JING LU

COMPUTATIONAL BIOLOGIST, POSTDOC

Leibniz Institute on Aging – Fritz Lipmann Institute (FLI), Jena, Germany

[+49(0)1625429432] [jing.lu@leibniz-fli.de] [GoogleScholar] [GitHub] [PersonalPress]

Profile_____

Accomplished computational biologist and bioinformatician with experience in data analysis, machine learning, and the development of bioinformatic pipelines. Currently a postdoctoral researcher at the Leibniz Institute on Aging – Fritz Lipmann Institute, with a strong background in multi-omics, data integration, and visualization. Proven track record of contributing to high-impact research projects, publishing in reputable scientific journals, and innovating bioinformatics solutions for clinical and research applications. Proficient in Python, R, and Linux environment management, with a keen interest in advancing the understanding of cellular senescence and aging. Seeking opportunities to leverage my expertise in computational biology to drive scientific discovery and innovation.

Education_____

Leibniz Institute on Aging – Fritz Lipmann Institute (FLI)   *Jena, Germany*

Postdoc in Machine learning and AI   *2023-Present*

University of Jena   *Jena, Germany*

Ph.D. in Bioinformatics   *2019-2022*

University of Chinese Academy of Sciences   *Beijing & Shenzhen, China*

M.Sc. in Genetics   *2012-2015*

GPA: 3.52/4.00 (4.00 is the best possible)

Experience_____

Leibniz Institute on Aging – Fritz Lipmann Institute (FLI)   *Jena, Germany*

Senior bioinformatician & Computational biologist   *2023-Present*

- Manage datasets and computational pipeline framework within the group
- Bioinformatic atlas research on cellular senescence
- Computational inference on causal gene network
- Interaction research on microbiome community

Leibniz Institute on Aging – Fritz Lipmann Institute (FLI)   *Jena, Germany*

Graduate researcher   *2019-2022*

- Characterise the aging change of stem cells in the mouse intestine both in vivo crypts and in vitro organoids in transcriptome level
- Multi-omics bioinformatic analysis for the lab including DNAseq, RNAseq, scRNAseq, ChIPseq, Metagenomics and 16s.
- Investigation of functional modules' conservation during embryo development process in mouse and human

- Developed a new gene panel for colon cancer diagnosis

3DMed Company   *Shanghai, China*

Junior researcher   *2015-2018*

- Developing, improving and validating bioinformatic pipelines for the business from Laboratory Developed Tests (LDT) and In Vitro Diagnostics (IVD), developed a software module to increase the detection accuracy by supplementing the main pipeline
- Innovating molecular biomarkers for medical use, offering scientific services to external partners, and collaborating on the registration work of new medical product
- Developed a bioinformatic software to detect and design neo-antigen vaccines in individual patients as part of the precision medicine

BGI   *Shenzhen, China*

Software engineer   *2013-2015*

- Developed a bioinformatic genotyping pipeline for the high-throughput multi-markers' amplicon sequencing platform in a low-cost way
- Developed a software tool set for individual identification and paternity testing in the forensic field
- Developed the bioinformatic software for the first version of genetic ID card of Chinese citizen

Skills_____

Programming and Software Development

  - Python: software and pipeline development, machine learning driven development

  - R: mathematical and statistical analysis, data visualization, and pipeline development

  - bash: pipeline framework and data management

  - ShinyApp: interactive application development

Data Analysis and Management

  - Reproducibility: Docker, Conda, renv

  - workflows: Snakemake, Nextflow

High-Performance Computing (HPC)

  - HPC environments: SGE (Sun Grid Engine)

  - Version control: Git

Interests_____

Platforming biology (big data and frame work), Causal statistics (MR, LCV), Network modules, Interaction system, Non-negative matrix factorization, Different aging clocks, Embryo development process, Cellular senescence, Technology application, Nanopore sequencing, Quantum computation, Artificial intelligence, Explainable machine learning, Drug repurposing

Languages_____

English and Chinese

Awards & Grants

Publications

1. **J. Lu**, F. Annunziata, D. Sirvinskas, O. Omrani, H. Li, S. M. M. Rasa, A. Krepelova, L. Adam, F. Neri, Establishment and evaluation of module-based immune-associated gene signature to predict overall survival in patients of colon adenocarcinoma. J Biomed Sci. 29 (2022), doi:10.1186/S12929-022-00867-2.

