BRIAN M. SCHILDER

Passionately pursuing multi-disciplinary research to improve human lives.

Imperial College London
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/microscropy.

• **Publications**: Strong writing skills as evidenced by **18** peer-reviewed scientific publications, **20** 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.

• **R**: Created **30** R packages to date, including on Bioconductor and CRAN. Experienced in created Shiny Apps and Rmarkdown reports.

• **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 **11**+ websites, web apps, and interactive reports. Developed templates to automatically render websites on-the-fly from CSVs using Javascript.

CONTACT

✉
brian_schilder@alumni.brown.edu
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+1 908-268-9859
📞 **UK**
+44 073-0653-7736
in **LinkedIn**
ⓘD **ORCID**
GitHub
🐦 **Twitter**
🌐 **Personal Website**
🌐 **Lab Website**

SUMMARY

💼 **14+ years of research experience.**
📄 **18 peer-reviewed publications & 5 preprints.**
🔧 **44 bioinformatics tools & databases developed.**
🖥 **12+ years of teaching & supervising experience.**

TABLE OF CONTENTS

 CV source code

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.
- **Version control**: Extensive and daily use of git, GitHub Issues, GitHub Projects.
- **Supervision**: Supervises numerous student research 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 Sneeboer, E Navarro, **BM Schilder**…T Raj
📰 **News**
- Microglial transcriptomics meets genetics: new disease leads (Nature Reviews Neurology, 2022)
- Mighty MiGA: Microglial Genomic Atlas Zeros in on Causal AD Risk Variants (ALZFORUM, 2022)
- Can a Human Microglial Atlas Guide Brain Disorder Research? (Mount Sinai Health System, 2022)
- Polygenic Scores Paint Microglia as Culprits in Alzheimer's (ALZFORUM, 2021)

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
📰 **News**
- Mount Sinai: Fighting Neurodegenerative Disorders (Mount Sinai Health System, 2019)

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-l 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
📰 **News**
- Researchers identify 64 regions of the genome that increase risk for bipolar disorder (EurekAlert, 2021)
- Largest Bipolar Disorder Genetics Study Doubles Genetic Risk Factors (Nordic Society of Human Genetics and Precision Medicine, 2021)

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
📰 **News**
- Chosen as 'Featured Frontmatter' article in Cell Systems

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
📰 **News**
- Geneshot: Piercing the Literature to Identify and Predict Relevant Genes (University of Pittsburgh Health Sciences Library System Update, 2019)
- The Future of AI at the Hasso Plattner Institute for Digital Health at Mount Sinai (Mount Sinai Health System, 2020)

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
📰 **News**
- Mount Sinai Faculty Spotlight: Ma'ayan Lab (Mount Sinai Health System, 2018)

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
📰 **News**
- Monkeys on a Treadmill? A Conversation with Dr. Kimberley Phillips (Why Social Science?)

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 ● **Artificial intelligence for dementia research methods optimization**
arxiv (2023) https://doi.org/10.48550/arXiv.2303.01949
M Bucholc, C James, AA Khleifat, A Badhwar, N Clarke, A Dehsarvi, CR Madan, SJ Marzi, C Shand, **BM Schilder**, S Tamburin, HM Tantiangco, I Lourida, DJ Llewellyn, JM Ranson

2023 ● **Identification of cell type-specific gene targets underlying thousands of rare diseases and subtraits**
medRxiv (2023) https://doi.org/10.1101/2023.02.13.23285820
KB Murphy, R Gordon-Smith, J Chapman, M Otani, **BM Schilder**, NG Skene

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; https://www.semanticscholar.org/paper/Trial-by-trial-adaptation-of-decision-making-a-EEG-Vugt-Simen/330371d08842ecd1bda332dd22351a7135b5cb1f
M van Vugt, P Simen, J Cohen

📄 REVIEWERSHIPS

2022 — **[Unpublished article]**
Bioinformatics (2022)

