# BRIAN M SCHILDER, PHD

**Passionately pursuing transdisciplinary research to advance human health and knowledge.**

Cold Spring Harbor Laboratory

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 phenome (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
Twitter
YouTube
Personal Website
Lab Website


## SUMMARY

16+ years of research
25 publications
7 preprints
41 software packages
11 databases & apps
24 talks
14+ years of teaching & team management

## TABLE OF CONTENTS



*Updated Sep-09-2025*

*Made with autoCV*

## CORE SKILLS

### Research

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

- **Publication record**: 25 publications, 7 preprints and 14 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.

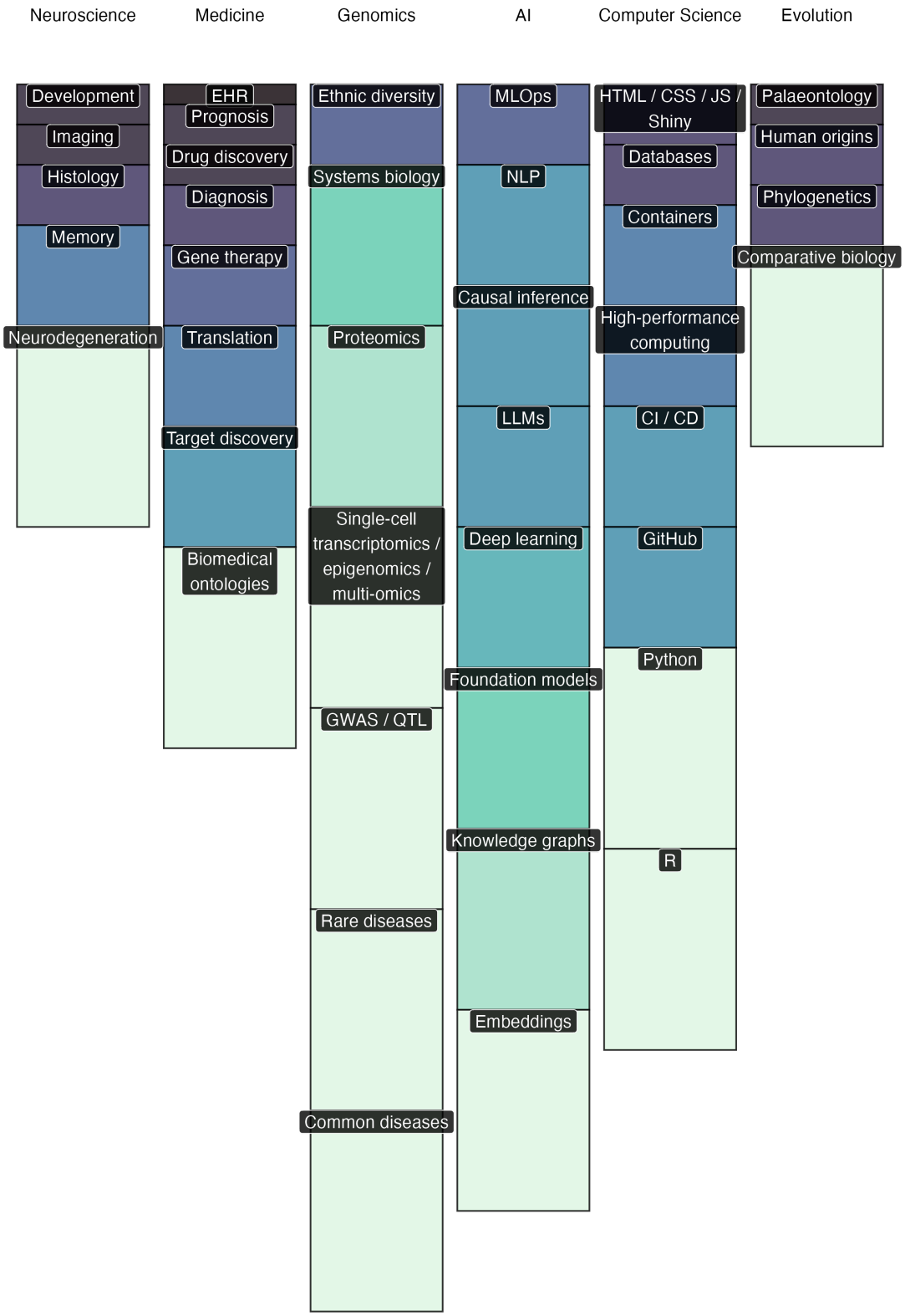
### Soft Skills

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

2025 **CUT&Tag recovers up to half of ENCODE ChIP-seq peaks**
*Nature Communications* (2025) (16):2993; https://doi.org/10.1038/s41467-025-58137-2
L Abbasova, P Urbanaviciute, D Hu, JN Ismail, **BM Schilder**, A Nott, NG Skene, SJ Marzi

