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Corresponding Author: Thomas L. Kash

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Supplementary Videos: 0

Reporting Checklist for Nature Neuroscience

This checklist is used to ensure good reporting standards and to improve the reproducibility of published results. For more information, please read Reporting Life Sciences Research.

Please note that in the event of publication, it is mandatory that authors include all relevant methodological and statistical information in the manuscript.

Statistics reporting, by figure

- Please specify the following information for each panel reporting quantitative data, and where each item is reported (section, e.g. Results, & paragraph number).
- Each figure legend should ideally contain an exact sample size (n) for each experimental group/condition, where n is an exact number and not a range, a clear definition of how n is defined (for example x cells from x slices from x animals from x litters, collected over x days), a description of the statistical test used, the results of the tests, any descriptive statistics and clearly defined error bars if applicable.
- For any experiments using custom statistics, please indicate the test used and stats obtained for each experiment.
- Each figure legend should include a statement of how many times the experiment shown was replicated in the lab; the details of sample collection should be sufficiently clear so that the replicability of the experiment is obvious to the reader.
- For experiments reported in the text but not in the figures, please use the paragraph number instead of the figure number.

Note: Mean and standard deviation are not appropriate on small samples, and plotting independent data points is usually more informative. When technical replicates are reported, error and significance measures reflect the experimental variability and not the variability of the biological process; it is misleading not to state this clearly.

		TEST USED		n			DESCRIPTIVE STATS (AVERAGE, VARIANCE)		P VALUE		DEGREES OF FREEDOM & F/t/z/R/ETC VALUE	
	FIGURE NUMBER	WHICH TEST?	SECTION & PARAGRAPH #	EXACT VALUE	DEFINED?	SECTION & PARAGRAPH #	REPORTED?	SECTION & PARAGRAPH #	EXACT VALUE	SECTION & PARAGRAPH #	VALUE	SECTION & PARAGRAPH #
example	1a	one-way ANOVA	Fig. legend	9, 9, 10, 15	mice from at least 3 litters/group	Methods para 8	error bars are mean +/- SEM	Fig. legend	p = 0.044	Fig. legend	F(3, 36) = 2.97	Fig. legend
example	results, para 6	unpaired t-test	Results para 6	15	slices from 10 mice	Results para 6	error bars are mean +/- SEM	Results para 6	p = 0.0006	Results para 6	t(28) = 2.808	Results para 6
+ -	1b	unpaired ttest	Fig legend	7,7	indiv mouse	Fig legend	err bars are mean +/- SEM	Fig legend	p = 0.0238	Fig legend	t(12)=2.586	Fig legend

