



Computational Neuroscience

Automated cognome construction and semi-automated hypothesis generation

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ARTICLE INFO

Article history:

Received 15 March 2012

Received in revised form 11 April 2012

Accepted 24 April 2012

Keywords:

Literature mining

Hypothesis generation

Semi-automated science

Cognome

Connectome

ABSTRACT

Modern neuroscientific research stands on the shoulders of countless giants. PubMed alone contains more than 21 million peer-reviewed articles with 40–50,000 more published every month. Understanding the human brain, cognition, and disease will require integrating facts from dozens of scientific fields spread amongst millions of studies locked away in static documents, making any such integration daunting, at best. The future of scientific progress will be aided by bridging the gap between the millions of published research articles and modern databases such as the Allen brain atlas (ABA). To that end, we have analyzed the text of over 3.5 million scientific abstracts to find associations between neuroscientific concepts. From the literature alone, we show that we can blindly and algorithmically extract a “cognome”: relationships between brain structure, function, and disease. We demonstrate the potential of data-mining and cross-platform data-integration with the ABA by introducing two methods for semi-automated hypothesis generation. By analyzing statistical “holes” and discrepancies in the literature we can find understudied or overlooked research paths. That is, we have added a layer of semi-automation to a part of the scientific process itself. This is an important step toward fundamentally incorporating data-mining algorithms into the scientific method in a manner that is generalizable to any scientific or medical field.

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1. Introduction

The scientific method begins with a hypothesis about our reality that can be tested via experimental observation. Hypothesis formation is iterative, building off prior scientific knowledge. Before one can form a hypothesis, one must have a thorough understanding of previous research to ensure that the path of inquiry is founded upon a stable base of established facts. But how can a researcher perform a thorough, unbiased literature review when over one million scientific articles are published annually (Björk et al., 2008)? The rate of scientific discovery has outpaced our ability to integrate knowledge in an unbiased, principled fashion. One solution may be via automated information aggregation (Akil et al., 2001). In this manuscript we show that, by calculating associations between concepts in the peer-reviewed literature, we can algorithmically synthesize scientific information and use that knowledge to help formulate plausible low-level hypotheses.

Neuroscience is a particularly complex discipline that relies upon expertise from many disparate fields (Akil et al., 2001). The aim of neuroscience is to understand relationships between brain,

behavior, and disease; yet, no one person or group can possibly unify all neuroscientific understanding into a coherent framework. In this paper, we show that the literature contains a hidden network of connected facts that, by definition, recapitulate known neuroscientific relationships. Neuroanatomical, behavioral, and disease associations can be quantified and visualized to speed research and education or to discover understudied research paths (Yarkoni et al., 2010; Wren et al., 2004; Bilder et al., 2009). Rather than allowing our limited ability to review the entire scientific literature bias our hypotheses, we can algorithmically integrate millions of scientific research papers in a principled fashion.

To accomplish this, we used a co-occurrence algorithm to calculate the pair-wise association index (AI) between neuroscientific terms (and their synonyms) contained within more than 3.5 million papers indexed in PubMed (see Section 2). The primary assumption is that the frequency with which terms appeared together across the titles or abstracts of manuscripts is proportional to their probability of association. That is, we assumed an underlying structure within the peer-reviewed neuroscientific literature that we could leverage to our advantage. We conceive of our system as a proof-of-concept tool for knowledge discovery limited only by the size and quality of the inputs. We believe that, in its current state, when combined with the website search and visualization system we created to accompany it (<http://www.brainscanr.com>), it acts as a more sophisticated complement to normal PubMed searches. Furthermore, it provides, for the first time, a method for quantifying

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the relationship between disparate neuroscientific concepts, paving the way for researchers to incorporate statistical decision making into their future research.

2. Methods

2.1. Data collection

We populated a dictionary with phrases for 124 brain regions, 291 cognitive functions, and 47 diseases. Brain region names and associated synonyms were selected from BrainInfo (2007) (Bowden et al., 2007), Neuroscience Division, National Primate Research Center, University of Washington (Bowden and Dubach, 2003). Cognitive functions were obtained from (<http://www.cognitiveatlas.org/>) (Poldrack et al., 2011). Disease names are from (<http://www.ninds.nih.gov/>). The initial population of the dictionary was meant to represent the broadest, most plausibly common search terms that are also relatively unique (and thus likely not to lead to spurious connections). The full list of terms and their synonyms are included in [Supporting List 1](#).

2.2. Association probabilities

We quantified the association between two terms using a weighted co-occurrence algorithm (Jaccard index) that highlights the unique relationship between term pairs. For any given pair of terms i and j , we define the association index,

$$AI_{i,j} = \frac{c_{i,j} \cap d_{i,j}}{c_{i,j} \cup d_{i,j}},$$

where the intersection between $c_{i,j}$ and $d_{i,j}$ was calculated using the following query of the PubMed database using the ESearch utility and the count return type (using the example c is “prefrontal cortex” and d is “striatum”): [http://eutils.ncbi.nlm.nih.gov/entrez/eutils/esearch.fcgi?db=pubmed&field=word&term=\(“prefrontal+cortex”+OR+“prefrontal+cortices”\)+AND+\(“striatum”+OR+“neostriatum”+OR+“corpus+striatum”\)&rettype=count](http://eutils.ncbi.nlm.nih.gov/entrez/eutils/esearch.fcgi?db=pubmed&field=word&term=(“prefrontal+cortex”+OR+“prefrontal+cortices”)+AND+(“striatum”+OR+“neostriatum”+OR+“corpus+striatum”)&rettype=count) The union was calculated using the sum of two separate queries:

[http://eutils.ncbi.nlm.nih.gov/entrez/eutils/esearch.fcgi?db=pubmed&field=word&term=\(“prefrontal+cortex”+OR+“prefrontal+cortices”\)+NOT+\(“striatum”+OR+“neostriatum”+OR+“corpus+striatum”\)&rettype=count](http://eutils.ncbi.nlm.nih.gov/entrez/eutils/esearch.fcgi?db=pubmed&field=word&term=(“prefrontal+cortex”+OR+“prefrontal+cortices”)+NOT+(“striatum”+OR+“neostriatum”+OR+“corpus+striatum”)&rettype=count)

[http://eutils.ncbi.nlm.nih.gov/entrez/eutils/esearch.fcgi?db=pubmed&field=word&term=\(“striatum”+OR+“neostriatum”+OR+“corpus+striatum”\)+NOT+\(“prefrontal+cortex”+OR+“prefrontal+cortices”\)&rettype=count](http://eutils.ncbi.nlm.nih.gov/entrez/eutils/esearch.fcgi?db=pubmed&field=word&term=(“striatum”+OR+“neostriatum”+OR+“corpus+striatum”)+NOT+(“prefrontal+cortex”+OR+“prefrontal+cortices”)&rettype=count)

Note that for these searches, all synonyms for a given term are included within the parentheses and each term is individually surrounded by quotation marks to limit the search to each exact phrase. Furthermore, the “field = word” modifier limits the search to the article’s title and abstract. This reduces instances of false associations due to name or journal title homographs (e.g., author name “Fear” or journal name “Language” as opposed to the behavioral terms “fear” or “language”).

