**NARPS – report of analysis and results**

**General information**

**Team ID**:

**A link to the private NeuroVault collection**:

**Results**

The hypotheses you were requested to test are:

Parametric effect of gain:

1. Positive effect in ventromedial PFC - for the equal indifference group
2. Positive effect in ventromedial PFC - for the equal range group
3. Positive effect in ventral striatum - for the equal indifference group
4. Positive effect in ventral striatum - for the equal range group

Parametric effect of loss:

1. Negative effect in VMPFC - for the equal indifference group
2. Negative effect in VMPFC - for the equal range group
3. Positive effect in amygdala - for the equal indifference group
4. Positive effect in amygdala - for the equal range group

Equal range vs. equal indifference:

1. Greater response to losses in amygdala for equal range condition vs. equal indifference condition.

For each hypothesis, please report your binary decision (confirmed- yes/no), how much you are confident about this result and how similar you think your result is to the results of the other analysis teams:

|  |  |  |  |
| --- | --- | --- | --- |
| **Hypothesis** | **Confirmed?** | **How confident are you about this result?** | **How similar do you think your result is to the other analysis teams?** |
| 1 |  |  |  |
| 2 |  |  |  |
| 3 |  |  |  |
| 4 |  |  |  |
| 5 |  |  |  |
| 6 |  |  |  |
| 7 |  |  |  |
| 8 |  |  |  |
| 9 |  |  |  |

**Anything else you would like to add regarding the results?**

The positive parametric effect of gains on vmPFC was observed before cluster mass correction in the EI group. The same was true for the ER group, but in ventral striatum.

**Analysis: General**

***Please report your analysis procedures and tools as thoroughly as possible.***

**Did you pre-register your analysis?**

**If so- please provide us with a link to the pre-registration form:**

**How did you define each of the pre-hypothesized regions (vmPFC, ventral striatum and amygdala) in order to decide whether the predicted effects were found in this region or not?**

Write your answer here

**Exclusions**

How many participants were included in the final analysis? 102

Which participants were excluded (provide the ID, e.g. sub-150) and why?

sub-048: missing data

sub-056: accept/reject responses were not in keeping with a positive weight on gains and a negative weight on losses (as determined by a logistic regression)

sub-016, sub-030, sub-088, sub-100, sub-116: exceeded movement thresholds (timepoints with framewise displacement exceeded 5%)

**Analysis: Pre-processing**

If you used the data pre-processed with fmriprep v1.1.4 that we provided, please indicate this in the relevant sections, but still provide full description of any pre-processing step you made to the fmripreped data.

Questions are based on COBIDAS report (http://www.humanbrainmapping.org/files/2016/COBIDASreport.pdf).

**Did you use the data pre-processed with fmriprep v1.1.4 that we provided?**

**Order of pre-processing steps:**

Please specify the order in which the pre-processing steps were performed

**We used fmriprep data, followed by smoothing of each individual's 4D functional volume with a 3mm gaussian kernel.**

**Software/s used**

For each software used, be sure to include version and revision number. If possible, include URL and Research Resource Identifier for each software used.

SPM: Version and other details

FSL: 6.0

AFNI: AFNI\_2011\_12\_21\_1014 (Apr 15 2015) [64-bit]

BrainVoyager: Version and other details

Other, please specify all: R 3.5.1 for behavioral analysis

**Brain extraction**

If performed, report:

* Name of software/method (e.g., BET, recon-all in FreeSurfer, etc).
* Parameter choices (e.g. BET’s fractional intensity threshold).

Any manual editing applied to the brain masks.

Describe brain extraction here

**Segmentation**

For structural images, method used to extract gray, white, CSF and other tissue classes.

Describe segmentation here

**Slice time correction**

If performed, report:

* Name of software/method.
* Whether performed after or before motion correction.
* Reference slice.

Interpolation type and order (e.g., 3rd order spline or sinc).

Describe slice time correction here

**Motion correction**

Report:

* Name of software/method.
* Use of non-rigid registration, and if so the type of transformation.
* Use of motion susceptibility correction (fieldmap-based unwarping), as well as the particular software/method.
* Reference scan (e.g. 1st scan or middle scan).
* Image similarity metric (e.g. normalized correlation, mutual information, etc).
* Interpolation type (e.g., spline, sinc), and whether image transformations are combined to allow a single interpolation.
* Use of any slice-to-volume registration methods, or integrated with slice
* time correction.

