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Review

Person-specific and precision neuroimaging: Current methods and future directions

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ABSTRACT

Most neuroimaging studies of brain function analyze data in normalized space to identify regions of common activation across participants. These studies treat interindividual differences in brain organization as noise, but this approach can obscure important information about the brain's functional architecture. Recently, a number of studies have adopted a person-specific approach that aims to characterize these individual differences and explore their reliability and implications for behavior. A subset of these studies has taken a precision imaging approach that collects multiple hours of data from each participant to map brain function on a finer scale. In this review, we provide a broad overview of how person-specific and precision imaging techniques have used resting-state measures to examine individual differences in the brain's organization and their impact on behavior, followed by how task-based activity continues to add detail to these discoveries. We argue that person-specific and precision approaches demonstrate substantial promise in uncovering new details of the brain's functional organization and its relationship to behavior in many areas of cognitive neuroscience. We also discuss some current limitations in this new field and some new directions it may take.

1. Introduction

Most functional magnetic resonance imaging (fMRI) studies normalize individual brains to a template, with the goal of finding common patterns of activation across a group that can be generalized to a given population. However, the shape and functional organization of brains differ greatly between individuals, and normalization can never completely compensate for these differences. Worse yet, the same functional region may not be in the same anatomical region in different participants, so even perfect alignment of anatomical features could still lead to averaging across regions that are functionally heterogeneous (Fedorenko et al., 2010; Fedorenko and Kanwisher, 2009; Frost and Goebel, 2012; Nieto-Castanon and Fedorenko, 2012).

Partially in response to these concerns, recent work has explored the use of more person-specific methods when analyzing fMRI data. Rather than treating individual differences in brain organization as noise, these studies aim to identify reliable patterns of activation or connectivity in individuals even if those patterns are unique and different from those of other participants. This body of work has provided evidence that individual differences in neural organization are reliable and may be relevant to individual differences in behavior (Braga and Buckner, 2017; Finn et al., 2017; Finn et al., 2015; Gordon et al., 2020; Kong et al., 2019). If so, a clearer understanding of the relationship between person-specific imaging results and person-specific behavior could shed light on how behavior is implemented in the brain and have practical implications for the treatment and prevention of clinical disorders.

This review provides a summary of recent explorations of person-specific imaging approaches, including the "precision" (also referred to as "deep" or "dense" sampling) neuroimaging approach (Gordon et al., 2020; Gratton et al., 2020; Smith et al., 2021). There have been a few other recent reviews of precision neuroimaging literature focused on specific subtopics (e.g., precision psychiatry or cognitive control; Gratton et al., 2020; Smith et al., 2021). This review is intended as a broad overview of how person-specific and precision approaches can improve our understanding of brain organization more generally. First, we discuss the problems associated with traditional group analyses, and how such practices may lead to blurred, or even misleading, results. Next, we review studies using person-specific and precision imaging approaches, first by examining work using resting-state measures, followed by studies that incorporate task-based activation. We define person-specific studies as those that explicitly examine differences in brain activity at the individual subject level, rather than combining subjects together and looking at group-level activation or connectivity patterns.

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For example, many person-specific studies have used methods such as connectome-based predictive modeling (CPM) to overcome limitations in the generalizability of traditional approaches and have attempted to relate individual differences in brain connectivity to individual differences in behavior. Other studies have used a precision neuroimaging approach, in which each individual is scanned for an extended period of time (typically more than two hours) in order to develop more reliable estimates of brain activity and organization at the individual subject level. Table 1 lists the studies reviewed in these sections by dataset (when available) to provide a quick reference to the work that has been done. The final section of this review discusses the limitations of current person-specific neuroimaging work and includes potential future directions that may provide greater insight into individual differences in brain organization and behavior.

2. Limitations of traditional imaging approaches

The functional organization of the human brain shares many commonalities across people. The primary visual cortex can reliably be found in the occipital lobe. The primary motor cortex can reliably be found in the precentral gyrus. The primary auditory cortex can reliably be found near Heschl's gyrus. And the list goes on. This commonality makes it possible to combine the neural activity in individual participants in a group analysis in order to identify activation that hopefully generalizes to the population from which the sample was drawn.

However, each individual brain differs in size and shape (Amunts and Zilles, 2015; Frost and Goebel, 2012; Gordon et al., 2017a; Gordon et al., 2017b; Kong et al., 2019; Salvo et al., 2021; Seitzman et al., 2019), and so most fMRI studies conduct a series of steps to make individual brains more similar to each other. One of the first such steps is normalization, which attempts to warp each individual's brain in such a way that the same anatomical location (e.g., the left lingual gyrus or the posterior part of the right superior gyrus) in different people will be aligned in normalized space. Although this approach can work relatively well for subcortical structures, the cortical surface is much more difficult to align across subjects due to the heterogeneity in cortical folding patterns (Frost and Goebel, 2012; Tucholka et al., 2012). Worse yet, many functional regions are in somewhat different anatomical locations in different people, meaning that even if normalization could perfectly align a set of brains structurally, they would still not be aligned functionally. For example, Frost and Goebel (2012) sought to determine the extent to which anatomical and functional brain areas correspond across individuals using a series of functional localizers. Despite using curvature-based cortical alignment, which incorporates individual folding patterns to improve anatomical alignment, they found that many functional areas, such as language areas and the fusiform face area, vary considerably in anatomical location across individuals. Likewise, Malikovic et al. (2007) found substantial variation across individual brains in the anatomical location of area V5/MT+. Based on these and similar results, Amunts and Zilles (2015) argued that new approaches to brain mapping are necessary to relate structure to function (e.g., Amunts and Zilles, 2015).

Recent advances have attempted to mitigate the problems associated with traditional alignment methods. For example, Multi-modal Surface Matching (MSM) methods allow for different combinations of input features to improve alignment, and hyperalignment aligns patterns of neural activity across individuals (Busch et al., 2021; Haxby et al., 2011; Haxby et al., 2020; Robinson et al., 2018; Robinson et al., 2014). What these methods have in common is that they attempt to address the fact that traditional group-averaged analyses can obscure individual differences in brain topology. Traditional group analyses implicitly assume that all subjects have the same functional regions in the same anatomical locations, but this assumption is often violated. And when it is, neural signals from functionally distinct areas will be mixed together during group analysis, which could lead to results that may not reflect any person in the group. This idea has been proven using the ergodic theorems and has long been recognized in many scientific fields, including psychology and neuroscience (Fisher et al., 2018; Molenaar and Campbell, 2009; Seghier and Price, 2018). The problem is that most psychological processes are not ergodic (i.e., processes where inter- and intraindividual variation are "asymptotically equivalent"; Molenaar and Campbell, 2009), and so group data may not accurately reflect psychological processes at an individual level. In fact, almost 70 years ago, Sidman (1952) demonstrated that a group-averaged curve often does not represent any of the individual curves from which the average was created. Because the averaged data will only be similar to individual data under specific conditions, he determined that averaged data cannot be used to make inferences at the individual level.

