Problematic Social Media Use in College Students: Risk Heterogeneity and Psychopathological Network Structures

Lin Luo, Junfeng Yuan

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Table of Contents

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Lin Luo[1, 2]; Junfeng Yuan[1]

[1]Guizhou Normal University, Huaxi District, Guiyang City, Guizhou Province Guizhou Normal University Guiyang CN
[2] Key Laboratory of Brain Function and Brain Disease Prevention and Treatment of Guizhou Province Guiyang CN

Corresponding Author:
Lin Luo
Guizhou Normal University, Huaxi District, Guiyang City, Guizhou Province
Guizhou Normal University
School of Physical Education, Guizhou Normal University, Guiyang, 550025, China
Guiyang
CN

Abstract

Background: With the increasing prevalence of social media use, the relationship between problematic social media use and mental health has received widespread attention.

Objective: To explore the psychopathological network characteristics of Chinese college students with different risk levels of problematic social media use (PSMU), and to reveal structural differences in symptom networks and their clinical implications.

Methods: Using a cross-sectional study design, we recruited a sample of Chinese college students (N=12,766). Psychological symptoms were assessed using the DSM-5 Cross-Cutting Symptom Measure (CCSM). Through Latent Profile Analysis (LPA) and network analysis methods, we systematically compared symptom network topology, centrality characteristics, and symptom transmission pathways between high- and low-risk PSMU groups. Key analytical metrics included network density, average degree, clustering coefficient, node centrality, and directed acyclic graph (DAG) analysis.

Results: The sample comprised 11,646 low-risk and 1,120 high-risk participants. The low-risk group demonstrated significantly higher network density, average degree, and clustering coefficient, indicating more tightly interconnected and organized symptom networks. The high-risk group exhibited relatively sparse network structures with heightened sensitivity to core symptom activation. Depressive and anxiety symptoms occupied central positions in both groups, but showed stronger interconnections in the high-risk group. Obsessive-compulsive and dissociative symptoms displayed significant mediating and bridging roles in symptom networks. DAG analysis revealed that the depression-anxiety pathway may constitute the core driving module in the high-risk group's symptom network.

Conclusions: This study elucidates the structural characteristics and differences in psychopathological networks among college students with varying PSMU risk levels. The organizational patterns of symptom networks reflect the complexity and dynamic nature of individual mental health statuses. For high-risk populations, we recommend focused attention on core symptoms including depression, anxiety, obsessive-compulsive tendencies, and dissociation, along with developing personalized intervention strategies based on network structural features.

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Lin Luo[12]*, Junfeng Yuan[1]
1School of Physical Education, Guizhou Normal University, Guiyang, 550025, China
2Key Laboratory of Brain Function and Brain Disease Prevention and Treatment of Guizhou Province，Guiyang, 550025, China
* Corresponding author: Lin Luo. Email: 460022831@gznu.edu.cn

Abstract

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Keywords: Problematic social media use; Network analysis; Psychopathological symptoms; College students; DSM-5 CCSM

1. Introduction

Problematic Social Media Use (PSMU) has emerged as a critical digital health concern attracting global attention (World Health Organization, 2015; Salari et al., 2025; Fioravanti et al., 2021). Epidemiological studies reveal its high prevalence among youth populations (Wang, 2024), particularly college students who demonstrate marked vulnerability due to their developmental stage and living environment (Salari et al., 2023; Roig-Vila et al., 2020; Ayar et al., 2018). While academic consensus on PSMU's conceptual boundaries remains elusive, researchers generally agree on its core manifestation as a maladaptive usage pattern that may lead to functional impairments across academic (Geng et al., 2018), social, and mental health domains (Scott & Woods, 2019; Orben, 2020; Cataldo et al., 2022). Crucially, PSMU's essence extends beyond quantitative metrics like usage duration to encompass behavioral regulation difficulties (Wegmann et al., 2020) and their multifaceted negative consequences (Li et al., 2016).

Although Griffiths' (2005) six-component model of behavioral addiction (salience, tolerance, mood modification, relapse, withdrawal, and conflict) has long informed PSMU conceptualization and assessment development (Andreassen, 2015), recent empirical studies challenge its applicability. Emerging evidence suggests PSMU's addictive components may not form a unitary construct (Fournier et al., 2023), with salience and tolerance dimensions showing weaker associations with psychopathological symptoms, potentially representing peripheral rather than core features. Conversely, conflict and mood modification dimensions have been identified as critical bridge symptoms linking PSMU to psychological distress (e.g., depression, anxiety, and stress) (Peng & Liao, 2023). Numerous studies report significant associations between PSMU and mental health issues including depression, anxiety, and sleep disturbances (Aydin et al., 2020; Hussain & Griffiths, 2018; Shannon et al., 2024). However, traditional approaches relying on scale total scores risk obscuring symptom heterogeneity (Fried & Nesse, 2015). Given PSMU's diverse manifestations and complex relationships with specific mental health problems, total score approaches or single models prove inadequate for capturing this complexity. Therefore, investigating distinct association patterns between PSMU risk subgroups and specific psychological distress symptoms holds crucial theoretical and clinical significance. This granular approach not only facilitates identification of high-risk PSMU populations needing intervention but also informs personalized strategies tailored to different PSMU manifestation patterns.

