

BRIAN M. SCHILDER


Passionately pursuing multi-disciplinary research to improve human lives.

PhD Candidate
ScB, MPhil

EDUCATION

2024


Imperial College London

PhD: Clinical Medical Research; Computational Neurogenomics  London, UK

Thesis: Multi-omic medicine: dissecting the cell-type-specific molecular mechanisms underlying neurodegenerative disease genomics

2017


The George Washington University

MPhil: Human Paleobiology; Evolutionary Neuroscience & Genomics  Washington, DC, USA

Thesis: The evolution of the hippocampus and adult neurogenesis: Novel insights into the origins of human memory

2011

Brown University

ScB: Cognitive Neuroscience; Neurological Diseases & Disorders  Providence, RI, USA

CORE SKILLS

Research

14+ years of highly multidisciplinary research experience. Creative and rapid hypothesis generation, project design, and problem solving.

- **Fields:** Including but not limited to: Neuroscience, systems biology, bioinformatics, machine learning, multi-omics, biomedicine, cognition, statistics, computer science, phylogenetics, paleoanthropology biomechanics, primatology, histology/microscopy.
- **Publications:** Strong writing skills as evidenced by **18** peer-reviewed scientific publications, 17 international conference posters and **10** successful grant applications.

Programming

Extensive experience in developing highly reproducible scripts and software packages to interrogate large and diverse data.

- **Bioinformatics:** Including but not limited to: GWAS, QTL, bulk/scRNA-seq & epigenomics, machine learning, high-performance computing, GitHub, GitHub Actions, Docker/Singularity containers, DockerHub, conda, Nextflow, reproducibility.
- **Python:** Regularly uses ML packages (e.g. sklearn, tensorflow, Keras). Developed and own IP for PubReporter, a software for extracting and conducting topic modelling/NLP on relevant scientific literature at scale.
- **JavaScript/HTML/CSS:** Created **10+** websites, web apps, and interactive reports. Developed templates to automatically render websites on-the-fly from CSVs using Javascript.
- **R:** Created **26** R packages to date, including on Bioconductor and CRAN. Experienced in created Shiny Apps and Rmarkdown reports.

CONTACT



brian_schilder@alumni.brown.edu

 [LinkedIn](#)


 [GitHub](#)

 [Twitter](#)


 [Personal Website](#)

 [Lab Website](#)

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 **UK: +44 073-0653-7736**

SUMMARY

 **14+ years of research experience.**

 **18 peer-reviewed publications to date.**

 **35 bioinformatics tools**

Communication

Effective and engaging scientific presentations to a variety of audiences.

- **Peers:** Extensive experience presenting research proposals/findings to both internal and external labs/conferences. Invited speaker at leading research institutions. Diverse, multi-disciplinary and global collaborative network.
- **Students:** Teaching assistant and/or guest lecturer for courses in diverse fields (biological anthropology, neuroscience, computational biology).
- **Public:** Developed and delivered numerous community engagement programs for a wide variety of stakeholders, including students (preschool through postgraduate), community members, and patients (e.g. Children's National Hospital, Parkinson's UK).

Project Management

Coordinates multiple independent projects at once with researchers of varying degrees of education and research experience. Effective handling of many projects at once.

- **Documentation:** Detailed and understandable in-code documentation is second-nature.
- **Supervision:** Supervises numerous student research projects.
- **Version control:** Extensive and daily use of git, GitHub Issues, GitHub Projects.



