

Disentangling large-scale brain dynamics and their links to behavior during the emotional face matching task

Corresponding Author: Dr Cole Korponay

This file contains all reviewer reports in order by version, followed by all author rebuttals in order by version.

Version 0:

Reviewer comments:

Reviewer #1

(Remarks to the Author)

The authors of the study used a powerful method - tensor independent component analysis – to investigate brain dynamics during emotional face matching task in the HCP sample. Such an approach represents an interesting research avenue thanks to the combination of a modern analytical tool and a large dataset of task-fMRI. Notably, the authors used the large sample size to split subjects into two groups for reproducibility assessment. As key findings, the authors describe 10 brain networks activated during the task. They delve into the spatial organization of these networks as well as their temporal profiles. Finally, the authors also describe inter-individual differences and link them to latent psychobehavioral phenotypes. The study is well-written and the methodology is timely and sound. However, I have several comments regarding the organization of the manuscript as well as some unexplained methodological steps.

Major:

The authors present 10 brain networks as the main result of the tICA analysis. However, it is not clear how these 10 were selected. The authors first ran tICA at varying model orders between $d = 5$ and $d = 25$ and identified an optimal model order to be $d = 20$. It is not clear based on which criteria this model order was selected.

In the next step, the time courses, power spectra and spatial maps of these 20 components were examined to identify those most likely to reflect task-related brain activity. Again, it is not clear how exactly were these components examined and what were the criteria for inclusion. I understand that one of the criteria was “spatial resemblance” of large-scale brain networks. Why? Which ones? What were the criteria for significant resemblance?

After the identification of 10 “significant” brain maps, the authors discuss the contribution of individual regions. Again, was some thresholding applied to select contributing regions? The authors state that 74% of cortex was recruited as a node in one or more of the large-scale networks during the EFMT. Does it mean the ICA weights in these 10 networks were exactly 0 for the remaining 26% of the cortex?

The discussion section currently contains 8 references. Most of the Discussion is a mere recapitulation of the Results section. The authors should better anchor the current study within the relevant literature. More focus should be on the comparison of obtained results with prior research.

Figure 3 does not do a good job of conveying the message. The choice of circular bar plots is rather unfortunate here. The majority of the figure is occupied by network names, where the name of each of the 17 networks is repeated 20 times. The magnitude of the similarity between the two networks is absolutely unreadable. Please consider a different type of plot that would be more suitable. In addition, what does the number “1” inside each plot represent?

The plots in Figure 3 display spatial overlap between the positive (red) and negative (blue) components of each EFMT-recruited network (Group 1 LR) and each of 17 canonical large-scale networks defined in the Gordon et al. parcellation. What do the authors mean by positive and negative components? Does it correspond to negative and positive ICA brain weights? If so, why are these analyzed separately?

The organization of the Results section is slightly confusing. The authors provide general results for each of their analytical steps and only then dive again into the results of each analytical step in a network-by-network fashion (i.e. Network Profiling

in Depth section). The authors could consider removing this section by moving the results to their respective previous Result section (i.e., description of temporal profile to FMT-Recruited Networks Have Diverse Temporal Dynamics section).

I read this study as a study of brain activity during EFMT rather than a study of brain pathophysiology. However, the first paragraph of the Introduction ends with the statement: “comprehensive review of such studies shows only sparse associations between these EFMT-based neurobiological phenotypes and psychopathology, despite the examination of multiple disorders and numerous variations of the task.” The end of the first paragraph should rather point to the main aim of the present manuscript.

Figure 1: The authors state that the analyses were conducted post-hoc on the subjects' loadings identified by tICA. Wasn't the hierarchical clustering applied to network time profiles?

Abstract: The claim that the networks more strongly explained individual differences in task performance compared contrast-based activation maps is hard to assess as no formal comparison was presented in the study

Minor:

The introduction is quite long. Space can be saved by reducing the text devoted to precision psychiatry which is not directly related to this study.

Line 253: Three participants were removed from the analysis due to low overall EFMT accuracy. When were these participants removed? If only at this stage, please explain why not previously.