Recognizing PSMU's complexity, this study employs Latent Profile Analysis (LPA) - a person-centered classification method (Spurk et al., 2020) - to explore PSMU's heterogeneous manifestations. Unlike variable-centered approaches, LPA identifies latent subgroups based on individuals' symptom configuration across multiple PSMU dimensions (Peng & Liao, 2023), offering insights into users' distinct "symptom profiles." This methodology advances understanding of PSMU heterogeneity while informing targeted intervention strategies. Concurrently, Network Analysis (NA) provides novel analytical tools to elucidate symptom interactions (Hevey, 2018), particularly through identification of "bridge symptoms" between mental disorders (Jones et al., 2021). Although LPA and NA have been widely applied to examine relationships between psychological distress and internet gaming disorder (IGD) or internet addiction (Cerniglia et al., 2019; Cai et al., 2021; Peng & Liao, 2023), their integrated application in PSMU research remains limited (Peng & Liao, 2023).

This investigation applies network analysis to Chinese college students, comparing symptom network structures across PSMU risk groups to achieve three objectives: (1) Identify pivotal symptom nodes in risk escalation processes; (2) Reveal culturally specific symptom association patterns; (3) Explore implications of network stability for intervention timing. Furthermore, Bayesian-directed acyclic graph construction enables detection of both direct symptom associations and potential causal pathways (Scutari & Nagarajan, 2013), offering novel theoretical perspectives and methodological support for PSMU mechanism research.

2. Methods

2.1 Participants

This study employed a convenience sampling method to recruit college students from multiple Chinese universities between October and November 2024. Collaborating with university faculty, recruitment notices were distributed through classroom announcements and online social platforms, ensuring geographical diversity across 12 provinces in Northern, Eastern, Southern, Central, and Northwestern China. Inclusion criteria required participants to be: (1) full-time undergraduate students; (2) consistent social media platform users over the past six months. Exclusion criteria removed invalid responses with completion times below 3 minutes (determined through pilot testing).

The final sample comprised 12,766 valid responses, with 58.71% female participants ($n = 7,491$). Age ranged from 18 to 29 years ($M = 20.99$, $SD = 1.16$), representing all undergraduate grades (freshmen to seniors). Data collection was conducted through the encrypted Maike CRM online survey platform, with voluntary anonymous participation. The study protocol received ethical approval from Guizhou Normal University Academic Ethics Committee (Approval No.: 2023030005). All procedures adhered to the Declaration of Helsinki ethical guidelines, including informed consent, privacy protection, and voluntary withdrawal rights.

2.2 Measures

2.2.1 Demographic Characteristics

A self-designed questionnaire collected participants' basic demographic information, including gender, age, academic year, major, and family residence location.

2.2.2 Problematic Social Media Use (PSMU)

The Chinese version of the Social Networking Addiction Scale (SNAS-C) was used to assess PSMU severity. Originally developed by Shahnawaz and Mehrotra (2020) based on core components of addictive behavior theory, the scale was translated and culturally adapted by Bi et al. (2024). The SNAS-C contains 29 items evaluating six dimensions: Salience, Mood Modification, Tolerance, Withdrawal Symptoms, Conflict, and Relapse. Responses are recorded on a 5-point Likert scale (0 = "Never" to 4 = "Always"), with total scores ranging from 0 to 116. Higher scores indicate greater PSMU severity. The scale demonstrated excellent internal consistency in our sample (Cronbach's α = 0.972). Full item descriptions are provided in Appendix A.

2.2.3 Psychopathological Symptoms

The Chinese adult version of the DSM-5 Self-Rated Level 1 Cross-Cutting Symptom Measure (CCSM) assessed psychological symptoms over the past two weeks (Bravo et al., 2018; Ma et al., 2021). This 23-item instrument evaluates 13 psychopathological domains:Depression (Items 1-3)□Mania (Items 4-5)□Anxiety (Items 6-8)□Somatic Symptoms (Items 9-10) □ Suicidal Ideation (Item 11) □ Psychotic Symptoms (Items 12-13) □ Sleep Problems (Item 14)□Memory Impairment (Item 15)□Obsessive-Compulsive Symptoms (Items 16-17)□Dissociative Symptoms (Item 18)□Personality Functioning (Items 19-20)□Substance Use (Items 21-23).Responses use a 5-point scale (0 = "None/Not at all" to 4 = "Severe/Nearly every day"). The measure showed strong psychometric properties in this study (Overall Cronbach's α = 0.958). Complete item descriptions are available in Appendix B.