PUBLICATIONS

- 2022 • **Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors**
Biological Psychiatry (2022) 91(3):313-327; <https://doi.org/10.1016/j.biopsych.2021.05.029>
N Mullins, J Kang, AI Campos,...**BM Schilder**, et al.
- 2022 • **Genetic analysis of the human microglial transcriptome across brain regions, aging and disease pathologies**
Nature Genetics (2022) <https://doi.org/10.1038/s41588-021-00976-y>
K de Paiva Lopes, G JL Snijders, J Humphrey, A Allan, M Sneebor, E Navarro, **BM Schilder**...T Raj
- 2021 • **Multi-omic insights into Parkinson's Disease: From genetic associations to functional mechanisms**
Neurobiology of Disease (2021) 105580; <https://doi.org/10.1016/j.nbd.2021.105580>
BM Schilder, E Navarro, T Raj
- 2021 • **Fine-Mapping of Parkinson's Disease Susceptibility Loci Identifies Putative Causal Variants**
Human Molecular Genetics (2021) ddab294; <https://doi.org/10.1093/hmg/ddab294>
BM Schilder, T Raj
- 2021 • **echolocatoR: An Automated End-to-End Statistical and Functional Genomic Fine-Mapping Pipeline**
Bioinformatics (2021) btab658; <https://doi.org/10.1093/bioinformatics/btab658>
BM Schilder, J Humphrey, T Raj
- 2021 • **MungeSumstats: A Bioconductor Package for the Standardisation and Quality Control of Many GWAS Summary Statistics**
Bioinformatics (2021) 37(23):4593-4596; <https://doi.org/10.1093/bioinformatics/btab665>
A Murphy, **BM Schilder**, NG Skene
- 2021 • **Dysregulation of mitochondrial and proteo-lysosomal genes in Parkinson's disease myeloid cells**
Nature Genetics (2021) <https://doi.org/10.1101/2020.07.20.212407>
E Navarro, E Udine, K de Paiva Lopes, M Parks, G Riboldi, **BM Schilder**...T Raj
- 2021 • **Phenome-wide and eQTL Associations of COVID-19 Genetic Risk Loci**
iScience (2021) <https://doi.org/10.1016/j.isci.2021.102550>
C Moon, **BM Schilder**, T Raj, K-I Huang

- 2020 • **Genome-Wide Association Study of over 40,000 Bipolar Disorder Cases Provides Novel Biological Insights**
Nature Genetics (2020) 53:817-829; <https://doi.org/10.1038/s41588-021-00857-4>
 N Mullins, AJ Forstner, KS O'Connell, B Coombes, JRI Coleman...**BM Schilder**... et al.
- 2020 • **Tensor decomposition of stimulated monocyte and macrophage gene expression profiles identifies neurodegenerative disease-specific trans-eQTLs**
PLOS Genetics (2020) 16(9):e1008549; <https://doi.org/10.1101/499509>
 S Ramdhani, E Navarro, E Udine, AG Efthymiou, **BM Schilder**, M Parks, A Goate, T Raj
- 2019 • **Evolutionary shifts dramatically reorganized the human hippocampal complex**
Journal of Comparative Neurology (2019) 528(17):3143-3170; <https://doi.org/10.1002/cne.24822>
BM Schilder, HM Petry, PR Hof
- 2019 • **FAIRshake: Toolkit to Evaluate the Findability, Accessibility, Interoperability, and Reusability of Research Digital Resources.**
Cell Systems (2019) 9; <https://doi.org/10.1016/j.cels.2019.09.011>
 D Clarke, L Wang, A Jones, M Wojciechowicz, D Torre, K Jagodnik, S Jenkins, P McQuilton, Z Flamholz, M Silverstein, **BM Schilder**...A Ma'ayan
- 2019 • **Geneshot: search engine for ranking genes from arbitrary text queries**
Nucleic Acids Research (2019) 47(W1):W571-W577; <https://doi.org/10.1093/nar/gkz393>
 A Lachmann, **BM Schilder**, ML Wojciechowicz, D Torre, MV Kuleshov, AB Keenan, A Ma'ayan
- 2018 • **eXpression2Kinases (X2K) Web: linking expression signatures to upstream cell signaling networks**
Nucleic Acids Research (2018) 46(W1):W171-W179; <https://doi.org/10.1093/nar/gky458>
 DJB Clarke, MV Kuleshov, **BM Schilder**, D Torre, ME Duffy, AB Keenan, A Lachmann, AS Feldmann, GW Gundersen, MC Silverstein, Z Wang
- 2015 • **Defining elemental imitation mechanisms: A comparison of cognitive and motor-spatial imitation learning across object- and computer-based tasks**
Journal of Cognition and Development (2015) 17(2):221-243; <https://doi.org/10.1080/15248372.2015.1053483>
 F Subiaul, L Zimmerman, E Renner, **BM Schilder**, R Barr
- 2015 • **Take the monkey and run**
Journal of Neuroscience Methods (2015) 248:28-31; <http://doi.org/10.1016/j.jneumeth.2015.03.023>
 KA Phillips, MK Hambright, K Hewes, **BM Schilder**, CN Ross, SD Tardif
- 2014 • **Becoming a high-fidelity - super - imitator: what are the contributions of social and individual learning?**
Developmental Science (2014) 18(6):1025-1035; <http://doi.org/10.1111/desc.12276>
 F Subiaul, EM Patterson, **BM Schilder**, E Renner, R Barr
- 2014 • **Working memory constraints on imitation and emulation**
Journal of Experimental Child Psychology (2014) 128:190-200; <http://doi.org/10.1016/j.jecp.2014.07.005>
 F Subiaul, **BM Schilder**



