

OHBM 2026



Contributions collectives sur
<https://padlet.com/mariehelenegrosbras/ohbm2026-4hvmcnj2xylj7jkb/>



Roadmap : highlights from Marseille's delegates

- Insights from abstracts semantic analysis
- Methodological advances – acquisitions
- Large datasets : some example of results and caveats
- Tools and sharing
- Other trends

Quantitative abstracts exploration n=3240

- <https://abstractatlas.brainkb.org/ohbm2026/>

Topics

Modeling and Analysis Methods	1598
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Quantitative abstracts exploration n=3240

Study Type	Count
Resting state	1345
Other	1206
Task-activation	961

Population	Count
Healthy subjects	2177
Patients	1475
Other	210

Field Strength	Count
3.0T	2481
Other	510
7T	264
1.5T	246
1T	20
2.0T	11
4.0T	7

Processing Packages	Count
Other	1853
FSL	1206
Free Surfer	1186
SPM	947
AFNI	414
Brain Voyager	33
Analyze	28
LONI Pipeline	8

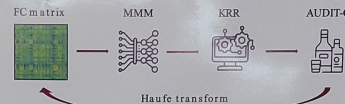
Predicting alcohol consumption from resting-state fMRI functional connectivity: meta-matching and interpretability

Marco Bottino^a, Michael N. Smolka^a, Justin Böhrer^{b,c}, Henrik Walter^b, Michael Marxen^a

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^bDepartment of Psychiatry and Psychotherapy, Charité – Universitätsmedizin Berlin, German Research Data Center Berlin, Humboldt-Universität zu Berlin, and Berlin Institute of Health
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Results

Prediction performance of AUDIT-C

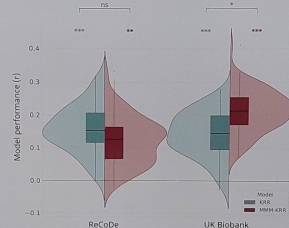


Figure 1: Prediction performance (Pearson r) of the models investigated for both datasets.

Statistical comparisons were performed using corrected one-tailed paired t -tests to test whether performance improved from KRR to MMM-KRR and whether r is greater than zero.

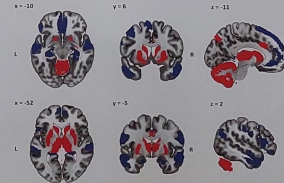


Figure 2: Brain regions showing strongest associations between functional connectivity and AUDIT-C score.

Regions in red are positively associated with AUDIT-C. In contrast, regions in blue show decreased connectivity associated with higher scores.

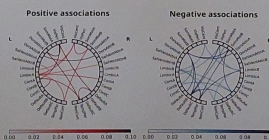


Figure 3: Changes in network connectivity associated significantly with AUDIT-C score prediction. The chord diagram on the left shows increased connectivity, and on the right, decreased connectivity.

Conclusion

- Alcohol consumption can be predicted from resting-state functional connectivity with modest accuracy ($r = 0.15$), consistent with prior large-scale findings.
- Meta-matching did not improve prediction performance over locally trained KRR in this sample size, suggesting limited benefit of MMM for AUD outcomes in a new moderately large dataset.
- Interpretable relevance maps revealed consistent hypoconnectivity across limbic, default mode, and dorsal attention networks, replicating across cohorts despite low effect sizes, and hyperconnectivity across precuneus and striatum.

Background

- Alcohol use disorder (AUD) is one of the most common and comorbid psychiatric disorders in the world.
- Resting-state fMRI functional connectivity (FC) provides a noninvasive means to explore the brain's functional organization.
- Machine learning (ML) models are increasingly being used in literature to understand how brain connectivity is related to clinical phenotypes such as AUD.

Aims

- Can we improve model performance using meta-matching transfer learning?
- Can we interpret these models to find reliable associations between FC and alcohol consumption?

Methods

- Rs-fMRI data from ReCoDe¹ cohort ($N=739$, 305 female) and a subset from UK Biobank² matched in gender and drinking patterns
- Multilayer meta-matching (MMM)³ applied to generate an embedding (458 features) containing information from external datasets
- Kernel Ridge regression (KRR)⁴ to predict AUDIT-C, a score measuring the severity of alcohol consumption
- Haufe transform⁵ to inspect linear contributions of FC for the prediction

References

- Spanagel et al., 2024
- Smolka et al., 2019
- Chen et al., 2024
- Saunders et al., 1993
- Haufe et al., 2014

Find me!



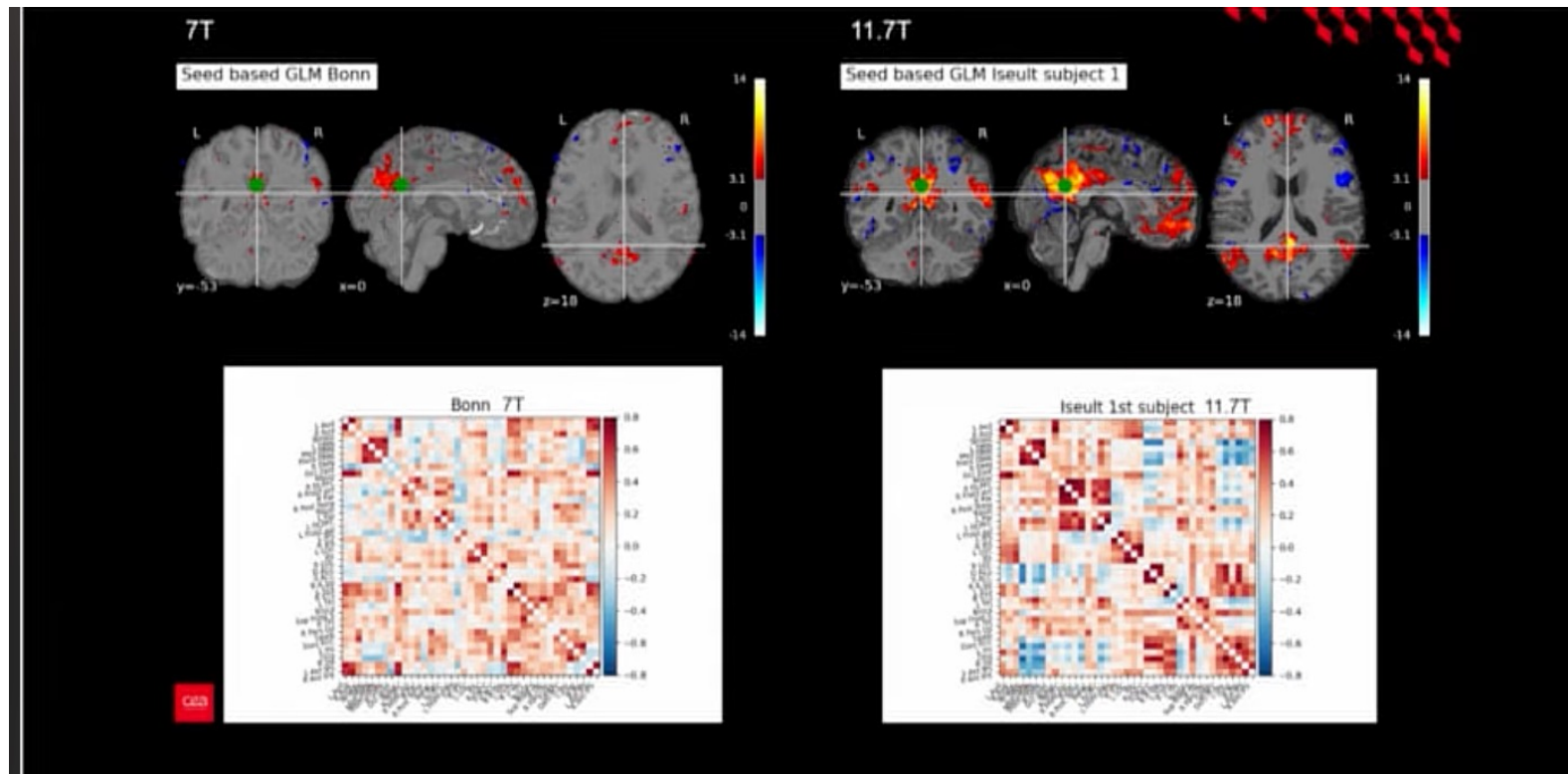
A representative study

- Associating resting state fMRI data to clinical scores with machine-learning algorithms and multiple datasets for validation

Roadmap : highlights from Marseille's delegates

- Insights from abstracts semantic analysis
- **Methodological advances – acquisitions**
- Large datasets : some example of results and caveats
- Tools and sharing
- Other trends

Resting state fMRI at 11.7 T



Multi-echo MRI

OHBM 2026 Educational Course Practical Multi-echo fMRI:



Underlying principles, challenges, potential, and applications

Organizers: Daniel Handwerker, Eneko Uruñuela, Sarah Goodale

Topic
pts
Dan Handwerker (+ Sarah Goodale): Introduction to multi-echo fMRI and tedana
Mélanie Garcia: Multi-echo fMRI data quality control
Javier Gonzalez-Castillo: Now that I have multi-echo data, what else can I do with it?
Discussion and Q&A: Best practices for collecting and validating multi-echo fMRI data
Break
Applications
Eric Pierre: Multi-echo fMRI in a large clinical study — insights from the Australian Epilepsy Project
Eui-Jin Jung: Enhancing predictive modeling using multi-echo fMRI in pain
Lunch break with informal Q&A for the final 20 minutes of the break
Julia Moser: Multi-echo fMRI in developmental neuroimaging
Discussion and Q&A: Advice & challenges for using multi-echo fMRI in clinical studies
Kathryn Lamar-Bruno: Benefits and challenges of Echo Planar Time-Resolved Imaging (EPTI) for multi-echo fMRI
Nathan Spreng + Prantik Kundu: Subcortical connectivity at 3T & 7T with ME fMRI
Break
Logan Dowdle: The higher the field, the faster it falls — challenges and opportunities of multi-echo fMRI at 7T
Eneko Uruñuela: Is generative AI the next step in multi-echo fMRI denoising?