2.3 Statistical Analysis

2.3.1 Descriptive Analysis

The study performed preliminary statistical analysis using SPSS 26.0 and conducted comprehensive descriptive statistics on the demographic characteristics of the sample, including gender, age, grade, etc.

2.3.2 Latent Profile Analysis

Based on the item scores of the six dimensions of the Social Network Addiction Scale (SNAS-C), the study conducted Latent Profile Analysis (LPA) using R software (version 4.2.2) to identify groups of participants with similar levels of Problematic Social Media Use (PSMU) risk. During the analysis, models with 2 to 5 latent profiles were estimated, and the optimal number of profiles was determined using the following integrated criteria: First, lower information criterion values indicate better model fit, including the Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC), and sample-size adjusted BIC (ssaBIC) (Nylund-Gibson & Choi, 2018). Second, entropy was used to evaluate classification accuracy, with a range from 0 to 1; values greater than 0.8 indicate high classification precision (Fonseca-Pedrero et al., 2017). Third, the model improvement was evaluated using the Bootstrap Likelihood Ratio Test (BLRT), where a BLRT p-value less than 0.05 indicates a significant improvement in model fit compared to a solution with one less category; conversely, non-significant BLRT results (p-value > 0.05) suggest that a k-class model is not superior to a k-1 class model. Finally, to avoid overfitting and ensure the practicality of the analysis results, each latent category should include at least 5% of the total sample (Nagin, 2005; Wendt et al., 2019; Zhang et al., 2018). The results were visualized using scatter plots (Masyn, 2013), and the latent profile model was cross-validated through two randomly split samples (training sample n=6,383 and validation sample n=6,383). In the validation phase, the model parameters were fixed based on the training sample's model, and the model from the validation sample was compared to assess its stability and reliability. Finally, the demographic characteristics, SNAS-C scores, and mental health indicators across PSMU risk groups were compared.

2.3.3 Network Analysis

Data analysis and visualization were conducted in an integrated environment using R (version 4.2.2), RStudio, and Python 3.9. Network estimation and basic visualization were primarily implemented using the qgraph and bootnet packages in R (Epskamp & Fried, 2018). For more sophisticated graphical presentations, advanced network visualizations were completed using Python 3.9 with libraries such as networkx and pyvis. Predictability analysis used the mgm package (Haslbeck & Waldorp, 2018), network structure comparison employed the NetworkComparisonTest package (van Borkulo et al., 2014), and directed acyclic graph (DAG) analysis was performed through the bnlearn package. In the Gaussian Graphical Model (GGM), nodes represent items from the DSM-5 CCSM, and edges denote the strength of associations between items. Based on the correlation matrix of 13 psychopathological dimensions and 23 items, a regularized partial correlation network was estimated. Specifically, the GGM was regularized using the graphical LASSO algorithm to effectively eliminate spurious associations and simplify weak redundant associations to zero, thereby constructing a sparse network structure (Friedman et al., 2008). In the qgraph package, model selection was based on the Extended Bayesian Information Criterion (EBIC), and the network with the lowest EBIC value was selected from 100 candidate networks, with tuning parameters λ set to 0.001 and the hyperparameter γ (gamma) set to 0.5 (Wysocki & Rhemtulla, 2021).

The study assessed the importance of nodes in the network by calculating node strength and predictability (Epskamp & Fried, 2018). Strength refers to the sum of absolute edge weights between a node and all other nodes, reflecting the node’s relative importance. Predictability quantifies the percentage of shared variance between a node and its adjacent nodes, measuring the node's absolute importance. Furthermore, the study employed a two-step expected influence measure as a bridging centrality indicator to assess the extent of influence transmission across different symptom communities (Jones et al., 2021).

Robustness analysis was conducted using the bootnet package (Epskamp et al., 2018). First, the 95% confidence intervals of edge weights were obtained through 5,000 bootstrap samples, where less overlap in the confidence intervals indicates higher accuracy of the undirected network estimation. Second, subsampling (5,000 bootstrap samples) was used to re-estimate the network, and the correlation between node centralities after removing certain individuals and the original estimates was compared to assess the stability of centrality measures. The study calculated the Centrality Stability (CS) coefficient as a key measure, where a CS coefficient >0.25 indicates acceptable stability, and a CS coefficient >0.5 indicates good stability (Epskamp & Fried, 2018).