		TEST USED		n			DESCRIPTIVE STATS (AVERAGE, VARIANCE)		P VALUE		DEGREES OF FREEDOM & F/t/z/R/ETC VALUE	
	FIGURE NUMBER	WHICH TEST?	SECTION & PARAGRAPH #	EXACT VALUE	DEFINED?	SECTION & PARAGRAPH #	REPORTED?	SECTION & PARAGRAPH #	EXACT VALUE	SECTION & PARAGRAPH #	VALUE	SECTION & PARAGRAPH #
+ -	1c	unpaired ttest	Fig legend	7,7	indiv mouse		err bars are mean +/- SEM		p = 0.8630		t(12)=0.1763	
+ -	1d	unpaired ttest	Fig legend	7,7	indiv mouse		err bars are mean +/- SEM		p = 0.7816		t(12)=0.2836	
+ -	1e	unpaired ttest	Fig legend	7,7	indiv mouse		err bars are mean +/- SEM		p = 0.7121		t(12)=0.3779	
+ -	1f	unpaired ttest	Fig legend	7,7	indiv mouse		err bars are mean +/- SEM		p = 0.4616		t(12)=0.7606	
+ -	1i	paired ttest, baseline vs washout	Fig legend	13	max 2 neurons/ mouse; 11 mice		err bars are mean +/- SEM		freq: p = 0.0051 amp: p = 0.2349		freq:t(12)=3.421 amp: t(12)=1.251	
+ -	1j	paired ttests, baseline vs washout	Fig legend	5	max 2 neurons/ mouse; 3 mice		err bars are mean +/- SEM		freq: p = 0.6322 amp: p = 0.0405		freq:t(4)=0.5174 amp: t(4)=2.987	
+ -	1k	paired ttests baseline vs washout	Fig legend	13,7,5,6, 6,5,6	max 2 neurons/ mouse; 11, 4,3,3,5,4,3 mice		err bars are mean +/- SEM		in order: frequency p = 0.0051 p = 0.5560 p = 0.1199 p = 0.8569 p = 0.0264 p = 0.8835 p = 0.0051 amplitude p = 0.2349 p = 0.5485 p = 0.2645 p = 0.1501 p = 0.0609 p = 0.5841 p = 0.0156		in order: frequency t(12)=3.421 t(6)=0.6233 t(4)=1.972 t(5)=0.1898 t(5)=3.115 t(4)=0.1562 t(5)=4.759 amplitude t(12)=1.251 t(6)=0.6356 t(4)=1.297 t(5)=1.699 t(5)=2.410 t(4)=0.5946 t(5)=3.600	
+ -	1l	paired ttest baseline vs washout	Fig legend	9	max 2 neurons/ mouse; 7 mice		err bars are mean +/- SEM		p = 0.0068		t(8)=3.614	
+ -	Supp 1b	unpaired ttest, Welch's corr	Fig legend	6,7	indiv mouse		err bars are mean +/- SEM		p = 0.6597		t(11)=0.4622	
+ -	S1c	unpaired ttest	Fig legend	7,7	indiv mouse		err bars are mean +/- SEM		p=0.2426		t(12)=1.229	
+ -	S1d	unpaired ttest	Fig legend	7,7	indiv mouse		err bars are mean +/- SEM		p=0.0020		t(12)=3.938	
+ -	S1e	unpaired ttest	Fig legend	7,5	indiv mouse		err bars are mean +/- SEM		p=0.4645		t(10)=0.7605	
+ -	S1f	unpaired ttest	Fig legend	7,5	indiv mouse		err bars are mean +/- SEM		p=0.4971		t(10)=0.7046	
+ -	S1g	unpaired ttest	Fig legend	7,6	indiv mouse		err bars are mean +/- SEM		p = 0.7967		t(11)=0.2640	
+ -	S1h	unpaired ttest	Fig legend	7,8	indiv mouse		err bars are mean +/- SEM		p = 0.2076		t(13)=1.326	
+ -	S1i	unpaired ttest	Fig legend	7,8	indiv mouse		err bars are mean +/- SEM		p = 0.0436		t(13)=2.235	

