



# BRIAN M SCHILDER, PHD

Passionately pursuing transdisciplinary research to advance human health and knowledge.



## 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



## CORE SKILLS

### Research

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

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

## CONTACT

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📞 UK

+44 073-0653-7736

🌐 LinkedIn

🆔 ORCID

🔍 Google Scholar

🐙 GitHub

🐦 Twitter

📺 YouTube

🌐 Personal Website

🌐 Lab Website

## SUMMARY

📅 **15+** years of research

📄 **23** publications

📄 **8** preprints

🔧 **41** software packages

🗄 **11** databases & apps

🗣 **23** talks

👤 **13+** years of teaching & team management

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🎓 Education

✓ Skills

✓ Expertise

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🗣 Posters

📅 Experience

👤 Teaching

🔧 Packages

🌐 Websites

🗄 Databases

💰 Grants

🏆 Awards

🏢 Affiliations

🔗 Data visualisation

🎮 Extracurricular

📅 Updated Jun-07-2024

📄 Made with autoCV

## 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](#).

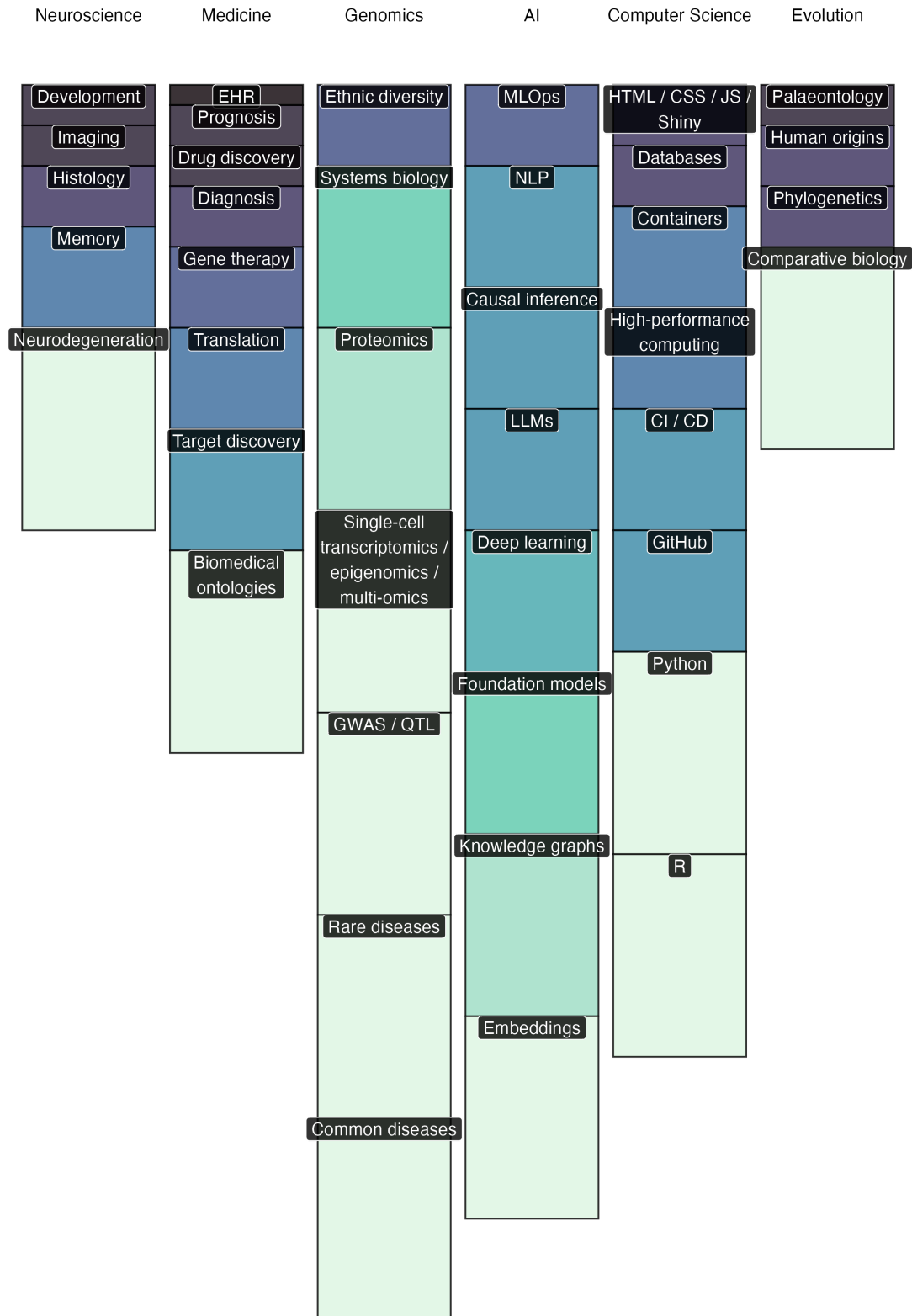
## Soft skills

Advances science through effective problem formulation, collaboration and communication.

- **Problem formulation:** Rapid hypothesis generation, project design, and creative problem solving.
- **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 my overall expertise in a given domain. The color and height of each rectangle are scaled to my relative level of expertise within each subdomain.





## PUBLICATIONS


- 2023 • **rworkflows: automating reproducible practices for the R community**  
*Nature Communications* (2023) 15(149); <https://doi.org/10.1038/s41467-023-44484-5>  
BM Schilder, AE Murphy, NG Skene  
 **News**  
- Featured in *Nature Communications* Editors' Highlights
- 2023 • **Artificial intelligence for neurodegenerative experimental models**  
*Alzheimer's & Dementia* (2023) <http://doi.org/10.1002/alz.13479>  
SJ Marzi, BM Schilder, A Nott, C Sala Frigerio, S Willaime-Morawek, M Bucholc, DP Hanger, C James, PA Lewis, I Lourida, W Noble, F Rodriguez-Algarra, JA Sharif, M Tsalenchuk, LM Winchester, U Yaman, Z Yao, DEMON Network, JM Ranson, DJ Llewellyn
- 2023 • **Artificial intelligence for dementia genetics and omics**  