PREPRINTS

- 2023 • **The rworkflows suite: automated continuous integration for quality checking, documentation website creation, and containerised deployment of R packages**
Research Square (2023) <https://doi.org/10.21203/rs.3.rs-2399015/v1>
BM Schilder, AE Murphy, NG Skene
- 2022 • **CUT&Tag recovers up to half of ENCODE ChIP-seq peaks**
bioRxiv (2022) <https://doi.org/10.1101/2022.03.30.486382>
 D Hu, L Abbasova, **BM Schilder**, A Nott, NG Skene, SJ Marzi

2022

EpiCompare: R package for the comparison and quality control of epigenomic peak files

bioRxiv (2022) <https://doi.org/10.1101/2022.07.22.501149>

S Choi, **BM Schilder**, L Abbasova, AE Murphy, NG Skene



ACKNOWLEDGEMENTS

2021

eQTL Catalogue: a compendium of uniformly processed human gene expression and splicing QTLs.

Nature Genetics (2021) 53:1290-1299; <https://doi.org/10.1038/s41588-021-00924-w>

N Kerimov, JD Hayhurst, K Peikova et al.

2020

Functionally-informed fine-mapping and polygenic localization of complex trait heritability

Nature Genetics (2020) <https://doi.org/10.1038/s41588-020-00735-5>

O Weissbrod...AL Price

2019

Wayfinding: The science and mystery of how humans navigate the world.

St. Martin's Press (2019) ISBN-13: 978-1250096968; <https://www.amazon.co.uk/Wayfinding-Science-Mystery-Humans-Navigate/dp/1250096960>

MR O'Connor

2012

EEG oscillations reveal neural correlates of evidence accumulation

Frontiers in Decision Neuroscience (2012) 6(106):Jan-13; <https://doi.org/10.3389/fnins.2012.00106>

M van Vugt, P Simen, L Nystrom, P Holmes, J Cohen

2011

Trial-by-trial adaptation of decision making performance: a model-based EEG analysis

Interdisciplinary Perspectives on Cognition, Education, and the Brain (2011) 7;

M van Vugt, P Simen, J Cohen



RESEARCH EXPERIENCE

2024

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2020

PhD Candidate

Imperial College London (UK Dementia Research Institute, Department of Brain Sciences)

📍 London, UK

- Thesis: Multi-omic medicine: dissecting the cell-type-specific molecular mechanisms underlying neurodegenerative disease genomics.
- Objective: Computationally dissect the subtraits, cell-types underlying the genomic signatures of Alzheimer's Disease and Parkinson's Disease.

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2019

Consultant

120/80 MKTG

📍 New York, NY, USA

- Offers consultation services to a wide portfolio of high-profile digital healthcare companies, with a focus on data analytics, research publication, and strategic transparency.
- Provides data-driven business intelligence reports using proprietary software scientific literature mining software that I have created.
- Professional company web design.

2020

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2018




Bioinformatician II

Icahn School of Medicine at Mount Sinai (Department of Neuroscience / Department of Neurology / Department of Genetics & Genomics / Ronald M. Loeb Center for Alzheimer's Disease)

📍 New York, NY, USA




- Developed machine learning systems to integrate large-scale multi-omics datasets (e.g. whole-genome sequencing, bulk and single-cell RNA-seq, epigenomics, clinical data) to uncover the molecular mechanisms underlying neurodegenerative diseases (e.g. Alzheimer's, Parkinson's, ALS).
- Computationally identified specific disease-causal variants, pathways and cell-types for subsequent functional wet lab validation (e.g. CRISPR-cas9 editing in patient-derived cell cultures, iPSCs and cerebral organoids).