Describe motion correction here

**Gradient distortion correction**

If not already described as part of motion susceptibility correction.

Describe gradient distortion correction here

**Function to ­structure (intra-subject) coregistration**

Report:

* Name of software/method.
* Type of transformation (rigid, nonlinear); if nonlinear, type of transformation
* Cost function (e.g., correlation ratio, mutual information, boundary-based registration, etc).
* Interpolation method (e.g., spline, linear).

Note this step might not be necessary if direct T2\* to a functional template registration is used.

Describe function to structure (intra-subject) coregistration here

**Distortion correction**

Use of any distortion correction due to field or gradient nonlinearity.

Describe distortion correction here

**Intersubject registration**

Report:

* Name of software/method (e.g., FSL flirt followed by fnirt, FreeSurfer, Caret, Workbench, etc)
* Whether volume and/or surface based registration is used (if not already clearly implied).
* Image types registered (e.g. T2\* or T1).
* Any preprocessing to images; e.g. for T1, bias field correction, or segmentation of gray matter; for T2\*, single image (specify image) or mean image.
* Template space (e.g., MNI, Talairach, fsaverage, FS\_LR), modality (e.g., T1, T2\*), resolution (e.g., 2mm, fsaverage5, 32k\_FS\_LR), and the specific name of template image used; note the domain of the template if not whole brain, i.e. cortical surface only, cerebellum only, CIFTI ‘grayordinates’ (cortical surface vertices + subcortical gray matter voxels), etc.
* Additional template transformation for reporting; e.g., if using a template in MNI space, but reporting coordinates in Talairach, clearly note and report method used (e.g., Brett’s mni2tal, Lancaster’s icbm\_spm2tal).
* Choice of warp (rigid, nonlinear); if nonlinear, transformation type (e.g., B­splines, stationary velocity field, momentum, non­parametric displacement field); if a parametric transformation is used, report resolution, e.g., 10x10x10 spline control points.
* Use of regularization, and the parameter(s) used to set degree of regularization.

Describe intersubject registration here

**Intensity correction**

Bias field corrections for structural MRI, but also correction of odd versus even slice intensity differences attributable to interleaved EPI acquisition without gaps.

Describe intensity correction here

**Intensity normalization**

Scan-by-scan or run-wide scaling of image intensities before statistical modelling. E.g. SPM scales each run such that the mean image will have mean intracerebral intensity of 100; FSL scales each run such that the mean image will have an intracerebral mode of 10,000.

Describe intensity normalization here

**Artifact and structured noise removal**

Use of physiological noise correction method.

Report:

* Name of software/method used (e.g. CompCor, ICA-FIX, ICA-AROMA, etc.).
* If using a nuisance regression method, specify regressors used; for each type, include key details, as follows:
  + Motion parameters.
    - Expansion basis and order (e.g. 1st temporal derivatives; Volterra kernel expansion)
  + Tissue signals.
    - Tissue type (e.g., whole brain, gray matter, white matter, ventricles).
    - Tissue definition (e.g., a priori seed, automatic segmentation, spatial regression).
    - Signal definition (e.g., mean of voxels, first singular vector,

etc.).

* + Physiological signals
    - e.g., heart rate variability, respiration.
    - Modeling choices (e.g. RETROICOR, cardiac and/or respiratory response functions) and number of computed regressors.

Describe artifact and structured noise removal here

**Volume censoring**

Remediation of problem scans, also known as “scrubbing” or “de-spiking”.

Report:

* Name of software/method.
* Criteria (e.g., frame-by-frame displacement threshold, percentage BOLD change).
* Use of censoring or interpolation; if interpolation, method used (e.g., spline, spectral estimation).

**Spatial smoothing**

If this preprocessing step is performed, report:

* Name of software/method.
* Size and type of smoothing kernel.
* Filtering approach, e.g., fixed kernel or iterative smoothing until fixed FWHM.
* Space in which smoothing is performed (i.e. native volume, native surface, MNI volume, template surface).

We performed spatial smoothing on each subject's MNI152-aligned data using a Gaussian kernel (FWHM of 3mm) using FSL (FSLmaths).

**Anything else you want to add regarding pre-processing?**

**Analysis: Statistical modeling and inference**

Questions are based on COBIDAS report (<http://www.humanbrainmapping.org/files/2016/COBIDASreport.pdf)>.

**Dependent variable: Data submitted to statistical modeling**

Report the number of time points, number of subjects; specify exclusions of time points / subjects, if not already specified.