2021 — **Most Pathways Can Be Related to the Pathogenesis of Alzheimer's Disease**
Alzheimer's Research & Therapy (2021) https://doi.org/10.3389/fnagi.2022.846902
SL Morgan, P Naderi, K Koler, Y Pita-Juarez, D Prokopenko, IS Vlachos, RE Tanzi, L Bertram, WA Hide

2021 — **CLIP: accurate prediction of disordered linear interacting peptides from protein sequences using co-evolutionary information**
Bioinformatics (2021) https://doi.org/10.1093/bib/bbac502
Z Peng, Z Li, Q Meng, B Zhao, L Kurgan

2020 — **Single-Cell Transcriptomics and In Situ Morphological Analyses Reveal Microglia Heterogeneity Across the Nigrostriatal Pathway**
Neurobiology of Disease (2020) https://doi.org/10.3389/fimmu.2021.639613
O Uriarte Huarte, D Kyriakis, T Heurtaux, Y Pires-Afonso, K Grzyb, R Halder, M Buttini, A Skupin, M Mittelbronn, A Michelucci

2019 — **Deconstructing cerebellar development cell by cell**
PLOS Genetics (2019) https://doi.org/10.1371/journal.pgen.1008630
MJ van Essen, S Nayler, EBE Becker, J Jacob

2019 — **[Unpublished article]**
Nature Neuroscience (2019)

🧑‍🏫 INVITED TALKS

2023 — **Multi-omics medicine: investigating shared genetic risk factors to better understand neurodegenerative disease**
Turing Omics Meeting
Omics Data Generation & Analysis Group
The Alan Turing Institute

2022 — **Decomposing the phenome: learning the latent genomic structure underlying thousands of diseases and traits**
Neuroepidemiology of Aging Webinar
RUSH Alzheimer's Disease Center (RADC)
RUSH University

2022 — **Drug (re)discovery in the age of genomics: multi-omic strategies for identifying disease treatments**
Department Seminar
3D (Drug, Disease, Delivery) Center / Department of Pharmaceutical Sciences
University of South Dakota

2020 — **Statistical and functional genetic fine-mapping across multiple disease**
Seminar
Alzheimer's Disease Sequencing Project
Columbia University / Icahn School of Medicine at Mount Sinai

2020 — **Statistical and functional genetic fine-mapping across multiple disease**
Laboratory of Neurogenetics Friday Workshop
National Institute on Aging
National Institutes of Health

CONFERENCE TALKS

2022 — **Systematic quantification of animal model viability across human diseases**
Informatics-Synapse Joint Early Career Researcher Meeting

UK Dementia Research Institute (UK DRI)

2020 — **Automated genetic fine-mapping of neurological disorders**
London Genetics Network

2019 — **Parkinson's disease derived monocytes show alteration in the phago-lysosomal pathway**
American Society of Human Genetics

Co-contributor

2016 — Marmoset Social

Society for Neuroscience

2016 — JB Johnston Club for Evolutionary Neuroscience

Society for Neuroscience

2014 — JB Johnston Club for Evolutionary Neuroscience

Society for Neuroscience

CONFERENCE POSTERS

2023 — **Systematic quantification of animal model viability across human disease**
UK Dementia Research Institute Scientific Advisory Board (2023)
BM Schilder, NG Skene

2022 — **Systematic quantification of animal model viability across human disease**
Rising Scientist Day at Imperial College London (2022)
BM Schilder, NG Skene

2022 — **A compehensive statistical and functional fine-mapping pipeline applied to Bipolar Disorder GWAS risk loci**
European Neuropsychopharmacology (2022) 63:e14; http://dx.doi.org/10.1016/j.euroneuro.2022.07.037
M Koromina, A Ravi, **BM Schilder**, B Muller, J Coleman, T Raj, N Mullins

2021 — **Genetic Effects on Human Microglia Transcriptome in Neuropsychiatric Diseases**
Biological Psychiatry (2021) 89(9):S84-S85; https://doi.org/10.1016/j.biopsych.2021.02.225
G Snijders, K de Paiva Lopes, J Humphrey, S Allan, M Sneeboer, R Navarro, **BM Schilder**, R Vialle, M Parks, R Missall, W van Zuiden, F Gigase, R Kubler, AB van Berlekom, C Bottcher, J Priller, R Kahn, L de Witte, T Raj