+ -	S1j	unpaired ttest	Fig legend	9,7	indiv mouse		err bars are mean +/- SEM		p = 0.9346		t(14)=0.08249	
+ -	S1k	unpaired ttest	Fig legend	9,7	indiv mouse		err bars are mean +/- SEM		p = 0.6695		t(14)=0.4359	
+ -	S1l	unpaired ttest	Fig legend	7,9	indiv mouse		err bars are mean +/- SEM		p = 0.0411		t(14)=2.249	
+ -	S1m	unpaired ttest	Fig legend	9,8	indiv mouse		err bars are mean +/- SEM		p = 0.4371		t(15)=0.7984	
+ -	S1n	unpaired ttest	Fig legend	9,8	indiv mouse		err bars are mean +/- SEM		p = 0.8356		t(15)=0.2112	
+ -	S1o	unpaired ttest	Fig legend	8,9	indiv mouse		err bars are mean +/- SEM		p = 0.3707		t(15)=0.9229	
+ -	S1p	unpaired ttest	Fig legend	8,9	indiv mouse		err bars are mean +/- SEM		p = 0.9214		t(15)=0.1003	
+ -	S1q	unpaired ttest	Fig legend	7,10	indiv mouse		err bars are mean +/- SEM		p = 0.2625		t(15)=1.164	
+ -	Supp 2a	unpaired ttest	Fig legend	8,6	indiv mouse		err bars are mean +/- SEM		p = 0.0286		t(12)=2.488	
+ -	S2b	unpaired ttest	Fig legend	6,9	indiv mouse		err bars are mean +/- SEM		p = 0.9404		t(13)=0.07628	
+ -	S2c	unpaired ttest	Fig legend	3,5	indiv mouse		err bars are mean +/- SEM		p = 0.7064		t(6)=0.3951	
+ -	S2d	unpaired ttest	Fig legend	3,4	indiv mouse		err bars are mean +/- SEM		p = 0.9704		t(5)=0.03903	
+ -	Supp 3a	paired ttests baseline vs washout	Fig legend	5,5	max 3 neurons/ mouse; 3,3 mice		err bars are mean +/- SEM		in order: p = 0.0092 p = 0.3865 p = 0.9611 p = 0.6660		in order: t(4)=4.721 t(4)=0.9710 t(4)=0.05190 t(4)=0.4652	
+ -	S3b	Sidaks multiple comparison test; all values compared to CON	Fig legend	26,11,7,11,20,13,8,10	max 4 neurons/ mouse; same # of mice as 1k		err bars are mean +/- SEM		in order: p = 0.9992 p = 0.0031 p > 0.9999 p = 0.2928 p = 0.0102 p = 0.6770 p = 0.8592		in order: t(35)=0.4669 t(31)=3.632 t(35)=0.3377 t(44)=2.000 t(37)=3.275 t(32)=1.454 t(34)=1.172	
+ -	S3c	paired ttest baseline vs washout	Fig legend	same cells as 1i	same as 1i		err bars are mean +/- SEM		p = 0.6424		t(12)=0.4763	
+ -	S3d	paired ttests baseline vs washout	Fig legend	6	max 3 neurons/ mouse; 3 mice		err bars are mean +/- SEM		freq: p = 0.0254 amp: p = 0.8892		freq:t(5)=3.150 amp: t(5)=0.1465	
+ -	2b	unpaired ttests	Fig legend	10,10	each N=1 mouse (avg of 5 slices)		err bars are mean +/- SEM		p = 0.4161		t(18)=0.8324	
+ -	2c	unpaired ttests	Fig legend	13,13; 13,12	max 2 neurons/ mouse; 7,7 mice		err bars are mean +/- SEM		sIPSC: p = 0.2845 mIPSC: p = 0.1857		sIPSC: t(24)=1.095 mIPSC: t(23)=1.364	
+ -	2d	unpaired ttests	Fig legend	same as E4c	same as 2c		err bars are mean +/- SEM		sIPSC: p = 0.3500 mIPSC: p = 0.3621		sIPSC: t(24)=0.9532 mIPSC: t(23)=0.9278	
+ -	2e	paired ttests baseline vs washout	Fig legend	13 (same as Fig 1i),6,5,6	max 2 neurons/ mouse; 11, 5,4,4 mice		err bars are mean +/- SEM		in order: p = 0.0051 (same as 1i) p = 0.0161 p = 0.9618 p = 0.5250		in order: t(12)=3.421 (same as 1i) t(5)=3.569 t(4)=0.05099 t(5)=0.6829	

