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
- 📞 **US** +1 908-268-9859
- 📞 **UK** +44 073-0653-7736
- 🔗 **LinkedIn**
- iD **ORCID**
- G **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**

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📅 *Updated May-28-2024*
📦 *Made with autoCV*

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✓ 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 anayses and AI model training (CPUs and GPUs).
- **Web development**: **6**+ websites, web apps, and interactive reports.

AI & Machine Learning

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

- **Causal variant effect prediction**: Used functional impact predictions from DNA sequence models (DeepSEA, Basenji, IMPACT) to validate SNPs prioritised with Bayesian fine-mapping. 📄
- **Foundation models**: Used transformer trained on >36M cells and protein sequence embeddings to uncover cell type-specific mechanisms of disease.
- **LLM knowledge extraction**: Developed framework to extract quantitative metrics of phenotype severity from GPT-4. 📄
- **Disease genomics embeddings**: Developed VAE/graph models to reveal joint latent representation of genomic signatures across all diseases and phenotypes.
- **NLP**: Created a suite of proprietary Python packages for advanced topic modelling of the PubMed literature to provide business intelligence to the world's largest digital health, biotech, and pharma companies (as a consultant with 120/80 Group).
- **Tensor decomposition**: Applied multi-condition factorisation to efficiently discover neurodegeneration-relevant *trans*-eQTLs 📄

Project Management

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

- **Documentation**: Defines obectives 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.
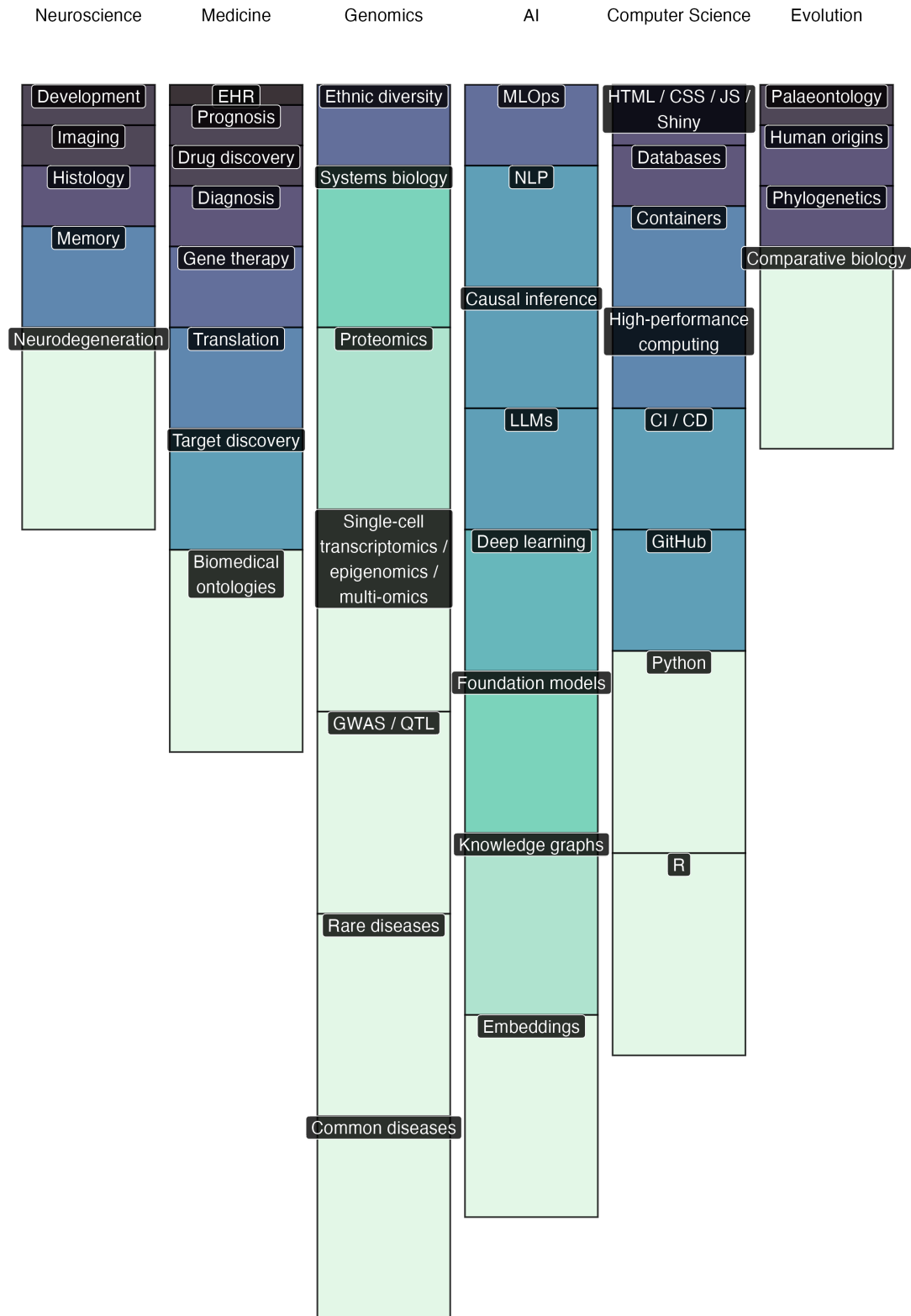
Soft skills

