



# BRIAN M. SCHILDER

Passionately pursuing transdisciplinary research to advance human health and knowledge.

**Imperial College London**  
**PhD Student**  
**MPhil, ScB**

## EDUCATION

2024



**Imperial College London / UK Dementia Research Institute /  
The Alan Turing Institute**  
**PhD:** Clinical Medical Research; Computational Neurogenomics 📍 [London, UK](#)

**Supervisors:** Nathan G. Skene, PhD; Paul M. Matthews, PhD

**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 Paleobiology; Evolutionary Neuroscience & Genomics  
📍 [Washington, DC, USA](#)

**Supervisors:** Chet C. Sherwood, PhD; Brenda J. Bradley, PhD

**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](#)

**Supervisors:** Sheila E. Blumstein, PhD; David L. Sheinberg, PhD

## CONTACT

✉ [brian\\_schilder \[at\] alumni.brown.edu](mailto: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

📅 **15+ years of research**  
 📄 **23 publications**  
 📄 **4 preprints**  
 🔧 **41 software packages**  
 🗄 **11 databases & apps**  
 🗣 **22 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 May-20-2024](#)  
 📄 [Made with autoCV](#)

## ✓ CORE SKILLS



### Research

**15+** years of deep expertise in a genomics, AI, evolutionary biology and biomedicine. Seamlessly fuses ideas and methods across multiple domains.

- **Publication record:** **23** publications, **4** 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 prediction:** Used functional impact predictions from DNA sequence models (DeepSEA, Basenji, IMPACT) to validate SNPs prioritised with Bayesian fine-mapping. 
- **Single-cell omics:** Used autoencoders that take RNA expression and ESM protein embeddings (SATURN, CellBLAST) to integrate and embed scRNA-seq atlases from multiple species.
- **LLM knowledge extraction:** Developed a framework to extract quantitative metrics of phenotype severity from GPT-4. 
- **Disease genomics embeddings:** Developed VAE- and graph-based dimensionality reduction models to create a joint latent representation of genome-wide signatures from all known diseases and phenotypes.
- **Topic modeling:** Created a suite of proprietary Python packages for NLP-based 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](#)).
- **Collaborative AI:** Uses generative AI assistants (GitHub Copilot) to accelerate and augment coding.

