NING LIU

Adelaide, SA 5000 | 0452382831 | ning.liu@adelaide.edu.au

Brief Biography

Dr Ning Liu is a bioinformatician and Senior Postdoctoral Researcher at the South Australian immunoGENomics Cancer Institute (SAiGENCI) and Adelaide Centre for Epigenetics (ACE), Adelaide University. He completed his PhD in Bioinformatics at the University of Adelaide in 2021 and has since developed computational methods for single-cell genomics, spatial transcriptomics, epigenomics and multi-omics analysis. His research focuses on understanding gene regulation, cell identity and tissue organisation in development and disease through statistical modelling, software development and AI-based approaches.

Dr Liu has developed several open-source bioinformatics tools, including standR, hoodscanR, scider, DOMINO, GRASP and vissE.Cloud, supporting spatial-omics analysis. His work has been published in leading journals including Nature, Nature Methods, Nucleic Acids Research, Genome Biology, Briefing in Bioinformatics, and Immunology. He also contributes to postgraduate genomics teaching, bioinformatics workshops, student supervision and national bioinformatics community activities.

Qualifications and Prizes

Qualifications

- **Ph.D.** of Medicine (Bioinformatics) University of Adelaide, 10/2021
  - Thesis title: Three-dimensional regulation: Establishing novel linkages between non-coding genetic variation and target genes.

- **Master** of Biotechnology (Bioinformatics) University of Adelaide, 07/2017
  - GPA 3.8 out of 4
  - Thesis title: Investigating computational analysis pipelines and genomic proximity interactions in T lymphocytes.

- **Bachelor** of Biotechnology (Biostatistics) Xia'men University, 06/2015

Prizes

- Audience Choice Award for the presentation from APBJC 2024 in Japan
- Dean's Commendation for Doctoral Thesis Excellence Award in 2021 from University of Adelaide
- Outstanding Academic Achievement Award in both 2015-2016 and 2016-2017 from University of Adelaide

Career Profile

Senior Postdoctoral Researcher 10/2023 to Present

Polo lab, Adelaide Centre of Epigenetics (ACE) and Cancer Epigenetics program, South Australian Immunogenomics Cancer Institute (SAiGENCI), University of Adelaide – Adelaide, SA

- Development of novel computational methods to address biological questions in the field of spatial transcriptomics and epigenetics with the context of cancer and cell development.
- Leveraged interpersonal and communication skills to mentor PhD, graduate and undergraduate students.

Research Officer 05/2021 to 10/2023

Bioinformatics Division, Walter And Eliza Hall Institute Of Medical Research (WEHI) – Melbourne, VIC

- Performed in-depth data analysis for spatial transcriptomics and proteomics data and single cell RNA-seq data.
- Developed computational packages for analyzing spatial transcriptomics data.
- Supervision of undergraduate students.

Publications

2026

1) Hao, Y., Sun, H., Ran, Z., Guo, X., Liu, M., Bi, Y., Polo, J.M., **Liu, N.*** and Li, F.*, 2026. Graph-based RNA structural representation reveals determinants of subcellular localization. bioRxiv, pp.2026-02. (Accepted in Briefing in Bioinformatics)

2) Wong, Y.Y., Harbison, J.E., Hassan, D., Gundsambuu, B., Hope, C.M., Wong, S.W., Couper, J.J., Gummow, J.A., Breen, J., **Liu, N.** and Pederson, S.M., 2026. Integrative epigenomic and transcriptomic profiling reveals dysregulated T cell regulatory networks in Stage 3 Type 1 diabetes.

3) Mengyuan, S.*, Yingnan, G.*, **Ning, L.***, Dharmesh, B., Michael, M., Juan, H., Jared, A., Edward, Y., Chen, Z., Nora, L. and Si, S., 2026. cellNexus: Quality control, annotation, aggregation and analytical layers for the Human Cell Atlas data. bioRxiv, pp.2026-04. (Accepted in Nature Methods)

2025

4) Li, M.*, Liu, N.*, Nguyen, Q.H. and Chen, Y., 2025. Preserving tissue structure through density-based spatial analysis with scider. bioRxiv, pp.2025-09.