+ -	2f	paired ttests baseline vs washout	Fig legend	11,5 4,4	max 2 neurons/ mouse; 10,3,4,3 mice		err bars are mean +/- SEM		in order: p = 0.2438 p = 0.9919 p = 0.1842 p = 0.0035		in order: t(10)=1.238 t(3)=0.01104 t(4)=1.603 t(3)=8.451	
+ -	3b	unpaired ttest with Welchs corr; unpaired ttest	Fig legend	8,12 15,12	max 3 neurons/ mouse; 5,5,7,6 mice		err bars are mean +/- SEM		sIPSC: p = 0.0399 mIPSC: p = 0.9624		sIPSC: t(18)=2.319 mIPSC: t(25)=0.04756	
+ -	3c	paired ttests baseline vs washout	Fig legend	7,6	1 neuron/mouse; 7,6 mice		err bars are mean +/- SEM		p = 0.6216 p = 0.0158		t(6)=0.5201 t(5)=3.583	
+ -	3d	paired ttests baseline vs washout	Fig legend	7,6	max 2 neurons/ mouse; 6,5 mice		err bars are mean +/- SEM		p = 0.8603 p = 0.0313		t(6)=0.1837 t(5)=2.965	
+ -	3e	unpaired ttest	Fig legend	10,7	each N=1 mouse (avg of 3-5 slices)		err bars are mean +/- SEM		p = 0.7544		t(15)=0.3186	
+ -	3f	unpaired ttest	Fig legend	9,6	each N=1 mouse (avg of 3-5 slices)		err bars are mean +/- SEM		p = 0.0010		t(13)=4.228	
+ -	3g	unpaired ttest	Fig legend	10,7	each N=1 mouse (avg of 3-5 slices)		err bars are mean +/- SEM		p = 0.0246		t(15)=2.498	
+ -	3k	paired ttests baseline vs washout	Fig legend	5,8 7,6,3 5,6 4,9	max 3 neurons/ mouse/monkey; 3,4 mice 7,6,2 mice 3,3 mice 3,5 monkeys		err bars are mean +/- SEM		in order: p = 0.9890 p = 0.3046 p = 0.6216 (same as 2c) p = 0.0158 (same as 2c) p = 0.3753 p = 0.5397 p = 0.0271 p = 0.5074 p = 0.0030		in order: t(4)=0.01473 t(7)=1.108 t(6)=0.5201 (same as 2c) t(5)=3.583 (same as 2c) t(2)=1.131 t(4)=0.6698 t(5)=3.092 t(3)=.0.7506 t(8)=4.205	
+ -	3h	Sidaks multiple comparison test; all values compared to CON	Fig legend	10,10,10	each n=1 mouse (avg of 3-5 slices)		err bars are mean +/- SEM		p = 0.0040 p < 0.0001		t(18)=3.577 t(18)=5.220	
+ -	Supp 4b	unpaired ttest	Fig legend	10,10	each N=1 mouse		err bars are mean +/- SEM		p = 0.9978		t(18)=0.005170	
+ -	S4c	unpaired ttest	Fig legend	10,10	each N=1 mouse		err bars are mean +/- SEM		p = 0.6749		t(18)=0.4264	
+ -	S4d	unpaired ttest	Fig legend	10,10	each N=1 mouse		err bars are mean +/- SEM		p = 0.7841		t(18)=0.2781	
+ -	4c	unpaired ttest	Fig legend	11,7	max 3 neurons/ mouse; 6,4 mice		err bars are mean +/- SEM		p = 0.2148		t(16)=1.292	
+ -	4d	unpaired ttest	Fig legend	same as 3c	same as 3c		err bars are mean +/- SEM		p = 0.0389		t(16)=2.250	
+ -	4e	paired ttests baseline vs washout	Fig legend	same as 3c	same as 3c		err bars are mean +/- SEM		p = 0.0178 p = 0.8733		t(10)=2.830 t(6)=0.1664	
+ -	4f	paired ttests baseline vs washout	Fig legend	same as 3c	same as 3c		err bars are mean +/- SEM		p = 0.0376 p = 0.9861		t(10)=2.395 t(6)=0.01822	
+ -	4g	paired ttests baseline vs washout	Fig legend	11,6	max 3 neurons/ mouse; 6,4 mice		err bars are mean +/- SEM		p = 0.0372 p = 0.5141		t(10)=2.401 t(5)=0.7018	