Line 240: The arbitrary sign flips between modes in the tensor ICA can be described in Methods rather than in Results. The authors could manually align modes in their analytical pipeline, which would lead to easier understanding of the Result section since the discussion of technical details would be omitted.

Line 238: Please remove the reference to the visual elements (i.e., Dashed lines of the time courses) in the figures as the Results should be readable without access to the figures.

Line 388: What is a trending relationship?

Line 158: How were the networks from the two scanning sessions matched?

Abstract: The abstract could contain the name of the used method.

Reviewer #2

(Remarks to the Author)

This study utilized tensor independent component analysis (tICA) to identify 10 large-scale brain networks with distinct temporal dynamics during an emotional face matching task (EFMT). The activity of these networks was primarily associated with individual differences in cognitive abilities, with only weak correlations to emotional traits. This suggests that the task may predominantly reflect cognitive processing rather than emotional processing. Overall, this paper demonstrates a degree of innovation by employing an advanced analytical method to explore the complex brain dynamics during the performance of EFMT and their relationships with behavior, cognition, and mental health. However, the manuscript still has several areas that require improvement. The main concerns and suggestions for revision are as follows:

1. The primary issue is the traditional idea or approach used to validate the superiority of the new method over the old one. This approach overlooks the possibility that the two methods may be suited to address different scientific questions, leading to alternative explanations for the findings derived from the new method, and potentially obscuring its most valuable contributions. First, because the contrast data and computational methods differ, the results obtained with the new method cannot directly refute previous findings using traditional methods. For instance, the study did not reliably detect activity in the amygdala and subgenual cingulate cortex, possibly due to the inherently weak signals in these regions which are hard to capture in whole-brain analyses. Therefore, conclusions regarding the EFMT's lack of emotional processing should be made with caution. Second, the traditional approach typically subtracts the strong cognitive signals to isolate emotion-induced activity, while the new method incorporates all condition information. This means that signals related to robust cognitive processes—which the traditional method might treat as noise—are retained in the tICA approach. Finally, while traditional subtraction methods (comparing experimental and control groups) are primarily used for localizing brain regions and testing a priori hypotheses (and can be useful for clinical targeting), the bottom-up, data-driven tICA focuses on exploring whole-brain information, emphasizing dynamic and individual differences. This approach is better suited for clinical diagnostic discrimination. Recommendation: The authors should further explore the data from the perspective of dynamic characteristics of brain networks and individualized prediction, rather than merely performing a simple correlation analysis between brain networks and cognitive-emotional functions. It is strongly recommended to employ complex algorithms, such as machine learning or computational modeling, to investigate which neural features across different temporal dynamics in various brain networks can accurately predict or distinguish emotional effects or other dependent variables in the EFMT. This would truly capitalize on the advantages of innovative methods like tICA for individualized prediction or diagnostic discrimination analysis.

2. The study finds that EFMT-related brain network activity is stably correlated with cognitive function, but it does not show significant associations with internalizing/negative emotions or happiness/positive emotions. Using this result to claim that the EFMT is not an emotion-related task requires further evidence. This lack of association might be due to the relatively low

emotional variability in the healthy, young HCP sample, or because the emotions elicited by the EFMT (anger, fear) do not capture the broader dimensions of negative or positive affect.

Recommendation: The authors should consider incorporating more refined behavioral indices, such as reaction time and accuracy differences for various emotional face types (anger vs. fear), or collect post-task subjective emotional experience reports. Additionally, grouping participants by their emotional states or traits and separately analyzing the neural responses to anger and fear stimuli could provide deeper insights into the relationship between neural activity, emotional processing, and cognitive function.

3. It is possible that the EFMT involves an interplay of both cognitive and emotional processes rather than being a purely cognitive task that poorly reflects emotional processing, as suggested by the current interpretation. Recommendation: The authors could leverage another major advantage of their new method to clarify this possibility by examining the neural activity changes and interaction mechanisms between emotional and cognitive processing throughout the EFMT from a whole-brain perspective. They should also consider that cognitive and emotional processing might operate at different temporal scales, which could explain why emotional processing signals are not as consistently detected.

