DataBases

*The following are databases of available, open-access data for **human** neural data, with a spatial dimension.*

OMEGA - MEG Data: https://omega.bic.mni.mcgill.ca/

Niso, G., Rogers, C., Moreau, J. T., Chen, L. Y., Madjar, C., Das, S., ... & Baillet, S. (2016). OMEGA: the open MEG archive. *NeuroImage*, *124*, 1182-1187.

Reference article for the OMEGA database. Did some source maps of frequency bands.

HCP - sMRI & MEG Data: http://www.humanconnectome.org

Van Essen, D. C., Smith, S. M., Barch, D. M., Behrens, T. E., Yacoub, E., Ugurbil, K., & WU-Minn HCP Consortium. (2013). The WU-Minn human connectome project: an overview. *Neuroimage*, *80*, 62-79.

Overview of the Human Connectome Project.

Van Essen, D. C., Ugurbil, K., Auerbach, E., Barch, D., Behrens, T. E. J., Bucholz, R., ... & Della Penna, S. (2012). The Human Connectome Project: a data acquisition perspective. *Neuroimage*, *62*(4), 2222-2231.

Overview of data collection for the Human Connectome Project.

ABHA Gene Atlas - Gene Expression Data:

Hawrylycz, M., Miller, J. A., Menon, V., Feng, D., Dolbeare, T., Guillozet-Bongaarts, A. L., ... & Glasser, M. F. (2015). Canonical genetic signatures of the adult human brain. *Nature neuroscience*, *18*(12) 1832-1844.

Reference article for the Allen Human Brain Atlas (AHBA), 6 brain dataset.

Hawrylycz, M. J., Lein, E. S., Guillozet-Bongaarts, A. L., Shen, E. H., Ng, L., Miller, J. A., ... & Abajian, C. (2012). An anatomically comprehensive atlas of the adult human brain transcriptome. *Nature*, *489*(7416), 391-399.

Initial AHBA analysis, for 2 subjects.

NeuroSynth - fMRI Meta-Analysis Data: http://neurosynth.org

Yarkoni, T., Poldrack, R. A., Nichols, T. E., Van Essen, D. C., & Wager, T. D. (2011). Large- scale automated synthesis of human functional neuroimaging data. *Nature methods*, *8*(8), 665-670.

Reference article for NeuroSynth.

Kang Dataset - Gene Expression Data:

Kang, H. J., Kawasawa, Y. I., Cheng, F., Zhu, Y., Xu, X., Li, M., ... & Guennel, T. (2011). Spatio-temporal transcriptome of the human brain. *Nature*, *478*(7370), 483-489.

Looking at the exon-level transcriptome across space and time - a group of locations across different developmental stages, in a group of 57 donor brains. Explore differential expression and network analysis of genes. Data is available.

NeuroVault - Statistical maps, parcellations and atlases: http://neurovault.org

Gorgolewski, K. J., Varoquaux, G., Rivera, G., Schwarz, Y., Ghosh, S. S., Maumet, C., ... & Yarkoni, T. (2015). NeuroVault. org: A web-based repository for collecting and sharing unthresholded statistical maps of the human brain. *Frontiers in neuroinformatics*, *9*, 8.

NeuroVault is a web based repository to store statistical maps of the human brain. Plugs in directly with NeuroSynth.

IMAGEN - s&fMRI, genotype, behaviour & neuropsychological battery: https://imagen-europe.com

Schumann, G., Loth, E., Banaschewski, T., Barbot, A., Barker, G., Büchel, C., ... & Garavan, H. (2010). The IMAGEN study: reinforcement-related behaviour in normal brain function and psychopathology. *Molecular psychiatry*, *15*(12), 1128-1139.

IMAGEN is a study of 2000 14 year old, followed longitudinally, who have behavioural, neuropsychological, functional and structural neuroimaging, and genotyping done. It's aim is to look for individual variability in emotion and motivation, and their relations to neuropsychiatric disease.

Cam-CAN - s&fMRI, MEG, behavioural: https://camcan-archive.mrc-cbu.cam.ac.uk/dataaccess/

Shafto, M. A., Tyler, L. K., Dixon, M., Taylor, J. R., Rowe, J. B., Cusack, R., ... & Henson, R. N. (2014). The Cambridge Centre for Ageing and Neuroscience (Cam-CAN) study protocol: a cross-sectional, lifespan, multidisciplinary examination of healthy cognitive ageing. *BMC neurology*, *14*(1), 1.