2020 — **Cell-type-specific reconstruction of primate evolution from genomic positive selection**
Rising Scientist Day at Imperial College London (2020)
K Murphy, **BM Schilder**, NG Skene

2019 — **Automated genetic and functional fine-mapping of Parkinson's Disease Loci.**
American Society of Human Genetics (2019)
BM Schilder, T Raj

2019 — **Parkinson's disease derived monocytes show alteration in the phago-lysosomal pathway**
American Society of Human Genetics (2019)
E Udine, E Navarro, …**BM Schilder**, …T Raj

2018 • **Learning X2K: Parameter Optimization via Genetic Algorithms to Calibrate the Expression2Kinases Pipeline**
Illuminating the Druggable Genome (2018)
BM Schilder, A Lachmann, M Kuleshov, A Ma'ayan

2018 • **Learning X2K: Parameter Optimization via Genetic Algorithms to Calibrate the Expression2Kinases Pipeline**
Big Data 2 Knowledge - Library of Integrated Network-Based Cellular Signatures (LINCS) (2018)
BM Schilder, A Lachmann, M Kuleshov, A Ma'ayan

2017 • **The evolution of the human hippocampus and neuroplasticity**
Association for American Physical Anthropologists (2017)
BM Schilder, BJ Bradley, CC Sherwood

2016 • **The molecular evolution of the primate hippocampus**
Society for Neuroscience (2016)
BM Schilder, BJ Bradley, CC Sherwood

2015 • **Effects of exercise on disease progression and cognition in the marmoset EAE model**
JB Johnston Club for Evolutionary Neuroscience (2015)
KA Phillips, MK Hambright, K Hewes, **BM Schilder**, B Jagessar, B t'Hart, SD Tardif

2015 • **The effects of climatic trends, variability, and rates of change on mammalian brain evolution**
Association for American Physical Anthropologists (2015)
BM Schilder, WA Barr, R Bobe, CC Sherwood

2015 • **Individual, Observational, and Imitation Learning in Orangutans and Children**
Association for American Physical Anthropologists (2015)
E Renner, **BM Schilder**, F Subiaul

2014 • **The helper hinderer task revisited: an infant eye tracking study**
The George Washington University Research Day (2014)
A Gokhale, **BM Schilder**, F Subiaul

2013 • **Dendritic morphology of pyramidal neurons across the visual stream: A direct comparison of chimpanzees and humans**
Society for Neuroscience (2013)
BM Schilder, O Adeyo

2013 • **The striatum in the evolution of learned vocalizations: Understanding the neurobiological precursors to human speech using a chimpanzee model**
Society for Neuroscience (2013)
S Bianchi, T Duka, G Muntane, **BM Schilder**, CD Stimpson, WD Hopkins

2013 • **Imitation & emulation in a novel box task**
Association for Psychological Science (2013)
L Zimmerman, N Brito, C Mendelson, R Barr, E Renner, **BM Schilder**, F Subiaul

2013 • **A study of imitation and working memory in 2- to 4- year-olds**
Association for Psychological Science (2013)
R Barr, F Subiaul, L Zimmerman, L Renner, **BM Schilder**, C Mendelson, L Golojuch

2013 • **The impact of wealth on sharing preferences in children**
Child Development Society (2013)
J Miller, **BM Schilder**, L Peizer, F Subiaul

🧳 RESEARCH EXPERIENCE

2024 | 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.

- | 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 | 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
- 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
- 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
- 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
- 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
- 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
· 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
· Performed dissection, histology, microscopy and quantitative stereology in post-mortem primate brain tissues.
· Trained junior and senior personnel on lab protocols.