Advances science through effective problem formulation, collaboration and communcation.

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

EXPERTISE BY FIELD

The total height of each column represents my overall expertise in a given domain. The color and height of each rectangle are scaled to my relative level of expertise within each subdomain.

Neuroscience	Medicine	Genomics	AI	Computer Science	Evolution

Neuroscience: Development, Imaging, Histology, Memory, Neurodegeneration

Medicine: EHR, Prognosis, Drug discovery, Diagnosis, Gene therapy, Translation, Target discovery, Biomedical ontologies

Genomics: Ethnic diversity, Systems biology, Proteomics, Single-cell transcriptomics / epigenomics / multi-omics, GWAS / QTL, Rare diseases, Common diseases

AI: MLOps, NLP, Causal inference, LLMs, Deep learning, Foundation models, Knowledge graphs, Embeddings

Computer Science: HTML / CSS / JS / Shiny, Databases, Containers, High-performance computing, CI / CD, GitHub, Python, R

Evolution: Palaeontology, Human origins, Phylogenetics, Comparative biology

📄 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 Khleifat, A Badhwar, N Clarke, A Dehsarvi, CR Madan, SJ Marzi, C Shand, **BM Schilder**, S Tamburin, HM Tantiangco, I Lourida, DJ Llewellyn, JM Ranson

2023 ● **EpiCompare: R package for the comparison and quality control of epigenomic peak files**
Bioinformatics Advances (2023) 13(1):vbad049; https://doi.org/10.1093/bioadv/vbad049
S Choi, **BM Schilder**, L Abbasova, AE Murphy, NG Skene

2022 ● **Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors**
Biological Psychiatry (2022) 91(3):313-327; https://doi.org/10.1016/j.biopsych.2021.05.029
N Mullins, J Kang, AI Campos,…**BM Schilder**, et al.

2022 ● **Genetic analysis of the human microglial transcriptome across brain regions, aging and disease pathologies**
Nature Genetics (2022) https://doi.org/10.1038/s41588-021-00976-y
K de Paiva Lopes, G JL Snijders, J Humphrey, A Allan, M Sneeboer, E Navarro, **BM Schilder**…T Raj
📰 **News**
- Microglial transcriptomics meets genetics: new disease leads (Nature Reviews Neurology, 2022)
- Mighty MiGA: Microglial Genomic Atlas Zeros in on Causal AD Risk Variants (ALZFORUM, 2022)
- Can a Human Microglial Atlas Guide Brain Disorder Research? (Mount Sinai Health System, 2022)
- Polygenic Scores Paint Microglia as Culprits in Alzheimer's (ALZFORUM, 2021)

2021 ● **Multi-omic insights into Parkinson's Disease: From genetic associations to functional mechanisms**
Neurobiology of Disease (2021) 105580; https://doi.org/10.1016/j.nbd.2021.105580
BM Schilder, E Navarro, T Raj

2021 ● **Fine-Mapping of Parkinson's Disease Susceptibility Loci Identifies Putative Causal Variants**
Human Molecular Genetics (2021) ddab294; https://doi.org/10.1093/hmg/ddab294
BM Schilder, T Raj

2021 ● **echolocatoR: An Automated End-to-End Statistical and Functional Genomic Fine-Mapping Pipeline**
Bioinformatics (2021) btab658; https://doi.org/10.1093/bioinformatics/btab658
BM Schilder, J Humphrey, T Raj

