



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

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🌐 LinkedIn

🆔 ORCID

🔍 Google Scholar

🔄 GitHub

🐦 Twitter

📺 YouTube

🌐 Personal Website

🌐 Lab Website

SUMMARY

📅 15+ years of research

📄 23 publications

📄 4 preprints

🔧 41 software packages

📄 11 databases & apps

🗣️ 22 talks

👤 13+ years of teaching & team management

TABLE OF CONTENTS

🎓 Education

✓ Skills

✓ Expertise

📄 Publications

📄 Preprints

📄 Acknowledgements

📄 Reviewerships

🗣️ Internal talks

🗣️ Invited talks

🗣️ Conference talks

🗣️ Posters

📄 Experience

👤 Teaching

🔧 Packages

🌐 Websites

📄 Databases

💰 Grants

🏆 Awards

🏛️ Affiliations

📊 Data visualisation

🧩 Extracurricular

📅 Updated May-20-2024

📄 Made with autoCV

✓ CORE SKILLS

Research

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

- **Publication record:** **23** publications, **4** preprints and **13** awarded grants.
- **Reproducibility:** Global leader in promoting and enabling reproducible scientific practices. [Writes 100% reproducible manuscripts programmatically.](#)
- **Bioinformatics:** Created **45** Python and R packages to address key challenges in biological research.
- **High-performance computing:** Highly parallelised analyses and AI model training (CPUs and GPUs).
- **Web development:** **6+** websites, web apps, and interactive reports.

AI & Machine Learning

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

- **Causal variant prediction:** Used functional impact predictions from DNA sequence models (DeepSEA, Basenji, IMPACT) to validate SNPs prioritised with Bayesian fine-mapping. [Writes 100% reproducible manuscripts programmatically.](#)
- **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. [Writes 100% reproducible manuscripts programmatically.](#)
- **Disease genomics embeddings:** Developed VAE- and graph-based dimensionality reduction models to create a joint latent representation of genome-wide signatures from all known diseases and phenotypes.
- **Topic modeling:** Created a suite of proprietary Python packages for NLP-based topic modelling of the PubMed literature to provide business intelligence to the world's largest digital health, biotech, and pharma companies (as a consultant with [120/80 Group](#)).
- **Collaborative AI:** Uses generative AI assistants (GitHub Copilot) to accelerate and augment coding.