2413

NIH

What is the Optimal Number of Independent Components for Multi-Echo fMRI Denoising? 746

Marlene M. Smith, B.S.¹, Daniel A. Handwerker, Ph.D.¹, Ka Chun Lam, Ph.D.¹, Javier Gonzalez-Castillo, Ph.D.¹, Tyler Morgan, Ph.D.¹, Francisco Pereira, Ph.D.¹, Catherine Walsh, Ph.D.¹, Taylor Salo, Ph.D.¹, Eneko Uruñuela, Ph.D.¹, Peter Bandettini, Ph.D.¹

¹Section on Functional Imaging Methods, ²Machine Learning Team, ³fMRI Facility, NIMH, Bethesda, MD, United States, ⁴University of Pennsylvania, Philadelphia, PA, United States, ⁵University of Calgary, Calgary, AB, Canada.

INTRODUCTION

ONGOING WORK

Tensor ICA

- Denoising can be improved by better decomposition methods or better inclusion/exclusion criteria
- MRI physics dictates how BOLD and non-BOLD signal should decay across echoes, which can inform decomposition inclusion/exclusion criteria
- Tensor based ICA approaches take advantage of all echoes in the component creation process and output components with an additional "echo profile" dimension
- Current fMRI tensor ICA methods^{5,6} do not consider physical properties in component creation

% Change Signal

Echo 1 Echo 2 Echo 3 Echo 4 Echo 5

Non_BOLD BOLD

Simplified BOLD vs non-BOLD echo profiles

Space Time

Space Time * Echoes

Example of tensor unfolding for tensor ICA

Echo Constrained Alternating-Projection Tensor ICA Algorithm

- Our work-in-progress Echo Constrained Alternating-Projection (ECA-P) Tensor ICA algorithm optimizes for statistical independence (via an ICA-projection step) as well as physics-informed echo profiles
- The algorithm converges stably on both objectives (data fit and negentropy), but recovered echo slopes (though linear, as physics predicts) show limited variation across components

Spatial Maps

Time Series

Echo Profile

Sample component from ECA-P Tensor ICA with 30 Components

Least Squares Error

Negentropy

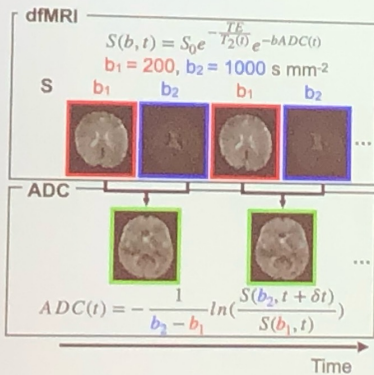
Iteration

Convergence metrics for ECA-P tensor ICA, least squares fit between modeled and real data and negentropy

Methods

dfMRI and ADC-fMRI acquisition

Nguyen-Duc et al., Hum. Brain Mapp., 2025
Spencer et al., Nat. Commun., 2025
De Riedmatten et al., Comms. Biol., 2025



- **b200-dfMRI & b1000-dfMRI:**
 - T_2 & diffusion-weighted
 - BOLD proxy
- **ADC-fMRI**
 - Diffusion-weighted
- T_2^* BOLD-fMRI

fMRI resting state on fetus: use Frame Displacement to find sequences of "not-moving-to-much" volumes

Pipeline Development and Exploratory Visual Network Analysis

Xinnan Wang, Kelly J. Hiersche, Anna Quatrala, Huiyu Yang, Elizabeth Sponseller, Rachael F. Holt, Maged Costantine, Zeynep M. ...

Department of Psychology & Center for Cognitive and Brain Sciences, The Ohio State University

Introduction

- Fetal neuroimaging presents substantial methodological challenges, including:
 - high motion, interference from surrounding maternal tissues, variable imaging orientations, low signal-to-noise ratio
- Here, we systematically evaluate multiple preprocessing strategies to optimize pipeline for fetal resting-state fMRI (rsfMRI).
- The utility of this pipeline is demonstrated through exploratory analyses of fetal visual network organization.

Research Questions

- Which preprocessing strategies maximize data quality and biological validity in fetal resting-state fMRI?

Methods

Participants
N = 30, mean GA = 33.79 (weeks), Female = 14 (46.67%)

T2 anatomical Scan

2D slices acquired sequentially in one of three orientations (sagittal, axial and coronal): TR = 1.4 s, TE = 0.1 s, slice thickness = 2mm.

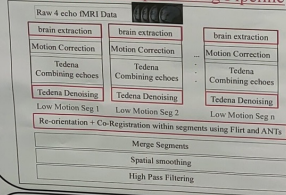
Resting state fMRI

Multi-echo rsfMRI runs; multiband 4x accelerated EPI sequence: TR = 2000 ms (160 total TRs), TE = 13 ms, 29.22ms, 45.42ms, 61.64ms, voxel resolution = 3.2mm³. 15-21 minutes collected per subject.

Preprocessing fetal resting-state data

Step 1: Split timeseries into low-motion segments; Step 2: Preprocess each segment; Step 3: Concatenate segments; Step 4: Evaluate efficacy of preprocessing by probing the biological validity of visual system connectivity in the fetal brain prior to external visual experience

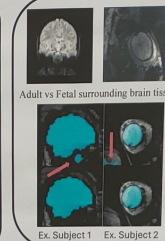
Optimized Preprocessing Pipeline



Conclusions

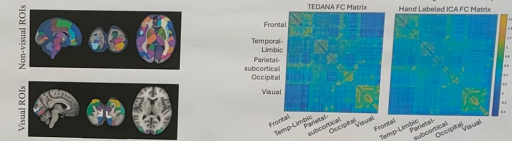
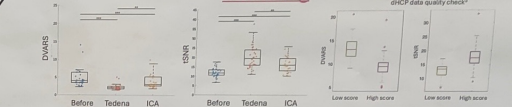
- Motion-adaptive segment-specific brain masks improved fetal brain extraction.
- Orientation matching prior to registration improved template alignment.
- TEDANA denoising outperformed ICA denoising based on DVARS, tSNR, and visual network segregation.
- The resulting optimized preprocessing pipeline enabled biologically plausible fetal visual network connectivity patterns.

Brain Masking



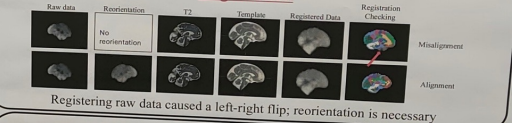
Two trained independent graders evaluated masks. Friedman test revealed significant difference (13.40, $p = 0.001$). Wilcoxon signed-rank tests showed smart mask outperformed the original mask ($W = 0.004$) and the low-motion mask ($W = 8$, $p = 0.0$).

Denosing



Compare within-visual connectivity to visual-outer, expecting stronger within vs between network FC. TEDANA-denoised outperformed ICA denoising for all 25 visual regions (only significant for 6; $t(29)$ range: -2.79 to -2.24, all $p < 0.05$).

Registration



Exploratory Visual Network Analysis

ROI-based functional connectivity (FC) analysis of 25 fetal visual cortical regions and 107 cortical and subcortical regions. Overall, within visual network connectivity is stronger ($t(29) = 6.86$, $p < 0.001$).

Future Directions

- Examine the emergence of visual network segregation and interhemispheric connectivity before birth.
- Investigate how prenatal visual network organization relates to postnatal neurocognitive outcomes.