2021

MungeSumstats: A Bioconductor Package for the Standardisation and Quality Control of Many GWAS Summary Statistics
Bioinformatics (2021) 37(23):4593-4596; https://doi.org/10.1093/bioinformatics/btab665
A Murphy, **BM Schilder**, NG Skene

2021

Dysregulation of mitochondrial and proteo-lysosomal genes in Parkinson's disease myeloid cells
Nature Genetics (2021) https://doi.org/10.1101/2020.07.20.212407
E Navarro, E Udine, K de Paiva Lopes, M Parks, G Riboldi, **BM Schilder**…T Raj
📖 **News**
- Mount Sinai: Fighting Neurodegenerative Disorders (Mount Sinai Health System, 2019)

2021

Phenome-wide and eQTL Associations of COVID-19 Genetic Risk Loci
iScience (2021) https://doi.org/10.1016/j.isci.2021.102550
C Moon, **BM Schilder**, T Raj, K-l Huang

2021

Genome-Wide Association Study of over 40,000 Bipolar Disorder Cases Provides Novel Biological Insights
Nature Genetics (2021) 53:817-829; https://doi.org/10.1038/s41588-021-00857-4
N Mullins, AJ Forstner, KS O'Connell, B Coombes, JRI Coleman…**BM Schilder**… et al.
📖 **News**
- Researchers identify 64 regions of the genome that increase risk for bipolar disorder (EurekAlert, 2021)
- Largest Bipolar Disorder Genetics Study Doubles Genetic Risk Factors (Nordic Society of Human Genetics and Precision Medicine, 2021)

2020

Tensor decomposition of stimulated monocyte and macrophage gene expression profiles identifies neurodegenerative disease-specific trans-eQTLs
PLOS Genetics (2020) 16(9):e1008549; https://doi.org/10.1371/journal.pgen.1008549
S Ramdhani, E Navarro, E Udine, AG Efthymiou, **BM Schilder**, M Parks, A Goate, T Raj

2019

Evolutionary shifts dramatically reorganized the human hippocampal complex
Journal of Comparative Neurology (2019) 528(17):3143-3170; https://doi.org/10.1002/cne.24822
BM Schilder, HM Petry, PR Hof

2019

FAIRshake: Toolkit to Evaluate the Findability, Accessibility, Interoperability, and Reusability of Research Digital Resources
Cell Systems (2019) 9; https://doi.org/10.1016/j.cels.2019.09.011
D Clarke, L Wang, A Jones, M Wojciechowicz, D Torre, K Jagodnik, S Jenkins, P McQuilton, Z Flamholz, M Silverstein, **BM Schilder**…A Ma'ayan
📖 **News**
- Chosen as 'Featured Frontmatter' article in Cell Systems

2019

Geneshot: search engine for ranking genes from arbitrary text queries
Nucleic Acids Research (2019) 47(W1):W571-W577; https://doi.org/10.1093/nar/gkz393
A Lachmann, **BM Schilder**, ML Wojciechowicz, D Torre, MV Kuleshov, AB Keenan, A Ma'ayan
📖 **News**
- Geneshot: Piercing the Literature to Identify and Predict Relevant Genes (University of Pittsburgh Health Sciences Library System Update, 2019)
- The Future of AI at the Hasso Plattner Institute for Digital Health at Mount Sinai (Mount Sinai Health System, 2020)

2018

eXpression2Kinases (X2K) Web: linking expression signatures to upstream cell signaling networks
Nucleic Acids Research (2018) 46(W1):W171-W179; https://doi.org/10.1093/nar/gky458
DJB Clarke, MV Kuleshov, **BM Schilder**, D Torre, ME Duffy, AB Keenan, A Lachmann, AS Feldmann, GW Gundersen, MC Silverstein, Z Wang
📖 **News**
- Mount Sinai Faculty Spotlight: Ma'ayan Lab (Mount Sinai Health System, 2018)

2015

Defining elemental imitation mechanisms: A comparison of cognitive and motor-spatial imitation learning across object- and computer-based tasks
Journal of Cognition and Development (2015) 17(2):221-243; https://doi.org/10.1080/15248372.2015.1053483
F Subiaul, L Zimmerman, E Renner, **BM Schilder**, R Barr

2015

Take the monkey and run
Journal of Neuroscience Methods (2015) 248:28-31; http://doi.org/10.1016/j.jneumeth.2015.03.023
KA Phillips, MK Hambright, K Hewes, **BM Schilder**, CN Ross, SD Tardif
📖 **News**
- Monkeys on a Treadmill? A Conversation with Dr. Kimberley Phillips (Why Social Science?)

