

Extensive sampling for complete models of individual brains

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In designing cognitive neuroscience experiments, resource limitations induce a fundamental trade-off between sampling variation across individual brains and sampling variation across experimental conditions. Here, we argue that extensive sampling of experimental conditions is essential for understanding how human brains process complex stimuli, that a model of how any one brain does this is likely to generalize to most other brains, and that introducing large numbers of subjects into an analysis pool is likely to introduce unnecessary and undesirable variance. Thus, contrary to conventional wisdom, we believe that sampling many individuals provides relatively few benefits and that extensive sampling of a limited number of subjects is more productive for revealing general principles. Furthermore, an emphasis on depth in individual brains is well-suited for capitalizing on the improvements in resolution and signal-to-noise ratio that are being achieved in modern neuroscientific measurement techniques.

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Introduction

When can cognitive neuroscientists stop doing experiments? Each experiment costs society time, money, and effort, and can pose risks to individual subjects, so it is worth considering what our end-goal is and how we would know when we have achieved it.

We assume that the end-goal is a complete model of the human brain [1–3]. A complete model would be both oracle and interpreter: it would predict with great accuracy the

brain activity and behavior that we would observe in response to arbitrary stimuli and task instructions, and would connect the observed responses to meaningful evolutionary, developmental, computational, psychological, and philosophical narratives.

The cognitive neuroscience of vision (where our interests lie) works toward this end-goal one stimulus at a time. Experimentalists present visual stimuli while measuring brain activity using one of many techniques for interrogating neural activity (e.g., fMRI, EEG, MEG, ECoG, electrophysiology). The cost of each experiment is the accumulated cost of measuring these responses across many stimuli. In this paper we consider whether it is better to accumulate cost by sampling variation across individuals, or by sampling variation across stimuli. Specifically, we ask which approach yields greater progress toward the ambitious end-goal of a complete model?

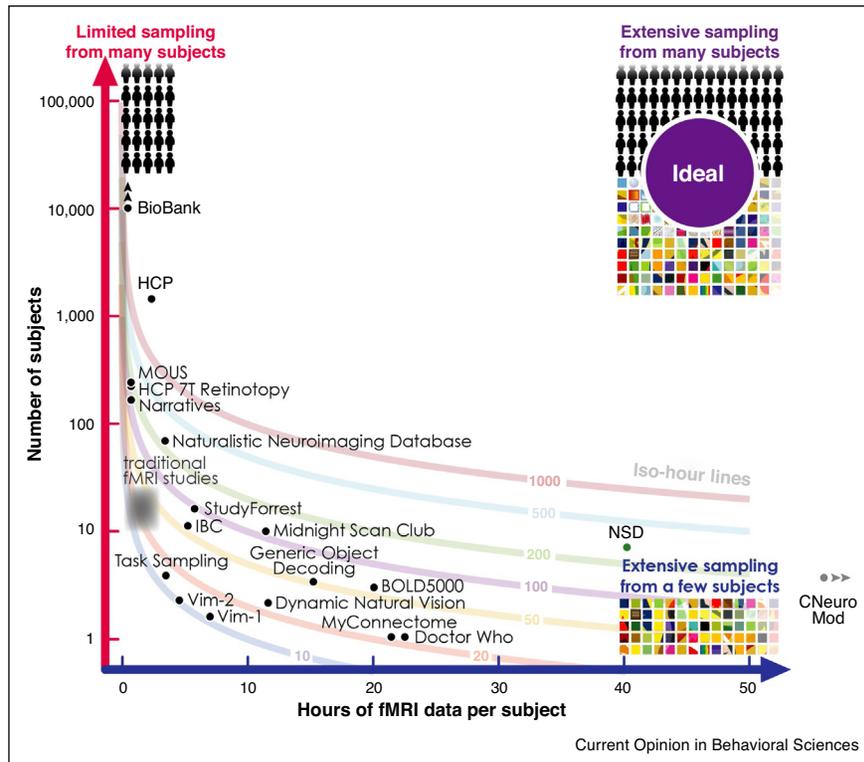
Fundamental trade-off between sampling individual variation and sampling stimulus variation

Resource constraints on experimental design impose a fundamental trade-off between sampling individual variation and sampling stimulus variation. We illustrate how a number of recent fMRI studies have managed this trade-off by plotting them in a two-dimensional space with number of individual subjects as the *y*-axis and number of hours of data per subject as the *x*-axis (Figure 1). We acknowledge that the number of hours of scanning per subject is only a proxy for how extensively a given experiment samples variation across stimuli (or, more generally, experimental conditions). We include resting-state fMRI data collection in this plot under the working premise that the ‘conditions’ that vary in this case are unmeasured endogenous (e.g., cognitive, affective) states.

