A data-driven approach to the automated study of cross-species homologies

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Abstract

Behavioral neuroscience has made great strides in developing animal models of human behavior and psychiatric disorders. Animal models allow for the formulation of hypotheses regarding the mechanisms underlying psychiatric disorders, and the opportunity to test these hypotheses using procedures that are too invasive for human participants. However, recent scientific reviews have highlighted the low success rate of translating results from animal models into clinical interventions in humans. One roadblock for increasing this success rate is an only incomplete bidirectional functional mapping between the human and rodent brain. In an attempt to narrow this gap we created a framework for performing large-scale automated synthesis of human neuroimaging data and behavioral neuroscience data. This framework enables region to region mapping of brain regions across species, as well as cross-species mapping of psychological functions. As a proof of concept, we utilize the framework to create a biredictional cross-species mapping between the amygdala and hippocampus for fear-related and spatial memories, respectively. We then proceed to address two open questions in the field: (1) Do rodents have a dorsolateral prefrontal cortex? (2) Which human brain region corresponds to the rodent prelimbic cortex?

The current understanding of the biological processes underlying brain disorders is strongly informed by animal models, in which mechanistic hy-

potheses can be tested using procedures that are too invasive for human subjects. However, uncertainty about whether analogous neural mechanisms are conserved in the human brain has undermined progress in identifying specific biological mechanisms and corresponding therapeutic targets [1]. Currently, research aimed at developing new treatments for brain disorders is under threat, as prominent pharmaceutical companies have cut research funding dedicated to developing drugs for psychiatric disorders [2].

For example, drug-addiction related expenditure alone is estimated at between 0.01% and 0.5% of GDP in Europe [3], and about 4% of GDP in the U.S.A. (including costs related to crime, lost work productivity and health care) [4]. One particularly fecund theoretical framing in this context is the distinction between goal-directed and habitual behavior. Human and non-human animals face a constant trade-off in decision-making (for a review, see [5]): they can either deploy cognitive effort to evaluate alternative ways of attaining desirable outcomes, or instead fall back on habits, which by definition involve no consideration of potential outcomes. Habits are often adaptive, allowing individuals to devote excess cognitive resources to more demanding challenges [6]. But there's no free lunch. Habits are also relatively inflexible, and therefore maladaptive when they no longer lead to desired outcomes [7, 8]. Dysfunctional persistence of habitual behavior is a candidate source of pathological substance use, as well as in various other clinical conditions, including eating-disorders, obsessive-compulsive disorder, and drug-use disorders [9]. Given that maladaptive habitual behaviors are implicated in debilitating addictions and clinical disorders, there is much interest in understanding the neural mechanisms governing deployment of habitual versus goal-directed behaviors.

However, most of the insights into the underlying mechanisms of drug addiction have been derived from animal models [10]. The central aim of the present work is therefore to develop a novel data-driven interdisciplinary approach, to systematically characterize cross-species homologies. To this end, we developed an extension, NeuroBabel, for an existing framework for brain mapping. This existing framework, NeuroSynth [11], was developed to perform large-scale automated synthesis of human neuroimaging data, by combining information regarding the location of reported brain activation with the frequency (term frequency–inverse document frequency, tf-idf) of scientific terms in each published neuroimaging study, to create a term-to-coordinate mapping. This mapping has been highly successful in synthesizing results from neuroimaging studies, by enabling large-scale automated meta-analyses and enabling the decoding of mental states [12, 13, 14, 15]. We critically expand on this existing framework by also including infor-

mation from published rodent studies. That is, we added coordinates of surgical procedures in the rodent brain, as well as the frequency of scientific terms in the companion articles. In addition to enabling the functionality of synthesizing the results of rodent studies, analogous to the functionality of NeuroSynth for human neuroimaging studies, this framework provides a formal quantitative link between the rodent and human neuroscience literature. By using the distribution of word frequencies of scientific terms shared by the two neuroscientific fields, this framework enables a bidirectional functional mapping between the rodent and the human brain.