These same concerns apply to neuroimaging research. For example, assume that there is a brain region that performs the same function in every individual subject, but that the location of that brain region does not overlap in any two participants after normalization. Group-level analyses looking for regions related to that function could then miss this area despite its relevance to the function of interest. In this case, generalizing the group result to every individual in the group, and the population from which the sample was drawn, is misleading and an example of the so-called ecological fallacy (Fisher et al., 2018).

3. Identifying individual variation with resting-state connectivity

3.1. Connectome fingerprinting and person-specific connectivity

Person-specific neuroimaging research aims to understand individual differences in the brain, rather than treat these differences as noise. Many of these studies use publicly-available datasets, such as the Human Connectome Project (HCP; Van Essen et al., 2013), which aims to examine individual differences, particularly in functional connectivity in the brain. While previous individual difference studies have attempted to correlate functional connectivity with behavioral performance, these measures often lacked reliability and were unlikely to be replicated (Marek et al., 2022; Noble et al., 2021; Shen et al., 2017). Finn et al. (2015) introduced the connectome-based predictive modeling (CPM) method, which attempts to overcome limitations in generalizability by using whole-brain information to identify predictive networks with built-in cross-validation, rather than simply finding correlations (Shen et al., 2017). They examined individual differences in resting-state functional connectivity (RSFC) in the HCP sample and demonstrated that an individual could be accurately identified from a group based on their connectivity patterns. Individual identification based on RSFC or "connectome fingerprinting" (Finn et al., 2015; Miranda-Dominguez et al., 2014; Xu et al., 2016) has been used repeatedly to examine individual differences in brain connectivity. For example, Airan et al. (2016) explored several metrics contributing to individual identification, and found that individual differences in connectivity were largest in association and frontoparietal networks, consistent with other findings (Chen et al., 2015; Mueller et al., 2013; Peña-Gómez et al., 2018). Additionally, whereas many studies compute a single, stable functional connectome, Liu et al. (2018) found that time-varying characteristics of RSFC (termed the "chronnectome" or dynamic functional connectivity) also reliably identify individuals from a group. Moreover, Chen and Hu (2018) used a recurrent neural network that incorporated temporal and spatial information to accurately identify individuals with only 72 seconds of data, and Byrge and Kennedy (2019) found that no specific sets of connections were necessary for accurate individual identification. These results suggest that connectivity in many different areas of the brain include person-specific features (features present in individuals despite their absence in group averages; also known as "trait-like" or "network variants"; Gordon et al., 2017a; Gratton et al., 2018; Seitzman et al., 2019).

Individual differences in functional connectivity have also been found to be stable over time. For example, Miranda-Dominguez and colleagues (2018) found that connectome fingerprinting remains accurate

Table 1
Literature review.

Citation	Dataset Number	Dataset Name	Sample	Population	Sessions	Tasks	RS-fMRI (min./session)	Dataset Availability
Resting-state fMRI studies								
Byrge and Kennedy (2019)	1	HCP	835 (NA)	Healthy	2	-	30	https://www.humanconnectome.org
	2	ABIDE	54 (11F)	Healthy, Autism Spectrum Disorder	2-3	1	32	http://fcon_1000.projects.nitrc.org/indi/abide/abide_II.html
Chen and Hu (2018)	1	HCP	100 (54F)	Healthy	2	-	30	https://www.humanconnectome.org
Demeter et al. (2020)	1	-	30 (9F)	Healthy pediatric	2	-	6-12	-
	2	MSC	20 (5F)	Healthy	2	-	30	https://openneuro.org/datasets/ds000224/versions/00001.
	3	-	30 (24F)	Healthy pediatric	1	-	6-12	-
	4	HCP	50 (26F)	Healthy	1	-	15-30	https://www.humanconnectome.org
	5	-	38 (16F)	Healthy pediatric	1	-	6-12	-
	6	HCP	50 (26F)	Healthy	1	-	15-30	https://www.humanconnectome.org
	7	-	34 (12F)	Healthy pediatric	1	-	15-30	-
Finn et al. (2015)	1	HCP	126 (86F)	Healthy	2	4	30	https://www.humanconnectome.org
	2	Yale	45 (17F)	Healthy	1	-	45	
Kashyap et al. (2019)	1	HCP	803 (NA)	Healthy	2	-	30	https://www.humanconnectome.org
Liu et al. (2018)	1	HCP	105 (68F)	Healthy	2	-	30	https://www.humanconnectome.org
Liu et al. (2019)	1	HCP	801 (443F)	Healthy	2	-	30	https://www.humanconnectome.org
	2	HCP	183 (81F)	Healthy	2	-	30	https://www.humanconnectome.org
Miranda-Dominguez et al. (2018)	1	-	159 (64F)	Healthy	1-3	-	5	
	2	HCP	198 (109F)	Healthy	2	-	30	https://www.humanconnectome.org
Noble et al. (2017)	1	-	12 (6F)	Healthy	4	-	36	-
	2	HCP	606 (NA)	Healthy	2	-	30	https://www.humanconnectome.org
Smith et al. (2015)	1	HCP	461 (271F)	Healthy	2	-	30	https://www.humanconnectome.org
Wang et al. (2021)	1	HCP	886 (NA)	Healthy	2	-	30	https://www.humanconnectome.org
Wang et al. (2015)	1	-	25 (9F)	Healthy	5	-	12	-
	2	HCP	100 (54F)	Healthy	2	7	30	https://www.humanconnectome.org
	3	GSP	104 (56F)	Healthy	1	-	6	https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/25833
	4	-	8 (5F)	Epilepsy	1	5	12	-
Badhwar et al. (2020)†	1	-	1 (0F)	Healthy	25	-	9-10	https://zenodo.org/record/3350885#.YUIUSJ1KiUk
	2	HNU	30 (15F)	Healthy	10	-	10	https://figshare.com/s/7dac285e153e176d90e8
Chen et al. (2015)	1	HNU	30 (15F)	Healthy	10	-	10	https://figshare.com/s/7dac285e153e176d90e8
Peña-Gómez et al. (2018)	1	HNU	30 (15F)	Healthy	10	-	10	http://fcon_1000.projects.nitrc.org/indi/CoRR/html/hnu_1.html
	2	GSP	40 (15F)	Healthy	2	-	6	https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/25833
Xu et al. (2016)	1	HNU	30 (15F)	Healthy	10	-	10	http://fcon_1000.projects.nitrc.org/indi/CoRR/html/hnu_1.html
	2	eNKI-TRT	20 (4F)	Representative Sample	2	-	10	http://fcon_1000.projects.nitrc.org/indi/pro/eNKI_RS_TRT/FrontPage.html
	3	QTIM	272 (204F)	Twins	1	-	5	https://imaginggenomics.net.au/projects/qtim/
Gordon et al. (2017c)	1	MSC	10 (5F)	Healthy	10	3	30	https://openneuro.org/datasets/ds000224/versions/00001
Gordon et al. (2020)	1	MSC	10 (5F)	Healthy	1-10	3	30	https://openneuro.org/datasets/ds000224/versions/00001.
Gratton et al. (2018)	1	MSC	10 (5F)	Healthy	10	3	30	https://openneuro.org/datasets/ds000224/versions/00001
Greene et al. (2020)	1	MSC	10 (5F)	Healthy	10	-	30	https://openneuro.org/datasets/ds000224/versions/00001.
Lynch et al. (2020)	1	-	4 (0F)	Healthy	12-24	-	174-348	-
	2	MSC	10 (5F)	Healthy	10	-	30	https://openneuro.org/datasets/ds000224/versions/00001.
	3	CAST	3 (1F)	Healthy	42-64	-	30	https://openneuro.org:443/datasets/ds002766
	4	MyConnectome	1 (0F)	Healthy	104	6	10	http://openfmri.org/dataset/ds000031
Sylvester et al. (2020)	1	MSC	10 (5F)	Healthy	10	-	30	https://openneuro.org/datasets/ds000224/versions/00001.
Poldrack et al. (2015)	1	MyConnectome	1 (0F)	Healthy	104	6	10	http://openfmri.org/dataset/ds000031
Laumann et al. (2015)	1	MyConnectome	1 (0F)	Healthy	84	6	10	http://openfmri.org/dataset/ds000031
	2	-	1 (0F)	Healthy	10	-	30	-
	3	WashU 120	120 (60F)	Healthy	1	-	14	https://legacy.openfmri.org/dataset/ds000243/