+ -	4h	paired ttests baseline vs washout	Fig legend	same as 3c	same as 3c		err bars are mean +/- SEM		75th percentile: CRF neurons: p = 0.0411 non-CRF neurons: p = 0.5556		75th percentile: CRF neurons: t(10)=2.343 non-CRF neurons: t(6)=0.6240	
+ -	5c	2x2 RM ANOVA; post-hoc ttests baseline vs CNO	Fig legend	12,11	indiv mouse		indiv data points		ANOVA: virus: p = 0.3880 CNO: p < 0.0001 interaction: p = 0.0138 posthocs: CON: p = 0.1169 Gi-DREADD: p < 0.0001		ANOVA: virus: F(1,21)=0.7771 CNO: F(1,21)=29.79 interaction: F(1,21)=7.265 posthocs: CON: t(11)=1.701 Gi-DREADD: t(10)=6.238	
+ -	5d	2x2 RM ANOVA; post-hoc ttests baseline vs CNO	Fig legend	same as 4c	same as 4c		indiv data points		ANOVA: virus: p = 0.1338 CNO: p = 0.4601 interaction: p = 0.0465 posthocs: CON: p = 0.6593 Gi-DREADD: p = 0.0103		ANOVA: virus: F(1,21)=2.433 CNO: F(1,21)=0.5664 interaction: F(1,21)=4.476 posthocs: CON: t(1)=0.4531 Gi-DREADD: t(10)=3.149	
+ -	5e	unpaired ttest	Fig legend	same as 4c	same as 4c		err bars are mean +/- SEM		p = 0.5480		t(21)=0.6107	
+ -	5h	2x2 RM ANOVA	Fig legend	12,7	indiv mouse		indiv data points		ANOVA: virus: p = 0.1728 CNO: p = 0.5467 interaction: p = 0.3546		ANOVA: virus: F(1,17)=2.025 CNO: F(1,17)=0.3783 interaction: F(1,17)=0.9057	
+ -	5i	2x2 RM ANOVA	Fig legend	same as 4h	same as 4h		indiv data points		ANOVA: virus: p = 0.5232 CNO: p = 0.0059 interaction: p = 0.8160		ANOVA: virus: F(1,17)=0.4249 CNO: F(1,17)=9.916 interaction: F(1,17)=0.05584	
+ -	5j	unpaired ttest	Fig legend	same as 4h	same as 4h		err bars are mean +/- SEM		p = 0.7074		t(17)=0.3817	
+ -	5k	unpaired ttest	Fig legend	9,5	indiv mouse		err bars are mean +/- SEM		p = 0.0362		t(12)=2.358	
+ -	Supp 5c	paired ttest baseline vs washout	Fig legend	9	max 4 cells/mouse; 4 mice		err bars are mean +/- SEM		p = 0.0038		t(8)=4.032	

Representative figures

1. Are any representative images shown (including Western blots and immunohistochemistry/staining) in the paper?

   If so, what figure(s)?

Rep traces from whole-cell voltage-clamp and current-clamp recordings:
Fig 1g,h,l
Fig3j
Fig 4b,g
Supp Fig. 5b

Rep images for fluorescence expression in reporter mice and Cre mice injected with virus:
Fig 4a
Fig. 5b,g

Rep images for immunohistochemistry:
Fig 2a

2. For each representative image, is there a clear statement of how many times this experiment was successfully repeated and a discussion of any limitations in repeatability?

   If so, where is this reported (section, paragraph #)?

Yes, n's for experiments represented always listed in figure legend. Images shown were replicated for every N in experiment.

Statistics and general methods

1. Is there a justification of the sample size?

   If so, how was it justified?

   Where (section, paragraph #)?

   Even if no sample size calculation was performed, authors should report why the sample size is adequate to measure their effect size.

Sample sizes for behavioral experiments were sufficiently large to allow for loss of Ns due to missed placements. Sample sizes for electrophysiology experiments were consistent with our lab's previously reported N's for the study of these drugs and peptides. This is reported in the Statistical Analysis methods section.

2. Are statistical tests justified as appropriate for every figure?

   Where (section, paragraph #)?

Yes, and they are described in statistical analysis section of Methods and are listed in Figure legends.

   a. If there is a section summarizing the statistical methods in the methods, is the statistical test for each experiment clearly defined?

yes

   b. Do the data meet the assumptions of the specific statistical test you chose (e.g. normality for a parametric test)?

      Where is this described (section, paragraph #)?

Yes, and corrections/alternate stats used when necessary.

   c. Is there any estimate of variance within each group of data?

      Is the variance similar between groups that are being statistically compared?

      Where is this described (section, paragraph #)?

