Cuiping Pan, Ph.D.

EDUCATION

2013-2014	Stanford Advanced Project Management	Certificate, Stanford University, USA
2005-2008	Ph.D. Biochemistry	Max-Planck Institute of Biochemistry, Germany
2003-2005	M.Sc. Biotechnology	University of Southern Denmark, Denmark
1999-2003	B.Sc. Biotechnology	Zhejiang University, China

RESEARCH FOCUS

2021.10-now	Principal Investigator	Greater Bay Area Institute of Precision Medicine, Fudan University, Guangzhou, China
2021.05-10	Associate Research Professor	Biomedical Pioneering Innovation Center, Peking University, China
2014-2021	Director of Bioinformatics	ERIC Center for Genomics, VA Palo Alto, USA
2013-2014	Research Associate	Department of Genetics, Stanford University, USA
2010-2013	Postdoctoral Fellow	Department of Genetics, Stanford University, USA
2009-2010	Project Assistant	Chinese Academy of Sciences, Tianjin/Beijing, China

RESEARCH FOCUS

My research focuses on:

(1) Multiomics for exploring disease mechanisms, biomarkers and risk prediction models.

(2) Big data computing techniques, such as cloud computing, parallel computing and machine learning.

(3) Personalized protocol for precision health management and disease treatment.

2021.10-present, Greater Bay Area Institute of Precision Medicine, Fudan University, China

- Cardiovascular system and immune system: *Annals of the Rheumatic Diseases* (2023)

2021.5-10, Biomedical Pioneering Innovation Center, Peking University, China

- Developed bioinformatic analysis for genetics- and epigenetics- based non-invasive *in intro* fertilization technologies

2014-2021, VA Palo Alto Healthcare System, USA

- Decoded the genome of abdominal aortic aneurysm: *Cell* (2018), *Circulation* (2020), *Circulation* (2021).
- Led a bioinformatics team to build computational infrastructure and develop methods for the Genomics Initiatives in the VA Million Veteran Program:
    - Intelligent data processing workflow, with the throughput of 600 whole genomes per day, and continuous process of 80,000 whole genomes for 5 months: *Scientific Reports* (2021)
    - Methods for integrative analysis of tens of thousands of whole genomes, for interactive query of terabytes of genotypes and for federal computing: *Bioinformatics* (2017), *IEEE BIBM Conference* (2020), *Bioinformatics* (2021), *PLoS Computational Biology* (2021).

2010-2014, Stanford University Genetics Department, Mentor: Prof. Michael Snyder

- Developed personal genome interpretation pipeline for the Stanford Clinical Genomics Program: *The Journal of the American Medical Association* (2014), *PLoS Genetics* (2015).
- Developed HPC-based scalable variant calling methods for large quantities of whole genome sequencing data: *Nature Biotechnology* (2012).

2004-2008, Max-Planck Institute of Biochemistry, Mentor: Prof. Matthias Mann

- Studied cell systems related to the type 2 diabetes, using the quantitative mass-spectrometry method SILAC LC-MS/MS: *Molecular & Cellular Proteomics* (2009)
- Studied small molecule inhibitors and drugs on cellular signaling pathways, using the SILAC TiO2-based LC-MS/MS phosphoproteomics approach: *Proteomics* (2008), *Molecular & Cellular Proteomics* (2009).
- Studied proteome of other systems using label-free quantification technologies: *Journal of proteome research* (2010), *Traffic* (2007).

2002-2003, Zhegjiang University，Mentor: Prof. Bo Zheng

- Applied the Detrended Fluctuation Analysis method to study electroencephalogram of Alzheimer's patients: *Physics Letters A* (2004), *Physica A: Statistical Mechanics and its Applications* (2006).