2.3. Data visualization and website creation

The brainSCANr website was created using the Google App Engine (Google, Inc.) framework. Graph connectivity plotting (see [Fig. 3C](#) for an example) was performed using the JavaScript InfoVis Toolkit (Nicolas Garcia Belmonte, <http://thejit.org/>). The full association database used in this study is available at that site for download. For [Fig. 2](#) the graph was plotted using the GraphViz (AT&T Research Labs) radial plot function.

Clustering was performed using an iterative (k -means) clustering algorithm (MATLAB® R2009b, Natick, MA; *kmeans.m*) and hierarchical clustering (*linkage.m*). For the brain structure and functions analyses, we used 20 clusters, and for the disease analysis we used 5 clusters. It is important to note that there are many techniques for clustering data (see Parsons et al., 2004), but the actual resulting clusters and dendrogram presented herein do not affect the results, but rather are included for display purposes.

2.4. Allen brain atlas

Gene expression data from the Allen brain atlas (ABA) were taken from subject H0351.2001 and visualized ([Fig. 4A](#)) on the ABA website. In order to allow for cross-database comparisons, raw expression intensity values for each gene g in brain region b was normalized across all n brain regions B in the ABA by converting them to a z -score such that,

$$z(g_b) = \frac{g_b - \mu_B}{\sigma_B}$$

To calculate a single expression value for broad neurochemical such as serotonin, which may have many genes coding receptors and transporters, we averaged normalized gene expression values across all relevant genes by searching the ABA genetic probe ontology for the neurochemical name. So, for example, the gene expression deviation value we report for serotonin represents the average across 208 serotonin-related genes. Because both the ABA and this manuscript use the same neuroanatomical naming ontology (Bowden and Dubach, 2003), we could compare brain region and gene expression data between databases.

For the analyses in [Fig. 5](#), gene expression deviation is defined as the absolute value of average gene expression z -scores, as both gene under- and over-expression are heavily researched. For the ABA/AI correlation analysis, we only correlated data where $AI > 0$ for a given neurochemical/brain region pair, yielding 1131 correlated pairs out of 1500 possible (25 neurochemicals times 60 brain regions). For surrogate correlation analyses ([Fig. 5B](#)), 10^4 surrogate correlations were calculated by extracting the correlation coefficient r between gene expression deviation and a random permutation of the AI data. This gave a distribution of possible r values against which the real correlation could be compared by calculating the z -score and associated p -value. For the surrogate difference analyses ([Fig. 5D](#)) the same technique was used as in the surrogate correlation analysis, however we compared the real difference with 10^4 surrogate differences, rather than correlation data. Surrogate difference scores were calculated by first combining all gene expression deviation values (for $AI > 0$ and for $AI = 0$) and then randomly drawing 1131 values (to represent data where $AI > 0$), calculating the mean, and comparing that against the mean of the remaining 369 values.

2.5. Semi-automated hypothesis generation

We introduce two methods for semi-automated hypothesis generation. The first relies on a simple “friend-of-a-friend should be a friend” concept wherein we assume that two terms that each strongly relate to a parent term should relate to one another. If they do not, then that relationship is flagged as a possible hypothesis. More technically, we considered each “parent” term and looked to find the terms the parent is strongly related to (more than 1000 joint publications between parent and “child”). If the parent had two or more such relationships we then examined the relations between each of these strong children. Any child/child pair that had a weak relationship (fewer than 30 publications) was flagged as a possible hypothesis. While the values used to define “strong” and “weak” relationships are somewhat arbitrary, we sought to keep