1 Results

1.1 Overview

The present extension was created in several steps. First, we built a web crawler to identify and download articles of studies that included a intracranial surgical intervention. Specifically, for this first release, we downloaded articles from ScienceDirect, if they were published after 1995 and included the keyword "bregma", which is often used as reference for stereotaxic intracranial surgery. Second, we developed a text-mining tool that would extract the target coordinates of the performed surgeries. Third, we calculated the word frequency of scientific terms in each study. Specifically, we calculated the term frequency–inverse document frequency (tf-idf), which is a measure intended to reflect the importance of a word to a text document. Fourth, we combined these data with the existing neurosynth dataset, including the word frequency of scientific terms from vocabulary shared between the included neuroimaging and behavioral neuroscience studies. This resulted in a data set with 2668 rodent studies with 5276 surgery coordinates (Figure 1), and 6579 neuroimaging studies with 236254 activation voci, and a shared vocabulary of 2579 scientific terms.

We then proceeded to systematically validate the ability of our framework to provide functionality for the rodent literature analogous to that provided for the human neuroimaging literature by NeuroSynth. That is, whether it was possible to meta-analytically decode the function of a brain area. Next, we tested whether it was possible to use this framework to characterize cross-species homologies in the functional architecture of human and rodent brains.

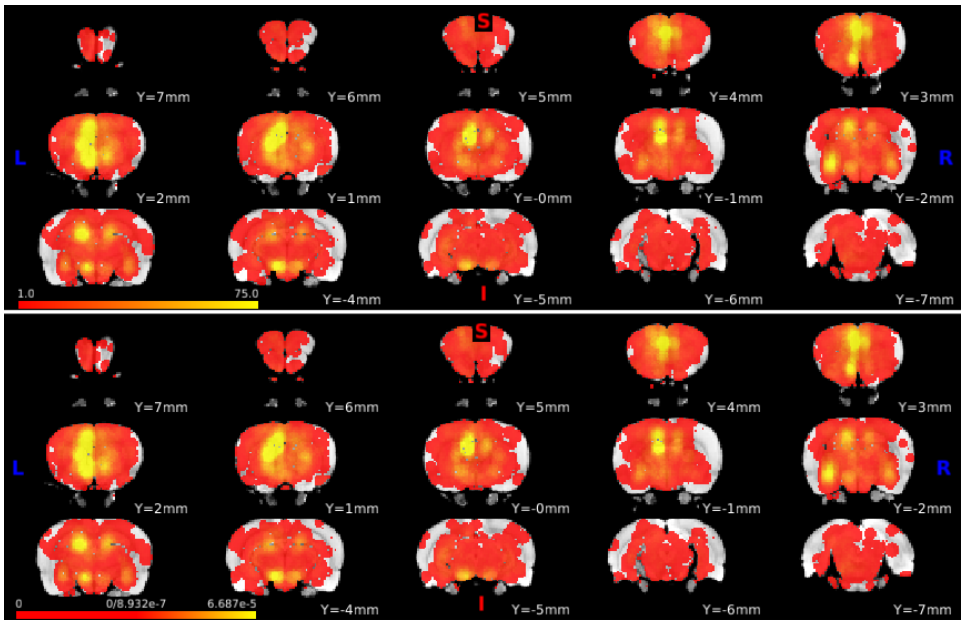

Figure 1: Distribution of extracted surgery coordinates. (Top) shows absolute count, in terms of number of studies, and (Bottom) shows the density, that is after dividing (Top) by the sum total of extracted surgery coordinates (n=5276). The figure shows that studies that used bregma as reference for intracranial surgery tended to focus on the rodent prelimbic and infralimbic cortex, the hippocampal region, amygdala, and hypothalamus.

1.2 Forward and Reverse Inference

One of the breakthrough functionalities of the NeuroSynth framework is that it enables quantitative reverse inference, in addition to forward inference, regarding the relationship between the psychological states of participants and activation across different areas of the brain. In contrast, most hypothesis-driven neuroimaging studies depend on forward inference, which answers important questions such as, "Which brain areas become active when participants view fearful facial expressions?" Although forward inference is a powerful tool, its explanatory power falls short of that of reverse inference [16, 11], which addresses critical, conceptually distinct questions about functional specialization; for example, "Can we infer that participants were viewing fearful facial expressions, given the pattern of activation across the brain?"

