



BRIAN M SCHILDER, PHD

Passionately pursuing transdisciplinary research to advance human health and knowledge.



Postdoctoral Research Scientist

EDUCATION

2024



Imperial College London / The Alan Turing Institute

PhD: Clinical Medical Research; Computational Genomics & Machine Learning

📍 London, UK

Thesis: Multi-omic medicine: dissecting the cell type-specific and pleiotropic mechanisms underlying disease genomics at scale

- **Aim 1)** Dissect the multi-scale mechanisms (e.g. genes, pathways, cell types, phenotypes) underlying all rare disease genomics.
- **Aim 2)** Decompose the genome (all diseases and traits) into a unified latent genomic space to identify pleiotropy and disease trajectories at scale.
- **Aim 3)** Demonstrate and facilitate FAIR (Findable, Accessible, Interoperable, Reproducible) practices.

2017



The George Washington University / Georgetown University

MPhil: Human Evolution; Comparative Neuroscience & Genomics

📍 Washington, DC, USA

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

- **Aim 1)** Identify human-specific features of hippocampal subfield organization, adult neurogenesis, and their ecological correlates.
- **Aim 2)** Identify human-specific patterns of hippocampal subfield gene expression.
- **Aim 3)** Identify the genetic mechanisms mediating the evolution of human hippocampal neuroanatomy and gene expression.

2011



Brown University / Princeton University

ScB: Cognitive Neuroscience; Neurological Diseases & Disorders

📍 Providence, RI, USA

CONTACT

✉ brian_schilder [at] alumni.brown.edu

📞 US

+1 908-268-9859

📞 UK

+44 073-0653-7736

🔗 LinkedIn

🆔 ORCID

🔗 Google Scholar

/github GitHub

🐦 Twitter

🎥 YouTube

🌐 Personal Website

🌐 Lab Website

SUMMARY

📘 15+ years of research

📄 23 publications

📄 8 preprints

🔧 41 software packages

💻 11 databases & apps

📢 23 talks

🧑‍🏫 13+ years of teaching & team management

TABLE OF CONTENTS

🎓 Education

✓ Skills

✓ Expertise

📄 Publications

📄 Preprints

📄 Acknowledgements

📄 Reviewerships

📢 Internal talks

📢 Invited talks

📢 Conference talks

📢 Posters

💼 Experience

🧑‍🏫 Teaching

🔧 Packages

💻 Websites

💻 Databases

💰 Grants

🏆 Awards

🏛️ Affiliations

🔊 Data visualisation

🗺️ Extracurricular

📅 Updated Nov-05-2024

📦 Made with autoCV

✓ CORE SKILLS

• Research

15+ years of deep expertise in genomics, AI, evolutionary biology and biomedicine. Strategically fuses concepts and methods across multiple domains.

- **Publication record:** 23 publications, 8 preprints and 13 awarded grants.
- **Reproducibility:** Global leader in promoting and enabling reproducible scientific practices. Writes 100% reproducible manuscripts programmatically.
- **Bioinformatics:** Created 45 Python and R packages to address key challenges in biological research.
- **High-performance computing:** Highly parallelised analyses and AI model training (CPUs and GPUs).
- **Web development:** 6+ websites, web apps, and interactive reports.

• AI & Machine Learning

Proficient in developing and deploying AI/ML models (PyTorch, tensorflow, Keras, sklearn and H2O) to solve complex biological problems. Applied examples include:

- **Causal variant effect prediction:** Used functional impact predictions from DNA sequence models (DeepSEA, Basenji, IMPACT) to validate SNPs prioritised with Bayesian fine-mapping.
- **Foundation models:** Used transformer trained on >36M cells and protein sequence embeddings to uncover cell type-specific mechanisms of disease.
- **LLM knowledge extraction:** Developed framework to extract quantitative metrics of phenotype severity from GPT-4.
- **Disease genomics embeddings:** Developed VAE/graph models to reveal joint latent representation of genomic signatures across all diseases and phenotypes.
- **NLP:** Created a suite of proprietary Python packages for advanced topic modelling of the PubMed literature to provide business intelligence to the world's largest digital health, biotech, and pharma companies (as a consultant with 120/80 Group).
- **Tensor decomposition:** Applied multi-condition factorisation to efficiently discover neurodegeneration-relevant *trans-eQTLs*

• Project Management

Efficient management strategies to define objectives, track progress and coordinate diverse teams.

