

# Dependency Networks of Emotional Facial-Expression in Mood and Anxiety Disorders

*Keywords: Dependency network analysis; Digital phenotyping; Facial expression analysis; Mood and anxiety disorders; Emotion dynamics;*

## Extended Abstract

Digital phenotyping based on facial expression analysis is a promising approach to measure mood and anxiety severity in the real world that is cheap, low-burden, and scalable. This approach will ultimately help individuals and clinicians monitor and manage symptoms in real-time. However, little work has examined facial features and their dynamics in a naturalistic context in relation to specific clinical symptoms. Here, we applied a graph theoretical approach to study facial expression dynamics during a naturalistic clinical evaluation. We hypothesized that the dynamic emotional network topological organization would distinguish between mood or anxiety disorders (MA) patients and healthy controls (HC).

A total of  $N=80$  participants, 68 with mood or anxiety disorder and 12 healthy controls (HC), completed audio-visual (AV) recordings during the Structured Clinical Interview for DSM-5 (SCID-5). The AV data was then processed via DeepFace, an open-source deep-learning facial recognition algorithm. Probability percentages of facial expression estimates (i.e., Happy, Sad, Fear, Angry, Surprise, and Disgust) were computed per frame, thus creating a time-series for each emotion. We then estimated facial expression dynamics over time via the dependency network analysis (DEPNA) [1, 2] graph theory model. DEPNA quantifies the 'Influencing Degree' (out-degree) and 'Influenced Degree' (in-degree) of each emotion-node according to its partial correlation with the rest of the network of emotion-nodes. Next, we conducted a between-group two-sample t-test for each node's degree of influence controlling for age, sex and SCID-5 duration (number of time-points). All influencing or influenced t-test results were corrected for multiple comparisons ( $N=7$ , number of nodes in the network) using false discovery rate (FDR) correction with  $p < 0.05$  threshold. To create network graph visualization (Figure 1), we used the pair-wise dependency connectivity matrix. A two-tailed t-statistic was computed to compare the two groups. We then connected only pair-wise nodes with dependencies that were significantly different between the two groups ( $p < 0.05$ , FDR corrected for number of tests) creating a simple graph visualization of the differences between the groups. Graph visualization was conducted using the NetworkX library in Python [3].

Compared with HC, MA patients showed significantly lower 'Influencing Degree' for *Neutral* expressions ( $t(78) = 3.70$ ,  $p = 0.003$  FDR corrected,  $Cohen's d = 1.37$ ), and significantly lower 'Influencing Degree' and 'Influenced Degree' for *Happy* expressions ( $t(78) = 3.12$ ,  $p = 0.005$  FDR corrected,  $Cohen's d = 1.23$ , and  $t(78) = 5.77$ ,  $p = 1.82E - 06$  FDR corrected,  $Cohen's d = 2.13$ , respectively). Specific significant directed influences are shown in Figure 1. In terms of specific, directed influence, *Sad* emotion-node significantly influenced *Fear*, *Angry*, and *Surprise* ( $p < 0.05$ , FDR-corrected), to a greater extent among the MA group compared to HC (Figure 1a). On the other hand, *Neutral* and *Happy* emotion-nodes both influenced each other and *Sad* to a greater extent among the HC group compared to MA ( $p < 0.05$ , FDR-corrected) (Figure 1a).

Our network analyses indicate that, relative to HC, MA patients show reduced positive (neutral and happy) expressions, consistent with blunted emotional expression, a transdiagnos-

tic feature linked to anhedonia and constrained affect and may serve as a digital biomarker for diagnosis and prediction in real-world settings

