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

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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
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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)
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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)
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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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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 andcollaboration 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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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)

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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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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.
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