### 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](#).

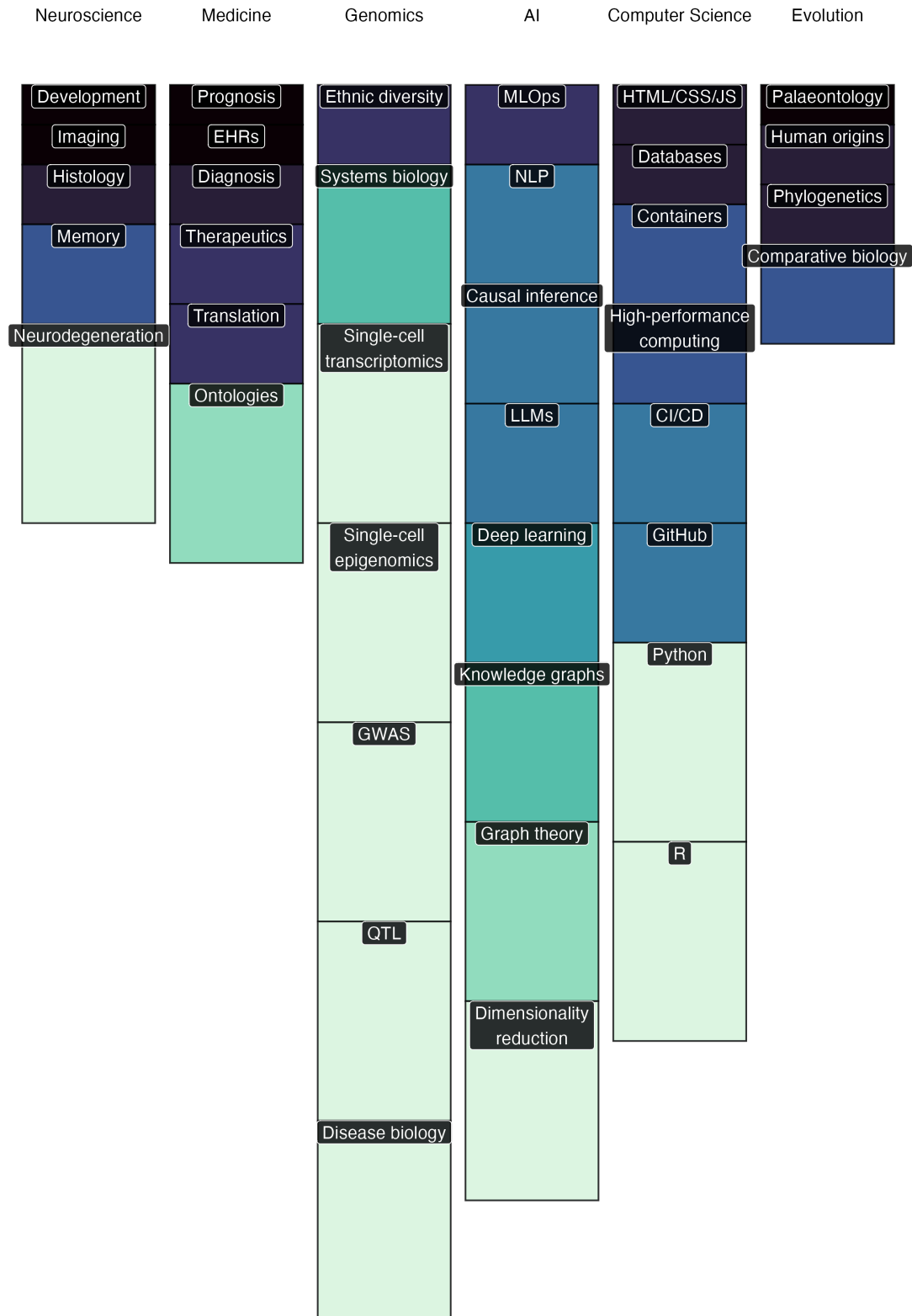
### Soft skills

Advances science through effective problem formulation, collaboration and communication.

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

## ✓ EXPERTISE BY FIELD






The total height of each column represents overall expertise in a given domain. Rectangles are scaled to the 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 Schwartzentruber, JA Botia, M Nalls, A Singleton, **BM Schilder**, J Humphrey, SJ Marzi, CE Toomey, AAI 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, AAI Kleifat, 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/10.1101/499509>  
 S Ramdhani, E Navarro, E Udine, AG Efthymiou, **BM Schilder**, M Parks, A Goate, T Raj
- 2019 • **Evolutionary shifts dramatically reorganized the human hippocampal complex**  
*Journal of Comparative Neurology* (2019) 528(17):3143-3170; <https://doi.org/10.1002/cne.24822>  
**BM Schilder**, HM Petry, PR Hof
- 2019 • **FAIRshake: Toolkit to Evaluate the Findability, Accessibility, Interoperability, and Reusability of Research Digital Resources**  
*Cell Systems* (2019) 9; <https://doi.org/10.1016/j.cels.2019.09.011>  
 D Clarke, L Wang, A Jones, M Wojciechowicz, D Torre, K Jagodnik, S Jenkins, P McQuilton, Z Flamholz, M Silverstein, **BM Schilder**...A Ma'ayan  
 **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 • **Harnessing AI to annotate the severity of all phenotypic abnormalities within the Human Phenotype Ontology**  
*medRxiv* (2024)  
 KB Murphy, **BM Schilder**, NG Skene
- 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 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 • **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 (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

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/ismbecb2023>  
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 Sneenboer, 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 Hambricht, 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