- **Documentation:** Defines objectives and tracks progress with GitHub Projects. Includes useful documentation in Issues, inline code and shareable reports.
- **Version control:** Extensive and daily use of GitHub, containers (*Docker, Singularity, virtual machines*), environments (*conda*) and pipelines (*Nextflow*).
- **Team management:** Led numerous collaborative research projects and supervised researchers at various career stages.

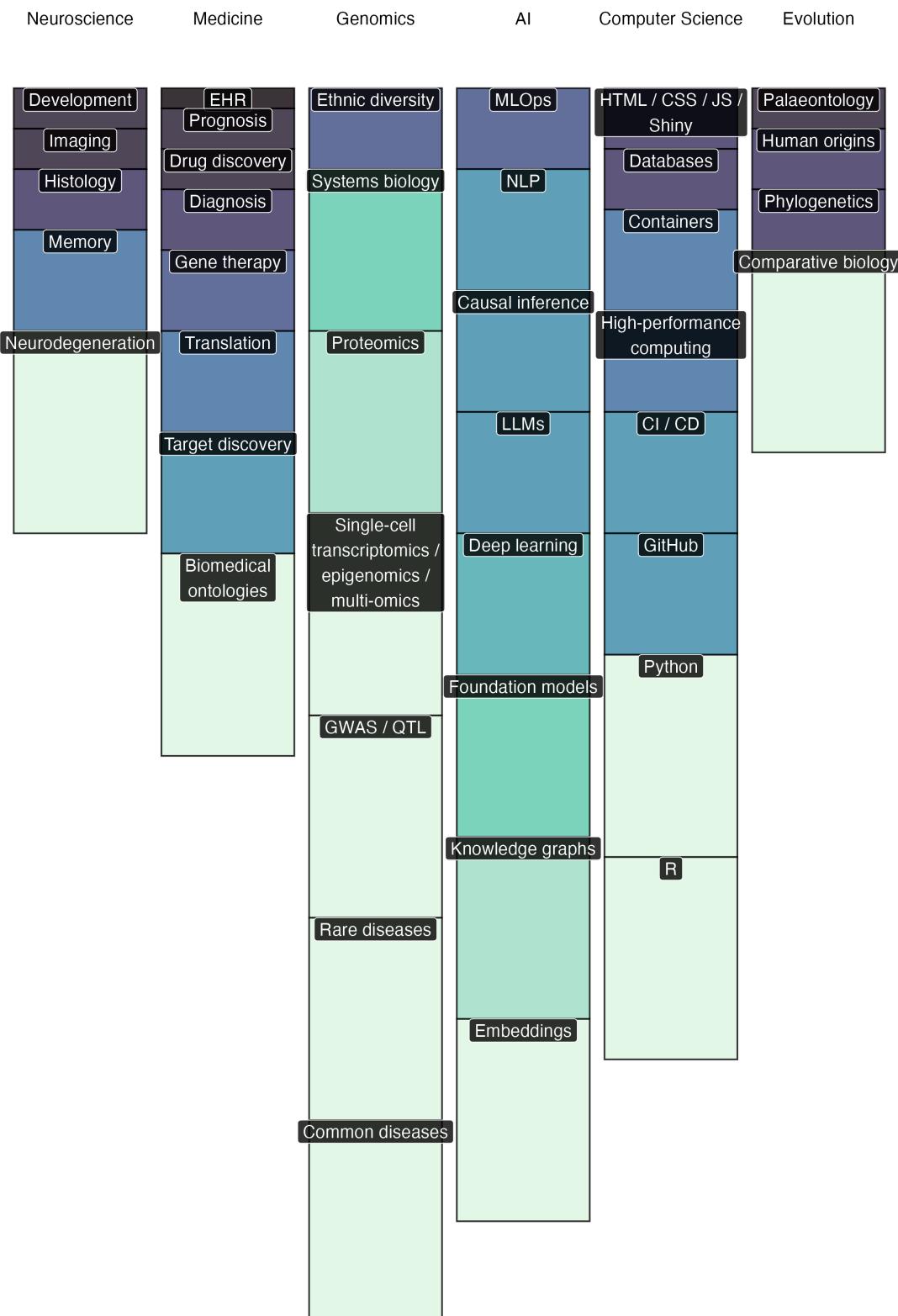
• Soft Skills

Advances science through effective problem formulation, collaboration and communication.