*Alzheimer's & Dementia* (2023) <http://doi.org/10.1002/alz.13427>  
C Bettencourt, NG Skene, S Bandres-Ciga, E Anderson, LM Winchester, IF Foote, J 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 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/10.1371/journal.pgen.1008549>  
 S Ramdhani, E Navarro, E Udine, AG Efthymiou, BM Schilder, M Parks, A Goate, T Raj
- 2019 • **Evolutionary shifts dramatically reorganized the human hippocampal complex**  
*Journal of Comparative Neurology* (2019) 528(17):3143-3170; <https://doi.org/10.1002/cne.24822>  
 BM Schilder, HM Petry, PR Hof
- 2019 • **FAIRshake: Toolkit to Evaluate the Findability, Accessibility, Interoperability, and Reusability of Research Digital Resources**  
*Cell Systems* (2019) 9; <https://doi.org/10.1016/j.cels.2019.09.011>  
 D Clarke, L Wang, A Jones, M Wojciechowicz, D Torre, K Jagodnik, S Jenkins, P McQuilton, Z Flamholz, M Silverstein, BM Schilder... A Ma'ayan  
 **News**  
 - Chosen as 'Featured Frontmatter' article in *Cell Systems*
- 2019 • **Geneshot: search engine for ranking genes from arbitrary text queries**  
*Nucleic Acids Research* (2019) 47(W1):W571-W577; <https://doi.org/10.1093/nar/gkz393>  
 A Lachmann, BM Schilder, ML Wojciechowicz, D Torre, MV Kuleshov, AB Keenan, A Ma'ayan  
 **News**  
 - Geneshot: Piercing the Literature to Identify and Predict Relevant Genes (University of Pittsburgh Health Sciences Library System Update, 2019)  
 - The Future of AI at the Hasso Plattner Institute for Digital Health at Mount Sinai (Mount Sinai Health System, 2020)
- 2018 • **eXpression2Kinases (X2K) Web: linking expression signatures to upstream cell signaling networks**  
*Nucleic Acids Research* (2018) 46(W1):W171-W179; <https://doi.org/10.1093/nar/gky458>  
 DJB Clarke, MV Kuleshov, BM Schilder, D Torre, ME Duffy, AB Keenan, A Lachmann, AS Feldmann, GW Gundersen, MC Silverstein, Z Wang  
 **News**  
 - Mount Sinai Faculty Spotlight: Ma'ayan Lab (Mount Sinai Health System, 2018)
- 2015 • **Defining elemental imitation mechanisms: A comparison of cognitive and motor-spatial imitation learning across object- and computer-based tasks**  
*Journal of Cognition and Development* (2015) 17(2):221-243; <https://doi.org/10.1080/15248372.2015.1053483>  
 F Subiaul, L Zimmerman, E Renner, BM Schilder, R Barr