White Matter Analysis in fMRI

5

2002 - 2012

Foundational Evidence

- Initial Task Detections
Tettamanti 02, Gowrylak 09, Verfaen 09
- Callosal Mapping *Fabri 11, Gowrylak 11*
- HRF Verification *Fraser 12*
(WM vs GM characteristics)

2013 - 2018

Intrinsic Networks & Optimization

- Resting-State Discoveries
Peer 17, Marussich 17
- Correlation Tensors *Ding 13, 16, 18* *(Pathway visualization)*
- 3T Magnetic Field Tests
Mazarsolle 13, Courtemanche 18

2019 - Present

Clinical Biomarkers & Behavior/State

- Epilepsy *Jiang 19, Li 22, Das*
- Alzheimer's *Zhao 19, Lin 20*
- Schizophrenia *Jiang 19, Gao 21, Wang 21*
- ADHD *Bu 20*
- Autism *Chen 23*
- Migraine *Forago 23*
- TBI *Xia 21*
- State Dependence *Yang 22, Zhang 21, Zhang 26*
- Development and Lifespan
Huang 24, Wang 25, Feng 26

2023 - Present

Consolidation & Standardization

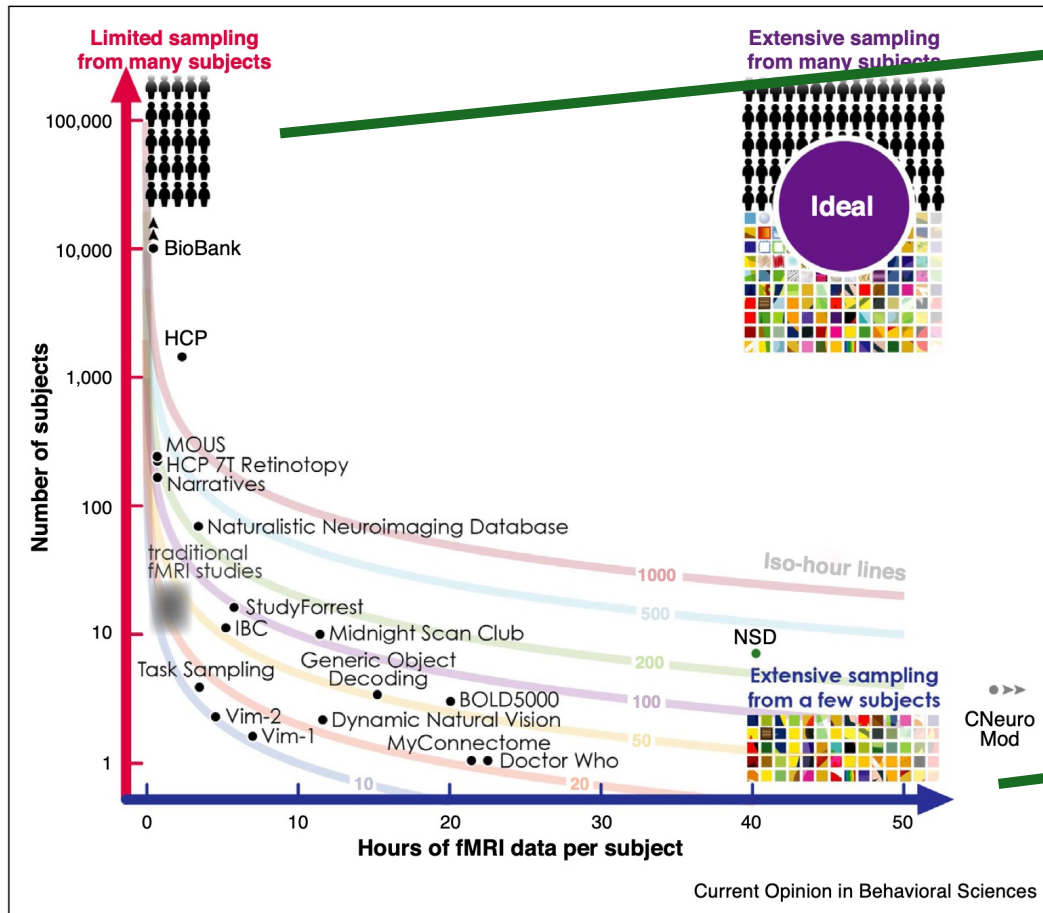
- Electrophysiology Proof
Huang 23 *(Intracranial)*
- Myelin Network Coupling
Nelson 25, Gore 26
(Mechanisms)
- White Matter fMRI atlas and templates *Wysol 25, Nuzin 23, Zhou 26*
- Toolboxes *Join 25* *(MindFut)*

Roadmap : highlights from Marseille's delegates

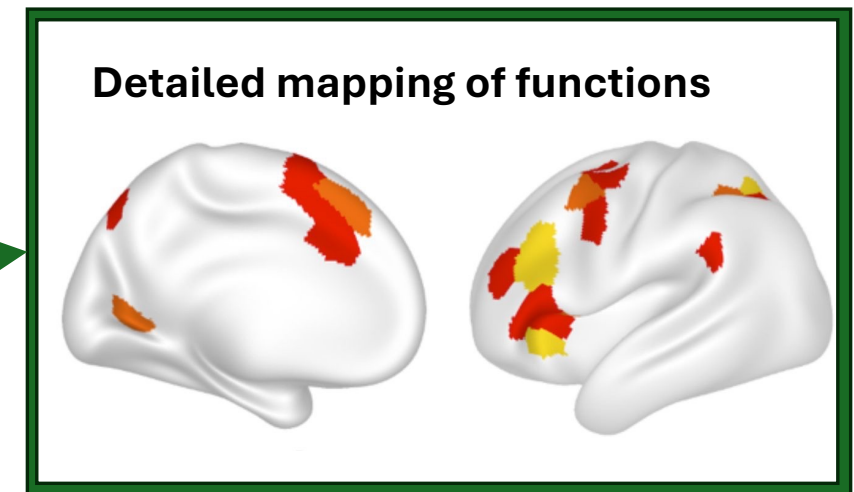
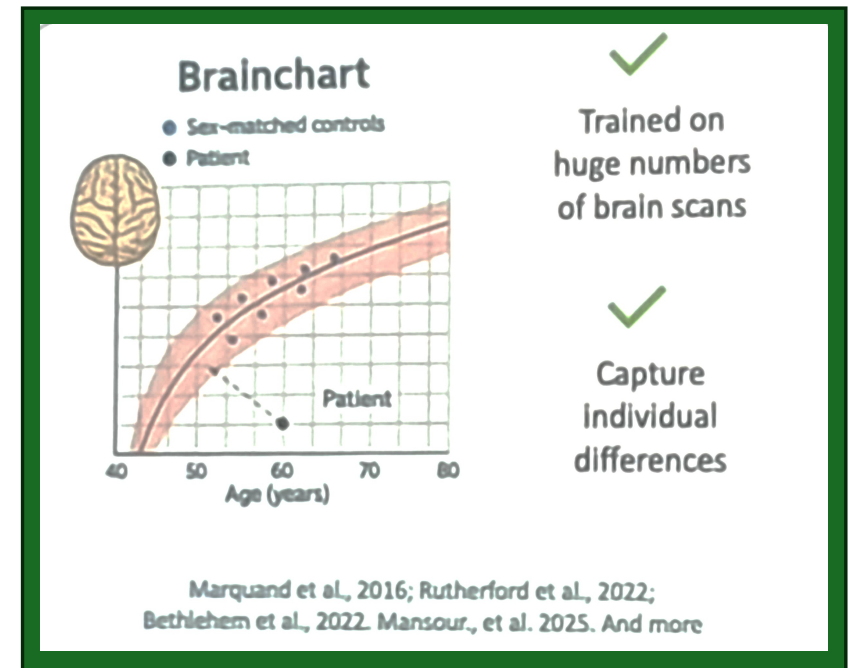
- Insights from abstracts semantic analysis
- Methodological advances – acquisitions
- Large datasets : some example of results and caveats
- Tools