- **Problem formulation:** Rapid hypothesis generation, project design, and creative problem solving.
- **Collaboration:** Diverse and global collaborative networking.
- **Communication:** Clear and concise distillation of complex results to a variety of audiences. Presented 25 conference posters.

✓ EXPERTISE BY FIELD

The total height of each column represents my overall expertise in a given domain. The color and height of each rectangle are scaled to my relative level of expertise within each subdomain.





PUBLICATIONS

- 2023 • **rworkflows: automating reproducible practices for the R community**
Nature Communications (2023) 15(149); <https://doi.org/10.1038/s41467-023-44484-5>
BM Schilder, AE Murphy, NG Skene
▣ News
- Featured in *Nature Communications* Editors' Highlights
- 2023 • **Artificial intelligence for neurodegenerative experimental models**
Alzheimer's & Dementia (2023) <http://doi.org/10.1002/alz.13479>
SJ Marzi, **BM Schilder**, A Nott, C Sala Frigerio, S Willaime-Morawek, M Bucholc, DP Hanger, C James, PA Lewis, I Lourida, W Noble, F Rodriguez-Algarra, JA Sharif, M Tsalenchuk, LM Winchester, U Yaman, Z Yao, DEMON Network, JM Ranson, DJ Llewellyn
- 2023 • **Artificial intelligence for dementia genetics and omics**
Alzheimer's & Dementia (2023) <http://doi.org/10.1002/alz.13427>
C Bettencourt, NG Skene, S Bandres-Ciga, E Anderson, LM Winchester, IF Foote, J Schwartzenruber, JA Botia, M Nalls, A Singleton, **BM Schilder**, J Humphrey, SJ Marzi, CE Toomey, A Al Kleifat, EL Harshfield, V Garfield, C Sandor, S Keat, S Tamburin, C Sala Frigerio, I Lourida, DEMON Network, JM Ranson, DJ Llewellyn
- 2023 • **Artificial intelligence for dementia research methods optimization**
Alzheimer's & Dementia (2023) <http://doi.org/10.1002/alz.13441>
M Bucholc, C James, A Al 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 • **EpiCompare: R package for the comparison and quality control of epigenomic peak files**
Bioinformatics Advances (2023) 13(1):vbad049; <https://doi.org/10.1093/bioadv/vbad049>
S Choi, **BM Schilder**, L Abbasova, AE Murphy, NG Skene
- 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 Sneboer, 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-I Huang
- 2021 • **Genome-Wide Association Study of over 40,000 Bipolar Disorder Cases Provides Novel Biological Insights**
Nature Genetics (2021) 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.
[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)
- 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/10.1371/journal.pgen.1008549>
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
[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

- 2024 • **Zero-shot transfer learning of genomic disease signatures using single-cell foundation models**
arXiv (2024)
BM Schilder
- 2024 • **Harnessing generative AI to annotate the severity of all phenotypic abnormalities within the Human Phenotype Ontology**
medRxiv (2024) <https://doi.org/10.1101/2024.06.10.24308475>
KB Murphy, **BM Schilder**, NG Skene
- 2024 • **Navigating the Phenomic Landscape: systematic characterisation of the latent genomic space underlying all traits and diseases**
bioRxiv (2024) <http://dx.doi.org/10.13140/RG.2.2.12144.26880>
BM Schilder, NG Skene
- 2024 • **Chromatin interactions and active histone mark signatures underpin TBXT expression in metastatic lung cancer**
SSRN (2024) <https://ssrn.com/abstract=4965385>
RM Yaa, **BM Schilder**, RD Acemel, FC Wardle
- 2024 • **Integrative multi-omics analysis of glial signatures associated with accelerated cognitive decline in Alzheimer's disease**
bioRxiv (2024)
E Schneegans, N Fancy, V Chau, TKD Cheung, E Adair, M Papageorgopoulou, **BM Schilder**, PM Matthews, JS Jackson
- 2023 • **Fine-mapping genomic loci refines bipolar disorder risk genes**
medRxiv (2023) <https://www.medrxiv.org/content/10.1101/2024.02.12.24302716v1>
M Koromina, A Ravi, G Panagiotaropoulou, **BM Schilder**, ... S Ripke, T Raj, JRI Coleman, N Mullins
 News
- Currently under journal review
- 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
- 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