- 2015 • **Take the monkey and run**  
*Journal of Neuroscience Methods* (2015) 248:28-31; <http://doi.org/10.1016/j.jneumeth.2015.03.023>  
 KA Phillips, MK Hambright, K Hewes, BM Schilder, CN Ross, SD Tardif  
 **News**  
 - [Monkeys on a Treadmill? A Conversation with Dr. Kimberley Phillips \(Why Social Science?\)](#)
- 2014 • **Becoming a high-fidelity - super - imitator: what are the contributions of social and individual learning?**  
*Developmental Science* (2014) 18(6):1025-1035; <http://doi.org/10.1111/desc.12276>  
 F Subiaul, EM Patterson, BM Schilder, E Renner, R Barr
- 2014 • **Working memory constraints on imitation and emulation**  
*Journal of Experimental Child Psychology* (2014) 128:190-200; <http://doi.org/10.1016/j.jecp.2014.07.005>  
 F Subiaul, BM Schilder



## PREPRINTS

- 2024 • **Zero-shot transfer learning of genomic disease signatures using single-cell foundation models**  
*arXiv* (2024)  
 BM Schilder
- 2024 • **Harnessing generative AI to annotate the severity of all phenotypic abnormalities within the Human Phenotype Ontology**  
*medRxiv* (2024)  
 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)  
 BM Schilder, NG Skene
- 2024 • **Active chromatin interaction and histone mark signatures underpin epigenetic TBXT expression in metastatic lung cancer**  
*bioRxiv* (2024)  
 RM Yaa, BM Schilder, RD Acemel, FC Wardle
- 2024 • **Integrative multi-omics analysis of glial signatures associated with accelerated cognitive decline in Alzheimer's disease**  
*bioRxiv* (2024)  
 E Schneegans, N Fancy, V Chau, T Ka, D Cheung, E Adair, M Papageorgopoulou, BM Schilder, PM Matthews, JS Jackson
- 2023 • **Fine-mapping genomic loci refines bipolar disorder risk genes**  
*medRxiv* (2023) <https://www.medrxiv.org/content/10.1101/2024.02.12.24302716v1>  
 M Koromina, A Ravi, G Panagiotaropoulou, BM Schilder, ... S Ripke, T Raj, JRI Coleman, N Mullins  
 **News**  
 - Currently under journal review
- 2023 • **Identification of cell type-specific gene targets underlying thousands of rare diseases and subtraits**  
*medRxiv* (2023) <https://doi.org/10.1101/2023.02.13.23285820>  
 KB Murphy, R Gordon-Smith, J Chapman, M Otani, BM Schilder, NG Skene
- 2022 • **CUT&Tag recovers up to half of ENCODE ChIP-seq peaks**  
*bioRxiv* (2022) <https://doi.org/10.1101/2022.03.30.486382>  
 D Hu, L Abbasova, BM Schilder, A Nott, NG Skene, SJ Marzi



