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## Shila Ghazanfar

Research Associate  
Royal Society-Newton International Fellow  
shila.ghazanfar@cruk.cam.ac.uk

## Curriculum Vitae

Cancer Research UK Cambridge Institute  
University of Cambridge, Cambridge, United Kingdom

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### Employment and Academic Positions

- 2/2019 – Royal Society-Newton International Fellow. *Leveraging spatially resolved single cell gene expression and single cell RNA-sequencing to understand cellular heterogeneity*. UK Co-applicant: Dr John Marioni (University of Cambridge/EMBL-EBI).
- 2/2019 – Research Associate, Cancer Research UK Cambridge Institute, University of Cambridge.
- 9/2017— 1/2019 Research Associate, Judith and David Coffey Life Lab, Charles Perkins Centre; School of Mathematics and Statistics, The University of Sydney.
- 5/2017— 8/2017 Research Associate, School of Life and Environmental Science (SOLES), The University of Sydney.
- 3/2017— 7/2017 Casual tutor, School of Mathematics and Statistics, The University of Sydney.
- 3/2013—11/2016 Postgraduate Teaching Fellow, School of Mathematics and Statistics, The University of Sydney.
- 3/2012—11/2012 Casual tutor, School of Mathematics and Statistics, The University of Sydney.

### Fellowships and Awards

- 2019 Royal Society Newton International Fellowship.
- 2013 CSIRO Office of the Chief Executive (OCE) Ph.D. Scholarship.
- 2013 Australian Postgraduate Award (Ph.D.).
- 2012 CSIRO Mathematics, Informatics, and Statistics (CMIS) Honours Scholarship.

### Academic Record and Qualifications

- Ph.D. Mathematical Statistics, University of Sydney, Australia, 2017. *Statistical approaches to harness high throughput sequencing data in diverse biological systems*. <http://hdl.handle.net/2123/17268>
- B.Sc (Adv. Mathematics) Majors in Statistics and Pure Mathematics, with First Class Honours, University of Sydney, Australia, 2012. *Statistical issues of integrative gene set approaches for biomedical data*.

### Prizes, Honours and Awards

Approximately \$315,000 AUD total funding through competitive awards and scholarships:

- 2019; £100,566.20 Royal Society Newton International Fellowship. NIF\R1\181950.
- 2018; \$200 Australian Bioinformatics and Computational Biology Society Travel Grant to attend ABACBS 2018 Conference.
- 2018; (expenses) Funded award to attend the MAGIC Mentoring and Guidance in Careers program for Women in Mathematical Sciences in Canberra, Australia.
- 2018; \$250 Oz Single Cells Data Analysis Challenge: “Utilising ambient RNA and damaged cell profiles for appropriate cell selection in droplet-based single cell transcriptomics”.
- 2016; \$100 2nd Oral Prize at AB3ACBS Conference.
- 2016; \$750 SSAI NSW Branch Travel Grant to attend the Australian Statistical Conference.
- 2015; \$75 2nd Poster Prize at COMBINE Symposium.
- 2015; \$500 SSAI NSW Branch Travel Grant to attend Young Statisticians Conference.
- 2014; \$100 University of Sydney Faculty of Science grant to attend EMBL Australia PhD Symposium.
- 2013; (expenses) Successful application to attend the EMBL Australia PhD Course.
- 2013; \$750 AMSI Travel Scholarship for BioInfoSummer.
- 2013; \$51,000 CSIRO OCE PhD Scholarship (Stipend \$7,000 p.a. with \$10,000 p.a. operating expenses for three years).
- 2013; \$950 University of Sydney School of Mathematics and Statistics PRSS Funding.
- 2013; \$86,000 Australian Postgraduate Award (approx. \$28,715 p.a. for three years and six months).
- 2012; \$3,000 CSIRO Mathematics, Informatics, and Statistics (CMIS) Honours Scholarship.

## Research mentorship and supervision

2021 – <i>current</i>	Elyas Heidari; Masters thesis student; Supervisor.
2020	Nicolas Huynh; Summer Research student successful in obtaining French Embassy Internship at EMBL-EBI. Deferred due to COVID-19; Supervisor under guidance by Dr John Marioni.
2019 – 2021	Tim Lohoff; PhD student; Collaborator and mentoring throughout first lead author publication.
2018	Andrew Lee; Summer Research Scholarship student; Supervisor under guidance by Prof Jean Yang and Prof Germaine Wong.
2017	Elise Bickley; BINF3101 Bioinformatics Project Unit of Study; Supervisor joint with Prof Jean Yang.
2017	Yingxin Lin; Honours student; Mentor.