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

- 2024 • **[Unpublished article]**
BMJ Open (2024)
- 2023 • **Multi-region brain transcriptomes uncover two subtypes of aging individuals with differences in Alzheimer risk and the impact of APOE ϵ 4**
Neuron (2023) <https://doi.org/10.1101/2023.01.25.524961>
AJ Lee, Y Ma, L Yu, RJ Dawe, C McCabe, K Arfanakis, R Mayeux, DA Bennett, HU Klein, PL De Jager
- 2023 • **Summary statistics-based association test for identifying the pleiotropic effects with set of genetic variants**
Bioinformatics (2023) <https://doi.org/10.1093/bioinformatics/btad182>
D Bu, X Wang, Q Li
- 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 Hock
- 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 • **Partitioning the genetic architecture of amyotrophic lateral sclerosis**
Nature Neuroscience (2019) <https://doi.org/10.1101/505693>
IJ Broce,... RS Desikan

ⓘ INTERNAL TALKS

- 2022 • **Drug (re)discovery in the age of genomics: multi-omic strategies for identifying disease treatments**
Seminar
Drug Discovery and Trials Optimisation Working Group
Deep Dementia Phenotyping Network (DEMON)
- 2021 • **We've tagged a lot of cells, and sorted them in wells, some of the reads were double, So we looked into the trouble**
Seminar
UK Dementia Research Institute
Imperial College London
- 2021 • **Beyond GWAS: getting more out of genomic data in the age of machine learning**
Methods Optimisation Working Group
Deep Dementia Phenotyping Network (DEMON)
- 2021 • **Interspecies translation of single-cell transcriptomic signatures**
Seminar
Experimental Models Working Group
Deep Dementia Phenotyping Network (DEMON)
- 2020 • **Automated consensus fine-mapping of neurological disorder genomics**
Seminar
UK Dementia Research Institute (UK DRI)

ⓘ INVITED TALKS

- 2024 • **Navigating the Phenomic Landscape: Systematic characterisation of the latent genomic space underlying all traits and diseases**
Mondo Outreach Call

Monarch Initiative
- 2024 • **Harnessing AI to annotate the severity of all phenotypic abnormalities within the Human Phenotype Ontology**
Turing Omics Meeting
Omics Data Generation & Analysis Group
The Alan Turing Institute
- 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 phenotype: learning the latent genomic structure underlying thousands of diseases and traits**
Neuroepidemiology of Aging Webinar
RUSH Alzheimer's Disease Center (RADeC)
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

- 2023 • **rworkflows: taming the Wild West of R packages**
EuroBioc2023

Bioconductor
[45-minute workshop.](#)
- 2023 • **rworkflows: taming the Wild West of R packages**
BioC2023

Bioconductor
[10-minute talk within the Infrastructure Track.](#)
- 2023 • **Navigating the rare diseases landscape: A comprehensive approach to identify gene therapy targets based on cell type-phenotype associations**
Intelligent Systems For Molecular Biology / European Conference on Computational Biology (ISMB/ECCB)

International Society for Computational Biology (ISMB)
[20-minute talk within the Bio-Ontologies COSI Track.](#)
- 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

The Genetics Society
[6-minute talk](#)
- 2019 • **Parkinson's disease derived monocytes show alteration in the phago-lysosomal pathway**
American Society of Human Genetics (ASHG) Annual Meeting

American Society of Human Genetics (ASHG)
Co-contributor
- 2017 • **Comparative neuroanatomy of navigational maps in primates**
JB Johnston Club for Evolutionary Neuroscience

Society for Neuroscience (SfN)
Co-contributor

- 2016 • **The evolution of human hippocampal gene expression**
JB Johnston Club for Evolutionary Neuroscience

Society for Neuroscience (SfN)
 - 2015 • **The neurobiological effects of exercise on marmoset models of Multiple Sclerosis**
Marmoset Social

Society for Neuroscience (SfN)
 - 2015 • **The neurobiological effects of exercise on marmoset models of Multiple Sclerosis**
JB Johnston Club for Evolutionary Neuroscience

