findings should be interpreted with this caveat in mind.

The present findings suggest that culturally adapted interventions should consider differences in symptomatology. In Japanese populations, the stronger Depressed Affect–Somatic connection suggests that body–mind treatments may be particularly relevant; culturally adapted cognitive-behavioral therapy programs have demonstrated feasibility, high completion rates, and substantial symptom reduction in Japanese clinical settings (Fujisawa et al., 2010), supporting the proposition that interventions tailored to local contexts can effectively engage Japanese patients. The functional independence of positive affect in Japanese samples also suggests that interventions targeting positive emotions may function differently across cultures.

4.5. Limitations

This study has several limitations. First, the MIDJA longitudinal sample ($N = 197$) was relatively small for network estimation, although the four-node subscale design and CS coefficients above 0.50 (Epskamp et al., 2018) supported reliability. MIDJA multivariate missingness exceeded the 10% threshold at T1 (12.04%) and approached it at T2 (9.45%); the random forest imputation sensitivity analysis (Supplementary Table S1) yielded networks highly congruent with the listwise estimates and preserved every substantive conclusion. Larger Japanese samples with lower attrition would nevertheless strengthen these findings.

Second, measurement intervals differed substantially (4–5 years for MIDJA vs. 8–18 years for MIDUS). As a structural consequence, MIDUS was on average older than MIDJA at T2 (M = 65.98 vs. M = 58.89; baseline T1 ages were equivalent). High stability despite these varying intervals can be interpreted as evidence of robust network structure, but future research with matched intervals would strengthen this conclusion.

Third, subscale-level networks may obscure detailed symptom connections; the supplementary 20-item analysis with MIDUS data showed similar temporal stability (edge $r = 0.803$), suggesting findings generalize across levels of granularity.

Fourth, the MIDJA sample was drawn from the Tokyo metropolitan area and may not generalize to rural Japan or other East Asian populations; although MIDUS used national probability sampling, selective attrition may have affected sample composition at follow-up (Radler and Ryff, 2010). Findings should therefore be interpreted as applying only to these midlife adult populations.

Finally, cross-sectional network structures do not establish causal relationships between symptoms. Although high temporal stability suggests consistent organization, it does not confirm causal influence. Longitudinal panel network models or intensive longitudinal designs are needed to examine temporal dynamics and potential causal relationships.

4.6. Future directions

Future research should pursue four directions: item-level measurement invariance analyses to distinguish true cultural differences from differential item functioning; intensive longitudinal designs to examine within-person dynamics; replication across additional cultures to test individualist–collectivist generalization; and clinical trials of culturally targeted somatic-symptom interventions.

5. Conclusion

This study provides the first longitudinal examination of depression symptom network stability across cultures. Networks demonstrated high temporal stability in both American and Japanese midlife adults, with edge weight correlations exceeding 0.90 in both samples, while consistent cross-cultural differences emerged in the role of Positive Affect and in the strength of the Depressed Affect–Somatic connection. These findings suggest that the overall pattern of depression-symptom associations is stable within cultures yet differs meaningfully between them, with implications for cross-cultural assessment and culturally adapted interventions.

CRediT authorship contribution statement

Takayuki Fujii: Writing – review & editing, Writing – original draft, Visualization, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Taiga Seo:** Writing – review & editing. **Yuji Nogami:** Writing – review & editing, Supervision.

Consent to participate

Informed consent was obtained from all participants included in the MIDUS and MIDJA studies.

Ethics approval and consent to participate

This study represents a secondary analysis of existing data from the Midlife in the United States (MIDUS) and Midlife in Japan (MIDJA) studies. The original MIDUS Biomarker Project received approval from the Institutional Review Boards at the University of Wisconsin-Madison, Georgetown University, and UCLA. The original MIDJA Biomarker Project was approved by the ethics committees of the University of Tokyo and Nihon University. All procedures performed in studies involving human participants were in accordance with the ethical standards of the institutional and/or national research committee and the 1964 Helsinki Declaration and its later amendments. This study used de-identified publicly available secondary data obtained from the ICPSR under data use agreements.

Declaration of Generative AI and AI-assisted technologies in the writing process

During the preparation of this manuscript, the authors used Paperpal in order to improve language and readability. After using this tool, the authors reviewed and edited the content as needed and take full responsibility for the content of the published article.

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Declaration of competing interest

The authors declare that they have no competing financial interests or personal relationships that could have influenced the work reported in this study.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.jad.2026.122029.

Data availability

The MIDUS 2 Biomarker Project data (Ryff et al., 2025; ICPSR Study 29282) can be accessed at doi:https://doi.org/10.3886/ICPSR29282.v11. The MIDUS 3 Biomarker Project data (Ryff et al., 2023; ICPSR Study 38837) can be accessed at doi:https://doi.org/10.3886/ICPSR38837.v1. The MIDJA 1 Biomarker Project data (Markus et al., 2020; ICPSR Study 34969) can be accessed at doi: https://doi.org/10.3886/ICPSR34969.v4. The MIDJA 2 Biomarker Project data (Ryff et al., 2018; ICPSR Study 36530) can be accessed at doi:https://doi.org/10.3886/ICPSR36530.v4. Access requires registration with the ICPSR and agreement to its terms of use. The study was preregistered on the Open Science Framework (https://osf.io/dnb6u/?view_only=a64eacb12e014cabb0aaca249ee95514). The complete R analysis code is available from the corresponding author upon reasonable request.

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