In an ideal world, all experiments would reside in the upper right (many subjects and many hours per subject). However, resource limitations force experimentalists to distribute their efforts along iso-hour contours that extend from the upper left (many subjects but few hours per subject) to the lower right (many hours per subject but few subjects). Traditional fMRI studies tend to collect one session of data on about 10–20 participants (see gray box). The studies illustrated in Figure 1 have deliberately pushed sampling strategies towards one extreme (more subjects) or the other (more data per subject).

Efforts that involve extensive data collection across large numbers of individual brains but small numbers of experimental conditions [4*,10,11*,24] are in line with cognitive

Figure 1



Trade-off between number of subjects and amount of data per subject.

In the context of basic-science fMRI studies with publicly available data, we select a few representative publications, biasing towards recent and/or influential studies. Selected publications include Biobank [4*], BOLD5000 [5**], CNeuroMod [6*], Doctor Who [7**], Dynamic Natural Vision [8], Generic Object Decoding [9], HCP [10], HCP 7T Retinotopy [11], IBC [12], Midnight Scan Club [13**], MOUS [14*], MyConnectome [15], Narratives [16*], Naturalistic Neuroimaging Database [17], NSD [18**], StudyForrest [19,20], Task Sampling [21**], Vim-1 [22], and Vim-2 [23]. For each publication, we plot the number of subjects scanned and the number of hours of task-based and resting-state fMRI conducted for each subject (estimated based on information provided in the publication). The green dot denotes a soon-to-be-released study that is discussed in further detail in this article, the gray dot denotes an upcoming study, and the thick 'iso-hour' lines indicate points that share the same number of total hours of fMRI data.

neuroscience's historical penchant for studies with large (more than 20) numbers of subjects [25–27]. The intuition behind this approach seems to be that inferring a complete model of *the* human brain requires generalizing over response patterns in the brains of many individual humans. However, we argue that a complete model of *the* human brain must be able to predict and interpret activity in any *one* human brain, and that a complete model of the brain of any one individual will bring us within striking distance of a complete model that adequately describes most individuals. This line of thinking has motivated us, and presumably several others, to explore the other end of the spectrum, sampling many stimuli (or experimental conditions) in just a few individuals [5**,6*,7**,15,18**].

Many reasons for extensive sampling of stimulus variation

The images of the natural world that the eye transmits to the brain are ambiguous and complex [28]. While we can learn much from probing the visual system with simple

stimuli [29], we ultimately want to understand how the brain solves the hard computational problem of interpreting natural scenes. We take for granted the many arguments that have been put forth in favor of using natural stimuli to probe the visual system [30–33].

Understanding how the human brain interprets natural images is likely to require extensive sampling of stimulus variation. Natural scenes are high-dimensional and, despite recent progress in modeling their statistical structure [34], it is not possible to adequately sample them by varying a small number of controllable parameters. Furthermore, visual (and auditory) features are often highly correlated in stimuli, both natural [35] and synthetic [36], and it is difficult to isolate individual features [37]. Correlation of stimulus features creates inferential challenges [38]: for example, an undersampled neuron that is strongly activated by the color yellow can easily be mistaken for a neuron that is strongly activated by bananas.

A complete model of the human visual system will have to specify how the high-dimensional space of natural stimuli is transformed and represented by the human brain. Such a model will necessarily be complex, with many potential stimulus features and free parameters [39]; fitting and adjudicating different models will therefore require substantial empirical data. Thus, we believe that to have any hope of achieving a complete model of the visual brain, extensive sampling of stimulus variation will be necessary.

Few reasons for sampling individual variation

For basic cognitive neuroscience, motivations for sampling a large number of subjects (while collecting modest data per subject) might include the following:

- 1 We might be concerned that what we observe to be true of one brain may not be true of others.
- 2 We might want to increase the statistical power of our analyses by adding more subjects.
- 3 We are actually interested in explaining individual variation (or variation across groups).

In this section, we consider each of these motivations in turn and suggest reasons why we nonetheless might want to prioritize the sampling of stimulus over individual variation. We acknowledge that there are other considerations that may constrain a given study: for example, extensive data collection might be impractical or too exhausting for a given subject population, or a given experiment might require novelty and cannot be repeated (e.g., one-shot experiments, drug or brain-stimulation treatments). We offer some thoughts on the issue of subject burden later in this article.

Complete models of individuals are likely to generalize

Suppose that by dedicating all available experimental resources, we are able to sample stimulus variation extensively enough to construct a complete model of an individual brain. Would this complete model of a single brain do more to mislead us about general principles than it would to reveal them?