Society for Neuroscience (SfN)
-  **CONFERENCE POSTERS**
- 2024 • **Navigating the Phenomic Landscape: systematic characterisation of the latent genomic space underlying all traits and diseases**
Target to Patient (2024) <https://www.ebi.ac.uk/industry/targettopatient/>
BM Schilder, NG Skene
 - 2023 • **CUT&Tag recovers up to half of ENCODE ChIP-seq peaks**
Connectome (UK Dementia Research Institute) (2023) <https://ukdri.ac.uk/>
J Ismail, D Hu, L Abbasova, BM Schilder, A Nott, NG Skene, SJ Marzi
 - 2023 • **Navigating the rare diseases landscape: A comprehensive approach to identify gene therapy targets based on cell type-phenotype associations**
Intelligent Systems For Molecular Biology / European Conference on Computational Biology (ISMB/ECCB) (2023) <https://www.iscb.org/ismbeccb2023>
BM Schilder, KB Murphy, R Gordon-Smith, J Chapman, M Otani, NG Skene
 - 2023 • **Identification of cell type-specific gene targets underlying thousands of rare diseases and clinical phenotypes**
Genomics of Rare Diseases (2023) <https://coursesandconferences.wellcomeconnectingscience.org/event/genomics-of-rare-disease-20230424/>
BM Schilder, KB Murphy, R Gordon-Smith, J Chapman, M Otani, NG Skene
 - 2023 • **Statistical and Functional Fine-Mapping as a Powerful Tool to Unravel the Biological Etiology of Bipolar Disorder**
Biological Psychiatry (2023) 93(9):S18; <https://doi.org/10.1016/j.biopsych.2023.02.063>
M Koromina, A Ravi, BM Schilder, B Muller, J Coleman, T Raj
 - 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 comprehensive 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 Sneboer, 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) <https://www.abstractsonline.com/pp8/index.html#/4071/presentation/4471>
BM Schilder, BJ Bradley, CC Sherwood
- 2016 • **The molecular evolution of plasticity and the human hippocampus**
Society for Neuroscience (2016) <https://www.abstractsonline.com/pp8/index.html#/4071/presentation/4471>
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	<ul style="list-style-type: none"> ● Imitation & emulation in a novel box task <i>Association for Psychological Science</i> (2013) L Zimmerman, N Brito, C Mendelson, R Barr, E Renner, BM Schilder, F Subiaul
R Barr, F Subiaul, L Zimmerman, L Renner, BM Schilder, C Mendelson, L Golozub 2013	<ul style="list-style-type: none"> ● A study of imitation and working memory in 2- to 4-year-olds • Association for Psychological Science* (2013) 2013
2013	<ul style="list-style-type: none"> ● The impact of wealth on sharing preferences in children <i>Child Development Society</i> (2013) J Miller, BM Schilder, L Peizer, F Subiaul

RESEARCH EXPERIENCE

- I 2024	<ul style="list-style-type: none"> ● Postdoctoral Research Scientist Cold Spring Harbor Laboratory (Quantitative Biology) Cold Spring Harbor, NY, USA • Advancing deep learning applications in genomics and biomedicine in the laboratory of Dr. Peter Koo. • Developing a genomic foundation model to map complex genome-phenome relationships and make highly accurate, personalized disease risk predictions.
- I 2019	<ul style="list-style-type: none"> ● Lead Data Scientist 120/80 Group New York, NY, USA • Offers data-driven consultation services to a wide portfolio of high-profile digital healthcare, pharmaceutical and biotech companies. • Developed a suite of proprietary softwares to extract customised business intelligence from the published literature to generate customised and interpretable reports to clients. • Provides clients guidance on strategic AI implementation, data analysis, publication and transparency.
2020 I 2018	<ul style="list-style-type: none"> ● 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 I 2017	<ul style="list-style-type: none"> ● 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	<ul style="list-style-type: none"> ● 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 I 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 (<i>Homo</i> , <i>Paranthropus</i>). • As Project Leader, investigated the running biomechanics of local Daasanach tribespeople while mentoring undergraduate students.	
2013 I 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 I 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 (<i>H. heidelbergensis</i> , <i>H. neanderthalensis</i>) 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 (<i>H. heidelbergensis</i>) and Sima de las Palomas (<i>H. neanderthalensis</i>) 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 I 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

-
I
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 genome-wide GWAS summary statistics'

2020
I
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
I
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 I 2013	Teaching Assistant The George Washington University (Department of Anthropology) • 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.	📍 Washington, DC, USA
2013 I 2012	Research Mentor The George Washington University (Department of Psychology) • Mentored students and affiliated projects: • Anushka Gokhale (BSc): 'Infants' Social Assessment of Characters Through Eye Gaze'	📍 Washington, DC, USA
2013 I 2011	Lab Protocol Trainer The George Washington University (Department of Anthropology) • Trained undergraduate, graduate, and post-doctoral researchers in Social Cognition Lab and Lab for Evolutionary Neuroscience in a variety of methodological research protocols.	📍 Washington, DC, USA

