

# LIZHONG CHEN

(+61)426810317 ◇ chen.l@wehi.edu.au ◇ lizhongc.github.io

## Education

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- The University of Melbourne** Doctor of Philosophy (PhD) in Statistics **02/2017 – 02/2022**  
Supervisors: A/Prof. Guoqi Qian, Prof. Yuriy Kuleshov, Dr Tingjin Chu  
Thesis: Model selection and averaging by Gibbs sampler with a tropical cyclone seasonal forecasting application
- Peking University** Master of Science (M.S.) in Mathematics **09/2013 – 07/2016**  
Mentor: A/Prof. Houhong Fan  
Thesis: A Report on Computations of Cohomology Rings and Homotopy Groups of Lie Groups
- Peking University** Bachelor of Science (B.S.) in Mathematics **09/2013 – 07/2016**

## Research Experience

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- Smyth Lab, WEHI** *Research Officer* **03/2022 – present**  
Supervisor: Prof. Gordon K Smyth

## Publications

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- [1] Yunshun Chen, Lizhong Chen, Aaron TL Lun, Pedro L Baldoni, and Gordon K Smyth. edgeR v4: powerful differential analysis of sequencing data with expanded functionality and improved support for small counts and larger datasets. *Nucleic Acids Research*, 53(2), 2025.
- [2] Pedro L Baldoni, Lizhong Chen, and Gordon K Smyth. Faster and more accurate assessment of differential transcript expression with Gibbs sampling and edgeR v4. *NAR Genomics and Bioinformatics*, 6(4), 2024.
- [3] Guoqi Qian, Lizhong Chen, and Yuriy Kuleshov. Improving methodology for tropical cyclone seasonal forecasting in the Australian and the South Pacific Ocean regions by selecting and averaging models via Metropolis-Gibbs sampling. *Remote Sensing*, 14(22):5872, 2022.
- [4] Pedro L Baldoni, Lizhong Chen, Mengbo Li, Yunshun Chen, and Gordon K Smyth. Dividing out quantification uncertainty enables assessment of differential transcript usage with diffSplice. *bioRxiv*, 2025.
- [5] Jianan Wang, Lizhong Chen, Daniel V Brown, Chris Chiu, and Terence P Speed. CMDdemux: an efficient single cell demultiplexing method. *bioRxiv*, 2025.
- [6] Jianan Wang, Lizhong Chen, Rachel Thijssen, Belinda Phipson, and Terence P Speed. GLMsim: a GLM-based single cell RNA-seq simulator incorporating batch and biological effects. *bioRxiv*, 2024.

## Talks and Presentations

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- edgeR quasi-likelihood: correcting deviance for bias** Bioinformatics division seminar, WEHI **08/2022**
- Extending edgeR for small counts and large samples** Bioinformatics division seminar, WEHI **05/2023**
- Applying edgeR for alternative splicing analysis** Bioinformatics division seminar, WEHI **04/2024**
- edgeRv4 with expanded functionality and improved support** Short talk, EuroBioC2025 **09/2025**
- Analyzing paired count data using edgeR** Bioinformatics division seminar, WEHI **09/2025**

## Teaching Experience

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- The University of Melbourne** *Tutor* **07/2017 - 02/2022**  
Linear Algebra, Accelerated Mathematics I/II, Complex Analysis, Multivariate Statistical Techniques
- The University of Melbourne** *Assignment and Exam Marker* **07/2018 - 07/2021**  
Statistical Modelling, Mathematical statistics
- Peking University** *Teaching assistant* **09/2013 - 07/2016**  
Mathematical analysis I/II, Calculus I, Advanced algebra I

## Honors and scholarships

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Melbourne Research Scholarship	The University of Melbourne	2017
Outstanding Graduate of Beijing		2016
Outstanding Graduate of Peking University	Peking University	2016
Guanghua Scholarship	Peking University	2015
National Scholarship	Peking University	2014
Second-Class Freshmen Scholarship	Peking University	2009

## Projects

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### **IBGS: Iterated Blockwise Gibbs Sampler**

IBGS is an MCMC search algorithm designed to find the best model in the high dimensional data given a model selection criterion such as AIC, BIC and so on. Moreover, it can identify those most important covariates having the significant influence on the response.

### **edgeR: Empirical Analysis of Digital Gene Expression Data in R**

We develop the new quasi-likelihood method for differential expression analysis using the exact calculation for unit deviance of Negative Binomial distribution.

### **statmod: Statistical Modeling**

We make the exact distributional calculations for unit deviances of Binomial, Poisson and Negative Binomial distributions.

### **limma: Linear Models for Microarray and Omics Data**

We update the estimation for the prior distribution in empirical Bayes approach.

## Referee services

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Applied mathematical modelling, Nucleic Acids Research, Australian & New Zealand Journal of Statistics