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Table 1 (*continued*)

Citation	Dataset Number	Dataset Name	Sample	Population	Sessions	Tasks	RS-fMRI (min./session)	Dataset Availability
Gordon et al. (2017a)	1	-	1 (NA)	Healthy	10	-	30	
	2	WashU 120	120 (60F)	Healthy	1	-	14	https://legacy.openfmri.org/dataset/ds000243/
Marek et al. (2019)	1	ABCD	2188 (1144F)	Healthy	1-2	-	20	https://nda.nih.gov/abcd
Lake et al. (2019)	1	ABIDE	1044 (NA)	Healthy, Autism Spectrum Disorder	2-3	1	8 ± 2 (mean ± SD)	https://fcon_1000.projects.nitrc.org/indi/abide/
	2	ADHD-200	776 (NA)	Healthy, ADHD	1	1	24	https://fcon_1000.projects.nitrc.org/indi/adhd200/
Horien et al. (2019)	1	SLIM	105 (49F)	Healthy	3	-	8	http://fcon_1000.projects.nitrc.org/
	2	CoRR	93 (45F)	Healthy	2-3	-	5	http://fcon_1000.projects.nitrc.org/indi/CoRR/html/samples.html
	3	CoRR	79 (58F)	Healthy	2	-	12	http://fcon_1000.projects.nitrc.org/indi/CoRR/html/samples.html
	4	CoRR	26 (0F)	Healthy	2	-	24	http://fcon_1000.projects.nitrc.org/indi/CoRR/html/samples.html
Filevich et al. (2017)	1	Day2Day	8 (6F)	Healthy	11-50	-	5	Available upon request
Jalbrzikowski et al. (2020)	1	FCON 1000	140 (73F)	Healthy	1-2	1	16	http://fcon_1000.projects.nitrc.org/
	2	FCON 1000	208 (104F)	Healthy	1-3	-	5	
Choe et al. (2015)	1	Kirby	1 (0F)	Healthy	158	-	7	http://www.nitrc.org/projects/kirbyweekly
	2	Kirby	21 (10F)	Healthy	1	-	7	http://www.nitrc.org/projects/multimodal
Airan et al. (2016)	1	KKI	21 (10F)	Healthy	2	-	30	http://fcon_1000.projects.nitrc.org/indi/pro/nki.html
	2	NKI	23 (6F)	Healthy	2	-	5	
	3	NKI	23 (6F)	Healthy	2	-	10	
	4	NKI	23 (6F)	Healthy	2	-	10	
Allen et al. (2022)	1	NSD	8 (6F)	Unreported	30-40	1	100-180	http://naturalscenesdataset.org/
Duchesne et al. (2019)†	1	SIMON	1 (0F)	Healthy	73	-	9-10	http://fcon_1000.projects.nitrc.org/indi/retro/SIMON.html
Braga and Buckner (2017)	1	-	4 (4F)	Healthy	24	-	7	-
Brennan et al. (2019)	1	-	41 (17F)	Obsessive-Compulsive Disorder	2	-	12	-
Dosenbach et al. (2010)	1	-	192 (115F)	Mixed	1	-	~5	-
Fan et al. (2021)	1	-	70 (NA)	First-episode adolescent-onset schizophrenia and age-matched controls	1	-	8	-
	2	-	183 (101F)	Mixed	1	-	~5	-
	3	-	143 (99F)	Mixed	1	-	~5	-
Gordon et al. (2017b)	1	-	120 (60F)	Healthy	1	-	14	-
	2	-	108 (69F)	Healthy	1	-	10	-
Gordon et al. (2018)	1	-	26 (5F)	TBI	2-5	-	5-44	-
Mueller et al. (2013)	1	-	25 (9F)	Healthy	2-5	-	12	-
Miranda-Dominguez et al. (2014)	1	-	27 (16F)	Healthy	1	-	6-23	-
	2	-	5 (NA)	Healthy	2	-	6-23	-
Newbold et al. (2020)	1	CAST	3 (1F)	Healthy	42-64	-	30	https://openneuro.org:443/datasets/ds002766
Ousdal et al. (2020)	1	-	75 (49F)	Healthy	2	-	8	Available upon request
Wang et al. (2020)	1	-	158 (84F)	Schizophrenia, Schizoaffective Disorder, Bipolar Disorder with psychosis	1	-	6-12	-
Task-based fMRI studies								
Avery et al. (2020)	1	HCP	502 (274F)	Healthy	2	1	30	https://www.humanconnectome.org
	2	-	157 (105F)	Healthy, Amnestic Mild Cognitive Impairment, Alzheimer's Disease	1	-	-	-
Cole et al. (2014)	1	-	15 (7F)	Healthy	1	64	10	-
	2	HCP	118 (NA)	Healthy	2	7	30	https://www.humanconnectome.org
Cole et al. (2016)	1	HCP	100 (54F)	Healthy	2	7	30	https://www.humanconnectome.org