4. The manuscript's discussion on not finding activity in the amygdala or anterior cingulate cortex could benefit from additional references to similar findings in previous studies (e.g., Feng et al., 2018, *NeuroImage*, 173, 258–274; Chen et al., 2018, *Brain Structure and Function*, 223, 3813–3840).

5. The study mentions that the tICA model order was set to $d = 20$, citing previous research.

Recommendation: The authors should clearly explain the method, rationale, and basis for choosing this model order. Please provide a brief explanation on whether the choice of $d = 20$ was based on component interpretability, correspondence with known brain networks, or some optimization criterion.

6. The clarity of the result presentation could be enhanced, as some legends and labels in the figures require further optimization. For example, ensure that the meaning of the color red is consistent across all figures (e.g., Figure 4 vs. other figures), and consider adding clearer labels to the radar chart in Figure 3. The authors should carefully review all figure labels, legends, and color codings to ensure that readers can easily understand and compare the results across different networks.

Version 1:

Reviewer comments:

Reviewer #1

(Remarks to the Author)

I would like to congratulate the authors on a well-executed revision. The manuscript is notably improved, and the responses to the reviewers' comments are thoughtful and comprehensive. I also thank the authors for the clarification regarding the model order selection process. That said, I suggest explicitly stating in the Methods section that the authors visually inspected the time course, power spectrum, and spatial map of each component to identify those most likely to reflect task-related brain activity—if this was indeed the case. This addition would help readers better understand the criteria behind the selection of $d = 20$ and the identification of the final task-relevant components.

Finally, I recommend briefly acknowledging the subjectivity inherent in this visual selection process in the Limitations section, as this has important implications for reproducibility and interpretation.

Reviewer #2

(Remarks to the Author)

The authors of this manuscript have answered my questions.

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Reviewer #1 (Remarks to the Author):

The authors of the study used a powerful method - tensor independent component analysis – to investigate brain dynamics during emotional face matching task in the HCP sample. Such an approach represents an interesting research avenue thanks to the combination of a modern analytical tool and a large dataset of task-fMRI. Notably, the authors used the large sample size to split subjects into two groups for reproducibility assessment. As key findings, the authors describe 10 brain networks activated during the task. They delve into the spatial organization of these networks as well as their temporal profiles. Finally, the authors also describe inter-individual differences and link them to latent psychobehavioral phenotypes. The study is well-written and the methodology is timely and sound. However, I have several comments regarding the organization of the manuscript as well as some unexplained methodological steps.

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The authors present 10 brain networks as the main result of the tICA analysis. However, it is not clear how these 10 were selected. The authors first ran tICA at varying model orders between $d = 5$ and $d = 25$ and identified an optimal model order to be $d = 20$. It is not clear based on which criteria this model order was selected.

We thank the reviewer for bringing this lack of clarity to our attention. We have now restructured and added more detail to this section to help clarify the model order selection process, including explanation of how model orders were identified as being too high or too low (pg. 26-27):

“Because the goal was to investigate large-scale canonical brain networks, the model order of the group ICA needed to be relatively low to result in a coarse spatial scale parcellation of the brain into networks. Model orders that are too low fail to fully disaggregate known canonical brain networks, while model orders that are too high produce finer spatial scale parcellations that reflect excessive segregation of known large-scale networks into individual or bilateral brain areas rather than networks. Therefore, we tested a range of model orders from 5 to 25 to identify which decomposition parcellated the brain into canonical network patterns while effectively unmixing any noise/artifacts into separate components. For each model order, we examined the time course, power spectrum and spatial map of each component to identify those most likely to reflect task-related brain activity (e.g., components with spatial patterns resembling large-scale brain networks and with temporal courses reflecting one or more aspects of the task time course). Ultimately, we identified $d = 20$ to be the optimal model order in our data that best achieved the balance between disaggregating large-scale canonical networks and not producing excessive segregation; this model order is also in line with previous reports examining the correspondence between task activation networks and canonical resting state brain networks^{48,49}.

