# Ruichen Rong
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## OBJECTIVE
An assistant professor with extensive experience in **computational biology, artificial intelligence, and software engineer** passion for advanced biomedical research.

## EDUCATION
- **Ph.D, Computational Biology** — Jan 2011 – Aug 2017
  University of North Texas, Denton, TX, USA
  *Research Area: biostatistics, applied mathematics*
- **M.S, Computer Sciences** — Jan 2013 – Aug 2016
  University of North Texas, Denton, TX, USA
  *Research Area: machine learning, data science, computer vision*
- **B.S, Biotechnology** — Sep 2005 – Jan 2010
  Shanghai Jiao Tong University, Shanghai, China

## EXPERIENCE
**1. UT Southwestern Medical Center**, Dallas, TX
**Assistant Professor** — Aug 2023 – Present
- Achievements:
  - Developed a digital pathology annotation and data collection tool I-viewer powered by HDYolo, SAM.
  - Developed pan-cancer models for TME features identification: tumor growth pattern, secondary structure, nucleus and cytoplasm morphologies, etc.
  - Developing Multimodal Large Language Model for pathological image reasoning with **LLaVA by** finetuning **BLIP2**, **ImageBind**, **LLaMA2** on high quality VQA dataset collected by I-viewer.
- Responsibilities:
  - Design and maintain backend infrastructure and coordinate AI model deployment.
  - Lead digital pathology projects, organize team efforts, and mentor students and post-docs.
  - Performed scientific writing for publications, grants, and patents.

**2. UT Southwestern Medical Center**, Dallas, TX
**Senior Data Scientist** — Mar 2018 – Aug 2023
- Achievements:
  - Developed a real-time nucleus segmentation and TME feature quantification pipeline for pathological images with GAN, Yolo, panoptic segmentation.
  - Developed NLP pipelines with BERT and LLMs to analyze doctor diagnosis and reports.
  - Developed transformer forecasting model to predict the risk of death for Covid19 ICU patients.
  - Developed GCN models to analyze genetic image relations for spatial transcriptomic data.
- Responsibilities:
  - Developed and maintained AI applications and pipelines.
  - Implemented many models in different fields: semantic segmentation, object detection, NER, relational analysis, sentimental analysis, collaborative filtering, forecasting, etc.
  - Collaborated with cross-functional teams and communicated with collaborators to identify solutions.

**3. Loyola University of Chicago**, Maywood, IL
**Associate Researcher** — Oct 2017– Feb 2018
- Improved brain tumor segmentation mIoU by 7% with semi-3D-UNet.
- Visualized the EMR trajectories and correlations with Cox-PH regression and Random Forest**.**

**4. Google Inc.**, Mountain View, CA
**Software Engineer Intern** — Jan 2016 – April 2016
- Increased nDCG by ~3% in Google Map semantic location recommender system by building a curriculum LSTM model on user longitudinal dataset with large number of unlabeled/mislabeled timepoint.
- Contributed over 8,000 lines of product code (Python/C++) into team infrastructure.

**5. University of North Texas**, Denton, TX
**Research Assistant** Jan 2011 – Aug 2015

- Established an automatic feature selection algorithm for metagenomics bio-diversity explanation.
- Built up geometry proof for elastic-net regularization and convex-hull optimization with KKT.

## SKILLS

- Computer Vision: image classification, semantic/panoptic segmentation (UNet, DeepLab, SAM), object detection/instance segmentation (MaskRCNN, Yolo, FCOS, DETR), GAN (VAE, GANs, Pix2pix), contrastive learning (MoCo, SimCLR, CLIP), graph-neural network (GCN, PointNet), Point Cloud 3D detection, universal imaging model (SAM), and generative AIs (StableDiffusion XL, LoRA).
- NLP: LLMs (LLaMA2, Bard, ChatGPT), BERT, Named Entity Recognition, Relational/Sentimental Analysis.
- Recommender system: collaborator filtering, content-based system, feature engineer.
- Machine learning frameworks: PyTorch, TensorFlow, Scikit-learn, Spacy, HuggingFace, OpenAI.
- Engineer: databases (SQL, HDFS), API and web developments (Flask, FastAPI, Javascript), MLOps (AWS SageMaker, Torch serve, BentoML, Docker, Kubernetes), programming (Python, Java, C++, R).

