# BIOGRAPHICAL SKETCH

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NAME: Xiaoyang, Ruan

eRA COMMONS USER NAME (credential, e.g., agency login): RUAN123

POSITION TITLE: Assistant Professor of Biomedical Informatics

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 *(if applicable)* | Completion Date MM/YYYY | FIELD OF STUDY |
|---|---|---|---|
| Shenyang Pharmaceutical University, Shenyang, China | B.S. | 09/2004 | Pharmacy |
| Beijing Hypertension League Institute, Beijing, China | M.S-Ph.D Joint-Training | 09/2009 | Population Genetics |
| Georgetown University, Washington DC. USA | Postdoctoral | 03/2011 | Bioinformatics |
| Mayo Clinic, Rochester, MN, USA | Postdoctoral | 06/2016 | Bioinformatics |

## A. Personal Statement

I am an assistant professor of the Center for Translational AI Excellence and Applications in Medicine (TEAM-AI) at McWilliams School of Biomedical Informatics, UTHealth Houston. I have an interdisciplinary educational background in the healthcare and pharmaceutical industries and extensive data science expertise. I have led several pioneering projects focused on dynamic risk modeling using real-world electronic health records. I also have a wealth of experience in designing and maintaining large-scale cloud-based data warehouses, as well as conducting related dynamic data collection, analysis, and presentation. These experiences have equipped me with a holistic perspective and a deep understanding of complex biomedical informatics challenges, and robust ability to extract valuable insights from vast and intricate datasets, applicable across diverse domains.

**Ongoing projects**

NIBIB R01 EB019403.
Hongfang Liu (PI); Role: Co-investigator
Explorative analysis of longitudinal deep learning for real-time risk modeling of various clinical outcomes.
Longitudinal deep learning for deep phenotyping and precision medicine

**Completed projects**

NIH (CA170357 and CA204013), Clinical Core of Mayo Clinic Center for Cell Signaling in Gastroenterology (P30DK084567).
Lisa Boardman (PI); Role: Co-investigator
Early genetic aberration in colorectal cancer vicinity normal and pre-cancerous tissue

NSF ABI: 0845523, NIH R01LM009959A1.
Hongfang Liu (PI); Role: Co-investigator
NCI60 cancer cell line genetic aberration study

F. Hoffmann-La Roche, the National Infrastructure Program of Chinese Genetic Resources (2005DKA21300) and Tsinghua-Yuyuan Medical Science Research Foundation.
Lisheng Liu, Xinyu Wang (PI); Role: Researcher
Delineates the association of polymorphism in the Chinese population with hypertension, obesity, and type II diabetes.

**Citations:**

1. **X Ruan**, S Fu, CB Storlie, et al. *Journal of Biomedical Informatics. 2022* Real-time risk prediction of colorectal surgery-related post-surgical complications using GRU-D model
2. **X Ruan**, L Wang, C Thongprayoon, et al. *Artificial Intelligence in Medicine 2023* GRU-D-Weibull: A Novel Real-Time Individualized Endpoint Prediction
3. **X Ruan**, L Wang, M Mai, et al. *https://arxiv.org/abs/2212.09606 2022* Discrimination, calibration, and point estimate accuracy of GRU-D-Weibull architecture for real-time individualized endpoint prediction
4. BR Druliner, **X Ruan**, Sicotte H, et al. *Mol Carcinog. 2018* Early genetic aberrations in patients with sporadic colorectal cancer.

## B. Positions, Scientific Appointments, and Honors

**Positions and Scientific Appointments**

2023-present Assistant Professor in Research, Data Science & AI, MC William School of Biomedical Informatics, UT Health, Houston, TX, US
2021-2023 Research Associate, AI & Informatics, Mayo Clinic, Rochester, MN, US
2018-2021 Senior data analysis consultant, JiangSu HengFengQiang Biotechnology LTD, JiangSu, China.
2016-Present Founder of Shanghai KaiNeng Information Technology Inc and Katelynn's Report
2011-2016 Research Fellow, Biomedical Statistical and Informatics, Mayo Clinic. Rochester, MN, US
2010-2011 Research Fellow, Department of Biostatistics, Bioinformatics and Biomath, Medical Center, Georgetown University. Washington DC. US
2010-2011 Special Volunteer, National Cancer Institute, National Institute of Health. Washington DC. US