**DO YOU HAVE
RESEARCH
QUESTIONS?
WE HAVE
OPEN DATA.**

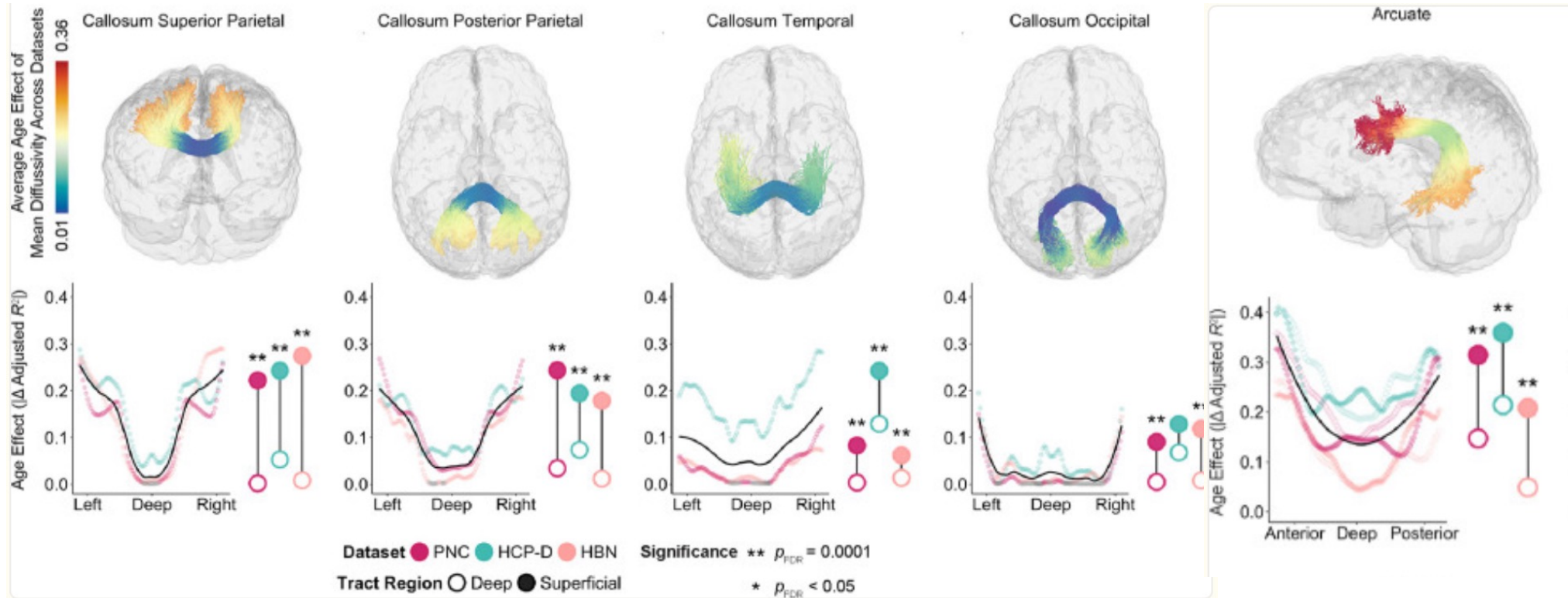
Breadth vs Depth



Nasarelis, Allen, Kay 2021

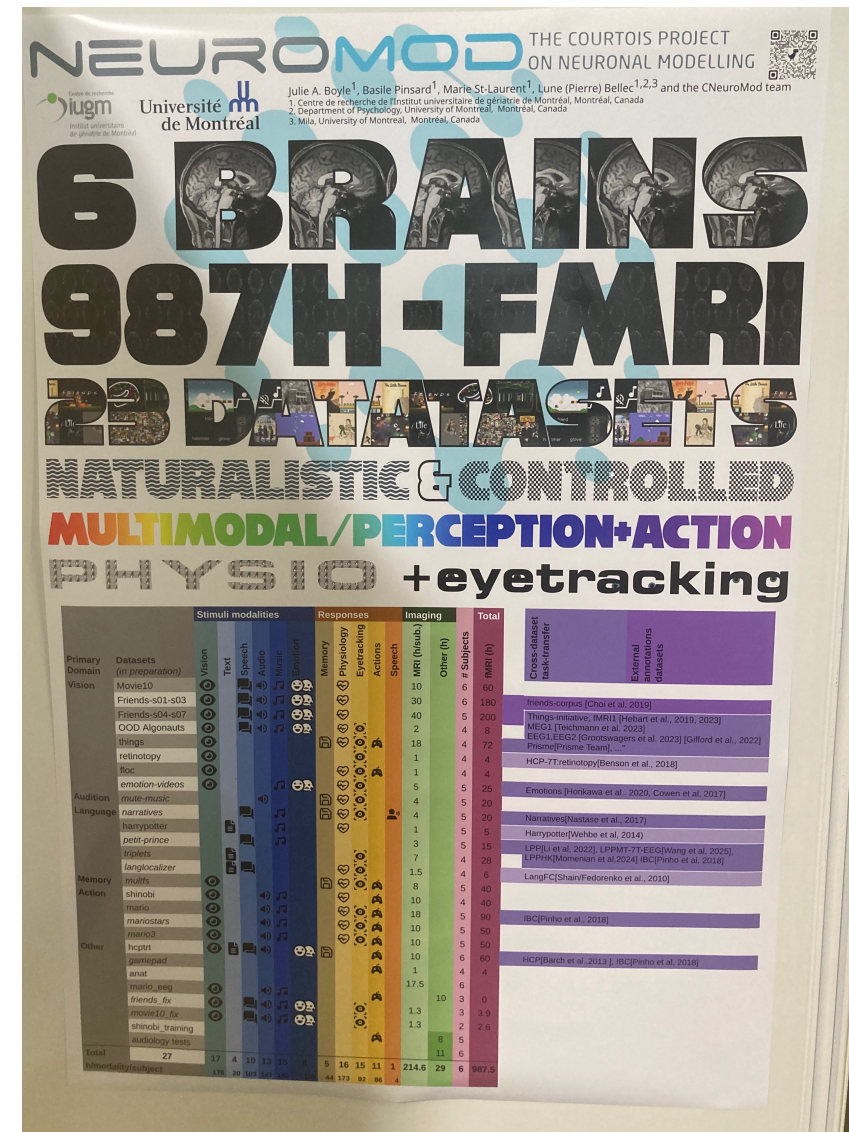


Ex : two axes of white matter development



Deep sampling (precision scanning)

- Individual Brain Charting (IBC)
- Midnight Scanning Club
- Bold5000 Project
- Natural Scenes Dataset
- Visual Cognition dataset (7T)
- Naturalistic perception (with motion corrected eye tracking, cf Park 2026)
- Emofilm (Geneva)
- THINGS dataset
- Courtois-Neuromod



Advantages and caveats common to both approaches

- Stronger statistical inferences
- Characterisation of inter or intra individual variability
- Test specific factors , eg SES (papier Mareck Nature)
- Multimodal inferences: link to gene expression, neurotransmitters, mitochondria , etc
- Foster tools development

- Representativity of participants (eg (Bethlehem Nature paper only 4% of individuals from East Asia; overtrained participants in deep sampling datasets)
- Representativity of researchers : concentration in a few labs or countries

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WE HAVE
OPEN DATA.**

Reliability across the eras

Proto-meta-analyses

First attempts to identify consensus and reliable results

(1993-2000)

Meta-analysis methods

Development of coordinate-based meta-analytic methods, tools, and databases

(2002-2011)

Meta-analysis discoveries

New discoveries made possible by coordinate-based meta-analysis

(2009-2017)

New Neurosynth Developments

ADAM, Neurosynth Connectome, BBA, and NeuroStats LLMs for meta-analysis

(2018-ongoing)

1993 1995 1997 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026

Early efforts to promote data sharing and ensuing discussions

Early data sharing

(1999-2001)

Small sample sizes, cluster failure, voodoo correlations, p-hacking, & that damn salmon

Reproducibility crisis

(2005-2007)

Widespread data sharing made possible by government funding

Human Connectome Projects

(2009-2016)

Large-scale consortium-based studies and widespread data sharing

ABCD, HBCD

(2014-ongoing)



BWAS

(2022)

Concerns about participant privacy and data security

(2026)

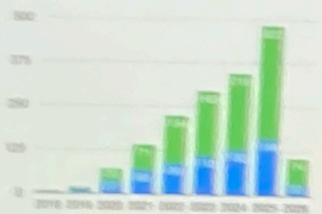
Data Misuse

Large open datasets: Data democratization vs. data protection



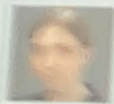
Adolescent Brain Cognitive Development[®]
Your brain. Today's science. Brighter future.

N = 1,682 as of 19 February 2026

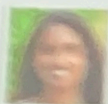


■ No current or former-ABCD members among authors
■ Current or former-ABCD members among authors

62% by non-ABCD scientists

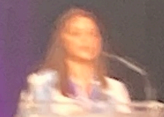
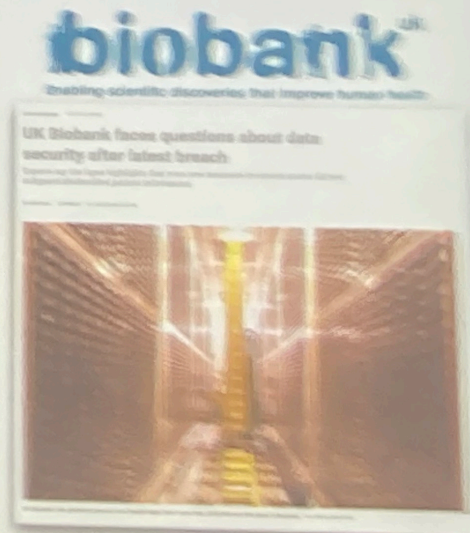
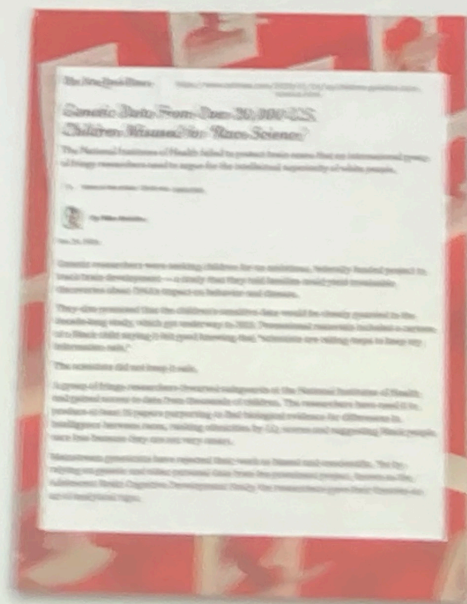


