




Li Xia

Instructor, Medicine - Oncology

 NIH Biosketch available Online

 Curriculum Vitae available Online

Bio

BIO

Dr. Xia is a hybrid computer scientist, statistician and bioinformatician who takes a general interest in genome sciences and medicine. His career goal is to advance the field of precision health, in particular precision cancer medicine, by integrating novel technology, big-data, and intelligent models. Dr. Xia worked extensively on microbiome and human multiomics data modeling and analysis. His publications addressed many methodological needs in commensal bacteria, structural variation, and cancer genomics analysis. He and his works were recognized by the career awards he received from the American Cancer Society and the Innovation in Cancer Informatics Fund. Find out more about his research at <https://profiles.stanford.edu/lixia>.

ACADEMIC APPOINTMENTS

- Instructor, Medicine - Oncology

HONORS AND AWARDS

- Postdoc Fellowship, American Cancer Society (2019)
- Scholar-In-Training Award, American Association for Cancer Research (2018)
- Travel Fellowship, Alzheimer's Association International Conference (2016)
- Reviewer's Choice Best Abstract, The American Society of Human Genetics Annual Meeting (2015)
- Travel Fellowship, Bayer International Computational Biology Workshop (2014)
- Dissertation Year Fellowship, University of Southern California (2012)
- Merit Fellowship, University of Southern California (2006-2007)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Program Committee Co-chair, COMMAND workshop of the IEEE Bioinformatics and Biomedicine Conference 2015 (2015 - 2015)

PROFESSIONAL EDUCATION

- Doctor of Philosophy, University of Southern California, Los Angeles, US , Bioinformatics and Computational Biology (2013)
- Master of Science, University of Southern California, Los Angeles, US , Statistics (2012)
- Master of Science, University of Southern California, Los Angeles, US , Computer Science (2008)
- Master of Science, Fudan University, Shanghai, China , Physics (Theoretical Physics) (2006)
- Bachelor of Science, Fudan University, Shanghai, China , Electronics Engineering (2003)

Publications

PUBLICATIONS

- **Explore mediated co-varying dynamics in microbial community using integrated local similarity and liquid association analysis.** *BMC genomics*
Ai, D., Li, X., Pan, H., Chen, J., Cram, J. A., Xia, L. C.
2019; 20 (Suppl 2): 185
- **Identifying Gut Microbiota Associated With Colorectal Cancer Using a Zero-Inflated Lognormal Model.** *Frontiers in microbiology*
Ai, D., Pan, H., Li, X., Gao, Y., Liu, G., Xia, L. C.
2019; 10: 826
- **SVEngine: an efficient and versatile simulator of genome structural variations with features of cancer clonal evolution.** *GigaScience*
Xia, L. C., Ai, D., Lee, H., Andor, N., Li, C., Zhang, N. R., Ji, H. P.
2018
- **Identification of large rearrangements in cancer genomes with barcode linked reads.** *Nucleic acids research*
Xia, L. C., Bell, J. M., Wood-Bouwens, C., Chen, J. J., Zhang, N. R., Ji, H. P.
2018; 46 (4): e19
- **Integrated metagenomic data analysis demonstrates that a loss of diversity in oral microbiota is associated with periodontitis.** *BMC genomics*
Ai, D., Huang, R., Wen, J., Li, C., Zhu, J., Xia, L. C.
2017; 18: 1041-?
- **A genome-wide approach for detecting novel insertion-deletion variants of mid-range size.** *Nucleic acids research*
Xia, L. C., Sakshuwong, S., Hopmans, E. S., Bell, J. M., Grimes, S. M., Siegmund, D. O., Ji, H. P., Zhang, N. R.
2016; 44 (15)
- **Statistical significance approximation in local trend analysis of high-throughput time-series data using the theory of Markov chains** *BMC BIOINFORMATICS*
Xia, L. C., Ai, D., Cram, J. A., Liang, X., Fuhrman, J. A., Sun, F.
2015; 16
- **Efficient statistical significance approximation for local similarity analysis of high-throughput time series data** *BIOINFORMATICS*
Xia, L. C., Ai, D., Cram, J., Fuhrman, J. A., Sun, F.
2013; 29 (2): 230-237
- **Extended local similarity analysis (eLSA) of microbial community and other time series data with replicates** *BMC SYSTEMS BIOLOGY*
Xia, L. C., Steele, J. A., Cram, J. A., Cardon, Z. G., Simmons, S. L., Vallino, J. J., Fuhrman, J. A., Sun, F.
2011; 5
- **Accurate Genome Relative Abundance Estimation Based on Shotgun Metagenomic Reads** *PLOS ONE*
Xia, L. C., Cram, J. A., Chen, T., Fuhrman, J. A., Sun, F.
2011; 6 (12)
- **Analysis of Whole-Exome Sequencing Data for Alzheimer Disease Stratified by APOE Genotype** *JAMA NEUROLOGY*
Ma, Y., Jun, G. R., Zhang, X., Chung, J., No, A. C., Chen, Y., Bellenguez, C., Hamilton-Nelson, K., Martin, E. R., Kunkle, B. W., Bis, J. C., DeStefano, S.,
DeStefano, et al
2019; 76 (9): 1099–1108
- **The statistical power of k-mer based aggregative statistics for alignment-free detection of horizontal gene transfer.** *Synthetic and systems biotechnology*
Huang, G., Liu, X., Huang, T., Xia, L.
2019; 4 (3): 150–56
- **Association network analysis identifies enzymatic components of gut microbiota that significantly differ between colorectal cancer patients and healthy controls** *PEERJ*
Ai, D., Pan, H., Li, X., Wu, M., Xia, L. C.
2019; 7
- **Identifying Gut Microbiota Associated With Colorectal Cancer Using a Zero-Inflated Lognormal Model** *FRONTIERS IN MICROBIOLOGY*