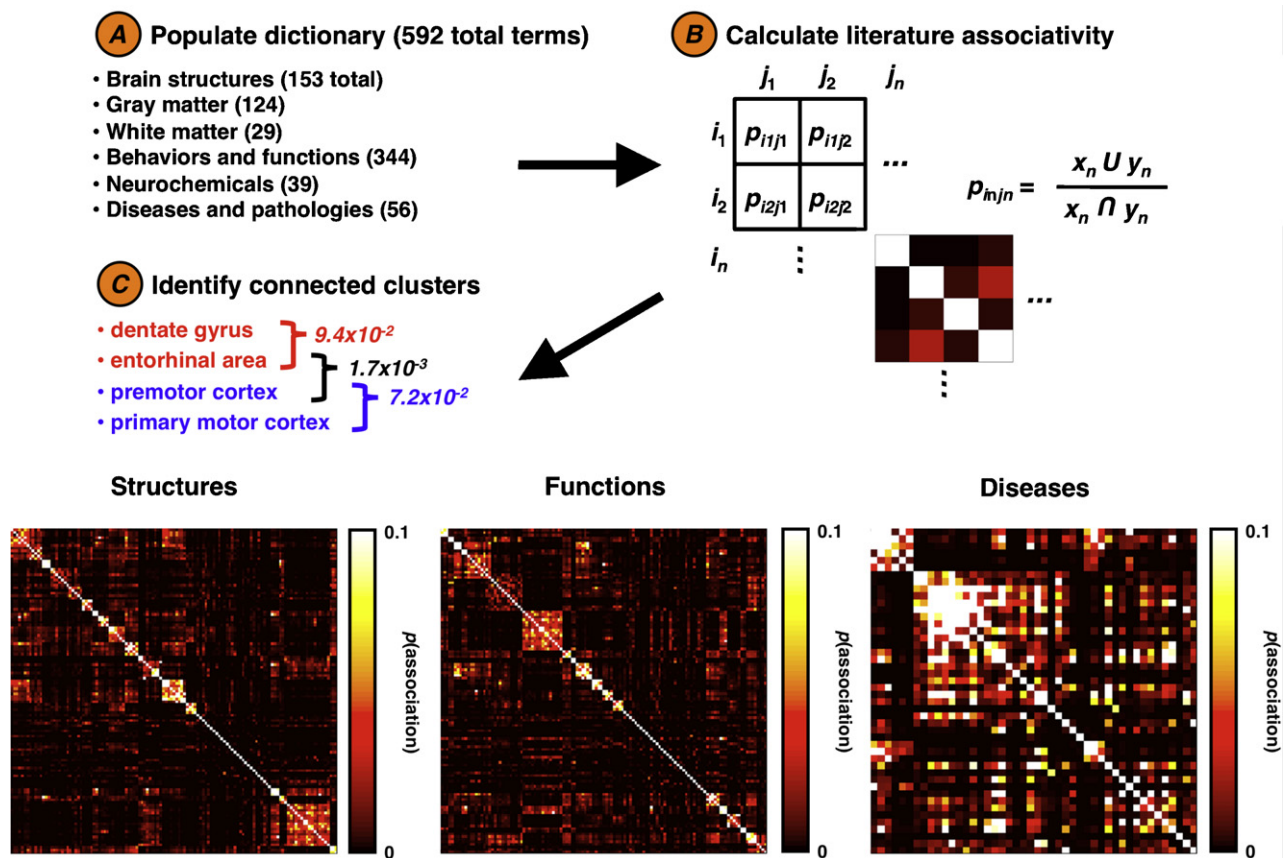


Fig. 1. Calculating brain structure, function, and disease relationships. We begin by (A) populating a database with search terms and their synonyms. From this we calculate, (B) the probability of association (p) between a term (i_n) and all other terms (j), giving us (C) a series of association matrices. Each row/column index in this matrix represents the probability of association between two terms as calculated from PubMed. For each matrix, data are sorted according to the clusters identified via k -means clustering using 20 structure clusters, 20 function clusters, and 5 disease clusters. This method highlights several within-cluster associations along the diagonal (see Supporting Tables for clusters).

the number of hypothesis candidates low. This choice of cutoffs yielded 896 hypotheses out of 175,528 total term pairs (0.51% rate).

The second method for hypothesis generation looks for discrepancies between actual gene expression data extracted from the ABA and the calculated neurochemical/brain relationship from PubMed. ABA gene expression values for each of the 25 neurochemicals were first sorted to find in which brain regions they are most strongly expressed. We then identified cases where brain regions were found to strongly express a given gene, yet had relatively few publications mentioning that region and gene.

3. Results

3.1. Cognome construction

In order to reconstruct this cognome, we calculated the probability of association between each term and every other term, giving an association matrix of size $(n^2 - n)/2$ (Fig. 1 and Section 2). Once the full association matrix was calculated we constructed a full brain connectivity graph (Fig. 2 and Supporting Fig. S1), limited only by the dictionary used to define the search terms (see Supporting List 1 for the full list). We find relatively strong associations between all brain region terms. For visualization purposes we classified each brain region as belonging to one of 8 pre-defined macroscale clusters and colored each node according to group membership. This coloring highlights the clustering of brain regions by type; cortical regions form distinct groups farther from

the central brainstem structures while thalamic and basal ganglia structures cluster together nearer the brainstem.

We then blindly clustered structures based upon their association weights (Fig. 1 and Table 1). These clusters—defined by their PubMed associations—recapitulate known neuroanatomical circuits. Several of these circuits are anatomically diffuse; for example, one cluster, a “visual” circuit, associates the lateral geniculate nucleus and pulvinar, the superior colliculus, and the primary visual and visual extrastriate cortices. We observe clusters of brainstem auditory and prosencephalic auditory circuits as well as oculomotor nuclei. These results show that there is an inherent structure to the peer-reviewed literature that can be algorithmically recovered. Note that differences in clustering methods yield different results, and that the clusters shown here are meant as illustrative examples of the structure inherent to the data. The full hierarchical dendrogram can be viewed in Supporting Fig. S2.

Just as we can identify clusters of associated brain regions, we can also cluster functions or diseases (see Fig. 1). Conceptually, clustering cognitive and behavioral functions provides a quantification of the relationship between two cognitive tasks or behavioral states (Yarkoni et al., 2011; Poldrack et al., 2009). For example, there is a known relationship between “visual working memory” and “delayed match to sample” tasks (Voytek and Knight, 2010; Voytek et al., 2010) that is recovered by our algorithm ($AI = 8.5 \times 10^{-3}$); similarly there is a weak association between “visual working memory” and “stress” ($AI = 6.1 \times 10^{-6}$), suggesting the two concepts are relatively unrelated. As can be seen in Table 2, there are two clusters of tasks identified as “executive functions” and

Table 1Brain structure clusters. Clusters identified via *k*-means clustering of the brain region association matrix. Cluster titles were defined post hoc based upon author's interpretation.

Unknown	Speech/motor	Basal ganglia	Thalamic
Cerebellum	Broca's area	Caudate nucleus	Centromedian nucleus
Cuneate nucleus of the medulla	Insula	Globus pallidus	Intralaminar nuclear group
Emboliform nucleus	Operculum	Nucleus accumbens	Reticular nucleus of the thalamus
Hippocampus	Premotor cortex	Putamen	Ventral anterior nucleus
Hypothalamus	Primary motor cortex	Substantia nigra	Ventral posterior nucleus
Orbital gyri	Supplementary motor cortex	Ventral tegmental area	Ventral posterolateral nucleus
Thalamus	Wernicke's area		Zona incerta
Basal ganglia II	Cingulate	Prefrontal	Heschls gyrus
Basal ganglia	Anterior cingulate gyrus	Medial prefrontal cortex	Planum temporale
Striatum	Cingulate gyrus	Prefrontal cortex	Transverse temporal gyrus
Subthalamic nucleus	Posterior cingulate gyrus		
Visual	Hippocampal	Amygdalar	Hypothalamic
Lateral geniculate nucleus	Dentate gyrus	Amygdala	Dorsomedial nucleus of the hypothalamus
Primary visual cortex	Entorhinal area	Basal forebrain nucleus	Medial dorsal nucleus
Pulvinar	Perirhinal area	Basal nucleus of the amygdala	Posterior nucleus of the hypothalamus
Superior colliculus	Subiculum	Diagonal band	Ventral posteromedial nucleus
Visual extrastriate		Stria terminalis	
Prosencephalic auditory	Brainstem auditory	Oculomotor	Cranial Nerve Nuclei
Inferior colliculus	Cochlear nuclei	Abducens nucleus	Dorsal motor nucleus of the vagus nerve
Medial geniculate body	Superior olive	Interstitial nucleus of Cajal	Hypoglossal nucleus
Primary auditory area	Trapezoid body	Oculomotor nuclear complex	Nucleus ambiguus
		Trochlear nucleus	Solitary nucleus
Brainstem	Cortical	Cortical (cont.)	Cortical (cont.)
Locus ceruleus	Angular gyrus	Medial frontal gyrus	Precuneus
Medulla	Fusiform gyrus	Medial parietal gyrus	Superior frontal gyrus
Periaqueductal	Inferior frontal gyrus	Middle frontal gyrus	Superior parietal lobule
Pons	Inferior parietal lobule	Middle temporal gyrus	Superior temporal gyrus
Raphe nuclei	Inferior temporal gyrus	Parahippocampal gyrus	
	Lingual gyrus	Postcentral gyrus	