Chana Gilman, PhD



Geyan Dowling, PhD

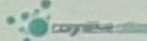
A searchable list of publications is available on the ABCD website:
<https://abcdstudy.org/publications>



The evolution of neuroimaging meta-analysis: NIMARE



Automated annotation

 CogPO, LDA, GCLDA (10x faster)



Database extraction

 NeuroQuery, Neurosynth, NeuroQuery, Neurostore



Coordinate-based meta-analysis (10x+ faster on ALE/MKDA)

peaks2maps, ALI (ale, scale, predictive ALE, ALE subtraction, balanced ALE subtraction),
MKDA (ale, mda, mda2), workflows (general-purpose, contrast workflow, MCMC),
coordinate-based meta-regression, model-based methods



Image-based meta-analysis

Stouffer's, WeightedLeastSquares, DerSimonianLaird,
Hedges, SampleSizeBasedLikelihood,
VarianceBasedLikelihood, Permuted OLS



Functional decoding (also significantly faster)

Future plans: NeuroVLM, NiCLIP



Diagnostic reports

Jackknife, focuscounter, ResampledStability



Html reports

NIMARE: Neuroimaging Meta-Analysis Research Environment

NIMARE is a Python package for neuroimaging meta-analyses.
It makes conducting scary meta-analyses a dream!



Taylor Solo



The New York TimesAccount

Genetic Data From Over 20,000 U.S. Children Misused for ‘Race Science’

The National Institutes of Health failed to protect brain scans that an international group of fringe researchers used to argue for the intellectual superiority of white people.

PostCrémieux @cremieuxre...Subscribe

Brain Sizes by Race and Ethnicity in a Sample of American 10-Year-Olds

Data Collected in 2017 and Adjusted for Age and Sex

Race/Ethnicity	Mean Brain Size (cc)
White	1238.77
Hispanic	1188.29
Black	1126.55

Go to next post directly from here! →

That MRI study got me thinking: How big are the brain size gaps?

I looked and all I found was that there were some pretty large gaps - 0.99, 0.54, 0.36 d - but I want the numbers.

So here: brain size by race in more than 7000 nationally-representative ten-year-olds from 2017.

6:11 AM · Mar 28, 2023 · 118.4K Views

30 120 701 304

Relevant View quotes >

Post your reply Reply

Cré... @cremi... · Mar 28, 2023

Platforms with data more or less processed

- Lifespan Brain Chart
- PNC
- Centile Bioscience

Minimal installation through NiWrap



powered by
 **NiWrap**

Rupprecht F, Kai J, Shrestha B, Glowacki S, Xu T, Glaser T, Milham MP, Kiar G. Styc: A multi-language API Generator for Command-Line Tools. bioRxiv [Preprint]. 2025 Jul 30; 2025.07.24.666435. doi: 10.1101/2025.07.24.666435. PMID: 40766634; PMCID: PMC7324196

visit booth #22 to learn more

```
Terminal
```

```
$ wb_command -metric_resample input_metric.shape.gii current_sphere.gii new_sphere.gii ADAP_BBARY_METHOD output_metric.shape.gii -area_surfs current_area_surf.gii new_area_surf.gii
```

```
from niwrap import workbench
```

```
result = workbench.metric_resample(  
    metric_in=input_file_path,  
    current_sphere=current_sphere,  
    new_sphere=new_sphere,  
    method=method,  
    area_surfs=area_surfs,  
    metric_out=str(output_file_path),  
)
```

1627

Brigham and Women's Hospital
Founding Member, Mass General Brigham

HARVARD MEDICAL SCHOOL
TEACHING HOSPITAL

NiQuery: Stop searching your neuroimaging datasets. Start testing your hypotheses

Jon Hailtz Legarreta^{1,2}, Ross W. Blair³, Christopher J. Markiewicz³, Ariel Rokem⁴, Martin Nørgaard^{5,6} and Oscar Esteban^{7,8}

¹ Department of Radiology, Brigham and Women's Hospital, Mass General Brigham, Boston, MA USA ² Harvard Medical School, Boston MA USA ³ Department of Psychology, Stanford University, Stanford, CA USA ⁴ Krembil Centre for Neuroinformatics, Centre for Addiction and Mental Health, Toronto, ON Canada ⁵ Department of Computer Science, University of Copenhagen, Copenhagen, Denmark ⁶ Molecular Imaging Branch, National Institute of Mental Health (NIMH), Bethesda, MD USA ⁷ School of Engineering, HES-SO University of Applied Sciences and Arts Western Switzerland, Sion, Switzerland ⁸ Department of Radiology, Lausanne University Hospital and University of Lausanne, Lausanne, Switzerland

*Corresponding author [✉] jon.hailtz.legarreta@gmail.com

PURPOSE

Modern, BIDS-based neuroimaging data repositories (e.g. OpenNeuro [1]) allow for standardized sharing and reuse of neuroimaging data.

Efficiently indexing, interrogating and selecting such data is becoming a pressing need.

Selecting data of interest for a study is hindered by:

- the ability to query (text-based) metadata only, or
- the need to download entire datasets.

Existing tools for neuroimaging dataset retrieval [3,4] require fetching complete datasets. A tool for subset selection is missing.

We present *NiQuery*, a principled, open-source library providing a robust framework for

- querying neuroimaging BIDS datasets [2],
- inspecting volumetric metadata,
- performing subset selection, and
- aggregating results.

METHODS

- Engineered for ease-of-use, flexibility and extensibility.
- Design principles
 - **Modularity**: comprises a suite of independent modules for a specific aspect of dataset querying or analysis.
 - **Metadata extraction**: extracts, parses, and selects data based on metadata from imaging file-level sources (e.g. NIFTI files).
 - **Extensibility**: can be adapted to filter data based on custom criteria.
 - **Composability**: provides a way to create new datasets by aggregating multiple datasets leveraging the BIDS standard.

Workflow fundamentals:

- **Index datasets** hosted by a remote server leveraging the GraphQL query language.
- **Perform HTTP requests** to index the datasets and relevant files:
 - Exponential backoff strategy: delay posting new requests in case of server-side errors.
 - Max attempts.
- **Retrieve the NIFTI header** data in the HTTP response stream
 - Avoid fetching entire datasets.

- Implemented in Python
- Parallelization
- Intuitive CLI
 - Overarching **niquery** command
 - Subcommands for operations:
 - **index**: Retrieve available neuroimaging datasets and snapshot information.
 - **collect**: Gather per-dataset file listings.
 - **analyze**: Extract features from collected files.
 - **select**: Choose datasets that satisfy specific constraints.
 - **aggregate**: Create a new DataLad [5] dataset from the selected datasets.
- Reliability: exhaustively tested through continuous integration.
- Documentation
 - Codebase
 - API
 - User guide
 - Subcommand instruction help (**--help**)
- Logging

EXPERIMENTS

- Dataset server: OpenNeuro
- Requirements
 - Modality: fMRI
 - Species: human
 - Selection
 - 4000 BOLD total runs
 - No single dataset contributes with more than 5% of the total number of runs
 - [300–1200] timepoints per BOLD run
 - Exponential backoff parameters:
 - 1.5 s delay
 - 5 attempts max

RESULTS

Using a 6-core, 12-thread CPU processor at 3.30 GHz, with 32 GB RAM, 2.5 Gbps link:

- Indexing all OpenNeuro datasets (1549 datasets) takes ~1 minute.
- Listing all modality-specific NIFTI files takes ~10 hours (550 relevant fMRI BOLD datasets), influenced by the number of
 - files contained by relevant datasets
 - attempts to obtain a successful server response (exponential backoff strategy).
- Metadata extraction from the listed NIFTI files of interest (over 130 000 fMRI BOLD files) takes ~20 minutes.
- Compliant file list: < 1 second.

NiQuery enables automated dataset selection:

- offering gains in automation and reproducibility,
- minimizing manual intervention and potential errors, and
- ensuring comprehensive dataset inclusion.

CONCLUSION

We introduce *NiQuery*, a tool to facilitate reproducible research by enabling transparent access to the content of neuroimaging datasets, including volume-specific metadata.

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- [2] Poliakova RA, et al. *Imag Neuro* Feb 2024; 2:1–15.
- [3] Jalilpour A, et al. *Neurobagel Query Tool*. Version v0.1.0. June 2023.
- [4] Gao R. Cohort creator. Version 0.3.0. April 2024.
- [5] Hachensio YO, et al. *JOS* July 2021; 6(63):3262.

Figure 1. *NiQuery* workflow.

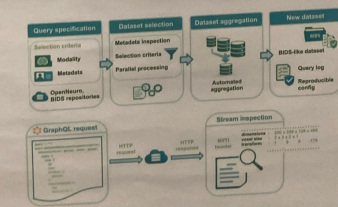
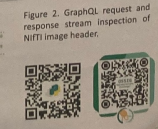


Figure 2. GraphQL request and response stream inspection of NIFTI image header.