🔧 SOFTWARE PACKAGES

1. **MSTExplorer** 
Multi-Scale Targets Explorer: Systematically identify, prioritise and visualise cell-type-specific gene therapy targets across the phenotype.
[🔗](https://github.com/neurogenomics/MSTExplorer) [📄](https://doi.org/10.1101/2023.02.13.23285820)
2. **HPOExplorer** 
Import, annotate and visualise the 18k+ hierarchically structured clinical phenotypes across the Human Phenotype Ontology.
[🔗](https://github.com/neurogenomics/HPOExplorer) [📄](https://doi.org/10.1101/2023.02.13.23285820)
3. **KGExplorer** 
Query, construct, and analyse large-scale biomedical knowledge graphs and ontologies.
[🔗](https://github.com/neurogenomics/KGExplorer)
4. **autoCV** 
Automatically generate and style your CV from tables.
[🔗](https://github.com/bschilder/autoCV)
5. **anndataR** 
Bring the power and flexibility of AnnData to the R ecosystem, allowing you to effortlessly manipulate and analyze your single-cell data.
[🔗](https://github.com/scverse/anndataR)
6. **gptPhD** 
Query Large Language Models for the purposes of systematically extracting biomedical knowledge.
[🔗](https://github.com/neurogenomics/gptPhD)
7. **ThreeWayTest** 
Summary statistics-based association test for identifying the pleiotropic effects with set of genetic variants.
[🔗](https://github.com/bschilder/ThreeWayTest)
8. **SCAVENGE** 
Variant to function mapping at single-cell resolution through network propagation.
[🔗](https://github.com/sankaranlab/SCAVENGE) [📄](https://doi.org/10.1038/s41587-022-01341-y)
9. **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)

11. ● **PeakyFinders** 
R package for mining, calling, and importing epigenomic peaks.
🔗 <https://github.com/neurogenomics/PeakyFinders>
12. ● **graphiti** 
Extract colour palettes from graffiti artworks.
🔗 <https://github.com/bschilder/graphiti>
13. ● **SkillNet** 
Creates user-specific contribution networks from GitHub Organization repositories.
🔗 <https://github.com/neurogenomics/SkillNet>
14. ● **phenoRx** 
Make cell type-specific predictions for patients based on clinical phenotypes and/or risk genes.
🔗 <https://github.com/neurogenomics/phenoRx>
15. ● **phenomix** 
R package for the exploration and analysis of many genotype-phenotype datasets at once.
🔗 <https://github.com/neurogenomics/phenomix>
16. ● **MAGMA.Celltyping** 
Identify cell types underlying the associations found in GWAS summary statistics.
🔗 https://github.com/neurogenomics/MAGMA_Celltyping
17. ● **EWCE** 
Expression Weighted Celltype Enrichment.
🔗 <https://github.com/NathanSkene/EWCE>
18. ● **EpiCompare** 
R package for QC and benchmarking epigenetic datasets.
🔗 <https://github.com/neurogenomics/EpiCompare>
📄 <https://doi.org/10.1101/2022.07.22.501149>
19. ● **orthogene** 
Interspecies gene mapping.
🔗 <https://github.com/neurogenomics/orthogene>
20. ● **MungeSumstats** 
Standardise the format of summary statistics from GWAS.
🔗 <https://github.com/neurogenomics/MungeSumstats>
📄 <https://doi.org/10.1093/bioinformatics/btab665>
21. ● **scNLP** 
Tools for applying natural language processing (NLP) techniques to single-cell (sc) omics data.
🔗 <https://github.com/neurogenomics/scNLP>
22. ● **scKirby** 
Automated ingestion and conversion of various single-cell data formats.
🔗 <https://github.com/neurogenomics/scKirby>
23. ● **geneshotR** 
R package for querying and processing results from Geneshot.
🔗 <https://github.com/bschilder/geneshotR>
24. ● **templateR** 
Self-updating template for developing R packages.
🔗 <https://github.com/neurogenomics/templateR>
📄 <https://doi.org/10.21203/rs.3.rs-2399015/v1>
25. ● **echoverseTemplate** 
Self-updating template for creating echoverse R packages.
🔗 <https://github.com/RajLabMSSM/echoverseTemplate/>
📄 <https://doi.org/10.1093/bioinformatics/btab658>
26. ● **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>