Across the 4 runs, all 256 trials were modeled for 102 subjects. We censored volumes based on three criteria: (1) a framewise displacement greater than 5 mm, (2) the first 3 volumes of each run to remedy early spiking in a considerable number of voxels that was unrelated to experimental manipulations, and (3) volumes from trials with no response. For (1) and (2), we passed a list of affected volumes to the -CENSOR flag in AFNI 3dDevconvolve for each subject's GLM. For (3), volumes were censored by regressing them out through a single predictor with 1 and 0s for each subject's GLM.

**Dependent variable: Spatial region modeled**

If not “Full brain”, give a specification of an anatomically or functionally defined mask. Please note that your final reported decisions regarding the hypotheses should be based on whole-brain corrected results.

Full brain

**Independent variables - first level**

For first level fMRI, specify:

* Event­related design predictors.
  + Modeled duration, if other than zero.
  + Parametric modulation.
* Block Design predictors.
  + Note whether baseline was explicitly modeled.
* HRF basis, typically one of:
  + Canonical only.
  + Canonical plus temporal derivative.
  + Canonical plus temporal and dispersion derivative.
  + Smooth basis (e.g. SPM “informed” or Fourier basis; FSL’s FLOBS).
  + Finite Impulse Response model.
* Drift regressors (e.g. DCT basis in SPM, with specified cut­off).
* Movement regressors; specify if squares and/or temporal derivative used.
* Any other nuisance regressors, and whether they were entered as interactions (e.g. with a task effect in 1st level fMRI, or with group effect).
* Any orthogonalization of regressors, and set of other regressors used to orthogonalize against.

Event-related:

-Intercept (4s duration)

-Reaction time (mean centered, parametric, 4s duration)

-Gain (mean centered, parametric, 4s duration)

-Loss (mean centered, parametric, 4s duration)

Block design: None

HRF:

-canonical only (AFNI 3dDeconvolve)

Drift:

-5 polynomial regressors (powers 1-5) per block

Movement:

-6 standard movement regressors per block

Other nuisance/orthogoalization:

-No response trials (0 reaction time), 4 second duration

-6 aCompCor principal components

**Independent variables - second and group level**

For second level fMRI or general group model, specify:

* Group effects (patients vs. controls).
* Clearly state whether or not covariates are split by group (i.e. fit as a group-by-covariate interaction).
* Other between subject effects (age, sex; for VBM, total GM or ICV).

For group model with repeated measures, specify:

* How condition effects are modeled (e.g. as factors, or as linear trends).
* Whether subject effects are modeled (i.e. as regressors, as opposed to with a covariance structure).

**We modeled effects for each group separately (equal range, equal indifference) using FSL randomise (except where indicated) with 5000 permutations per contrast. Inidividual subject coefficient maps for each predictor were separately modeled to derive main effects. We used a mask encompassing voxels present in 85% of subjects (derived from both groups combined). We performed spatial smoothing on each subject's coefficient map using a Gaussian kernel (FWHM of 4mm) using FSL (FSLmaths). We used an additional 5mm variance smoothing for the t-statistics. We computed one sample one-sided t-stats for each contrast (positive and negative). We applied cluster-mass thresholding at t=2.68 (based on the smaller group size of 48 [minus 1] for equal range), indicating a one-tailed FWE-corrected p-value of 0.005. This threshold was 2.62 (102 - 1) for the contrast between ER and EI groups.**

**Model type**

Some suggested terms include:

* “Mass Univariate”.
* “Multivariate” (e.g. ICA on whole brain data).
* “Mass Multivariate” (e.g. MANOVA on diffusion or morphometry tensor data).
* “Local Multivariate” (e.g. “searchlight”).
* “Multivariate, intra-subject predictive” (e.g. classify individual trials in event­related fMRI).
* “Multivariate inter-subject predictive” (e.g. classify subjects as patient vs. control).
* “Representational Similarity Analysis”.

Mass Univariate

**Model settings**

The essential details of the model. For mass-univariate, first level fMRI, these include:

* Drift model, if not already specified as a dependent variable (e.g. locally linear detrending of data & regressors, as in FSL).
* Autocorrelation model (e.g. global approximate AR(1) in SPM; locally regularized autocorrelation function in FSL).

