fMRI analysis - agency/decision making

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Contents

Preprocessing	1
Steps & Settings	1
Subjects excluded after prepro	3
Art repair	3
First-level analysis	4
With art repair, without motion regressors	4
Repetition of first-level analysis with art repair AND motion regressors	6
Repetition of first-level analysis with motion regressors but NO art repair	7
Second-level analysis	7
Filenames and location	7
Settings	7
Pictures	8
Interpretation of active brain areas	11
Participant information	11
Excluded for data when art repair is used	11
Excluded when art repair is not used	11
Block order	11
Unusual, but still included	11

Preprocessing

Steps & Settings

The following pipeline was used:

 $1.\ \, {\rm Motion\ correction\ (folder:}\ \, Realignment).$

Settings:

Estimate

• Quality: 0.9

• Separation: 4

- Smoothing (FWHM): 5
- Num passes: Register to mean
- Interpolation: 2nd Degree B-Spline
- Wrapping: No wrapWeighting: 0 files

Reslice

- Resliced images: All images + mean image
- Interpolation: 4th Degree B-Spline
- Wrapping: No wrap Masking: mask images
- 2. Coregistration (folder: Coregistration)

Settings: **Estimate**

- Objective function: mutual information
- Separation: [4 2]
- Tolerances: left as default 1x12 array
- Histogram smoothing: [5 5]

Reslice

- Interpolation: trilinear
- Wrapping: no wrap
- Masking: Don't mask images
- 3. Segmentation (of structural only; folder: Segmentation)

Settings: Output files

- Grey matter: native space
- White matter: native space
- CSF: native space
- Bias corrected: Save bias corrected
- Clean up partitions: don't do cleanup

Custom

- Tissue probability maps: 3 files
- Gaussians per class: [2 2 2 4]
- Affine regularization: ICBM space template European brains
- Warping regularization: 1
- Warp frequency cutoff: 25
- Bias regularization: very light (0.0001)
- Bias FWHM: 60 mm cutoff
- Sampling distance: 3
- Masking image: none

4. Normalization (folder: Normalization)

Settings:

Estimation options

• Template image: T1.nii,1

• Template weighting image: 0 files

• Source image smoothing: 8

• Template image smoothing: 0

• Affine regularization: ICBM space template

• Nonlinear frequency cutoff: 25

Nonlinear iterations: 16Nonlinear regularization: 1

Writing options

• Perserve: concentrations

• Bounding box: [-78 -112 -50]

Voxel sizes: [2 2 2]Interpolation: trilinearWrapping: no wrap

5. Smoothing (folder: *Smoothing*) Settings:

• FWHM: [4 4 4]; note that this is different from the default 6

Data type: sameImplicit masking: no

Each step was checked visually before progressing to the next one.

Subjects excluded after prepro

- 2 for oddly shaped brain/failed motion correction
- 9 for failed motion correction
- 10 for abnormally large ventricles
- 26 for behavioral abnormalities
- \bullet 32 for uncorrectable rotation

Art repair

Artifact repair was done using the Gabrieli lab's ArtRepair toolbox, available for free online. As Lester suggested, I used the *art global* script to repair the already preprocessed images.

Because the end-stage preprocessed images are found in the "Smoothing" folder, the artifact repaired images appear in "Smoothing" for each subject, but they have a "v" added to the prefix.

Note: this program needs to be run separately for each scan; that means it has to be run 4 times for each subject.

I created a matlab script, now found in the Art Repair folder on the Acropolis server (mnt/ide0/share/hcnlab/spm8/ArtRepair v5b), called *artglobal loop*. This script loops through each subject and through each of the 4 scans, running *art global* separately, with defaults in place, each time. It spits out warnings when over 25% of the data in that scan were repaired (as per Lester's suggestion of 25%) so that the user can go back, change the threshold, and re-run those separately.

Only a few subjects showed runs that exceeded this threshold:

- Subject 12 run 3; based on Lester's notes and the high but below threshold number of corrected volumes in other runs, I am going to exclude this subject from further analysis.
- Subject 17 run 3; re-ran with a different threshold.

Some other subjects showed lots of corrected volumes but below threshold. These included:

- Subject 16 runs 3 and 4; based on Lester's notes it seems like a good idea to exclude this one.
- Subject 20 run 1 only; I will keep this subject unless things look strange.