5) Kulasinghe, A., Berrell, N., Tan, C.W., Kilgallon, A., Monkman, J., Bidgood, C., Janke, C., Donovan, M., Liu, N., Embaye, K. and Yunis, J., 2025. Spatial Multiomic Profiling Identifies Metabolic and Inflammatory Signatures Driving Recurrence in Adjuvant-Treated NSCLC.

6) **Liu, N.**, Martin, J., Bhuva, D.D., Chen, J., Li, M., Lee, S.C., Kharbanda, M., Cheng, J., Mohamed, A., Kulasinghe, A. and Chen, Y., 2024. hoodscanR: profiling single-cell neighborhoods in spatial transcriptomics data. bioRxiv, pp.2024-03. (reviewing in Bioinformatics)

7) Jia, P., Liu, N.W., Ran, Z., Maiolo, S., Zhang, T., Mohenska, M., Guo, X., Wang, C., Walter, E., Ricciardelli, C., Lokman, N.A., Morrow, R., Oehler, M., Polo, J.M.*, **Liu, N.*** and Li, F.Y.*, 2025. DOMINO: diffusion-optimised graph learning identifies domain

structures with enhanced accuracy and scalability. bioRxiv, pp.2025-12. (reviewing in Nature Communication)

2024

8) Sadeghirad, H., Monkman, J., Tan, C.W., **Liu, N.**, Yunis, J., Donovan, M.L., Moradi, A., Jhaveri, N., Perry, C., Adams, M.N. and O'Byrne, K., 2024. Spatial dynamics of tertiary lymphoid aggregates in head and neck cancer: insights into immunotherapy response. Journal of Translational Medicine, 22(1), pp.1-13.

9) Bhuva, D.D., Tan, C.W., Salim, A., Marceaux, C., Pickering, M.A., Chen, J., Kharbanda, M., Jin, X., **Liu, N.**, Feher, K. and Putri, G., 2024. Library size confounds biology in spatial transcriptomics data. Genome Biology, 25(1), p.99.

10) Huang, W., O'Hara, S.E., Xie, C., **Liu, N.**, Rayner, C.K., Nicholas, L.M. and Wu, T., 2024. Effects of a bitter substance, denatonium benzoate, on pancreatic hormone secretion. American Journal of Physiology-Endocrinology and Metabolism, 326(4), pp.E537-E544.

11) Tan, C.W., Chen, J., **Liu, N.**, Bhuva, D.D., Blick, T., Monkman, J., Cooper, C., Kharbanda, M., Feher, K., Phipson, B. and Killingbeck, E.E., 2024. In situ single-cell profiling sheds light on IFI27 localisation during SARS-CoV-2 infection. eBioMedicine, 101.

12) Bhuva, D.D., Tan, C.W., **Liu, N.**, Whitfield, H.J., Papachristos, N., Lee, S.C., Kharbanda, M., Mohamed, A. and Davis, M.J., 2024. vissE: A versatile tool to identify and visualise higher-order molecular phenotypes from functional enrichment analysis. BMC bioinformatics, 25(1), pp.1-22.

13) **Liu, N.,** Bhuva, D.D., Mohamed, A., Bokelund, M., Kulasinghe, A., Tan, C.W. and Davis, M.J., 2024. standR: spatial transcriptomic analysis for GeoMx DSP data. Nucleic Acids Research, 52(1), pp.e2-e2.

2023

14) Buckberry, S., Liu, X., Poppe, D., Tan, J.P., Sun, G., Chen, J., Nguyen, T.V., de Mendoza, A., Pflueger, J., Frazer, T. and Vargas-Landín, D.B., Paynter, J.M., Smits, N., **Liu, N.**, Ouyang, J.F., Rossello, F.J., Chy, H.S., Rackham, O.J.L., Laslett, A.L., Breen, J., Faulkner, G.J., Nefzger, C.M., Polo, J.M. & Lister, R. 2023. Transient naive reprogramming corrects hiPS cells functionally and epigenetically. Nature, pp.1-10.

15) Mohamed, A., Bhuva, D.D., Lee, S., **Liu, N.**, Tan, C.W. and Davis, M.J., 2023. vissE. cloud: a webserver to visualise higher order molecular phenotypes from enrichment analysis. Nucleic Acids Research, p.gkad337.