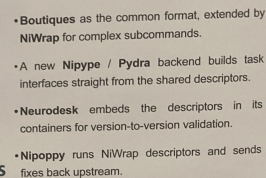


Try it ! `pip install niquery`

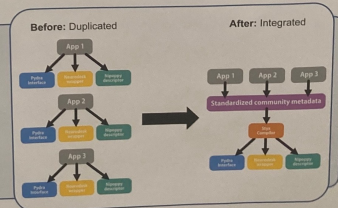
Child Mind
Institute
& Friends



- Imagecimating tools need interfaces for many platforms: workflow engines, dataset managers, container environments.
- BIDS, Pydra, Neurodesk, Nipopy, and NiWrap each solved part of this on their own.
- The same tool gets re-wrapped five times, with duplicated maintenance and inconsistent behavior.
- These platforms now share one set of tool descriptors. Any platform can adopt them, and we welcome new collaborators.



- **Add a tool:** contribute one Boutiques descriptor and it works across every platform.
- **Building a platform?** Write a Styx backend and reuse the whole catalog.
- **Report interface bugs:** a fix to a shared descriptor reaches everyone.
- Find the repos and docs at the QR code, or **come talk to us**.



- One descriptor, many platforms: **less duplicated work, consistent behavior.**
- **Cross-platform testing surfaces** interface bugs, and fixes reach everyone.
- Each platform keeps its own strengths.

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Rantan AJ, Das TC, Johnson JT, et al. NeuroGen: an accessible, flexible and portable data analysis environment for reproducible neuroimaging. *Nat Methods*. 2024;21(3):304–310.

Alyssa De, Sebastian Urita, Brett B. Levenson, Shree Poo, Eric M. de Hempt, Eder Engelmann, Kar A. Lemstra, Thomas Pham, Jacob Brown, Muhammad, Mohammed Mostafiz, Anjan Chakrabarti, Matthew Calkins, Akshat Jain, Austin Macdonald, Ihsa Rabbie, Ashley Steiner, Matthew Juchow, Ian De Castro, Gabriel A. Daverny, Steven S. Caiafa, Benjamin Nee, Johannes Paulus, Michael W. Vassar, M. Stefan Balkrishna, Neel Arachchige, David M Thompson, Richard M. Lister, Chaitanya Vasavada, O. Harishankar, Vishal D. van der Walt, Janneke Boelele-Peters.

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Ecosystem

The diagram illustrates the CLBATOOLKIT ecosystem as a series of concentric layers surrounding a central core. The layers are as follows:

- Foundation:**
 - 1. Foundation
 - 2. Numerical core & data management
 - 3. Neuroimaging
 - 4. CLBATOOLKIT modules
- Core Layer (Python 3.9):**
 - NumPy
 - SciPy
 - Pandas
 - h5py
 - DIPY
- Second Layer:**
 - NiBabel
 - NetworkX
 - scikit-image
 - Pydicom
 - PyVista
- Third Layer (Specialized Tools):**
 - Surfaces & Parcels:** (surfstat, parcellatools, brainstat, Neurostat)
 - Diffusion Weighted Images:** (dwibots, tractools)
 - Connectivity & Networks:** (connectivitytools, networktools)
 - Image & QC:** (SimpleElastic, scikit-image, morphometrics, morphotools, morphotools)
 - Visualization & Plots:** (visualfontools, plottools, colortools)
 - Pipelines & Utilities:** (pipelines, microtools)
- Other Tools:**
 - BIDS & DICOM (bids-validator, dicom-validator)
 - Imageio

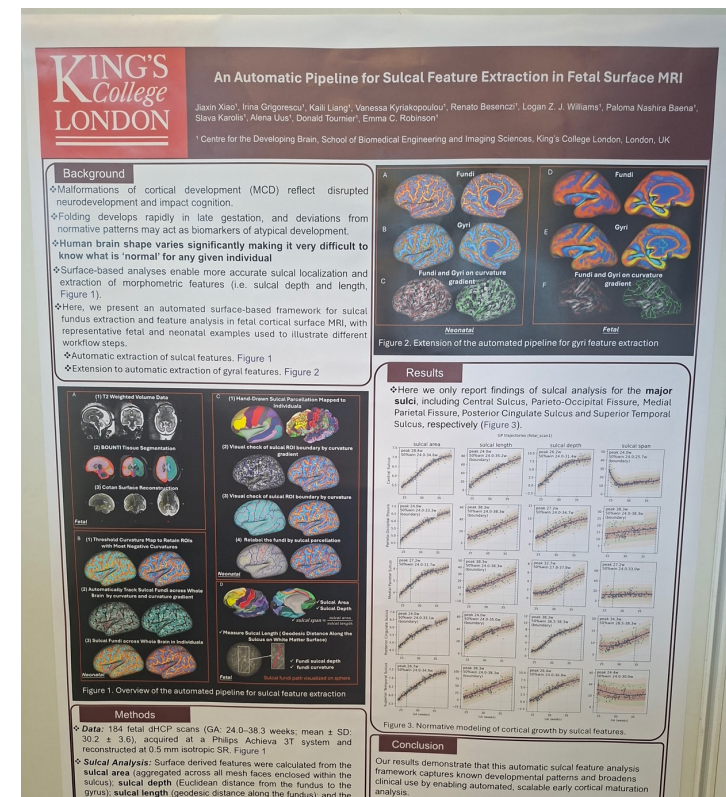
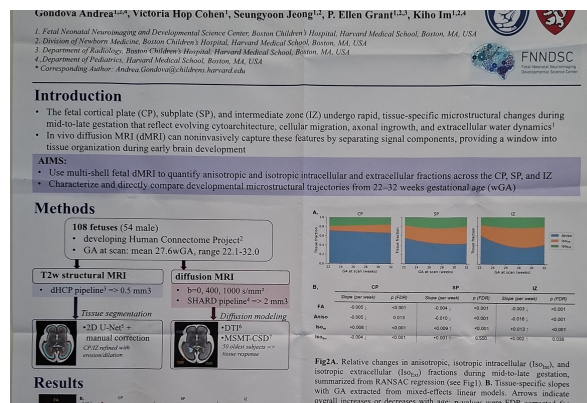
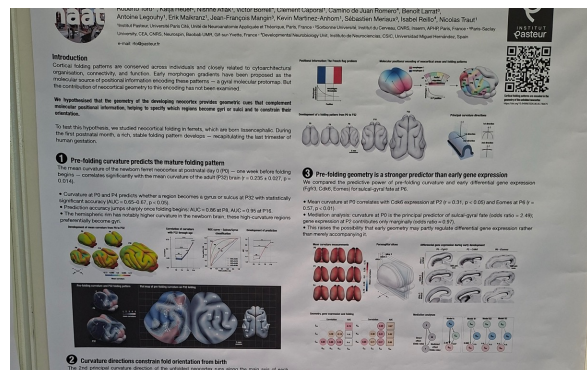
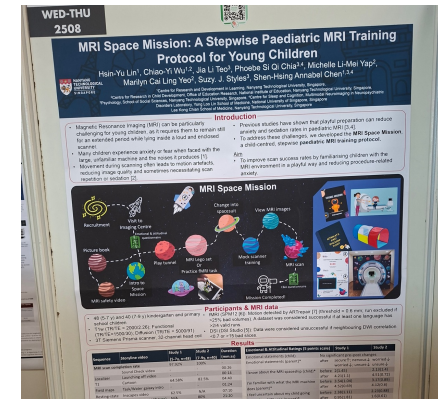
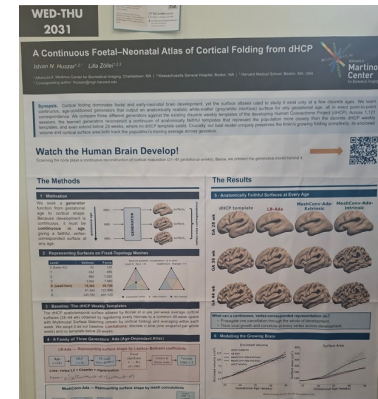
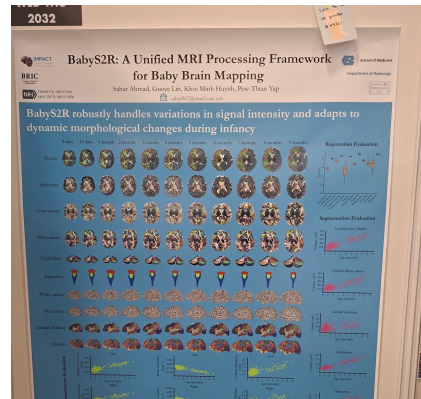
Figure 1: Overview of the ecosystem and its software dependencies.