27. ● **echodata** 
Examples of fine-mapped GWAS summary statistics, data formatting functions, and API access to the echolocateR Fine-mapping Portal.
↳ <https://github.com/RajLabMSSM/echodata>
📄 <https://doi.org/10.1093/bioinformatics/btab658>
28. ● **echoannot** 
Functions for annotating genomic data with annotations and epigenomic data.
↳ <https://github.com/RajLabMSSM/echoannot>
📄 <https://doi.org/10.1093/bioinformatics/btab658>
29. ● **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>
30. ● **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>
31. ● **echotabix** 
Tabix indexing and querying.
↳ <https://github.com/RajLabMSSM/echotabix>
📄 <https://doi.org/10.1093/bioinformatics/btab658>
32. ● **echoLD** 
LD downloading and processing.
↳ <https://github.com/RajLabMSSM/echoLD>
📄 <https://doi.org/10.1093/bioinformatics/btab658>
33. ● **echofinemap** 
Statistical and functional fine-mapping functions.
↳ <https://github.com/RajLabMSSM/echofinemap>
📄 <https://doi.org/10.1093/bioinformatics/btab658>
34. ● **echodeps** 
Creates interactive dependency networks for R packages.
↳ <https://github.com/RajLabMSSM/echodeps>
📄 <https://doi.org/10.1093/bioinformatics/btab658>
35. ● **echogithub** 
Access and process metadata from GitHub.
↳ <https://github.com/RajLabMSSM/echogithub>
📄 <https://doi.org/10.1093/bioinformatics/btab658>
36. ● **devoptera** 
Practical tools for R developers.
↳ <https://github.com/RajLabMSSM/devoptera>
📄 <https://doi.org/10.1093/bioinformatics/btab658>
37. ● **downloadR** 
Single- and multi-threaded downloading functions.
↳ <https://github.com/RajLabMSSM/downloadR>
📄 <https://doi.org/10.1093/bioinformatics/btab658>
38. ● **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>
39. ● **TopicModeler** 
Proprietary Python package to run advanced topic modeling on text corpuses.

40. ● **LinkReporter** 
Proprietary Python package to extract job postings and company employee listings from LinkedIn and generate interactive business intelligence reports.
41. ● **PubReporter** 
Proprietary Python package to extract relevant scientific literature, gather citations, and generate 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** 🎨 Python JS HTML CSS
 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** 🎨 Python JS HTML CSS
 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** HTML CSS JS
 ↗ <https://github.com/bmschilder/BMSchilder>
 ↗ <https://bmschilder.github.io/BMSchilder>
2. **Official Raj Lab Website** HTML CSS JS
 ↗ https://github.com/RajLabMSSM/RajLab_website
 ↗ <http://www.rajlab.org>

