



CURRICULUM VITAE

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A Permanent Resident of the United States of America

(Prepared: 04/01/2019)

Specialties and Interests:

Bioinformatics, Biostatistics, Biomedical Big Data, Precision Medicine, Multiomics and Metagenomics Analysis

Education:

- 2013 Ph.D. University of Southern California, *in Bioinformatics and Comp. Biol.* (Advisor. **Fengzhu Sun**)
- 2012 M.S. University of Southern California, *in Statistics*
- 2008 M.S. University of Southern California, *in Computer Science*
- 2006 M.S. Fudan University, *in Theoretical Physics* (Advisor. **Bailin Hao**)
- 2003 B.S. Fudan University, *in Electronics Engineering*

Research Grants (Role: PI):

- 01/19 – 12/20 **Innovation for Cancer Informatics Fund.** Funded for developing a cancer microbiome datahub to characterize the determinants of cancer immune microenvironment (<http://www.the-ici-fund.org>).
- 01/19 – 12/19 ACS 132922-PF-18-184-01-TBG. **American Cancer Society Postdoc Fellowship.** Funded for developing single cell/molecule analysis to characterize determinants of immune-escaping tumors.

Professional Appointments (Primary):

- 08/18 – now *Instructor*, Department of Medicine, Stanford University
- 04/18 – 08/18 *Research Scientist*, Department of Medicine, Stanford University
- 04/13 – 03/18 *Postdoc Research Associate*, Department of Medicine, Stanford University (Adv. **Nancy Zhang & Hanlee Ji**)
- 08/06 – 05/13 *Graduate Research Assistant*, Department of Biology, University of Southern California

Teaching and Mentoring Experiences:

- 09/13 – 01/18 *Research Mentor of* S. Sakshuwong, A. Montgomery, R. Huang and 5 others, Stanford University
- 08/09 – 08/11 *Graduate Teaching Assistant*, Department of Biology, University of Southern California
- 09/04 – 06/05 *Graduate Teaching Assistant*, Department of Physics, Fudan University

Professional Appointments (Other):

- 08/13 – now *Visiting Scholar*, Department of Statistics, Wharton School, University of Pennsylvania
- 05/12 – 08/12 *Statistician*, School of Social Works, University of Southern California
- 10/05 – 02/06 *Research Intern*, Global Development Lab, IBM

Research Articles (selected):

1. D Ai, X Li, H Pan, J Chen, J Cram[#], **LC Xia**[#]. Explore mediated co-varying dynamics in microbial community using integrated local similarity and liquid association analysis. *BMC Genomics*, 20(S2):185, 2019 (**#corresponding**)
2. **LC Xia**, D Ai, H Lee, N Andor, C Li, NR Zhang, HP Ji. SVEngine: an efficient and versatile simulator of genome structural variations with features of cancer clonal evolution. *GigaScience*, 7, gij081, 2018
3. **LC Xia**, JM Bell, C Wood-Bouwens, JJ Chen, NR Zhang, HP Ji. Identification of large rearrangements in cancer genomes with barcode linked reads. *Nucleic Acids Research*, 46(4): e19, 2018
4. D Ai, R Huang, J Wen, C Li, J Zhu, **LC Xia**[#]. Integrated metagenomic data analysis demonstrates that a loss of diversity in oral microbiota is associated with Periodontitis. *BMC Genomics*, 18(S1):1041, 2017 (**#corresponding**)

5. **LC Xia**, S Sakshuwong, ES Hopmans, JM Bell, SM Grimes, DO Siegmund, HP Ji, NR Zhang. A genome-wide approach for detecting the full spectrum of insertion-deletion variants. *Nucleic Acids Research*, 44(15): e126, 2016
6. **LC Xia***, D Ai*, JA Cram, JA Fuhrman, F Sun. Efficient statistical significance approximation for local association analysis of high-throughput time series data. *Bioinformatics*, 29(2), 230-237, 2013 (***first**)
7. **LC Xia**, JA Cram, T Chen, JA Fuhrman, F Sun. Accurate genome relative abundance estimation based on shotgun metagenomic reads. *PLoS One*, 6(12): e27992, 2011

Research Articles (as a primary author):