16) Kulasinghe, A.*, **Liu, N.***, Tan, C.W., Monkman, J., Sinclair, J.E., Bhuva, D.D., Godbolt, D., Pan, L., Nam, A., Sadeghirad, H. and Sato, K., 2023. Transcriptomic profiling of cardiac tissues from SARS-CoV-2 patients identifies DNA damage. Immunology, 168(3), pp.403-419.

17) Sadeghirad, H.*, **Liu, N.***, Monkman, J., Ma, N., Cheikh, B.B., Jhaveri, N., Tan, C.W., Warkiani, M.E., Adams, M.N., Nguyen, Q. and Ladwa, R., Compartmentalised spatial profiling of the tumour microenvironment in head and neck squamous cell carcinoma identifies immune checkpoint molecules and tumour necrosis factor receptor superfamily members as biomarkers of response to immunotherapy. Frontiers in Immunology, 14, p.1384.

18) Aldersey, J.E., **Liu, N.**, Tearle, R., Low, W.Y., Breen, J., Williams, J.L. and Bottema, C.D.K., 2023. Topologically associating domains in the POLLED region are the same for Angus-and Brahman-specific Hi-C reads from F1 hybrid fetal tissue. Animal Genetics.

19) Wong, Y.Y., Harbison, J.E., Hope, C.M., Gundsambuu, B., Brown, K.A., Wong, S.W., Brown, C.Y., Couper, J.J., Breen, J., **Liu, N.** and Pederson, S.M., 2023. Parallel recovery of chromatin accessibility and gene expression dynamics from frozen human regulatory T cells. Scientific Reports, 13(1), p.5506.

2022

20) **Liu, N.**, Sadlon, T., Wong, Y.Y., Pederson, S., Breen, J. and Barry, S.C., 2022. 3DFAACTS-SNP: using regulatory T cell-specific epigenomics data to uncover candidate mechanisms of type 1 diabetes (T1D) risk. Epigenetics & Chromatin, 15(1), pp.1-21.

2021

21) **Liu, N.**, Low, W. Y., Alinejad-Rokny, H., Pederson, S., Sadlon, T., Barry, S., & Breen, J. (2021). Seeing the forest through the trees: prioritising potentially functional interactions from Hi-C. Epigenetics & Chromatin, 14(1), 1-17.

2020

22) Brown, C.Y., Sadlon, T., Hope, C.M., Wong, Y.Y., Wong, S., **Liu, N.**, Withers, H., Brown, K., Bandara, V., Gundsambuu, B. and Pederson, S., 2020. Molecular Insights Into Regulatory T-Cell Adaptation to Self, Environment, and Host Tissues: Plasticity or Loss of Function in Autoimmune Disease. Frontiers in Immunology, 11, p.1269.

2019

23) Wan, Q., Leemaqz, S.Y.L., Pederson, S.M., McCullough, D., McAninch, D.C., Jankovic-Karasoulos, T., Smith, M.D., Bogias, K.J., **Liu, N.**, Breen, J. and Roberts, C.T., 2019. Quality control measures for placental sample purity in DNA methylation array analyses. Placenta, 88, pp.8-11.

Software Packages, and Web Apps

Bioconductor packages

1) scider (2023) over 3,800 downloads
2) hoodscanR (2023) over 4,500 downloads
3) standR (2022) over 8,000 downloads

Web apps

4) vissE.Cloud (2023) over 70,000 accesses (from 42 countries)

Deep learning-based python libraries

5) DOMINO (2025)
6) GRASP (2026)

Adwards & Funding

Grant	Funding Organization	Chief Investigators	Status	Amount
BioPlatforms Australia South Australian Framework Initiative: Dissecting molecular mechanisms underpinning a new cytokine signalling axis governing leukaemia stemness.	South Australia Genomics Centre	Dr Winnie Kan Dr Adrienne Sullivan **Dr Ning Liu** Professor Jose Polo Professor Angel Lopez Associate Professor Luciano Martelotto Associate Professor Daniel Thomas	2025-2026	$ 125,000
MRF2031100 METASPATIAL Study: Metabolic Spatial Analysis of Lung Cancer study	Medical Research Future Fund (MRFF)	Dr. Arutha Kulasinghe Dr. Dharmesh D Bhuva Dr. Amelia Parker Prof. Gabrielle Belz Prof. Melissa Davis Dr. Sophie Curio Dr. Chin Wee Tan Dr. Mark Adams **Dr. Ning Liu** Dr. Qiutong Huang Prof. Ken O'Byrne Prof. Brett Hughes Dr. Jenny Gunter Dr. Charles Bidgood A/Prof. Haitham Tuffaha	2024-2028	$ 1,999,650
Australian Bioinformatics and Computational Biology Society (ABACBS) – Best poster talk	ABACBS	Ning Liu	2019	$ 500
ABACBS travel grant	Illumina, Inc.	Ning Liu	2019	$ 500
ABACBS travel grant	ABACBS	Ning Liu	2018	$ 500
EMBL Australia PhD Course grant	EMBL Australia	Ning Liu	2018	$ 5000
Adelaide Graduate Research Scholarship	The University of Adelaide	Ning Liu	2017-2021	$ 150,000 fee waiver + 24,000 stipend p.a.

