



陳俊杰博士

數智科技學系 | 助理教授

個人簡介

陳俊杰博士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 (含博士後)

- 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)

o 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)
7. Chan CKK, Rosic N, Lorenc MT, Visendi P, Lin M, Kaniewska P, et al. A differential k-mer analysis pipeline for comparing RNA-Seq transcriptome and meta-transcriptome datasets without

- a reference. *Funct Integr Genomics*. 2019;19:363–71. doi:10.1007/s10142-018-0647-3. (IF: 2.745)
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*. 2019;17:789–800. doi:10.1111/pbi.13015. (IF: 8.154)
 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)
 11. Yuan Y, Bayer PE, Scheben A; Chan CKK and Edwards D: BioNanoAnalyst: A visualisation tool to assess genome assembly quality using BioNano data. *BMC Bioinformatics*. 2017;18 1:323. doi:10.1186/s12859-017-1735-4. (IF: 2.448)
 12. Lim DKY, Schuhmann H, Thomas-Hall SR, Chan CKK, Wass TJ, Aguilera F, Adarme-Vega TC, Dal’Molin CGO, Thorpe GJ, Batley J, Edwards D, Schenk PM: RNA-Seq and metabolic flux analysis of Tetraselmis sp. M8 1 during nitrogen starvation reveals a 2 two-stage lipid accumulation mechanism. *Bioresource Technology*. 2017;doi:http://dx.doi.org/10.1016/j.biortech.2017.06.003 (IF: 5.651)
 13. Bayer PE, Hurgobin B, Golicz A, Chan CKK, Yuan Y, Lee HT, Renton M, Meng J, Li R, Long Y, Zou J, Bancroft I, Chalhoub B, King G, Batley J, Edwards D: Assembly and comparison of two closely related Brassica napus genomes. *Plant Biotechnology Journal*. 2017; doi:10.1111/pbi.12742. (IF: 6.305)
 14. Montenegro JDM, Golicz AA, Bayer PE, Hurgobin B, Lee HT, Chan CKK, Visendi P, Lai K, Doležel J, Batley J, Edwards D: The pan-genome of modern hexaploid bread wheat. *The Plant Journal*. 2017, doi:10.1111/tbj.13515 (IF: 5.901) 1/4
 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)
 16. Lee H, Golicz AA, Bayer PE, Jiao Y, Tang H, Paterson AH, Sablok G, Krishnaraj RR, Chan CKK, Batley J, Edwards D: The Genome of a Southern Hemisphere Seagrass Species (*Zostera muelleri*). *Plant Physiol* 2016, 172(1):272-283. (IF: 6.280)
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 18. Kaniewska P, Chan CKK, Kline D, Ling EYS, Rosic N, Edwards D, Hoegh-Guldberg O, Dove S: Transcriptomic Changes in Coral Holobionts Provide Insights into Physiological Challenges of Future Climate and Ocean Change. *PLoS ONE* 2015, 10(10):e0139223. (IF: 2.806)
 19. Bayer P, Ruperao P, Mason A, Stiller J, Chan CKK, Hayashi S, Long Y, Meng J, Sutton T, Visendi P et al: High-resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in *Cicer arietinum* and *Brassica napus*. *Theor Appl Genet* 2015:1-9. (IF: 3.264)
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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)
22. Rosic N, Ling EYS, Chan CKK, Lee HC, Kaniewska P, Edwards D, Dove S, Hoegh-Guldberg O: Unfolding the secrets of coral-algal symbiosis. *ISME J* 2014. (IF: 9.302)
23. Ruperao P, Chan CKK, Azam S, Karafiátová M, Hayashi S, Čížková J, Saxena RK, Šimková H, Song C, Vrána J et al: A chromosomal genomics approach to assess and validate the desi and kabuli draft chickpea genome assemblies. *Plant Biotechnology Journal* 2014, 12(6):778-786. (IF: 5.752)
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會議論文發表

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5. Chan CKK, Lam G, Guru SM, Halgamuge MN, Fernando S: Development of a SMARTBOLT prototype with energy model for clustered sensor systems. In: FSKD'02: Nov 18-22 2002; Singapore; 2002: 280-284.

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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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10. Montenegro J, Lee HT, Hurgobin B, Visendi P, Chan K, et al.: Improved methods for reassembly and analysis of the 17 Gb bread wheat genome. In: PAG XXIV Conference, Jan 9-13, San Diego, CA, USA (2016)
11. Bayer P, Ruperao P, Montenegro J, Chan K, Sutton T, et al.: Improving genome assemblies and capturing genome variation data for applied crop improvement. In: PAG Asia 2015, Jul 13-15, Singapore (2015)

12. Golicz AA, Schliep M, Lee HT, Bayer PE, Larkum AWD, Dolferus R, Batley J, Chan CKK, et al.: Genomic characterisation of seagrass (*Zostera muelleri*), a plant adapted to life in the submerged marine environment. In: PAG Asia 2015, Jul 13-15, Singapore (2015)
13. Montenegro MD, Hurgobin B, Golicz A, Martinez P, Muhindira PV, Lee J, Bayer PE, Ruperao P, Chan K, et al.: Wheat genome assessment and reassembly. In: PAG Asia 2015, Jul 13-15, Singapore (2015)
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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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19. Tollenaere R, Alamery S, Saad NSM, Hayward AC, Bayer PE, Dalton-Morgan J, Chan K, et al.: Identification and Characterisation of Candidate Genes for Blackleg Resistance in *Brassica napus* Using Next Generation Sequencing. In: PAG XXII Conference, Jan 10-15, San Diego, CA, USA (2014)
20. Batley J, Tollenaere R, Alamery S, Saad NSM, Hayward AC, Bayer PE, Dalton-Morgan J, Chan K, et al.: Identification and Characterisation of Candidates for Blackleg Resistance QTLs in *Brassica napus* Using Next Generation Sequencing. In: PAG XXII Conference, Jan 10-15, San Diego, CA, USA (2014)
21. Lim DKY, Schuhmann H, Thomas-Hall SR, Chan K, Edwards D, et al.: Identifying the bottlenecks of microalgal lipid production: a new transcriptional profiling approach. In: IMBC 2013, Nov 11-15, Brisbane Australia (2013)
22. Chan CKK, He K, Lv L, Wu X, Sun J., et al.: In-house rice genome browser. In: TCM 2010 (Monsanto internal conference), Jun 08-11, St. Louis, MO, USA (2010)
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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25. Zhang R, Lv L, Chan CKK, Sun J, He K, et al.: GE-Atlas: A graphical visualization tool for viewing and mining gene expression patterns. In: TCM 2010 (Monsanto internal conference), Jun

08-11, St. Louis, MO, USA (2010)

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1. Yuan, Y., Scheben, A., Chan, CKK, Edwards, D. (2017). Databases for Wheat Genomics and Crop Improvement. In *Methods in molecular biology* (Clifton, N.J.) (Vol. 1679, pp. 277–291). https://doi.org/10.1007/978-1-4939-7337-8_18
2. Ghosh S, Chan CKK: Analysis of RNA-Seq Data Using TopHat and Cufflinks. In: *Plant Bioinformatics: Methods and Protocols*. Edited by Edwards D. New York, NY: Springer New York; 2016: 339-361.
3. Tseng C-H, Chan CKK, Hsu AL, Halgamuge SK, Tang S-L: Binning Sequences Using Very Sparse Labels Within a Metagenome. In: *Encyclopedia of Metagenomics*. Edited by Nelson EK. New York, NY: Springer New York; 2013: 1-13.
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