Project Management

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

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

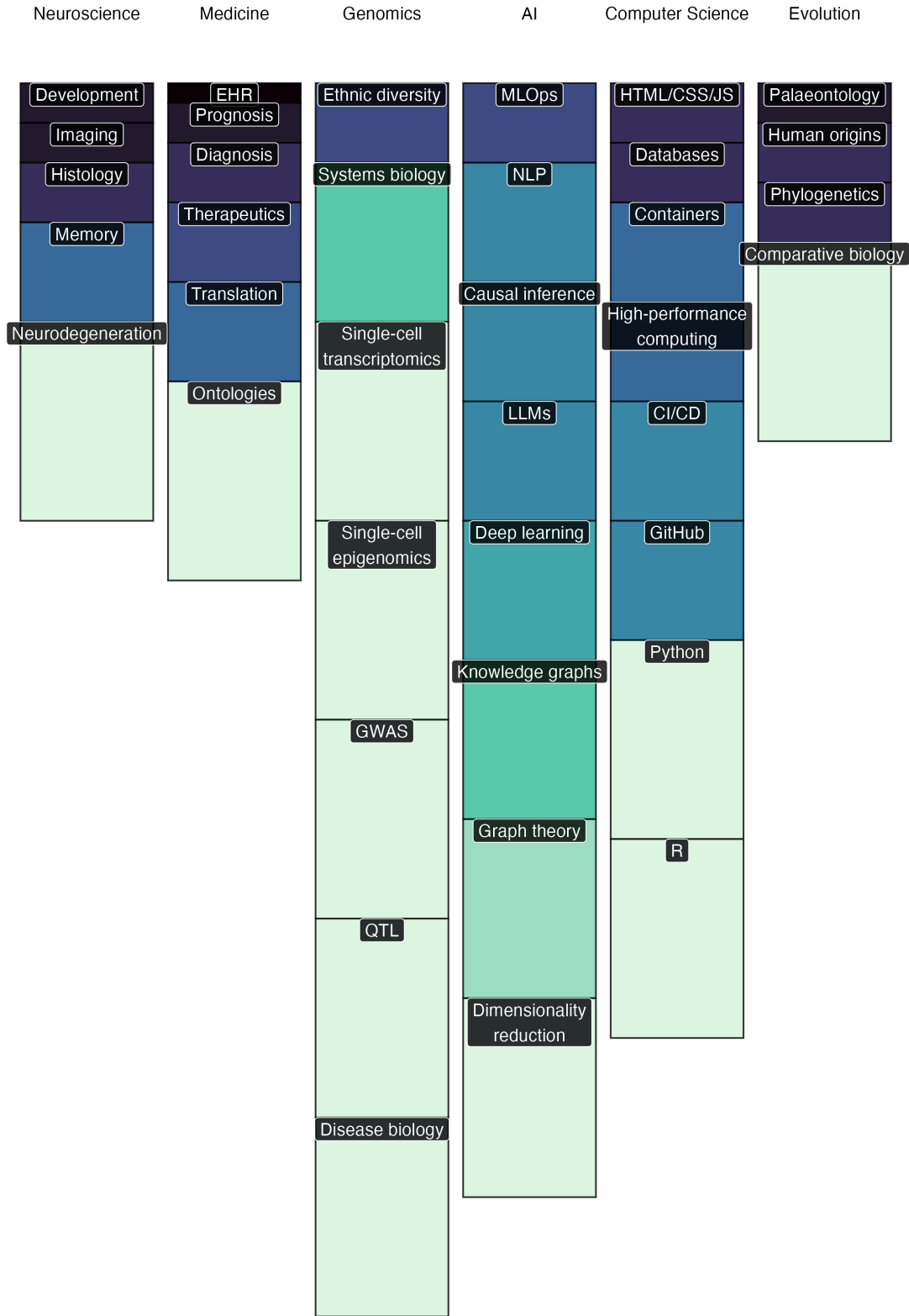
Soft skills

Advances science through effective problem formulation, collaboration and communication.

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

✓ EXPERTISE BY FIELD

The total height of each column represents overall expertise in a given domain. Rectangles are scaled to the relative level of expertise within each subdomain.







PUBLICATIONS

- 2023 ● **rworkflows: automating reproducible practices for the R community**
Nature Communications (2023) 15(149); <https://doi.org/10.1038/s41467-023-44484-5>
BM Schilder, AE Murphy, NG Skene
 News
- Featured in *Nature Communications* Editors' Highlights
- 2023 ● **Artificial intelligence for neurodegenerative experimental models**
Alzheimer's & Dementia (2023) <http://doi.org/10.1002/alz.13479>
SJ Marzi, BM Schilder, A Nott, C Sala Frigerio, S Willaime-Morawek, M Bucholc, DP Hanger, C James, PA Lewis, I Lourida, W Noble, F Rodriguez-Algarra, JA Sharif, M Tsalenchuk, LM Winchester, U Yaman, Z Yao, DEMON Network, JM Ranson, DJ Llewellyn
- 2023 ● **Artificial intelligence for dementia genetics and omics**
Alzheimer's & Dementia (2023) <http://doi.org/10.1002/alz.13427>
C Bettencourt, NG Skene, S Bandres-Ciga, E Anderson, LM Winchester, IF Foote, J Schwartzentruber, JA Botia, M Nalls, A Singleton, BM Schilder, J Humphrey, SJ Marzi, CE Toomey, 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 Sneebouer, E Navarro, BM Schilder... T Raj
 News
- Microglial transcriptomics meets genetics: new disease leads (*Nature Reviews Neurology*, 2022)
- Mighty MiGA: Microglial Genomic Atlas Zeros in on Causal AD Risk Variants (*ALZFORUM*, 2022)
- Can a Human Microglial Atlas Guide Brain Disorder Research? (*Mount Sinai Health System*, 2022)
- Polygenic Scores Paint Microglia as Culprits in Alzheimer's (*ALZFORUM*, 2021)
- 2021 ● **Multi-omic insights into Parkinson's Disease: From genetic associations to functional mechanisms**
Neurobiology of Disease (2021) 105580; <https://doi.org/10.1016/j.nbd.2021.105580>
BM Schilder, E Navarro, T Raj
- 2021 ● **Fine-Mapping of Parkinson's Disease Susceptibility Loci Identifies Putative Causal Variants**
Human Molecular Genetics (2021) ddab294; <https://doi.org/10.1093/hmg/ddab294>
BM Schilder, T Raj
- 2021 ● **echolocator: An Automated End-to-End Statistical and Functional Genomic Fine-Mapping Pipeline**
Bioinformatics (2021) btab658; <https://doi.org/10.1093/bioinformatics/btab658>
BM Schilder, J Humphrey, T Raj