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Table 1 (*continued*)

Citation	Dataset Number	Dataset Name	Sample	Population	Sessions	Tasks	RS-fMRI (min./session)	Dataset Availability
Cole et al. (2019)	1	HCP	75 (NA)	Healthy	2	7	30	https://www.humanconnectome.org
Finn et al. (2017)	1	HCP	716 (392F)	Healthy	2	7	30	https://www.humanconnectome.org
Gao et al. (2019)	1	HCP	515 (274F)	Healthy	1	7	30	https://www.humanconnectome.org
	2	PNC	571 (320F)	Healthy	1	2	6	https://www.nitrc.org/projects/pnc
Greene et al. (2018)	1	HCP	515 (274F)	Healthy	1	7	30	https://www.humanconnectome.org
	2	PNC	571 (320F)	Healthy	1	2	6	https://www.nitrc.org/projects/pnc
Jiang et al. (2020)	1	HCP	463 (269F)	Healthy	1	7	15	https://www.humanconnectome.org
Salehi et al. (2020)	1	-	1 (0F)	Healthy	33	6	14	-
	2	MSC	10 (5F)	Healthy	10	3	30	https://openneuro.org/datasets/ds000224/versions/00001.
	3	HCP	514 (NA)	Healthy	2	7	30	https://www.humanconnectome.org
Seitzman et al. (2019)	1	MSC	10 (5F)	Healthy	10	2	30	https://openneuro.org/datasets/ds000224/versions/00001.
	2	MyConnectome	1 (0F)	Healthy	84	-	10	http://myconnectome.org/wp/
	3	HCP	384 (174F)	Healthy	2	-	30	https://www.humanconnectome.org
	4	WashU 120	120 (60F)	Healthy	1	-	14	https://legacy.openfmri.org/dataset/ds000243/
Shah et al. (2016)	1	HCP	476 (280F)	Healthy	2	7	30	https://www.humanconnectome.org
Tavor et al. (2016)	1	HCP	98 (NA)	Healthy	2	7	30	https://www.humanconnectome.org
Wu et al. (2020)	1	HCP	922 (NA)	Healthy	1	7	-	https://www.humanconnectome.org
Kraus et al. (2021)	1	MSC	DS1: 10 (5F)	Healthy	10	3	30	https://openneuro.org/datasets/ds000224/versions/00001.
Marek et al. (2018)	1	MSC	10 (5F)	Healthy	10	3	30	https://openneuro.org/datasets/ds000224/versions/00001.
Pinho et al. (2018)	1	IBC	12 (2F)	Healthy	9-30	12	-	https://openneuro.org/datasets/ds002685/versions/1.3.1
Pinho et al. (2021)	1	IBC	13 (2F)	Healthy	9-30	12	-	https://openneuro.org/datasets/ds002685/versions/1.3.1
Rosenberg et al. (2016)	1	-	25 (13F)	Healthy	1	1	12	-
	2	ADHD-200	113 (35F)	Healthy, ADHD	1	1	24	http://preprocessed-connectomes-project.org/adhd200/
Geerligs et al. (2015)	1	Cam-CAN	632 (320F)	Healthy	1	2	8.5	https://www.cam-can.org/index.php?content=dataset
Anderson et al. (2011)	1	-	1 (0F)	Healthy	1-10	1	50	-
	2	-	36 (20F)	Healthy (inc. adolescents)	1	-	8	-
Braga et al. (2020)	1	-	7 (5F)	Healthy	4-24	1-2	14-21	-
DiNicola et al. (2020)	1	-	6 (4F)	Healthy	4	1-2	112	-
	2	-	6 (4F)	Healthy	4	1-2	112	-
Epstein and Kanwisher (1998)	1	-	9 (NA)	Healthy	1	1	-	-
	2	-	6 (NA)	Healthy	1	1	-	-
Fedorenko et al. (2010)	1	-	37 (26F)	Unreported	1	2	-	-
Fong et al. (2019)	1	-	25 (17F)	Healthy	1	3	12	-
	2	-	44 (NA)	Healthy	1	1	12	-
	3	-	116 (74F)	Healthy (experimental and control groups)	1	1	10	-
Kanwisher et al. (1997)	1	-	15 (9F)	Healthy	1-2	3	-	-
Osher et al. (2019)	1	-	9 (3F)	Healthy	1-2	1	12-18	-
Parker Jones et al. (2017)	1	-	103 (53F)	Healthy, Pre-surgical patients	1	1	5	-
Rosenberg et al. (2018)	1	-	44 (29F)	Healthy	1	1	12	-
Spiridon et al. (2006)	1	-	14 (7F)	Healthy	1	1	-	-
Tobyne et al. (2018)	1	-	9 (5F)	Healthy	1	1	6-11	-
	2	-	14 (6F)	Healthy	1	1	12-18	-
Vanderwal et al. (2017)	1	-	31 (17F)	Healthy	1	2	7	-

Note. Table is separated into two categories: (1) studies reporting resting-state fMRI findings and (2) studies reporting task-based fMRI findings. Citations are organized by dataset, in descending order by number of mentions in the review. Citations using the same dataset are organized in alphabetical order. DS = data set, F = females, NA = not available), HCP = Human Connectome Project, ABIDE = Autism Brain Imaging Data Exchange, MSC = Midnight Scan Club, GSP = Brain Genomics Superstruct Project, HNU = Hangzhou Normal University test–retest dataset, eNKI-TRT = Enhanced NKI-Rockland Sample test–retest dataset, QTIM = Queensland Twin Imaging, WashU 120 = 120 participants from Washington University, ABCD = Adolescent Brain Cognitive Development Study, SLIM = Southwest University Longitudinal Imaging Multimodal Dataset, CoRR = Consortium for Reliability and Reproducibility, FCON 1000 = 1000 Functional Connectomes Project, KKI = Kennedy Krieger Institute, NKI = Nathan Kline Institute, NSD = Natural Scenes Dataset, SIMON = Single Individual volunteering for Multiple Observations across Networks, PNC = Philadelphia Neurodevelopment Cohort, IBC = Individual Brain Charting, Cam-CAN = Cambridge Centre for Aging and Neuroscience

† Multi-site study, where scan time may vary based on site.

in both adults and children over a two-year time period, a finding that has since been corroborated by other groups (Jalbrzikowski et al., 2020; Marek et al., 2019; Ousdal et al., 2020). Horien et al. (2019) then used four longitudinal datasets to demonstrate that the same frontoparietal and association networks that have previously been shown to be most predictive of individual subjects also best distinguish individual connectivity patterns years later.