In the next step, the time courses, power spectra and spatial maps of these 20 components were examined to identify those most likely to reflect task-related brain activity. Again, it is not clear how exactly were these components examined and what were the criteria for inclusion. I understand that one of the criteria was “spatial resemblance” of large-scale brain networks. Why? Which ones? What were the criteria for significant resemblance?

We thank the reviewer for bringing this lack of clarity to our attention. Components were evaluated not only by their spatial map (i.e., does it resemble one or more canonical large-scale networks and was overlap with the Gordon network parcellation confirmed with the NCT toolbox), but also by their power spectrum (are there peaks outside the low-frequency range that correspond to the frequencies of the task stimulation?), and time course (does it track with one or more components of the task time course?). Moreover, this was complemented by a process of elimination of components whose properties resembled physiological or movement-related noise sources, in line with best practices for hand-identification of ICA-derived noise components (Griffanti et al., NeuroImage 2017). We have added this information to the section on page 27.

After the identification of 10 “significant” brain maps, the authors discuss the contribution of individual regions. Again, was some thresholding applied to select contributing regions? The authors state that 74% of cortex was recruited as a node in one or more of the large-scale networks during the EFMT. Does it mean the ICA weights in these 10 networks were exactly 0 for the remaining 26% of the cortex?

For this analysis, each of the 10 components was thresholded using a Gaussian-Gamma mixture model (which is suitable for maximally non-Gaussian ICA spatial maps) with $p=0.5$. Using this threshold, equal weight is given to identifying a voxel as being in the signal vs being in the noise and thus represents a somewhat liberal threshold. As such, this does not mean ICA weights were exactly 0 in the remaining 26% of cortex. Rather, it indicates that even with the threshold $p=0.5$ (which is the default in FSL MELODIC), the remaining 26% of cortex did not have a statistically significant ICA weight across any of the 10 components. We have added more details on this thresholding procedure on page 7.

The discussion section currently contains 8 references. Most of the Discussion is a mere recapitulation of the Results section. The authors should better anchor the current study within the relevant literature. More focus should be on the comparison of obtained results with prior research.

We thank the Reviewer for this recommendation. We have now removed the “Network Profiling In-Depth” section from the Results to accommodate a more critical and less redundant treatment of this content in the Discussion section that also engages more comprehensively with prior literature.

Figure 3 does not do a good job of conveying the message. The choice of circular bar plots is rather unfortunate here. The majority of the figure is occupied by network names, where the name of each of the 17 networks is repeated 20 times. The magnitude of the similarity between the two networks is absolutely unreadable. Please consider a different type of plot that would be more suitable. In addition, what does the number “1” inside each plot represent?

We agree with the Reviewer (this figure was generated by the newly developed Network Correspondence Toolbox). We have manually created a new figure (using a heatmap format) from the toolbox’s output that we anticipate readers will find simpler and more readable.

The plots in Figure 3 display spatial overlap between the positive (red) and negative (blue) components of each EFMT-recruited network (Group 1 LR) and each of 17 canonical large-scale networks defined in the Gordon et al. parcellation. What do the authors mean by positive and negative components? Does it correspond to negative and positive ICA brain weights? If so, why are these analyzed separately?

Correct, these refer to the suprathreshold positive and suprathreshold negative ICA weight maps for each of the 10 components. These were analyzed separately because we observed visually that the positive and negative parts of each component typically represented distinct networks (e.g., for Component 5, the positive part involved the default mode network, whereas the negative part involved the lateral visual network). More generally, the tensor ICA can identify states comprised of anti-correlated network patterns that have been reported by others during both resting state and task performance (see for example Li et al. 2021 (Neuroimage 227:117680)) as an important characteristic of brain organization. As such, the positive and negative parts were analyzed separately to determine their distinct network makeups. We have now clarified this in the text.

The organization of the Results section is slightly confusing. The authors provide general results for each of their analytical steps and only then dive again into the results of each analytical step in a network-by-network fashion (i.e. Network Profiling in Depth section). The authors could consider removing this section by moving the results to their respective previous Result section (i.e., description of temporal profile to FMT-Recruited Networks Have Diverse Temporal Dynamics section).

We thank the Reviewer for this recommendation. We have now distributed this content to respective Results sections, with expanded commentary in the Discussion section.