- Ai, D., Pan, H., Li, X., Gao, Y., Liu, G., Xia, L. C.
2019; 10
- **Constructing the Microbial Association Network from Large-Scale Time Series Data Using Granger Causality** *GENES*
Ai, D., Li, X., Liu, G., Liang, X., Xia, L. C.
2019; 10 (3)
 - **Constructing the Microbial Association Network from Large-Scale Time Series Data Using Granger Causality.** *Genes*
Ai, D., Li, X., Liu, G., Liang, X., Xia, L. C.
2019; 10 (3)
 - **Association of Rare Coding Mutations With Alzheimer Disease and Other Dementias Among Adults of European Ancestry** *JAMA NETWORK OPEN*
Patel, D., Mez, J., Vardarajan, B. N., Staley, L., Chung, J., Zhang, X., Farrell, J. J., Rynkiewicz, M. J., Cannon-Albright, L. A., Teerlink, C. C., Stevens, J., Corcoran, C., Murcia, et al
2019; 2 (3): e191350
 - **Using Decision Tree Aggregation with Random Forest Model to Identify Gut Microbes Associated with Colorectal Cancer.** *Genes*
Ai, D., Pan, H., Han, R., Li, X., Liu, G., Xia, L. C.
2019; 10 (2)
 - **Targeted short read sequencing and assembly of re-arrangements and candidate gene loci provide megabase diplotypes.** *Nucleic acids research*
Shin, G., Greer, S. U., Xia, L. C., Lee, H., Zhou, J., Boles, T. C., Ji, H. P.
2019
 - **Association network analysis identifies enzymatic components of gut microbiota that significantly differ between colorectal cancer patients and healthy controls.** *PeerJ*
Ai, D., Pan, H., Li, X., Wu, M., Xia, L. C.
2019; 7: e7315
 - **High-quality CNV segments from low-coverage whole genome sequencing from FFPE cancer biopsies based on an evaluation of multiple CNV tools**
Lee, H., Xia, L., Greer, S., Bell, J., Grimes, S. M., Bouwens, C., Shin, G., Lau, B. C., Johnson, L., Andor, N., Day, K., Miller, M., Escobar, et al
AMER ASSOC CANCER RESEARCH.2018
 - **Linked read whole genome sequencing reveals pervasive chromosomal level instability and novel rearrangements in brain metastases from colorectal cancer**
Xia, L. C., Bell, J. M., Wood-Bouwens, C., King, D. A., Shin, G., Greer, S., Connolly, I. D., Gephart, M. H., Ji, H. P.
AMER ASSOC CANCER RESEARCH.2018
 - **CoreProbe: A Novel Algorithm for Estimating Relative Abundance Based on Metagenomic Reads.** *Genes*
Ai, D., Pan, H., Huang, R., Xia, L. C.
2018; 9 (6)
 - **Chromosome-scale mega-haplotypes enable digital karyotyping of cancer aneuploidy** *NUCLEIC ACIDS RESEARCH*
Bell, J. M., Lau, B. T., Greer, S. U., Wood-Bouwens, C., Xia, L. C., Connolly, I. D., Gephart, M. H., Ji, H. P.
2017; 45 (19): e162
 - **CRISPR-Cas9-targeted fragmentation and selective sequencing enable massively parallel microsatellite analysis** *NATURE COMMUNICATIONS*
Shin, G., Grimes, S. M., Lee, H., Lau, B. T., Xia, L. C., Ji, H. P.
2017; 8
 - **Correlation detection strategies in microbial data sets vary widely in sensitivity and precision** *ISME JOURNAL*
Weiss, S., Van Treuren, W., Lozupone, C., Faust, K., Friedman, J., Deng, Y., Xia, L. C., Xu, Z. Z., Ursell, L., Alm, E. J., Birmingham, A., Cram, J. A., Fuhrman, et al
2016; 10 (7): 1669-1681
 - **SCAN STATISTICS ON POISSON RANDOM FIELDS WITH APPLICATIONS IN GENOMICS** *ANNALS OF APPLIED STATISTICS*
Zhang, N. R., Yakir, B., Xia, L. C., Siegmund, D.
2016; 10 (2): 726-755
 - **Pan-cancer analysis of the extent and consequences of intratumor heterogeneity** *NATURE MEDICINE*
Andor, N., Graham, T. A., Jansen, M., Xia, L. C., Aktipis, C. A., Petritsch, C., Ji, H. P., Maley, C. C.