**Honors**

2021-present JMIR reviewer
2022 AMIA AI summit poster presenter

## C. Contribution to Science

### 1. Clinical predictive modeling with real-world EHR data (2021-present)

Risk modeling with real-world EHR data has important implications for both patients and healthcare providers in many aspects including early detection of high-risk patients, personalized treatment plan, efficient resource allocation, reducing hospital readmission, medication management, enhanced follow-up and post-discharge care. I am the primary investigator of several projects exploiting longitudinal deep learning architectures for individualized real-time risk assessment with highly diversified data quality. The findings will ultimately lead to bedside tools that significantly improve patient outcomes.

a. **X Ruan**, S Fu, CB Storlie, et al. *Journal of Biomedical Informatics. 2022*
Real-time risk prediction of colorectal surgery-related post-surgical complications using GRU-D model
b. X Ruan, L Wang, C Thongprayoon, et al. *Artificial Intelligence In Medicine 2023*
GRU-D-Weibull: A Novel Real-Time Individualized Endpoint Prediction
c. **X Ruan**, L Wang, M Mai, et al. *https://arxiv.org/abs/2212.09606 2022*
Discrimination, calibration, and point estimate accuracy of GRU-D-Weibull architecture for real-time individualized endpoint prediction
d. H Xu, M Aldrich, … **X Ruan**, et al. *JAMIA 2014* Validating drug repurposing signals using electronic health records: a case study of metformin associated with reduced cancer mortality

### 2. Early genetic aberration in cancer patients (2010-2016)

Research into early genetic aberrations in cancer patients holds immense potential to revolutionize the cancer clinical field. By identifying genetic mutations and abnormalities at the earliest stages of cancer development, clinicians can diagnose the disease more accurately and design highly targeted treatment strategies. This precision medicine approach allows for the selection of therapies tailored to an individual's unique genetic profile, increasing treatment efficacy while minimizing side effects. My research ultimately enhances patient outcomes and quality of life, and also paves the way for the development of novel therapies and early intervention strategies that have the potential to transform the landscape of cancer care.

a. **X Ruan**, JP Kocher, Y Pommier, et al. *PLoS ONE 2012* Mass homozygotes accumulation in the NCI-60 cancer cell lines as compared to HapMap trios, and relation to fragile site location
b. **X Ruan**, H Liu, Boardman L, et al. *PLoS ONE 2014* Genome-wide analysis of loss of heterozygosity in breast infiltrating ductal carcinoma distant normal tissue highlights arm specific enrichment and expansion across tumor
c. BR Druliner, **X Ruan**, Sicotte H, et al. *Mol Carcinog. 2018* Early genetic aberrations in patients with sporadic colorectal cancer.
d. S Rashtak, **X Ruan**, BR Druliner, et al. *Clinical Colorectal Cancer 2017* Peripheral Neutrophil to Lymphocyte Ratio Improves Prognostication in Colon Cancer.

**3. Population genetics study in Chinese obesity population (2005-2009)**

Obesity is an important public health concern which significantly impacts quality of life, life expectancy. It is associated with an increased risk of various chronic conditions, including type 2 diabetes, cardiovascular diseases, hypertension, and certain types of cancer. Moreover, obesity places a substantial burden on healthcare systems, leading to higher healthcare costs and reduced workforce productivity. My research is supported by Hoffmann-La Roche AG as part of the effort to develop genetically engineering Apolipoprotein A dimer for treating obesity and related diseases.

a. **X Ruan**, L Ma, S Wang, et al. *Obesity 2009* Association of Two CETP Polymorphisms With HDL Levels in the Chinese Obese Population
b. **X Ruan**, L Ma, S Wang, et al. *ActaDiabetol. 2010* TAQIB and I405V polymorphisms of CETP are moderately associated with obesity risk in the Chinese adult population
c. X Liu, X Wang, Y Shen, L Wu, **X Ruan**, et al, The functional variant rs1048990 in PSMA6 is associated with susceptibility to myocardial infarction in a Chinese population
d. X Ruan, Z Li, Y Zhang, et al. J Cell Mol Med. 2011 Apolipoprotein A-I possesses an anti-obesity effect associated with increase of energy expenditure and up-regulation of UCP1 in brown fat

**Published Work in MyBibliography**
https://www.ncbi.nlm.nih.gov/myncbi/18yUqaeBFaHcsv/bibliography/public/