Conference/Seminar Presentations

1. **National invited speaker**, Australian Bioinformatics and Computational Biology Society (ABACBS) Conference, Adelaide, Australia, Dec 2025.

2. WEHI Spatial Technology Symposium 2025, Melbourne, Australia, Jun 2025
3. Bioconductor Asia 2024, Sydney, Australia, Nov 2024
4. 1st Asia & Pacific Bioinformatics Joint Conference (APBJC) 2024, Okinawa, Japan, Oct 2024
5. **Invited speaker**, Researcher Seminar at Institute of Evolution & Marine Biodiversity, Ocean University of China, China, April 2024.
6. Adelaide Bioinformatics Meeting at CCB, Adelaide, Australia, March 2024.
7. **Invited speaker**, Australian Lung Cancer Conference, Gold coast, Australia, Feb 2023.
8. Bioinformatics seminar, Walter Eliza Hall Institute, Melbourne, Australia, Oct 2022.
9. Australian Bioinformatics and Computational Biology Society (ABACBS) Conference, Sydney, Australia, Dec 2019.
10. Australian Bioinformatics and Computational Biology Society (ABACBS) Conference, Melbourne, Australia, Nov 2018.
11. Lorne Genome Conference, Lorne, Australia, Feb 2018.

Workshops Delivered

1. Bioinformatics workshop, ABACBS 2025 conference, Adelaide, Dec 2025.
2. Bioinformatics workshop, ABACBS 2023 conference, Brisbane, Dec 2023.
3. Bioinformatics workshop, Monash Bioinformatics Platform, Monash University, Melbourne, Sep 2023.
4. Bioinformatics workshop, ABACBS 2022 conference, Melbourne, Dec 2022.
5. Bioinformatics workshop, Fall into bioinformatics, Adelaide, 2019.
6. Bioinformatics workshop, Spring into bioinformatics, Adelaide, 2019.
7. Bioinformatics workshop, RAdelaide workshop, Adelaide, 2017 & 2019.

Professional Contributions

Professional memberships:

- Member of International Society of Computational Biology (ISCB) (2024 - present).
- Member of the Australian Bioinformatics and Computational Biology Society (ABACBS) (2016 - present).

Organization committee:

- Postdoctoral Executive committee, ABACBS, 2025 & 2026.
- Conference committee, COMBINE symposium, 2017 & 2018.
- Executive committee, COMBINE, 2018 & 2019.

Act as a reviewer in the following journals:

- Genome Biology
- Bioinformatics
- Briefing in Bioinformatics
- PLOS Computational Biology
- Journal of Translational Medicine
- Genome Medicine

Supervision and mentoring

- PhD student for cell development and epigenome in Marsupial model: Elly Walters (Adelaide University)
- Honor students: Xinqi Peng, Xianzhe Hu (Adelaide University)
- Master student: Yuanzhen (Jennifer) Tan (Adelaide University)
- Undergraduate students: Boya Lv (China Agricultural University), Micah Bokelund (The University of Melbourne)

Teaching activities

1. Course designer and lecturer of undergraduate course Science Process and Practice in 2024-2026, Haide College, Ocean University of China and the University of Adelaide.
2. Course workshop designer and instructor of postgraduate course Genomics Applications (BIOINF 7150) in 2020, University of Adelaide.
3. Workshop tutor of postgraduate course Bioinformatics and Systems Modelling (BIOTECH 7005) in 2018, University of Adelaide.