Moreover, evidence suggests that individual connectomes may be partially determined by genetics. Miranda-Dominguez et al. (2018) found that fingerprinting analyses distinguished siblings from unrelated individuals. Demeter et al. (2020) further showed that functional connectome fingerprints can be used to identify pairs of identical twins and that identification accuracy decreases as genetic similarity decreases.

In addition to individual connectomes being stable and reliable, they are also associated with multiple aspects of behavior, including fluid intelligence (Finn et al., 2015), personality (Kashyap et al., 2019; Liu et al., 2019), lifestyle (Smith et al., 2015), cognitive flexibility, and processing speed (Wang et al., 2021). They may also be a useful tool for understanding brain pathology. For example, Dosenbach et al. (2010) used RSFC to predict "brain age," a level of brain maturity based on functional organization. Additionally, Ousdal et al. (2020) found an association between increased connectome stability over 2-3 years and reduced memory performance among middle-aged and older adults. They speculated that increased stability reflects the brain's decreased ability to adapt to age-related changes, which may affect overall cognitive function and result in memory deficits. Additionally, individual functional connectomes predict social and behavioral symptom scores in children with autism spectrum disorder and attention deficit/hyperactivity disorder, suggesting that functional connectivity may be used to inform future research on these disorders (Lake et al., 2019). Brennan et al. (2019) also demonstrated that RSFC-based biomarkers could be used to predict treatment-based improvement as well as the severity of various obsessive-compulsive behaviors, such as checking and washing. Furthermore, person-specific studies of psychosis have used RSFC to predict symptom severity and identify biomarkers better than traditional approaches (Fan et al., 2021; Wang et al., 2020). These studies all found that abnormalities in between-network functional connectivity were important in predicting symptom scores, suggesting that these disorders might be related to dysfunctional interactions between higher-order networks. In short, person-specific imaging has uncovered details about psychiatric disorders as well as the relationship between functional connectomes and behavior that had previously been undetected in group-level research.

3.2. Precision neuroimaging and the resting state

A number of recent person-specific studies have adopted a "precision" neuroimaging approach, collecting a substantial amount of data from each participant (at least two hours, and often much more) (Allen et al., 2022; Gordon et al., 2017c; Gratton et al., 2020; Gratton et al., 2018; Laumann et al., 2015). Many traditional fMRI studies collect relatively little data (sometimes only 5-10 minutes) from each subject and then conduct a group analysis. However, with such small quantities of data, the test-retest reliability of fMRI measures is low and confounded by variables such as head motion (Anderson et al., 2011; Gordon et al., 2017c; Laumann et al., 2015; Laumann et al., 2017; Lynch et al., 2020; Noble et al., 2021). Precision neuroimaging studies address these concerns by collecting high-quality individual measurements through repeated sampling, giving rise to alternative terms like "dense sampling" or "deep sampling." Some of the earliest of these studies provided the foundation for person-specific neuroimaging by collecting fMRI data from a small number of people over many sessions (Choe et al., 2015; Filevich et al., 2017; Gordon et al., 2017c; Laumann et al., 2015; Noble et al., 2017; Poldrack et al., 2015). For example, Poldrack et al. (2015) collected one of the largest single-human datasets to date, with eighty-four resting-state scans (totaling about 14 hours) over the course of 532 days. Laumann et al. (2015) then compared these data with group data and found that the functional organization of the individual's brain included distinct features not seen in the group. The authors suggested that smaller amounts of data may not accurately capture these person-specific features. Gordon et al. (2017a) examined three resting-state datasets and determined that many individuals exhibit person-specific features and that these features are reliable even though they are unique. Furthermore, after scanning ten individuals repeatedly at midnight (the Midnight Scan Club dataset; MSC) over almost two months and obtaining 15 hours of data from each participant, Gordon et al. (2017c) determined that several of their participants displayed person-specific features that were not present in the group average, supporting the idea that meaningful information is obscured by group averaging (see Gordon and Nelson (2021) for a review).

Expanding upon these findings, other work has provided further evidence for the stability of connectomes over time. Badhwar et al. (2020) scanned a single individual over 2.5 years, across multiple sites and scanners. While comparing across sites and/or scanners significantly decreased fingerprinting accuracy, the participant's connectome was stable across scans conducted at the same site and scanner.

Precision imaging is becoming increasingly popular, not only to further study intraindividual variability across time (e.g., Duchesne et al., 2019, who have scanned a single individual for over 15 years) but also to expand upon the study of person-specific features. Such studies have found that functionally-defined regions can vary in size in predictable ways and that person-specific features that are not present in group averages can nevertheless be consistent across a subset of participants (Gordon et al., 2017a). For example, Braga and Buckner's (2017) analysis of individual brain networks revealed that the default network may instead be two distinct networks, but the fine spatial scale needed to observe this distinction cannot be achieved with group-level analyses. They also found similar results in other traditional functional networks, suggesting that group-level analyses do not capture essential information about individual brain organization. Gordon et al. (2020) then built upon these results and found that the default mode network was fractionated into nine subnetworks with different functions, further demonstrating that precision imaging approaches provide a finer-grained examination of brain organization than is possible in traditional approaches.

Precision neuroimaging can also be readily applied to the study of psychopathology. Poldrack et al.'s (2015) characterization of a single human brain demonstrated how changes in activity can be measured over time and are connected to physiological measures, which could potentially reveal details related to illness. More recently, Gratton et al. (2020) pointed out that one reason treatments for psychiatric disorders are often inadequate (Kilbourne et al., 2018; Wang et al., 2002) could be the high variability in patient symptomatology within disorders. They argued that precision neuroimaging might be one way to characterize individual differences within disorders in order to tailor treatments to individual patients more effectively. Consistent with this idea, evidence suggests that the quantity of data that is typically collected in neuroimaging studies is not sufficient to accurately characterize psychopathology at the individual level (Liu et al., 2020). Partly in response to this concern, Sylvester et al. (2020) used the MSC dataset to examine connectivity between the amygdala and resting-state networks. They identified three separate subdivisions within the amygdala that exhibit differential patterns of connectivity and argued that precision datasets will enable researchers to better understand the neural mechanisms underlying mental illnesses. Similarly, Greene et al. (2020) used a precision neuroimaging approach to characterize connectivity with the thalamus and basal ganglia, finding that some subcortical areas serve as "integration zones" for larger networks. Some zones were shared across all participants, while others were person-specific. The authors suggest that these individual differences in brain organization may ex-

plain variation in clinical outcomes and serve as potential treatment targets. Consistent with this idea, Gordon et al. (2018) applied precision fMRI to the study of veterans with post-traumatic stress disorder (PTSD). They found that having had a traumatic brain injury decreased RSFC, and that decreased RSFC was associated with increased PTSD symptom severity—an effect that the authors demonstrated would not be apparent without large amounts of data.