Re-run of subject 17, run 3

Used the GUI to adjust the threshold as follows:



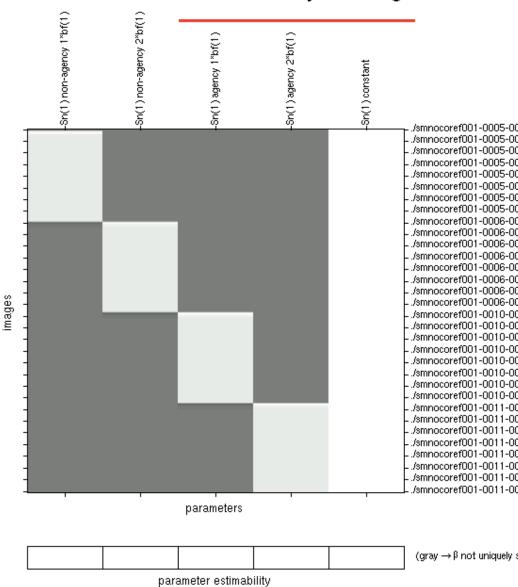
First-level analysis

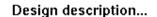
With art repair, without motion regressors

The options I used were:

- Units: seconds
- Interscan interval: 2 (same as TR)
- Microtime resolution: 16 (default)
- Microtime onset: 1 (default)
- High pass filter: 420 seconds
- Basis functions: canonical HRF with no derivatives
- Volterra: do not model interactions
- Global normalization: none
- Explicit mask: none
- Serial correlations: AR(1)

Statistical analysis: Design





Basis functions: hrf
Number of sessions: 1
Trials per session: 4
Interscan interval: 2.00 {s}
High pass Filter: Cutoff: 840 {s}
Global calculation: mean voxel value

Grand mean scaling: session specific Global normalisation: None

The design matrix looks like this:

This shows that each run of 210 scans was treated as a separate condition.

Making the "multiple conditions" .mat file

- One file for agency first condition, one for non-first condition
- Names set to cell array with "agency 1", "agency 2", "non-agency 1", and "non-agency 2" blocks for agency first; flipped for non-agency first.
- Onsets set to 0, 420, 840, and 1260
- Durations set to 420 only
- Saved as /mnt/ide0/share/hcnlab/agency/nifti/001/Specify model 1/params_aq_first.mat, and /mnt/ide0/share/hcnlab/agency/nifti/001/Specify model 1/params_ nonag_ first.mat

Running batch option

This stage can be run as a loop through subjects using the batch firstlevel.m script found in mnt/ide0/share/hcnlab/agency/nifti/001/Specify model 1.

First-pass examination of level 1 results

3 "contrasts" defined

1. Agency > non-agency (subtracts activation from non-agency from activation from agency condition, showing where the brain is MORE active, as measured by blood flow, for agency).

For agency first, vector is: [1 1 -1 -1 0]

For non-agency first, vector is: [-1 -1 1 1 0]

- 2. Agency vs. baseline (shows where brain is active for agency, regardless of other conditions) For agency first, vector is: [1 1 0 0 0]
 - For non-agency first, vector is: [0 0 1 1 0]
- 3. Non-agency vs. baseline (shows where brain is active for non-agency, regardless of other conditions) For agency first, vector is: [0 0 1 1 0] For non-agency first, vector is: [1 1 0 0 0]

Other options

- Apply masking: none
- p value adjustment: none
- Threshold T/p value: 0.001
- Extent threshold: 0 voxels (will count ANY activation, doesn't have to be a certain size)

Repetition of first-level analysis with art repair AND motion regressors

Even though the results made sense without the motion regressors I was curious to see if they would be improved or changed by adding motion regressors (e.g. using the rp*.txt files generated at the Realign phase of preprocessing as multiple regressors).

Batch processing

To do this, I edited the batch—firstlevel.m script to loop through all the subjects but add the regressors.

Results

I examined the same contrasts as before, with the same options.

Repetition of first-level analysis with motion regressors but NO art repair

Based on some odd-looking brains that came out of the first-level analysis with art repair, I decided to try this again but not do art repair, instead excluding subjects that had motion issues. See below for the expanded list of excluded subjects.

Batch processing

To do this, I edited the $batch_$ firstlevel.m script to loop through all the subjects but add the regressors.

Results

I examined the same contrasts as before, with the same options.