Cam-CAN study overview. The aim is to investigate how age-related changes to neural structure and function relate to cognitive abilities across the lifespan. 700 participants will be included in the stage of the study in which structural and functional imaging will be recorded (sMRI, fMRI & MEG).

Taylor, J. R., Williams, N., Cusack, R., Auer, T., Shafto, M. A., Dixon, M., ... & Henson, R. N. (2015). The Cambridge Centre for Ageing and Neuroscience (Cam-CAN) data repository: structural and functional MRI, MEG, and cognitive data from a cross-sectional adult lifespan sample. *Neuroimage*.

Overview of the data repository. Database has raw and processed data for structural and functional MRI, MEG from tasks and resting state, a battery of cognitive tests, and demographic and neuropsychological data from about 700 subjects, evenly spread across an age range of 18-87 years old.

BrainMap - MRI: http://www.brainmap.org

Fox, P. T., & Lancaster, J. L. (2002). Mapping context and content: the BrainMap model. *Nature Reviews Neuroscience*, *3*(4), 319-321.

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Laird, A. R., Lancaster, J. J., & Fox, P. T. (2005). Brainmap. *Neuroinformatics*, *3*(1), 65-77.

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Cross-Modality Database Integration

*The following papers are data integration papers in which data from different modalities, collected from **existing databases** reflecting **different participants** is connected and analyzed together.*

Cioli, C., Abdi, H., Beaton, D., Burnod, Y., & Mesmoudi, S. (2014). Differences in human cortical gene expression match the temporal properties of large-scale functional networks. *PloS one*, *9*(12), e115913.

Compare functional organization of the cortex to gene expression, from the ABA. Look at two large functional network, Visuo-Sensorimotor-Auditory and Parieto-Temporo-Frontal. Show patterns of gene expression of the genes that vary the most across the cortex match these two large networks. Specific gene groups were associated with each network.

Crossley, N. A., Fox, P. T., & Bullmore, E. T. (2016). Meta-connectomics: human brain network and connectivity meta-analyses. *Psychological medicine*, *46*(05), 897-907.

A review of what they call 'meta-connectomics' - combining connectivity with other brain characteristics. Consider network analysis of task based neuroimaging, and linking MRI abnormalities to the normative connectome, and also incorporating cellular and transcriptional data.

Krienen, F. M., Yeo, B. T., Ge, T., Buckner, R. L., & Sherwood, C. C. (2016). Transcriptional profiles of supragranular-enriched genes associate with corticocortical network architecture in the human brain. *Proceedings of the National Academy of Sciences*, *113*(4), E469-E478.

Want to test if changes in molecular architecture can explain larger, interconnected brain regions in humans. Use genetic data from the ABA, compare expression values to mouse expression datasets, and compare regional gene expression to structural tracing from primates and functional connectivity in fMRI. Report that the topography of gene expression relates to these functional and structural networks.

Richiardi, J., Altmann, A., Milazzo, A. C., Chang, C., Chakravarty, M. M., Banaschewski, T., ... & Conrod, P. (2015). Correlated gene expression supports synchronous activity in brain networks. *Science*, *348*(6240), 1241-1244.

Compare resting-state activity from fMRI, to gene expression from the ABA, using a network modelling approach, asking whether gene expression networks are grouped into functional networks from fMRI. Find a set of genes that relate, that are enriched for channel genes. Do follow up work, showing polymorphisms in these genes affect functional connectivity in an adolescent sample, and show that expression levels of these genes are related to axonal connections in the mouse.

Vértes, P. E., Rittman, T., Whitaker, K. J., Romero-Garcia, R., Váša, F., Kitzbichler, M. G., ... & Goodyer, I. M. (2016). Gene transcription profiles associated with inter-modular hubs and connection distance in human functional magnetic resonance imaging networks. *Phil. Trans. R. Soc. B*, *371*(1705), 20150362.

Estimate functional connectivity from fMRI data. Look for relationships between this data, and ABA gene data. Find components linking gene clusters to functional networks.

Wang, G. Z., Belgard, T. G., Mao, D., Chen, L., Berto, S., Preuss, T. M., ... & Konopka, G. (2015). Correspondence between resting-state activity and brain gene expression. *Neuron*, *88*(4), 659-666.

Investigating whether gene expression in the cortex is correlated to functional connectivity in fMRI data, focusing on the DMN in particular. Report on a group of 38 genes that have significant correlations, and explore these genes a bit, for example finding some of them are also implicated in autism.

Whitaker, K. J., Vértes, P. E., Romero-Garcia, R., Váša, F., Moutoussis, M., Prabhu, G., ... & Tait, R. (2016). Adolescence is associated with genomically patterned consolidation of the hubs of the human brain connectome. *Proceedings of the National Academy of Sciences*, *113*(32), 9105-9110.