## Selected Presentations

I have given over 30 conference, seminar, and workshop presentations (8 talks in 2020 and 4 in 2021 thus far), including invitations to 15 international conferences, workshops and departmental seminars, 4 of which were fully funded.

(v) indicates a virtual presentation.

### International conferences:

Invited Speaker (v)	<i>Integrating molecule-resolved spatial gene expression and single cell RNA-sequencing data.</i> Single Cell Genomics Day. March 2021.
Invited Speaker (v)	<i>Molecule-resolved spatial reference maps for mouse organogenesis.</i> ISSCR digital Computational Stem Cell Biology - Reference maps for stem cell biology. March 2021.
Selected Speaker (v)	<i>Interrogating highly multiplexed spatially resolved gene expression of mouse embryogenesis.</i> Cold Spring Harbor Laboratory Biology of Genomes. May 2020.
Invited Speaker*	EuroBioc in Brussels, Belgium in December 2019 [declined due to schedule conflict].
Invited Speaker*	<i>Investigating second order interactions in single cell data.</i> Joint Statistical Meeting special session on Single Cell Genomics in Denver, USA, in July 2019.

### National conferences:

Invited Speaker*	<i>Investigating higher order interactions in single cell data with scHOT.</i> BioCAsia lecture in Sydney, Australia December 2019.
Invited Speaker*	<i>scMerge: Integration of multiple single-cell transcriptomics datasets leveraging stable expression and pseudo-replication.</i> BioInfoSummer in Perth, Australia, in December 2018.
Invited Speaker	<i>Differential correlation across ranked samples for single cell RNA-sequencing data.</i> ComBio meeting in Sydney, Australia, 2018.

### Workshops and short courses:

Invited Presenter	EMBL-EBI RNA-Seq analysis course lecture on single cell sequencing analysis in Cambridge UK, April 2020
Invited Workshop*	BioInfoSummer, Sydney, Australia, December 2019.
Invited Workshop*	BioInfoSummer, Perth, Australia, December 2018.

\* indicate fully or partially funded.

## Education Funding

2015 The University of Sydney DVC Education/Small Educational Innovation Grant - Improving Statistical Efficacy through Engaged Enquiry and Student-Driven Research in a large First Year Unit.

## Teaching

### *Subjects lectured:*

MATH1005 Statistics (S2 2015, S2 2016, Winter School 2014, 2015) ~300 students per stream totalling ~1,200 students, ~80-100 in Winter School.  
PHAR1811 Foundations of Pharmacy (S1 2014, S1 2015) ~280 students each year.  
STAT2911 Probability and Statistical Models (Advanced) (S1 2015) – lectures on parametric bootstrap and conditional expectation (~40 students).

### *Subjects tutored:*

STAT3014 Applied Statistics (S2 2013, S2 2014);  
STAT3012 Applied Linear Models (S1 2016);  
STAT2911 Probability and Statistical Models (Advanced) (S1 2015);  
STAT2011 Statistical Models (S1 2015, S1 2017);  
STAT2012 Statistical Tests (S2 2014);  
PHAR2813 Therapeutic Principles (S1 2014, S1 2016);  
PHAR2821 Drug Discovery and Design B (S2 2013, S2 2014, S2 2016);  
MATH1905 Statistics (Advanced) (S2 2014);  
PHAR1811 Foundations of Pharmacy (S1 2014);  
MATH1005 Statistics (S2 2012, S2 2013, Winter School 2014, Winter School 2015, S2 2015, S2 2016);  
MATH1015 Biostatistics (S1 2013, S1 2014);  
MATH1011 Applications of Calculus (S1 2012, Summer School 2014, Summer School 2017, S1 2017);  
MATH1111 Introduction to Calculus (S1 2013, S1 2014).

### *Other:*

Computer demonstrations using R statistical software.  
Duty tutoring: weekly consultation hour for any first-year mathematics and statistics unit (S1 2013, S2 2013, S1 2014).  
Designing and marking final exams in statistics.  
Designing and marking assignments in mathematics and statistics.  
Marking computer lab reports in statistics.  
Designing and marking quizzes in mathematics and statistics.  
Designing and marking project-based assignments in statistics.