Second-level analysis

Filenames and location

Files for second-level analysis are the contrasts created in first-level. These are numbered as follows:

```
For agency > non-agency contrast: con\_\ 0001\_\ subj\#.img \ is \ saved \ in \ /mnt/ide0/hcnlab/agency/nifti/2ndlev\_\ 1/ag\_\ over\_\ no/ For agency vs. baseline: con\_\ 0002\_\ subj\#.img \ is \ saved \ in \ /mnt/ide0/hcnlab/agency/nifti/2ndlev\_\ 1/ag\_\ vs\_\ base/ For non-agency vs. baseline: con\_\ 0003\_\ subj\#.img \ is \ saved \ in \ /mnt/ide0/hcnlab/agency/nifti/2ndlev\_\ 1/no\_\ vs\_\ base/
```

Settings

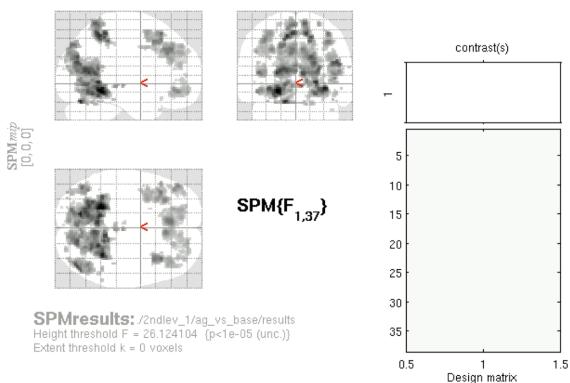
To obtain the second-level contrasts, I followed the tutorial in the SPM8 manual closely. For each condition (e.g. agency vs. baseline), I made an F contrast with weights matrix = 1.

- Apply masking: none
- p value adjustment: none
- Threshold T/p value: 0.000001 for comparisons with baseline; 0.025 for agency > non-agency contrast
- Extent threshold: 0 voxels for comparisons with baseline; 5 voxels for agency > non-agency contrast because so many one or two-voxel locations were lighting up

Pictures

Agency vs. baseline

agency vs. baseline



Statistics: p-values adjusted for search volume

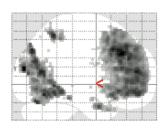
set-lev	vel	C	:luster-lev	el			mm mm mm						
D C	D FWE-com	q FDR-com	^k E	Duncorr	D FWE-com	q _{FDR-corr} F		(Z _≡)	Duncorr				
0.000 74			3943		0.000	0.009	80.71	6.40	0.000	-22	-48	-1	
						0.000	0.015	70.48	6.13	0.000	32	-46	-
						0.000	0.015	70.14	6.12	0.000	-14	-72	-2
				325		0.000	0.027	63.80	5.94	0.000	-12	-50	5
						0.005	0.062	47.06	5.35	0.000	-4	-52	6
						0.013	0.100	42.64	5.16	0.000	-12	-52	6
				251		0.001	0.032	57.80	5.75	0.000	10	-44	5
						0.002	0.044	51.07	5.51	0.000	8	-54	6
						0.003	0.048	49.45	5.45	0.000	16	-40	4
				406		0.001	0.032	55.83	5.68	0.000	46	-76	2
						0.010	0.091	43.74	5.21	0.000	44	-64	
						0.013	0.101	42.51	5.16	0.000	44	-72	
				177		0.004	0.051	48.97	5.43	0.000	36	22	5
						0.006	0.069	46.08	5.31	0.000	36	16	4
						0.162	0.500	30.57	4.55	0.000	32	12	3
				190		0.004	0.051	48.68	5.42	0.000	-44	-70	1
						0.065	0.275	34.84	4.79	0.000	-38	-88	1
						0.081	0.310	33.82	4.73	0.000	-38	-82	1
				895		0.006	0.068	46.35	5.32	0.000	-6	34	3
						0.008	0.077	45.04	5.27	0.000	6	28	3
						0.037	0.187	37.41	4.92	0.000	-20	36	3
				487		0.008	0.077	45.22	5.28	0.000	-38	22	4
						0.012	0.098	42.99	5.18	0.000	-30	26	3
						0.025	0.150	39.40	5.02	0.000	-32	18	54
				10		0.010 naxima more ti	0.091	43.84	5.22	0.000	6	-44	_

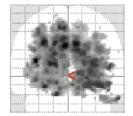
Height threshold: F = 26.12, p = 0.000 (0.404)
Extent threshold: k = 0 voxels, p = 1.000 (0.404)
Expected voxels per cluster, <k> = 3.396
Expected number of clusters, <c> = 0.52
FWEp: 36.043, FDRp: 49.454