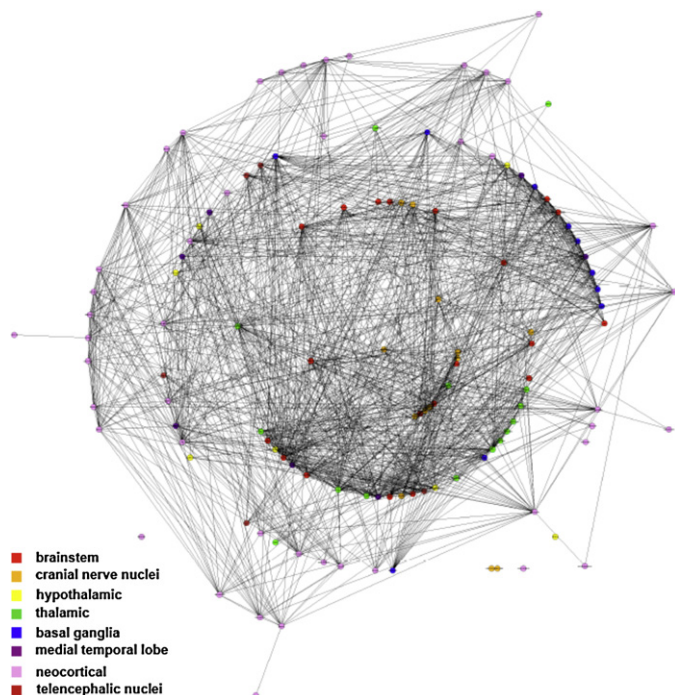


Fig. 2. Inferred systems-level connectome. Based upon a pre-defined dictionary of 124 brain regions and their 703 synonyms, we calculated the probability of association between all pairs of brain regions based upon their co-occurrence in the scientific literature indexed via PubMed. This method recovers known neuroanatomical relationships (see Supporting Table 1). In the center rings, brainstem structures cluster together, with telencephalic/neocortical structures arranged in the outside rings. Note the clustering of thalamic and basal ganglia structures in the middle rings. Graphic visualization was performed using GraphViz (AT&T Research Labs) with a connectivity threshold of 0.095.

“monitoring and control” clusters. The former contains 9 tasks such as the Stroop and Wisconsin card sorting tasks, as well as working memory. The latter cluster contains tasks such as go/no-go, stop signal, and antisaccade. These tasks are known to be functionally related and interdependent. In Table 3 we outline clusters of diseases identified from their associations. This results in a cluster of psychiatric disorders including bipolar disorder, schizophrenia, and obsessive-compulsive disorder, as well as a cluster of agnosias such as Broca's and Wernicke's aphasia, apraxia, and prosopagnosia.

While these classifications provide important data on within-category clustering, by combining structural, functional, and disease terms in a unified matrix we can calculate cross-category clusters (see Table 4). We observe cross-category relationships for language terms including language comprehension, Wernicke's area, and Wernicke's aphasia. We also find a Parkinson's disease cluster containing terms such as Parkinson's disease, caudate nucleus, and substantia nigra. Such cross-category clustering demonstrates the utility of this method for integrating and unifying complex interrelationships across a broad range of neuroscientific fields.

3.2. Hypothesis generation

While known relationships can be captured automatically, we can identify statistical “holes” in the literature using a method we call “semi-automated hypothesis generation”. In Fig. 3 we outline the algorithm used to find these statistical discrepancies, based on a simple “friend-of-a-friend should be a friend” concept. For example, in Fig. 3A we show a hypothetical relationship between a parent term *a* and its two children: *a_i* and *a_j*. In this case, both *a_i* and *a_j* are strongly related to their parent, but weakly related to one another. This is the basis for our hypothesis-finding algorithm (Fig. 3C). In Fig. 3D we show one real-world example (out of 896 identified) wherein both *striatum* and *migraine* are strongly related to *serotonin* (>2900 publications for each relationship), yet the striatum

Table 2
Functional clusters. Clusters identified via *k*-means clustering of the functions association matrix. Cluster titles were defined post hoc based upon author's interpretation.