- |  
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	<b>Bioinformatician II</b> Icahn School of Medicine at Mount Sinai (Department of Pharmacological Sciences)  <a href="#">New York, NY, USA</a> <ul style="list-style-type: none"> <li>• Conducted computational systems biology research. Integrated and analyzed large-scale genomic and biomedical data (e.g. Python, R, JavaScript).</li> <li>• Developed evolutionary algorithm to optimize gene network kinase regulator prediction (eXpression2Kinases).</li> <li>• Developed and deployed computational tools, software, databases and web applications for basic and clinical research, resulting in 3 peer-reviewed publications.</li> </ul>
2017	<b>Participant</b> Technische Universität Dresden / eMed (Summer School in Systems Medicine)  <a href="#">Frauenchiemsee, Germany</a> <ul style="list-style-type: none"> <li>• Attended lectures and extended skills in extraction and analysis of big data from biomedical and neurogenomic resources.</li> <li>• Developed, performed and wrote manuscript for collaborative bioinformatics research project in less than one week.</li> </ul>
2016	<b>Participant</b> Icahn School of Medicine at Mount Sinai (Scientific Computing & Data Science)  <a href="#">New York, NY, USA</a> <ul style="list-style-type: none"> <li>• Intensive summer school in high-performance computing, coding, genome database utilization and bioinformatics methods including transcriptomics and genetic association testing.</li> </ul>
2017   2014	<b>Collaborator</b> Trinity University / Southwestern National Primate Research Center (Department of Neuroscience)  <a href="#">San Antonio, TX, USA</a> <ul style="list-style-type: none"> <li>• Investigated the neurobiological mechanisms underlying the ameliorating effects of exercise on relapse-remitting Multiple Sclerosis.</li> </ul>
2014	<b>Teaching Assistant / Project Leader</b> The George Washington University / Rutgers University (Department of Anthropology)  <a href="#">Ileret, Kenya</a> <ul style="list-style-type: none"> <li>• Served as Teaching Assistant while excavating Lower Paleolithic hominin sites (Homo, Paranthropus).</li> <li>• As Project Leader, investigated the running biomechanics of local Daasanach tribespeople while mentoring undergraduate students.</li> </ul>
2013   2011	<b>Research Assistant</b> The George Washington University (Department of Anthropology)  <a href="#">Washington, DC, USA</a> <ul style="list-style-type: none"> <li>• Performed dissection, histology, microscopy and quantitative stereology in post-mortem primate brain tissues.</li> <li>• Trained junior and senior personnel on lab protocols.</li> </ul>
2013   2011	<b>Senior Lab Manager</b> The George Washington University (Department of Speech, Language & Hearing Sciences)  <a href="#">Washington, DC, USA</a> <ul style="list-style-type: none"> <li>• 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.</li> </ul>
2012	<b>Volunteer Researcher</b> University of Winnipeg / University of Belgrade (Department of Anthropology / Department of Archaeology)  <a href="#">Sićevo, Serbia</a> <ul style="list-style-type: none"> <li>• Excavated Paleolithic fossils and tools (H. heidelbergensis, H. neanderthalensis) at Mala Balanica, Velika Balanica, and Pešturina sites.</li> </ul>
2011	<b>Volunteer Researcher</b> Universidad de Murcia (Department of Zoology & Physical Anthropology)  <a href="#">Murcia, Spain</a> <ul style="list-style-type: none"> <li>• Excavated Paleolithic fossils and tools from Cueva Negra (H. heidelbergensis) and Sima de las Palomas (H. neanderthalensis) with an international research team.</li> </ul>
2011	<b>Volunteer Research Intern</b> American Museum of Natural History (Division of Anthropology)  <a href="#">New York, NY, USA</a> <ul style="list-style-type: none"> <li>• Contributed to paleoanthropological research on primate fossils using 3D morphometry imaging equipment including Minolta, Microscribe and CT.</li> </ul>
2010	<b>Paid Research Intern</b> Princeton University (Princeton Neuroscience Institute)  <a href="#">Princeton, NJ, USA</a> <ul style="list-style-type: none"> <li>• Investigated the neural basis of decision-making in humans.</li> <li>• Recruited participants, recorded EEG and analyzed data in MATLAB.</li> </ul>