\$ GRANTS

Total (all grants): \$2,949,872
Total (as primary applicant): \$311,382

- 2023 **EuroBioc2023 Scholarship, Bioconductor**
Project: 'rworkflows: taming the Wild West of R packages'
 ↗ **News**
 - Awarded to support attending the [EuroBioc2023 meeting](#).
 • **Role:** Primary applicant • **Amount:** \$250
 • **PI:** BM Schilder
- 2023 **BioC2023 Scholarship, Bioconductor**
Project: 'rworkflows: taming the Wild West of R packages'
 ↗ **News**
 - Awarded to support attending the [BioC2023 meeting](#). Additionally included free lodging.
 • **Role:** Primary applicant • **Amount:** \$1500
 • **PI:** BM Schilder
- 2023 **Junior Scientist Conference Grant, The Genetics Society**
Project: 'Identification of cell type-specific gene targets underlying thousands of rare diseases and subtraits'
 • **Role:** Primary applicant • **Amount:** £750
 • **PI:** BM Schilder
- 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 I 2022	Turing Community Award, Alan Turing Institute Project: 'Multi-omic medicine: dissecting the cell-type-specific molecular mechanisms underlying neurodegenerative disease genomics'	<ul style="list-style-type: none"> • Role: Primary applicant • PI: BM Schilder <ul style="list-style-type: none"> • Amount: £1,500
2022	National Institutes of Health Project: 'Statistical and functional fine-mapping of bipolar disorder genetic risk loci'	<ul style="list-style-type: none"> • 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'	<ul style="list-style-type: none"> • Role: Co-applicant • PI: D Hu, NG Skene <ul style="list-style-type: none"> • Amount: £12,790
2020	National Institutes of Health Project: "Cognitive Systems Analysis of Alzheimer's Disease Genetic and Phenotypic Data"	<ul style="list-style-type: none"> • Role: Co-applicant • PI: T Raj, D Knowles <ul style="list-style-type: none"> • Amount: \$2,523,431
2024 I 2020	UK Dementia Research Institute Project: 'UK DRI at Imperial Distinguished Studentship'	<ul style="list-style-type: none"> • Role: Primary applicant • PI: BM Schilder <ul style="list-style-type: none"> • Amount: £217,000
2019 I 2017	The Michael J. Fox Foundation Project: "The Role of Peripheral Myeloid Cells in Parkinson's Disease"	<ul style="list-style-type: none"> • Role: Fundee • PI: T Raj
2020 I 2017	The Michael J. Fox Foundation Project: 'Functional Fine-Mapping of LRRK2 Locus'	<ul style="list-style-type: none"> • 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'	<ul style="list-style-type: none"> • Role: Primary applicant • PI: BM Schilder <ul style="list-style-type: none"> • Amount: \$31,543
2017	Wenner-Gren Project: 'The evolution of the hippocampus and adult neurogenesis: insights into the origins of human memory'	<ul style="list-style-type: none"> • Role: Primary applicant • PI: BM Schilder <ul style="list-style-type: none"> • Amount: \$19,512
2016	Leakey Foundation Project: 'The evolution of the hippocampus and adult neurogenesis: Novel insights into the origins of human memory'	<ul style="list-style-type: none"> • Role: Primary applicant • PI: BM Schilder <ul style="list-style-type: none"> • Amount: \$15,000
2016	COSMOS Club Project: 'The evolution of adult neurogenesis across primates'	<ul style="list-style-type: none"> • Role: Primary applicant • PI: BM Schilder <ul style="list-style-type: none"> • Amount: \$3,250

AWARDS

- 2023 • **Prize for Computational Reproducibility in Dementia Research, UK Dementia Research Institute**
Project: 'rworkflows: taming the Wild West of R packages'
 News
- Awarded honourable mention.
- 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 • **Poster Competition, Rising Scientist Day**
Project: 'Systematic quantification of animal model viability across human diseases'
 News
- Awarded prize for research poster competition.
- 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



- Fellow



- Member



- Society of Technological Advancement Member



- Synapse Working Group
- Informatics Working Group



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



- Turing Enrichment Scheme
- Turing-Roche Strategic Partnership
- Turing Omics Data Generation & Analysis Interest Group
- Turing Clinical AI Interest Group



- Bipolar Disorder Working Group



- Chair of the Bioconductor Cloud Methods Working Group
- Lead of the Bioconductor GitHub Actions Subgroup



IMPERIAL
ENTREPRENEURS

- Member

DATA VISUALISATION / ARTWORK PORTFOLIO

2022	echoverse Dependency Graph	London, UK
	<ul style="list-style-type: none">• Interactive graph showing the dependency structure of all packages within the echoverse suite.	
2020	Hex stickers	London, UK
	<ul style="list-style-type: none">• All hex stickers for R packages I've helped develop.	
2023	3D Human Phenotype Ontology	London, UK
	<ul style="list-style-type: none">• 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
	<ul style="list-style-type: none">• Network of systematically prioritised gene therapy targets for rare diseases• Associated preprint	
2023	Curriculum Vitae Connexa	London, UK
	<ul style="list-style-type: none">• Term co-occurrence network generated by analysing all data that went into this CV.	
2021	Experiments with Generative AI	London, UK
	<ul style="list-style-type: none">• 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
	<ul style="list-style-type: none">• 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	Pacophage	London, UK
	<ul style="list-style-type: none">• Colocalised genetic loci ...but shaped as Pac-Man!• Associated study	

2020	Circos	 London, UK
	<ul style="list-style-type: none"> • Colocalised genetic loci across a variety of neurological disease GWAS and cell-type-specific QTLs. • Associated study 	
2019	Wildfire Circle	 New York, NY, USA
	<ul style="list-style-type: none"> • 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
	<ul style="list-style-type: none"> • 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
	<ul style="list-style-type: none"> • 3D model of my brain generated from MRI scans. 	

EXTRACURRICULAR EXPERIENCE

2003	Competitive Running Career	 Earth
	<ul style="list-style-type: none"> • 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. 	
1995	Music Production	 Earth
	<ul style="list-style-type: none"> • 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. 	