Publications

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* Equal contributions # Corresponding author

1. Gao H*, Liu S*, Mai Y, Wang Y, Zhang X, Zheng S, Luo C#, **Pan C#**. Combined Therapy of Prednisone

and mTOR Inhibitor Sirolimus for Treating Retroperitoneal Fibrosis. *Ann Rheum Dis.* 2023 Feb; doi:10.1136/ard-2022-223736

2. Guo X*, Xu W*, Zhang W, **Pan C**, Thalacker-Mercera AE, Zheng H, Gu Z. High-frequency and functional mitochondrial DNA mutations at the single-cell level. *Proc Natl Acad Sci.* 2023 Jan 3;120(1):e2201518120.
3. Billing-Ross P, Song J, Tsao PS#, **Pan C#**. Trellis for Efficient Data and Task Management in VA Million Veteran Program. *Sci Rep.* 2021 Dec; 11, 23229.
4. Bahmani A*, Ferriter K*, Krishnan V, Alavi A, Alavi A,Tsao PS, Snyder MP#, **Pan C#**. Swarm: A Federated Cloud Framework for Large-Scale Variant Analysis. *PLoS Comput Biol.* 2021 May 12;17(5):e1008977.
5. **Pan C#**, Tsao PS. Response by Pan and Tsao to Letter Regarding Article, "Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program". *Circulation.* 2021 Apr 27;143(17):e873-e874.
6. Bahmani A*, Xing Z*, Krishnan V*, Ray U*, Mueller F, Alavi AA, Tsao PS, Snyder MP#, **Pan C#**. Hummingbird: Efficient Performance Prediction for Executing Genomic Applications in the Cloud. *Bioinformatics.* 37 (17), 2537-2543.
7. Ferriter K, Mueller F#, Bahmani A#, **Pan C#**. VCFC: Structural and Semantic Compression and Indexing of Genetic Variant Data. (full access) Conference paper for The IEEE International Conference on Bioinformatics and Biomedicine 2020. *BIBM 2020.* 200-203. 2020 Dec.
8. Klarin D, Verma SS, Judy R, Dikilitas O, Wolford B, Paranjpe I, Levin MG, **Pan C**, Tcheandjieu C, Spin J, Lynch J, Assimes TL, Nyrønning LÅ, Mattsson E, Edwards TL, Denny J, Larson E, Lee MAM, Carrell D, Zhang Y, Jarvik G, Gharavi A, Harley J, Jarvik G, Mentch F, Pacheco JA, Skogholt AH, Thomas L, Gabrielsen ME, Hveem K, Nielsen JB, Zhou W, Fritsche K, Huang J, Natarajan P, Sun YS, DuVall SL, Rader DJ, Cho K, Chang KM, Wilson PWF, O'Donnell CJ, Kathiresan S, Scali ST, Berceli SA, Willer C, Jones GT, Bown MJ, Nadkarni G, Kullo I, Ritchie M, Damrauer SM*, Tsao PS* on behalf of the VA Million Veteran Program. Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. *Circulation.* 2020 Sep 28. doi: 10.1161/CIRCULATIONAHA.120.047544.
9. Hunter-Zinck H, Shi Y, Li M, Gorman BR, Ji SG, Sun N, Webster T, Liem A, Hsieh P, Devineni P, Karnam P, Gong X, Radhakrishnan L, Schmidt J, Assimes TL, Huang J, **Pan C,** Humphries D, Brophy M, Moser J, Muralidhar S, Huang GD, Przygodzki R, Concato J, Gaziano JM, Gelernter J, O'Donnell CJ, Hauser ER, Zhao H, O'Leary TJ; VA Million Veteran Program, Tsao PS, Pyarajan S. Genotyping Array Design and Data Quality Control in the Million Veteran Program. *Am J Hum Genet.* 2020 Apr 2;106(4):535-548.
10. Li J*, **Pan C***, Zhang S*, Spin JM, Deng A, Leung LLK, Dalman RL, Tsao PS, Snyder M. Decoding the Genomics of Abdominal Aortic Aneurysm. *Cell.* 2018 Sep 174 (6): 1361-1372.
11. Pan C*, McInnes G*, Deflaux N*, Snyder M, Bingham J, Datta S, Tsao PS. Cloud-based Interactive Analytics for Terabytes of Genomic Variants Data. *Bioinformatics.* 2017 Dec 1;33(23):3709-3715.
12. Dewey FE, Grove ME, Priest JR, Waggott D, Batra P, Miller CL, Wheeler M, Zia A, **Pan C**, Karzcewski KJ, Miyake C, Whirl-Carrillo M, Klein TE, Datta S, Altman RB, Snyder M, Quertermous T, Ashley EA.