1. D Ai#, H Pan, X Li, Y Gao, G Liu, **LC Xia#**. Identifying Gut Microbiota Associated with Colorectal Cancer Using a Zero-Inflated Lognormal Model. *Frontiers in Microbiology*, 10, 826, 2019 (**#corresponding**)
2. D Ai#, X Li, G Liu, X Liang, **LC Xia#**. Constructing the microbial association network from large-scale time series data using Granger causality. *Genes* 10(3), 216, 2019 (**#corresponding**)
3. D Ai#, H Pan, R Han, X Chen, **LC Xia#**. Using decision tree aggregation with random forest model to identify gut microbes associated with colorectal cancer. *Genes* 10(2), 112, 2019 (**#corresponding**)
4. D Ai#, H Pan, R Huang, **LC Xia#**. CoreProbe: a novel algorithm for estimating relative abundance based on metagenomic reads. *Genes*, 9(6), 313, 2018 (**#corresponding**)
5. **LC Xia**, D Ai, JA Cram, X Liang, JA Fuhrman, F Sun. Statistical significance approximation in local trend analysis of high-throughput time-series data using the theory of Markov chains. *BMC Bioinformatics*, 16:301, 2015
6. **LC Xia**, JA Steele, JA Cram, ZG Cardon, S. Simmons, JJ Vallino, JA Fuhrman, F Sun. Extended local similarity analysis of microbial community and other time series data with replicates. *BMC Systems Biology*, 5(S2): S15, 2011
7. **LC Xia***, Chan Zhou*. Phase transition in sequence unique reconstruction. *Journal of Systems Science and Complexity*, 20:18-29, 2007 (***first**)

Research Articles (as a co-author):

8. XL Zhang, ..., **LC Xia** (70 of 163), ..., LA Farrer. A rare missense variant of CASP7 is associated with familial late-onset Alzheimer's disease. *Alzheimer's & dementia: the journal of the Alzheimer's Association*, 15: 441, 2019
9. JM Bell, BT Lau, SU Greer, C Wood-Bouwens, **LC Xia**, ID Connolly, MH Gephart, HP Ji. Chromosome-scale mega-haplotypes enable digital karyotyping of cancer aneuploidy. *Nucleic Acids Research*, 45: e162, 2017
10. GW Shin, SM Grimes, H Lee, BT Lau, **LC Xia**, HP Ji. CRISPR-Cas9-targeted fragmentation and selective sequencing enable massively parallel microsatellite analysis. *Nature Communications*, 8: 14291, 2017
11. N Andor, T Graham, M Jansen, **LC Xia**, C Aktipis, C Petritsch, HP Ji, C Malay. Pan-cancer analysis of the extent and consequences of intra-tumor heterogeneity. *Nature Medicine*, 22:105-113, 2016
12. NR Zhang, B Yakir, **LC Xia**, D Siegmund. Scan statistics on Poisson random fields with applications in genomics. *Annals of Applied Statistics*, 10 (2), 726-755, 2016
13. S Weiss, WV Treuren, C Lozupone, K Faust, J Friedman, Y Deng, **LC Xia**, Z Xu, L Ursell, E Alm, A Birmingham, JA Cram, JA Fuhrman, J Raes, F Sun, J Zhou, R Knight. Correlation detection strategies in microbial datasets vary widely in sensitivity and precision. *The ISME Journal*, 9 (12), 2573-2586, 2016 (**ELSA: the best performer**)
14. A Cushing, A Kamali, M Winters, E Hopmans, J Bell, SM Grimes, **LC Xia**, NR Zhang, R Moss, M Holodniy, HP Ji. Emergence of hemagglutinin mutations during the course of Influenza infection. *Scientific Reports*, 5:16178, 2015
15. JA Cram, **LC Xia**, DM Needham, R Sachdeva, F Sun, JA Fuhrman. Cross-depth analysis of marine bacterial networks suggests downward propagation of temporal changes. *The ISME Journal*, 9 (12):2573-2586, 2015
16. Q Wang, M Li, **LC Xia**, G Wen. Genetic analysis of differentiation of T-helper lymphocytes. *Genetics and Molecular Research*, 12 (2), 972-987, 2013
17. Q Wang, M Li, H Zu, M Gao, **LC Xia**. A quantitative valuation of health care system in US, China, and Sweden. *Health Med*, 7 (4), 1064-1074, 2013
18. JA Steele, PD Countway, **LC Xia**, PD Vigil, JM Beman, DY Kim, CET Chow, R Sachdeva, AC Jones, MS Schwalbach, JM Rose, I Hewson, A Patel, F Sun, DA Caron, JA Fuhrman. Marine bacterial, archaeal and protistan association networks reveal ecological linkages. *The ISME Journal*, 5:1414-1425, 2011
19. S Zhang, Y Li, **LC Xia**, Q Pan. PPLook: an automated data mining tool for protein-protein interaction. *BMC Bioinformatics*, 11:326, 2010
20. P He, **LC Xia**: Oligonucleotide profiling for discriminating bacteria in bacterial communities. *Combinatorial Chemistry and High-throughput Screening*, 10(4):247-55, 2007