Compare structural MRI, in particular cortical thickness and myelination, from a group aged 14-24, to gene expression from the ABA. Find that adolescent cortical myelination and shrinkage were associated with a spatially patterned group of genes, enriched for genes related to the synapse, oligodendricites and schizophrenia.

Cross-Modality Imaging Papers

*The following papers are cross-modal, data integration papers, but done by collecting data (or using existing data) in which multiple modalities of data are collected within the **same participants**.*

Chu, C. J., Tanaka, N., Diaz, J., Edlow, B. L., Wu, O., Hämäläinen, M., ... & Kramer, M. A. (2015). EEG functional connectivity is partially predicted by underlying white matter connectivity. *NeuroImage*, *108*, 23-33.

Looking at how functional networks and oscillations, all from EEG, relate to structural connections from DTI, all recorded in the same subjects. Find that cortical networks derived from EEG seem to reflect underlying white matter connectivity, across all frequency bands. Note: subjects are all young with epilepsy.

Hunt, B. A., Tewarie, P. K., Mougin, O. E., Geades, N., Jones, D. K., Singh, K. D., ... & Brookes, M. J. (2016). Relationships between cortical myeloarchitecture and electrophysiological networks. *Proceedings of the National Academy of Sciences*, *113*(47), 13510-13515.

Test the hypothesis that gray-matter myelin is related to electrophysiological connectivity. Use high-field MRI for structural analysis, and MEG to record functional networks. Show a significant relationship exists between functional and structural networks.

Mišić, B., Betzel, R. F., de Reus, M. A., van den Heuvel, M. P., Berman, M. G., McIntosh, A. R., & Sporns, O. (2016). Network-level structure-function relationships in human neocortex. *Cerebral Cortex*, bhw089.

Use HCP data, comparing functional networks (from resting fMRI) to structural networks from DTI data. Find relations between them, supporting that the structural organization of the cerebral cortex supports functional network architecture.

Yang, Z., Qiu, J., Wang, P., Liu, R., & Zuo, X. N. (2016). Brain structure–function associations identified in large-scale neuroimaging data. *Brain Structure and Function*, 1-16.

Looking at cross-individual covariance among structural and functional neuroimaging data, all from MRI. Build a database how each of 12 metrics they examine co-vary.

Source of the MEG Signal

Okada, Y. C., Wu, J., & Kyuhou, S. (1997). Genesis of MEG signals in a mammalian CNS structure. *Electroencephalography and clinical neurophysiology*, *103*(4), 474-485.

Recording magnetic fields of cell slices. Report that MEFs were produced by currents along the longitudinal axis of the pyramidal cells. Pharmacological investigation suggested a predominance of excitatory connections in generating the MEF. Variation of the waveform with stimulation site suggested the contribution of many factors, both synaptic and voltage-sensitive conductances, to the overall waveform.

Zhu, Z., Zumer, J. M., Lowenthal, M. E., Padberg, J., Recanzone, G. H., Krubitzer, L. A., ... & Disbrow, E. A. (2009). The relationship between magnetic and electrophysiological responses to complex tactile stimuli. *BMC neuroscience*, *10*(1), 4.

Comparing magnetic and electrophysiological (LFP & MUA) responses to complex tactile stimuli. Signal intensity inversely related to rate of stimulation, to different degrees for each method. Intensity and latency of the MEG signal were better correlated with the LFP than the MUA, so they suggest that the MEG signal reflects primarily synaptic currents rather than spiking activity.

Reliability & Consistency of the EEG/MEG Signal

Fingelkurts, A. A., Fingelkurts, A. A., Ermolaev, V. A., & Kaplan, A. Y. (2006). Stability, reliability and consistency of the compositions of brain oscillations. *International Journal of Psychophysiology*, *59*(2), 116-126.

Looking at EEG oscillations in rest and memory task. Within sessions, oscillations are found to be fairly stable, and reproducible between sessions. Test-retest reliability of oscillations depends on task.

Fingelkurts, A. A., & Fingelkurts, A. A. (2014). EEG oscillatory states: universality, uniqueness and specificity across healthy-normal, altered and pathological brain conditions. *PloS one*, *9*(2), e87507.

Looking at EEG across 13 different conditions, covering healthy, altered and pathological brain states. Looking at 'spectral patterns'. Suggest that there is a limited repertoire of spectral activity within any given state, with some differences across the different conditions.

