



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](#)
 📄 [Publications](#)
 📄 [Preprints](#)
 📄 [Acknowledgements](#)
 📄 [Reviewerships](#)
 🗣️ [Internal talks](#)
 🗣️ [Invited talks](#)
 🗣️ [Conference talks](#)
 🗣️ [Posters](#)
 📄 [Experience](#)
 👤 [Teaching](#)
 🔧 [Packages](#)
 📄 [Websites](#)
 📄 [Databases](#)
 💰 [Grants](#)
 🏆 [Awards](#)
 🏢 [Affiliations](#)
 📊 [Data visualisation](#)
 🎮 [Extracurricular](#)

📅 [Updated May-13-2024](#)
 🏠 [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.

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/10.1101/499509>
 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 Hambricht, 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 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 Sneebauer, 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 • **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 <ul style="list-style-type: none"> • 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 <ul style="list-style-type: none"> • 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 <ul style="list-style-type: none"> • Investigated the neurobiological mechanisms underlying the ameliorating effects of exercise on relapse-remitting Multiple Sclerosis.
2014	Teaching Assistant / Project Leader The George Washington University / Rutgers University (Department of Anthropology)  Ileret, Kenya <ul style="list-style-type: none"> • Served as Teaching Assistant while excavating Lower Paleolithic hominin sites (Homo, Paranthropus). • As Project Leader, investigated the running biomechanics of local Daasanach tribespeople while mentoring undergraduate students.
2013 2011	Research Assistant The George Washington University (Department of Anthropology)  Washington, DC, USA <ul style="list-style-type: none"> • Performed dissection, histology, microscopy and quantitative stereology in post-mortem primate brain tissues. • Trained junior and senior personnel on lab protocols.
2013 2011	Senior Lab Manager The George Washington University (Department of Speech, Language & Hearing Sciences)  Washington, DC, USA <ul style="list-style-type: none"> • Organized and trained dozens of undergraduates to conduct weekly cognitive development research; designed and/or directly contributed to over 15 research projects in two years.
2012	Volunteer Researcher University of Winnipeg / University of Belgrade (Department of Anthropology / Department of Archaeology)  Sićevo, Serbia <ul style="list-style-type: none"> • Excavated Paleolithic fossils and tools (H. heidelbergensis, H. neanderthalensis) at Mala Balanica, Velika Balanica, and Pešturina sites.
2011	Volunteer Researcher Universidad de Murcia (Department of Zoology & Physical Anthropology)  Murcia, Spain <ul style="list-style-type: none"> • Excavated Paleolithic fossils and tools from Cueva Negra (H. heidelbergensis) and Sima de las Palomas (H. neanderthalensis) with an international research team.
2011	Volunteer Research Intern American Museum of Natural History (Division of Anthropology)  New York, NY, USA <ul style="list-style-type: none"> • Contributed to paleoanthropological research on primate fossils using 3D morphometry imaging equipment including Minolta, Microscribe and CT.
2010	Paid Research Intern Princeton University (Princeton Neuroscience Institute)  Princeton, NJ, USA <ul style="list-style-type: none"> • Investigated the neural basis of decision-making in humans. • Recruited participants, recorded EEG and analyzed data in MATLAB.
2010 2009	Student Researcher Brown University (Department of Cognitive, Linguistic & Psychological Sciences)  Providence, RI, USA <ul style="list-style-type: none"> • Experimental Analysis of Animal Behavior & Cognition: Conducted various operant conditioning experiments on rats. Gained experience in animal behavioral training, data collection, and data analysis in MATLAB. • Laboratory in Genes and Behavior: Tested transgenic mice with modified N-type voltage-gated calcium channel subunits in a battery of cognitive and sensorimotor tasks. Results were published.



TEACHING / MENTORING EXPERIENCE

- |
2020

Research Mentor
Imperial College London (Department of Brain Sciences / Department of Life Sciences) 📍 London, UK