Inferring general principles from relatively small numbers of observations is a practice taken for granted in other domains. For example, in physics, consider Kepler's deduction of the laws of planetary motion from a limited set of observations. As another example, in neuroanatomy, consider the insights into structure-function relationships provided by Cajal's exquisitely detailed drawings of individual neurons. Whether these types of generalizations succeed in cognitive neuroscience remains an open question. However, we point out that most of what we have learned about the organization of mammalian visual systems suggests that a complete model of an individual brain would yield useful insights. Many principles of visual organization in human brains—

such as retinotopic organization [40] and face-selectivity [41]—not only generalize across individuals, but for the most part generalize across species [42,43]. Beyond sensory processing, there is even some evidence that cortical organization of high-level task representations [21**] and semantic processing [44] exhibits consistent structure across individuals. We furthermore point out that generalization is an existential assumption of animal models in systems neuroscience: it is assumed that the brains of other species have much to teach us about our own.

If we were to achieve a complete model of an individual, it would certainly be important to test generalization of the model. This could be done relatively quickly and cheaply by testing a second or third subject. We would not need to gather enough samples from the additional subjects to derive complete models of their brains from scratch—we would need just enough to test the generalization of the model from the first subject, tweaking it to account for local differences.

To be clear, we are arguing here that the most useful insights for cognitive neuroscience lie in identifying general principles that govern how functional activity arises in the brain and how functional properties are anatomically organized. To achieve this, we believe that extensive sampling of individuals is essential. We acknowledge that such an approach is not suitable for assessing differences in the exact size or layout of maps or functional properties across the population at large: we feel it is more pressing to identify the axes that characterize brain function as opposed to characterizing the distribution of individuals along such axes.

More subjects = more 'noise'

There are two radically different stances towards characterizing function in brains [45]. In the group-oriented stance, which perhaps is more typical in cognitive studies, statistical variability (error) is computed across subjects and effects are established at the group level. This approach lends itself well to brain measurements conducted at low spatial resolution and analyses that involve deliberate spatial smoothing of neuroimaging data and/or averaging of functional activity across subjects in a common anatomical space [46]. Accumulating samples of brain activity in this fashion will certainly improve reliability of group-average measures, but is likely to preserve only the simplest and most coarse patterns of activity. This is because the structural and functional organization of the brain varies considerably across individuals at the fine scale [47]. While surface-based approaches for registering cerebral cortex across individuals are more accurate than volume-based approaches [48,49], substantial variability still remains [50]. It is possible, of course, to adopt strategies that avoid direct averaging of activity in a common space, such as manually defining well-established regions-of-interest in individual

subjects [51] or characterizing activity at a more abstract level before averaging [16,52,53], but these strategies come with their own limitations.

In the individual-oriented stance, which perhaps is more typical in sensory studies, statistical variability (error) is computed across stimuli or trials (or scan sessions) for a given subject. By doing so, variability is quantified at the most precise unit of measurement (e.g., voxels, neurons, electrodes). Additional brain measurements contribute directly to additional information about the nature of the computation occurring at each unit, and does so without incurring any cost of intersubject variability. The aim is to establish effects in individual subjects and reproduce the effects on additional subjects if necessary. Notably, this general approach of measurement and characterization of a small number of subjects is rooted in classic studies in human psychophysics [54,55], neuroimaging [56,57], and animal electrophysiology [58].

Our contention is that adding subjects to increase statistical power makes sense only if one adopts the group-oriented stance where group-averaging of activity is performed. If we switch stances and instead characterize effects in individual subjects, the problem of intersubject variability is largely avoided. In a sense, the choice to study and analyze group-average activity actually adds unnecessary ‘noise’ to the analysis. We therefore suggest that increased sampling of stimulus variation (within an individual) is a preferable method for improving statistical power compared to increased sampling of individual variation.

Complete models of individual brains may reveal the most interesting forms of individual variation

We think that the most compelling reason for sampling individual variation is if we are actually interested in understanding person-to-person variation in some cognitive function [59], or differences between populations grouped by a shared pathology or mental illness [60]. For these purposes, studies involving large numbers of subjects are appropriate and may be highly useful for developing predictive biomarkers for various behavioral phenotypes [61]. However, we contend that in neurotypical subject pools, many of the most interesting forms of individual variation are subjective mental events like dreams, mental images, and recalled memories [62,63]. It is likely that a deep understanding of how these events are mediated by brain activity will require sophisticated models of individual brains spanning perception, attention, memory, and cognition—and therefore require extensive sampling of stimulus and task variation. Functional brain measurements are notoriously noisy (reflecting either instrumental or true neural variation), and relating brain responses to precise measures of behavior is a challenging endeavor that requires substantial

amounts of data, assuming we are careful not to overestimate the robustness of our measures [64].