2025 **Chromatin Interaction and Histone Mark Signatures Associated With TBXT Expression in Metastatic Lung Cancer**
*Genes Chromosomes Cancer,* (2025) (64):e70041; https://doi.org/10.1002/gcc.70041
RM Yaa, **BM Schilder**, RD Acemel, FC Wardle

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 Schwartzentruber, 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 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-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

2022 **Mondo: Integrating Disease Terminology Across Communities**
*medRxiv* (2022) https://doi.org/10.1101/2022.04.13.22273750
NA Vasilevsky, … **BM Schilder**, …,PN Robinson, CJ Mungall, A Hamosh, MA Haendel

2025 **Cell type-specific contextualisation of the human phenome: towards the systematic treatment of all rare diseases**
*medRxiv* (2025) https://doi.org/10.1101/2023.02.13.23285820
**BM Schilder**, KB Murphy, H Dash, Y Zhang, R Gordon-Smith, J Chapman, M Otani, NG Skene

2025 **Gene expression patterns of the developing human face at single cell resolution reveal cell type contributions to normal facial variation and disease risk**
*bioRxiv* (2025) https://www.biorxiv.org/content/10.1101/2025.01.18.633396v1
N Khouri-Farah, EW Winchester, **BM Schilder**, K Robinson, SW Curtis, NM Skene, E Leslie-Clarkson, J Cotney

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 **Integrative multi-omics analysis of glial signatures associated with accelerated cognitive decline in Alzheimer's disease**
*bioRxiv* (2024) https://doi.org/10.1101/2024.08.27.24312641
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

## 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):13-Jan; 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

2025 **Mixture of Experts Enable Efficient and Effective Protein Understanding and Design**
*Nature Methods* (2025)
N Sun, S Zou, T Tao, S Mahbub, D Li, Y Zhuang, H Wang, X Cheng, L Song, EP Xing

2025 **Compressing the collective knowledge of ESM into a single protein language model**
*Nature Methods* (2025)
T Dinh, S Jang, N Zaitlen, V Ntranos

2025 **Large language models identify causal genes in complex trait GWAS**
*Nature Communications* (2025)
SS Shringarpure, W Wang, S Karagounis, X Wang, AC Reisetter, A Auton, AA Khan

2025 **ENCORE: a practical implementation to improve reproducibility and transparency of computational research**
*Nature Communications* (2025)
AHC van Kampen, U Mahamune, A Jongejan, BDC van Schaik, D Balashova, D Lashgari, M Pras-Raves, EJM Wever, AD Dane, R García-Valiente, PD Moerland

2025 **L2G: Repurposing Language Models for Genomics Tasks**
*ISMB/ECCB* (2025) https://doi.org/10.1101/2024.12.09.627422
W Cheng, J Shen, M Khodak, J Ma, A Talwalkar

2025 **Enhancing regulatory variant prioritization via long-range DNA sequences and multi-task learning**
*The American Journal of Human Genetics* (2025)
Y Takahashi, QS Wang, T Hasegawa, H Namkoong, F Inoue, K Fukunaga, S Imoto, S Miyano, Y Okada, Japan COVID-19 Task Force

2024 **Deciphering the tissue-specific functional effect of Alzheimer risk SNPs with deep genome annotation**
*BioData Mining* (2024) https://doi.org/10.1186/s13040-024-00400-1
PV Pugalenthi, B He, L Xie, K Nho, AJ Saykin, J Yan

2024 **A genetic and transcriptomic assessment of the KTN1 gene in Parkinson's disease risk**
*Neurobiology of Aging* (2024) https://doi.org/10.1016/j.neurobiolaging.2023.11.001
A Moore, PW Crea, M Makarious, S Bandres-Ciga, C Blauwendraat, M Diez-Fairen

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 APOEε4**
*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.iclibezp1.cc.ic.ac.uk/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 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 **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 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

2025 **Evaluating the sensitivity of genomic foundation models to interindividual variation using biobank-scale personalized genomes**
AI x Bio

Wellcome Genome Campus

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 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) 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 **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

**Postdoctoral Research Scientist**
Cold Spring Harbor Laboratory (Simons Center for 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.