## Professional Service and Experience

2020	Attended EMBO Lab Leadership for Postdocs Course in February 2020.
2020	Member of Bioconductor Technical Advisory Board since 2020.
2019	Attended Royal Society Leadership Effectiveness Course in November 2019.
2019	Wellcome Trust Mouse Gastrulation Consortium Meetings organiser since 2019.
2019	Member of GIW 2019 program committee.
2019	Judged oral presentation at 2019 COMBINE Symposium in Sydney, Australia.
2018	Coordinated The University of Sydney Statistical Bioinformatics Seminar in 2018, ensuring a 50/50 balance along gender and EMCR status among seminar speakers.
2018	Invited to judge oral presentations at the 2018 COMBINE Symposium in Melbourne.
2018	Attended Mentoring and Guidance in Careers Workshop in October 2018. This was a week-long workshop with a competitive application process for mentoring of female and gender diverse early career researchers in Mathematics and Physics.
2018	Attended Charles Perkins Centre EMCR workshop on 'Manuscripts and Grant Reviewing' in June 2018.
2018	Present a talk at The University of Sydney Faculty of Science Higher Degree by Research Supervisor Forum: Supervising 21st Century Style: New Challenges and Opportunities in June 2018.
2018	Attended workshop on 'Effective data presentation at conferences' in March 2018.
2017	Volunteer for University of Sydney Open Day August 2017.
2017	Executive member of the COMBINE student and early-career researcher organisation in 2017, part of the COMBINE National Committee Media and Communications team.
2016	Member of organising committee for COMBINE Student Symposium in October 2016.
2015 – 2017	Student member of AustMS November 2015 - 2017.
2013 – 2017	Student member of the Statistical Society of Australia (SSAI) since November 2013.
2015 – 2017	Member of University of Sydney School of Mathematics and Statistics Publicity and Outreach Committee.
2015	Chaired a session at the COMBINE Symposium in October 2015.
2015	Volunteer for University of Sydney Open Day August 2015.
2015	Presented a talk at School of Mathematics and Statistics 'Thank You to Teachers' evening in August 2015.
2015	Attended 'Data Visualisation Masterclass' at Charles Perkins Centre in June 2015.
2015	Completed 'High Performance Computing Intermediate Training' at University of Sydney in March 2015.
2014	Attended 'UCSC Genome Browser' workshop in September 2014.
2014	Volunteer for University of Sydney Info Day January 2014.
2013	Participated in the inaugural EMBL Australia PhD Course, a two week intensive course on molecular biology and bioinformatics held at the University of Melbourne in June 2013.
2013	Involved in the CSIRO Vacation Scholarship Program from January to March 2013.
2012	Involved in the Charles Perkins Centre Summer Vacation Scholarship Program from December 2011 to February 2012.
2009	Volunteer for School Tutoring Program at the University of Sydney in 2009.
2007	Involved in Peer Tutoring at Macarthur Girls High School in 2007.

## Peer review

Ongoing	Refereeing for international journals such as Nature Methods and Bioinformatics. I have reviewed a total of 23 manuscripts thus far. Publons: <a href="https://publons.com/a/1038599/">publons.com/a/1038599/</a>
2019	Program Committee for Genome Informatics Workshop, Sydney, Australia.

## Software

I have contributed to 7 software items, below is a selected list of software for which I have led the development:

- 2020 **Spatial Mouse Atlas**: an R/Shiny web application to interrogate spatially resolved expression of mouse organogenesis (Lohoff\*, Ghazanfar\*, et al, Nature Biotechnology, in press).  
<https://marionilab.cruk.cam.ac.uk/SpatialMouseAtlas/>
- 2020 **scHOT**: an R/Bioconductor package for single cell higher order testing (Ghazanfar et al, Nature Methods, 2020). (License: GPL-3)  
<https://bioconductor.org/packages/scHOT>
- 2018 **DCARS**: an R package for testing differential correlation across ranked samples (Ghazanfar et al, Bioinformatics, 2018). (License: GPL-3)  
<https://github.com/shazanfar/DCARS>
- 2018 **cellAggregator**: an R package for simulating cell-cell aggregation assays using Markov chains (Bisogni et al, eLife, 2018). (License: MIT)  
<https://github.com/shazanfar/cellAggregator>
- 2016 **PACMEN**: an R/Shiny web application for joint analysis of cancer mutation and gene expression network analysis, published as proceedings to the Asia Pacific Bioinformatics Conference (Ghazanfar and Yang, Computational Biology and Chemistry, 2016).  
<http://shiny.maths.usyd.edu.au/PACMEN/>