- 2021 ● **MungeSumstats: A Bioconductor Package for the Standardisation and Quality Control of Many GWAS Summary Statistics**
Bioinformatics (2021) 37(23):4593-4596; <https://doi.org/10.1093/bioinformatics/btab665>
 A Murphy, **BM Schilder**, NG Skene
- 2021 ● **Dysregulation of mitochondrial and proteo-lysosomal genes in Parkinson's disease myeloid cells**
Nature Genetics (2021) <https://doi.org/10.1101/2020.07.20.212407>
 E Navarro, E Udine, K de Paiva Lopes, M Parks, G Riboldi, **BM Schilder**...T Raj
 📰 News
 - [Mount Sinai: Fighting Neurodegenerative Disorders](#) (Mount Sinai Health System, 2019)
- 2021 ● **Phenome-wide and eQTL Associations of COVID-19 Genetic Risk Loci**
iScience (2021) <https://doi.org/10.1016/j.isci.2021.102550>
 C Moon, **BM Schilder**, T Raj, K-I Huang
- 2021 ● **Genome-Wide Association Study of over 40,000 Bipolar Disorder Cases Provides Novel Biological Insights**
Nature Genetics (2021) 53:817-829; <https://doi.org/10.1038/s41588-021-00857-4>
 N Mullins, AJ Forstner, KS O'Connell, B Coombes, JRI Coleman...**BM Schilder**... et al.
 📰 News
 - [Researchers identify 64 regions of the genome that increase risk for bipolar disorder](#) (EurekAlert, 2021)
 - [Largest Bipolar Disorder Genetics Study Doubles Genetic Risk Factors](#) (Nordic Society of Human Genetics and Precision Medicine, 2021)
- 2020 ● **Tensor decomposition of stimulated monocyte and macrophage gene expression profiles identifies neurodegenerative disease-specific trans-eQTLs**
PLOS Genetics (2020) 16(9):e1008549; <https://doi.org/10.1101/499509>
 S Ramdhani, E Navarro, E Udine, AG Efthymiou, **BM Schilder**, M Parks, A Goate, T Raj
- 2019 ● **Evolutionary shifts dramatically reorganized the human hippocampal complex**
Journal of Comparative Neurology (2019) 528(17):3143-3170; <https://doi.org/10.1002/cne.24822>
BM Schilder, HM Petry, PR Hof
- 2019 ● **FAIRshake: Toolkit to Evaluate the Findability, Accessibility, Interoperability, and Reusability of Research Digital Resources**
Cell Systems (2019) 9; <https://doi.org/10.1016/j.cels.2019.09.011>
 D Clarke, L Wang, A Jones, M Wojciechowicz, D Torre, K Jagodnik, S Jenkins, P McQuilton, Z Flamholz, M Silverstein, **BM Schilder**...A Ma'ayan
 📰 News
 - [Chosen as 'Featured Frontmatter' article in Cell Systems](#)
- 2019 ● **Geneshot: search engine for ranking genes from arbitrary text queries**
Nucleic Acids Research (2019) 47(W1):W571-W577; <https://doi.org/10.1093/nar/gkz393>
 A Lachmann, **BM Schilder**, ML Wojciechowicz, D Torre, MV Kuleshov, AB Keenan, A Ma'ayan
 📰 News
 - [Geneshot: Piercing the Literature to Identify and Predict Relevant Genes](#) (University of Pittsburgh Health Sciences Library System Update, 2019)
 - [The Future of AI at the Hasso Plattner Institute for Digital Health at Mount Sinai](#) (Mount Sinai Health System, 2020)
- 2018 ● **eXpression2Kinases (X2K) Web: linking expression signatures to upstream cell signaling networks**
Nucleic Acids Research (2018) 46(W1):W171-W179; <https://doi.org/10.1093/nar/gky458>
 DJB Clarke, MV Kuleshov, **BM Schilder**, D Torre, ME Duffy, AB Keenan, A Lachmann, AS Feldmann, GW Gundersen, MC Silverstein, Z Wang
 📰 News
 - [Mount Sinai Faculty Spotlight: Ma'ayan Lab](#) (Mount Sinai Health System, 2018)
- 2015 ● **Defining elemental imitation mechanisms: A comparison of cognitive and motor-spatial imitation learning across object- and computer-based tasks**
Journal of Cognition and Development (2015) 17(2):221-243; <https://doi.org/10.1080/15248372.2015.1053483>
 F Subiaul, L Zimmerman, E Renner, **BM Schilder**, R Barr