2. **J. Lu**, A. Krepelova, S. M. M. Rasa, F. Annunziata, O. Husak, L. Adam, S. Nunna, F. Neri, Characterization of an in vitro 3D intestinal organoid model by using massive RNAseq-based transcriptome profiling. Scientific Reports 2021 11:1. 11, 1–14 (2021).

3. Omrani, O., Krepelova, A., Rasa, S. M. M., Sirvinskas, D., **Lu, J.**, Annunziata, F., Garside, G., Bajwa, S., Reinhardt, S., Adam, L., Käppel, S., Ducano, N., Donna, D., Ori, A., Oliviero, S., Rudolph, K. L., & Neri, F. (2023). IFNγ-Stat1 axis drives aging-associated loss of intestinal tissue homeostasis and regeneration. *Nature Communications*, *14*(1), 6109. https://doi.org/10.1038/s41467-023-41683-y

4. D. Širvinskas, O. Omrani, **J. Lu**, M. Rasa, A. Krepelova, L. Adam, S. Kaeppel, F. Sommer, F. Neri, Single-cell atlas of the aging mouse colon. iScience. 25, 104202 (2022).

5. T. Schomann, K. Mirzakhani, J. Kallenbach, **J. Lu**, S. M. M. Rasa, F. Neri, A. Baniahmad, Androgen-Induced MIG6 Regulates Phosphorylation of Retinoblastoma Protein and AKT to Counteract Non-Genomic AR Signaling in Prostate Cancer Cells. Biomolecules. 12 (2022), doi:10.3390/BIOM12081048.

6. Z. Wang, J. Duan, S. Cai, M. Han, H. Dong, J. Zhao, B. Zhu, S. Wang, M. Zhuo, J. Sun, Q. Wang, H. Bai, J. Han, Y. Tian, **J. Lu**, T. Xu, X. Zhao, G. Wang, X. Cao, F. Li, D. Wang, Y. Chen, Y. Bai, J. Zhao, Z. Zhao, Y. Zhang, L. Xiong, J. He, S. Gao, J. Wang, Assessment of Blood Tumor Mutational Burden as a Potential Biomarker for Immunotherapy in Patients With Non-Small Cell Lung Cancer With Use of a Next-Generation Sequencing Cancer Gene Panel. JAMA Oncol. 5, 696–702 (2019).

7. D. Su, D. Zhang, K. Chen, **J. Lu**, J. Wu, X. Cao, L. Ying, Q. Jin, Y. Ye, Z. Xie, L. Xiong, W. Mao, F. Li, High performance of targeted next generation sequencing on variance detection in clinical tumor specimens in comparison with current conventional methods. J Exp Clin Cancer Res. 36 (2017), doi:10.1186/S13046-017-0591-4.

8. W. Zhuang, J. Ma, X. Chen, G. Wang, **J. Lu**, Y. Chen, H. Dong, S. Cai, Y. Zhang, X. Zhao, Y. Zhu, C. Xu, Y. Huang, Z. Huang, X. Zhu, H. Jiang, Z. Wang, The Tumor Mutational Burden of Chinese Advanced Cancer Patients Estimated by a 381-cancer-gene Panel. J Cancer. 9, 2302–2307 (2018).

9. K. Zhang, S. Fei, **J. Lu**, Q. Yang, J. Yang, Y. Zeng, Y. Liu, G. Xiong, X. Jiao, Y. Tao, Z. Yuan, G. Wei, Z. Wei, D. Liu, T. Xu, S. Cai, F. Li, R. Cao, L. Liu, Analysis of Tumour Mutation Burden (TMB) in Chinese Lung Adenocarcinoma: Implications for Clinical Practice. SSRN Electronic Journal(2020), doi:10.2139/SSRN.3207876.

10. **J. Lu**, J. Lu, X. F. Li, H. Jiang, Complete mitochondrial genome of the Saker falcon, Falco cherrug (Falco, Falconidae). Mitochondrial DNA A DNA Mapp Seq Anal. 27, 3226–3227 (2016).