Yes, except where noted and corrected when necessary. This is reported in stats description and during reporting of individual results in Figure legends.

   d. Are tests specified as one- or two-sided?

Yes, reported and always conducted as two-sided.

e. Are there adjustments for multiple comparisons?	Yes, primarily Sidak's multiple comparisons test; This is reported when used.
3. Are criteria for excluding data points reported? Was this criterion established prior to data collection? Where is this described (section, paragraph #)?	Yes, described in methods section. For behavior, only mice with missed injections/cannulae placements were excluded; for electrophysiology, excluders included only outliers over 2.5 standard deviations from the mean for baseline measurements or neurons for which membrane properties drifted (common exclusion criteria for slice physiology).
4. Define the method of randomization used to assign subjects (or samples) to the experimental groups and to collect and process data. If no randomization was used, state so. Where does this appear (section, paragraph #)?	For behavioral pharmacology exps, drug/vehicle groups were randomly assigned such that baseline pre-surgery consumption levels were similar between groups. For experiments with Cre mice, mice were randomly assigned to groups such that age and bodyweight were counterbalanced between groups such that litters were represented in all groups. For all other experiments, WT mice were randomly assigned to groups because mice were ordered so that age and bodyweight were similar.
5. Is a statement of the extent to which investigator knew the group allocation during the experiment and in assessing outcome included? If no blinding was done, state so. Where (section, paragraph #)?	Experimenters were always blind to condition. Statements are made throughout the methods section as needed.
6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included? Where (section, paragraph #)?	Yes, beginning of methods section.
7. Is the species of the animals used reported? Where (section, paragraph #)?	Yes, beginning of methods section.
8. Is the strain of the animals (including background strains of KO/ transgenic animals used) reported? Where (section, paragraph #)?	Yes, in methods section.
9. Is the sex of the animals/subjects used reported? Where (section, paragraph #)?	Yes, beginning of methods section and throughout as needed.
10. Is the age of the animals/subjects reported? Where (section, paragraph #)?	Yes, beginning of methods section.
11. For animals housed in a vivarium, is the light/dark cycle reported? Where (section, paragraph #)?	Yes, in methods section.
12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported? Where (section, paragraph #)?	Mice were singly housed for home cage drinking experiments, as described in methods.

13. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)?

    Where (section, paragraph #)?

Yes, always reported, as this is critical to results.

14. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported?

    Where (section, paragraph #)?

Yes, with time lines of experimental procedures included in figures and described in detail in methods section.

    a. If multiple behavioral tests were conducted in the same group of animals, is this reported?

       Where (section, paragraph #)?

Yes, with time lines of experimental procedures included in figures and described in detail in methods section.

15. If any animals/subjects were excluded from analysis, is this reported?

    Where (section, paragraph #)?

Yes, described in methods section. For behavior, only mice with missed injections/cannulae placements were excluded; for electrophysiology, excluders included only outliers over 2.5 standard deviations from the mean for baseline measurements or neurons for which membrane properties drifted (common exclusion criteria for slice physiology). All exclusions are reported.

    a. How were the criteria for exclusion defined?

       Where is this described (section, paragraph #)?

    b. Specify reasons for any discrepancy between the number of animals at the beginning and end of the study.

       Where is this described (section, paragraph #)?

Reagents

1. Have antibodies been validated for use in the system under study (assay and species)?

Yes, and reported with citations in text.

    a. Is antibody catalog number given?

       Where does this appear (section, paragraph #)?

    b. Where were the validation data reported (citation, supplementary information, Antibodypedia)?

       Where does this appear (section, paragraph #)?

2. If cell lines were used to reflect the properties of a particular tissue or disease state, is their source identified?

    Where (section, paragraph #)?

    a. Were they recently authenticated?

       Where is this information reported (section, paragraph #)?

Data deposition

Data deposition in a public repository is mandatory for:

a. Protein, DNA and RNA sequences
b. Macromolecular structures
c. Crystallographic data for small molecules
d. Microarray data

Deposition is strongly recommended for many other datasets for which structured public repositories exist; more details on our data policy are available here. We encourage the provision of other source data in supplementary information or in unstructured repositories such as Figshare and Dryad.