Newbold et al. (2020) casted the right arms of three participants for two weeks and scanned them every day for six to nine weeks. RSFC significantly decreased between the left primary motor cortex and other somatomotor areas during the cast period, while spontaneous pulses began occurring throughout circuits associated with the disused arm. Yet after cast removal, RSFC quickly returned to pre-cast levels, and the pulses began to disappear. These findings suggest that when faced with sufficient change, the brain's functional organization can be altered by behavior, which could change the way we understand brain plasticity in the context of disease (Newbold and Dosenbach, 2021; Newbold et al., 2020). These insights would not have been possible without the fine-grained detail afforded by precision approaches.

4. Task-based activity may improve person-specific characterization

4.1. Task-based activity and individual differences

The person-specific studies already discussed focused on resting-state fMRI rather than task-based activity. One of the motivations for using the resting state is that functional organization is similar across different brain states (Cole et al., 2016; Mars et al., 2018; Salvo et al., 2021; Shah et al., 2016; Tavor et al., 2016) and therefore is able to index who you are, rather than what you are doing (Finn and Constable, 2016; Gordon and Nelson, 2021; Gratton et al., 2018). For example, using 64 different tasks, Cole et al. (2014) found that functional organization is primarily determined by an "intrinsic" structure that changes little between rest or across tasks. Though the authors did find that functional connectivity changes across tasks, these changes were small, and Cole et al. (2019) suggest that such changes may be due to confounding factors, such as task timing or head motion.

RSFC can also be used to predict patterns of task activity. For example, Tobyne et al. (2018) used connectome fingerprinting to predict activations in lateral frontal cortex related to visual and auditory working memory and attention, and Osher et al. (2019) further predicted dorsal attention network activation from RSFC. It is therefore natural to ask whether RSFC is all one needs to capture individual differences in neural organization, especially given that RSFC is relatively simple to obtain (Dubois and Adolphs, 2016; Finn et al., 2017; Parker Jones et al., 2017; Tobyne et al., 2018).

Nevertheless, there are reasons to suspect that resting state connectivity alone may not be sufficient for characterizing some aspects of individual variability. First, rest is an unconstrained state, and so differences in what people do during that unconstrained time could introduce noise and obscure reliable person-specific patterns of activity. Participants' minds may wander as they become bored, or they may move around or even fall asleep. These issues are even more pronounced in clinical populations, older adults, and children (Anderson et al., 2011; Eickhoff et al., 2020; Greene et al., 2018). To mitigate these problems, some studies have sought to compare activation during rest with activation during naturalistic viewing conditions (e.g., watching movie clips) in hopes of constraining brain state across participants. In one such study, Vanderwal et al. (2017) found that the inclusion of movies improved fingerprinting accuracy over rest alone.

A second concern is that resting state connectivity alone may miss important aspects of neural organization (Geerligs et al., 2015). For example, by scanning the same subjects while they viewed a variety of different visual stimuli, Kanwisher and colleagues were able to identify regions in ventral visual cortex that were associated with specific functions (e.g., the fusiform face area [FFA], the parahippocampal place area [PPA]) (Epstein and Kanwisher, 1998; Fedorenko and Kanwisher, 2009; Kanwisher et al., 1997; Spiridon et al., 2006). This work led to the use of task-based functional localizers, which are now routinely used to identify functional regions that vary in location from person to person (Fedorenko, 2021; Fedorenko et al., 2010; Nieto-Castanon and Fedorenko, 2012). While resting-state data can often predict task-based activations (e.g., Tavor et al., 2016; also see Section 4.2), resting state data alone would not have been able to determine that the FFA is involved in face processing or that the PPA is involved in place processing.

Using tasks to change brain state might also provide further insights into the brain's functional organization, even when examining resting-state connectivity. Finn and Constable (2017) use the analogy of a cardiac stress test, which aims to bring out differences that may be abnormal, but too slight to observe at rest. Similarly, using cognitive tasks to expose a process of interest may magnify individual differences that are unseen during rest. For example, by manipulating brain state, Greene et al. (2018) were better able to predict individual traits from functional connectivity measurements, suggesting that the tasks induced changes in connectivity that magnified relevant individual differences. Moreover, models that include task states also predict a variety of behavioral measures more accurately than those that only include resting state data (Jiang et al., 2020), including measures of working memory (Avery et al., 2020) and attention (Fong et al., 2019; Rosenberg et al., 2016; Rosenberg et al., 2018). Including multiple task states has been found to further improve behavioral predictions (Gao et al., 2019; Greene et al., 2018; Wu et al., 2020), but incorporating them into a single connectome could potentially blur important differences between states. Gao et al. (2019) therefore proposed creating separate connectomes for each task state and then combining them into a multidimensional connectome, which further improved prediction accuracy.

4.2. Task-based activity in precision techniques

A number of studies have also incorporated task-based activity in a precision neuroimaging framework and collected extensive amounts of data. In some cases, adding task data did not affect the results significantly. For example, Gratton et al. (2018) found that functional organization is primarily determined by individual, trait-like qualities, rather than those due to task state. Additionally, Braga et al. (2020) repeatedly scanned a small set of individuals in order to characterize the language network in each person and found that their connectivity-defined language network changed little based on what state was used to create it. On the other hand, they also found that this network is one of several distinct association networks that have specialized functions, and they also identified some functional regions that had not been found in previous work. Marek et al. (2018), using the MSC dataset, found consistent individual variation in the functional architecture of the cerebellum that corresponded to parcellations derived from resting state data, and multiple others have found that rs-fMRI can reproduce similar person-specific regions and networks as those produced by task-based functional localizers (Gordon et al., 2017c; Laumann et al., 2015).