The Network Comparison Test (NCT) was used to evaluate the differences in network structure between high-risk and low-risk groups for social network addiction (van Borkulo et al., 2017). This test assessed three key dimensions: network structure invariance (evaluating the overall difference between the two groups' network structures), edge strength invariance (evaluating whether there are differences in edge weights between the groups), and global strength invariance (assessing the difference in overall network connectivity between the two groups). To ensure the reliability of statistical inference, the study used 1,000 permutation tests ($p<0.05$) to determine the statistical significance of the differences.

2.3.4 Directed Acyclic Graphs (DAG)

Finally, the study used the hill-climbing algorithm from the bnlearn package to calculate and visualize the Bayesian network (Gámez et al., 2007). In the random restart process, the algorithm optimizes the Bayesian Information Criterion (BIC) by adding, deleting, or reversing edges, thus identifying potential edges and their directions between nodes. The average network was obtained through 5,000 bootstrap samples, and only edges with consistent directionality in at least 85% of the bootstrap networks were retained to ensure the stability and reliability of the network structure (Adhitama & Saputro, 2022).

3. Results

3.1 LPA Analysis Results

As shown in Table 1, the results of Latent Profile Analysis (LPA) indicate a continuous decline in the model fit indices (AIC, BIC, aBIC) with an increasing number of latent categories, indicating a better fit and suggesting an improvement in model quality. However, when evaluating classification effectiveness, both the category probability distribution and entropy must be considered. The Scree Plot in Appendix D further supports the selection of the three-profile model: when the number of categories is three, the aBIC value shows a significant decrease, with subsequent additions of categories leading to much smaller improvements in aBIC, clearly forming an 'inflection point' where the fit improvement plateaus. Furthermore, the Cohen's d values between groups of the three-profile model (see Appendix E) all exceed 0.80, indicating strong group differentiation and high classification accuracy.

Based on the severity of PSMU, the three latent profiles were identified as the No-risk PSMU group, the Low-risk PSMU group, and the At-risk PSMU group. To better observe the psychological symptom differences across risk levels, and in line with previous research (Luo et al., 2024), the No-risk and Low-risk groups were merged into a single Low-risk group, while the At-risk group was classified as the High-risk group. The distribution of SNAS-C scores for college students with different PSMU risk levels is shown in Appendix E.

Table 1: Fit statistics for latent profile analysis and the corresponding profile probabilities.

Model	k	G^2/LL	AIC	BIC	aBIC	Entropy	Profile Probability(%)
1-profile	1	-281911.176	563906.351	564206.934	564073.464	-	100%
2-profile	2	-248075.123	496278.247	496736.277	496532.895	0.979	21.48%/78.52%
3-profile	3	-233432.876	467037.752	467653.231	467379.937	0.970	19.08%/66.40%/14.53%
4-profile	4	-226875.013	453966.027	454738.953	454395.746	0.969	7.52%/16.40%/13.94%/ 62.14%
5-profile	5	-224057.905	448375.811	449306.186	448893.066	0.967	7.39%/ 6.93%/ 11.87%/ 59.96%/ 13.93%
6-profile	6	-221702.621	443709.241	444797.064	444314.032	0.967	7.39%/11.73%/58.09%/6.88%/ 14.32%/1.60%

3.2 Descriptive Analysis of Observed Variables for College Students at Different PSMU Risk Levels

The demographic characteristics of college students at different PSMU risk levels are detailed in Appendix C. Table 2 presents a comparison of DSM-5 CCSM scores across risk groups, including means (M), standard deviations (SD), and effect sizes for the differences between groups. The data analysis shows that the High-risk group has significantly higher average scores than the Low-risk group across all mental health symptom dimensions ($p < 0.001$). This suggests that the High-risk PSMU group may face more extensive and severe mental health challenges.

Effect size (Cohen's d) analysis reveals that the practical significance of the differences between the two groups ranges from small to moderate, with the most significant intergroup differences observed in the dimension related to obsessive-compulsive symptoms. This finding is particularly noteworthy, as it suggests a potential link between PSMU risk levels and compulsive behavior patterns. The differences between groups on all dimensions reached statistical significance ($p < 0.001$), indicating that the study's findings are both robust and consistent. Overall, the results support the hypothesis of a systematic relationship between PSMU risk levels and multidimensional mental health symptoms.