## ACKNOWLEDGEMENTS

- 2021 • **eQTL Catalogue: a compendium of uniformly processed human gene expression and splicing QTLs.**  
*Nature Genetics* (2021) 53:1290-1299; <https://doi.org/10.1038/s41588-021-00924-w>  
 N Kerimov, JD Hayhurst, K Peikova et al.
- 2020 • **Functionally-informed fine-mapping and polygenic localization of complex trait heritability**  
*Nature Genetics* (2020) <https://doi.org/10.1038/s41588-020-00735-5>  
 O Weissbrod...AL Price
- 2019 • **Wayfinding: The science and mystery of how humans navigate the world.**  
*St. Martin's Press* (2019) ISBN-13: 978-1250096968; <https://www.amazon.co.uk/Wayfinding-Science-Mystery-Humans-Navigate/dp/1250096960>  
 MR O'Connor
- 2012 • **EEG oscillations reveal neural correlates of evidence accumulation**  
*Frontiers in Decision Neuroscience* (2012) 6(106):Jan-13; <https://doi.org/10.3389/fnins.2012.00106>  
 M van Vugt, P Simen, L Nystrom, P Holmes, J Cohen
- 2011 • **Trial-by-trial adaptation of decision making performance: a model-based EEG analysis**  
*Interdisciplinary Perspectives on Cognition, Education, and the Brain* (2011) 7; <https://www.semanticscholar.org/paper/Trial-by-trial-adaptation-of-decision-making-a-EEG-Vugt-Simen/330371d08842ecd1bda332dd22351a7135b5cb1f>  
 M van Vugt, P Simen, J Cohen



## REVIEWERSHIPS

- 2024 • **[Unpublished article]**  
*BMJ Open* (2024)
- 2023 • **Multi-region brain transcriptomes uncover two subtypes of aging individuals with differences in Alzheimer risk and the impact of 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 Naylor, 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

- 2023 • **rworkflows: taming the Wild West of R packages**  
EuroBioc2023  
  
Bioconductor  
[45-minute workshop.](#)
- 2023 • **rworkflows: taming the Wild West of R packages**  
BioC2023  
  
Bioconductor  
[10-minute talk within the Infrastructure Track.](#)
- 2023 • **Navigating the rare diseases landscape: A comprehensive approach to identify gene therapy targets based on cell type-phenotype associations**  
Intelligent Systems For Molecular Biology / European Conference on Computational Biology (ISMB/ECCB)  
  
International Society for Computational Biology (ISMB)  
[20-minute talk within the Bio-Ontologies COSI Track.](#)
- 2022 • **Systematic quantification of animal model viability across human diseases**  
Informatics-Synapse Joint Early Career Researcher Meeting  
  
UK Dementia Research Institute (UK DRI)
- 2020 • **Automated genetic fine-mapping of neurological disorders**  
London Genetics Network  
  
The Genetics Society  
[6-minute talk](#)
- 2019 • **Parkinson's disease derived monocytes show alteration in the phago-lysosomal pathway**  
American Society of Human Genetics (ASHG) Annual Meeting  
  
American Society of Human Genetics (ASHG)  
Co-contributor
- 2017 • **Comparative neuroanatomy of navigational maps in primates**  
JB Johnston Club for Evolutionary Neuroscience  
  
Society for Neuroscience (SfN)  
Co-contributor

- 2016 • **The evolution of human hippocampal gene expression**  
JB Johnston Club for Evolutionary Neuroscience  
  
Society for Neuroscience (SfN)
- 2015 • **The neurobiological effects of exercise on marmoset models of Multiple Sclerosis**  
Marmoset Social  
  
Society for Neuroscience (SfN)
- 2015 • **The neurobiological effects of exercise on marmoset models of Multiple Sclerosis**  
JB Johnston Club for Evolutionary Neuroscience  
  
Society for Neuroscience (SfN)



