



陳俊杰博士

數智科技學系 | 助理教授

個人簡介

陳俊杰，博士、助理教授、碩士生導師。是一位資深的生物信息學與人工智能（AI）專家，擁有超過 20 年跨越學術界與工業界的深厚經驗。他精通大規模基因組數據解析，並具備長達 30 年的軟體開發與系統架構專業背景。陳博士擅長領導跨學科團隊，管理涵蓋 AI+ 農業、環境微生物學及轉化醫學等領域的複雜科研項目。他目前致力於將深度學習模型應用於多組學數據解析，推動科研成果從實驗室轉向臨床與產業應用。

工作經歷

- 澳門中西創新學院，助理教授
- 澳門大學，高級行政主任
- 澳門大學，訪問講師
- 澳洲 AGRF，生物信息學經理
- 澳洲西澳大利亞大學/昆士蘭大學，高級研究員
- 北京孟山都生物技術研究中心，生物信息學科學家及數據經理

- Objectiva (北京), 商業分析師
- 微軟 (北京), 軟體開發工程師

教育背景

- 墨爾本大學, 工程博士 (專攻機器學習和生物信息學)
- 墨爾本大學, 機電一體化學士 (一級榮譽)
- 墨爾本大學, 計算機科學學士

研究興趣

生成式 AI、多模態大模型、智慧農業與精準育種、宏基因組「暗物質」挖掘、轉化醫學。

任教課程

人工智能碩士及博士課程。

相關榮譽

墨爾本研究獎學金、Universitas 21 研究高級學位流動獎學金。

研究成果

論文發表：

1. Nie S, Li F., Li R., Wang J., Ma Y., Chan C-KK*, Zhao J.*, Hu H.*, Challenges in bringing pangenome research into breeding: a case study in rice, *Plant Biotechnology Journal*, Feb. 2026, doi: 10.1111/pbi.70591 *co-corresponding author (IF:10.5)
2. Huerlimann R, Cowley JA, Wade NM, Wang Y, Kasinadhuni N, Chan C-KK, et al. Genome assembly of the Australian black tiger shrimp (*Penaeus monodon*) reveals a novel fragmented IHNV EVE sequence. *G3 Genes|Genomes|Genetics*. 2022;12. doi:10.1093/G3JOURNAL/JKAC034. (IF: 3.154)
3. Liu H, Mullan D, Zhao S, Zhang Y, Ye J, Wang Y, Zhang A, Zhao X, Liu G, Zhang C, Chan K, Lu Z, Yan G (2022). Genomic regions controlling yield-related traits in spring wheat: a mini review and a case study for rainfed environments in Australia and China. *Genomics*, 114 (2), 110268. <https://doi.org/10.1016/J.YGENO.2022.110268> (IF = 5.736)
4. Schliebs O, Chan CKK, Bayer PE, Petereit J, Singh A, Hassani-Pak K, Batley J, Edwards D (2021). Daisychain: Search and Interactive Visualisation of Homologs in Genome Assemblies. *Agronomy* 2021, Vol. 11, Page 2587, 11(12), 2587. <https://doi.org/10.3390/AGRONOMY11122587> (IF: 2.24)
5. Yuan Y, Bayer PE, Anderson R, Lee HT, Chan CKK, Zhao R, Batley J, Edwards D. RefKA: A fast and efficient long-read genome assembly approach for large and complex genomes, *bioRxiv* 2020.04.17.035287; doi: <https://doi.org/10.1101/2020.04.17.035287>
6. Scheben A, Verpaalen B, Lawley CT, Chan CKK, Bayer PE, Batley J, et al. CropSNPdb: a database of SNP array data for Brassica crops and hexaploid bread wheat. *Plant J*. 2019;98:142–52. doi:10.1111/tpj.14194. (IF: 5.775)
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8. Bayer PE, Golicz AA, Tirnaz S, Chan CKK, Edwards D, Batley J. Variation in abundance of

predicted resistance genes in the Brassica oleracea pangenome. *Plant Biotechnol J*.

