# BRIAN M. SCHILDER



Passionately pursuing multi-disciplinary research to improve human lives.

Imperial College London **PhD Candidate** ScB, MPhil



## EDUCATION

2024

#### Imperial College London

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 Mendelian and complex disease genomics.
- Aim 2) Decompose multi-trait disease genomics and identify the multi-scale mechanisms underlying each latent component.
- Aim 3) Demonstrate reproducibility and make reproducible best practices accessible to others.

2017

#### The George Washington 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**

ScB: Cognitive Neuroscience; Neurological Diseases & Disorders

Providence, RI, USA

Supervisors: Sheila E Blumstein, PhD; David L. Sheinberg, PhD



## **CORE SKILLS**

#### Research

- 14+ years of highly multidisciplinary research experience. Creative and rapid hypothesis generation, project design, and problem solving.
- Fields: Including but not limited to: Neuroscience, systems biology, bioinformatics, machine learning, multiomics, biomedicine, rare diseases, complex diseases, cognition, statistics, computer science, phylogenetics,
- paleoanthropology biomechanics, primatology, histology/microscropy.
- · Publications: Strong writing skills as evidenced by 22 peer-reviewed scientific publications, 23 international conference posters and 13 successful grant applications.

#### CONTACT

- **☑** brian\_schilder [at] alumni.brown.edu
- C US
- +1 908-268-9859
- **UK**
- +44 073-0653-7736
- in LinkedIn
- (D) ORCID
- **GitHub**
- **₩** Twitter
- Personal Website
- Lab Website

#### SUMMARY

- 11 14+ years of research
- = 22 publications
- 3 preprints
- **№** 39 software packages
- = 11 databases & apps
- i□ 20 talks
- 12+ years of teaching
- & team management

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- **☎** Education
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- = Publications
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- \$ Grants
- **Q** Awards
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- **X** Extracurricular
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- Updated Sep-30-2023

#### **Programming**

Extensive experience in developing highly reproducible scripts and software packages to interrogate large and diverse data.

- Bioinformatics: Including but not limited to: GWAS, QTL, Python: Regularly uses ML packages (e.g. sklearn, bulk/scRNA-seq & epigenomics, machine learning, highperformance computing, GitHub, GitHub Actions, Docker/Singularity containers, DockerHub, conda, Nextflow, reproducibility.
- R: Created 36 R packages to date, including on Bioconductor and CRAN. Experienced in created Shiny Apps and Rmarkdown reports.
- tensorflow, Keras). Developed and own IP for PubReporter, a software for extracting and conducting topic modelling/NLP on relevant scientific literature at scale.
- Javascript/HTML/CSS: Created 6+ websites, web apps, and interactive reports. Developed templates to automatically render websites on-the-fly from CSVs using Javascript.

#### Communication

Effective and engaging scientific presentations to a variety of audiences.

- Peers: Extensive experience presenting research proposals/findings to both internal and external labs/conferences. Invited speaker at leading research institutions. Diverse, multi-disciplinary and global collaborative network.
- Students: Teaching assistant and/or guest lecturer for courses in diverse fields (biological anthropology,
- neuroscience, computational biology).
- Public: Developed and delivered numerous community engagement programs for a wide variety of stakeholders, including students (preschool through postgraduate), community members, and patients (e.g. Children's National Hospital, Parkinson's UK).

#### **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.

- Documentation: Detailed and understandable in-code documentation is second-nature.
- Version control: Extensive and daily use of git, GitHub Issues, GitHub Projects.
- · Supervision: Supervises numerous student research projects.