Research Articles (in submission):

21. **LC Xia**, K Day, HJ Lee, J Bell, S Grimes, M Kubit, M Miller, G Shin, C Wood-Bouwens, S Greer, H Escobar, D Haslem, PA Van Hummelen, HP Ji, LD. Nadauld. Loss of TP53 is a prognostic biomarker of poor survival in stage III colorectal cancer patients. (**in revision**)
22. D Ai#, M Wu, **LC Xia**#. Metabolic association network analysis identifies enzymatic components of gut microbiota that significantly differ between colorectal cancer patients and healthy people. (**in revision**)
23. X Liu, W Li, G Huang, T Huang, **LC Xia**#. SeqDistK: a novel tool for alignment-free phylogenetic analysis. (**in revision**)
24. G Huang, X Liu, T Huang, S Hu, **LC Xia**#. The statistical power of k-mer based aggregative statistics for alignment-free detection of horizontal gene transfer. (**under review**)
25. GW Shin, SU Greer, **LC Xia**, J Zhou, CT Boles, HP Ji. Structural variation and haplotypes from CRISPR-targeted sequencing of intact sub-Megabase DNA. (**under review**)

Invited Book Chapters:

1. F Sun, **LC Xia**. Extended local similarity analysis (ELSA) of biological data. in *Encyclopedia of metagenomics* 2014, ed: Karen E. Nelson. Springer. New York.
2. F Sun, **LC Xia**. Accurate genome relative abundance estimation based on shotgun metagenomic reads. in *Encyclopedia of metagenomics* 2014, ed: Karen E. Nelson. Springer. New York.

Dissertations and Thesis:

1. **LC Xia**. Developing statistical and algorithmic methods for shotgun metagenomics and time series analysis. Ph.D. dissertation, University of Southern California. (Committee: Profs. Fengzhu Sun of CompBio/Math, Jed Fuhrman of Bio, C.C. Jay Kuo of E.E.)
2. **LC Xia**. Efficient statistical significance approximation for local association analysis of high-throughput time series data. Master Thesis. University of Southern California. (Committee: Profs. Fengzhu Sun of CompBio/Math, Alan Schumitzky of Math, Jianfeng Zhang of Math)
3. **LC Xia**. Discovering taxon-specific oligomer repeats in microbial genomes. Master Thesis. Fudan University. (Committee: Profs. Bailin Hao of Physics, Haiping Fang of Physics, Baorong Lu of Bio, Wenju Zhang of Bio)

Honors and Awards:

- 2018 *Postdoc Fellow*, American Cancer Society
- 2018 *Scholar-in-Training Award*, American Association for Cancer Research
- 2017 *Finalist*, Pacific Biosciences 'Open Your Eyes to Isoform Diversity' Challenge
- 2016 *Travel Fellowship*, Alzheimer's Association International Conference
- 2015 *Reviewer's Choice Award*, American Society of Human Genetics Annual Meeting
- 2014 *Travel Award*, Bayer International Computational Biology Workshop
- 2011 – 2012 *Dissertation Year Fellowship*, University of Southern California
- 2006 – 2007 *Merit Fellowship*, University of Southern California
- 1999 – 2003 *People's Scholarship*, 3 times, Fudan University

Invited Lectures, Seminars and Presentations:

1. Minisymposium Speaker. **International Congress on Industrial and Applied Mathematics (ICIAM 2019)**, Valencia, Spain, July 2019
2. Explore mediated co-varying dynamics in microbial community using integrated local similarity and liquid association analysis. **Asian Pacific Bioinformatics Conference (APBC2019)**, Wuhan, China, Jan 2019
3. High performance discovery of complex genome-wide rearrangements with single molecule-based barcoded sequence reads. **American Society of Human Genetics Meeting (ASHG2016)**, Vancouver, Canada, Oct 2016
4. Integrated metagenomic data analysis demonstrates that a loss of diversity in oral microbiota is associated with Periodontitis. **27th International Conference on Genome Informatics (GIW2016)**, Shanghai, China, Oct 2016
5. Structural variation (SV) in heterogenous whole-genome sequencing data from 111 families at risk for Alzheimer disease: Alzheimer disease sequencing project SV study. **Alzheimer Association International Conference (AAIC2016)**, Toronto, Canada, Jul 2016

6. SWAN: a genome-wide structural variant analysis pipeline. **Bayer International Computational Biology Workshop**, 2014, Boston, USA, Sep 2014
7. High-throughput metagenomic data analysis with GRAMMy and ELSA. **J Craig Venter Institute**, San Diego, USA, Jun 2012
8. Extended local similarity analysis of microbial community and other time series data with replicates. **22nd International Conference on Genome Informatics (GIW2011)**, Pusan, Korea, Dec 2011

Scientific Program Committee:

Co-chair: computational methods for analyzing metagenomics data workshop within the IEEE Int'l Conference on Bioinformatics and Biomedicine (BIBM2015)

Journal Editorial Service:

Editorial Board: Computers in Biology and Medicine (2014-2015), Informatics in Medicine Unlocked (2015-2016)

Guest Editor: Evolutionary Bioinformatics (2014-2017)

Ad Hoc External Reviewer:

Conferences: Conference on Research in Computational Molecular Biology (RECOMB), Intelligent Machine in Molecular Biology Conference (ISMB), IEEE Int'l Conference on Bioinformatics and Biomedicine (BIBM), Asian Pacific Bioinformatics Conference (APBC)

Journals: Bioinformatics, Briefings in Bioinformatics, J of Medical Genetics, Database, Plos Medicine, Plos One, BMC Bioinformatics, BMC Research Notes, Microbial Informatics and Experimentation, Frontiers in Microbiology, Statistical Applications in Genetics and Molecular Biology, Peerj, Statistical Methods in Medical Research, Computers in Biology and Medicine, Evolutionary Bioinformatics

Research Grants (Role: non-PI)

07/17 – 06/20 NIH/NHGRI R01HG006137-07. Genomic and cellular variation from single molecules to single cells. Role: Key Person (Research Scientist)

07/14 – 06/17 NIH/NHGRI R01HG006137-04. Statistical models and analysis of complex genomic variation in clonal mixtures. Role: Key Person (Research Associate)

07/11 – 06/14 NIH/NHGRI R01HG006137-01. Statistical models for genome sequencing and association. Role: Research Associate

08/11 – 01/16 NSF OCE-1136818. Dimensions: Pattern and process in marine bacterial, archaeal, and protistan biodiversity, and effects of human impacts. Role: Research Assistant

09/07 – 08/13 NSF MCB-0703159. MO: assembly of marine microbial communities. Role: Research Assistant

Conference Abstracts and Posters:

1. **LC Xia**, D Ai, M Guo, HP Ji. iGRAMMy: Cloud-based characterization of microbial landscape in colorectal cancers. American Association for Cancer Research Meeting (AACR2019), Chicago, USA, Apr 2019
2. D Ai, X Li, H Pan, J Chen, J Cram, **LC Xia**. Explore mediated co-varying dynamics in microbial community using integrated local similarity and liquid association analysis. Asian Pacific Bioinformatics Conference (APBC2019), Wuhan, China, Jan 2019
3. PA Van Hummelen, **LC Xia**, K Day, H Lee, J Bell, S Grimes, M Kubit, M Miller, G Shin, C Wood-Bouwens, S Greer, H Escobar, D Haslem, HP Ji, LD Nadauld. Loss of TP53 is a prognostic biomarker of poor survival in stage III colorectal cancer patients. American Society of Clinical Oncology Meeting (ASCO2018), Chicago, USA, June 2018
4. **LC Xia**, J Bell, C Wood-Bouwens, DA King, A Renschler, GW Shin, S Greer, ID Connolly, MH Gephart, HP Ji. Linked read whole genome sequencing reveals pervasive chromosomal level instability and novel rearrangements in brain metastases from colorectal cancer. American Association for Cancer Research Meeting (AACR2018), Chicago, USA, Apr 2018
5. H Lee*, **LC Xia***, S Greer, JM Bell, S Grimes, M Kubit, C Wood-Bouwens, G Shin, L Johnson, N Andor, K Day, M Miller, H Escobar, L Nadauld, H Ji, PA Van Hummelen. High-quality CNV segments from low-coverage whole