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](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 for 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://github.com/neurogenomics/rare_disease_celltyping_apps)  
[https://neurogenomics.github.io/rare\\_disease\\_celltyping\\_apps/home](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://github.com/RajLabMSSM/PD_omics_review)  
[https://rajlabmssm.github.io/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](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://github.com/RajLabMSSM/Fine_Mapping_Shiny)  
[https://rajlab.shinyapps.io/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://github.com/RajLabMSSM/Tensor_myeloid)  
[https://rajlab.shinyapps.io/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://github.com/bschilder/Hippo_Eco)  
[https://bschilder.github.io/Hippo\\_Eco/HPsubfield\\_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](https://github.com/RajLabMSSM/RajLab_website)  
<http://www.rajlab.org>

## GRANTS

- Total (all grants): \$2,949,872**  
**Total (as primary applicant): \$311,382**
- 
- |      |   |
|------|---|
| 2023 | <ul style="list-style-type: none"><li><b>EuroBioc2023 Scholarship, Bioconductor</b><br/><b>Project:</b> 'rworkflows: taming the Wild West of R packages'<br/> <b>News</b><br/>- Awarded to support attending the <a href="#">EuroBioc2023 meeting</a>.<br/><br/><div style="display: flex; justify-content: space-between;"><div><ul style="list-style-type: none"><li>• <b>Role:</b> Primary applicant</li><li>• <b>PI:</b> BM Schilder</li></ul></div><div><ul style="list-style-type: none"><li>• <b>Amount:</b> \$250</li></ul></div></div></li></ul>                              |
| 2023 | <ul style="list-style-type: none"><li><b>BioC2023 Scholarship, Bioconductor</b><br/><b>Project:</b> 'rworkflows: taming the Wild West of R packages'<br/> <b>News</b><br/>- Awarded to support attending the <a href="#">BioC2023 meeting</a>. Additionally included free lodging.<br/><br/><div style="display: flex; justify-content: space-between;"><div><ul style="list-style-type: none"><li>• <b>Role:</b> Primary applicant</li><li>• <b>PI:</b> BM Schilder</li></ul></div><div><ul style="list-style-type: none"><li>• <b>Amount:</b> \$1500</li></ul></div></div></li></ul> |

2023	<b>Junior Scientist Conference Grant, The Genetics Society</b> <b>Project:</b> 'Identification of cell type-specific gene targets underlying thousands of rare diseases and subtraits' • <b>Role:</b> Primary applicant • <b>Amount:</b> £750 • <b>PI:</b> BM Schilder
2023	<b>Imperial UK Research Institute Impact Acceleration Account, Imperial College London</b> <b>Project:</b> 'Creating commercial kit solutions for single cell epigenetic profiling of histone marks and transcription factors' • <b>Role:</b> Co-applicant • <b>Amount:</b> £80,000 • <b>PI:</b> NG Skene
2024   2022	<b>Turing Community Award, Alan Turing Institute</b> <b>Project:</b> 'Multi-omic medicine: dissecting the cell-type-specific molecular mechanisms underlying neurodegenerative disease genomics' • <b>Role:</b> Primary applicant • <b>Amount:</b> £1,500 • <b>PI:</b> BM Schilder
2022	<b>National Institutes of Health</b> <b>Project:</b> 'Statistical and functional fine-mapping of bipolar disorder genetic risk loci' • <b>Role:</b> Co-applicant • <b>PI:</b> N Mullins
2021	<b>Collaborative Single Cell and Spatial Transcriptomics Studies Award Programme, UK Dementia Research Institute</b> <b>Project:</b> 'Amplifying genome coverage of single cell epigenetic profiling of the human brain' • <b>Role:</b> Co-applicant • <b>Amount:</b> £12,790 • <b>PI:</b> D Hu, NG Skene
2020	<b>National Institutes of Health</b> <b>Project:</b> "Cognitive Systems Analysis of Alzheimer's Disease Genetic and Phenotypic Data" • <b>Role:</b> Co-applicant • <b>Amount:</b> \$2,523,431 • <b>PI:</b> T Raj, D Knowles
2024   2020	<b>UK Dementia Research Institute</b> <b>Project:</b> 'UK DRI at Imperial Distinguished Studentship' • <b>Role:</b> Primary applicant • <b>Amount:</b> £217,000 • <b>PI:</b> BM Schilder
2019   2017	<b>The Michael J. Fox Foundation</b> <b>Project:</b> "The Role of Peripheral Myeloid Cells in Parkinson's Disease" • <b>Role:</b> Fundee • <b>PI:</b> T Raj
2020   2017	<b>The Michael J. Fox Foundation</b> <b>Project:</b> 'Functional Fine-Mapping of LRRK2 Locus' • <b>Role:</b> Fundee • <b>PI:</b> T Raj
2017	<b>National Science Foundation</b> <b>Project:</b> 'The evolution of the hippocampus and adult neurogenesis: novel insights into the origins of human memory' • <b>Role:</b> Primary applicant • <b>Amount:</b> \$31 543 • <b>PI:</b> BM Schilder
2017	<b>Wenner-Gren</b> <b>Project:</b> 'The evolution of the hippocampus and adult neurogenesis: insights into the origins of human memory' • <b>Role:</b> Primary applicant • <b>Amount:</b> \$19,512 • <b>PI:</b> 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