- | 2019

**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 | 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 | 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 | 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 | 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

- | 2020

**Research Mentor**
Imperial College London (Department of Brain Sciences / Department of Life Sciences) London, UK
- Mentored students and affiliated projects:
- Kitty Murphy (PhD): 'Evolutionary pressures on cell types: leveraging species differences to gain insight into neurodegenerative disease risk'
- Sheen Lei (BSc): 'Benchmarking cell-type-specific enrichment of genome-wide disease signatures'
- Ted Reese (MSc): 'Computational cell-type annotation of single-cell epigenomics data'
- Xindong Sun (MSc): 'Benchmark of Targeted insertion of promoters sequencing (TIP-seq) on histone modification H3K27ac and H3K27me3 in K562 cell line'
- Shuhan Shen (MSc): 'Evaluation and optimisation of methods for identifying the cell types underlying genetic disease signatures'
- Lusheng Li (MSc): 'Genetic identification of cell types underlying mammalian phenotypes'
- Sera Choi (BSc): 'EpiCompare: R package for QC and benchmarking epigenetic datasets'
- Emilie Cottard (MSc) & Will Lunt (BSc): 'A meta-analysis of selective cell-type vulnerability in Parkinson's Disease neuropathology'
- Jai Chapman (BSc): 'Expression Weighted Cell Type Enrichment as a Tool for Identifying Cell Types Underlying Rare Disease Phenotypes'
- Bobby Gordon-Smith (MSc): 'Identification of cell types involved in rare disease-associated human phenotypes'
- Leyla Abbasova (MSc): 'Analysis and optimisation of CUT&Tag for epigenomic profiling of the brain'
- Barney Hill (BSc): 'Identification of cell-types associated with latent factors inferred from phenome-wide GWAS summary statistics'

2020 | 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.

**MSTExplorer**
Multi-Scale Targets Explorer: Systematically identify, prioritise and visualise cell-type-specific gene therapy targets across the phenome.
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

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

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 echolocatoR 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**
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): $3,049,872**
**Total (as primary applicant): $311,382**

---

2025 | 2024

**Cancer Center Pilot Awards Program,**
**Cold Spring Harbor Laboratory Cancer Center**
**Project**: 'Exploiting interpretable AI to uncover the genetic basis of cellular reprogramming in cancer'
- **Role**: Co-applicant
- **PI**: DM McCandlish
- **Amount**: $100,000

2023

**EuroBioc2023 Scholarship,**
**Bioconductor**
**Project**: 'rworkflows: taming the Wild West of R packages'
**News**
- Awarded to support attending the EuroBioc2023 meeting.

- **Role**: Primary applicant
- **PI**: BM Schilder
- **Amount**: $250

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
- **PI**: BM Schilder
- **Amount**: $1,500

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
- **PI**: BM Schilder
- **Amount**: £750

2023

**Imperial UK Research Institute Impact Acceleration Account,**
**Imperial College London**
**Project**: 'Creating commercial kit solutions for single cell epigenetic profiling of histone marks and transcription factors'
- **Role**: Co-applicant
- **PI**: NG Skene
- **Amount**: £80,000

2024 | 2022

**Turing Community Award,**
**Alan Turing Institute**
**Project**: 'Multi-omic medicine: dissecting the cell-type-specific molecular mechanisms underlying neurodegenerative disease genomics'
- **Role**: Primary applicant
- **PI**: BM Schilder
- **Amount**: £1,500

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

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

NHS England

- Member

SOTA

- Society of Technological Advancement Member

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
- Turing Omics Data Generation & Analysis Interest Group
- Turing Clinical AI Interest Group

PGC
Psychiatric Genomics Consortium

- Bipolar Disorder Working Group

Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

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


• Member

## DATA VISUALISATION / ARTWORK PORTFOLIO

2022 — **echoverse Dependency Graph**

London, UK

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

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

-
|
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

.

-
|
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

.