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

PREPRINTS

- 2024 ● **Harnessing AI to annotate the severity of all phenotypic abnormalities within the Human Phenotype Ontology**
medRxiv (2024)
 KB Murphy, **BM Schilder**, NG Skene
- 2023 ● **Fine-mapping genomic loci refines bipolar disorder risk genes**
medRxiv (2023) <https://www.medrxiv.org/content/10.1101/2024.02.12.24302716v1>
 M Koromina, A Ravi, G Panagiotaropoulou, **BM Schilder**, ... S Ripke, T Raj, JRI Coleman, N Mullins
 **News**
 - Currently under journal review
- 2023 ● **Identification of cell type-specific gene targets underlying thousands of rare diseases and subtraits**
medRxiv (2023) <https://doi.org/10.1101/2023.02.13.23285820>
 KB Murphy, R Gordon-Smith, J Chapman, M Otani, **BM Schilder**, NG Skene
- 2022 ● **CUT&Tag recovers up to half of ENCODE ChIP-seq peaks**
bioRxiv (2022) <https://doi.org/10.1101/2022.03.30.486382>
 D Hu, L Abbasova, **BM Schilder**, A Nott, NG Skene, SJ Marzi

ACKNOWLEDGEMENTS

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

- 2011 ● **Trial-by-trial adaptation of decision making performance: a model-based EEG analysis**
Interdisciplinary Perspectives on Cognition, Education, and the Brain (2011) 7; <https://www.semanticscholar.org/paper/Trial-by-trial-adaptation-of-decision-making-a-EEG-Vugt-Simen/330371d08842ecd1bda332dd22351a7135b5cb1f>
M van Vugt, P Simen, J Cohen



REVIEWERSHIPS

- 2024 ● **[Unpublished article]**
BMJ Open (2024)
- 2023 ● **Multi-region brain transcriptomes uncover two subtypes of aging individuals with differences in Alzheimer risk and the impact of APOE ϵ 4**
Neuron (2023) <https://doi.org/10.1101/2023.01.25.524961>
AJ Lee, Y Ma, L Yu, RJ Dawe, C McCabe, K Arfanakis, R Mayeux, DA Bennett, HU Klein, PL De Jager
- 2023 ● **Summary statistics-based association test for identifying the pleiotropic effects with set of genetic variants**
Bioinformatics (2023) <https://doi-org.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 ● **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 Sneebouer, 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

 - Attended lectures and extended skills in extraction and analysis of big data from biomedical and neurogenomic resources.
 - Developed, performed and wrote manuscript for collaborative bioinformatics research project in less than one week.