## PUBLICATIONS

Google Scholar: https://scholar.google.com/citations?hl=en&user=pIvmT_UAAAAJ

| | All | Since 2018 |
|---|---|---|
| Publications | 34 | 25 |
| Citations | 2103 | 1605 |
| h-index | 13 | 13 |
| i10-index | 15 | 15 |

Patent:
Systems and methods for characterizing a tumor microenvironment using pathological images. G Xiao, Y Xie, R Rong, S Wang - US Patent App. 17/998,037, 2023

Recent Publications:

1. Wang, S., Rong, R., Zhou, Q., Yang, D. M., Zhang, X., Zhan, X., ... & Xiao, G. (2023). Deep learning of cell spatial organizations identifies clinically relevant insights in tissue images. *Nature communications*, *14*(1), 7872.
2. Wen, Z., Luo, D., Wang, S., Rong, R., Evers, B. M., Jia, L., ... & Xiao, G. (2023). Deep learning-based H-score quantification of immunohistochemistry-stained images. *Modern Pathology*, 100398.
3. Yang, S., Wang, S., Wang, Y., Rong, R., Li, B., Koh, A. Y., ... & Zhan, X. (2023). A Generalized Supervised Contrastive Learning Framework for Integrative Multi-omics Prediction Models. *bioRxiv*, 2023-11.
4. Wang, S., Rong, R., Gu, Z., Fujimoto, J., Zhan, X., Xie, Y., & Xiao, G. (2023). Unsupervised domain adaptation for nuclei segmentation: Adapting from hematoxylin & eosin stained slides to immunohistochemistry stained slides using a curriculum approach. *Computer Methods and Programs in Biomedicine*, *241*, 107768.
5. Rong, R., Sheng, H., Jin, K. W., Wu, F., Luo, D., Wen, Z., ... & Xiao, G. (2023). A Deep Learning Approach for Histology-Based Nucleus Segmentation and Tumor Microenvironment Characterization. *Modern Pathology*, 100196.
6. Rong, R., Wei, Y., Wang, T., Zhu, H., Wang, Y., & Xiao, G. (2023). Image-based quantification of histological features as a function of spatial location using the Tissue Positioning System. *eBioMedicine,* under review.
7. Wen, Z., Lin, Y. H., Wang, S., Fujiwara, N., Rong, R., Jin, K. W., ... & Xiao, G. (2023). Deep-Learning-Based Hepatic Ploidy Quantification Using H&E Histopathology Images. *Genes*, *14*(4), 921.
8. Rong, R., Wang, S., Zhang, X., Wen, Z., Cheng, X., Jia, L., ... & Xiao, G. (2023). Enhanced Pathology Image Quality with Restore-GAN. *The American Journal of Pathology*.
9. Wang, S., Rong, R., Yang, D. M., Fujimoto, J., Bishop, J. A., Yan, S., ... & Xie, Y. (2023). Features of tumor-microenvironment images predict targeted therapy survival benefit in patients with EGFR-mutant lung cancer. *The Journal of Clinical Investigation*, *133*(2).
10. Yang, S., Wang, S., Wang, Y., Rong, R., Kim, J., Li, B., ... & Zhan, X. (2022). MB-SupCon: Microbiome-based Predictive Models via Supervised Contrastive Learning. *Journal of Molecular Biology*, *434*(15), 167693.
11. Zhang, X., Wang, S., Rudzinski, E. R., Agarwal, S., Rong, R., Barkauskas, D. A., ... & Leavey, P. (2022). Deep learning of rhabdomyosarcoma pathology images for classification and survival outcome prediction. *The American Journal of Pathology*, *192*(6), 917-925.
12. Rong, R., Jiang, S., Xu, L., Xiao, G., Xie, Y., Liu, D. J., ... & Zhan, X. (2021). MB-GAN: microbiome simulation via generative adversarial network. *GigaScience*, *10*(2), giab005.

13. Zhang, L., Rong, R., Li, Q., Yang, D. M., Yao, B., Luo, D., ... & Xiao, G. (2021). A deep learning-based model for screening and staging pneumoconiosis. *Scientific reports*, *11*(1), 1-7.
14. Yan, J., Rong, R., Xiao, G., & Zhan, X. (2020). HiddenVis: a Hidden State Visualization Toolkit to Visualize and Interpret Deep Learning Models for Time Series Data. *bioRxiv*, 2020-12.
15. Wang, S., Rong, R., Yang, D. M., Fujimoto, J., Yan, S., Cai, L., ... & Xiao, G. (2020). Computational staining of pathology images to study the tumor microenvironment in lung cancer. *Cancer research*, *80*(10), 2056-2066.
16. Wang, S., Yang, D. M., Rong, R., Zhan, X., Fujimoto, J., Liu, H., ... & Xiao, G. (2019). Artificial intelligence in lung cancer pathology image analysis. *Cancers*, *11*(11), 1673.
17. Wang, S., Yang, D. M., Rong, R., Zhan, X., & Xiao, G. (2019). Pathology image analysis using segmentation deep learning algorithms. *The American journal of pathology*, *189*(9), 1686-1698.