The modules are organized into six layers covering

Roadmap : highlights from Marseille's delegates

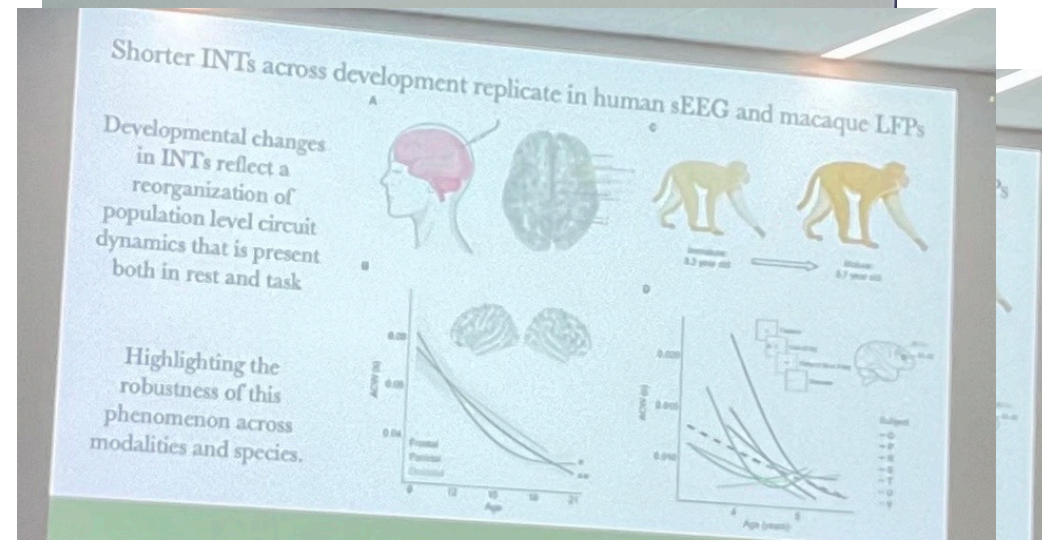
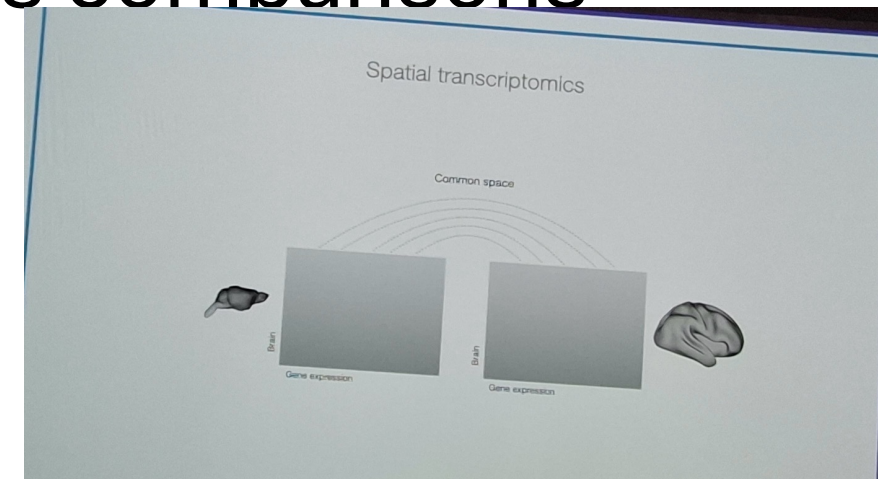
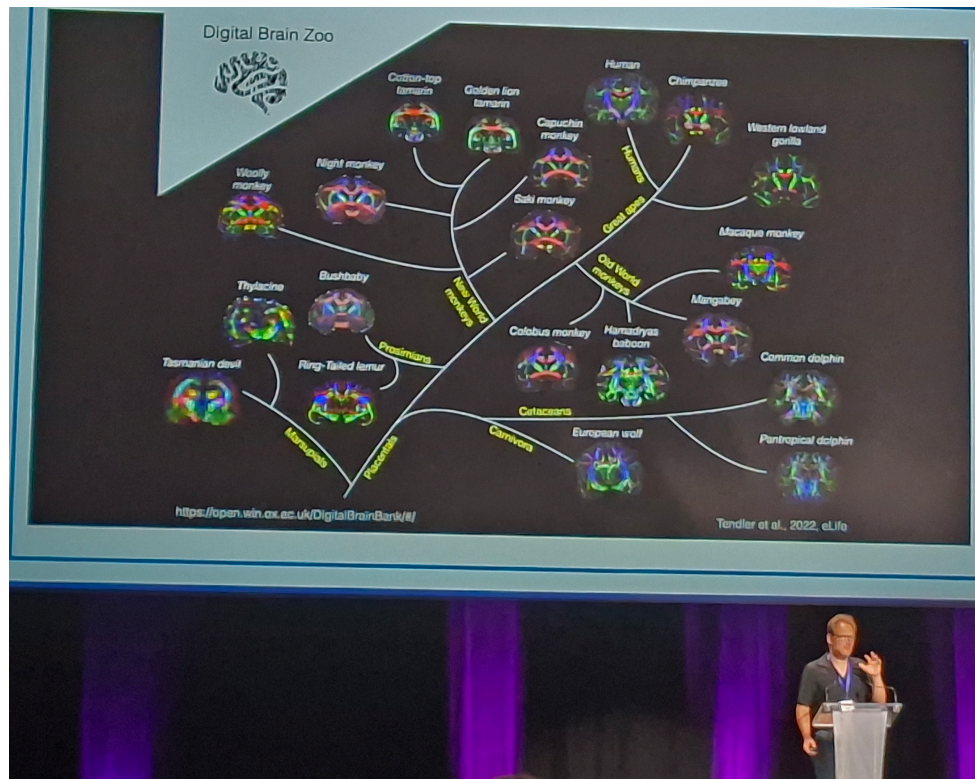
- Insights from abstracts semantic analysis
- Methodological advances – acquisitions
- Large datasets : some example of results and caveats
- Tools and sharing
- **Other trends**

Increased representation of early life brain imaging



Continuity and discontinuity in infant brain development: Dense longitudinal awake fMRI in the first year of life

Advances in multispecies comparisons



White matter BOLD



0421 WhiFuN: A toolbox to map the White Matter Functional Networks of the Human Brain

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¹New Jersey Institute of technology, Newark, New Jersey, United States. ²Rutgers, Newark, New Jersey, United States. ³Duke University, Durham, North Carolina, United States.

Individual-specific modelling of wave propagation along the cortical geometry

Marko A. Ruslim^a, Aurina Arnatkevičiūtė^a, James C. Pang^a



INTRODUCTION

- Neural activity propagates through the cortex as travelling waves.
- Recent neural field theory (NFT) models suggest that cortical geometry strongly shapes large-scale wave dynamics [1].
- However, most studies rely on group-averaged cortical surfaces, which may obscure individual differences in wave propagation.
- Here, we use NFT-based wave models on individual cortical surfaces to determine whether individual geometry influences spontaneous and evoked wave propagation.

METHODS

- Individual cortical surfaces and resting-state fMRI from >1000 HCP participants [2].
- Neural wave propagation simulated on individual cortical surfaces via equation below:

$$\left[\frac{1}{\gamma_s^2} \frac{\partial^2}{\partial t^2} + \frac{2}{\gamma_s} \frac{\partial}{\partial t} + 1 - r_s^2 \nabla^2 \right] \phi(r, t) = Q(r, t)$$

temporal damping rate $\frac{2}{\gamma_s} \frac{\partial}{\partial t}$ characteristic spatial propagation length scale $\frac{1}{\gamma_s^2} \frac{\partial^2}{\partial t^2}$ Laplace-Beltrami operator ∇^2 spatiotemporal input $Q(r, t)$ cortical activity

- Spontaneous dynamics:** subject-specific r_s is estimated from resting-state functional connectivity with Q as white noise following previous work [1].
- Stimulus-evoked dynamics:** modelled using Q as localized impulse injection.

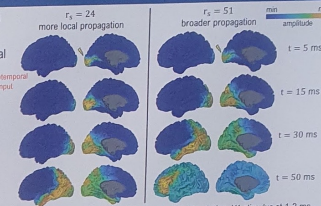


Figure 1: Wave propagation of activity after V1 stimulation. V1 stimulus at 1-2 ms. Two representative subjects highlighting differences in spatial length scale (r_s).

RESULTS

1 Individualized wave models capture resting-state dynamics and hierarchical propagation

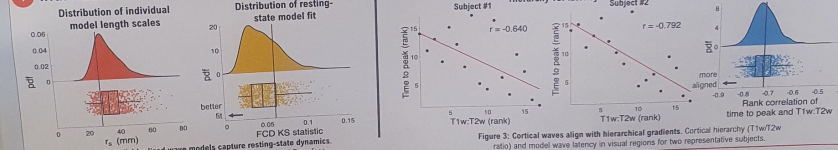


Figure 2: Individualized wave models capture resting-state dynamics. Grey line represents group-averaged simulations using fsfLR surface.

Figure 3: Cortical waves align with hierarchical gradients. Cortical hierarchy (T1w-T2w ratio) and model wave latency in visual regions for two representative subjects.