2013
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2011 ● **Senior Lab Manager**
The George Washington University (Department of Speech, Language & Hearing Sciences)
📍 Washington, DC, USA
· 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
· 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
· 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

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 | 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
- 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
- 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
- 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
- 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
· 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
· 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
· 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

1.
ThreeWayTest
Summary statistics-based association test for identifying the pleiotropic effects with set of genetic variants
🐙 https://github.com/bschilder/ThreeWayTest

2.
SCAVENGE
Variant to function mapping at single-cell resolution through network propagation
🐙 https://github.com/neurogenomics/SCAVENGE
📄 https://doi.org/10.1038/s41587-022-01341-y

3.
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

4.
TIPseeker
R package for post-processing [single-cell] TIP-seq data
🐙 https://github.com/neurogenomics/TIPseeker

5.
PeakyFinders
R package for mining, calling, and importing epigenomic peaks
🐙 https://github.com/neurogenomics/PeakyFinders

6.
SkillNet
Creates user-specific contribution networks from GitHub Organization repositories
🐙 https://github.com/neurogenomics/SkillNet

7.
phenomix
R package for the exploration and analysis of many genotype-phenotype datasets at once
🐙 https://github.com/neurogenomics/phenomix

8.
MAGMA_Celltyping
Identify cell types underlying the associations found in GWAS summary statistics
🐙 https://github.com/neurogenomics/MAGMA_Celltyping

9.
EWCE
Expression Weighted Celltype Enrichment
🐙 https://github.com/NathanSkene/EWCE

10.
EpiCompare
R package for QC and benchmarking epigenetic datasets
🐙 https://github.com/neurogenomics/EpiCompare
📄 https://doi.org/10.1101/2022.07.22.501149

11.
MultiEWCE
R package for analysing multiple gene lists using EWCE
🐙 https://github.com/neurogenomics/MultiEWCE
📄 https://doi.org/10.1101/2023.02.13.23285820

12. **HPOExplorer**
Functions for working with the Human Phenotype Ontology data
 https://github.com/neurogenomics/HPOExplorer
 https://doi.org/10.1101/2023.02.13.23285820

13. **orthogene**
Interspecies gene mapping
 https://github.com/neurogenomics/orthogene

14. **MungeSumstats**
Standardise the format of summary statistics from GWAS
 https://github.com/neurogenomics/MungeSumstats
 https://doi.org/10.1093/bioinformatics/btab665

15. **scNLP**
Tools for applying natural language processing (NLP) techniques to single-cell (sc) omics data
 https://github.com/neurogenomics/scNLP

16. **scKirby**
Automated ingestion and conversion of various single-cell data formats
 https://github.com/neurogenomics/scKirby

17. **templateR**
Self-updating template for developing R packages
 https://github.com/neurogenomics/templateR
 https://doi.org/10.21203/rs.3.rs-2399015/v1

18. **echoverseTemplate**
Self-updating template for creating echoverse R packages.
 https://github.com/RajLabMSSM/echoverseTemplate/
 https://doi.org/10.1093/bioinformatics/btab658

19. **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

20. **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
 https://doi.org/10.1093/bioinformatics/btab658

21. **echoannot**
Functions for annotating genomic data with annotations and epigenomic data
 https://github.com/RajLabMSSM/echoannot
 https://doi.org/10.1093/bioinformatics/btab658

22. **echoplot**
R package for LocusZoom-inspired GWAS/QTL visualization, with API access to LD panels
 https://github.com/RajLabMSSM/echoplot
 https://doi.org/10.1093/bioinformatics/btab658

23. **echoconda**
Various utility functions to find, build, and use conda environments from within R
 https://github.com/RajLabMSSM/echoconda
 https://doi.org/10.1093/bioinformatics/btab658

24. **echotabix**
Tabix indexing and querying
 https://github.com/RajLabMSSM/echotabix
 https://doi.org/10.1093/bioinformatics/btab658

25. **echoLD**
LD downloading and processing.
 https://github.com/RajLabMSSM/echoLD
 https://doi.org/10.1093/bioinformatics/btab658