Martín‐Buro, M. C., Garcés, P., & Maestú, F. (2016). Test‐retest reliability of resting‐state magnetoencephalography power in sensor and source space. *Human brain mapping*, *37*(1), 179-190.

Do test-retest reliability of MEG power in resting-state at sensor and source level. Three resting state scans, divided into frequency bands and compared with intraclass correlation coefficient (ICC). Overall, theta, alpha and low beta was fairly high (ICC > 0.6) while delta and gamma power was lower.

McEvoy, L. K., Smith, M. E., & Gevins, A. (2000). Test–retest reliability of cognitive EEG. *Clinical Neurophysiology*, *111*(3), 457-463.

Investigating the reliability of task related EEG activity (WM & psychomotor task). Found that task-related EEG was highly reliable within and between sessions.

Näpflin, M., Wildi, M., & Sarnthein, J. (2007). Test–retest reliability of resting EEG spectra validates a statistical signature of persons. *Clinical Neurophysiology*, *118*(11), 2519-2524.

Looking at reliability of resting state EEG recordings. Able to identify spectral EEG parameters as a signature of particular subjects over multiple recordings.

Tan, H. R., Gross, J., & Uhlhaas, P. J. (2015). MEG—measured auditory steady-state oscillations show high test–retest reliability: A sensor and source-space analysis. *NeuroImage*, *122*, 417-426.

Investigating the stability of task-related oscillatory activity in MEG, at both sensor and source level, using test-retest within a group of subject on the same auditory task. Spectral power and phase consistency of auditory steady state evoked potentials are highly reproducible.

Gene Analysis

The following papers relate to gene expression data, either analysis of them, relevant (non-human) databases and/or neuroinformatics tools, all of which could be useful for understanding gene results.

Cahoy, J. D., Emery, B., Kaushal, A., Foo, L. C., Zamanian, J. L., Christopherson, K. S., ... & Thompson, W. J. (2008). A transcriptome database for astrocytes, neurons, and oligodendrocytes: a new resource for understanding brain development and function. *The Journal of Neuroscience*, *28*(1), 264-278.

Do gene expression analysis of cell-type isolated samples of neurons, astrocytees and oligodendrocytes. Characterize cell type specific gene expression patterns. Done in mouse. Data is available.

Huang, D. W., Sherman, B. T., & Lempicki, R. A. (2009). Bioinformatics enrichment tools: paths toward the comprehensive functional analysis of large gene lists. *Nucleic acids research*, *37*(1), 1-13.

Survery of ~70 bioinformatics tools for understanding the function of large gene lists.

Huang, D. W., Sherman, B. T., & Lempicki, R. A. (2009). Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. *Nature protocols*, *4*(1), 44-57.

DAVID is a tool that integrates biological data and allows for analysis aimed at extracted biological meaning from large gene/protein lists.

Kuncheva, Z., Krishnan, M. L., & Montana, G. (2016). Exploring brain transcriptomic patterns: a topological analysis using spatial expression networks. *arXiv preprint arXiv:1610.02548*.

Looking to cluster gene expression activity, proposing a new representation of gene clusters. Find three large clusters of genes.

Mahfouz, A., Huisman, S. M., Lelieveldt, B. P., & Reinders, M. J. (2016). Brain transcriptome atlases: a computational perspective. *Brain Structure and Function*, 1-24.

A review of computational methods used to analyze brain transcriptome atlases.

Mancarci, B. O., Toker, L., Tripathy, S., Li, B., Rocco, B., Sibille, E., & Pavlidis, P. (2016). NeuroExpresso: A cross-laboratory database of brain cell-type expression profiles with applications to marker gene identification and bulk brain tissue transcriptome interpretation. *bioRxiv*, 089219.

Assembled a database of mouse brain cell-type specific gene expression datasets. Look for marker genes highly expressed in individual cell types, find some new ones not previously reported in the literature.

Zhang, Y., Chen, K., Sloan, S. A., Bennett, M. L., Scholze, A. R., O'Keeffe, S., ... & Deng, S. (2014). An RNA-sequencing transcriptome and splicing database of glia, neurons, and vascular cells of the cerebral cortex. *The Journal of Neuroscience*, *34*(36), 11929-11947.

Gene expression analysis of cell type specific samples, including eight different neural cell types. Identify thousands of cell type enriched genes. Done in mouse. Data is available.

Other

Darvas, F., Pantazis, D., Kucukaltun-Yildirim, E., & Leahy, R. M. (2004). Mapping human brain function with MEG and EEG: methods and validation. *NeuroImage, 23*, S289-S299.

Survey/overview of source projection for MEG & EEG.