Table 2 Summary of descriptive analysis in both samples

Domain	Number	Items	Low-risk Group Mean	Low-risk Group SD	High-risk Group Mean	High-risk Group SD	Cohen's d	p
Depression	1	De1	0.985	0.830	1.396	0.922	0.489	<0.001
	2	De2	0.700	0.779	1.129	0.909	0.543	<0.001
Anger	3	An	0.784	0.758	1.200	0.868	0.541	<0.001
Mania	4	Ma1	0.898	0.821	1.204	0.905	0.370	<0.001
	5	Ma2	0.661	0.733	0.926	0.806	0.358	<0.001
Anxiety	6	An1	0.805	0.776	1.25	0.905	0.564	<0.001
	7	An2	0.644	0.739	1.036	0.849	0.523	<0.001
	8	An3	0.81	0.774	1.171	0.834	0.463	<0.001
Somatic	9	So1	0.726	0.756	1.075	0.853	0.456	<0.001
	10	So2	0.500	0.723	0.870	0.887	0.501	<0.001
Suicidal	11	Su	0.312	0.626	0.546	0.797	0.364	<0.001
Psychotic	12	Ps1	0.352	0.634	0.591	0.811	0.366	<0.001
	13	Ps2	0.404	0.677	0.67	0.85	0.383	<0.001
Sleep disturbance	14	Sle	0.708	0.815	1.109	0.963	0.483	<0.001
Memory	15	Me	0.608	0.767	1.004	0.932	0.507	<0.001
Obsessive-Compulsive Disorder	16	OCD1	0.597	0.742	1.038	0.925	0.581	<0.001
	17	OCD2	0.507	0.719	0.936	0.926	0.579	<0.001
Dissociation	18	Di	0.464	0.689	0.826	0.873	0.512	<0.001
Personality	19	Pe1	0.462	0.721	0.849	0.937	0.522	<0.001
	20	Pe2	0.516	0.747	0.929	0.924	0.540	<0.001
Alcoho lUse	21	Al	0.264	0.588	0.399	0.718	0.226	<0.001
Tobacco Use	22	To	0.307	0.741	0.429	0.865	0.162	<0.001

Substance Use	23	Sub	0.142	0.454	0.216	0.557	0.160	<0.001

3.2Network estimation

The network estimation results (see Appendix E) indicate systematic differences in the network structures between the two groups, with the Low-risk group generally exhibiting stronger network connectivity. Among the symptoms, depressive symptoms (De1, De2) showed the most significant differences between the groups (differences of -1.8732 and -1.3525, p = 0.005, respectively). Anger and anxiety-related symptoms (An1, An2, An3) also showed significant differences ($p < 0.05$), while the differences between groups for substance use (Sub) and tobacco use (To) symptoms were minimal and not statistically significant.

Figure 1 illustrates the 23-node symptom network structure based on LASSO regularization. Network edge analysis (see Appendix F) reveals that the Low-risk group generally has higher Bridge values than the High-risk group, indicating more closely linked interactions between symptoms. The strongest bridging connections occurred in dissociation (Dissociation: Low-risk group 12.647 vs. High-risk group 11.852) and obsessive-compulsive symptoms (OCD1: Low-risk group 12.471 vs. High-risk group 11.824; OCD2: Low-risk group 12.461 vs. High-risk group 11.613). In contrast, the weakest bridging connections were observed in tobacco use (To: Low-risk group 6.811 vs. High-risk group 6.728) and substance use (Sub: Low-risk group 8.570 vs. High-risk group 6.696).

The Predictability analysis of network centrality (see Appendix G) shows that dissociation (Di) had the highest predictability in both groups (Low-risk group 0.718, High-risk group 0.701), and anxiety symptoms (An1) also showed relatively high predictability (Low-risk group 0.697, High-risk group 0.718). In contrast, the predictability of manic symptoms (Ma1) was relatively low (Low-risk group 0.410, High-risk group 0.336), while tobacco use (To) showed the lowest predictability in the Low-risk group (0.361). These results highlight the distinctive characteristics of symptom network structures at different risk levels.