## **PUBLICATIONS**

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

#### 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

#### 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

#### 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

### 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, Al Campos,...BM Schilder, et al.



2023

2023

2023

2023

2022

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, <b>BM Schilder</b> T Raj	
- Microglial transcriptomics meets genetics: new disease leads (Nature Reviews Neurology, 2022)	
<ul> <li>Mighty MiGA: Microglial Genomic Atlas Zeros in on Causal AD Risk Variants (ALZFORUM, 2022)</li> <li>Can a Human Microglial Atlas Guide Brain Disorder Research? (Mount Sinai Health System, 2022)</li> </ul>	
- Polygenic Scores Paint Microglia as Culprits in Alzheimer's (ALZFORUM, 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	
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	
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 M	any
GWAS Summary Statistics Bioinformatics (2021) 37(23):4593-4596; https://doi.org/10.1093/bioinformatics/btab665	
A Murphy, <b>BM Schilder</b> , NG Skene	
Dysregulation of mitochondrial and proteo-lysosomal genes in Parkinson's disease myeloic Nature Genetics (2021) https://doi.org/10.1101/2020.07.20.212407	d cells
E Navarro, E Udine, K de Paiva Lopes, M Parks, G Riboldi, <b>BM Schilder</b> T Raj	
<ul> <li>■ News</li> <li>- Mount Sinai: Fighting Neurodegenerative Disorders (Mount Sinai Health System, 2019)</li> </ul>	
Phenome-wide and eQTL Associations of COVID-19 Genetic Risk Loci	
<i>iScience</i> (2021) https://doi.org/10.1016/j.isci.2021.102550 C Moon, <b>BM Schilder</b> , T Raj, K-I Huang	
Civiouri, Bir Schilder, T Raj, K-i ridang	
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 ColemanBM Schilder et al.	
<ul><li>■ News</li><li>- Researchers identify 64 regions of the genome that increase risk for bipolar disorder (EurekAlert, 2021)</li></ul>	
<ul> <li>Largest Bipolar Disorder Genetics Study Doubles Genetic Risk Factors (Nordic Society of Human Genetics and Precision Medicine, 2021)</li> </ul>	d
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	
5 . Camanani, E Navario, E Gaine, AG Entrymod, Diff Golindor, Wir and, A Godie, 1 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  BM Schilder, HM Petry, PR Hof	
Sin Schilder, Their edy, Fix hor	

## 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

I

■ 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

- 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

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

2023

## 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

BM Schilder, AE Murphy, 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 WeissbrodAL 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		<b>EEG oscillations reveal neural correlates of evidence accumulation</b> 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
2023		[Unpublished article] Neuron (2023)
2022		[Unpublished article] Bioinformatics (2022)
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	•	[Unpublished article] Nature Neuroscience (2019)

## Multi-omics medicine: investigating shared genetic risk factors to better understand 2023 neurodegenerative disease **Turing Omics Meeting** Omics Data Generation & Analysis Group The Alan Turing Institute Decomposing the phenome: learning the latent genomic structure underlying thousands of 2022 diseases and traits Neuroepidemiology of Aging Webinar RUSH Alzheimer's Disease Center (RADC) **RUSH University** Drug (re)discovery in the age of genomics: multi-omic strategies for identifying disease 2022 treatments Department Seminar 3D (Drug, Disease, Delivery) Center / Department of Pharmaceutical Sciences University of South Dakota Statistical and functional genetic fine-mapping across multiple disease 2020 Seminar Alzheimer's Disease Sequencing Project Columbia University / Icahn School of Medicine at Mount Sinai Statistical and functional genetic fine-mapping across multiple disease 2020 Laboratory of Neurogenetics Friday Workshop National Institute on Aging National Institutes of Health **†**CONFERENCE TALKS rworkflows: taming the Wild West of R packages 2023 EuroBioc2023 Bioconductor 45-minute workshop. rworkflows: taming the Wild West of R packages 2023 BioC2023 Bioconductor 10-minute talk within the Infrastructure Track. Navigating the rare diseases landscape: A comprehensive approach to identify gene therapy 2023 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. Systematic quantification of animal model viability across human diseases 2022 Informatics-Synapse Joint Early Career Researcher Meeting UK Dementia Research Institute (UK DRI) Automated genetic fine-mapping of neurological disorders 2020

The Genetics Society

London Genetics Network

**忙** INVITED TALKS

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
2016	Marmoset Social
	Society for Neuroscience (SfN)
2016	JB Johnston Club for Evolutionary Neuroscience
	Society for Neuroscience (SfN)
2014	JB Johnston Club for Evolutionary Neuroscience
	Society for Neuroscience (SfN)
	CONFERENCE POSTERS
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	<ul> <li>Identification of cell type-specific gene targets underlying thousands of rare diseases and clinical phenotypes</li> </ul>
	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, <b>BM Schilder</b> , 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	<ul> <li>Systematic quantification of animal model viability across human disease</li> <li>Rising Scientist Day at Imperial College London (2022)</li> </ul>
	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

