



陳俊杰博士

智慧旅遊學系 | 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)
- 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：

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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)
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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.
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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.
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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/tpj.13515 (IF: 5.901) 1/4
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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)
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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)
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napus Using Next Generation Sequencing. In: PAG XXII Conference, Jan 10-15, San Diego, CA, USA (2014)

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Brassica napus Using Next Generation Sequencing. In: PAG XXII Conference, Jan 10-15, San Diego, CA, USA (2014)

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

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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