Reverse inference is a powerful tool for synthesizing results across neuroimaging studies for at least two reasons. First and foremost, reverse inference takes results from studies into account that may have targeted the same brain region, but were motivated by questions from different subfields of human neuroscience. This is for example the case for the dorsal anterior cingulate region, where consensus regarding its function is only slowly emerging (for a discussion, see e.g. [13] and [17]). However, a second reason for the power of reverse inference is that neuroimaging studies often report activation in parts of the brain that were not the primary region of interest of the study. For example, a recent meta-analysis of the human striatum has reported that the anterior putamen was associated with social and language functions [15], but also that there was no single mention of the striatum in the most characteristic study for this region, in terms of striatal activation voci and decoded psychological function [18].

While it is unlikely that a behavioral neuroscientist performed surgery in a brain region that was not relevant to the primary study aims, reverse inference still enables the synthesis of results across diverse subfields of behavioral neuroscience. To demonstrate this, we compared the results of forward and reverse inferences with the psychological term "fear" from the above example. That is, forward inference asks whether it is possible to predict where surgery was performed, given the importance of the word "fear" in an article. On the other hand, reverse inference asks whether it was possible to predict whether the term fear would appear in an article, given that surgery was performed in a particular part of the brain. Given the well-established role of the amygdala in fear conditioning [19], one would predict that both, forward and reverse inference would point towards this region.

Furthermore, it is also well-established that the hippocampal region is involved in fear conditioning, especially in contextual fear conditioning [20]. However, because this region is involved more generally in diverse forms of memory, such as spatial and episodic memory [21, 22], reverse inference should predict a relative low probability of the word fear in an article, given that surgery was performed in this region. As shown in Fig. 2 this is exactly what we found.

1.3 Cross-species mapping of psychological functions

The central aim for developing the present framework was to create a quantitative link between findings in behavioral neuroscience and human neuroimaging studies. This data-driven approach can be utilized to investigate cross-species homologies. This quantitative link was created in two sequential steps: First, we would query which scientific terms are associated with the brain region of interest in one species. Second, we would query which regions of the brain in the other species are associated with these terms (see Methods subsection "Cross-species mapping of psychological functions").

1.3.1 Validation of approach

To validate our approach, we performed a test query for two well-established results in the human and animal literature, that (1) the amygdala is critically involved in fear-related functions, such as recognizing fearful facial expressions in humans [23] and during fear conditioning [20], and that (2) the hippocampus supports spatial memory [21, 22].

We proceeded by first performing separate reverse inferences using the terms "fear" and "spatial memory" for rodents: For each voxel of the rodent brain, we asked given that surgery was performed in this voxel, what is the probability that the term appeared in the article. This resulted in a statistical map, which we would then project into the human brain, using the two step approach described above.

As expected, reverse inference in the rodent brain revealed a selective association of the amygdala with fear, and the hippocampal region with spatial memory (Figure 3, left). We then applied the two-step approach for projecting these regions into the human brain. As expected, we found that the rodent statistical map for fear was projected onto the human amygdala, while the statistical map for spatial memory was projected onto the human hippocampus (Figure 3, right). The center panel of Figure 3 further shows that the top ten scientific terms linking the two species are consistent