Other studies have found that including task-based activity in precision datasets can reveal within-individual differences between brain states. Anderson et al. (2011) found that they could discriminate functional connectivity derived from resting-state scans from connectivity derived from naturalistic viewing scans with exceptional accuracy when including more than 10 minutes of data. Their results suggest that functional connectivity during a task is somewhat different than during rest, and that state-related differences may only be discernible with precision approaches because of the increase in reliability they provide. Kraus et al. (2021) followed up this idea with an examination of trait-like variants that had previously only been found using resting-state data (Gordon et al., 2017c; Gratton et al., 2018; Seitzman et al., 2019). They found that though variants are more similar within individuals

across states than across individuals, they also demonstrated some dependence on brain state. Furthermore, task-based precision neuroimaging has revealed that specific default mode subnetworks are activated by different tasks (DiNicola et al., 2020; Gordon et al., 2020). Importantly, Salehi et al. (2020) found that the brain reconfigures the same way when completing the same task, indicating that the resting state alone does not provide a complete picture of the brain's functional architecture. In fact, the authors claimed that there is "no single atlas," and that subject-specific, state-specific atlases will be important in gaining a more complete understanding of the brain and its functions.

The Individual Brain Charting Project (Pinho et al., 2021; Pinho et al., 2018; Thirion et al., 2021) has demonstrated that increasing the number of cognitive tasks improves characterization of specific brain areas and their functions. Similarly, the Natural Scenes Dataset scanned individuals as they viewed thousands of different scene images (Allen et al., 2022). Such approaches are based on the idea that studying the functional architecture of a few individual brains in detail will provide new insight into neural organization more generally. Doing so will require studying individual brains in as many contexts as possible (Naselaris et al., 2021; Thirion et al., 2021).

5. Limitations and future directions

While person-specific imaging has provided important insights regarding individual differences in the brain, the field is still in its infancy. Here, we outline a few current limitations as well as potential directions for future research.

5.1. Using large task batteries to densely image cognition

The bulk of the research on individual variability has used resting state data, but recent evidence indicates that adding task states may be helpful. For example, Finn et al. (2017) suggested that because the resting state is noisier, task states may require less scanning time than rest to produce reliable within-subject measurements. However, very few studies have directly tested this hypothesis, and multi-echo fMRI may provide another solution (see Section 5.5). Furthermore, one task may not be optimal; the inclusion of more than one task state can be used to improve behavioral predictions (Gao et al., 2019; Greene et al., 2018; Wu et al., 2020), as any individual task may miss important aspects of functional architecture that could be observed using other tasks (Finn et al., 2017; Geerligs et al., 2015; Jiang et al., 2020; Pinho et al., 2021). Given a finite amount of time, one encounters a tradeoff between collecting more tasks versus collecting multiple runs of a single task. However, measuring brain activity from the same participants in as wide a variety of contexts as possible will provide a more complete picture of the neural organization of cognition. For example, studying the brain in different contexts has led to discoveries of many specialized brain regions, such as the fusiform face area, parahippocampal place area, and language areas (Epstein and Kanwisher, 1998; Fedorenko et al., 2012; Fedorenko et al., 2010; Kanwisher et al., 1997). Precision imaging presents a unique opportunity to study brain function at a finer scale through the incorporation of task states. The Individual Brain Charting (IBC) project (Pinho et al., 2020; Pinho et al., 2018), is one such attempt to map a wide domain of perceptual and cognitive functions by collecting data from twelve individuals as they complete approximately 30 tasks, while the Natural Scenes Dataset collected data from individuals as they viewed thousands of images (Allen et al., 2022). Approaches like these may be instrumental in furthering our understanding of functional brain architecture at an individual level.

5.2. Limitations of assuming shared topology

We have reviewed many studies that used person-specific imaging methods, but many of them still used a group-derived parcellation to map the brain and model its function (Eickhoff et al., 2018). In particular, many functional connectivity studies adopt a single, shared parcellation across participants For example, Finn et al. (2015) used a group-wise clustering algorithm on 45 participants to create a parcellation and then applied it to all subjects in their analyses. This method implicitly assumes that the parcels neither vary across individuals nor change within individuals based on tasks, which may be unrealistic (Salehi et al., 2020). In fact, the precision imaging literature reviewed previously has extensively demonstrated that group-based parcellations do not accurately represent the functional organization of every person in the group (Braga and Buckner, 2017; Gordon et al., 2020; Laumann et al., 2015; Poldrack et al., 2015). Future research could use function-based parcellation approaches, as suggested by Salehi et al. (2020), or create new parcellations that account for individual differences in neural architecture.

One promising alternative to traditional normalization is hyperalignment (Busch et al., 2021; Feilong et al., 2018; Guntupalli et al., 2016; Haxby et al., 2011). Here, patterns of activation in each participant are transformed into a common representational space such that voxels from different participants that share functional properties are mapped into nearby parts of a high-dimensional space. This approach makes it possible to analyze groups of participants in a common space while addressing the inherent variability in the spatial location of functional regions across participants.

5.3. Generalizability in person-specific imaging

One potential concern with person-specific and precision neuroimaging is generalizability. The studies discussed above have repeatedly found that individual brains are heterogeneous, so how can these results be generalized to individuals not in the study? Importantly, many of these studies have discovered features of the brain's neural architecture that are shared across many, if not all brains. For example, Braga and Buckner (2017) and Gordon et al. (2020) found that the default network may consist of multiple networks that were invisible with traditional approaches, but that nevertheless exist in almost every brain. Precision neuroimaging offers the ability to view the brain with a clarity that was not previously possible and will likely continue to reveal details about neural organization that have yet to be discovered. However, both the person-specific and precision imaging research reviewed here primarily use a small pool of datasets, such as the Human Connectome Project (HCP; Van Essen et al., 2013) or the Midnight Scan Club dataset (Gordon et al., 2017c) (Table 1). The subjects in such datasets are typically healthy, educated young adults and, in the case of precision imaging datasets, include individuals who co-authored the studies. Because either collecting data from many subjects or collecting large amounts of data from individuals is difficult and costly (Gratton et al., 2018; Lynch et al., 2021; Tobyne et al., 2018), these datasets are valuable resources. But the repeated use of such a small number of datasets may eventually lead to overfitting, where the models we create inevitably include the idiosyncrasies of those datasets (Grootswagers and Robinson, 2021). This issue poses a significant challenge for neuroimaging research, which already suffers from a replication crisis. The fact that these datasets are difficult to obtain is even more reason that they should be shared, and an increase in the number of person-specific and precision imaging datasets will allow for both the replication of previous work and the testing of new hypotheses. We hope that bringing attention to this limitation will prevent the problems associated with the overuse of a small pool of data, particularly as it pertains to the study of person-specific brain organization.