Social/emotional	Attention	Cognition/consciousness	Language
Affect recognition	Attentional capacity	Anticipation	Language comprehension
Emotional perception	Attentional shifting	Arousal	Language processing
Emotional recognition	Attentional blink	Association learning	Language production
Face perception	Attentional resources	Awareness	Lexical processing
Face recognition	Auditory attention	Classical conditioning	Lexical retrieval
Facial expression	Divided attention	Cognition	Phonological encoding
Familiarity	Focused attention	Consciousness	Picture naming
Happiness	Inhibition of return	Decision making	Semantic processing
Long term memory	Oddball	Fear	Sentence comprehension
Memory consolidation	Selective attention	Intelligence	Sentence production
Memory storage	Spatial attention	Pain	Syntactic processing
Memory trace	Sustained attention	Pavlovian conditioning	Word comprehension
Object recognition	Target detection	Reward	Word production
Recognition memory	Target processing	Stress	
Reconsolidation	Visual attention	Uncertainty	
Social cognition	Visual search		
Spatial memory			
Theory of mind			
Monitoring and control	Executive functioning	Learning and memory	Learning and memory II
Antisaccade	Delayed recall	Declarative memory	Autobiographical memory
Behavioral inhibition	Digit span	Habit learning	Episodic memory
Cognitive control	Executive function	Habit memory	Memory retrieval
Deductive reasoning	Set shifting	Procedural learning	Semantic knowledge
Error detection	Stroop	Procedural memory	Semantic memory
Executive control	Trail making	Skill learning	
Go/no-go	Verbal memory		
Inductive reasoning	Visual memory		
Performance monitoring	Wisconsin card sorting		
Stop signal			
Task switching			
Working memory	Phonological processes	Knowledge	Perception
Central executive	Phonological buffer	Declarative knowledge	Auditory perception
Phonological loop	Phonological discrimination	Nondeclarative knowledge	Color perception
Short term memory	Phonological working memory	Nondeclarative memory	Form perception
Spatial working memory	Word repetition	Procedural knowledge	Visual perception
Working memory			
Speech	Implicit/explicit learning	Analogical processes	Implicit/explicit memory
Articulation	Explicit knowledge	Analogical problem solving	Explicit memory
Speech perception	Explicit learning	Analogical reasoning	Implicit memory
Speech production	Implicit knowledge		
Eye movement	Sequence learning	Intelligence	
Eye movement	Motor sequence learning	Crystallized intelligence	
Saccade	Sequence learning	Fluid intelligence	

and migraines have few shared publications (only 16). While the lack of association may be due to a publication bias wherein null results go unreported, there may be a true association between the two concepts that is understudied. Using this method, the process of uncovering new research paths could drastically speed knowledge discovery (the full list of identified hypotheses is available in [Supporting List 2](#)).

We can extend this hypothesis discovery technique by incorporating gene expression data from the ABA ([Lein et al., 2007](#)). In [Fig. 4](#) we show comparisons between regional human gene expression data for serotonin-related genes versus the relationship between *serotonin* and those brain regions in PubMed. We find a significant discrepancy between actual gene expression data and literature

associations. For example, serotonin-related genes are most highly expressed in the zona incerta, yet there are only 42 papers that discuss the zona incerta in relation to serotonin. In contrast, there are 1584 papers that discuss the nucleus accumbens and serotonin. While the first method finds statistical holes in the literature, this method identifies biases in neurochemical research.

3.3. Data validation

We sought to validate our data by correlating the AI calculated from PubMed associations with real data. Because the Allen brain atlas uses the same neuroanatomical naming ontology as used by our database, we could more easily compare these two

Table 3
Disease clusters. Clusters identified via *k*-means clustering of the disease association matrix. Cluster titles were defined post hoc based upon author's interpretation.

Psychiatric Disorders	Agnosias	Alzheimer's	Eating Disorders
Anxiety	Agnosia	Alzheimer's disease	Anorexia
Bipolar disorder	Aphasia	Dementia	Bulimia
Depression	Apraxia		
Obsessive compulsive disorder	Broca's aphasia		
Panic disorder	Prosopagnosia		
Schizophrenia	Wernicke's aphasia		
Social phobia			

Table 4Cross-category clusters. Clusters identified via *k*-means clustering of the entire association matrix. Cluster titles were defined post hoc based upon author's interpretation.

Visual cognition	Language	Learning and reward	Speech production
Antisaccade	Language comprehension	Association learning	Articulation
Attentional shifting	Sentence comprehension	Classical conditioning	Speech perception
Auditory attention	Syntactic processing	Reward	Speech production
Cognitive control	Broca's aphasia	Medial prefrontal cortex	Word recognition
Divided attention	Wernicke's aphasia	Nucleus accumbens	Aphasia
Executive control	Broca's area	Prefrontal cortex	Apraxia
Focused attention	Wernicke's area	Ventral tegmental area	Dyslexia
Inhibition of return			
Selective attention	Consciousness	Parkinson's	Facial Perception
Spatial attention	Consciousness	Parkinson's disease	Face perception
Sustained attention	Ataxia	Caudate nucleus	Face recognition
Task switching	Coma	Globus pallidus	Agnosia
Visual attention	Cerebellum	Putamen	Prosopagnosia
Visual search	Medulla	Substantia nigra	
Frontal eye field	Pons		
Visual extrastriate			
TMS	Alzheimer's	fMRI	Medical EEG
Transcranial magnetic stimulation	Cognition	Functional magnetic resonance imaging	Electroencephalography
Premotor cortex	Alzheimer's disease	Inferior frontal gyrus	Epilepsy
Primary motor cortex	Dementia	Insula	
Supplementary motor cortex			