2018 2017	Bioinformatician II Icahn School of Medicine at Mount Sinai (Department of Pharmacological Sciences) 📍 New York, NY, USA <ul style="list-style-type: none"> • Conducted computational systems biology research. Integrated and analyzed large-scale genomic and biomedical data (e.g. Python, R, JavaScript). • Developed evolutionary algorithm to optimize gene network kinase regulator prediction (eXpression2Kinases). • Developed and deployed computational tools, software, databases and web applications for basic and clinical research, resulting in 3 peer-reviewed publications.
2017	Participant Technische Universität Dresden / eMed (Summer School in Systems Medicine) 📍 Frauenchiemsee, Germany <ul style="list-style-type: none"> • Attended lectures and extended skills in extraction and analysis of big data from biomedical and neurogenomic resources. • Developed, performed and wrote manuscript for collaborative bioinformatics research project in less than one week.
2016	Participant Icahn School of Medicine at Mount Sinai (Scientific Computing & Data Science) 📍 New York, NY, USA <ul style="list-style-type: none"> • Intensive summer school in high-performance computing, coding, genome database utilization and bioinformatics methods including transcriptomics and genetic association testing.
2017 2013	Graduate Student The George Washington University (Department of Anthropology) 📍 Washington, DC, USA <ul style="list-style-type: none"> • Thesis: Evolution of the Hippocampus and Adult Neurogenesis Research • Investigated the evolution of human-specific cognitive abilities and neurological disease susceptibilities (e.g. Alzheimer's Disease). • Focused on neuroanatomical, transcriptomic and genomic evolution of the human hippocampus and memory.
2017 2014	Collaborator Trinity University / Southwestern National Primate Research Center (Department of Neuroscience) 📍 San Antonio, TX, USA <ul style="list-style-type: none"> • Investigated the neurobiological mechanisms underlying the ameliorating effects of exercise on relapse-remitting Multiple Sclerosis.
2014	Teaching Assistant / Project Leader The George Washington University / Rutgers University (Department of Anthropology) 📍 Ileret, Kenya <ul style="list-style-type: none"> • Served as Teaching Assistant while excavating Lower Paleolithic hominin sites (Homo, Paranthropus). • As Project Leader, investigated the running biomechanics of local Daasanach tribespeople while mentoring undergraduate students.
2013 2011	Research Assistant The George Washington University (Department of Anthropology) 📍 Washington, DC, USA <ul style="list-style-type: none"> • Performed dissection, histology, microscopy and quantitative stereology in post-mortem primate brain tissues. • Trained junior and senior personnel on lab protocols.
2013 2011	Senior Lab Manager The George Washington University (Department of Speech, Language & Hearing Sciences) 📍 Washington, DC, USA <ul style="list-style-type: none"> • Organized and trained dozens of undergraduates to conduct weekly cognitive development research; designed and/or directly contributed to over 15 research projects in two years.
2012	Volunteer Researcher University of Winnipeg / University of Belgrade (Department of Anthropology / Department of Archaeology) 📍 Sićevo, Serbia <ul style="list-style-type: none"> • Excavated Paleolithic fossils and tools (H. heidelbergensis, H. neanderthalensis) at Mala Balanica, Velika Balanica, and Pešturina sites.
2011	Volunteer Researcher Universidad de Murcia (Department of Zoology & Physical Anthropology) 📍 Murcia, Spain <ul style="list-style-type: none"> • Excavated Paleolithic fossils and tools from Cueva Negra (H. heidelbergensis) and Sima de las Palomas (H. neanderthalensis) with an international research team.