 - Mentored students and affiliated projects:
 - Kitty Murphy (PhD): 'Evolutionary pressures on cell types: leveraging species differences to gain insight into neurodegenerative disease risk'
 - Sheen Lei (BSc): 'Benchmarking cell-type-specific enrichment of genome-wide disease signatures'
 - Ted Reese (MSc): 'Computational cell-type annotation of single-cell epigenomics data'
 - Xindong Sun (MSc): 'Benchmark of Targeted insertion of promoters sequencing (TIP-seq) on histone modification H3K27ac and H3K27me3 in K562 cell line'
 - Shuhan Shen (MSc): 'Evaluation and optimisation of methods for identifying the cell types underlying genetic disease signatures'
 - Lusheng Li (MSc): 'Genetic identification of cell types underlying mammalian phenotypes'
 - Sera Choi (BSc): 'EpiCompare: R package for QC and benchmarking epigenetic datasets'
 - Emilie Cottard (MSc) & Will Lunt (BSc): 'A meta-analysis of selective cell-type vulnerability in Parkinson's Disease neuropathology'
 - Jai Chapman (BSc): 'Expression Weighted Cell Type Enrichment as a Tool for Identifying Cell Types Underlying Rare Disease Phenotypes'
 - Bobby Gordon-Smith (MSc): 'Identification of cell types involved in rare disease-associated human phenotypes'
 - Leyla Abbasova (MSc): 'Analysis and optimisation of CUT&Tag for epigenomic profiling of the brain'
 - Barney Hill (BSc): 'Identification of cell-types associated with latent factors inferred from phenome-wide GWAS summary statistics'
- 2020
|
2019

Research Mentor
Icahn School of Medicine at Mount Sinai (Department of Neuroscience / Department of Neurology / Department of Genetics & Genomics / Ronald M. Loeb Center for Alzheimer's Disease) 📍 New York, NY, USA

 - Mentored MS, MD, and PhD students in projects focused on computational exploration of phenotype clustering and genomic regulation of neurodegenerative diseases.
- 2018

Research Co-mentor
Icahn School of Medicine at Mount Sinai (Department of Pharmacological Sciences) 📍 New York, NY, USA

 - Mentored students and affiliated projects:
 - Vivian Utti (BSc): 'ChEA3: Transcription Factor Enrichment Analysis' as part of the Summer Research Training Program in Biomedical Big Data Science.
 - Mary Duffy (PhD): 'Predicting upstream kinase regulators from interaction network databases'
 - Zach Flamholz (BSc): 'modEnrichr: a suite of gene set enrichment analysis tools for model organisms'
- 2018

Guest Lecturer
Icahn School of Medicine at Mount Sinai (Department of Pharmacological Sciences) 📍 New York, NY, USA

 - Lectured on data visualization in Python and Jupyter notebooks in the PhD/MD course 'Programming for Big Data Biomedicine'.
- 2017
|
2016

Research Mentor
The George Washington University (Department of Anthropology) 📍 Washington, DC, USA

 - Mentored students and affiliated projects:
 - Jamie Kleiner (BSc): 'Animal model simulating MS and exercise's impact on adult hippocampal neurogenesis'
- 2015

Teaching Assistant
The George Washington University (Department of Anthropology) 📍 Washington, DC, USA

 - Course: 'Human Brain Evolution'
 - Guest lectured, graded all assignments and exams, and provided additional educational support during office hours.
- 2014
















Teaching Assistant
The George Washington University (Department of Psychology) 📍 Washington, DC, USA



















 - Course: 'Biological Psychology'
 - Led undergraduates in article discussions, graded all assignments and exams, and provided additional educational support during office hours.



















- 2014
|
2013
- **Teaching Assistant**
The George Washington University (Department of Anthropology) 📍 Washington, DC, USA
• Course: 'Biological Anthropology'
• Led undergraduate students in two, 2-hour lab sessions per week, graded lab assignments and exams, and provided additional educational support during office hours.
- 2013
|
2012
- **Research Mentor**
The George Washington University (Department of Psychology) 📍 Washington, DC, USA
• Mentored students and affiliated projects:
• Anushka Gokhale (BSc): 'Infants' Social Assessment of Characters Through Eye Gaze'
- 2013
|
2011
- **Lab Protocol Trainer**
The George Washington University (Department of Anthropology) 📍 Washington, DC, USA
• Trained undergraduate, graduate, and post-doctoral researchers in Social Cognition Lab and Lab for Evolutionary Neuroscience in a variety of methodological research protocols.