5.4. The reliability paradox

One of the key advantages of precision imaging studies is that collecting a lot of data in each participant increases within-subject reliability. These higher-quality measurements allow researchers to be confident

that the person-specific features observed in a given individual are real and are not due to noise. That said, although within-subject reliability is necessary, it is not sufficient if our ultimate goal is to relate individual differences in brain organization to individual differences in behavior. To achieve that goal, the individual differences *between* subjects must also be reliable.

In most neuroimaging research, a reliable task produces the same effect across subjects and therefore has low between-subject variability. However, if the goal is to relate individual differences in neural measures to individual differences in behavioral measures, then low between-subject variability is actually a problem. As Hedge et al. (2018) argue, low between-subject variability means low reliability of individual differences, undermining the ability to identify reliable correlations between individual difference measures. This "reliability paradox" will become increasingly relevant to study designs as researchers attempt to examine brain-behavior relationships, as establishing both within- and between-subject reliability will be important in order to produce more replicable results and further inform new theories of cognitive processing (Hedge et al., 2018).

5.5. Incorporating brain stimulation techniques into person-specific imaging

Transcranial magnetic stimulation (TMS), a form of non-invasive brain stimulation, is well-suited to the study of individual differences because it makes it possible to experimentally manipulate activity in person-specific functional regions. Most neuroimaging research is inherently correlational, and so the addition of TMS to person-specific imaging studies would allow for the causal manipulation of brain activity in person-specific functional regions. Fortunately, brain stimulation is also moving towards person-specific methods. Stimulation sites were previously often chosen based on anatomical locations or International 10/20 electrode scalp positions, but because the functional organization of the brain differs across individuals, these standardized targets produce different effects in different people (Lynch et al., 2019; Sack et al., 2009). Instead, using functional connectivity to locate stimulation sites that are highly connected to an area of interest have been shown to be replicable and have promise in improving TMS-based treatments for a range of disorders. For example, TMS stimulation at person-specific sites highly connected to the hippocampus have been shown to improve memory performance, and frontal stimulation sites based on fMRI task data have been used to elucidate the organization of regions involved in perceptual decision making and cognitive control (Freedberg et al., 2019; Nee and D'Esposito, 2017; Rahnev et al., 2016; Wang et al., 2014). Ozdemir et al. (2020) used TMS to stimulate specific brain networks and then measured the propagation of activity to other regions. They found that the propagation patterns were unique to individuals and predicted individual differences in behavioral performance that were missed by traditional resting-state measures.

These person-specific approaches have further demonstrated promise in providing more effective treatments for disorders such as Alzheimer's disease and depression (Bagattini et al., 2021; Fox et al., 2012; Fox et al., 2012; Fox et al., 2013; Siddiqi et al., 2019). In fact, Siddiqi et al. (2019) demonstrated that people with different patterns of depressive symptoms responded better to different person-specific stimulation sites, suggesting that person-specific stimulation has the potential to improve the treatment of many different psychiatric disorders.

However, while several studies have mentioned the utility of this work in precision psychiatry (Braga and Buckner, 2017; Gratton et al., 2020; Greene et al., 2020), to our knowledge only a few studies have used TMS in conjunction with highly-sampled, precision datasets. Lynch et al. (2019) used the MSC dataset to determine that connector hubs, or areas connected to multiple networks, are individual-specific and can be mapped with large amounts of data. They then applied TMS to person-specific hub and non-hub stimulation sites in an independent dataset, finding that continuous theta burst stimulation to a hub target impaired working memory performance compared to stimulation of a non-hub target. Their results demonstrate that combining precision neuroimaging with TMS can provide unique opportunities to further our understanding of brain-behavior relationships.

5.6. New analytical techniques

A substantial amount of work has been done using connectome fingerprinting to identify individuals and predict patterns of activation and individual traits. This work could shed light on differences in cognition across healthy and clinical populations and identify those at risk of developing future disorders. Much of the current literature on predicting individual differences has used an approach called connectome-based predictive modeling (CPM), which derives models that predict brain-behavior relationships using cross-validation (Finn et al., 2015). However, other connectome fingerprinting techniques have also been successfully used to identify individuals by their structural (Osher et al., 2016; Saygin et al., 2012) and functional connectivity (Cai et al., 2019; Chen and Hu, 2018; Osher et al., 2019; Tobyne et al., 2018; Venkatesh et al., 2020). New methods have also become available, like the recent multidimensional CPM method, which combines connectomes from multiple different states, rather than using one state to predict others (Gao et al., 2019). Few studies directly compare these different methods, but those that do have found differences in their results (Gao et al., 2019; Yoo et al., 2019). For example, Finn et al. (2015) found that fingerprinting accuracy was worst when using less than 6 minutes of data, but Chen et al. (2018) reported that 72 seconds was sufficient for individual identification when using recurrent neural networks. A greater understanding of how these methods differ in their ability to identify individuals and predict behavior will be important to informing future research, as it could potentially limit inconsistencies due to "researcher degrees of freedom" (Poldrack et al., 2017).

In addition, one of the challenges associated with precision imaging methods is the need for large amounts of data. However, recent work has demonstrated the promise of multi-echo fMRI in shortening the scan time needed to produce reliable single-subject measurements. Lynch et al. (2020) found that 10 minutes of "optimally combined" multi-echo timeseries (OC-ME) data combined with Kundu et al.'s (2012) ME-ICA denoising technique provided more reliable estimates of single-subject functional connectivity than 30 minutes of traditional single-echo data. These methods may make precision imaging considerably more feasible in the study of psychiatric and neurological disorders (Lynch et al., 2021; Lynch et al., 2020). In a later review, these same authors argued that single-echo data should not be overlooked, because some cortical areas do demonstrate good reliability with only 15-30 minutes of data (Lynch et al., 2021).

6. Conclusion

Person-specific and precision neuroimaging will allow researchers to obtain a more precise understanding of the brain's functional architecture than ever before. Though this field is still in its early stages, studies have made substantial progress in recent years. This research suggests solutions to the well-known problems associated with group analyses and could lead to new insights into the functional organization of the human brain. They also provide meaningful evidence that "precision" imaging approaches can uncover fine-grained details of the brain that can only be seen when collecting substantial amounts of data from each individual. These person-specific approaches demonstrate substantial promise in uncovering the functional organization of the brain and its relationship to behavior.

Data and code availability

This review article does not include the use of original data and/or code. For information regarding the data and code from studies cited within, please see the original article.

Data Availability

This review does not present original data/code. When available, data availability for the studies cited within are provided in Table 1.

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