## 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

#### **Lead Data Scientist**

120/80 MKTG

New York, NY, USA

2019

- · Offered data-driven consultation services to a wide portfolio of high-profile digital healthcare, pharmaceutical and biotech companies.
- · Developed a suite of propietary softwares to extract customised business intelligence from the published literature. Generated customised and interpetable reports to clients.
- · Provided clients guidance on strategic 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.

#### Research Assistant 2013 The George Washington University (Department of Anthropology) Washington, DC, USA 2011 Performed dissection, histology, microscopy and quantitative stereology in post-mortem primate brain tissues. • Trained junior and senior personnel on lab protocols. Senior Lab Manager 2013 The George Washington University (Department of Speech, Language & Hearing Sciences) 2011 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. Volunteer Researcher 2012 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. Volunteer Researcher 2011 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. **Volunteer Research Intern** 2011 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. Paid Research Intern 2010 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. Student Researcher 2010 Brown University (Department of Cognitive, Linguistic & Psychological Sciences) Providence, RI, USA 2009 • Experimental Analysis of Animal Behavior & Cognition: Conducted various operant conditioning experiments on rats.

- 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)

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

#### **Teaching Assistant** 2014 The George Washington University (Department of Anthropology) Washington, DC, USA 2013 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. **Research Mentor** 2013 The George Washington University (Department of Psychology) Washington, DC, USA 2012 · Mentored students and affiliated projects: · Anushka Gokhale (BSc): 'Infants' Social Assessment of Characters Through Eye Gaze' **Lab Protocol Trainer** 2013 The George Washington University (Department of Anthropology) Washington, DC, USA 2011 • 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 anndataR 😱 🕏 1. Bring the power and flexibility of AnnData to the R ecosystem, allowing you to effortlessly manipulate and analyze your single-cell data. nttps://github.com/scverse/anndataR gptPhD 😱 2. Query Large Language Models for the purposes of systematically extracting biomedical knowledge. https://github.com/neurogenomics/gptPhD 3. ThreeWayTest R Summary statistics-based association test for identifying the pleiotropic effects with set of genetic variants https://github.com/bschilder/ThreeWayTest SCAVENGE R 4. Variant to function mapping at single-cell resolution through network propagation https://github.com/sankaranlab/SCAVENGE https://doi.org/10.1038/s41587-022-01341-y rworkflows 🖫 👨 5. 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 TIPseeker 😱 6. R package for post-processing [single-cell] TIP-seq data https://github.com/neurogenomics/TIPseeker 7. PeakyFinders R R package for mining, calling, and importing epigenomic peaks https://github.com/neurogenomics/PeakyFinders 8. graphiti 😱 Extract colour palettes from graffiti artworks. https://github.com/bschilder/graphiti 9. SkillNet R Creates user-specific contribution networks from GitHub Organization repositories https://github.com/neurogenomics/SkillNet phenoRx R

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

https://github.com/neurogenomics/phenomix

Make cell type-specific predictions for patients based on clinical phenotypes and/or risk genes.

10.

11.