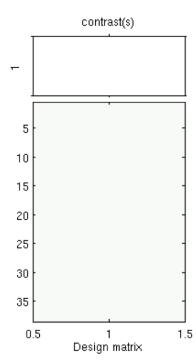
Degrees of freedom = [1.0, 37.0] FWHM = 10.6 10.3 9.5 mm mm mm; 5.3 5.2 4.7 (voxels) Volume: 1347416 = 168427 voxels = 1203.5 resels Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 129.36 voxels) Page 1

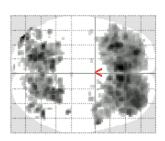


non-agency vs. baseline









 $\mathsf{SPM}\{\mathsf{F}_{1,37}^{}\}$

SPMresults: /2ndlev_1/no_vs_base/results Height threshold F = 34.231435 {p<1e-06 (unc.)} Extent threshold k = 0 voxels

Statistics: p-values adjusted for search volume

set-lev	/el	С	luster-lev	el			roro.		- -				
D	С	D FWE-corr	q FDR-corr	k _E	D _{uncorr}	D FWE-com	Q FDR-cor	_r F	(Z _≡)	D _{uncorr}	111111	mm m	
0.000	62			15981		0.000	0.021	88.44	6.58	0.000	-6	28	3
						0.000	0.024	81.88	6.43	0.000	8	30	3
						0.000	0.024	78.68	6.35	0.000	-30	26	3
				161		0.000	0.021	87.43	6.56	0.000	-40	-88	1
						0.000	0.029	64.19	5.95	0.000	-38	-82	1
						0.002	0.060	54.09	5.62	0.000	-50	-78	1
				3443		0.000	0.024	75.85	6.28	0.000	-18	-66	1
						0.000	0.024	75.67	6.27	0.000	-30	-64	-1
						0.000	0.024	74.95	6.25	0.000	-14	-74	-2
				160		0.000	0.026	71.58	6.16	0.000	-12	-52	5
						0.001	0.060	54.43	5.63	0.000	-14	-44	5
						0.026	0.427	39.39	5.01	0.000	-8	-62	6
				192		0.000	0.026	68.86	6.09	0.000	48	-64	. :
						0.001	0.051	56.22	5.69	0.000	38	-78	1
						0.004	0.112	48.39	5.41	0.000	40	-80	1
				229		0.000	0.027	64.64	5.96	0.000	58	2	-2
						0.002	0.070	52.62	5.57	0.000	42	-2	-2
						0.004	0.111	48.60	5.41	0.000	46	12	-3
				10		0.001	0.047	57.02	5.72	0.000	46	-34	-1
				62		0.002	0.061	53.58	5.60	0.000	-28	-80	1
				14		0.003	0.098	49.62	5.45	0.000	-46	-56	:
				38		0.005	0.115	48.20	5.40	0.000	10	-44	5
				7		0.005	0.128	47.33	5.36	0.000	40	-66	-
				4		0.007	0.152	46.07	5.31	0.000	-6	-98	10
			ta	13 ble sho	ws 3 local n	0.009 naxima more ti	0.187 han 8.0mm	44.59 n apart	5.25	0.000	-22	-92	2

Height threshold: F = 34.23, p = 0.000 (0.079) Extent threshold: k = 0 voxels, p = 1.000 (0.079)

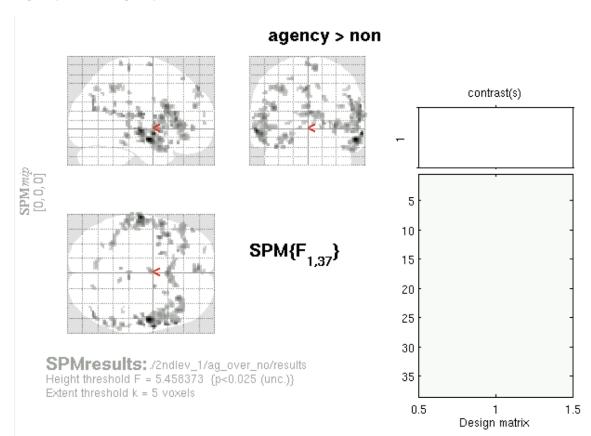
Expected voxels per cluster, <k> = 2.100 Expected number of clusters, <c> = 0.08 FWEp: 36.366, FDRp: 56.452

Degrees of freedom = [1.0, 37.0] FWHM = 10.4 10.0 9.3 mm mm mm; 5.2 5.0 4.6 (voxels) Volume: 1347416 = 168427 voxels = 1294.9 resels Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 120.23 voxels)