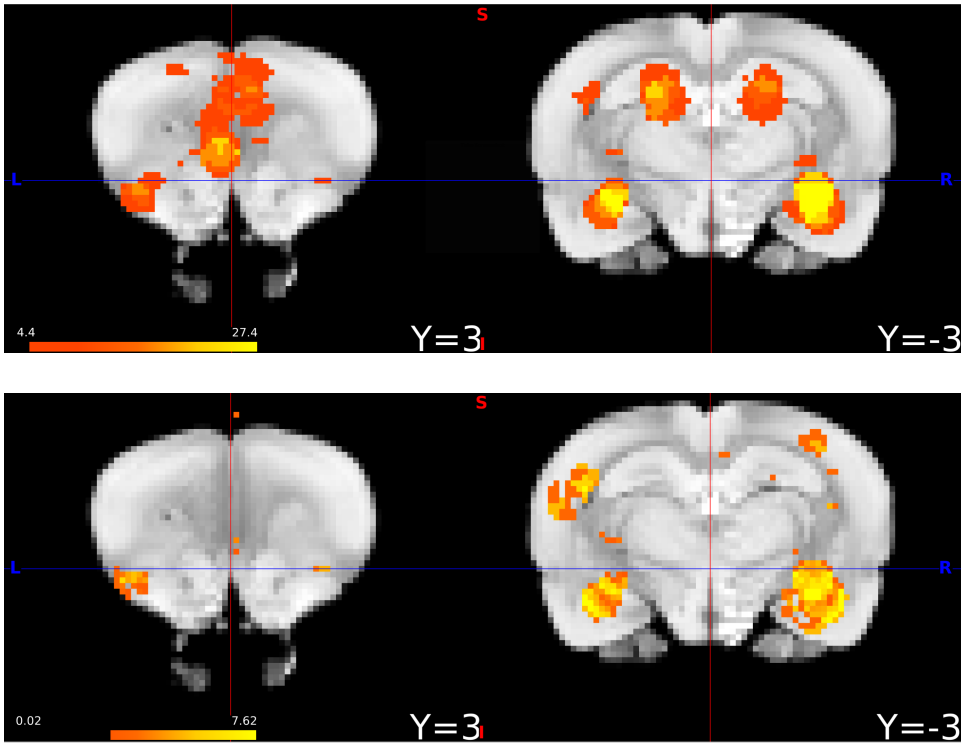

Figure 2: Forward and reverse inference for the term "fear". (Top) Results (z-scores) of forward inference, that is: Given the term "fear" appeared in an article, what is the probability of intracranial surgery having been performed in each voxel of the rodent brain? (Bottom) Results of reverse inference, that is: Given that surgery was performed in a particular voxel of the rodent brain, what is probability that the term "fear" appeared in the article. One notable difference is that the hippocampal only appears during forward inference, but not during reverse inference. While this may be partially due to overall weaker results for reverse inference, it may also reflects the fact that the in comparison to the amygdala, the hippocampal formation supports spatial and contextual memory in general, while the amygdala is more specifically involved in fear-related processes. Note: different scales were used for forward and reverse inference results.

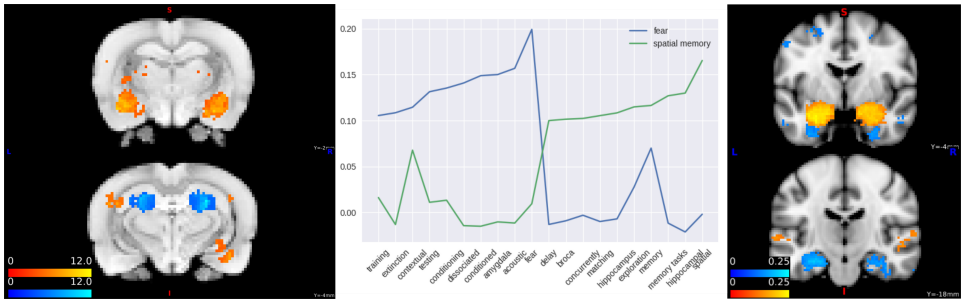

Figure 3: Cross-species mapping of "fear" and "spatial memory" from the rodent to the human brain. (Left) Results (z-scores) of reverse inference for "fear" (orange-yellow) and "spatial memory" (blue-lightblue). (Center) Top-ten scientific terms associated with brain regions identified via reverse inference for the same terms. (Right) Human brain regions associated with the psychological terms in the center panel. Overlays show Pearson correlations.

with the well-established functions of these two regions in either species. In summary, these results suggest that our approach represents a data-driven framework for investigating cross-species homologies.

1.3.2 Projection of rat prelimbic cortical map onto the human brain

After this validation of our approach, we proceeded to address an open question in decision neuroscience: What human brain regions correspond to the rodent prelimbic cortex? Research in rodents has accrued a wealth of evidence that this regions interacts with the dorsomedial striatum to support the acquisition and performance of goal-directed behavior [24, 25, 26]. Recent reviews of cross-species homologies have suggested that the human ventromedial prefrontal cortex may serve psychological functions similar to those functions associated with the rodent prelimbic cortex [27, 28], as the human ventromedial prefrontal cortex and the rodent prelimbic cortex seem to be similarly involved in discovering action - reward contingencies in the service of goal-directed behavior [29].