11. X. Li, J. Lu, **J. Lu**, X. Hu, Z. Huang, The complete mitochondrial genome of the American crow, Corvus brachyrhynchos (Passeriformes, Corvidae). Mitochondrial DNA A DNA Mapp Seq Anal. 27, 4213–4214 (2016).

Patents_____

No.	Patent Title	Type	Accepted date	Patent ID	Author List
1	用于鉴定多个生物样本之间身份关系的方法和系统 A new methods and System used for identifying multiple biological samples	PCT	Oct.2014	P2014-1-0204.WO-PIDC14754	**Jing Lu**, Haojun Jiang, Xiongbin Kang, Fang Chen, Ping Liu, Hui Jiang
2	个体单核苷酸多态性位点分型方法及装置 A new Method and Installation used for SNP genotype	PCT	Oct.2014	P2014-1-0195.WO-14P20730	**Jing Lu**, Haojun Jiang, Xiongbin Kang, Ping Liu, Fang Chen, Hui Jiang
3	一种单体型分型测序文库的构建方法、分型方法和试剂 A new library-construction method used for haplotype typing	PCT	Nov.2014	P2014-1-0297.WO	**Jing Lu**, Sheng Li, Haojun Jiang, Xiongbin Kang, Fang Chen, Hui Jiang
4	一种基于STR分型技术在无创产前亲子鉴定中应用的检测方法和系统 A new method used for noninvasive paternity test based on STR genotyping	PCT	Sep.2014	CN2014/087987	Haojun Jiang, **Jing Lu**, Fang Chen, Hui Jiang, Xiongbin Kang, Ping Liu
5	一种胎儿DNA浓度的检测方法 A new method used for fetal DNA concentration detection	PCT	Aug.2014	P2014-1-0145.WO	Xiongbin Kang, **Jing Lu**, Fang Chen, Ping Liu, Huixin Xu, Haojun Jiang

Posters_____

Title	Published
Unveiling Lifespan Regulators: From Knock-Out Phenotype Correlation to Large-Scale Gene Network Inference	2024 FLI Retreat
Deconvolution of senescent cells from bulk RNAseq	2023 GRC
Deconvolution of senescent cells from bulk RNAseq	2023 DGfA
Batch effects from different single-cell RNA-seq studies are not negligible	2019 FLI Retreat
A theoretical model and clinical validation of blood tumor mutation burden (bTMB) detection for cancer	2018 ASCO
The comparison of tumor mutational burden in patients with early and late stage lung adenocarcinoma in China	2018 ASCO
TMB analysis for 1812 samples of Chinese malignant solid tumor	2017 CSCO

Presentations

Title	Published
Machine learning-based classification of senescent cells using SPiDER-Sorted scRNAseq data	2024 FLI Retreat
Unveiling senescence: a comprehensive approach from single-cell RNAseq to senescence atlas compendium	2024 FLI WIP
Establishment and evaluation of module-based immune-associated gene signature to predict overall survival in patients of colon adenocarcinoma	2022 FLI WIP
Exploration of aging feature profiles in vivo and their validation with a good in-vitro model	2019 FLI WIP

Cooperations

Project	Cooperators
Senescence atlas research	Dr. Katarzyna Winek, Dr. Julia von Maltzahn, Prof. Claudia Waskow, Prof. Christoph Englert, Prof. Helen Morrison, Dr. Adrian Press
ChIPseq analysis on AKT-AR pathways	Prof. Baniahmad Aria, Julia Kallenbach, Elmira Keramatfar
The impact of gut microbiome on PiZ disease	Dr. Francesco Annunziata, Prof. Nunzia Pastore
The comparison of Facal microbiome between VitA-deficient diet in mouse	Prof. K. Lenhard Rudolph, Dr. Friedrich Becker
Regeneration-relevant transcriptome change after intestine damage	Dr. Alessandro Ori, Alberto Minetti
Single cell analysis on the intestine aging	Dr. Omid Omrani, Dr. Dovydas Syrvinskas
Organoids characterisation	Dr. Anna Krepelova