- 2016

● **Participant**
Icahn School of Medicine at Mount Sinai (Scientific Computing & Data Science) 📍 New York, NY, USA

 - Intensive summer school in high-performance computing, coding, genome database utilization and bioinformatics methods including transcriptomics and genetic association testing.

- 2017
|
2014

● **Collaborator**
Trinity University / Southwestern National Primate Research Center (Department of Neuroscience) 📍 San Antonio, TX, USA

 - Investigated the neurobiological mechanisms underlying the ameliorating effects of exercise on relapse-remitting Multiple Sclerosis.

- 2014

● **Teaching Assistant / Project Leader**
The George Washington University / Rutgers University (Department of Anthropology) 📍 Ileret, Kenya

 - Served as Teaching Assistant while excavating Lower Paleolithic hominin sites (Homo, Paranthropus).
 - As Project Leader, investigated the running biomechanics of local Daasanach tribespeople while mentoring undergraduate students.

- 2013
|
2011

● **Research Assistant**
The George Washington University (Department of Anthropology) 📍 Washington, DC, USA

 - Performed dissection, histology, microscopy and quantitative stereology in post-mortem primate brain tissues.
 - Trained junior and senior personnel on lab protocols.

- 2013
|
2011

● **Senior Lab Manager**
The George Washington University (Department of Speech, Language & Hearing Sciences) 📍 Washington, DC, USA

 - Organized and trained dozens of undergraduates to conduct weekly cognitive development research; designed and/or directly contributed to over 15 research projects in two years.

- 2012

● **Volunteer Researcher**
University of Winnipeg / University of Belgrade (Department of Anthropology / Department of Archaeology) 📍 Sicevo, Serbia

 - Excavated Paleolithic fossils and tools (H. heidelbergensis, H. neanderthalensis) at Mala Balanica, Velika Balanica, and Pešturina sites.

- 2011

● **Volunteer Researcher**
Universidad de Murcia (Department of Zoology & Physical Anthropology) 📍 Murcia, Spain

 - Excavated Paleolithic fossils and tools from Cueva Negra (H. heidelbergensis) and Sima de las Palomas (H. neanderthalensis) with an international research team.

- 2011

● **Volunteer Research Intern**
American Museum of Natural History (Division of Anthropology) 📍 New York, NY, USA


 - Contributed to paleoanthropological research on primate fossils using 3D morphometry imaging equipment including Minolta, Microscribe and CT.

- 2010

● **Paid Research Intern**
Princeton University (Princeton Neuroscience Institute) 📍 Princeton, NJ, USA

 - Investigated the neural basis of decision-making in humans.
 - Recruited participants, recorded EEG and analyzed data in MATLAB.


2010
|
2009

Student Researcher
Brown University (Department of Cognitive, Linguistic & Psychological Sciences)  Providence, RI, USA

- Experimental Analysis of Animal Behavior & Cognition: Conducted various operant conditioning experiments on rats. Gained experience in animal behavioral training, data collection, and data analysis in MATLAB.
- Laboratory in Genes and Behavior: Tested transgenic mice with modified N-type voltage-gated calcium channel subunits in a battery of cognitive and sensorimotor tasks. Results were published.