## CONFERENCE POSTERS









- 2024 • **Navigating the Phenomic Landscape: systematic characterisation of the latent genomic space underlying all traits and diseases**  
*Target to Patient* (2024) <https://www.ebi.ac.uk/industry/targettopatient/>  
BM Schilder, NG Skene
- 2023 • **CUT&Tag recovers up to half of ENCODE ChIP-seq peaks**  
*Connectome (UK Dementia Research Institute)* (2023) <https://ukdri.ac.uk/>  
J Ismail, D Hu, L Abbasova, BM Schilder, A Nott, NG Skene, SJ Marzi
- 2023 • **Navigating the rare diseases landscape: A comprehensive approach to identify gene therapy targets based on cell type-phenotype associations**  
*Intelligent Systems For Molecular Biology / European Conference on Computational Biology (ISMB/ECCB)* (2023) <https://www.iscb.org/ismbeccb2023>  
BM Schilder, KB Murphy, R Gordon-Smith, J Chapman, M Otani, NG Skene
- 2023 • **Identification of cell type-specific gene targets underlying thousands of rare diseases and clinical phenotypes**  
*Genomics of Rare Diseases* (2023) <https://coursesandconferences.wellcomeconnectingscience.org/event/genomics-of-rare-disease-20230424/>  
BM Schilder, KB Murphy, R Gordon-Smith, J Chapman, M Otani, NG Skene
- 2023 • **Statistical and Functional Fine-Mapping as a Powerful Tool to Unravel the Biological Etiology of Bipolar Disorder**  
*Biological Psychiatry* (2023) 93(9):S18; <https://doi.org/10.1016/j.biopsych.2023.02.063>  
M Koromina, A Ravi, BM Schilder, B Muller, J Coleman, T Raj
- 2023 • **Systematic quantification of animal model viability across human disease**  
*UK Dementia Research Institute Scientific Advisory Board* (2023)  
BM Schilder, NG Skene
- 2022 • **Systematic quantification of animal model viability across human disease**  
*Rising Scientist Day at Imperial College London* (2022)  
BM Schilder, NG Skene
- 2022 • **A comprehensive statistical and functional fine-mapping pipeline applied to Bipolar Disorder GWAS risk loci**  
*European Neuropsychopharmacology* (2022) 63:e14; <http://dx.doi.org/10.1016/j.euroneuro.2022.07.037>  
M Koromina, A Ravi, BM Schilder, B Muller, J Coleman, T Raj, N Mullins
- 2021 • **Genetic Effects on Human Microglia Transcriptome in Neuropsychiatric Diseases**  
*Biological Psychiatry* (2021) 89(9):S84-S85; <https://doi.org/10.1016/j.biopsych.2021.02.225>  
G Snijders, K de Paiva Lopes, J Humphrey, S Allan, M 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

- |  
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	<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	<b>Student Researcher</b> Brown University (Department of Cognitive, Linguistic & Psychological Sciences)  <a href="#">Providence, RI, USA</a> <ul style="list-style-type: none"> <li>• Experimental Analysis of Animal Behavior &amp; Cognition: Conducted various operant conditioning experiments on rats. Gained experience in animal behavioral training, data collection, and data analysis in MATLAB.</li> <li>• 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.</li> </ul>



## TEACHING / MENTORING EXPERIENCE

- 2020  
|  
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

- 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>
- 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>
- KGExplorer**   
 Query, construct, and analyse large-scale biomedical knowledge graphs and ontologies.  
<https://github.com/neurogenomics/KGExplorer>
- autoCV**   
 Automatically generate and style your CV from tables.  
<https://github.com/bschilder/autoCV>
- 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>
- gptPhD**   
 Query Large Language Models for the purposes of systematically extracting biomedical knowledge.  
<https://github.com/neurogenomics/gptPhD>
- ThreeWayTest**   
 Summary statistics-based association test for identifying the pleiotropic effects with set of genetic variants.  
<https://github.com/bschilder/ThreeWayTest>
- 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>
- 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 corporuses.
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 **EuroBioc2023 Scholarship, Bioconductor**  
**Project:** 'rworkflows: taming the Wild West of R packages'  
 **News**  
- Awarded to support attending the [EuroBioc2023 meeting](#).  
  
• **Role:** Primary applicant • **Amount:** \$250  
• **PI:** BM Schilder
- 2023 **BioC2023 Scholarship, Bioconductor**  
**Project:** 'rworkflows: taming the Wild West of R packages'  
 **News**  
- Awarded to support attending the [BioC2023 meeting](#). Additionally included free lodging.  
  