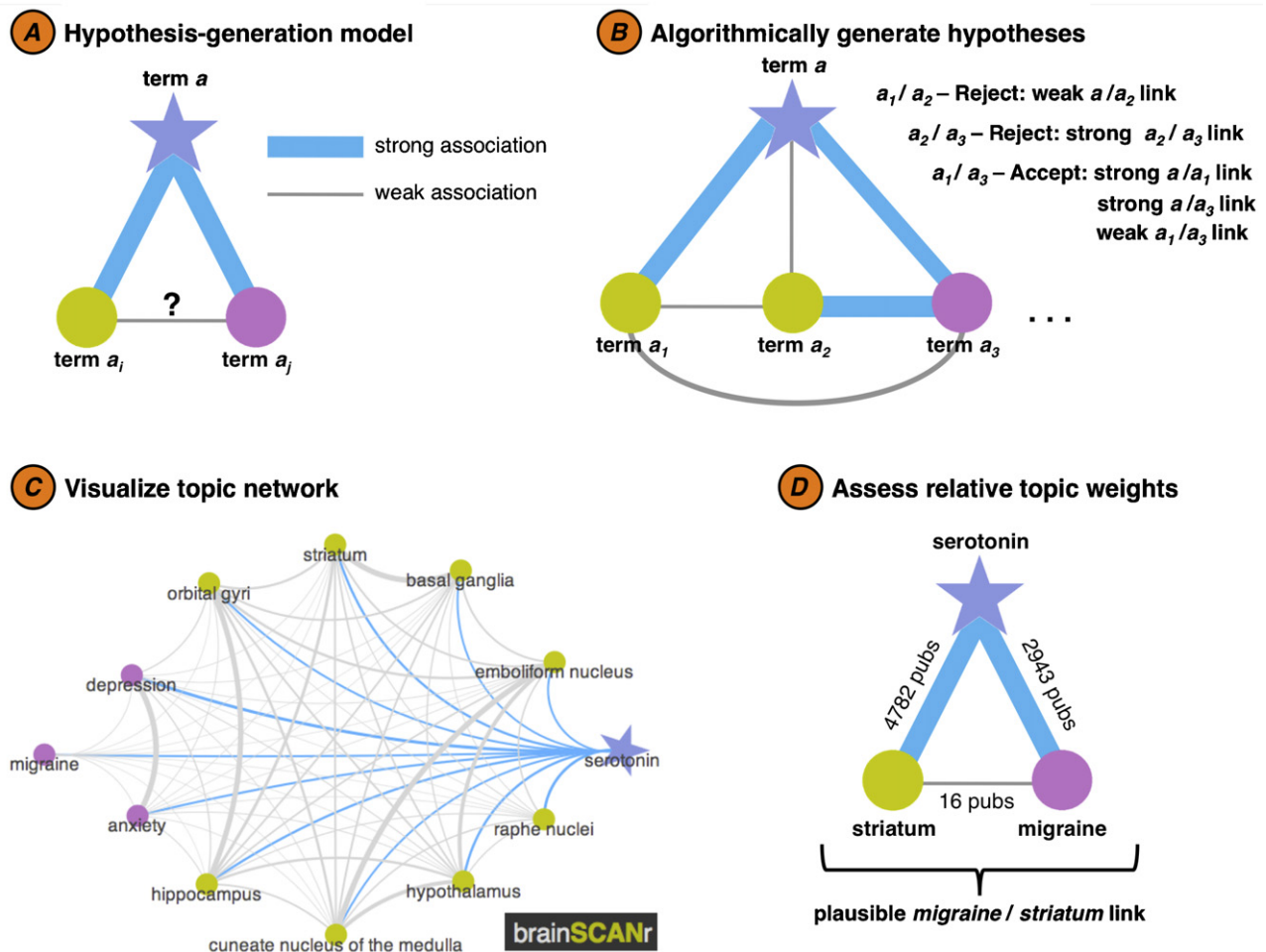


Fig. 3. Semi-automated hypothesis generation. A simple algorithm is used to evaluate possible novel or under-studied research topics based upon statistical discrepancies in the scientific literature. In the example above, we algorithmically determine a possible relationship between *migraine* and *serotonin*-related brain regions such as the *striatum* (for a full list of possible hypotheses, see [Supporting List 2](#)). (A) The hypothesis generation model is based on a simple “friend-of-a-friend should be a friend” concept: if term *a* is strongly associated with two terms (a_i and a_j), yet the association between a_i and a_j is weak, then perhaps we are (scientifically) missing a relationship between a_i and a_j . (B) In order for the algorithm to flag a relationship as a plausible hypothesis, three conditions must be met: terms a_i and a_j each need to have a strong relationship with their parent term, *a*, and the relationship between a_i and a_j should be weak. (C) The topic network for term *a* can be visualized (here using <http://www.brainSCANr.com>) to highlight relative associations between terms (main term *a*: blue star; brain regions: gold circles; diseases: purple circles). (D) An example of an algorithmically defined hypothesis. Here, the term *serotonin* is strongly associated with two terms: *striatum* (2943 joint publications) and *migraine* (4782 joint publications). In contrast, however, there are only 16 publications (at the time of this writing) that jointly mention *striatum* and *migraine*. Given that serotonin is so strongly related to these two topics, perhaps there is a missing association between migraines and the striatum.