2014

Becoming a high-fidelity - super - imitator: what are the contributions of social and individual learning?
Developmental Science (2014) 18(6):1025-1035; http://doi.org/10.1111/desc.12276
F Subiaul, EM Patterson, **BM Schilder**, E Renner, R Barr

2014

Working memory constraints on imitation and emulation
Journal of Experimental Child Psychology (2014) 128:190-200; http://doi.org/10.1016/j.jecp.2014.07.005
F Subiaul, **BM Schilder**

📑 PREPRINTS

2024

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 compehensive statistical and functional fine-mapping pipeline applied to Bipolar Disorder GWAS risk loci**
European Neuropsychopharmacology (2022) 63:e14; http://dx.doi.org/10.1016/j.euroneuro.2022.07.037
M Koromina, A Ravi, BM Schilder, B Muller, J Coleman, T Raj, N Mullins

2021   **Genetic Effects on Human Microglia Transcriptome in Neuropsychiatric Diseases**
Biological Psychiatry (2021) 89(9):S84-S85; https://doi.org/10.1016/j.biopsych.2021.02.225
G Snijders, K de Paiva Lopes, J Humphrey, S Allan, M Sneeboer, R Navarro, BM Schilder, R Vialle, M Parks, R Missall, W van Zuiden, F Gigase, R Kubler, AB van Berlekom, C Bottcher, J Priller, R Kahn, L de Witte, T Raj

2020   **Cell-type-specific reconstruction of primate evolution from genomic positive selection**
Rising Scientist Day at Imperial College London (2020)
K Murphy, BM Schilder, NG Skene

2019   **Automated genetic and functional fine-mapping of Parkinson's Disease Loci**
American Society of Human Genetics (2019)
BM Schilder, T Raj

2019   **Parkinson's disease derived monocytes show alteration in the phago-lysosomal pathway**
American Society of Human Genetics (2019)
E Udine, E Navarro, …BM Schilder, …T Raj

2018   **Learning X2K: Parameter Optimization via Genetic Algorithms to Calibrate the Expression2Kinases Pipeline**
Illuminating the Druggable Genome (2018)
BM Schilder, A Lachmann, M Kuleshov, A Ma'ayan

2018   **Learning X2K: Parameter Optimization via Genetic Algorithms to Calibrate the Expression2Kinases Pipeline**
Big Data 2 Knowledge - Library of Integrated Network-Based Cellular Signatures (LINCS) (2018)
BM Schilder, A Lachmann, M Kuleshov, A Ma'ayan

2017   **The evolution of the human hippocampus and neuroplasticity**
Association for American Physical Anthropologists (2017) https://www.abstractsonline.com/pp8/index.html#!/4071/presentation/4471
BM Schilder, BJ Bradley, CC Sherwood

2016   **The molecular evolution of plasticity and the human hippocampus**
Society for Neuroscience (2016) https://www.abstractsonline.com/pp8/index.html#!/4071/presentation/4471
BM Schilder, BJ Bradley, CC Sherwood

2015 • **Effects of exercise on disease progression and cognition in the marmoset EAE model**
JB Johnston Club for Evolutionary Neuroscience (2015)
KA Phillips, MK Hambright, K Hewes, BM Schilder, B Jagessar, B t'Hart, SD Tardif

2015 • **The effects of climatic trends, variability, and rates of change on mammalian brain evolution**
Association for American Physical Anthropologists (2015)
BM Schilder, WA Barr, R Bobe, CC Sherwood

2015 • **Individual, Observational, and Imitation Learning in Orangutans and Children**
Association for American Physical Anthropologists (2015)
E Renner, BM Schilder, F Subiaul

2014 • **The helper hinderer task revisited: an infant eye tracking study**
The George Washington University Research Day (2014)
A Gokhale, BM Schilder, F Subiaul

2013 • **Dendritic morphology of pyramidal neurons across the visual stream: A direct comparison of chimpanzees and humans**
Society for Neuroscience (2013)
BM Schilder, O Adeyo

2013 • **The striatum in the evolution of learned vocalizations: Understanding the neurobiological precursors to human speech using a chimpanzee model**
Society for Neuroscience (2013)
S Bianchi, T Duka, G Muntane, BM Schilder, CD Stimpson, WD Hopkins

