

BIOGRAPHICAL SKETCH

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NAME: Jun Jiang

eRA COMMONS USER NAME (credential, e.g., agency login): JJiang124

POSITION TITLE: Research Associate

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE	Completion Date	FIELD OF STUDY
Southern Medical University Guangzhou, China	B.S.	06/2009	Electronic Informatics
Southern Medical University Guangzhou, China	PH.D.	06/2014	Biomedical Engineering
Mayo Clinic Rochester, MN. USA	postdoctoral	-	Computational histopathology

A. Personal Statement

My research focuses on developing novel methods and creative tools for biomedical image analytics, especially for histopathology in recent years. I started to work in this field when I was a Ph.D. candidate. At the early stage of my research, most of my work was related to image-guided radiotherapy using multimodality of radiology images. With hands-on experience on AI modeling and feature engineering, I developed serials of image registration and segmentation models to enable automatic tumor boundary contouring for efficient and reproducible therapy. My studies are significant to assist radiologists to achieve accurate cancer diagnosis and customized treatment.

After joining Mayo Clinic in March 2018, my research field has been extended to computational histopathology as more detailed information about cancer development and molecular profiles can be identified within histopathology images. By generalizing my previous work to whole slide images (WSIs) scanned from different tissue types and staining protocols, I have developed many tools for histopathology analysis, including but not limited to WSI registration, cell annotation and detection, tissue segmentation and classification, and staining color normalization. With increasing domain knowledge in cancer biology, I have been collaborating with creative colleagues in Mayo Clinic to devise and leverage deep learning models for characterizing complex tumor-immune microenvironment in histopathology images. Specifically, I have established effective pipelines to quantify cellular composition and regional texture information within H&E slide to differentiate ovarian cancer subtypes and evaluate extent of tumor stroma reactions. I found some immune phenotypes measuring tumor stroma reaction is strongly associated with inferior patient outcomes and positively related to cancer signaling aberrations associated pathways. Moreover, I have been working on combining multimodal histopathology images by establishing the spatial correlation between cells from different modalities. The enriched cell profiles can be integrated with other data types (such as protein, transcript, and medical records) to enable AI enhanced co-learning for optimized model prediction.

Overall, I have been contributing my efforts to advance the histopathology image characterization using computational and data-driven approaches. By establishing correlations between cancer profiles and imaging phenotypes, my research can push the boundaries of understanding to inner mechanism of cancer and consequently lead to optimal patient treatments.

On-going Research Projects

Eric & Wendy Schmidt Fund for AI Research & Innovation, Mayo Clinic

Wang (PI) Role: co-Investigator 01/31/2023 – 01/30/2025

Development of AI-Empowered Spatial Multiomics Integrations to Discover Tumor Microenvironment Culprits for Ovarian Cancer Treatment Resistance

Ovarian SPORE pilot project

Wang (PI)

Role: co-Investigator

Ovarian SPORE, Mayo Clinic

2022 - 2023

Spatial Discoveries of Tumor-Immune Microenvironment Characteristics Determining Platinum Resistance in High-Grade Serous Ovarian Cancer

B. Positions, Scientific Appointments, and Honors

Positions and Employment

2014 - 2015 System Research Scientist, Mindray Bio-Medical Electronics. Shenzhen, China

2015 - 2017 Research Assistant, Southern Medical University, Guangzhou, China

2018 - 2022 Research Fellow, Mayo Clinic, Rochester, MN. USA

2023 - present Research Associate, Mayo Clinic, Rochester, MN. USA

Honors

2019 - present Mayo Clinic Ventures Inventor

2019 - present Member of Association for Pathology Informatics

2013 - 2014 Scholarship, Outstanding Doctoral Student

C. Contribution to Science

1. Developing deep learning models and digital pathology infrastructure for health research

My contribution to computational histopathology for cancer research can be summarized into two aspects: 1) Developing scalable and generalizable deep learning models for the objective assessment of pathological feature within whole slide images. Trained from annotations from pathologists, the developed models can be applied to large research cohort to enable novel findings by associating image patterns with cancer biological characteristics. 2) Constructing analytic infrastructures to facilitate the computational analysis of histopathology images. This includes the development of pipelines for quantifying tumor stroma reaction, cell/tissue annotation and feature extraction, whole slide image normalization, registration and quality checking, as well as image file management and conversion. These studies not only provide insightful references for other research scientists, but also lay a solid foundation for my further research endeavors.

- a. **Jiang, Jun**, Raymond Moore, Brenna Novotny, Leo Liu, Zachary Fogarty, Ray Guo, Markovic Svetomir, and Chen Wang. "Towards H&E Referenced Multiplex Immunofluorescence Interpretation: Spatial Co-localization, Cell Feature Validation, and Virtual H&E Generation." *Nature Communication*. *Under review* (2024).
- b. **Jiang, Jun**, Raymond Moore, Brenna Novotny, Leo Liu, Zachary Fogarty, Ray Guo, Markovic Svetomir, and Chen Wang. "Multimodal Alignment of Histopathological Images

Using Cell Segmentation and Point Set Matching for Integrative Cancer Analysis." *arXiv preprint arXiv:2410.00152* (2024).