• **Role:** Primary applicant • **Amount:** \$1500  
• **PI:** BM Schilder
- 2023 **Junior Scientist Conference Grant, The Genetics Society**  
**Project:** 'Identification of cell type-specific gene targets underlying thousands of rare diseases and subtraits'  
  
• **Role:** Primary applicant • **Amount:** £750  
• **PI:** BM Schilder

2023	<ul style="list-style-type: none"> <li> <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>PI:</b> NG Skene         </li> </ul>	<ul style="list-style-type: none"> <li>• <b>Amount:</b> £80,000</li> </ul>
2024   2022	<ul style="list-style-type: none"> <li> <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>PI:</b> BM Schilder         </li> </ul>	<ul style="list-style-type: none"> <li>• <b>Amount:</b> £1,500</li> </ul>
2022	<ul style="list-style-type: none"> <li> <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         </li> </ul>	<ul style="list-style-type: none"> <li>• <b>PI:</b> N Mullins</li> </ul>
2021	<ul style="list-style-type: none"> <li> <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>PI:</b> D Hu, NG Skene         </li> </ul>	<ul style="list-style-type: none"> <li>• <b>Amount:</b> £12,790</li> </ul>
2020	<ul style="list-style-type: none"> <li> <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>PI:</b> T Raj, D Knowles         </li> </ul>	<ul style="list-style-type: none"> <li>• <b>Amount:</b> \$2,523,431</li> </ul>
2024   2020	<ul style="list-style-type: none"> <li> <b>UK Dementia Research Institute</b>  <b>Project:</b> 'UK DRI at Imperial Distinguished Studentship'            • <b>Role:</b> Primary applicant            • <b>PI:</b> BM Schilder         </li> </ul>	<ul style="list-style-type: none"> <li>• <b>Amount:</b> £217,000</li> </ul>
2019   2017	<ul style="list-style-type: none"> <li> <b>The Michael J. Fox Foundation</b>  <b>Project:</b> "The Role of Peripheral Myeloid Cells in Parkinson's Disease"            • <b>Role:</b> Fundee         </li> </ul>	<ul style="list-style-type: none"> <li>• <b>PI:</b> T Raj</li> </ul>
2020   2017	<ul style="list-style-type: none"> <li> <b>The Michael J. Fox Foundation</b>  <b>Project:</b> 'Functional Fine-Mapping of LRRK2 Locus'            • <b>Role:</b> Fundee         </li> </ul>	<ul style="list-style-type: none"> <li>• <b>PI:</b> T Raj</li> </ul>
2017	<ul style="list-style-type: none"> <li> <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>PI:</b> BM Schilder         </li> </ul>	<ul style="list-style-type: none"> <li>• <b>Amount:</b> \$31 543</li> </ul>
2017	<ul style="list-style-type: none"> <li> <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>PI:</b> BM Schilder         </li> </ul>	<ul style="list-style-type: none"> <li>• <b>Amount:</b> \$19,512</li> </ul>
2016	<ul style="list-style-type: none"> <li> <b>Leakey 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>PI:</b> BM Schilder         </li> </ul>	<ul style="list-style-type: none"> <li>• <b>Amount:</b> \$15,000</li> </ul>

2016

### **COSMOS Club**

**Project:** 'The evolution of adult neurogenesis across primates'

- **Role:** Primary applicant
- **PI:** BM Schilder

• **Amount:** \$3,250



## **AWARDS**

2023

### **Prize for Computational Reproducibility in Dementia Research, UK Dementia Research Institute**

**Project:** 'rworkflows: taming the Wild West of R packages'

**News**

- [Awarded honourable mention.](#)

2022

### **Prize for Computational Reproducibility in Dementia Research, UK Dementia Research Institute**

**Project:** 'MungeSumstats: A Bioconductor package for the standardisation and quality control of many GWAS summary statistics'

**News**

- Awarded honourable mention.

2022

### **Poster Competition, Rising Scientist Day**

**Project:** 'Systematic quantification of animal model viability across human diseases'

**News**

- Awarded prize for research poster competition.

2022

### **Award for Outstanding Contribution, NEUROHACK, Deep Dementia Phenotyping Network (DEMON)**

**Project:** 'Predicting ALS drug targets using integrative multi-modal deep learning'

**News**

- [Individually awarded](#) for outstanding contributions during the NEUROHACK 2022, a competitive 4-day hackathon to apply AI in finding ALS therapeutic solutions.