2013 • **Imitation & emulation in a novel box task**
Association for Psychological Science (2013)
L Zimmerman, N Brito, C Mendelson, R Barr, E Renner, BM Schilder, F Subiaul

2013 • **A study of imitation and working memory in 2- to 4- year-olds**
Association for Psychological Science (2013)
R Barr, F Subiaul, L Zimmerman, L Renner, BM Schilder, C Mendelson, L Golojuch

2013 • **The impact of wealth on sharing preferences in children**
Child Development Society (2013)
J Miller, BM Schilder, L Peizer, F Subiaul

💼 RESEARCH EXPERIENCE

-
|
2019 • **Lead Data Scientist**
120/80 Group   📍 New York, NY, USA
• Offers data-driven consultation services to a wide portfolio of high-profile digital healthcare, pharmaceutical and biotech companies.
• Developed a suite of proprietary softwares to extract customised business intelligence from the published literature to generate customised and interpretable reports to clients.
• Provides clients guidance on strategic AI implementation, data analysis, publication and transparency.

2020
|
2018 • **Bioinformatician II**
Icahn School of Medicine at Mount Sinai (Department of Neuroscience / Department of Neurology / Department of Genetics & Genomics / Ronald M. Loeb Center for Alzheimer's Disease)
📍 New York, NY, USA
• Developed machine learning systems to integrate large-scale multi-omics datasets (e.g. whole-genome sequencing, bulk and single-cell RNA-seq, epigenomics, clinical data) to uncover the molecular mechanisms underlying neurodegenerative diseases (e.g. Alzheimer's, Parkinson's, ALS).
• Computationally identified specific disease-causal variants, pathways and cell-types for subsequent functional wet lab validation (e.g. CRISPR-cas9 editing in patient-derived cell cultures, iPSCs and cerebral organoids).

2018 | 2017

Bioinformatician II
Icahn School of Medicine at Mount Sinai (Department of Pharmacological Sciences)   📍 New York, NY, USA
- Conducted computational systems biology research. Integrated and analyzed large-scale genomic and biomedical data (e.g. Python, R, JavaScript).
- Developed evolutionary algorithm to optimize gene network kinase regulator prediction (eXpression2Kinases).
- Developed and deployed computational tools, software, databases and web applications for basic and clinical research, resulting in 3 peer-reviewed publications.

2017

Participant
Technische Universität Dresden / eMed (Summer School in Systems Medicine)   📍 Frauenchiemsee, Germany
- Attended lectures and extended skills in extraction and analysis of big data from biomedical and neurogenomic resources.
- Developed, performed and wrote manuscript for collaborative bioinformatics research project in less than one week.

2016

Participant
Icahn School of Medicine at Mount Sinai (Scientific Computing & Data Science)   📍 New York, NY, USA
- Intensive summer school in high-performance computing, coding, genome database utilization and bioinformatics methods including transcriptomics and genetic association testing.

2017 | 2014

Collaborator
Trinity University / Southwestern National Primate Research Center (Department of Neuroscience)
   📍 San Antonio, TX, USA
- Investigated the neurobiological mechanisms underlying the ameliorating effects of exercise on relapse-remitting Multiple Sclerosis.

2014

Teaching Assistant / Project Leader
The George Washington University / Rutgers University (Department of Anthropology)   📍 Ileret, Kenya
- Served as Teaching Assistant while excavating Lower Paleolithic hominin sites (Homo, Paranthropus).
- As Project Leader, investigated the running biomechanics of local Daasanach tribespeople while mentoring undergraduate students.

2013 | 2011

Research Assistant
The George Washington University (Department of Anthropology)   📍 Washington, DC, USA
- Performed dissection, histology, microscopy and quantitative stereology in post-mortem primate brain tissues.
- Trained junior and senior personnel on lab protocols.

2013 | 2011

Senior Lab Manager
The George Washington University (Department of Speech, Language & Hearing Sciences)
   📍 Washington, DC, USA
- Organized and trained dozens of undergraduates to conduct weekly cognitive development research; designed and/or directly contributed to over 15 research projects in two years.

2012

Volunteer Researcher
University of Winnipeg / University of Belgrade (Department of Anthropology / Department of Archaeology)
   📍 Sićevo, Serbia
- Excavated Paleolithic fossils and tools (H. heidelbergensis, H. neanderthalensis) at Mala Balanica, Velika Balanica, and Pešturina sites.