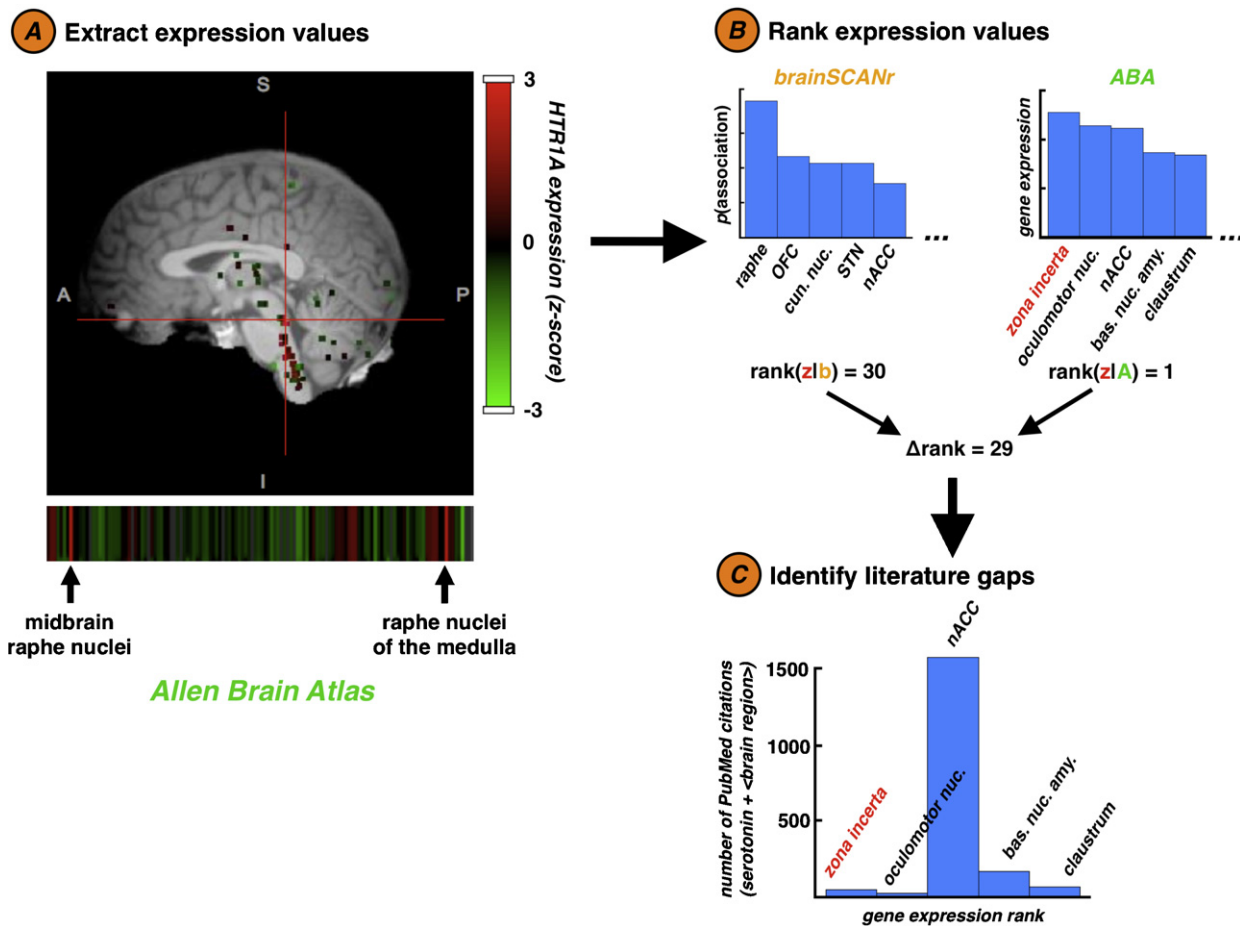


Fig. 4. Allen brain atlas integration. A second approach toward semi-automated hypothesis generation is accomplished via integrating our data with the Allen brain atlas (ABA). (A) From the ABA we extract real gene expression values for a sub-selection of human brain regions (60 were used in our ABA analyses). Here we show an expression map for *HTR1A*, the gene that encodes the 5-HT1A receptor. (B) We begin by ranking the brain regions that most strongly express genes related to a specific neurochemical (here, *serotonin*). According to the ABA (A, green), *serotonin*-related genes are most strongly expressed in the *zona incerta* (z, red). However according to our data (b, orange), *serotonin* is most strongly associated with the brain region *raphe nuclei*; the *zona incerta* ranks 30th out of 60 brain regions. (C) When we examine the number of publications in PubMed that discuss *serotonin* with the 5 brain regions that most strongly express *serotonin*-related genes, we find that the *nucleus accumbens* has orders of magnitude more publications than the other regions (1584 publications), whereas only 42 papers discuss *serotonin* and the *zona incerta*, despite the fact that the *zona incerta* expresses *serotonin*-related genes most strongly. This discrepancy suggests that the role of the *zona incerta* in serotonergic processes and *serotonin*-related functions is poorly understood. Our method demonstrates that such holes in our understanding may be identified automatically and algorithmically.

datasets than we could with other external sources. We find that the calculated AI for neurochemical/brain region relationships is significantly correlated ($r_{1131} = 0.11$, $p < 0.001$) with the gene expression magnitude for the same gene expression/brain region pairings (Fig. 5A), and that this correlation is unlikely due to an artifact of our calculation and integration methods (Fig. 5B). Furthermore, as would be expected, actual gene expression magnitude is lower for pairings where we find no neurochemical/brain region relationship in the literature (AI = 0) than for when there is a relationship (AI > 0) ($t_{1498} = 2.36$, $p = 0.018$), and that this effect is unlikely due to differences in the amount of data between the two groupings (Fig. 5D).

4. Discussion

In this manuscript we demonstrate that, by mining the peer-review literature for associations between neuroscientific terms, we can recapitulate known scientific relationships. Furthermore, we introduce an algorithm for semi-automated hypothesis generation that can be used to speed research discovery. Although the current analysis is restricted to a limited dictionary of terms, the association and visualization methods are applicable to any search

term or phrase found in PubMed, meaning that our method can be more broadly generalized to any scientific field using any peer-review database. Of course, there are limitations to our method. While we show that calculated AI does significantly correlate with real gene expression data, the correlation is relatively weak and explains only about 1% of the variance. This may be caused by several underlying factors, including, but not limited to, a loss of specificity as a result of averaging across a wide range of genes, inaccuracies in our text-mining approach or in the literature itself, the reliance upon gene expression data from a single human subject, or an incompatibility between the IA metric and gene expression data. Nevertheless the significance suggests that literature mining can capture real relationships (Fig. 5A).

Furthermore, our calculations are by definition based upon the existing literature, thus associations may reflect publication biases (though there is a well-described publication bias such that negative results are underreported (Begg and Berlin, 1989; Dirnagl and Lauritzen, 2010; Ioannidis et al., 1997; Stern and Simes, 1997). Furthermore, our method does not differentiate positive from negative results: if a paper states that the amygdala does *not* relate to fear, that paper is weighted equally to a paper that finds a positive relationship. Despite these limitations, our associations map onto known relationships with remarkable accuracy.