26. **echodeps**
Creates interactive dependency networks for R packages
https://github.com/RajLabMSSM/echodeps
https://doi.org/10.1093/bioinformatics/btab658

27. **echogithub**
Access and process metadata from GitHub
https://github.com/RajLabMSSM/echogithub
https://doi.org/10.1093/bioinformatics/btab658

28. **devoptera**
Practical tools for R developers
https://github.com/RajLabMSSM/devoptera
https://doi.org/10.1093/bioinformatics/btab658

29. **downloadR**
Single- and multi-threaded downloading functions
https://github.com/RajLabMSSM/downloadR
https://doi.org/10.1093/bioinformatics/btab658

30. **catalogueR**
R package for rapid API-access and colocalization of summary statistics from eQTL Catalogue
https://github.com/RajLabMSSM/catalogueR
https://doi.org/10.1093/bioinformatics/btab658

31. **PubReporter**
Proprietary Python package for extracting relevant scientific literature and citations, performing topic modelling, and generating interactive business intelligence reports.

🗄 DATABASES / WEB APPS

1. **EpiArchives**
Public archive for EpiCompare reports.
https://github.com/neurogenomics/EpiArchives
https://doi.org/10.1101/2022.07.22.501149

2. **Rare Disease Celltyping Portal**
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
https://neurogenomics.github.io/rare_disease_celltyping_apps/home
https://doi.org/10.1101/2023.02.13.23285820

3. **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

4. **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

5. **MAGMA Files Public**
Gene enrichment files for hundreds of GWAS generated with Multi-marker Analysis of GenoMic Annotation (MAGMA) for use in downstream analyses
https://github.com/neurogenomics/MAGMA_Files_Public

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. **COVID-19 Patient Tracker**
Web app for summarizing and visualizing real-time EHR data of COVID-19 patients within the Mount Sinai Health System

8. **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

9. **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

10. **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

11. **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

🖥️ 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): $2,947,192
Total (as primary applicant): $308,702

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   • **Amount**: £80,000
• **PI**: NG Skene

2024 | 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   • **Amount**: £1,500
• **PI**: BM Schilder

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   • **Amount**: £12,790
• **PI**: D Hu, NG Skene

2020 ● **National Institutes of Health**
Project: "Cognitive Systems Analysis of Alzheimer's Disease Genetic and Phenotypic Data"
• **Role**: Co-applicant   • **Amount**: $2,523,431
• **PI**: T Raj, D Knowles

2024 | 2020 ● **UK Dementia Research Institute**
Project: 'UK DRI at Imperial Distinguished Studentship'
• **Role**: Primary applicant   • **Amount**: £217,000
• **PI**: BM Schilder

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,**
UK Dementia Research Institute
Project: 'MungeSumstats: A Bioconductor package for the standardisation and quality control of many GWAS summary statistics'
▣ **News**
- Awarded honourable mention

2022   **Award for Outstanding Contribution,**
NEUROHACK, Deep Dementia Phenotyping Network (DEMON)
Project: 'Predicting ALS drug targets using integrative multi-modal deep learning'
📰 **News**
- Individually awarded for outstanding contributions during the NEUROHACK 2022, a competitive 4-day hackathon to apply AI in finding ALS therapeutic solutions.

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'
📰 **News**
- Winners announced for UK DRI's first 'Prize for Computational Reproducibility in Dementia Research (UK Dementia Research Institute, 2021)
- Jointly awarded inaugural prize with Kitty Murphy.

2021   **Centre Photography Competition,**
UK Dementia Research Institute
Project: 'Wildfire Circle, Golden Brain, Wildfire, Geneshot, Geology of Biology, Neon Brain'
📰 **News**
- One of the winners of the scientific image competition.

2019   **Art of the Brain,**
Friedman Brain Institute, Icahn School of Medicine
Project: 'Wildfire'
📰 **News**
- Awarded 2nd place and Featured on the cover of Biological Psychiatry: Volume 87, Issue 12 (2020). Exhibited and auctioned at the Grady Alexis Gallery (New York City), where all proceeds were voluntarily donated to the Diversity in Neuroscience Initiative.