SOFTWARE PACKAGES

1. **MSTExplorer** 
Multi-Scale Targets Explorer: Systematically identify, prioritise and visualise cell-type-specific gene therapy targets across the phenome.
<https://github.com/neurogenomics/MSTExplorer>
<https://doi.org/10.1101/2023.02.13.23285820>
2. **HPOExplorer** 
Import, annotate and visualise the 18k+ hierarchically structured clinical phenotypes across the Human Phenotype Ontology.
<https://github.com/neurogenomics/HPOExplorer>
<https://doi.org/10.1101/2023.02.13.23285820>
3. **KGExplorer**  
Query, construct, and analyse large-scale biomedical knowledge graphs and ontologies.
<https://github.com/neurogenomics/KGExplorer>
4. **autoCV**    
Automatically generate and style your CV from tables.
<https://github.com/bschilder/autoCV>
5. **anndataR**  
Bring the power and flexibility of AnnData to the R ecosystem, allowing you to effortlessly manipulate and analyze your single-cell data.
<https://github.com/scverse/anndataR>
6. **gptPhD** 
Query Large Language Models for the purposes of systematically extracting biomedical knowledge.
<https://github.com/neurogenomics/gptPhD>
7. **ThreeWayTest** 
Summary statistics-based association test for identifying the pleiotropic effects with set of genetic variants.
<https://github.com/bschilder/ThreeWayTest>
8. **SCAVENGE** 
Variant to function mapping at single-cell resolution through network propagation.
<https://github.com/sankaranlab/SCAVENGE>
<https://doi.org/10.1038/s41587-022-01341-y>
9. **rworkflows**  
Continuous integration for R packages. Automates testing, documentation website building, and containerised deployment.
<https://github.com/neurogenomics/rworkflows>
<https://doi.org/10.21203/rs.3.rs-2399015/v1>









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










26. **echolocator**  
R package for end-to-end statistical and functional fine-mapping with extensive dataset access.
<https://github.com/RajLabMSSM/echolocator>
<https://doi.org/10.1093/bioinformatics/btab658>
27. **echodata** 
Examples of fine-mapped GWAS summary statistics, data formatting functions, and API access to the echolocator Fine-mapping Portal.
<https://github.com/RajLabMSSM/echodata>
<https://doi.org/10.1093/bioinformatics/btab658>
28. **echoannot** 
Functions for annotating genomic data with annotations and epigenomic data.
<https://github.com/RajLabMSSM/echoannot>
<https://doi.org/10.1093/bioinformatics/btab658>
29. **echoplot** 
R package for LocusZoom-inspired GWAS/QTL visualization, with API access to LD panels.
<https://github.com/RajLabMSSM/echoplot>
<https://doi.org/10.1093/bioinformatics/btab658>
30. **echoconda**  
Various utility functions to find, build, and use conda environments from within R.
<https://github.com/RajLabMSSM/echoconda>
<https://doi.org/10.1093/bioinformatics/btab658>
31. **echotabix**  
Tabix indexing and querying.
<https://github.com/RajLabMSSM/echotabix>
<https://doi.org/10.1093/bioinformatics/btab658>
32. **echoLD**  
LD downloading and processing.
<https://github.com/RajLabMSSM/echoLD>
<https://doi.org/10.1093/bioinformatics/btab658>
33. **echofinemap**  
Statistical and functional fine-mapping functions.
<https://github.com/RajLabMSSM/echofinemap>
<https://doi.org/10.1093/bioinformatics/btab658>
34. **echodeps** 
Creates interactive dependency networks for R packages.
<https://github.com/RajLabMSSM/echodeps>
<https://doi.org/10.1093/bioinformatics/btab658>
35. **echogithub** 
Access and process metadata from GitHub.
<https://github.com/RajLabMSSM/echogithub>
<https://doi.org/10.1093/bioinformatics/btab658>
36. **devoptera** 
Practical tools for R developers.
<https://github.com/RajLabMSSM/devoptera>
<https://doi.org/10.1093/bioinformatics/btab658>
37. **downloadR** 
Single- and multi-threaded downloading functions.
<https://github.com/RajLabMSSM/downloadR>
<https://doi.org/10.1093/bioinformatics/btab658>
38. **catalogueR** 
R package for rapid API-access and colocalization of summary statistics from eQTL Catalogue.
<https://github.com/RajLabMSSM/catalogueR>
<https://doi.org/10.1093/bioinformatics/btab658>

