BRIAN M. SCHILDER

PhD Candidate
ScB, MPhil

🎓 EDUCATION

- **Imperial College London**
  PhD: Clinical Medical Research; Computational Neurogenomics
  London, UK 2024 **Thesis**: Multi-omic medicine: dissecting the cell-type-specific molecular mechanisms underlying neurodegenerative disease genomics

The George Washington University

MPhil: Human Paleobiology; Evolutionary Neuroscience & Genomics Washington, DC,USA 2017 **Thesis**: The evolution of the hippocampus and adult neurogenesis: Novel insights into the origins of human memory

Brown University

ScB: Cognitive Neuroscience; Neurological Diseases & Disorders Providence, RI,USA 2011

💻 RESEARCH EXPERIENCE

Graduate Research Assistant

Beijing Institute of Genomics, Chinese Academy of Sciences

Beijing, China

2011 - 2014

- Performed computational biology research towards understanding regulation of alternative splicing in human and mouse transcriptome.
- Found EGFR pathway related mutations, aimed to understand the impacts of cancer mutations on EGFR signaling pathway.

Bioinformatican

My Health Gene Technology Co., Ltd.

Beijing, China

2015 - 2016

- Investigated how cancer cells spread to other parts of the body at the single cell level.

Visiting Scientist

University of Alabama at Birmingham

AL, USA

2016 - 2018

- Investigated the role of mitochondria in development of cancer.

CONTACT INFO

✉
brian_schilder@alumni.brown.edu

in LinkIn

GitHub

Twitter

🌐 Professional Website

📞 **US**: +1 908-268-9859

📞 **UK**: +44 073-0653-7736

CORE SKILLS

Programming: Extensive experience in developing scripts and software packages to interrogate large data effectively, efficiently, and reproducibly. Active contributor to the open-source bioinformatics community.

Research: 12+ years of highly multidisciplinary research experience. Creative and rapid hypothesis generation, project design, and problem solving.

Communication: Effective and engaging scientific presentations to a variety of audiences.

Project Management: Coordinates multiple independent projects at once with researchers of varying degrees of education and research experience. Effective handling of many projects at once.

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- Investigated the evolution of genome architecture and its role in important evolutionary events.
- Detected thrombotic thrombocytopenic purpura related mutations in mutiple patients' blood genome.

🎒 PROFESSIONAL EXPERIENCE

Data Scientist, intern

SupStat Inc.

Beijing, China

2014

- Taught R language to beginners.
- Wrote Shiny app demos.
- Converted statistical tutorials from SPSS to R language.

Bioinformatician

My Health Gene Technology Co., Ltd.

Beijing, China

2015 - 2016

- Analyzed whole-exome sequencing data.
- Wrote analysis pipelines of ChIP-seq, single cell DNA-seq and single cell RNA-seq.
- Studied tumor metastasis and wrote research reports.
- Also did case studies to identify the genetic defect causing rare disease.

🖥 TEACHING EXPERIENCE

Introduction to R Language for Beginners.

Instructor of R and Data Mining Training Courses at SupStat Inc.

Beijing, China

2014

Computational Biology and Bioinformatics.

Teaching assistant of GBS CB2-201 courses at UAB

AL, USA

2016 - 2017

📄 SELECTED PUBLICATIONS

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/A

2022

N Mullins, J Kang, AI Campos,…**BM Schilder**, et al.