We encourage publication of Data Descriptors (see Scientific Data) to maximize data reuse.

1. Are accession codes for deposit dates provided?

   Where (section, paragraph #)?

Computer code/software

Any custom algorithm/software that is central to the methods must be supplied by the authors in a usable and readable form for readers at the time of publication. However, referees may ask for this information at any time during the review process.

1. Identify all custom software or scripts that were required to conduct the study and where in the procedures each was used.

2. If computer code was used to generate results that are central to the paper's conclusions, include a statement in the Methods section under "**Code availability**" to indicate whether and how the code can be accessed. Include version information as necessary and any restrictions on availability.

Human subjects

1. Which IRB approved the protocol?

   Where is this stated (section, paragraph #)?

2. Is demographic information on all subjects provided?

   Where (section, paragraph #)?

3. Is the number of human subjects, their age and sex clearly defined?

   Where (section, paragraph #)?

4. Are the inclusion and exclusion criteria (if any) clearly specified?

   Where (section, paragraph #)?

5. How well were the groups matched?

   Where is this information described (section, paragraph #)?

6. Is a statement included confirming that informed consent was obtained from all subjects?

   Where (section, paragraph #)?

7. For publication of patient photos, is a statement included confirming that consent to publish was obtained?

   Where (section, paragraph #)?

fMRI studies

For papers reporting functional imaging (fMRI) results please ensure that these minimal reporting guidelines are met and that all this information is clearly provided in the methods:

1. Were any subjects scanned but then rejected for the analysis after the data was collected?

   a. If yes, is the number rejected and reasons for rejection described?

      Where (section, paragraph #)?

2. Is the number of blocks, trials or experimental units per session and/or subjects specified?

   Where (section, paragraph #)?

3. Is the length of each trial and interval between trials specified?

4. Is a blocked, event-related, or mixed design being used? If applicable, please specify the block length or how the event-related or mixed design was optimized.

5. Is the task design clearly described?

   Where (section, paragraph #)?

6. How was behavioral performance measured?

7. Is an ANOVA or factorial design being used?

8. For data acquisition, is a whole brain scan used?

   If not, state area of acquisition.

   a. How was this region determined?

9. Is the field strength (in Tesla) of the MRI system stated?

    a. Is the pulse sequence type (gradient/spin echo, EPI/spiral) stated?

    b. Are the field-of-view, matrix size, slice thickness, and TE/TR/flip angle clearly stated?

10. Are the software and specific parameters (model/functions, smoothing kernel size if applicable, etc.) used for data processing and pre-processing clearly stated?

11. Is the coordinate space for the anatomical/functional imaging data clearly defined as subject/native space or standardized stereotaxic space, e.g., original Talairach, MNI305, ICBM152, etc? Where (section, paragraph #)?

12. If there was data normalization/standardization to a specific space template, are the type of transformation (linear vs. nonlinear) used and image types being transformed clearly described? Where (section, paragraph #)?

13. How were anatomical locations determined, e.g., via an automated labeling algorithm (AAL), standardized coordinate database (Talairach daemon), probabilistic atlases, etc.?

14. Were any additional regressors (behavioral covariates, motion etc) used?

15. Is the contrast construction clearly defined?

16. Is a mixed/random effects or fixed inference used?

    a. If fixed effects inference used, is this justified?

17. Were repeated measures used (multiple measurements per subject)?

    a. If so, are the method to account for within subject correlation and the assumptions made about variance clearly stated?

18. If the threshold used for inference and visualization in figures varies, is this clearly stated?

19. Are statistical inferences corrected for multiple comparisons?

    a. If not, is this labeled as uncorrected?

20. Are the results based on an ROI (region of interest) analysis?

    a. If so, is the rationale clearly described?

    b. How were the ROI's defined (functional vs anatomical localization)?

21. Is there correction for multiple comparisons within each voxel?

22. For cluster-wise significance, is the cluster-defining threshold and the corrected significance level defined?

Additional comments

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