2021

### **Prize for Computational Reproducibility in Dementia Research, UK Dementia Research Institute**

**Project:** 'echolocator: an automated end-to-end statistical and functional genomic fine-mapping pipeline'

**News**

- [Winners announced for UK DRI's first 'Prize for Computational Reproducibility in Dementia Research \(UK Dementia Research Institute, 2021\)](#)

- [Jointly awarded inaugural prize with Kitty Murphy.](#)

2021

### **Centre Photography Competition, UK Dementia Research Institute**

**Project:** 'Wildfire Circle, Golden Brain, Wildfire, Geneshot, Geology of Biology, Neon Brain'

**News**

- [One of the winners of the scientific image competition.](#)

2019

### **Art of the Brain, Friedman Brain Institute, Icahn School of Medicine**

**Project:** 'Wildfire'

**News**

- [Awarded 2nd place](#) and Featured on the [cover of Biological Psychiatry: Volume 87, Issue 12 \(2020\)](#). Exhibited and auctioned at the Grady Alexis Gallery (New York City), where all proceeds were voluntarily donated to the Diversity in Neuroscience Initiative.

## AFFILIATIONS



- Society of Technological Advancement member



- 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](#)





• Member

## DATA VISUALISATION / ARTWORK PORTFOLIO

- |      |  |  |
|------|--|--|
| 2022 | <ul style="list-style-type: none"> <li>• <b><a href="#">echoverse Dependency Graph</a></b> <ul style="list-style-type: none"> <li>• Interactive graph showing the dependency structure of all packages within the <a href="#">echoverse</a> suite.</li> </ul> </li> </ul>  |  <a href="#">London, UK</a>   |
| 2020 | <ul style="list-style-type: none"> <li>• <b><a href="#">Hex stickers</a></b> <ul style="list-style-type: none"> <li>• All hex stickers for R packages I've helped develop.</li> </ul> </li> </ul>  |  <a href="#">London, UK</a>   |
| 2023 | <ul style="list-style-type: none"> <li>• <b><a href="#">3D Human Phenotype Ontology</a></b> <ul style="list-style-type: none"> <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> </li> </ul>   |  <a href="#">London, UK</a>   |
| 2023 | <ul style="list-style-type: none"> <li>• <b><a href="#">Multi-scale Rare Disease Mechanisms</a></b> <ul style="list-style-type: none"> <li>• Network of systematically prioritised gene therapy targets for rare diseases</li> <li>• <a href="#">Associated preprint</a></li> </ul> </li> </ul>  |  <a href="#">London, UK</a> |
| 2023 | <ul style="list-style-type: none"> <li>• <b><a href="#">Curriculum Vitae Connexa</a></b> <ul style="list-style-type: none"> <li>• Term co-occurrence network generated by analysing all data that went into this CV.</li> </ul> </li> </ul>  |  <a href="#">London, UK</a> |
| 2021 | <ul style="list-style-type: none"> <li>• <b><a href="#">Experiments with Generative AI</a></b> <ul style="list-style-type: none"> <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> </li> </ul> |  <a href="#">London, UK</a> |
| 2021 | <ul style="list-style-type: none"> <li>• <b><a href="#">Lights in the dark genome: the current state of Parkinson's research</a></b> <ul style="list-style-type: none"> <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> </li> </ul>   |  <a href="#">London, UK</a> |
| 2020 | <ul style="list-style-type: none"> <li>• <b><a href="#">Pacrophage</a></b> <ul style="list-style-type: none"> <li>• Colocalised genetic loci ...but shaped as Pac-Man!</li> <li>• <a href="#">Associated study</a></li> </ul> </li> </ul>  |  <a href="#">London, UK</a> |

- 2020 • **Circos**
  - Colocalised genetic loci across a variety of neurological disease GWAS and cell-type-specific QTLs.
  - [Associated study](#)

📍 London, UK
- 2019 • **Wildfire Circle**
  - 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.](#)

📍 New York, NY, USA
- 2019 • **Wildfire**
  - 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.

📍 New York, NY, USA
- 2019 • **3D Brain Model**
  - 3D model of my brain generated from MRI scans.

📍 New York, NY, USA



## 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