For mass-univariate second level fMRI these include:

* Fixed effects (all subjects’ data in one model).
* Random or mixed-effects model, implemented with:
  + Ordinary least squares (OLS, aka unweighted summary statistics approach; SPM default, FSL FEAT’s “Simple OLS”).
  + Weighted least squares (i.e. FSL FEAT’s “FLAME 1”), using voxel-wise estimate of between subject variance.
  + Global weighted least squares (i.e. SPM’s MFX).

With any group (multi-subject) model, indicate any specific variance structure, e.g.

* Un-equal variance between groups (and if globally pooled, as in SPM).
* If repeated measures, the specific covariance structure assumed (e.g.

compound symmetric, or arbitrary; if globally pooled).

For local-multivariate report:

* The number of voxels in the local model.
* Local model used (e.g. Canonical Correlation Analysis) with any constraints (e.g. positive weights only).

Describe model settings

**Inference: Contrast/effect**

* Specification of the precise effect tested, often as a linear contrast of parameters in a model. When possible, define these in terms of the task or stimulus conditions instead of psychological concepts (See *Task Specification* in *Experimental Design Reporting*).
* Provide tables/figures on main effects (e.g. in supplement), not just differences or interactions. For example, an inference on a difference of two fMRI conditions, A­B, doesn’t indicate if both A & B induced positive changes; likewise, to fully interpret an interaction requires knowledge of the main effects.
* Indicate any use of any omnibus ANOVA tests.
* All contrasts explored as part of the research should be fully described in the methods section, whether or not they are considered in the results.
* If performing a two-sided test via two one-sided tests, double the one-sided p-values to convert them into two-sided p-values. For example, if looking at both a contrast [-1 1] and [1 -1] together, each with cluster-forming threshold p=0.001, double the FWE cluster p-values from each contrast to obtain two-sided inferences.

Describe inference: Contrast/effect

**Inference: Search region**

* Whole brain or “small volume”; carefully describe any small volume correction used for each contrast.
* If a small-volume correction mask is defined anatomically, provide named anatomical regions from a publicly available ROI atlas.
* If small-volume correction mask is functionally defined, clearly describe the functional task and identify any risk of circularity.
* All small-volume corrections should be fully described in the methods section, not just mentioned in passing in the results.

We determined whether the whole-brain test results encompassed the hypothesized regions of interest by using the Bartra, McGuire, & Kable (2013) vmPFC and ventral striatum masks. The amygdala mask was taken from Smith, Gseir, Speer, & Delgado (2016) through NeuroVault.

**Inference: Statistic type**

Typically, one of:

* Voxel-wise (aka peak-wise in SPM).
* Cluster-wise.
  + - Cluster size.
    - Cluster mass.
    - Threshold-free Cluster Enhancement (TFCE).

For cluster size or mass, report:

* Cluster-forming threshold.

For all cluster-wise methods, report:

* Neighborhood size used to form clusters (e.g. 6, 18 or 26).

For TFCE, report:

* Use of non-default TFCE parameters.

We performed a cluster mass correction for all tests as part of FSL's randomise command. The cluster-forming threshold was a t-value of 2.62 (0.995th quantile for n = 48 - 1) for each single tailed test (hypotheses 1-8), and 2.68 (n = 102 - 1) for ER vs EI (hypothesis 9)

**Inference: P-value computation**

Report if anything but standard parametric inference used to obtain (uncorrected) P-values. If nonparametric method was used, report method (e.g. permutation or bootstrap) and number of permutations/samples used.

We used FSL's randomise to permute the cluster generation 5000 times. P-values were generated based on the resulting null distribution.

**Inference: Multiple testing correction**

For mass-univariate, specify the type of correction and how it is obtained, especially if not the typical usage. Usually one of:

* Familywise Error.
  + Random Field Theory (typical).
  + Permutation.
  + Monte Carlo.
  + Bonferroni.
* False Discovery Rate.
  + Benjamini & Hochberg FDR (typical).
  + Positive FDR.
  + Local FDR.
  + Cluster-level FDR.
* None / Uncorrected

If permutation or Monte Carlo, report the number of permutations/samples. If Monte Carlo, note the brain mask and smoothness used, and how smoothness was estimated.

FSL's randomise was used as part of the correction (5000 permutations)

**Anything else you want to add regarding analysis?**

**Thank you very much for thoroughly reporting your analysis!**

**Please make sure you filled all relevant fields with full descriptions.**

Please contact us if you have any questions: narpsimaging@gmail.com

**If you have any other general comments, please add them here. Thank you!**