## References

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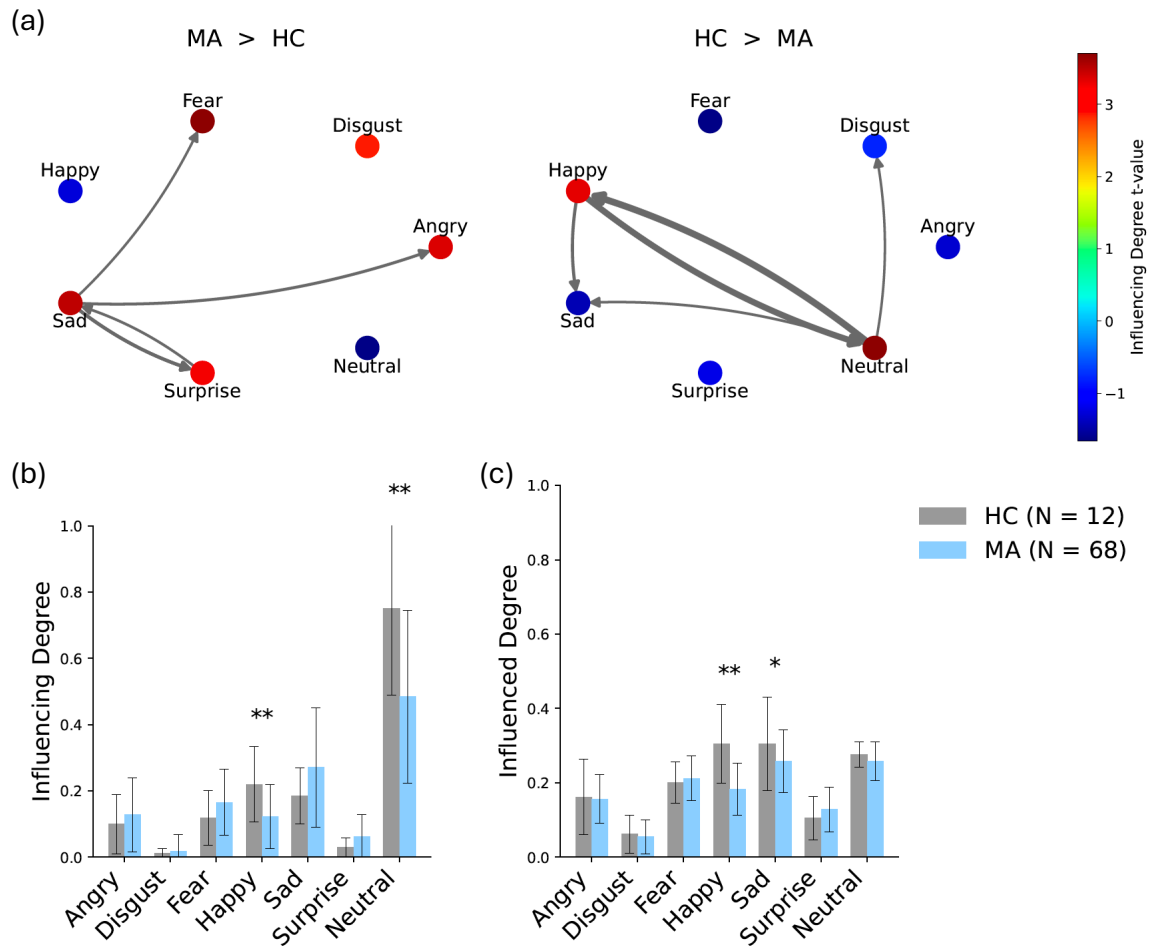


Figure 1: **Dependency network analysis of facial expression dynamics over time.** a) A network illustration of the ‘influencing degree’ of emotional facial expressions in the MA group against HC. Each region is color-coded according to the t-statistic value from the t-test between the ‘Influencing Degree’ of the two groups. All pair-wise ROIs with connections, significant at the  $p < 0.05$  level, are plotted as edges. Each edge is color-coded according to the t-test sign as light or dark gray with the arrows representing the direction of influence. b) The nodes’ averaged ‘Influencing Degree’ and c) ‘Influenced Degree’. \* $p < 0.05$ , \*\* $p < 0.05$  FDR-corrected.