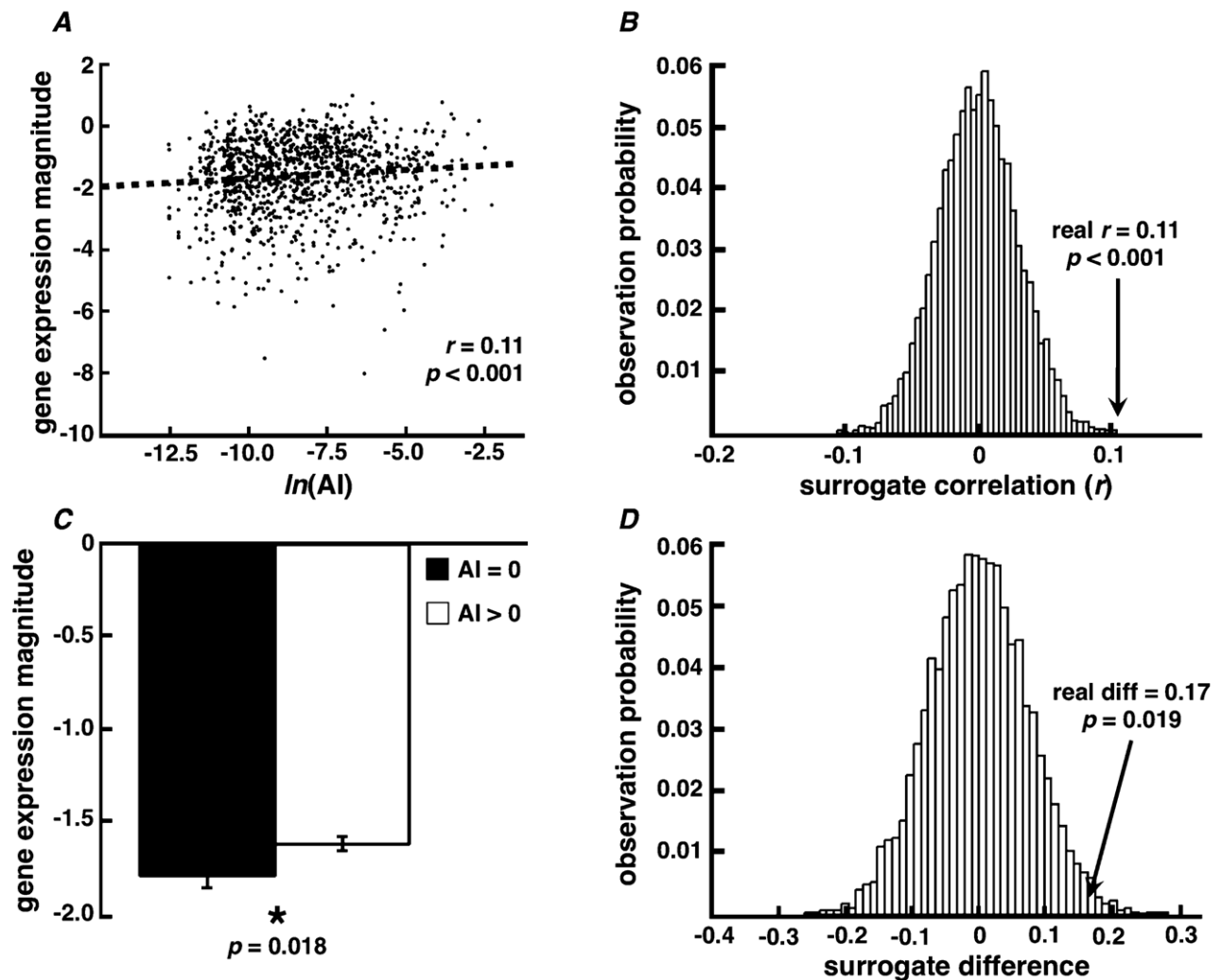


Fig. 5. Allen brain atlas/brainSCANr validation. We validated PubMed association probabilities by comparing them to brain/gene expression data from the ABA. (A) We find a significant correlation between association index (AI) and gene expression magnitude from the ABA for 1131 brain/gene expression relationships. (B) Resampling statistics suggest that the observed correlation ($r = 0.11$) is unlikely due to an artifact caused by AI or gene expression magnitude calculation techniques (see Section 2). (C) ABA gene expression magnitude is lower when the PubMed association probability equals zero. That is, when there are no published manuscripts relating a given brain region with a specific neurochemical, the magnitude of actual gene expression is likely to be lower than for cases where brain/neurochemical relationships do exist in PubMed (two-sample t -test, $p = 0.018$). (D) Resampling statistics suggest that the observed difference between the mean gene expression magnitudes when AI equals zero ($n = 369$) versus when AI is greater than zero ($n = 1131$; real diff = 0.17) is also unlikely due to an artifact caused by a difference in the number of trials between groups.

Given the matrix of association values for each brain region, we show that we can recreate known neuroanatomical circuits using blind, automated clustering algorithms. These algorithms identify physically diffuse but functionally associated networks such as subcortical-cortical visual pathways, brainstem auditory nuclei, and even behavioral circuits involved in speech and other high-level cognitive processes. By clustering cognitive functions, we can quantify the relationship between a variety of cognitive tasks commonly used in neuroscientific research, such as the relationships between tasks used to study executive functioning or cognitive control, similar to automated meta-analytic methods (Yarkoni et al., 2011). Finally, searching across all brain structures, functions, and diseases, we show that we can uncover statistical discrepancies in the literature to aid in scientific discovery. While we cannot confirm that such algorithmically identified hypotheses are correct without conducting actual experiments, the search space in the biomedical sciences is so vast that we believe that any principled methods to reduce that space can only help speed discovery, as even ruling out incorrect relationships is helpful. That is, these hypotheses are not meant

to represent a teleological endpoint, but rather a stepping-stone for researchers to help unmask possibly hidden mediating factors.

There is currently a massive scientific effort to identify the human connectome (Sporns et al., 2005; Modha and Singh, 2010; Editors, 2010). Even at the relatively macroscopic scale of systems and networks, the intricacies of neuroanatomical interconnectivity and how brain regions give rise to cognition and relate to disease are difficult to comprehend and visualize. Often these connectivity data are spread across dozens of research manuscripts, brain atlases, websites, and other repositories in static formats not openly accessible to all researchers. While fields such as genetics have put great effort into ontological projects (Zhang et al., 2010), the adoption of ontologies for neuroanatomy and cognition has been slow (but see (Bowden et al., 2007; Bohland et al., 2009; Larson and Martone, 2009; Stephan et al., 2000)). While the semantic associations we present herein appear to work well for the biomedical and psychological sciences, they may have more limited use in the physical sciences, for example, where the ontological weight is carried less by textual relationships.

Nevertheless, we can leverage the power of millions of publications to bootstrap informative relationships (Michel et al., 2011) and uncover scientific “metaknowledge” (Evans and Foster, 2011). Furthermore, the use of network mapping of textual relationships has recently been used in a variety of psychological and neuroscientific domains, including an analysis of comorbidity in psychiatric disorders based upon DSM-IV diagnostic criteria (Borsboom et al., 2011) and relationships between genes (Alako et al., 2005). By mining these relationships, we show that it is possible to add a layer of intelligent automation to the scientific method as has been demonstrated for the data modeling stage (Schmidt and Lipson, 2009). By implementing a connection-finding algorithm, we believe we can speed the process of discovering new relationships. So while the future of scientific research does not rely on these tools, we believe it will be greatly aided by them. This is a small step toward a future of semi-automated, algorithmic scientific research.

Acknowledgements

We thank Curtis Chambers for technical assistance, and Leon Deouell, Amitai Shenhav, Avgusta Shestyuk, Kirstie Whitaker, and many brainSCANr beta testers for technical discussions. BV is funded by the National Institute of Neurological Disorders and Stroke (NS21135-22S1) and a National Institutes of Health Institutional Research and Academic Career Development Award (IRACDA)(GM081266-05).

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.jneumeth.2012.04.019>.

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