12. MAGMA Celltyping R Identify cell types underlying the associations found in GWAS summary statistics https://github.com/neurogenomics/MAGMA Celltyping **EWCE** 13. **Expression Weighted Celltype Enrichment** nttps://github.com/NathanSkene/EWCE EpiCompare R 14. R package for QC and benchmarking epigenetic datasets https://github.com/neurogenomics/EpiCompare https://doi.org/10.1101/2022.07.22.501149 MultiEWCE R 15. R package for analysing multiple gene lists using EWCE https://github.com/neurogenomics/MultiEWCE https://doi.org/10.1101/2023.02.13.23285820 **HPOExplorer** • R 16. Functions for working with the Human Phenotype Ontology data https://github.com/neurogenomics/HPOExplorer https://doi.org/10.1101/2023.02.13.23285820 orthogene R 17. Interspecies gene mapping https://github.com/neurogenomics/orthogene MungeSumstats R 18. Standardise the format of summary statistics from GWAS https://github.com/neurogenomics/MungeSumstats https://doi.org/10.1093/bioinformatics/btab665 scNLP 😱 19. Tools for applying natural language processing (NLP) techniques to single-cell (sc) omics data https://github.com/neurogenomics/scNLP scKirby 😱 👨 20. Automated ingestion and conversion of various single-cell data formats https://github.com/neurogenomics/scKirby geneshotR R 21. R package for querying and processing results from Geneshot. https://github.com/bschilder/geneshotR templateR R 22. Self-updating template for developing R packages https://github.com/neurogenomics/templateR https://doi.org/10.21203/rs.3.rs-2399015/v1 echoverseTemplate R 23. Self-updating template for creating echoverse R packages. https://github.com/RajLabMSSM/echoverseTemplate/ https://doi.org/10.1093/bioinformatics/btab658 24. 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 echodata 😱 25. 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

echoannot R 26. Functions for annotating genomic data with annotations and epigenomic data https://github.com/RajLabMSSM/echoannot https://doi.org/10.1093/bioinformatics/btab658 27. 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 echoconda 😱 락 28. 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 echotabix 🗬 🕏 29. Tabix indexing and querying https://github.com/RajLabMSSM/echotabix https://doi.org/10.1093/bioinformatics/btab658 echoLD 😱 락 30. LD downloading and processing. https://github.com/RajLabMSSM/echoLD https://doi.org/10.1093/bioinformatics/btab658 echofinemap 😱 👨 31. Statistical and functional fine-mapping functions. https://github.com/RajLabMSSM/echofinemap https://doi.org/10.1093/bioinformatics/btab658 32. echodeps R Creates interactive dependency networks for R packages https://github.com/RajLabMSSM/echodeps https://doi.org/10.1093/bioinformatics/btab658 echogithub R 33. Access and process metadata from GitHub https://github.com/RajLabMSSM/echogithub https://doi.org/10.1093/bioinformatics/btab658 devoptera R 34 Practical tools for R developers https://github.com/RajLabMSSM/devoptera https://doi.org/10.1093/bioinformatics/btab658 downloadR R 35. Single- and multi-threaded downloading functions https://github.com/RajLabMSSM/downloadR https://doi.org/10.1093/bioinformatics/btab658 catalogueR R 36. 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 TopicModeler 😎 37. Proprietary Python package to run advanced topic modeling on text corpuses. 38 JobReporter 😴

Proprietary Python package to extract job postings and company employee listings and generate interactive

business intelligence reports.

# PubReporter 5

Proprietary Python package for extract relevant scientific literature, gather citations, and generate interactive business intelligence reports.



#### DATABASES / WEB APPS

EpiArchives R 1.

Public archive for EpiCompare reports.

- https://github.com/neurogenomics/EpiArchives
- https://doi.org/10.1101/2022.07.22.501149

#### 2. Rare Disease Celltyping Portal R

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 R

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 metaanalysed cell counts manually curated and harmonised from the Parkinson's Disease literature

https://github.com/neurogenomics/SelectiveVulnerabilityMetaAnalysis

#### MAGMA Files Public R 5.

6.

7.

8.

9.

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

# echolocatoR Fine-mapping Portal R

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

# COVID-19 Patient Tracker

Web app for summarizing and visualizing real-time EHR data of COVID-19 patients within the Mount Sinai Health System

# 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

# 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

#### Geneshot 👙 🕏 🤠 🗒 10.

Flexible tool to identify genes associated with any biomedical term and to predict novel target genes

https://doi.org/10.1093/nar/gkz393

http://amp.pharm.mssm.edu/geneshot

11. **X2K ② ♣ ७ ७ ७** 

eXpression 2 Kinases (X2K) Web: Automated computational pipeline to infer kinase regulators from weighted or unweighted gene lists

♦ http://amp.pharm.mssm.edu/X2K

https://doi.org/10.1093/nar/gky458

# **WEBSITES**

1. Personal Website 😇 💆 🗓

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

2. Official Raj Lab Website 😇 💆 🗓

↑ https://github.com/RajLabMSSM/RajLab\_website 

↑ https://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'

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■ 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'

I News

2023

2023

2024

2022

- Awarded to support attending the BioC2023 meeting. Additionally included free lodging.