- 2011 • **Volunteer Research Intern**
American Museum of Natural History (Division of Anthropology)  [New York, NY, USA](#)
- Contributed to paleoanthropological research on primate fossils using 3D morphometry imaging equipment including Minolta, Microscribe and CT.
- 2010 • **Paid Research Intern**
Princeton University (Princeton Neuroscience Institute)  [Princeton, NJ, USA](#)
- Investigated the neural basis of decision-making in humans.
 - Recruited participants, recorded EEG and analyzed data in MATLAB.
- 2010
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2009 • **Student Researcher**
Brown University (Department of Cognitive, Linguistic & Psychological Sciences)  [Providence, RI, USA](#)
- Experimental Analysis of Animal Behavior & Cognition: Conducted various operant conditioning experiments on rats. Gained experience in animal behavioral training, data collection, and data analysis in MATLAB.
 - Laboratory in Genes and Behavior: Tested transgenic mice with modified N-type voltage-gated calcium channel subunits in a battery of cognitive and sensorimotor tasks. Results were published.



TEACHING / MENTORING EXPERIENCE

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2020 • **Research Mentor**
Imperial College London (Department of Brain Sciences / Department of Life Sciences)  [London, UK](#)
- Mentored students and affiliated projects:
 - Kitty Murphy (PhD): 'Evolutionary pressures on cell types: leveraging species differences to gain insight into neurodegenerative disease risk'
 - Sheen Lei (BSc): 'Benchmarking cell-type-specific enrichment of genome-wide disease signatures'
 - Ted Reese (MSc): 'Computational cell-type annotation of single-cell epigenomics data'
 - Xindong Sun (MSc): 'Benchmark of Targeted insertion of promoters sequencing (TIP-seq) on histone modification H3K27ac and H3K27me3 in K562 cell line'
 - Shuhan Shen (MSc): 'Evaluation and optimisation of methods for identifying the cell types underlying genetic disease signatures'
 - Lusheng Li (MSc): 'Genetic identification of cell types underlying mammalian phenotypes'
 - Sera Choi (BSc): 'EpiCompare: R package for QC and benchmarking epigenetic datasets'
 - Emilie Cottard (MSc) & Will Lunt (BSc): 'A meta-analysis of selective cell-type vulnerability in Parkinson's Disease neuropathology'
 - Jai Chapman (BSc): 'Expression Weighted Cell Type Enrichment as a Tool for Identifying Cell Types Underlying Rare Disease Phenotypes'
 - Bobby Gordon-Smith (MSc): 'Identification of cell types involved in rare disease-associated human phenotypes'
 - Leyla Abbasova (MSc): 'Analysis and optimisation of CUT&Tag for epigenomic profiling of the brain'
 - Barney Hill (BSc): 'Identification of cell-types associated with latent factors inferred from phenome-wide GWAS summary statistics'
- 2020
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2019 • **Research Mentor**
Icahn School of Medicine at Mount Sinai (Department of Neuroscience / Department of Neurology / Department of Genetics & Genomics / Ronald M. Loeb Center for Alzheimer's Disease)  [New York, NY, USA](#)
- Mentored MS, MD, and PhD students in projects focused on computational exploration of phenotype clustering and genomic regulation of neurodegenerative diseases.
- 2018 • **Research Co-mentor**
Icahn School of Medicine at Mount Sinai (Department of Pharmacological Sciences)  [New York, NY, USA](#)
- Mentored students and affiliated projects:
 - Vivian Utti (BSc): 'ChEA3: Transcription Factor Enrichment Analysis' as part of the Summer Research Training Program in Biomedical Big Data Science.
 - Mary Duffy (PhD): 'Predicting upstream kinase regulators from interaction network databases'
 - Zach Flamholz (BSc): 'modEnrichr: a suite of gene set enrichment analysis tools for model organisms'

