# Dear Lydia,

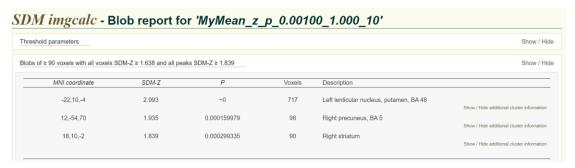
It's really honor for me to use SDM, and receiving your reply for several times made me encouraged. I have some questions about the use of SDM set out below:

- 1. <u>In 5.15 version</u>, dose "MyMean\_z\_p\_0.005\_1.000\_10" represents the main results rather than "MyMean\_z\_QH\_p\_0.005\_1.000\_10", and the difference between them whether means heterogeneity, that is to say the brain areas both existed in the "MyMean\_z\_p" and "MyMean\_z\_QH\_p" represents these areas exhibit a good reproducibility, but the areas produced in the "MyMean\_z\_p" did not exist in the "MyMean\_z\_QH\_p" means these brain areas had heterogeneity?
  - <u>In 6.21 version</u>, dose "uncorrected p=0.005" is equal to "MyMean\_z\_p\_0.005\_1.000\_10", and "TFCE p=0.05" is approximately equal to "MyMean\_z\_QH\_p\_0.005\_1.000\_10"? I'm not sure I'm right about what is said above.
- 2. When I tried to run the data of tutorial, I found that the results I got was different from the article *Voxel-wise meta-analysis of grey matter changes in obsessive—compulsive disorder*, and the results from two version were diverse from each other as well.

# The results from the article:

		Maximum			Cluster
	Talairach coordinates	SDM value	Uncorrected P	Number of voxels	Breakdown (number of voxels)
Clusters of increased grey matter Left lenticular nucleus (mainly anterior putamen)	-18, 8, 0	0.248	0.000005		Left lenticular nucleus (464) Left caudate nucleus (41) Left subcallosal gyrus (1)
Right superior parietal lobule and precuneus	14, -60, 62	0.210	0.00009	75	Right Brodmann area 7 (75)
Right lenticular nucleus (mainly anterior putamen)	14, 10, -2	0.187	0.0003	68	Right lenticular nucleus (54) Right caudate nucleus (14)
Clusters of decreased grey matter Right/left dorsal medial frontal gyri/anterior cingulate gyri	4, 28, 36	-0.278	0.00002		Right Brodmann area 8 (93) Right Brodmann area 32 (96) Right Brodmann area 6 (34) Right Brodmann area 9 (22) Left Brodmann area 8 (59) Left Brodmann area 32 (41) Left Brodmann area 6 (26) Left Brodmann area 9 (14)

# 5.15version, Uncorrected p=0.001



Р	Voxels	Description	
~0	1505	Right anterior cingulate / paracingulate gyri, BA 32	Show / Hide additional cluster information
0.000624478	62	Left gyrus rectus, BA 11	Show / Hide additional cluster information

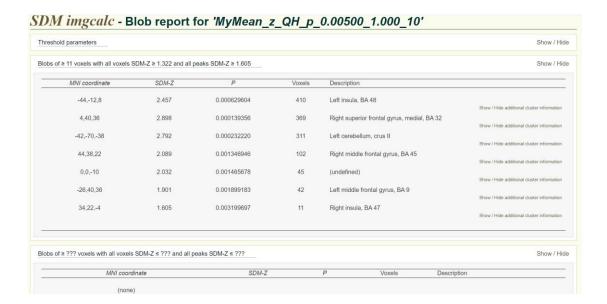
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# 5.15version, Uncorrected p=0.005

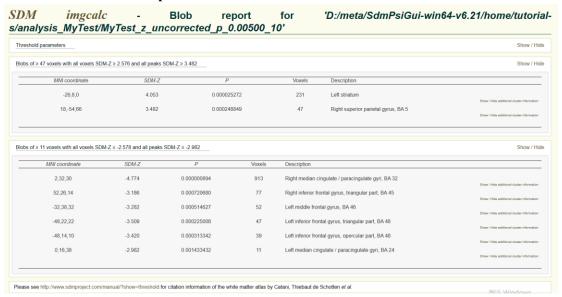
# SDM imgcalc - Blob report for 'MyMean\_z\_p\_0.00500\_1.000\_10'

≥ 24 voxels with all voxels S	DM-Z ≥ 1.319 and all pe	aks SDM-Z ≥ 1.477			Show / I
MNI coordinate	SDM-Z	P	Voxels	Description	
-22,10,-4	2.993	~0	1066	Left lenticular nucleus, putamen, BA 48	Show / Hide additional cluster informati
18,10,-2	1.839	0.000299335	436	Right striatum	Show / Hide additional cluster informat
-18,-54,-12	1.547	0.001527607	337	Left lingual gyrus, BA 19	Show / Hide additional cluster informat
12,-54,70	1.935	0.000159979	231	Right precuneus, BA 5	Show / Hide additional cluster informati
-18,-46,70	1.477	0.002327502	24	Left postcentral gyrus, BA 5	Show / Hide additional cluster informat