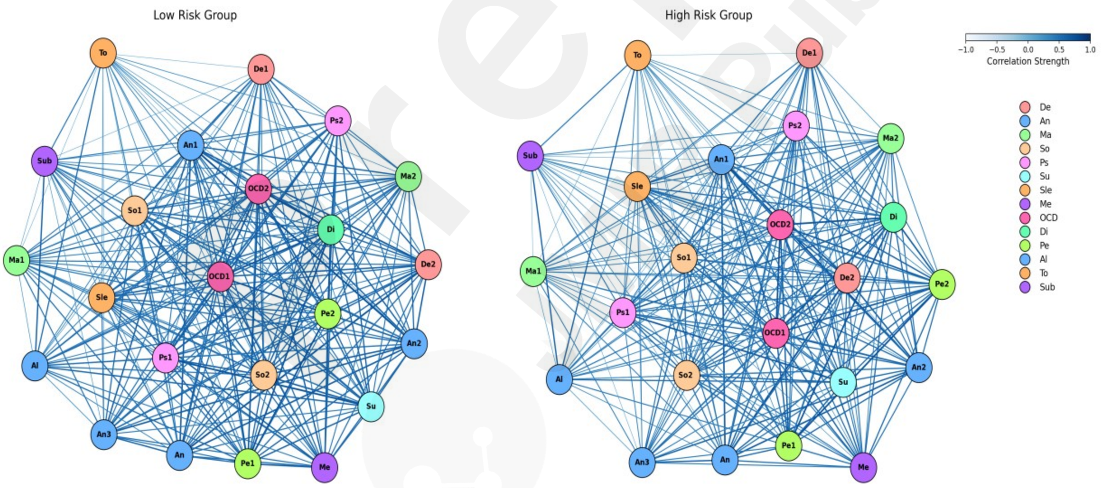

Figure 1. Item-level Network Structures for Both Groups□De1□Depression 1□De2□Depression 2□An□Anger□Ma1□Mania 1□Ma2□Mania 2□An1□Anxiety 1□An2□Anxiety 2□An3□Anxiety 3□So1□Somatic 1□So2□Somatic 2□Su□Suicidal□Ps1□Psychotic 1□Ps2□Psychotic 2□Sle□Sleep disturbance□Me□Memory□OCD1□Obsessive-Compulsive Disorder 1□OCD2□Obsessive-Compulsive Disorder 2□Di□Dissociation□Pe1□Personality 1□Pe2□Personality 2□Al□Alcohol Use□To□Tobacco Use□Sub□Substance Use□

Based on the results of the Network Comparison Test (NCT) (Appendix H), there were significant differences between the low-risk and high-risk groups in terms of network density, average degree, and clustering coefficient. The low-risk group exhibited a higher network density, indicating closer associations between symptoms; a higher average degree, suggesting stronger connections between individual symptoms and others; and a higher clustering coefficient, reflecting a greater tendency for symptoms to form tightly connected subgroups. These results suggest that the symptom network structure in the low-risk group is more compact and cohesive, potentially indicating greater resilience, while the network structure in the high-risk group is relatively more diffuse.

3.3 DAG analysis

The DAG （see Figure 2）analysis of the low-risk group revealed a relatively complex network of interconnections, where depressive symptoms (De1, De2) and anxiety symptoms (An1, An2, An3) formed a tightly connected core group. There was a bidirectional influence between manic symptoms (Ma1, Ma2) and somatic symptoms (So1, So2), while obsessive-compulsive symptoms (OCD1, OCD2) primarily served as mediators linking other symptom groups. In terms of edge strength distribution, the connection between depressive and anxiety symptoms was the strongest, followed by the connection between somatic and manic symptoms, while connections between other symptoms were relatively weaker.

In contrast, the network structure of the high-risk group, although sparser, showed stronger key path connections. In this network, depressive symptoms became a more prominent core node, directly influencing multiple other symptoms. The influence of anxiety symptoms expanded, establishing direct links with more symptoms. The connection between obsessive-compulsive symptoms and other symptoms was notably stronger. Regarding edge strength characteristics, the connection strength of the depressive-anxiety path was further enhanced, and the connection strength between obsessive-compulsive symptoms and other symptoms also significantly increased. Overall, the edge strength in the high-risk group was generally higher than that in the low-risk group. These findings suggest that the symptom associations in the high-risk group are more tightly connected, with more direct symptom transmission paths. Particularly, core symptoms (depression and anxiety) have a greater influence, and the associations between somatic symptoms and other symptoms have strengthened, potentially serving as important risk indicators.