2018	Guest Lecturer Icahn School of Medicine at Mount Sinai (Department of Pharmacological Sciences) 📍 New York, NY, USA <ul style="list-style-type: none"> Lectured on data visualization in Python and Jupyter notebooks in the PhD/MD course 'Programming for Big Data Biomedicine'.
2017 2016	Research Mentor The George Washington University (Department of Anthropology) 📍 Washington, DC, USA <ul style="list-style-type: none"> Mentored students and affiliated projects: Jamie Kleiner (BSc): 'Animal model simulating MS and exercise's impact on adult hippocampal neurogenesis'
2015	Teaching Assistant The George Washington University (Department of Anthropology) 📍 Washington, DC, USA <ul style="list-style-type: none"> Course: "'Human Brain Evolution'" Guest lectured, graded all assignments and exams, and provided additional educational support during office hours.
2014	Teaching Assistant The George Washington University (Department of Psychology) 📍 Washington, DC, USA <ul style="list-style-type: none"> Course: "'Biological Psychology'" Led undergraduates in article discussions, graded all assignments and exams, and provided additional educational support during office hours.
2014 2013	Teaching Assistant The George Washington University (Department of Anthropology) 📍 Washington, DC, USA <ul style="list-style-type: none"> Course: "'Biological Anthropology'" Led undergraduate students in two, 2-hour lab sessions per week, graded lab assignments and exams, and provided additional educational support during office hours.
2013 2012	Research Mentor The George Washington University (Department of Psychology) 📍 Washington, DC, USA <ul style="list-style-type: none"> Mentored students and affiliated projects: Anushka Gokhale (BSc): 'Infants' Social Assessment of Characters Through Eye Gaze'
2013 2011	Lab Protocol Trainer The George Washington University (Department of Anthropology) 📍 Washington, DC, USA <ul style="list-style-type: none"> Trained undergraduate, graduate, and post-doctoral researchers in Social Cognition Lab and Lab for Evolutionary Neuroscience in a variety of methodological research protocols.



SOFTWARE PACKAGES

- rworkflows**
 Continuous integration for R packages. Automates testing, documentation website building, and containerised deployment
<https://github.com/neurogenomics/rworkflows>
<https://doi.org/10.21203/rs.3.rs-2399015/v1>
- TIPseeker**
 R package for post-processing [single-cell] TIP-seq data
<https://github.com/neurogenomics/TIPseeker>
- PeakyFinders**
 R package for mining, calling, and importing epigenomic peaks
<https://github.com/neurogenomics/PeakyFinders>
- SkillNet**
 Creates user-specific contribution networks from GitHub Organization repositories
<https://github.com/neurogenomics/SkillNet>
- phenomix**
 R package for the exploration and analysis of many genotype-phenotype datasets at once
<https://github.com/neurogenomics/phenomix>

6. **MAGMA_Celltyping**
Identify cell types underlying the associations found in GWAS summary statistics
https://github.com/neurogenomics/MAGMA_Celltyping
7. **EWCE**
Expression Weighted Celltype Enrichment
<https://github.com/NathanSkene/EWCE>
8. **EpiCompare**
R package for QC and benchmarking epigenetic datasets
<https://github.com/neurogenomics/EpiCompare>
9. **MultiEWCE**
R package for analysing multiple gene lists using EWCE
<https://github.com/neurogenomics/MultiEWCE>
10. **HPOExplorer**
Functions for working with the Human Phenotype Ontology data
<https://github.com/neurogenomics/HPOExplorer>
11. **orthogene**
Interspecies gene mapping
<https://github.com/neurogenomics/orthogene>
12. **MungeSumstats**
Standardise the format of summary statistics from GWAS
<https://github.com/neurogenomics/MungeSumstats>
<https://doi.org/10.1093/bioinformatics/btab665>
13. **scNLP**
Tools for applying natural language processing (NLP) techniques to single-cell (sc) omics data
<https://github.com/neurogenomics/scNLP>
14. **scKirby**
Automated ingestion and conversion of various single-cell data formats
<https://github.com/neurogenomics/scKirby>
15. **templateR**
Template for developing R packages
<https://github.com/neurogenomics/templateR>
<https://doi.org/10.21203/rs.3.rs-2399015/v1>
16. **echolocator**
R package for end-to-end statistical and functional fine-mapping with extensive dataset access
<https://github.com/RajLabMSSM/echolocator>
<https://doi.org/10.1093/bioinformatics/btab658>
17. **echodata**
Examples of fine-mapped GWAS summary statistics, data formatting functions, and API access to the echolocator Fine-mapping Portal
<https://github.com/RajLabMSSM/echodata>
18. **echoannot**
Functions for annotating genomic data with annotations and epigenomic data
<https://github.com/RajLabMSSM/echoannot>
19. **echoplot**
R package for LocusZoom-inspired GWAS/QTL visualization, with API access to LD panels
<https://github.com/RajLabMSSM/echoplot>
20. **echoconda**
Various utility functions to find, build, and use conda environments from within R
<https://github.com/RajLabMSSM/echoconda>
21. **echotabix**
Tabix indexing and querying
<https://github.com/RajLabMSSM/echotabix>