- c. **Jiang Jun**, Tekin Burak, Yuan Lin, Armasu Sebastian, Winham Stacey J., Goode Ellen L., Liu Hongfang, Huang Yajue, Guo Ruifeng, Wang Chen. "Computational tumor stroma reaction evaluation led to novel prognosis-associated fibrosis and molecular signature discoveries in high-grade serous ovarian carcinoma" *Frontiers in Medicine* 9 (2022).
- d. **Jiang, Jun**, Tekin Burak, Guo Ruifeng, Liu Hongfang, Huang Yajue, and Wang Chen. "Digital pathology-based study of cell-and tissue-level morphologic features in serous borderline ovarian tumor and high-grade serous ovarian cancer." *Journal of Pathology Informatics* 12 (2021).
- e. **Jiang, Jun**, Naresh Prodduturi, David Chen, Qiangqiang Gu, Thomas Flotte, Qianjin Feng, and Steven Hart. "Image-to-image translation for automatic ink removal in whole slide images." *Journal of Medical Imaging* 7, no. 5 (2020): 057502.
- f. **Jiang, Jun**, Nicholas B. Larson, Naresh Prodduturi, Thomas J. Flotte, and Steven N. Hart. "Robust hierarchical density estimation and regression for re-stained histological whole slide image co-registration." *Plos one* 14, no. 7 (2019): e0220074.
- g. Gu, Qiangqiang, Naresh Prodduturi, **Jun Jiang**, Thomas J. Flotte, and Steven N. Hart. "Dicom_wsi: A python implementation for converting whole-slide images to digital imaging and Communications in Medicine compliant files." *Journal of Pathology Informatics* 12, no. 1 (2021).

2. Medical Image Segmentation for Image Guided Radiotherapy:

My early work centered on pioneering novel computational methods for automatically contouring Gross Tumor Volume (GTV). As an important procedure of image-guided radiotherapy (IR), tumor boundary is usually delineated by radiologists for guiding the dosage delivery. However, this manual process is labor-intensive and lacks reproducibility. To address this, I developed series of models that automated GTV delineation by incorporating tumor localization constraints and introducing innovative imaging modalities. These advanced approaches achieved efficient and reproducible GTV contouring, thereby enhancing the accuracy of IR and ultimately improving treatment outcomes.

- a. Zhao, Lijun, Zixiao Lu, **Jun Jiang**, Yujia Zhou, Yi Wu, and Qianjin Feng. "Automatic nasopharyngeal carcinoma segmentation using fully convolutional networks with auxiliary paths on dual-modality PET-CT images." *Journal of digital imaging* 32, no. 3 (2019): 462-470.
- b. Huang, Meiyang, Wei Yang, Yao Wu, **Jun Jiang**, Wufan Chen, and Qianjin Feng. "Brain tumor segmentation based on local independent projection-based classification." *IEEE transactions on biomedical engineering* 61, no. 10 (2014): 2633-2645.
- c. **Jiang, Jun**, Yao Wu, Meiyang Huang, Wei Yang, Wufan Chen, and Qianjin Feng. "3D brain tumor segmentation in multimodal MR images based on learning population-and patient-specific feature sets." *Computerized Medical Imaging and Graphics* 37, no. 7-8 (2013): 512-521.
- d. Huang, Meiyang, Wei Yang, **Jun Jiang**, Yao Wu, Yu Zhang, Wufan Chen, Qianjin Feng, and Alzheimer's Disease Neuroimaging Initiative. "Brain extraction based on locally linear representation-based classification." *Neuroimage* 92 (2014): 322-339.

- e. **Jiang, Jun**, Hubing Wu, Meiyang Huang, Yao Wu, Quanshi Wang, Jianqi Zhao, Wei Yang, Wufan Chen, and Qianjin Feng. "Variability of gross tumor volume in nasopharyngeal carcinoma using 11 C-choline and 18 F-FDG PET/CT." PLoS One 10, no. 7 (2015): e0131801.

Complete List of Published Work in My Bibliography:

<https://www.ncbi.nlm.nih.gov/myncbi/1JwnYMhlqn0soc/bibliography/public/>

D. Additional Information: Research Support and/or Scholastic Performance

1. Book chapter:

2023 – 2024 “Spatial Multiplexed Immunofluorescence Imaging in Exploring Tumor Immune Microenvironment of Melanoma” in book “Emerging Technologies for Cancer Detection and Diagnosis”. Lead by National Cancer Institute, Division of Cancer Treatment and Diagnosis (DCTD) and Mayo Clinic, Department of Oncology. Under review.

2. Journal reviewer:

2018 - present	Reviewer, Journal of Medical Imaging
2019 - present	Reviewer, Journal of Pathology Informatics
2020 - present	Reviewer, Journal of Medical System
2021 - present	Reviewer, Frontiers in Neuroscience
2022 - present	Review Editor, Cancer Genetics