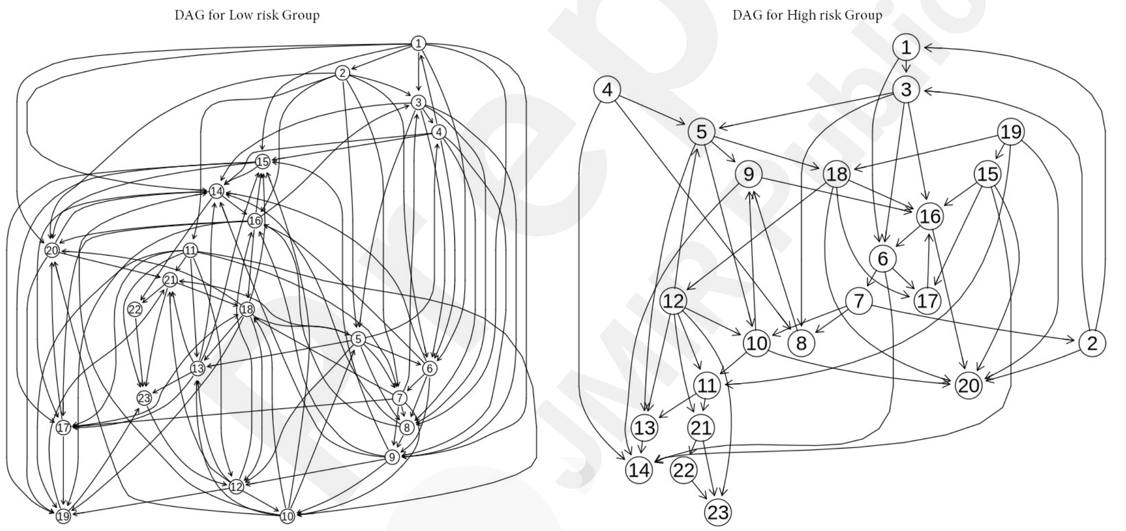

Figure 2 The directed acyclic graphs (DAGs) of the two groups.（1）Depression 1（2）Depression 2（3）Anger（4）Mania 1（5）Mania 2（6）Anxiety 1（7）Anxiety 2（8）Anxiety 3（9）Somatic 1（10）Somatic 2（11）Suicidal（12）Psychotic 1（13）Psychotic 2（14）Sleep disturbance（14）Memory（16）Obsessive-Compulsive Disorder 1（17）Obsessive-Compulsive Disorder 2（18）Dissociation（19）Personality 1（20）Personality 2（21）Alcohol Use（22）Tobacco Use（23）Substance Use）

4. Discussion

This study systematically explored the network characteristics of psychological symptoms in university students with different levels of problematic smartphone use (PSMU) risk, using Latent Profile Analysis (LPA) and network analysis methods. The findings revealed significant differences in the symptom network structure between the high- and low-risk PSMU groups, providing novel perspectives and empirical evidence for both clinical intervention and theoretical research.

First, the network analysis highlighted the fundamental differences in the overall network topology between the high- and low-risk groups. The low-risk group exhibited higher levels on key metrics such as network density, average degree, and clustering coefficient, indicating that their symptom network had a more tightly connected and organized structure. This high-density network structure may reflect stronger psychological resilience and self-regulation abilities in this group (Wen et al., 2025), aligning with the stability characteristics of the "healthy" networks reported in previous studies (Sturmberg et al., 2019). Notably, the network structure of the high-risk group displayed relatively looser characteristics, which could suggest that this group is more sensitive to the activation of core symptoms (Chen et al., 2023). From a network theory perspective, this characteristic could be interpreted as a "tipping point" effect: once a key node is activated, its impact may rapidly spread along the network edges, leading to symptom exacerbation or an increased risk of comorbidity (Barthélemy et al., 2004). In clinical practice, this finding underscores the importance of early identification and intervention for high-risk individuals.

Furthermore, at the core symptom level, the study found that depression (De1, De2) and anxiety (An1, An2, An3) occupied central positions in both the high- and low-risk groups, with a notably tighter and stronger connection between them in the high-risk group. This "emotional connectivity effect" may accelerate the accumulation and transmission of negative emotions within the individual's psychological system, further exacerbating the course of the disorder (Kiecolt-Glaser et al., 2002; Cox et al., 2019). Meanwhile, the mediating role of obsessive-compulsive symptoms (OCD1, OCD2) in the network structure is also noteworthy, as it may serve as a connecting bridge between core symptoms such as depression and anxiety and other related symptoms (e.g., somatization, sleep disorders). Early identification and intervention in obsessive-compulsive symptoms could help block or weaken the reciprocal activation between negative symptom networks (Fontenelle et al., 2022). Additionally, dissociative symptoms (Dissociation) exhibited significant "bridging centrality," suggesting they may be key connection points between different symptom clusters (Fayad et al., 2024).

In the comparison between high- and low-risk groups, the study observed significant differences in symptom transmission pathways. Although the overall network in the high-risk group was relatively sparse, certain key pathways, particularly the depression-anxiety pathway, showed stronger connection strengths. Notably, the link between somatic symptoms and other symptom clusters was significantly enhanced in the high-risk group, possibly indicating a heightened sensitivity to the interaction between physiological and psychological factors in this group. Directed Acyclic Graph (DAG) analysis further revealed that the depression-anxiety pathway in the high-risk group might become the "core driving module" of the entire network, making this group more susceptible to entering a vicious cycle of emotional disruption and symptom generalization.