To address this question, we first created an anatomical mask for the rodent prelimbic cortex [30] (not shown), to then use the above two-step approach to project this region into the human brain. We found that this resulted in a distributed set of clusters in the human brain, including the lat-

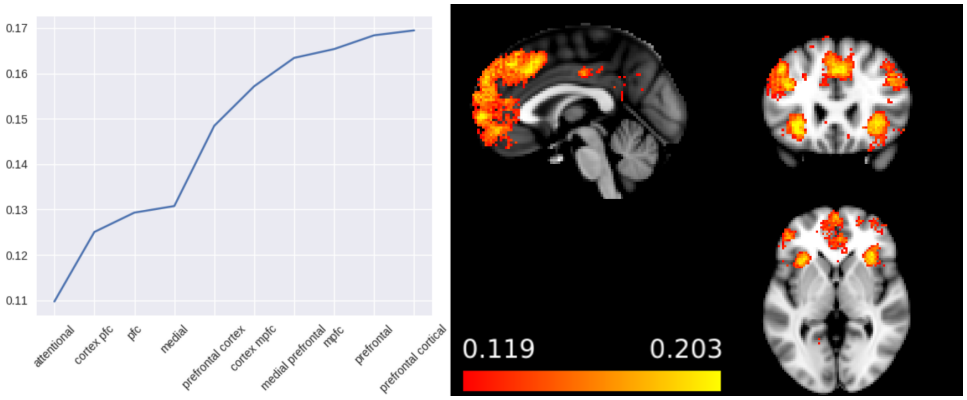

Figure 4: Cross-species mapping of the rodent prelimbic cortex into the human brain. (Left) Top-ten scientific terms identified in the decoding of the anatomical region of the prelimbic cortex in rodents. (Right) The cross-species mapping identified a distributed set of clusters, including the medial dorsal and ventral frontal cortices, dorsolateral prefrontal cortex, as well as anterior insular cortex. Overlay shows Pearson correlations.

eral prefrontal cortex, anterior amygdala, and dorsomedial prefrontal cortex (Figure 4, right). Interestingly, despite this distributed set of brain regions, we found that the top ten scientific terms associated with the rodent prelimbic cortex were predominantly anatomical terms referring to the (medial) prefrontal cortex 4, left).

1.3.3 Projection of human dorsolateral prefrontal cortex onto the rat brain

Next, we utilized our framework to query it for the rodent homologue of the human dorsolateral prefrontal cortex. Whether rodents have a homologue of the human dorsolateral prefrontal cortex is still a matter of debate. It has been argued that based on anatomical and functional characteristics, the rodent prelimbic cortex, dorsal anterior cingulate cortex, and frontal cortical area 2 may constitute a rodent homologue of dorsolateral prefrontal cortex (for a review, see [31]). To address this questions, we followed an approach analogous to the above query regarding the human homologue of the rodent prelimbic cortex. We created an anatomical mask of the middle frontal gyrus, according to the Harvard-Oxford human anatomical atlas [32, 33]. Next, we decoded the psychological function of this area in humans, to

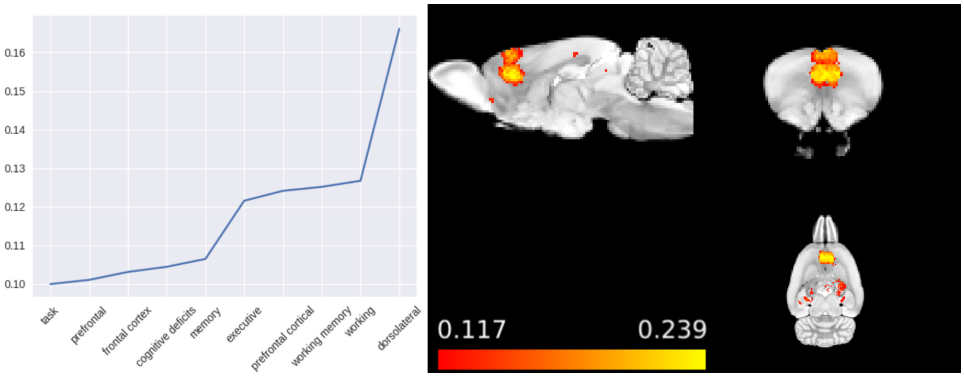

Figure 5: Cross-species mapping of the human medial frontal gyrus into the rodent brain. (Left) Top-ten scientific terms associated with an anatomical map of the human medial frontal gyrus. (Right) The cross-species mapping identified the rodent prelimbic and anterior cingulate cortex to correspond to the human medial frontal gyrus. Overlay shows Pearson correlations.

then investigate which regions in the rodent brain are associated with these psychological functions. We found that this procedure lead to an almost exclusive selection of the rodent prelimbic cortex and the anterior cingulate cortex (see Figure 5).