A case study

We have argued that extensive sampling of stimulus variation is essential for modeling brain activity and that allocating samples to one or a few individual brains is more effective than spreading them across many brains. But these are mere generalities—how many subjects should one actually use?

To make our discussion more concrete, we briefly address specific choices we made for the Natural Scenes Dataset (NSD, <http://naturalscenesdataset.org>). NSD is a massive sampling of high-resolution whole-brain 7T fMRI responses that will soon be publicly released [18**]. The unique scale of the dataset makes possible analyses that are difficult to carry out in smaller datasets, such as end-to-end training of a neural network-based encoding model of visual responses. Indeed, one of the overarching goals of NSD was to generate a dataset that can be used to develop and validate complete models of individual brains. In designing NSD, we had to move from general considerations to concrete choices about the number of stimuli to sample, the number of repetitions per stimulus, and the number of individual brains across which to distribute these samples.

NSD samples brain activity in response to roughly 73 000 distinct natural scenes aggregated across subjects. There is no general principle or rule one can consult to select the total number of images sampled; it may be the case that neuroscientists are destined to be starved for data relative to the dimensionality of visual stimuli. However, we were guided by the numbers of samples needed for data-hungry deep-learning techniques [65,66]. State-of-the-art techniques typically require tens of thousands of samples, and so we took this rough figure as our goal.

NSD samples each image three times within a given subject. Stimulus repeats are not a strict requirement for all analyses, since there is considerable overlap in the kinds of visual features that appear across images. However, stimulus repeats make it possible to entertain analyses of variation across trials, allowing one to study issues such as repetition and memory effects [67]. In addition, stimulus repeats enable the use of cross-validation methods for data denoising [68]. Finally, in the NSD experiment, subjects were asked to report on each trial if they remembered seeing the displayed stimulus on any previous trial. This added a cognitive dimension that enriches the analysis potential of the dataset.

NSD includes eight subjects. Why this design? One motivation comes from statistical considerations. If we assume that the researcher is equipped to demonstrate

effects in individual subjects, the availability of eight subjects provides statistical power to guard against incidental findings. For example, using a two-sided sign test, demonstration of a consistent sign of an effect in six out of eight subjects corresponds to a p -value of 0.03125.

Our primary consideration for recruiting eight subjects, however, was the demand on the subjects and the time required to acquire the full dataset. Although allocating the full set of 73 000 images to a single subject might not be an unreasonable proposition from the perspective of scientific value, subjects already had to commit to nearly a year of regularly scheduled scan sessions. If a single subject had been used, the dataset would have taken eight years to collect as opposed to one. Moreover, we speculate that a year of scanning may already be near the upper limit of what most subjects can be asked to tolerate, at least in the context of strenuous fMRI experiments where high performance is expected from scan subjects. Indeed, in light of these considerations, we took special care when acquiring the NSD dataset to minimize the burden of participation and to make the experience as pleasant as possible for the subjects. This included communicating clear expectations, sharing the scientific motivation and excitement of the dataset, instituting a bonus incentive structure for good performance, streamlining day-to-day scanning procedures, offering refreshments, maintaining an amicable relationship, continually assessing subject well-being, and soliciting subject feedback. While subjects had the option of halting participation at any time, all eight continued until the end.

Future outlook

Currently, there are few human fMRI datasets involving extremely deep and rich sampling of cognitive phenomena. But we imagine that the utility of and demand for such datasets will only increase as the field targets more sophisticated questions about the brain. Indeed, such datasets seem a necessity if we are attempting to derive deep principles of intelligence from brain data and incorporate these into artificial systems [69*]. Given the expense of neuroimaging data, collecting these datasets and making them publicly available are critical for scientific progress. In particular, we are excited by the prospect of different research groups comparing different models and analyses on common benchmark datasets [70*,71]. Finally, we note that a shift to extensive sampling of individuals goes hand-in-hand with improvements in our ability to collect brain measurements at high spatial and temporal resolution [72], our ability to handle, store, and compute on large datasets [73,74], and our ability to apply data-driven machine-learning techniques that can exploit large amounts of data [75,76].

Conflict of interest statement

Nothing declared.

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The Midnight Scan Club collected six hours of resting-state fMRI and five hours of task-based fMRI from each of ten human participants in order to obtain a deeper understanding of functional brain connectivity at the level of the individual. The study contends that precision individual connectomics is superior to the more standard group-averaging approach.

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