2016; 22 (1): 105-?

- **Pan-cancer analysis of the extent and consequences of intratumor heterogeneity.** *Nature medicine*
Andor, N., Graham, T. A., Jansen, M., Xia, L. C., Aktipis, C. A., Petritsch, C., Ji, H. P., Maley, C. C.
2016; 22 (1): 105-113
- **Cross-depth analysis of marine bacterial networks suggests downward propagation of temporal changes** *ISME JOURNAL*
Cram, J. A., Xia, L. C., Needham, D. M., Sachdeva, R., Sun, F., Fuhrman, J. A.
2015; 9 (12): 2573-2586
- **A new multiple feature approach for rapid and highly accurate somatic structural variation discovery from whole cancer genome sequencing**
Xia, L. C., Bell, J., Chen, J., Zhang, N. R., Ji, H. P.
AMER ASSOC CANCER RESEARCH.2015
- **Emergence of Hemagglutinin Mutations During the Course of Influenza Infection.** *Scientific reports*
Cushing, A., Kamali, A., Winters, M., Hopmans, E. S., Bell, J. M., Grimes, S. M., Xia, L. C., Zhang, N. R., Moss, R. B., Holodniy, M., Ji, H. P.
2015; 5: 16178-?
- **Extended Local Similarity Analysis (eLSA) of Biological Data** *Encyclopedia of Metagenomics: Genes, Genomes and Metagenomes. Basics, Methods, Databases and Tools*
Sun, F., Xia, L.
edited by Nelson, K.
Springer.2014
- **Accurate Genome Relative Abundance Estimation Based on Shotgun Metagenomic Reads** *Encyclopedia of Metagenomics: Genes, Genomes and Metagenomes. Basics, Methods, Databases and Tools*
Sun, F., Xia, L. C.
edited by Nelson, K.
Springer.2014
- **A Quantitative Evaluation of Health Care System in US, China, and Sweden** *Health Med*
Wang, Q., Li, M., Zu, H., Gao, M., Cao, C., Xia, L. C.
2013; 7 (4)
- **Genetic analysis of differentiation of T-helper lymphocytes** *GENETICS AND MOLECULAR RESEARCH*
Wang, Q., Li, M., Xia, L. C., Wen, G., Zu, H., Gao, M.
2013; 12 (2): 972-987
- **Marine bacterial, archaeal and protistan association networks reveal ecological linkages** *ISME JOURNAL*
Steele, J. A., Countway, P. D., Xia, L., Vigil, P. D., Beman, J. M., Kim, D. Y., Chow, C. T., Sachdeva, R., Jones, A. C., Schwalbach, M. S., Rose, J. M., Hewson, I., Patel, et al
2011; 5 (9): 1414-1425
- **PPLook: an automated data mining tool for protein-protein interaction** *BMC BIOINFORMATICS*
Zhang, S., Li, Y., Xia, L., Pan, Q.
2010; 11
- **Oligonucleotide profiling for discriminating bacteria in bacterial communities** *COMBINATORIAL CHEMISTRY & HIGH THROUGHPUT SCREENING*
He, P., Xia, L.
2007; 10 (4): 247-255
- **Phase transition in sequence unique reconstruction** *JOURNAL OF SYSTEMS SCIENCE & COMPLEXITY*
Xia, L., Zhou, C.
2007; 20 (1): 18-29