 **TEACHING / MENTORING EXPERIENCE**

-
|
2020

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


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

2020
|
2019

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


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

2018

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


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

2018

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


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

2017
|
2016

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

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














2015




















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



















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


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


SOFTWARE PACKAGES


1. • **MSTExplorer** 
Multi-Scale Targets Explorer: Systematically identify, prioritise and visualise cell-type-specific gene therapy targets across the phenome.
[🔗 https://github.com/neurogenomics/MSTExplorer](https://github.com/neurogenomics/MSTExplorer)
[📄 https://doi.org/10.1101/2023.02.13.23285820](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://github.com/neurogenomics/HPOExplorer)
[📄 https://doi.org/10.1101/2023.02.13.23285820](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](https://github.com/neurogenomics/KGExplorer)
4. • **autoCV**    
Automatically generate and style your CV from tables.
[🔗 https://github.com/bschilder/autoCV](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](https://github.com/scverse/anndataR)
6. • **gptPhD** 
Query Large Language Models for the purposes of systematically extracting biomedical knowledge.
[🔗 https://github.com/neurogenomics/gptPhD](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](https://github.com/bschilder/ThreeWayTest)
8. • **SCAVENGE** 
Variant to function mapping at single-cell resolution through network propagation.
[🔗 https://github.com/sankaranlab/SCAVENGE](https://github.com/sankaranlab/SCAVENGE)
[📄 https://doi.org/10.1038/s41587-022-01341-y](https://doi.org/10.1038/s41587-022-01341-y)


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

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

- 38. **catalogueR** 


R package for rapid API-access and colocalization of summary statistics from eQTL Catalogue.
<https://github.com/RajLabMSSM/catalogueR>
<https://doi.org/10.1093/bioinformatics/btab658>
- 39. **TopicModeler** 


Proprietary Python package to run advanced topic modeling on text corpuses.
- 40. **LinkReporter** 


Proprietary Python package to extract job postings and company employee listings from LinkedIn and generate interactive business intelligence reports.
- 41. **PubReporter** 


Proprietary Python package 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
 - **PI:** BM Schilder
 - **Amount:** \$250
- 2023 **BioC2023 Scholarship, Bioconductor**
Project: ‘rworkflows: taming the Wild West of R packages’
 **News**
 - Awarded to support attending the [BioC2023 meeting](#). Additionally included free lodging.
- **Role:** Primary applicant
 - **PI:** BM Schilder
 - **Amount:** \$1500

- 2023

• **Junior Scientist Conference Grant, The Genetics Society**
Project: 'Identification of cell type-specific gene targets underlying thousands of rare diseases and subtraits'
 • **Role:** Primary applicant • **Amount:** £750
 • **PI:** BM Schilder
- 2023

• **Imperial UK Research Institute Impact Acceleration Account, Imperial College London**
Project: 'Creating commercial kit solutions for single cell epigenetic profiling of histone marks and transcription factors'
 • **Role:** Co-applicant • **Amount:** £80,000
 • **PI:** NG Skene
- 2024
|
2022

• **Turing Community Award, Alan Turing Institute**
Project: 'Multi-omic medicine: dissecting the cell-type-specific molecular mechanisms underlying neurodegenerative disease genomics'
 • **Role:** Primary applicant • **Amount:** £1,500
 • **PI:** BM Schilder
- 2022

• **National Institutes of Health**
Project: 'Statistical and functional fine-mapping of bipolar disorder genetic risk loci'
 • **Role:** Co-applicant • **PI:** N Mullins
- 2021

• **Collaborative Single Cell and Spatial Transcriptomics Studies Award Programme, UK Dementia Research Institute**
Project: 'Amplifying genome coverage of single cell epigenetic profiling of the human brain'
 • **Role:** Co-applicant • **Amount:** £12,790
 • **PI:** D Hu, NG Skene
- 2020

• **National Institutes of Health**
Project: "Cognitive Systems Analysis of Alzheimer's Disease Genetic and Phenotypic Data"
 • **Role:** Co-applicant • **Amount:** \$2,523,431
 • **PI:** T Raj, D Knowles
- 2024
|
2020

• **UK Dementia Research Institute**
Project: 'UK DRI at Imperial Distinguished Studentship'
 • **Role:** Primary applicant • **Amount:** £217,000
 • **PI:** BM Schilder
- 2019
|
2017