🏛 AFFILIATIONS

Imperial College London

- Department of Brain Sciences
- Faculty of Medicine

UK Dementia Research Institute

- Synapse Working Group
- Informatics Working Group

DEMON Network
Data science and AI for dementia

- Genetics & Omics Working Group
- Experimental Models Working Group
- Drug Discovery & Trials Optimisation Working Group

The Alan Turing Institute

- Turing Enrichment Scheme
- Turing-Roche Strategic Partnership

PGC Psychiatric Genomics Consortium

- Bipolar Disorder Working Group

Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

- Bioconductor Cloud Methods Working Group
- Active developer

🚀 DATA VISUALISATION / ARTWORK PORTFOLIO

2022

echoverse Dependency Graph

📍 London, UK

- Interactve graph showing the dependency structure of all packages within the echoverse suite.

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2020

Hex stickers

📍 London, UK

- All hex stickers for R packages I've helped develop.

2023

3D Human Phenotype Ontology

📍 London, UK

- 3D force-directed graph of the Human Phenotype Ontology (clouds above) with kernel density estimation projected from the x/y planes (mountains below). Connections represent the hierarchical relationships between rare diseases and their associated symptoms/phenotypes.
- Associated preprint

2023

Multi-scale Rare Disease Mechanisms

📍 London, UK

- Network of systematically prioritised gene therapy targets for rare diseases
- Associated preprint

2023

Curriculum Vitae Connexa

📍 London, UK

- Term co-occurrence network generated by analysing all data that went into this CV.

2021

Experiments with Generative AI

📍 London, UK

- wombo.art: 'Multi-omic medicine: dissecting the cell-type-specific mechanisms in neurodegeneration genomics'
- wombo.art: 'Multi-omic medicine: neurodegenerative disease genomics'
- wombo.art: 'Multi-omic medicine: neurodegeneration'
- wombo.art: 'Neurodegeneration'

2021

Lights in the dark genome: the current state of Parkinson's research

📍 London, UK

- The majority of PD genetics research has focused on a relatively small number of genes. Above, are the top 75 most commonly mentioned genes in the PD literature, extracted using Geneshot.
- Associated study

2020

Pacrophage

📍 London, UK

- Colocalised genetic loci …but shaped as Pac-Man!
- Associated study

2020

Circos

📍 London, UK

- Colocalised genetic loci across a variety of neurological disease GWAS and cell-type-specific QTLs.
- Associated study

2019

Wildfire Circle

📍 New York, NY, USA

- Awarded 2nd place in the 2019 Art of the Brain competition, put on by the Mount Sinai's Friedman Brain Institute.
- Exhibited and auctioned at the Grady Alexis Gallery (New York City), where all proceeds were donated to the Diversity in Neuroscience Initiative .
- Featured on cover of Biological Psychiatry.

2019

Wildfire

📍 New York, NY, USA

- Transcriptomic data from 16k+ individual brain cells (shown as points) after reducing the dimensionality with an autoencoder and UMAP. 5 million tracts are shown interconnecting these cells, where shorter tract length represents greater similarity in their molecular profiles.

2019

3D Brain Model

📍 New York, NY, USA

- 3D model of my brain generated from MRI scans.

🎔🎜📷⚡ EXTRACURRICULAR EXPERIENCE

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|
2003

Competitive Running Career
- 8+ years of varsity and Division I cross country, winter track, and spring track throughout high school and college.
- Year-round, daily training and travel to weekly competitions necessitated a dedicated and regimented lifestyle in order to succeed as a student-athlete
- Running remains a passion of mine and I enjoy training for ultra-marathons in my free time.
- This passion, work ethic and self-insight have carried over to all aspects of my life, including my career as a researcher.

📍 Earth

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1995

Music Production
- Writes, records, produces and performs original music.
- Instruments: keys, percussion, vocals, etc.
- Proficient in Logic Pro X Digital Audio Workstation (DAW).
- Experiments with generative AI.

📍 Earth

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