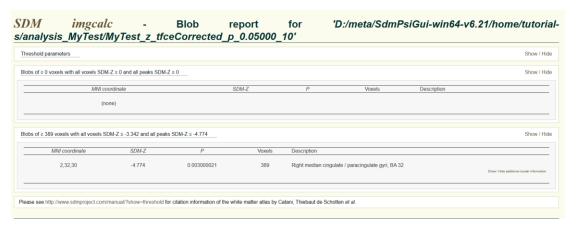
MNI coordinate	SDM-Z	Р	Voxels	Description	
6,36,24	-3.072	~0	2571	Right anterior cingulate / paracingulate gyri, BA 32	Show / Hide additional cluster info
0,36,-18	-2.164	0.000624478	501	Left gyrus rectus, BA 11	Show / Hide additional cluster info
-48,6,4	-1.860	0.001852751	87	Left rolandic operculum, BA 48	
-42.524	-1.841	0.002028227	50	Left middle frontal gyrus, orbital part, BA 46	Show / Hide additional cluster info



# 6.21 version uncorrected p=0.005



# Tfce corrected p=0.05

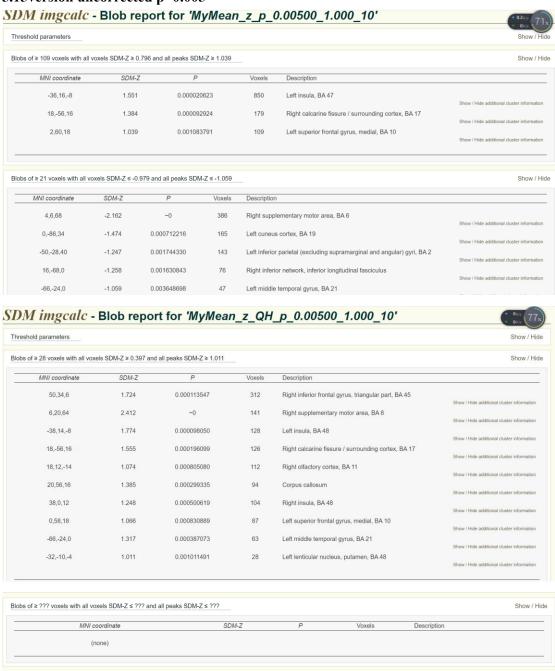


I was wondering why this would happen, I had no idea about it.

**3.** Similar to the situation above, diverse results from two version not only exist in the data of tutorial, but also in the data of mine. When I used 6.21 version, there were null results which were totally different from those in 5.15 results.

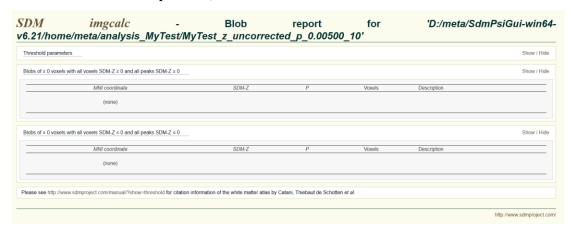
# My results from two version:

# 5.15version uncorrected p=0.005



# 6.21 version

# When I use uncorrected p = 0.005, there was no results.



# When I use uncorrected p=0.05, there was a result, which would be vanished in the transfer of p=0.05.



The causes of the problems described above are uncertain, thus I am really expect to receive a response so that I can determine which results are more useful.

**4. Heterogeneity**: In 5.15 version, my heterogeneity results are show as below:

	Po	sitive correl	ation	Negative correlation							
	Left insula (BA47)	Right calcarine fissure / surrounding cortex (BA17)	Left superior frontal gyrus, medial (BA10)	Right supplementary motor area (BA6)	Left cuneus cortex BA (19)	Left inferior parietal (excluding supramarginal and angular) gyri (BA2)	Right inferior network, inferior longitudinal fasciculus	Left middle temporal gyrus (BA21)	Right superior frontal gyrus, dorsolateral (9)		
Yoon, L. 2022	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes		
Li, J. 2021	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes		
Zou, L, 2018	Yes (BA48)	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes		
Yajing Pang 2015	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes		
Ikeda, 2017	Yes (BA48)	Yes	No , L2R	No	No	No	No	No	No		
Wei et al., 2014	Yes (BA48)	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes		
Sampaio, A. 2014	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes		
Aghajani, M. 2014	No	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes		
Wei et al., 2011	No	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes		
Cunisato et I.,	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes		
Kumari et al., 2004	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes		
Ruffle 2015	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes		

There is a highly heterogeneous article "**Ikeda 2017**", but I am not sure if the reason of high heterogeneity is the sample size. Therefore I have no idea about how to report this results. **Included studies:** 