Page 1



Agency > non-agency



Statistics: p-values adjusted for search volume

set-level	cluster-level				peak-level						mm mm mn		
	D FWE-com	q FDR-corr	ŔΕ	Duncorr	D FWE-com	q FDR-cor	r F	(Z _≡)	Duncorr	1111111			
55			229		0.949	0.996	18.91	3.71	0.000	54	-6	-1	
					1.000	0.996	14.91	3.33	0.000	62	0		
					1.000	0.996	10.27	2.77	0.003	58	6	-:	
			219		0.999	0.996	15.95	3.43	0.000	-62	-16	-	
					1.000	0.996	10.70	2.83	0.002	-54	8	:	
					1.000	0.996	9.47	2.66	0.004	-54	-14	-:	
			59		1.000	0.996	11.74	2.97	0.002	60	14		
					1.000	0.996	8.79	2.56	0.005	58	12	:	
					1.000	0.996	8.16	2.46	0.007	50	16		
			220		1.000	0.996	11.49	2.93	0.002	58	26		
					1.000	0.996	10.62	2.82	0.002	30	28		
					1.000	0.996	9.59	2.68	0.004	44	28		
			36		1.000	0.996	11.23	2.90	0.002	58	-16		
					1.000	0.996	8.48	2.51	0.006	50	-14	:	
			53		1.000	0.996	10.94	2.86	0.002	-42	16	2	
					1.000	0.996	6.98	2.26	0.012	-54	12	;	
			91		1.000	0.996	10.38	2.79	0.003	2	16	:	
					1.000	0.996	8.42	2.50	0.006	10	18	:	
					1.000	0.996	7.59	2.36	0.009	14	24	:	
			42		1.000	0.996	10.27	2.77	0.003	-4	52	•	
					1.000	0.996	7.31	2.32	0.010	-2	52	3	
			26		1.000	0.996	10.06	2.74	0.003	48	-72	:	
					1.000	0.996	9.55	2.67	0.004	50	-72	2	
					1.000	0.996	6.43	2.16	0.015	42	-74	3	
			14		1.000 naxima more ti	0.996	9.94	2.73	0.003	-38	6	-2	

Height threshold: F = 5.46, p = 0.025 (1.000) Extent threshold: k = 5 voxels, p = Expected voxels per cluster, <k> = 43.286 Expected number of clusters, <c> =

FWEp: 35.494, FDRp: Inf

Degrees of freedom = [1.0, 37.0] FWHM = 11.3 10.2 10.3 mm mm mm; 5.6 5.1 5.1 {voxels} Volume: 1347416 = 168427 voxels = 1061.6 resels Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 146.64 voxels) Page 1



Interpretation of active brain areas

The "versus baseline" contrasts give us a nice reality check. Because this task involves reading information on a screen, we should see activity in visual areas, which is obvious in both agency vs. baseline and non-agency vs. baseline. Because it involves pretty sophisticated decision-making, we should also see a great deal of frontal activation, which we also see in both "versus baseline" cases.

Converting MNI to TAL and area lookup

The coordinates in SPM are MNI coordinates. These need to be converted to Talairach in order to look them up in the Brede database. I used a website from the BioImage suite at Yale to convert MNI to TAL.

I then used the Brede database to look up the TAL coordinates and what areas they correspond with in the literature.

Areas implicated in literature The following papers (from Shoham) are being used as a guide.

- Hutcherson et. al. 2015 A neurocomputational model of altruistic choice and its implications
- Strombach et. al. 2015 Social discounting involves modulation of neural value signals by temporoparietal junction
- Fehr & Camerer 2007 Social neuroeconomics: the neural circuitry of social preferences

I looked at the names of the main areas implicated in these papers, then did a literature search to define the borders of these areas. I then compared the coordinates identified in my second-level analysis to the lists of coordinates as defined in many different papers.

Another approach is to use **Neurosynth** to generate automated meta-analyses; I am looking into this currently.

Participant information

Excluded for data when art repair is used

2, 9, 10, 12, 16, 26, 32

Excluded when art repair is not used

2, 9, 10, 12, 16, 17, 26, 32, 37, 38, 43, 45 (everyone on Lester's list of people who may have had motion issues)

Block order

Agency first: 2, 4, 6, 8, 10, 12, 14, 16, 18, 19, 21, 23, 25, 26, 28, 30, 32, 34, 36, 39, 41, 43

Non-agency first: 1, 3, 5, 7, 9, 11, 13, 15, 17, 20, 22, 24, 27, 29, 31, 33, 35, 37, 38, 40, 42, 44, 45

Unusual, but still included

- 13: had only 13 scans in run 4
- 35: had only 171 scans in run 4