22. ● **echoLD**
LD downloading and processing.
<https://github.com/RajLabMSSM/echoLD>
23. ● **echodeps**
Creates interactive dependency networks for R packages.
<https://github.com/RajLabMSSM/echodeps>
24. ● **echogithub**
Access and process metadata from GitHub
<https://github.com/RajLabMSSM/echogithub>
25. ● **downloadR**
Single- and multi-threaded downloading functions
<https://github.com/RajLabMSSM/downloadR>
26. ● **catalogueR**
R package for rapid API-access and colocalization of summary statistics from eQTL Catalogue
<https://github.com/RajLabMSSM/catalogueR>
27. ● **PubReporter**
Proprietary Python package for extracting relevant scientific literature and citations, performing topic modelling, and generating interactive business intelligence reports.



WEB APPS

1. ● **Geneshot**
Flexible tool to identify genes associated with any biomedical term and to predict novel target genes
<http://amp.pharm.mssm.edu/geneshot>
<https://doi.org/10.1093/nar/gkz393>
2. ● **X2K**
eXpression 2 Kinases (X2K) Web: Automated computational pipeline to infer kinase regulators from weighted or unweighted gene lists
<http://amp.pharm.mssm.edu/X2K>
<https://doi.org/10.1093/nar/gky458>
3. ● **Rare Disease Celltyping Apps**
Web portal connecting to multiple R Shiny apps to explore, visualize, and download cell type-specific enrichment results and systematically prioritised gene targets for over 6,000 rare disease phenotypes.
https://github.com/neurogenomics/rare_disease_celltyping_apps
4. ● **Parkinson's Disease Omics Review**
Data and code associated with the Parkinson's Disease review paper by Schilder, Navarro & Raj (Neurobiology of Disease, 2021)
https://github.com/RajLabMSSM/PD_omics_review
https://rajlabmssm.github.io/PD_omics_review/
<https://doi.org/10.1016/j.nbd.2021.105580>
5. ● **Selective Vulnerability Meta-analysis**
Selective Vulnerability Meta-analysis: Shiny app dedicated to the exploration and dissemination of meta-analysed cell counts manually curated and harmonised from the Parkinson's Disease literature
<https://github.com/neurogenomics/SelectiveVulnerabilityMetaAnalysis>
6. ● **echolocatoR Fine-mapping Portal**
Access to interactive plots and fine-mapping results across many GWAS/QTL datasets using echolocatoR
https://github.com/RajLabMSSM/Fine_Mapping_Shiny
https://rajlab.shinyapps.io/Fine_Mapping_Shiny
<https://doi.org/10.1093/bioinformatics/btab658>
7. ● **Tensor Decomposition Shiny App**
Interactive application to explore and download all results and plots from Ramdhani et al. (PLOS Genetics, 2020)
https://github.com/RajLabMSSM/Tensor_myeloid
https://rajlab.shinyapps.io/Tensor_myeloid
<https://doi.org/10.1101/499509>

8.
- Hippocampal Evolution**

Interactive code, results and visualization for the manuscript "Evolutionary selective pressures dramatically expanded and reorganized the human hippocampal complex"

https://github.com/bschilder/Hippo_Eco

https://bschilder.github.io/Hippo_Eco/HPsubfield_eco

<https://doi.org/10.1002/cne.24822>



WEBSITES

1.
- Personal Website**

<https://github.com/bschilder/BMSchilder>

<https://bschilder.github.io/BMSchilder>
2.
- Official Raj Lab Website**

https://github.com/RajLabMSSM/RajLab_website

<http://www.rajlab.org>



GRANTS

- Total (all grants): \$2,949,052**

Total (as primary applicant): \$310,562
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- 2023