• Role: Primary applicant

• PI: BM Schilder

#### 1. Bivi Schilder

The Genetics Society

**Junior Scientist Conference Grant,** 

Project: 'Identification of cell type-specific gene targets underlying thousands of rare diseases and subtraits'

• Role: Primary applicant

• PI: BM Schilder

• Amount: £750

• Amount: \$1500

# 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

# **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

**National Institutes of Health** 2022 Project: 'Statistical and functional fine-mapping of bipolar disorder genetic risk loci' · Role: Co-applicant • PI: N Mullins Collaborative Single Cell and Spatial Transcriptomics Studies Award Programme, 2021 **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 **National Institutes of Health** 2020 Project: "Cognitive Systems Analysis of Alzheimer's Disease Genetic and Phenotypic Data" · Role: Co-applicant Amount: \$2,523,431 • PI: T Raj, D Knowles **UK Dementia Research Institute** 2024 Project: 'UK DRI at Imperial Distinguished Studentship' 2020 · Role: Primary applicant • Amount: £217.000 • PI: BM Schilder The Michael J. Fox Foundation 2019 Project: "The Role of Peripheral Myeloid Cells in Parkinson's Disease" 2017 • Role: Fundee • PI: T Raj The Michael J. Fox Foundation 2020 Project: 'Functional Fine-Mapping of LRRK2 Locus' 2017 • Role: Fundee PI: T Raj **National Science Foundation** 2017 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 Wenner-Gren 2017 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 **Leakey Foundation** 2016 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 **COSMOS Club** 2016 Project: 'The evolution of adult neurogenesis across primates' · Role: Primary applicant • Amount: \$3.250 • PI: BM Schilder AWARDS Prize for Computational Reproducibility in Dementia Research, 2022 **UK Dementia Research Institute** Project: 'MungeSumstats: A Bioconductor package for the standardisation and quality control of many GWAS summary statistics' ■ News - Awarded honourable mention

### 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'

- 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

# **Imperial College** London

- Department of Brain Sciences
- · Faculty of Medicine



- Synapse Working Group
- · Informatics Working Group



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



· Bipolar Disorder Working Group



- Bioconductor Cloud Methods Working Group
- · Active developer

# DATA VISUALISATION / ARTWORK PORTFOLIO

echoverse Dependency Graph

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

♠ London, UK

**Hex stickers** 

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

O London, UK

#### 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

#### **Multi-scale Rare Disease Mechanisms**

◆ London, UK

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

2023

2022

2020

2023

19

**Curriculum Vitae Connexa** 2023 London, UK Term co-occurrence network generated by analysing all data that went into this CV. **Experiments with Generative AI** 2021 **Q** 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' Lights in the dark genome: the current state of Parkinson's research 2021 **Q** 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 **Pacrophage** 2020 **Q** London, UK Colocalised genetic loci ...but shaped as Pac-Man! · Associated study **Circos** 2020 **Q** London, UK Colocalised genetic loci across a variety of neurological disease GWAS and cell-type-specific QTLs. Associated study Wildfire Circle 2019 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. Wildfire 2019 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. **3D Brain Model** 2019 New York, NY, USA • 3D model of my brain generated from MRI scans. **S** EXTRACURRICULAR EXPERIENCE **Competitive Running Career** · 8+ years of varsity and Division I cross country, winter track, and spring track throughout high school and 2003 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.

researcher.

This passion, work ethic and self-insight have carried over to all aspects of my life, including my career as a

20

Earth

#### -| 1995

## **Music Production**

• Writes, records, produces and performs original music.

• Instruments: keys, percussion, vocals, etc.

- Proficient in Logic Pro X Digital Audio Workstation (DAW).
- Experiments with generative AI.

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Earth