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9. Scheben A., Chan CKK, Mansueto L., Mauleon R., Larmande P, Alexandrov N., Wing RA, McNally KL, Quesneville H. Edwards D., Progress in single-access information systems for wheat and rice crop improvement, *Briefings in Bioinformatics*, Volume 20, Issue 2, March 2019, Pages 565–571, <https://doi.org/10.1093/bib/bby016> (IF: 8.990)

10. Hurgobin B, Golicz AA, Bayer PE, Chan CKK, et al. Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid Brassica napus. *Plant Biotechnol J*. 2018;16(7):1265–1274. doi:10.1111/pbi.12867. (IF: 6.840)

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15. Golicz AA, Bayer PE, Barker GC, Edger PP, Kim H, Martinez PA, Chan CKK, Severn-Ellis A, McCombie WR, Parkin IAP et al: The pan-genome of an agronomically important crop plant Brassica oleracea. *Nature Communications* 2016, 7:13390. (IF: 12.124)

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21. Rosic N, Kaniewska P, Chan CKK, Ling E, Edwards D, Dove S, Hoegh-Guldberg O: Early transcriptional changes in the reef-building coral *Acropora aspera* in response to thermal and nutrient stress. *BMC Genomics* 2014, 15(1):1052. (IF: 3.729)
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會議論文發表

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2. Jabbari J, Kasinadhuni N, Stevens M, Siemering K, Chan K: Comparison of microbial community diversity inference by sequencing full-length and variable regions of the 16S rRNA gene using different PCR approaches on PacBio Sequel and Illumina MiSeq. In: AGTA 2019, Oct 7-9, Melbourne, Australia (2019)
3. Kasinadhuni K, Noune C, Crockett J, Chan K: Evaluation of internal controls on V1-V3 & V3-V4 primer sequences across various AGRF nodes on different MiSeq machines. In: AGTA 2018, Nov 4-7, Adelaide, Australia (2018)
4. Bayer PE, Chan CKK, Lee HT, Yuan Y, Edwards D: A fast long-read assembly method for the wheat genome. In: PAG XXVI Conference, Jan 13-17, San Diego, CA, USA (2018)
5. Chan K, Bayer P, Davey R, Alaux M, Pommier C, et al.: Development of WheatIS and collaboration between plant information systems. In: PAG XXV Conference, Jan 14-18, San

Diego, CA, USA (2017)

6. Kaur P, Chan CKK, Bayer PE, Edwards D, Erskine W: TrifoliGATE Subterranean Clover Genomic Resources: Building A Comprehensive User-Friendly Platform For Future Forage Legume Breeding. In ICLGG 2017, Sep 18-22, Siófok, Hungary (2017)

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15. Ruperao P, Bayer P, Chan CKK, Azam S, Karafiátová M, et al.: A chromosomal genomics approach to assess and validate the desi and kabuli draft chickpea genome assemblies. In: PAG XXII Conference, Jan 10-15, San Diego, CA, USA (2014)
16. Bayer PE, Lorenc M, Martinez P, Chan K, Visendi P, et al.: Genome assembly validation and trait association using skim based genotyping by sequencing in canola. In: PAG XXII Conference, Jan 10-15, San Diego, CA, USA (2014)
17. Visendi P, Stankova H, Hayashi S, Berkman P, Chan K, et al.: An optimised approach to sequence and assemble BACs: application to bread wheat chromosome arm 7DS. In: PAG XXII Conference, Jan 10-15, San Diego, CA, USA (2014)
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23. Sun J, Chan CKK, Tao N, Blanchard M, Cao Y: TE-Viewer: A visualization tool for examine molecular quality of transgenic events in our biotech plant testing pipeline. In: TCM 2010 (Monsanto internal conference), Jun 08-11, St. Louis, MO, USA (2010)
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26. Guru SM, Chan CKK, Halgamuge SK: Advanced Networked Sensor System. In: Knowledge Commercialisation Australasia Forum & Fair of Ideas, Mar 26-28, Sydney, Australia (2003)

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