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

N/A

2022

K de Paiva Lopes, G JL Snijders, J Humphrey, A Allan, M Sneeboer, E Navarro, **BM Schilder**…T Raj

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

N/A

2021

BM Schilder, E Navarro, T Raj

Fine-Mapping of Parkinson's Disease Susceptibility Loci Identifies Putative Causal Variants

Human Molecular Genetics (2021) ddab294; https://doi.org/10.1093/hmg/ddab294

N/A

2021

BM Schilder, T Raj

echolocatoR: An Automated End-to-End Statistical and Functional Genomic Fine-Mapping Pipeline

Bioinformatics (2021) btab658; https://doi.org/10.1093/bioinformatics/btab658

N/A

2021

BM Schilder, J Humphrey, T Raj

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

N/A

2021

A Murphy, **BM Schilder**, NG Skene

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

N/A

2021

E Navarro, E Udine, K de Paiva Lopes, M Parks, G Riboldi, **BM Schilder**…T Raj

Phenome-wide and eQTL Associations of COVID-19 Genetic Risk Loci

iScience (2021) https://doi.org/10.1016/j.isci.2021.102550

N/A

2021

C Moon, **BM Schilder**, T Raj, K-I Huang

Genome-Wide Association Study of over 40,000 Bipolar Disorder Cases Provides Novel Biological Insights

Nature Genetics (2020) 53:817-829; https://doi.org/10.1038/s41588 021 00857 4

N/A

2020

N Mullins, AJ Forstner, KS O'Connell, B Coombes, JRI Coleman…**BM Schilder**… et al.

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

N/A

2020

S Ramdhani, E Navarro, E Udine, AG Efthymiou, **BM Schilder**, M Parks, A Goate, T Raj

Evolutionary shifts dramatically reorganized the human hippocampal complex

Journal of Comparative Neurology (2019) 528(17):3143-3170; https://doi.org/10.1002/cne.24822

N/A

2019

BM Schilder, HM Petry, PR Hof

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

2019

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

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

N/A

2019

A Lachmann, **BM Schilder**, ML Wojciechowicz, D Torre, MV Kuleshov, AB Keenan, A Ma'ayan

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

N/A

2018

DJB Clarke, MV Kuleshov, **BM Schilder**, D Torre, ME Duffy, AB Keenan, A Lachmann, AS Feldmann, GW Gundersen, MC Silverstein, Z Wang

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

N/A

2015

F Subiaul, L Zimmerman, E Renner, **BM Schilder**, R Barr

Take the monkey and run

Journal of Neuroscience Methods (2015) 248:28-31; http://doi.org/10.1016/j.jneumeth.2015.03.023

N/A

2015

KA Phillips, MK Hambright, K Hewes, **BM Schilder**, CN Ross, SD Tardif

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

N/A

2014

F Subiaul, EM Patterson, **BM Schilder**, E Renner, R Barr

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

N/A

2014

F Subiaul, **BM Schilder**

PREPRINTS

The rworkflows suite: automated continuous integration for quality checking, documentation website creation, and containerised deployment of R packages

Research Square (2023) https://doi.org/10.21203/rs.3.rs 2399015/v1

N/A

2023

BM Schilder, AE Murphy, NG Skene

CUT&Tag recovers up to half of ENCODE ChIP-seq peaks

bioRxiv (2022) https://doi.org/10.1101/2022.03.30.486382

N/A

2022

D Hu, L Abbasova, **BM Schilder**, A Nott, NG Skene, SJ Marzi

EpiCompare: R package for the comparison and quality control of epigenomic peak files

bioRxiv (2022) https://doi.org/10.1101/2022.07.22.501149

N/A

2022

S Choi, **BM Schilder**, L Abbasova, AE Murphy, NG Skene

ACKNOWLEDGEMENTS

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/A

2021

N Kerimov, JD Hayhurst, K Peikova et al.

Functionally-informed fine-mapping and polygenic localization of complex trait heritability

Nature Genetics (2020) https://doi.org/10.1038/s41588 020 00735 5

N/A

2020

O Weissbrod…AL Price

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

N/A

2019

MR O'Connor

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

N/A

2012

M van Vugt, P Simen, L Nystrom, P Holmes, J Cohen

Trial-by-trial adaptation of decision making performance: a model-based EEG analysis

Interdisciplinary Perspectives on Cognition, Education, and the Brain (2011) 7;

N/A

2011

M van Vugt, P Simen, J Cohen