Imperial UK Research Institute Impact Acceleration Account, Imperial College London

Project: 'Creating commercial kit solutions for single cell epigenetic profiling of histone marks and transcription factors'

• **Role:** Co-applicant

• **PI:** NG Skene

• **Amount:** £80,000

2024
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2022

Turing Community Award, Alan Turing Institute

Project: 'Multi-omic medicine: dissecting the cell-type-specific molecular mechanisms underlying neurodegenerative disease genomics'

• **Role:** Primary applicant

• **PI:** BM Schilder

• **Amount:** £3,000

2022

National Institutes of Health

Project: 'Statistical and functional fine-mapping of bipolar disorder genetic risk loci'

• **Role:** Co-applicant

• **PI:** N Mullins

2021

Collaborative Single Cell and Spatial Transcriptomics Studies Award Programme, UK Dementia Research Institute

Project: 'Amplifying genome coverage of single cell epigenetic profiling of the human brain'

• **Role:** Co-applicant

• **PI:** D Hu, NG Skene

• **Amount:** £12,790

2020

National Institutes of Health

Project: 'Cognitive Systems Analysis of Alzheimer's Disease Genetic and Phenotypic Data'

• **Role:** Co-applicant

• **PI:** T Raj, D Knowles

• **Amount:** \$2,523,431

2024
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2020

UK Dementia Research Institute

Project: 'UK DRI at Imperial Distinguished Studentship'

• **Role:** Primary applicant

• **PI:** BM Schilder

• **Amount:** £217,000

2019 2017	The Michael J. Fox Foundation Project: 'The Role of Peripheral Myeloid Cells in Parkinson's Disease' • Role: Fundee • PI: T Raj
2020 2017	The Michael J. Fox Foundation Project: 'Functional Fine-Mapping of LRRK2 Locus' • Role: Fundee • PI: T Raj
2017	National Science Foundation Project: 'The evolution of the hippocampus and adult neurogenesis: novel insights into the origins of human memory' • Role: Primary applicant • Amount: \$31,543 • PI: BM Schilder
2017	Wenner-Gren Project: 'The evolution of the hippocampus and adult neurogenesis: insights into the origins of human memory' • Role: Primary applicant • Amount: \$19,512 • PI: BM Schilder
2016	Leakey Foundation Project: 'The evolution of the hippocampus and adult neurogenesis: Novel insights into the origins of human memory' • Role: Primary applicant • Amount: \$15,000 • PI: BM Schilder
2016	COSMOS Club Project: 'The evolution of adult neurogenesis across primates' • Role: Primary applicant • Amount: \$3,250 • PI: BM Schilder



AWARDS

2022	Prize for Computational Reproducibility in Dementia Research (honourable mention), UK Dementia Research Institute Project: 'MungeSumstats: A Bioconductor package for the standardisation and quality control of many GWAS summary statistics' Individually awarded for outstanding contributions during the NEUROHACK 2022, a competitive 4-day hackathon to apply AI in finding ALS therapeutic solutions.
2022	Award for Outstanding Contribution, NEUROHACK, Deep Dementia Phenotyping Network (DEMON) Project: 'Predicting ALS drug targets using integrative multi-modal deep learning' Jointly awarded inaugural prize with Kitty Murphy.
2021	Prize for Computational Reproducibility in Dementia Research, UK Dementia Research Institute Project: 'echolocator: an automated end-to-end statistical and functional genomic fine-mapping pipeline'
2021	Centre Photography Competition, UK Dementia Research Institute Project: 'Wildfire Circle, Golden Brain, Wildfire, Geneshot, Geology of Biology, Neon Brain' One of the winners of the scientific image competition.
2019	Art of the Brain, Friedman Brain Institute, Icahn School of Medicine Project: 'Wildfire' Awarded 2nd place and Featured on the cover of <i>Biological Psychiatry: Volume 87, Issue 12 (2020)</i> . Exhibited and auctioned at the Grady Alexis Gallery (New York City), where all proceeds were voluntarily donated to the Diversity in Neuroscience Initiative.