**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](#)



Psychiatric Genomics Consortium

- 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	<ul style="list-style-type: none"> <li><b>echoverse Dependency Graph</b></li> <li>• Interactive graph showing the dependency structure of all packages within the <a href="#">echoverse</a> suite.</li> </ul>	📍 London, UK
-   2020	<ul style="list-style-type: none"> <li><b>Hex stickers</b></li> <li>• All hex stickers for R packages I've helped develop.</li> </ul>	📍 London, UK
2023	<ul style="list-style-type: none"> <li><b>3D Human Phenotype Ontology</b></li> <li>• 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.</li> <li>• <a href="#">Associated preprint</a></li> </ul>	📍 London, UK
2023	<ul style="list-style-type: none"> <li><b>Multi-scale Rare Disease Mechanisms</b></li> <li>• Network of systematically prioritised gene therapy targets for rare diseases</li> <li>• <a href="#">Associated preprint</a></li> </ul>	📍 London, UK
2023	<ul style="list-style-type: none"> <li><b>Curriculum Vitae Connexa</b></li> <li>• Term co-occurrence network generated by analysing all data that went into this CV.</li> </ul>	📍 London, UK
2021	<ul style="list-style-type: none"> <li><b>Experiments with Generative AI</b></li> <li>• <a href="#">wombo.art</a>: 'Multi-omic medicine: dissecting the cell-type-specific mechanisms in neurodegeneration genomics'</li> <li>• <a href="#">wombo.art</a>: 'Multi-omic medicine: neurodegenerative disease genomics'</li> <li>• <a href="#">wombo.art</a>: 'Multi-omic medicine: neurodegeneration'</li> <li>• <a href="#">wombo.art</a>: 'Neurodegeneration'</li> </ul>	📍 London, UK
2021	<ul style="list-style-type: none"> <li><b>Lights in the dark genome: the current state of Parkinson's research</b></li> <li>• 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 <a href="#">Geneshot</a>.</li> <li>• <a href="#">Associated study</a></li> </ul>	📍 London, UK
2020	<ul style="list-style-type: none"> <li><b>Pacrophage</b></li> <li>• Colocalised genetic loci ...but shaped as Pac-Man!</li> <li>• <a href="#">Associated study</a></li> </ul>	📍 London, UK
2020	<ul style="list-style-type: none"> <li><b>Circos</b></li> <li>• Colocalised genetic loci across a variety of neurological disease GWAS and cell-type-specific QTLs.</li> <li>• <a href="#">Associated study</a></li> </ul>	📍 London, UK
2019	<ul style="list-style-type: none"> <li><b>Wildfire Circle</b></li> <li>• Awarded 2nd place in the <a href="#">2019 Art of the Brain</a> competition, put on by the Mount Sinai's Friedman Brain Institute.</li> <li>• Exhibited and auctioned at the <a href="#">Grady Alexis Gallery (New York City)</a>, where all proceeds were donated to the Diversity in Neuroscience Initiative .</li> <li>• <a href="#">Featured on cover of Biological Psychiatry</a>.</li> </ul>	📍 New York, NY, USA



- 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

Earth

• 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

• 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.

23