2 Discussion

The aim of this work was to create an easily expandable extension of the well-established NeuroSynth framework for human neuroimaging data, to provide (1) analogous analytic tools for the rodent literature, and (2) a data-driven tool for characterizing cross-species homologies between human and rodent brains.

Despite the emerging view in the field that the human ventromedial prefrontal cortex shares functional similarities with the rodent prelimbic cortex [27], our transcoding procedure selected a distributed set of cortical regions. While a previous review [31] suggested that the medial surface of the rodent frontal cortex is more differentiated in humans and distributed across the lateral prefrontal cortex, our results go beyond this by including the anterior insular cortex. Future analyses may be able to disentangle whether this divergence is caused simply by difference in the functional architectures across species, or whether it is a fundamental short-coming of

the present approach, which relies on how scientist describe the methods, results, and goal of their studies.

Several critical limitations of our dataset and approach should be kept in mind. These are largely the same as for the original NeuroSynth framework. Most critically, the results depend largely on the consensus in the field regarding the function of a brain region. For example, consider the case that only a small number of studies have uncovered the true psychological function of a brain region, while a large number of studies on a brain region assign a different, potentially more specific and appropriate, function to the same brain region. In this case, the results from applying the present approach would most likely be dominated by the large number of studies that reached an inaccurate consensus regarding the psychological function of this region, rather than by the small number of studies which have uncovered the true psychological function of a brain region.

A further limitation of the present dataset is that it only includes surgery coordinates, if they were presented with bregma as reference. This limitation can be easily overcome in future data releases, which can also include surgery coordinates with other anatomical references (e.g. interaural). However, this limitation is substantial, and should be kept in mind when interpreting the results of forward and reverse inference, as well as of the transcoding procedure.

Related to the previous limitation, the present dataset is limited by where in the brain researchers have performed intracranial surgery. This limitation is largely absent for the original neurosynth dataset, because neuroimaging studies often collect functional data from the whole brain, even if the aim of a research project is focused on a particular part of the brain.

This difference between the present dataset and the original dataset is also important when interpreting diverging results of forward and reverse inference. In the original NeuroSynth dataset, this divergence is driven by two factors. First, by the fact that reverse inference is relatively more apt at integrating findings across studies from different neuroimaging subfields, which may investigate the role of a particular brain region across a diverse set of psychological functions. Second, human neuroimaging studies oftentimes include tables reporting activation coordinates in parts of the brain that were not the focus of the study. Both these factors contribute to the strength of reverse inference as provided by the Neurosynth framework. In contrast, in the present dataset only the first of the two factors contributes to different results from forward and reverse inference.

We consider the present results a demonstration of some of the capabilities provided by the current dataset. Several extension and improvements

are plausible and easily attainable.

Similar to how the original Neurosynth dataset has grown in size since its initial conception, the automated nature of aggregating studies, extracting surgery coordinates, and text-mining of companion articles will also allow the present dataset to evolve over time. Furthermore, as mentioned above, future release should also consider surgery coordinates that are not reported with bregma as reference.

Furthermore, the dataset will enable scientists to ask research questions beyond the demonstrations presented here. For example, this dataset could be used by scientists from one field of neuroscience to determine which scientists in the other field may be interested in collaborations. Another application of this dataset could be to not only consider where surgery was performed, but also which manipulation (e.g. micro-infusion versus lesion), or which pharmacological manipulation was performed.

Finally, the present demonstration was limited to the well-established methods often applied for the original neurosynth dataset. Advanced machine learning techniques could be applied to the present dataset as well. For example, rather than relying simply on the word frequency (tf-idf) of scientific terms, the present dataset would allow the application of more advanced natural language processing algorithms.

Overall, the results presented here demonstrate the feasibility of a natural extension of the neurosynth framework to also include rodent studies. We believe that this approach could lead to increased collaboration between the fields of human and behavioral neuroscience. In particular, it may facilitate efforts of determining to which degree findings from animal models may translate into human neuroscience. This could lead to the development of novel targeted psychiatric interventions.