39. **TopicModeler** 
Proprietary Python package to run advanced topic modeling on text 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://neurogenomics.github.io/rare_disease_celltyping_apps/home
<https://doi.org/10.1101/2023.02.13.23285820>
3. **Parkinson's Disease Omics Review** 
Data and code associated with the Parkinson's Disease review paper by Schilder, Navarro & Raj (Neurobiology of Disease, 2021).
https://github.com/RajLabMSSM/PD_omics_review
https://rajlabmssm.github.io/PD_omics_review/
<https://doi.org/10.1016/j.nbd.2021.105580>
4. **Selective Vulnerability Meta-analysis** 
Selective Vulnerability Meta-analysis: Shiny app dedicated to the exploration and dissemination of meta-analysed cell counts manually curated and harmonised from the Parkinson's Disease literature.
<https://github.com/neurogenomics/SelectiveVulnerabilityMetaAnalysis>
5. **MAGMA Files Public** 
Gene enrichment files for hundreds of GWAS generated with Multi-marker Analysis of GenoMic Annotation (MAGMA) for use in downstream analyses.
https://github.com/neurogenomics/MAGMA_Files_Public
6. **echolocator Fine-mapping Portal** 
Access to interactive plots and fine-mapping results across many GWAS/QTL datasets using echolocator.
https://github.com/RajLabMSSM/Fine_Mapping_Shiny
https://rajlab.shinyapps.io/Fine_Mapping_Shiny
<https://doi.org/10.1093/bioinformatics/btab658>
7. **COVID-19 Patient Tracker** 
Web app for summarizing and visualizing real-time EHR data of COVID-19 patients within the Mount Sinai Health System.
8. **Tensor Decomposition Shiny App** 
Interactive application to explore and download all results and plots from Ramdhani et al. (PLOS Genetics, 2020).
https://github.com/RajLabMSSM/Tensor_myeloid
https://rajlab.shinyapps.io/Tensor_myeloid
<https://doi.org/10.1101/499509>


9. **Hippocampal Evolution** 
Interactive code, results and visualization for the manuscript "Evolutionary selective pressures dramatically expanded and reorganized the human hippocampal complex".
https://github.com/bschilder/Hippo_Eco
https://bschilder.github.io/Hippo_Eco/HPsubfield_eco
<https://doi.org/10.1002/cne.24822>
10. **Geneshot**    
Flexible tool to identify genes associated with any biomedical term and to predict novel target genes.
<http://amp.pharm.mssm.edu/geneshot>
<https://doi.org/10.1093/nar/gkz393>
11. **X2K**    
eXpression 2 Kinases (X2K) Web: Automated computational pipeline to infer kinase regulators from weighted or unweighted gene lists.
<http://amp.pharm.mssm.edu/X2K>
<https://doi.org/10.1093/nar/gky458>

WEBSITES

1. **Personal Website**   
<https://github.com/bschilder/BMSchilder>
<https://bschilder.github.io/BMSchilder>
2. **Official Raj Lab Website**   
https://github.com/RajLabMSSM/RajLab_website
<http://www.rajlab.org>

\$ GRANTS

- Total (all grants): \$2,949,872**
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"> Imperial UK Research Institute Impact Acceleration Account, Imperial College London Project: 'Creating commercial kit solutions for single cell epigenetic profiling of histone marks and transcription factors' • Role: Co-applicant • PI: NG Skene • Amount: £80,000
2024 2022	<ul style="list-style-type: none"> Turing Community Award, Alan Turing Institute Project: 'Multi-omic medicine: dissecting the cell-type-specific molecular mechanisms underlying neurodegenerative disease genomics' • Role: Primary applicant • PI: BM Schilder • Amount: £1,500
2022	<ul style="list-style-type: none"> National Institutes of Health Project: 'Statistical and functional fine-mapping of bipolar disorder genetic risk loci' • Role: Co-applicant • PI: N Mullins
2021	<ul style="list-style-type: none"> Collaborative Single Cell and Spatial Transcriptomics Studies Award Programme, UK Dementia Research Institute Project: 'Amplifying genome coverage of single cell epigenetic profiling of the human brain' • Role: Co-applicant • PI: D Hu, NG Skene • Amount: £12,790
2020	<ul style="list-style-type: none"> National Institutes of Health Project: "Cognitive Systems Analysis of Alzheimer's Disease Genetic and Phenotypic Data" • Role: Co-applicant • PI: T Raj, D Knowles • Amount: \$2,523,431
2024 2020	<ul style="list-style-type: none"> UK Dementia Research Institute Project: 'UK DRI at Imperial Distinguished Studentship' • Role: Primary applicant • PI: BM Schilder • Amount: £217,000
2019 2017	<ul style="list-style-type: none"> The Michael J. Fox Foundation Project: "The Role of Peripheral Myeloid Cells in Parkinson's Disease" • Role: Fundee • PI: T Raj
2020 2017	<ul style="list-style-type: none"> The Michael J. Fox Foundation Project: 'Functional Fine-Mapping of LRRK2 Locus' • Role: Fundee • PI: T Raj
2017	<ul style="list-style-type: none"> National Science Foundation Project: 'The evolution of the hippocampus and adult neurogenesis: novel insights into the origins of human memory' • Role: Primary applicant • PI: BM Schilder • Amount: \$31 543
2017	<ul style="list-style-type: none"> Wenner-Gren Project: 'The evolution of the hippocampus and adult neurogenesis: insights into the origins of human memory' • Role: Primary applicant • PI: BM Schilder • Amount: \$19,512
2016	<ul style="list-style-type: none"> Leakey Foundation Project: 'The evolution of the hippocampus and adult neurogenesis: Novel insights into the origins of human memory' • Role: Primary applicant • PI: BM Schilder • Amount: \$15,000