I read this study as a study of brain activity during EFMT rather than a study of brain pathophysiology. However, the first paragraph of the Introduction ends with the statement: “comprehensive review of such studies shows only sparse associations between these EFMT-based neurobiological phenotypes and psychopathology, despite the examination of multiple disorders and numerous variations of the task.” The end of the first paragraph should rather point to the main aim of the present manuscript.

We have now revised the end of this paragraph to better reflect the study aims.

Figure 1: The authors state that the analyses were conducted post-hoc on the subjects' loadings identified by tICA. Wasn't the hierarchical clustering applied to network time profiles?

We thank the reviewer for catching this error. Yes, the hierarchical clustering was applied to the correlation matrix from the network time courses, not to the subject loadings. We have now corrected this in the text (Figure 1 caption).

Abstract: The claim that the networks more strongly explained individual differences in

task performance compared contrast-based activation maps is hard to assess as no formal comparison was presented in the study

We have now added more details to the “Comparisons to Amygdala Connectivity and Activation during the EFMT” Results sections to fortify this claim, including that none of the links between task performance and contrast-based activation or connectivity surpassed corrected statistical significance (while those from the tICA network-based analysis did), and that the effect sizes of these associations were smaller than those from the tICA network-based analysis.

Minor:

The introduction is quite long. Space can be saved by reducing the text devoted to precision psychiatry which is not directly related to this study.

We have now streamlined the introduction and removed text (e.g., about precision psychiatry) that is not directly relevant to the study aims.

Line 253: Three participants were removed from the analysis due to low overall EFMT accuracy. When were these participants removed? If only at this stage, please explain why not previously.

These subjects still had high-quality and non-outlier brain imaging data and so were included in the tICA analysis to derive the task-relevant network maps. These subjects were only excluded from the brain-behavior analyses given that their behavioral scores were outliers.

Line 240: The arbitrary sign flips between modes in the tensor ICA can be described in Methods rather than in Results. The authors could manually align modes in their analytical pipeline, which would lead to easier understanding of the Result section since the discussion of technical details would be omitted.

Upon further investigation of the networks being referenced here (network 8 in Groups 1 and 2), rather than being sign-flipped manifestations of the same network state in both groups, the data better indicate that these are different networks. That is, while they both contain a positive component in the motor network, only one contains a negative component in the visual network. These networks may therefore represent different dynamic states of motor activity during the task. We have adjusted the relevant figures and results to reflect this change in interpretation of this network.

Line 238: Please remove the reference to the visual elements (i.e., Dashed lines of the time courses) in the figures as the Results should be readable without access to the figures.

We have now removed this text.

Line 388: What is a trending relationship?

The section referencing this term has been removed.

Line 158: How were the networks from the two scanning sessions matched?

Networks were matched by computing spatial map correlations and time course correlations across all networks and identifying those with the highest spatiotemporal correspondence. We have now clarified this in the text on page 5.

Abstract: The abstract could contain the name of the used method.

We have now included the name of the method in the abstract.

Reviewer #2 (Remarks to the Author):

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1. The primary issue is the traditional idea or approach used to validate the superiority of the new method over the old one. This approach overlooks the possibility that the two methods may be suited to address different scientific questions, leading to alternative explanations for the findings derived from the new method, and potentially obscuring its most valuable contributions. First, because the contrast data and computational methods differ, the results obtained with the new method cannot directly refute previous findings using traditional methods. For instance, the study did not reliably detect activity in the amygdala and subgenual cingulate cortex, possibly due to the inherently weak signals in these regions which are hard to capture in whole-brain analyses. Therefore, conclusions regarding the EFMT's lack of emotional processing should be made with caution. Second, the traditional approach typically subtracts the strong cognitive signals to isolate emotion-induced activity, while the new method incorporates all condition information. This means that signals related to robust cognitive processes—which the traditional method might treat as noise—are retained in the tICA approach. Finally, while traditional subtraction methods (comparing experimental and control groups) are primarily used for localizing brain regions and testing a priori hypotheses (and can be useful for clinical targeting), the bottom-up, data-driven tICA focuses on exploring whole-brain information, emphasizing dynamic and individual differences. This approach is better suited for clinical diagnostic discrimination. Recommendation: The authors should further explore the data from the perspective of dynamic characteristics of brain networks and individualized prediction, rather than merely performing a simple correlation analysis between brain networks and