## Publications

\*indicates equal first author

+indicates corresponding author

ORCID ID: 0000-0001-7861-6997

Google Scholar: <https://scholar.google.com/citations?user=D9Btwb8AAAAJ>

1. Lohoff T\*, **Ghazanfar S\***, Missarova A, Koulina N. Highly multiplexed spatially resolved gene expression profiling of mouse organogenesis. *Nature Biotechnology*. 2021. (in press)
2. Barile M, Imaz-Rosshandler I, Inzani I, **Ghazanfar S**, Nichols J, Marioni JC, et al. Coordinated Changes in Gene Expression Kinetics Underlie both Mouse and Human Erythroid Maturation. *Genome Biology*. 2021. (in press)
3. Francis D\*, **Ghazanfar S\***, Havula E, Krycer JR, Strbenac D, Senior A, et al. Genome wide analysis in Drosophila reveals diet by gene interactions and uncovers diet-responsive genes. *G3 Genes—Genomes—Genetics*. 2021.
4. Su X, Zhao L, Shi Y, Zhang R, Long Q, Bai S, ... **Ghazanfar S**, ... et al. Clonal evolution in liver cancer at single-cell and single-variant resolution. *J Hematol Oncol*. 2021.
5. Muus C, Luecken MD, Eraslan G, Sikkema L, Waghray A, Heimberg G, ..., **Ghazanfar S**, ... et al. Single-cell meta-analysis of SARS-CoV-2 entry genes across tissues and demographics. *Nature Medicine*. 2021.
6. Guibentif C, Griffiths JA, Imaz-Rosshandler I, **Ghazanfar S**, Nichols J, Wilson V, et al. Diverse Routes toward Early Somites in the Mouse Embryo. *Developmental Cell*. 2021.
7. Lau M-T, **Ghazanfar S**, Parkin A, Chou A, Rouaen JR, Littleboy JB, et al. Systematic functional identification of cancer multi-drug resistance genes. *Genome Biology*. 2020.
8. **Ghazanfar S**, Lin Y, Su X, Lin DM, Patrick E, Han ZG. Investigating higher-order interactions in single-cell data with scHOT. *Nature Methods*. 2020.
9. Su X, Long Q, Bo J, Shi Y, Zhao L-N, Lin Y, **Ghazanfar S**, et al. Mutational and transcriptomic landscapes of a rare human prostate basal cell carcinoma. *Prostate*. 2020.
10. Rood JE, Stuart T\*, **Ghazanfar S\***, Biancalani T\*, Fisher E, Butler A, et al. Toward a Common Coordinate Framework for the Human Body. *Cell*. 2019.
11. Lin Y, **Ghazanfar S**, Wang KYX, Gagnon-Bartsch JA, Lo KK, Su X, et al. scMerge leverages factor analysis, stable expression, and pseudoreplication to merge multiple single-cell RNA-seq datasets. *Proceedings of the National Academy of Sciences USA*. 2019.
12. Lim SY, Lee JH, Gide TN, Menzies AM, Guminski A., **Ghazanfar S**, et al. Circulating cytokines predict immune-related toxicity in melanoma patients receiving anti-PD-1-based immunotherapy. *Clinical Cancer Research*. 2019.
13. HuBMAP Consortium. The human body at cellular resolution: the NIH Human Biomolecular Atlas Program. *Nature*. 2019.

14. Lin Y, **Ghazanfar S**, Strbenac D, Wang A, Patrick E, Lin DM, et al. Evaluating stably expressed genes in single cells. *Gigascience*. 2019.
  15. Bisogni AJ, **Ghazanfar S**, Williams EO, Marsh HM, Yang JY, Lin DM. Tuning of delta-protocadherin adhesion through combinatorial diversity. *Elife*. 2018.
  16. Sykes EK, McDonald CE, **Ghazanfar S**, Mactier S, Thompson JF, Scolyer RA, et al. A 14-protein signature for rapid identification of poor prognosis stage III metastatic melanoma. *Proteomics Clinical Applications*. 2018.
  17. **Ghazanfar S**+, Strbenac D, Ormerod JT, Yang JYH, Patrick E. DCARS: differential correlation across ranked samples. *Bioinformatics*. 2019.
  18. **Ghazanfar S**, Vuocolo T, Morrison JL, Nicholas LM, McMillen IC, Yang JYH, et al. Gene expression allelic imbalance in ovine brown adipose tissue impacts energy homeostasis. *PLoS One*. 2017.
  19. **Ghazanfar S**, Bisogni AJ, Ormerod JT, Lin DM, Yang JYH. Integrated single cell data analysis reveals cell specific networks and novel coactivation markers. *BMC Systems Biology*. 2016.
  20. **Ghazanfar S**, Yang JYH. Characterizing mutation-expression network relationships in multiple cancers. *Computational Biology and Chemistry*. 2016.
  21. Yang P, Patrick E, Humphrey SJ, **Ghazanfar S**, James DE, Jothi R, et al. KinasePA: Phosphoproteomics data annotation using hypothesis driven kinase perturbation analysis. *Proteomics*. 2016.
- Preprints:*
22. Righelli D, Weber LM, Crowell HL, Pardo B, **Ghazanfar S** et al. SpatialExperiment: infrastructure for spatially resolved transcriptomics data in R using Bioconductor. *bioRxiv*. 2021.