2011

Volunteer Researcher
Universidad de Murcia (Department of Zoology & Physical Anthropology)   📍 Murcia, Spain
- Excavated Paleolithic fossils and tools from Cueva Negra (H. heidelbergensis) and Sima de las Palomas (H. neanderthalensis) with an international research team.

2011

Volunteer Research Intern
American Museum of Natural History (Division of Anthropology)   📍 New York, NY, USA
- Contributed to paleoanthropological research on primate fossils using 3D morphometry imaging equipment including Minolta, Microscribe and CT.

2010

Paid Research Intern
Princeton University (Princeton Neuroscience Institute)   📍 Princeton, NJ, USA
- Investigated the neural basis of decision-making in humans.
- Recruited participants, recorded EEG and analyzed data in MATLAB.

2010 | 2009

Student Researcher

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

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

🖳 TEACHING / MENTORING EXPERIENCE

- | 2020

Research Mentor

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

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

2020 | 2019

Research Mentor

Icahn School of Medicine at Mount Sinai (Department of Neuroscience / Department of Neurology / Department of Genetics & Genomics / Ronald M. Loeb Center for Alzheimer's Disease)

📍 New York, NY, USA

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

2018

Research Co-mentor

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

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

2018

Guest Lecturer

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

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

2017 | 2016

Research Mentor

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

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

2015

Teaching Assistant

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

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

2014 Teaching Assistant
The George Washington University (Department of Psychology) 📍 Washington, DC, USA
   • Course: 'Biological Psychology'
   • Led undergraduates in article discussions, graded all assignments and exams, and provided additional educational support during office hours.

2014
|
2013 Teaching Assistant
The George Washington University (Department of Anthropology) 📍 Washington, DC, USA
   • Course: 'Biological Anthropology'
   • Led undergraduate students in two, 2-hour lab sessions per week, graded lab assignments and exams, and provided additional educational support during office hours.

2013
|
2012 Research Mentor
The George Washington University (Department of Psychology) 📍 Washington, DC, USA
   • Mentored students and affiliated projects:
   • Anushka Gokhale (BSc): 'Infants' Social Assessment of Characters Through Eye Gaze'

2013
|
2011 Lab Protocol Trainer
The George Washington University (Department of Anthropology) 📍 Washington, DC, USA
   • Trained undergraduate, graduate, and post-doctoral researchers in Social Cognition Lab and Lab for Evolutionary Neuroscience in a variety of methodological research protocols.

🔧 SOFTWARE PACKAGES

1. **MSTExplorer** Ⓡ
Multi-Scale Targets Explorer: Systematically identify, prioritise and visualise cell-type-specific gene therapy targets across the phenome.
   https://github.com/neurogenomics/MSTExplorer
   https://doi.org/10.1101/2023.02.13.23285820

2. **HPOExplorer** Ⓡ
Import, annotate and visualise the 18k+ hierarchically structured clinical phenotypes across the Human Phenotype Ontology.
   https://github.com/neurogenomics/HPOExplorer
   https://doi.org/10.1101/2023.02.13.23285820

3. **KGExplorer** Ⓡ 🐍
Query, construct, and analyse large-scale biomedical knowledge graphs and ontologies.
   https://github.com/neurogenomics/KGExplorer

4. **autoCV** Ⓡ 🄷 🄲 🄹
Automatically generate and style your CV from tables.
   https://github.com/bschilder/autoCV

5. **anndataR** Ⓡ 🐍
Bring the power and flexibility of AnnData to the R ecosystem, allowing you to effortlessly manipulate and analyze your single-cell data.
   https://github.com/scverse/anndataR

6. **gptPhD** Ⓡ
Query Large Language Models for the purposes of systematically extracting biomedical knowledge.
   https://github.com/neurogenomics/gptPhD

7. **ThreeWayTest** Ⓡ
Summary statistics-based association test for identifying the pleiotropic effects with set of genetic variants.
   https://github.com/bschilder/ThreeWayTest

8. **SCAVENGE** Ⓡ
Variant to function mapping at single-cell resolution through network propagation.
   https://github.com/sankaranlab/SCAVENGE
   https://doi.org/10.1038/s41587-022-01341-y

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

11. **PeakyFinders** R
R package for mining, calling, and importing epigenomic peaks.
○ https://github.com/neurogenomics/PeakyFinders

12. **graphiti** R
Extract colour palettes from graffiti artworks.
○ https://github.com/bschilder/graphiti