• **The Michael J. Fox Foundation**
Project: "The Role of Peripheral Myeloid Cells in Parkinson's Disease"
 • **Role:** Fundee • **PI:** T Raj
- 2020
|
2017

• **The Michael J. Fox Foundation**
Project: 'Functional Fine-Mapping of LRRK2 Locus'
 • **Role:** Fundee • **PI:** T Raj
- 2017

• **National Science Foundation**
Project: 'The evolution of the hippocampus and adult neurogenesis: novel insights into the origins of human memory'
 • **Role:** Primary applicant • **Amount:** \$31 543
 • **PI:** BM Schilder
- 2017

• **Wenner-Gren**
Project: 'The evolution of the hippocampus and adult neurogenesis: insights into the origins of human memory'
 • **Role:** Primary applicant • **Amount:** \$19,512
 • **PI:** BM Schilder

2016 ● **Leakey Foundation**
Project: 'The evolution of the hippocampus and adult neurogenesis: Novel insights into the origins of human memory'
• **Role:** Primary applicant • **Amount:** \$15,000
• **PI:** BM Schilder

2016 ● **COSMOS Club**
Project: 'The evolution of adult neurogenesis across primates'
• **Role:** Primary applicant • **Amount:** \$3,250
• **PI:** BM Schilder



AWARDS

2023 ● **Prize for Computational Reproducibility in Dementia Research, UK Dementia Research Institute**
Project: 'workflows: 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](#)



- Bipolar Disorder Working Group



- [Chair of the Bioconductor Cloud Methods Working Group](#)
- [Lead of the Bioconductor GitHub Actions Subgroup](#)



IMPERIAL
ENTREPRENEURS

- Member



DATA VISUALISATION / ARTWORK PORTFOLIO

- 2022

 - echoverse Dependency Graph**

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

📍 London, UK
- |

2020

 - Hex stickers**

 - All hex stickers for R packages I've helped develop.

📍 London, UK
- 2023

 - 3D Human Phenotype Ontology**

 - 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](#)

📍 London, UK
- 2023

 - Multi-scale Rare Disease Mechanisms**

 - Network of systematically prioritised gene therapy targets for rare diseases
 - [Associated preprint](#)

📍 London, UK
- 2023

 - Curriculum Vitae Connexa**

 - Term co-occurrence network generated by analysing all data that went into this CV.

📍 London, UK
- 2021

 - Experiments with Generative AI**

 - [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'

📍 London, UK
- 2021

 - Lights in the dark genome: the current state of Parkinson's research**

 - 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](#)

📍 London, UK
- 2020

 - Pacrophage**

 - Colocalised genetic loci ...but shaped as Pac-Man!
 - [Associated study](#)

📍 London, UK
- 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** 📍 New York, NY, USA

- Transcriptomic data from 16k+ individual brain cells (shown as points) after reducing the dimensionality with an autoencoder and UMAP. 5 million tracts are shown interconnecting these cells, where shorter tract length represents greater similarity in their molecular profiles.

2019 ● **3D Brain Model** 📍 New York, NY, USA

- 3D model of my brain generated from MRI scans.



EXTRACURRICULAR EXPERIENCE

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2003 ● **Competitive Running Career** 📍 Earth

- 8+ years of varsity and Division I cross country, winter track, and spring track throughout high school and college.
- Year-round, daily training and travel to weekly competitions necessitated a dedicated and regimented lifestyle in order to succeed as a student-athlete
- Running remains a passion of mine and I enjoy training for ultra-marathons in my free time.
- This passion, work ethic and self-insight have carried over to all aspects of my life, including my career as a researcher.

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1995 ● **Music Production** 📍 Earth

- Writes, records, produces and performs original music.
- Instruments: keys, percussion, vocals, etc.
- Proficient in Logic Pro X Digital Audio Workstation (DAW).
- Experiments with generative AI.