These network characteristics provide multiple insights for clinical practice. First, during the assessment and monitoring process, particular attention should be given to core symptoms (depression, anxiety, obsession) and high centrality symptoms (dissociation), as they may not only serve as early warning indicators of PSMU but also as key entry points for targeted PSMU interventions. Second, for the high-risk PSMU population, clinical interventions should fully consider the network structure characteristics and key transmission pathways, focusing on blocking or weakening the nodes and edges that may accelerate symptom diffusion. For example, when depression and anxiety exhibit a "mutual activation" trend, integrated psychological therapies may be more effective in preventing emotional dysregulation from spreading to other areas of functioning. At the same time, the mediating role of obsessive-compulsive symptoms in the network suggests that intervention designs should particularly focus on their positive and negative feedback effects on other emotional and behavioral symptoms, and accordingly incorporate cognitive-behavioral therapy or impulse control techniques.

Although this study has provided valuable insights into the symptom structure of different PSMU risk groups through Latent Profile Analysis (LPA) and network analysis, the conclusions should still be interpreted with caution. First, the limitations of the measurement tools require special attention—the SNAS-C used in this study is not a clinical diagnostic tool for PSMU; while the DSM-5 Self-Rated Level 1 Cross-Cutting Symptoms

Measure for adults has clinical utility, its assessment of dimensional mental symptoms is relatively simplified and may not fully capture the complexity and subtle changes of symptoms. Second, the methodological limitations should also be considered. This study recruited participants through a convenience sampling method, potentially introducing sample selection bias; the cross-sectional study design inherently presents only a static structure of symptom networks, and cannot effectively infer causal relationships or dynamic evolution processes between symptoms. In terms of sample representativeness, the participants were primarily university students, which may limit the generalizability of the findings. Additionally, insufficient control of potential confounding variables is another key limitation. Important environmental factors, such as the quality of social support networks, family economic status, and family interaction patterns, may moderate or mediate the relationship between PSMU and mental symptoms, thereby influencing the observed network structure characteristics. However, these factors were not included in the analysis framework of this study. Based on these limitations, future research should focus on: (1) using more comprehensive, multidimensional PSMU assessment tools and mental symptom measurement methods; (2) designing longitudinal tracking studies to reveal the dynamic evolution of symptom networks; (3) expanding the sample size and including participants from more diverse demographic and socio-cultural backgrounds to enhance the external validity of the study; (4) incorporating important environmental and socio-psychological factors into the analytical model to construct a more complete theoretical framework, thus more accurately understanding the complex relationship mechanisms between PSMU and mental health issues.

5. Conclusion

The findings of this study provide a new perspective for understanding the relationship between PSMU and mental health. The tighter symptom network in the low-risk group may reflect stronger psychological resilience, while the more scattered network structure in the high-risk group may facilitate symptom spread. In both groups, depression and anxiety symptoms occupied central positions, while obsessive-compulsive and dissociative symptoms played a bridging role. These findings have practical implications: priority should be given to enhancing emotional regulation abilities in the high-risk PSMU group, particularly in relation to depression-anxiety symptoms; meanwhile, the value of obsessive-compulsive and dissociative symptoms as warning indicators should also be emphasized. Additionally, differentiated mental health service strategies can be implemented for different risk-level groups. However, the study's conclusions should be interpreted with caution. The SNAS-C used in this study is not a diagnostic tool for PSMU, and symptom measurement is relatively simplified; the cross-sectional design and convenience sampling limit causal inference and the generalizability of the results; moreover, potential confounding variables, such as social support, were not adequately controlled.

Supplementary Materials

Appendix A: Chinese Version of Social Networking Addiction Scale among College Students（SNAS-C）

Appendix B: Chinese Version of DSM-5 CCSM

Appendix C: Sample descriptive statistics of all variables included in the analyses

Appendix D: presents the scree plot based on AIC, BIC, aBIC, and Entropy metrics, illustrating the trend of changes from 1 to 6 profiles.

Appendix E: provides descriptive information for each profile based on the optimal three latent profiles.

Appendix F: Node Strength Difference Test Results Between Groups

Appendix G: Between-Group Comparison of Node Predictability and Bridge Analysis Results

Appendix H: Results of the Network Comparison Test (NCT) between the two groups.

Conflict of Interest Statement

There are no conflicts of interest to declare.

Data Availability Statement

The dataset generated in this study is available upon request from the corresponding author.

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Author Contribution Statement
L.L: Resource writing, project management, formal analysis, data management, writing the initial draft.
Y.J.: Survey, data management.

Ethical Statement
The study was approved by the Academic Ethics Committee of Guizhou Normal University (Approval No: 20230300005).

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Supplementary Files

Multimedia Appendixes

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