13. **SkillNet** R
Creates user-specific contribution networks from GitHub Organization repositories.
○ https://github.com/neurogenomics/SkillNet

14. **phenoRx** R
Make cell type-specific predictions for patients based on clinical phenotypes and/or risk genes.
○ https://github.com/neurogenomics/phenoRx

15. **phenomix** R 🐍
R package for the exploration and analysis of many genotype-phenotype datasets at once.
○ https://github.com/neurogenomics/phenomix

16. **MAGMA.Celltyping** R
Identify cell types underlying the associations found in GWAS summary statistics.
○ https://github.com/neurogenomics/MAGMA_Celltyping

17. **EWCE** R
Expression Weighted Celltype Enrichment.
○ https://github.com/NathanSkene/EWCE

18. **EpiCompare** R
R package for QC and benchmarking epigenetic datasets.
○ https://github.com/neurogenomics/EpiCompare
📄 https://doi.org/10.1101/2022.07.22.501149

19. **orthogene** R
Interspecies gene mapping.
○ https://github.com/neurogenomics/orthogene

20. **MungeSumstats** R
Standardise the format of summary statistics from GWAS.
○ https://github.com/neurogenomics/MungeSumstats
📄 https://doi.org/10.1093/bioinformatics/btab665

21. **scNLP** R
Tools for applying natural language processing (NLP) techniques to single-cell (sc) omics data.
○ https://github.com/neurogenomics/scNLP

22. **scKirby** R 🐍
Automated ingestion and conversion of various single-cell data formats.
○ https://github.com/neurogenomics/scKirby

23. **geneshotR** R
R package for querying and processing results from Geneshot.
○ https://github.com/bschilder/geneshotR

24. **templateR** R
Self-updating template for developing R packages.
○ https://github.com/neurogenomics/templateR
📄 https://doi.org/10.21203/rs.3.rs-2399015/v1

25. **echoverseTemplate** R
Self-updating template for creating echoverse R packages.
 https://github.com/RajLabMSSM/echoverseTemplate/
 https://doi.org/10.1093/bioinformatics/btab658

26. **echolocatoR** R 🐍
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** R
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** R
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
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** R 🐍
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** R 🐍
Tabix indexing and querying.
 https://github.com/RajLabMSSM/echotabix
 https://doi.org/10.1093/bioinformatics/btab658

32. **echoLD** R 🐍
LD downloading and processing.
 https://github.com/RajLabMSSM/echoLD
 https://doi.org/10.1093/bioinformatics/btab658

33. **echofinemap** R 🐍
Statistical and functional fine-mapping functions.
 https://github.com/RajLabMSSM/echofinemap
 https://doi.org/10.1093/bioinformatics/btab658

34. **echodeps** R
Creates interactive dependency networks for R packages.
 https://github.com/RajLabMSSM/echodeps
 https://doi.org/10.1093/bioinformatics/btab658

35. **echogithub** R
Access and process metadata from GitHub.
 https://github.com/RajLabMSSM/echogithub
 https://doi.org/10.1093/bioinformatics/btab658

36. **devoptera** R
Practical tools for R developers.
 https://github.com/RajLabMSSM/devoptera
 https://doi.org/10.1093/bioinformatics/btab658

37. **downloadR** R
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** R
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** R
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** ☕ 🐍 JS HTML CSS
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** ☕ 🐍 JS HTML CSS
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** HTML CSS JS

   ○ https://github.com/bschilder/BMSchilder
   ⊘ https://bschilder.github.io/BMSchilder

2. **Official Raj Lab Website** HTML CSS JS

   ○ 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 • **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: 'rworkflows: taming the Wild West of R packages'
📖 **News**
- Awarded honourable mention.

2022 • **Prize for Computational Reproducibility in Dementia Research,**
UK Dementia Research Institute
Project: 'MungeSumstats: A Bioconductor package for the standardisation and quality control of many GWAS summary statistics'
📖 **News**
- Awarded honourable mention.

2022 • **Poster Competition,**
Rising Scientist Day
Project: 'Systematic quantification of animal model viability across human diseases'
📖 **News**
- Awarded prize for research poster competition.

2022 • **Award for Outstanding Contribution,**
NEUROHACK, Deep Dementia Phenotyping Network (DEMON)
Project: 'Predicting ALS drug targets using integrative multi-modal deep learning'
📖 **News**
- Individually awarded for outstanding contributions during the NEUROHACK 2022, a competitive 4-day hackathon to apply AI in finding ALS therapeutic solutions.