genome sequencing from FFPE cancer biopsies based on an evaluation of multiple CNV tools. American Association for Cancer Research Meeting (AACR2018), Chicago, USA, Apr 2018 (***co-first**)

6. **LC Xia**, Linked-read, whole genome sequencing reveals pervasive chromosomal-level instability and novel rearrangements in brain metastases from colorectal cancer. Biomedical Computation at Stanford Symposium, Stanford, USA, Apr 2018
7. **LC Xia**, D Ai, R Huang, J Wen, C Li, J Zhu. Integrated metagenomic data analysis demonstrates that a loss of diversity in oral microbiota is associated with Periodontitis. International Conference on Genome Informatics (GIW2016), Shanghai, China, Oct 2016 (**selected for oral presentation**)
8. **LC Xia**, C Wood, B Lau, NR Zhang, HP Ji. High performance discovery of complex genome-wide rearrangements with single molecule-based barcoded sequence reads. American Society of Human Genetics Meeting (ASHG2016), Vancouver, Canada, Oct 2016 (**selected for oral presentation**)
9. **LC Xia**, Structural variation (SV) in heterogenous whole-genome sequencing data from 111 families at risk for Alzheimer disease: Alzheimer disease sequencing project SV study. Alzheimer Association International Conference (AAIC2016), Toronto, Canada, July 2016 (**selected for oral presentation**)
10. N Andor, TA Graham, M Jansen, **LC Xia**, A Aktipis, C Petritsch, HP Ji, CC Maley. Pan-cancer analysis of clonal evolution reveals the costs and adaptive benefits of genomic instability. American Association for Cancer Research Meeting (AACR2016), New Orleans, USA, Apr 2016
11. **LC Xia**, D Ai, R Huang, J Wen, C Li, J Zhu. Integrated metagenomic data analysis demonstrates that a loss of diversity in oral microbiota is associated with Periodontitis. Stanford Microbiome Symposium, Stanford, USA, May 2016
12. **LC Xia**, D Ai, R Huang, J Wen, C Li, J Zhu. Integrated metagenomic data analysis demonstrates that a loss of diversity in oral microbiota is associated with Periodontitis. Big Data in Biomedicine Conference, Stanford, USA, May 2016
13. **LC Xia**, HP Ji, NR Zhang. A multiple feature approach for robust and accurate structural variation discovery for whole genome sequencing data of varied designs. American Society of Human Genetics Meeting (ASHG2015), Baltimore, USA, Oct 2015. (**reviewer's choice award**)
14. **LC Xia**, J Bell, J Chen, NR Zhang, HP Ji. A new multiple feature approach for rapid and highly accurate somatic structural variation discovery from whole cancer genome sequencing. American Association for Cancer Research Meeting (AACR2015), Philadelphia, USA, Apr 2015.
15. **LC Xia**, JA Fuhrman, F Sun. Extended local similarity analysis of microbial community and other time series data with replicates. 22nd International Conference on Genome Informatics (GIW2011), Pusan, Korea, Dec 2011 (**selected for oral presentation**)
16. **LC Xia**, JA Fuhrman, F Sun. The GRAMMy analysis of metagenomic data sets. International Conference on Genome Informatics (GIW2011), Pusan, Korea, 2011
17. **LC Xia**, JA Fuhrman, F Sun. LSA: A web service for local similarity analysis of time sequence data. International Conference of Intelligent Systems for Molecular Biology (ISMB2010), Boston, USA, July 2010
18. **LC Xia**, JA Fuhrman, F Sun. Inferring pair and triplet interactions from time series ecological data. International Conference of Research in Computational Molecular Biology (RECOMB2009), Tuson, USA, May 2009