cognitive-emotional functions. It is strongly recommended to employ complex algorithms, such as machine learning or computational modeling, to investigate which neural features across different temporal dynamics in various brain networks can accurately predict or distinguish emotional effects or other dependent variables in the EFMT. This would truly capitalize on the advantages of innovative methods like tICA for individualized prediction or diagnostic discrimination analysis.

We thank the Reviewer for this nuanced perspective on the differences between and respective values of traditional contrast-based approaches and the data-driven tICA approach used in this study. We do want to emphasize that it is not our intention to suggest that the EFMT does not draw on emotion-related processing in the brain or that it refutes the findings of contrast-based analyses. Indeed, consistent with contrast-based analyses, 6 of our 10 identified networks recruit the amygdala, as detailed in the “EFMT Reproducibly Recruits 10 Large-Scale Networks” section of the Results. Our claims are that 1) the current approach extends, rather than refutes, findings from contrast-based analyses by being able to detect more nuanced task-relevant brain processes, and 2) that it is specifically individual differences in brain responsivity to the task that are predominantly related to individual differences in cognition, not that the task itself does not rely on emotional processing. In this revision we have clarified this at relevant points in the texts.

Nonetheless, we have now augmented our Discussion to consider the perspectives raised by the Reviewer (e.g., the possible influence of signal drop-out) in the context of our findings. Moreover, we thank the Reviewer for recommending these additional analyses to better leverage the advantages of the tICA approach for individualized prediction. We have now included several new machine learning analyses, accompanied by SHapley Additive exPlanations (SHAP), to ascertain the ability of brain network dynamics during the EFMT to make individualized predictions of cognitive-emotional functions and to quantify the feature importance of each network/behavioral measure.

2. The study finds that EFMT-related brain network activity is stably correlated with cognitive function, but it does not show significant associations with internalizing/negative emotions or happiness/positive emotions. Using this result to claim that the EFMT is not an emotion-related task requires further evidence. This lack of association might be due to the relatively low emotional variability in the healthy, young HCP sample, or because the emotions elicited by the EFMT (anger, fear) do not capture the broader dimensions of negative or positive affect.

Recommendation: The authors should consider incorporating more refined behavioral indices, such as reaction time and accuracy differences for various emotional face types (anger vs. fear), or collect post-task subjective emotional experience reports. Additionally, grouping participants by their emotional states or traits and separately analyzing the neural responses to anger and fear stimuli could provide deeper insights into the relationship between neural activity, emotional processing, and cognitive function.

We thank the Reviewer for raising these considerations. As noted in the manuscript, our use of a largely healthy sample may reduce our ability to observe associations between network loadings and variability in affect measures. Nevertheless, in a separate manuscript in preparation, we find and report that in HCP-YA, negative affect/internalizing and positive affect/well-being actually

have higher variability across subjects than cognition scores. As such, this can't explain the weaker brain network associations with emotions relative to cognition. Still, we undertook the Reviewer's recommended action of examining more fine-grained behavioral indices of emotion. To do so, we set up a machine learning analysis with the 87 neurocognition/neuropsychiatric assessments from the HCP as features to predict subject loadings on the EFMT brain networks, and then used SHAP to quantify feature importance for each of the 10 networks. This allowed us to evaluate whether certain subdomains of negative affect/internalizing and EFMT task performance (e.g., accuracy on emotional face trials, accuracy on shapes trials, etc.) might be more closely tied to the brain networks than the aggregate negative affect/internalizing measure. Consistent with our original interpretation, these analyses showed the overwhelming link between EFMT brain networks and cognition-related measurements. Few emotion-related measures were amongst the top ten most important predictive features across all networks, but we have highlighted those that were. We note that data on reaction time and accuracy for specific emotion types (i.e., angry faces versus fearful face) are not available in the HCP-YA dataset, nor are post-task subjective emotional experience reports.