2021 • **Prize for Computational Reproducibility in Dementia Research,**
UK Dementia Research Institute
Project: 'echolocatoR: an automated end-to-end statistical and functional genomic fine-mapping pipeline'
📖 **News**
- Winners announced for UK DRI's first 'Prize for Computational Reproducibility in Dementia Research (UK Dementia Research Institute, 2021)
- Jointly awarded inaugural prize with Kitty Murphy.

2021 • **Centre Photography Competition,**
UK Dementia Research Institute
Project: 'Wildfire Circle, Golden Brain, Wildfire, Geneshot, Geology of Biology, Neon Brain'
📖 **News**
- One of the winners of the scientific image competition.

2019 • **Art of the Brain,**
Friedman Brain Institute, Icahn School of Medicine
Project: 'Wildfire'
📖 **News**
- Awarded 2nd place and Featured on the cover of Biological Psychiatry: Volume 87, Issue 12 (2020). Exhibited and auctioned at the Grady Alexis Gallery (New York City), where all proceeds were voluntarily donated to the Diversity in Neuroscience Initiative.

🏛 AFFILIATIONS

UK Dementia Research Institute

- Synapse Working Group
- Informatics Working Group

DEMON Network
Data science and AI for dementia

- Genetics & Omics Working Group
- Experimental Models Working Group
- Drug Discovery & Trials Optimisation Working Group

The Alan Turing Institute

- Turing Enrichment Scheme
- Turing-Roche Strategic Partnership
- Turing Omics Data Generation & Analysis Interest Group
- Turing Clinical AI Interest Group

PGC Psychiatric Genomics Consortium

- Bipolar Disorder Working Group

Bioconductor OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

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

IMPERIAL ENTREPRENEURS

- Member

🛰 DATA VISUALISATION / ARTWORK PORTFOLIO

2022

echoverse Dependency Graph
📍 London, UK

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

-
|
2020

Hex stickers
📍 London, UK

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

2023

3D Human Phenotype Ontology
📍 London, UK

• 3D force-directed graph of the Human Phenotype Ontology (clouds above) with kernel density estimation projected from the x/y planes (mountains below). Connections represent the hierarchical relationships between rare diseases and their associated symptoms/phenotypes.
• Associated preprint

2023

Multi-scale Rare Disease Mechanisms
📍 London, UK

• Network of systematically prioritised gene therapy targets for rare diseases
• Associated preprint

2023

Curriculum Vitae Connexa
📍 London, UK

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

2021

Experiments with Generative AI
📍 London, UK

• wombo.art: 'Multi-omic medicine: dissecting the cell-type-specific mechanisms in neurodegeneration genomics'
• wombo.art: 'Multi-omic medicine: neurodegenerative disease genomics'
• wombo.art: 'Multi-omic medicine: neurodegeneration'
• wombo.art: 'Neurodegeneration'

2021

Lights in the dark genome: the current state of Parkinson's research
📍 London, UK

• The majority of PD genetics research has focused on a relatively small number of genes. Above, are the top 75 most commonly mentioned genes in the PD literature, extracted using Geneshot.
• Associated study

2020

Pacrophage
📍 London, UK

• Colocalised genetic loci …but shaped as Pac-Man!
• Associated study

2020

Circos
📍 London, UK

• Colocalised genetic loci across a variety of neurological disease GWAS and cell-type-specific QTLs.
• Associated study

2019

Wildfire Circle
📍 New York, NY, USA

• Awarded 2nd place in the 2019 Art of the Brain competition, put on by the Mount Sinai's Friedman Brain Institute.
• Exhibited and auctioned at the Grady Alexis Gallery (New York City), where all proceeds were donated to the Diversity in Neuroscience Initiative .
• Featured on cover of Biological Psychiatry.

2019 ● **Wildfire**

📍 New York, NY, USA

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

2019 ● **3D Brain Model**

📍 New York, NY, USA

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

EXTRACURRICULAR EXPERIENCE

● **Competitive Running Career**

– | 2003

• 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

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● **Music Production**

– | 1995

• Writes, records, produces and performs original music.

📍 Earth

• Instruments: keys, percussion, vocals, etc.
• Proficient in Logic Pro X Digital Audio Workstation (DAW).
• Experiments with generative AI.

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