3 Methods

3.1 Automated coordinate extraction

Surgery coordinates were extracted algorithmically, by first identifying the method section of an article, followed by an identification of sentences which included the keyword "bregma". Bregma is an anatomical landmark, which is frequently used as reference during intracranial surgeries. Coordinates were then extracted using regular expressions, working under the assumption that coordinates would be expressed in numbers, in between the keywords "anterior " or "posterior", "medial" or "lateral", and "dorsal" or "ventral". An ordered sequence of more relaxed regular expression was tested consec-

utively, until a match was found. Please refer to the github repository for details: https://github.com/wmpauli/ACE/.

The present data set does not take into account the age or weight of rodents included in each of the studies. While this should ideally be done, to achieve a higher accuracy for surgery coordinates, we argue that due to the large number of included studies, the effect of age and weight of rodents should not introduce a systematic bias.

3.2 Correction for different habits of performing surgery

After coordinate extraction, we identified studies in which the depth of the surgery coordinates were expressed in distance from dura or skull, rather than the more common approach to rely on bregma as dorsal/ventral reference. In these studies, we applied a non-linear correction of the reported coordinates to take into account the medial-lateral and anterior-posterior curvature of the surface of the rodent skull. The amount of adjustment was determined using an anatomical atlas [30].

3.3 Data Preparation

After extraction of surgery coordinates, coordinates where converted to the Waxholm Space Atlas of the Sprague Dawley Rat Brain [34], to enable the application of standard neuroimaging libraries for data analysis. A 1mm boxcar smoothing kernel was applied to surgery coordinates.

3.4 Vocabulary of psychological terms

For the purpose of the present analyses, we only included psychological terms that were included in the 2015 data release of neurosynth (version 0.6), but also occurred in the behavioral neuroscience studies included in the present data set (term frequency–inverse document frequency (tf-idf) threshold of 0.001). A total of 2579 psychological terms was included.

3.5 Anatomical ROIs

Anatomical regions of interest (ROIs) were determined according to an anatomical atlas [30].

3.6 Forward and Reverse inference

The present extension of the neurosynth data set was developed with the explicit intend that the all of the existing analysis tools of the neurosynth framework could be leveraged to perform analogous forward and reverse inference analyses, as has been done successfully for neuroimaging data [11]. We refer to the original publication and neurosynth.org for details of the approach. Briefly, for forward inference we calculated the probability that surgery was performed at a given coordinate, given that a psychological term appeared in the companion article (i.e. $P(xyz|term)$). For reverse inference, we calculated $P(term|xyz)$. We present the results of these analyses using the standard approach of neurosynth, i.e. z-scores reflecting the probability that a Mappable has a feature given that activation is present. For display purposes we applied a uncorrected threshold of p=0.001 to statistical maps.

3.7 Cross-species mapping of psychological function

To perform cross-species mappings, we decided to follow an approach that entirely relies on Pearson correlations. We made this choice for two reasons: (1) consistency of this analysis approach with existing methods implemented in the neurosynth framework (decode method), and (2) because of the intuitive understanding of Pearson correlation by a broad readership. The cross-species mapping was performed in two steps. First, we decoded the psychological function of each voxel, by calculating the Pearson correlation between activity/surgery in each voxel and the occurrence (tf-idf) of each scientific term across studies. This was done separately for each species, yielding two (one per species) v_s x t voxel-by-term matrices X_s, where v_s is the number of voxels in a species s, and t is the number of scientific terms in the vocabulary shared between human and animal literature (this step was performed using the "decode" function of the neurosynth framework). To perform the functional cross-species mapping of a brain region of interest in one species to the other species, we first normalized each matrix X_s, by subtracting the row-means, and then dividing by the square-root of row-sum of squares. This allowed us to calculate Pearson correlations with dot products of matrices. We decoded the function of a region of interest, by calculating the dot product of the associated 1 x v_s brain mask M_s and X_s, yielding a 1 x t term vector T. Next, we determined which brain voxels in the other species were associated with this term vector, by calculating the dot product of the (normalized) term vector T and the transpose of the voxel-by-term matrix X_s of the other species. This yielded a 1 x v_s vector, indicating how

strongly the function of each voxel in the second species correlated with the function of the region of interest in the first species. In addition, this analysis produced the term vector T, representing a functional/quantitative link between the two statistical maps.

3.8 Code Availability

The source code for creating the data set and performing the analyses reported here will are available as a github repository:
https://github.com/wmpauli/neurosynth.

3.9 Data Availability

The above repository also includes the present release of the dataset.

4 Acknowledgments

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