3. It is possible that the EFMT involves an interplay of both cognitive and emotional processes rather than being a purely cognitive task that poorly reflects emotional processing, as suggested by the current interpretation. Recommendation: The authors could leverage another major advantage of their new method to clarify this possibility by examining the neural activity changes and interaction mechanisms between emotional and cognitive processing throughout the EFMT from a whole-brain perspective. They should also consider that cognitive and emotional processing might operate at different temporal scales, which could explain why emotional processing signals are not as consistently detected.

We agree with the Reviewer that the EFMT involves both cognitive and emotional processes. As discussed above, we did not intend to suggest that the EFMT does not draw on emotion-related processing in the brain and have clarified this in the relevant areas of the text. We also agree with the Reviewer that cognitive and emotional processing may operate at different temporal scales. However, one of the advantages of tICA is that it is highly sensitive to and captures processes with distinct temporal dynamics and trajectories, and thus is likely capturing all of the relevant large-scale network-level processes operating during the task (6 of the 10 networks recruited the amygdala, highlighting the interplay between cognition and emotion).

4. The manuscript's discussion on not finding activity in the amygdala or anterior cingulate cortex could benefit from additional references to similar findings in previous studies (e.g., Feng et al., 2018, *NeuroImage*, 173, 258–274; Chen et al., 2018, *Brain Structure and Function*, 223, 3813–3840).

While we did find amygdala activity (6 of the 10 networks included the amygdala as a node), we have now included a point incorporating these references in relation to the absence of cingulate findings in our results (Discussion, page 22).

5. The study mentions that the tICA model order was set to $d = 20$, citing previous research.

Recommendation: The authors should clearly explain the method, rationale, and basis for choosing this model order. Please provide a brief explanation on whether the choice of $d = 20$ was based on component interpretability, correspondence with known brain networks, or some optimization criterion.

We thank the Reviewer for calling for greater clarity on this issue. We have now restructured and added more detail to this section to help clarify the model order selection process, including explanation of how model orders were identified as being too high or too low (pg. 29).

6. The clarity of the result presentation could be enhanced, as some legends and labels in the figures require further optimization. For example, ensure that the meaning of the color red is consistent across all figures (e.g., Figure 4 vs. other figures), and consider adding clearer labels to the radar chart in Figure 3. The authors should carefully review all figure labels, legends, and color codings to ensure that readers can easily understand and compare the results across different networks.

We thank the Reviewer for highlighting this. We have now overhauled Figure 3 to improve its interpretability and adjusted color schemes where feasible to improve consistency across figures.

RE: Manuscript COMMSBIO-25-0118A

Dear Editors,

We are grateful for your in-principle acceptance of our manuscript, “Concurrent large-scale brain dynamics during the emotional face matching task and their links to cognition and affect” at *Communications Biology*.

Both reviewers provided thoughtful and comprehensive guidance that improved the manuscript. We are pleased to have addressed and incorporated the remaining feedback from Reviewer 1 (these additions are highlighted in red in the marked up revised manuscript):

I suggest explicitly stating in the Methods section that the authors visually inspected the time course, power spectrum, and spatial map of each component to identify those most likely to reflect task-related brain activity—if this was indeed the case.

We have added the word “visual” to this section to explicitly convey that the inspection was visual.

Finally, I recommend briefly acknowledging the subjectivity inherent in this visual selection process in the Limitations section, as this has important implications for reproducibility and interpretation.

We have added the following sentence to the Limitations section in the Discussion: “First, while tICA is a purely data-driven technique, its use involves some subjective decision points as described in the Methods, including the choice of model order and the classification of noise and signal components.”

We look forward to the publication of our manuscript in *Communications Biology*!

Sincerely,

Cole Korponay, Julia E. Cohen-Gilbert, You Cheng, Poornima Kumar, Nathaniel G. Harnett, Adrian A. Medina, Brent P. Forester, Kerry J. Ressler, Jure Demsar, Blaise B. Frederick, Christian F. Beckmann, David G. Harper, Lisa D. Nickerson