Study	Sample size(F/M)	t值		Age (Mean±SD	personality measure	Scanner Type	Imaging technique	Statistical analysis	Thresshold	Software Type	Coordinate
Yoon, L. 2022	70(34/36)	-1.667239		13.64	The 44-item Big Five Inventory	3T Siemens Trio	FC	Amygdala Seed-Based Connectivity Analysis; Whole-Brain Connectivity	FDR corrected	Conn toolbox	No connection AAL-MNI
Li, J. 2021	32(20/12)	-1.695519	p < 0.05 GRF correction	11.69 ± 1.86 years	The modified Chinese Junior Eysenck Personality Questionnaire (EPQ)	3T Siemens Trio	fALFF(at the whole-brain level.) ROI-ROI FC	Correlation	GRF correction	SPM12 DPARSF toolkits	√ MNI
Zou. L. 2018	100 (50, 50)	-1660391	p < 0.05, FWE corrected	21.91+2.29	Eysenck Personality Questionnaire-Revised Short Scale for Chinese (EPQ-RSC)	3T Siemens Trio	FCD	Pearson's linear correlation multiple regression analyses	PWE corrected	SPM8 DPARSF v4.1	√ MNI
Yajing Pang 2015	71 (37/34)	-1.666914	p < .05 (the combined uncorrected individual voxel p < .01, and the minimum cluster size of the short- and long- range FCD was identified as 456 and 509 voxels, respectively	224±15	EPQ-RSC)	3T Siemens Trio	FCD Seed-based RSFC analysis	One-sample t-test Pearson correlation	AlphaSim corrected	SPM8	√ MNI
Ikeda. 2017	835 (348/487)	-1.646683	PWEcorrected p < 0.05	20.7 ± 1.8	NEO-FFI	3-T Philips Intera Achieva scanner	fALFF	Multiple regression	FWE corrected	SPM8	MNI
Wei et al. 2014	87 (39/48)	-1.662765	P < 0.05	23.5 ± NA	EPQ-RSC	3T Siemens Trio	fALFF	Multiple regression	AlphaSim corrected	SPMB	√ MNI
Sampaio, A. 2014	49 (30/19)	-1.677224	p < 0.05	25.0±5.3	NEO-FFI	Siemens Magnetom Avanto 1.5 T	ICA	Multiple regression	FWE corrected	SPM8	√ MNI
Aghajani, M. 2014	50 (32/18)	-1.676551	p < 0.05	40.51±9.45	NEO-FFI	Philips 3.0-T MRI scanners	Whole-brain analysis of amygdala RSFC	Multiple regression	cluster-corrected threshold of p < .05 with an initial cluster-forming threshold of Z > 2.3		√ MNI
Wei et al., 2011	87 (39/48)	-1.662765	p < 0.05	23.5 ± NA	EPQ-RSC	3T Siemens Trio	ReHo	Multiple regression	AlphaSim corrected	SPM8	√ MNI
Kunisato et al. 2011	24 (15/9)	-1.713872	p < 0.05	23.1 ± 1.9	NEO-FFI	GE Signa EXCITE HD 3.0T scanner	fALFF	Simple regression	Uncorrected	SPM8	√ MNI
Kumari et al., 2004	11 (0/11)	-1.812461	p < 0.05	25.4 ± 1.2	EPQ-R	1.5 T GE Signa system	signal intensity	Linear regression	Uncorrected	SPM99	√
Ruffle, 2015	33 (16/17)	-3.37	p=0.001	17.06 ± 0.73	EPQ-R	General Electric Signa Excite HDxt II 3.0 Tesla scanner	BOLD signal			XBAM version 4.1	Talairach

5. In 5.15 version, when we create the mask for the data of tutorial, why we type the coordinate as (X = -24, Y = 10, Z = -2)? Can we use another coordinate?

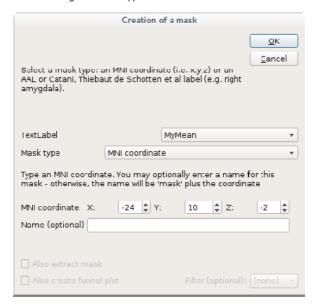
#### Assessment of heterogeneity and potential publication bias

We strongly recommend extracting values from relevant peaks, inspecting the corresponding  $\ell$  statistics (or other heterogeneity estimates) and check their funnel plots. You may also use extracted values to create meta-regression plots with Microsoft Excel, R or similar software.

You should first create a mask that includes the voxel or region from where you want to extract the values, and then extract these values using the mask. Fortunately, the "Thresholding" automatically creates the masks for the peaks.

> To create the mask, click the [Create a mask] button, select [MNI coordinate], click [OK], type the coordinate (X = -24, Y = 10, Z = -2), and click [OK].

A dialog similar to the following one should appear:



This will create a file named "analysis\_MyMean/masks/mask\_24\_10\_-2.nii.gz" which contains the mask. Note that you can copy this file to the folder of another meta-analysis in order to avoid creating it again.

# Looking forward to receiving your reply.

# **Best Wishes!**