Sequence to Medical Phenotypes: A Framework for Interpretation of Human Whole Genome DNA Sequence Data. *PLoS Genet.* 2015 Oct 8;11(10).

13. Hellmuth S*, Boettger F*, **Pan C**, Mann M, Stemmann O. PP2A Delays APC/C-dependent Degradation of Separase-associated but not Free Securin. *EMBO J.* 2014 May 16;33(10):1134-47.
14. Dewey FE*, Grove ME*, **Pan C***, Goldstein BA, Bernstein J, Chaib H, Goldfeder RL, Ormond KE, Caleshu C, Kingham K, Klein TE, Whirl-Carillo M, Sakamoto K, Wheeler MT, Butte AJ, Merker JD, Ford J, Boxer L, Loannidis JPA, Yeung AC, Altman RA, Assimes TL, Snyder M*, Ashley EA*, Quertermous T*. Clinical Interpretation and Implications of Whole Genome Sequencing. *JAMA.* 2014;311(10):1035-1045
15. Merker JD, Roskin KM, Ng D, **Pan C**, Fisk DG, King JJ, Hoh R, Stadler M, Okumoto LM, Abidi P, Hewitt R, Jones CD, Gojenola L, Clark MJ, Zhang B, Cherry AM, George TI, Cherry M, Snyder M, Boyd SD, Zehnder JL, Fire AZ*, Gotlib J*. Comprehensive Whole-genome Sequencing of An Early-stage Primary Myelofibrosis Patient Defines Low Mutational Burden and Non-recurrent Candidate Genes. *Haematologica.* 2013; Nov;98(11):1689-96
16. Lam HY, **Pan C**, Clark MJ, Lacroute P, Chen R, Haraksingh R, O'Huallachain M, Gerstein MB, Kidd JM, Bustamante CD, Snyder M. Detecting and Annotating Genetic Variations Using the HugeSeq Pipeline. *Nat Biotechnol.* 2012; 30 (3): 226-9
17. Sun N, **Pan C**, Nickell S, Mann M, Baumeister W, and Nagy I. Quantitative Proteomic and Transcriptomic Analysis of Thermoplasma Acidophilum Cultured under Aerobic and Anaerobic Conditions. *J Proteome Res.* 2010; 9 (9): 4839-50
18. **Pan C**, Olsen JV, Daub H, and Mann M. Global Effects of Kinase Inhibitors on Signaling Networks Revealed by Quantitative Phosphoproteomics. *Mol Cell Proteomics.* 2009 Dec;8(12):2796-808
19. **Pan C***, Kumar C*, Bohl S, Klingmü U, and Mann M. Comparative Proteomic Phenotyping of Cell lines and Primary Cells to Assess Preservation of Cell Type Specific Functions. *Mol Cell Proteomics.* Mar 01, 2009; 8: 443-450 (Journal cover story; Highlighted by Journal of Proteome Research, December 2008)
20. **Pan C**, Gnad F, Olsen JV, and Mann M. Quantitative Phosphoproteome Analysis of a Liver Cell Line Reveals Specificity of Phosphatase Inhibitors. *Proteomics.* 2008 Nov;8(21):4534-46
21. Schroder B, Wrocklage C, **Pan C**, Jager R, Kosters B, Schafer H, Elsasser HP, Mann M, Hasilik A. Integral and Associated Lysosomal Membrane Proteins. *Traffic* 2007 8:12 1676-86.
22. Yuan JW, ZhengB, **Pan CP**, Wu YZ, Trimper S. Dynamic Scaling Behavior of Human Brain Electroencephalogram. *Physica A: Statistical Mechanics and its Applications. 364. 315-323.*
23. **Pan CP**, Zheng B, Wu YZ, Wang Y, and Tang XW. Detrended Fluctuation Analysis of Human Brain Electroencephalogram. *Physics Letters A*, 2004, Volume 329, Issue 1-2, p.130-135.