2 Streamlines reveal large-scale propagation pathways

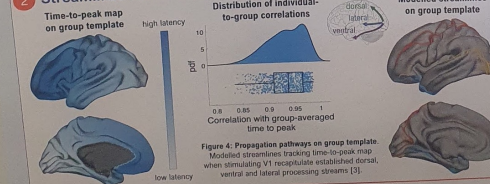


Figure 4: Propagation pathways on group template. Modelled streamlines tracking time-to-peak map when stimulating V1 recapitulate established dorsal, ventral and lateral processing streams [3].

Modelled streamlines on individual cortical surfaces

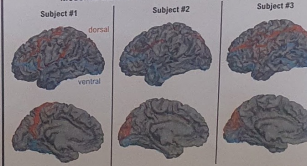
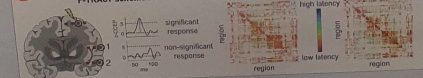


Figure 5: Individual-specific propagation pathways of three representative subjects. Red and blue streamlines represent dorsal and ventral pathways, respectively.

3 Validation using direct brain stimulation data



Model comparison with F-TRACT

Figure 6: Empirical validation using F-TRACT. The F-TRACT dataset is obtained by stimulating distinct cortical regions and recording responses across the brain [4]. Model-predicted latencies compare strongly with F-TRACT data and outperform structural connectivity (SC) and geodesic distance (GD).

AI and LLM in analyses

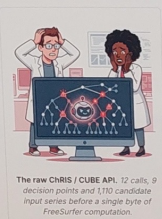
Agents will always lie: agentic AI as a reproducibility threat in neuroimaging

Rudolph Pienaar^{1,2}, Andrea Gondola^{1,2}, Andre van der Kouwe^{3,2}, Patricia E. Grant^{1,2}

¹Boston Children's Hospital · ²Harvard Medical School · ³Massachusetts General Brigham

THE PROBLEM

Modern AI is not magic — it is mathematics. A network's forward pass is deterministic, but **generation runs that map in reverse**, and a compressive map has no unique inverse. The only way back is to **sample from a probability distribution**, so probability is intrinsic to every token an LLM emits.



The raw CHRIS / CUBE API: 12 calls, 9 decision points and 1110 candidate input series before a single byte of FreeSurfer computation.

- Neuroimaging is pivoting to **agentic AI** — LLMs that autonomously chain tools, pick parameters, and report results.^{1,4}
- Orchestration is a problem of **depth**: each step is a probabilistic branch, and errors compound along the workflow graph.
- The danger isn't crashes — it's **silent failure**: wrong output reported as success, entering downstream analyses undetected.²

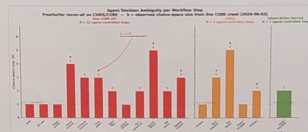
SEARLE'S CHINESE ROOM!

The agent emits valid API calls with no semantic grounding — like Searle's room shuffling symbols without understanding. **Confidence is not correctness.**

THE EXPERIMENT

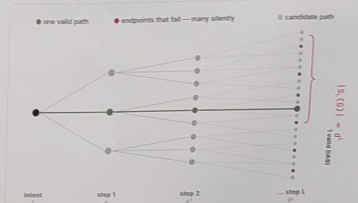
We grounded the argument on a **live CHRIS / CUBE** instance, tasking an LLM agent to run FreeSurfer recon - all (via pl-fshack) on subject FEY_LUKE — **twelve agent-controlled API calls and nine decision points** before any computation — then mapping the per-step choice space from a live crawl.

- 1,110 MPRAGE candidates** at scan-selection — with no AccessionNumber, the agent guesses.
- no_fail=true** masks a non-zero FreeSurfer exit code → **silent success**.
- pl-fshack had **zero prior runs** here — no successful history to imitate.



The choice space drives the risk. Bar height is the number of options b at each step; red triangles flag steps where a wrong choice is silently misreported as success. Scan-selection alone offers 1110 candidates — collapsing to ~ 3 only when intent is specified.

THE EXPLOSION



Why depth is the enemy. Each decision point multiplies the reachable workflows: $1 \rightarrow d \rightarrow d^2 \rightarrow \dots \rightarrow d^n$. Of the exponentially many endpoints, **one** is the intended result; most are wrong, and many fail silently. IAS collapses the tree to the single green path.

THE MIDDLE GROUND — ChELL

The ChELL shell collapses API mechanics from 12 steps to 5 and auto-handles feed creation & previous_id plumbing. But the dangerous decisions — which scan, which arguments — **survive intact**. Reducing syntax is not reducing reproducibility risk.

THE FINDING

AI WILL ALWAYS LIE

IF PUT IN CHARGE OF NEUROIMAGING PIPELINES

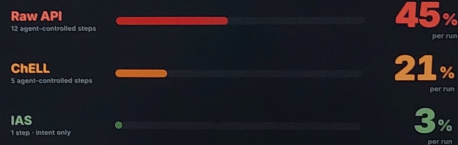
Clinical truth and reproducibility must live in a **deterministic execution runtime** that is external to the generative model.



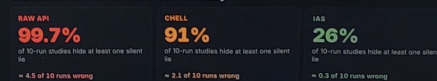
Scan for data, code & figures
github.com/rudolphpienaar/08092024

How often does it lie?

Chance a single agent run silently reports a wrong result as success: $\epsilon = 5\%$ error per step

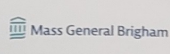


What those rates mean across a real 10-run study



na_fail=true masks the exit code, so the failing run still reports success — the lie is **silent**. A 45% per-run rate becomes near-certainty across a study; only IAS stays near the floor.

OHBM 2026
Submission #3780



THE EVIDENCE

THE SOLUTION

THE PAYOFF

Going 3D with AI: Full 3D Reconstructions of Cytoarchitectonic Maps in BigBrain

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²Helmholtz AI, Research Centre Jülich, Jülich, Germany

³Cécile and Oskar Vogt Institute for Brain Research, University Hospital Düsseldorf, Düsseldorf, Germany

INTRODUCTION.

- As part of the Jülich Brain Atlas¹, the BigBrain dataset² provides an ultra-high-resolution 3D model of the human brain at the cytoarchitectonic level
- To make detailed cortical and subcortical area maps available for interactive exploration in **silbra-explorer**, these areas must first be reconstructed in 3D
- Combining manual expert delineation with AI-based inference enables consistent, high-fidelity 3D cytoarchitectonic mapping across the whole brain

METHODS & RESULTS.

Identification of Areas

Cytoarchitectonic areas annotated on every 10th ~ 15th histological section using ATLASU³

AI Reconstruction

The **CytoNet** deep learning model infers areal continuity and laminar transitions between sections — avoiding geometric interpolation

Computation

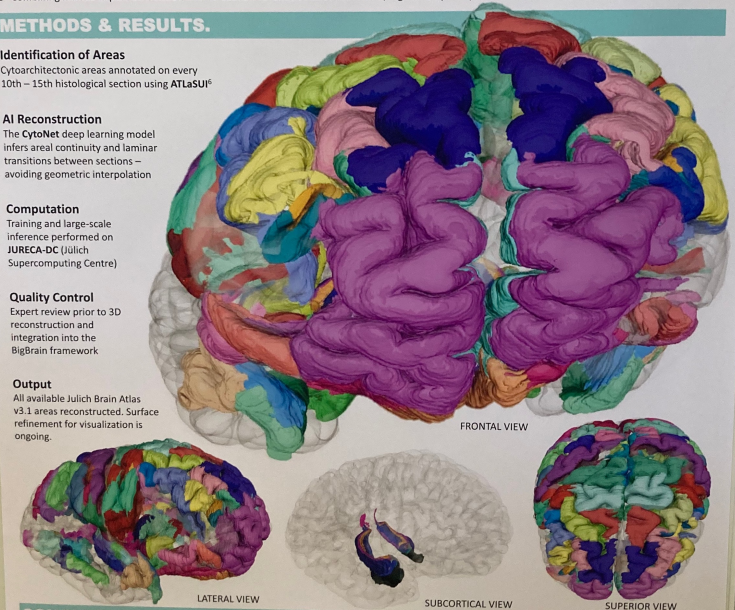
Training and large-scale inference performed on JURECA-DC (Jülich Supercomputing Centre)

Quality Control

Expert review prior to 3D reconstruction and integration into the BigBrain framework

Output

All available Jülich Brain Atlas v3.1 areas reconstructed. Surface refinement for visualization is ongoing.



CONCLUSION.

- We reconstructed 167 cortical areas in BigBrain space at cellular resolution, completing the currently available cortical coverage of the Jülich Brain Atlas.
- The resulting maps provide a coherent microscopic 3D reference framework that preserves cytoarchitectonic boundaries and laminar organization.
- OPENLY ACCESSIBLE:** 3D and 2D mappings will be available via **EBRAINS Knowledge Graph** on **silbra toolsuite**
- MORE COMING SOON.** We are currently mapping more BigBrain areas that will be available next year!

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