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



- 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

[echoverse Dependency Graph](#)

- Interactive graph showing the dependency structure of all packages within the [echoverse](#) suite.

- 2020	<ul style="list-style-type: none"> • Hex stickers 	<ul style="list-style-type: none"> • All hex stickers for R packages I've helped develop. 	<ul style="list-style-type: none"> 📍 London, UK
2023	<ul style="list-style-type: none"> • 3D Human Phenotype Ontology 	<ul style="list-style-type: none"> • 3D force-directed graph of the Human Phenotype Ontology (clouds above) with kernel density estimation projected from the x/y planes (mountains below). Connections represent the hierarchical relationships between rare diseases and their associated symptoms/phenotypes. • Associated preprint 	<ul style="list-style-type: none"> 📍 London, UK
2023	<ul style="list-style-type: none"> • Multi-scale Rare Disease Mechanisms 	<ul style="list-style-type: none"> • Network of systematically prioritised gene therapy targets for rare diseases • Associated preprint 	<ul style="list-style-type: none"> 📍 London, UK
2023	<ul style="list-style-type: none"> • Curriculum Vitae Connexa 	<ul style="list-style-type: none"> • Term co-occurrence network generated by analysing all data that went into this CV. 	<ul style="list-style-type: none"> 📍 London, UK
2021	<ul style="list-style-type: none"> • Experiments with Generative AI 	<ul style="list-style-type: none"> • wombo.art: 'Multi-omic medicine: dissecting the cell-type-specific mechanisms in neurodegeneration genomics' • wombo.art: 'Multi-omic medicine: neurodegenerative disease genomics' • wombo.art: 'Multi-omic medicine: neurodegeneration' • wombo.art: 'Neurodegeneration' 	<ul style="list-style-type: none"> 📍 London, UK
2021	<ul style="list-style-type: none"> • Lights in the dark genome: the current state of Parkinson's research 	<ul style="list-style-type: none"> • The majority of PD genetics research has focused on a relatively small number of genes. Above, are the top 75 most commonly mentioned genes in the PD literature, extracted using Geneshot. • Associated study 	<ul style="list-style-type: none"> 📍 London, UK
2020	<ul style="list-style-type: none"> • Pacrophage 	<ul style="list-style-type: none"> • Colocalised genetic loci ...but shaped as Pac-Man! • Associated study 	<ul style="list-style-type: none"> 📍 London, UK
2020	<ul style="list-style-type: none"> • Circos 	<ul style="list-style-type: none"> • Colocalised genetic loci across a variety of neurological disease GWAS and cell-type-specific QTLs. • Associated study 	<ul style="list-style-type: none"> 📍 London, UK
2019	<ul style="list-style-type: none"> • Wildfire Circle 	<ul style="list-style-type: none"> • Awarded 2nd place in the 2019 Art of the Brain competition, put on by the Mount Sinai's Friedman Brain Institute. • Exhibited and auctioned at the Grady Alexis Gallery (New York City), where all proceeds were donated to the Diversity in Neuroscience Initiative . • Featured on cover of Biological Psychiatry. 	<ul style="list-style-type: none"> 📍 New York, NY, USA
2019	<ul style="list-style-type: none"> • Wildfire 	<ul style="list-style-type: none"> • Transcriptomic data from 16k+ individual brain cells (shown as points) after reducing the dimensionality with an autoencoder and UMAP. 5 million tracts are shown interconnecting these cells, where shorter tract length represents greater similarity in their molecular profiles. 	<ul style="list-style-type: none"> 📍 New York, NY, USA
2019	<ul style="list-style-type: none"> • 3D Brain Model 	<ul style="list-style-type: none"> • 3D model of my brain generated from MRI scans. 	<ul style="list-style-type: none"> 📍 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