

# Peng Yang

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🔗 <https://github.com/pengyang0411>

## EDUCATION

- **Rice University** Jan. 2020 - Dec. 2024  
*Ph.D. in Statistics, GPA: 3.98/4.00*  
- Advisor: Dr. Ying Yuan, Dr. Liang Li, Dr. Ziyi Li.  
Houston, TX
- **Rice University** Aug. 2018 - Dec. 2019  
*Master in Statistics*  
Houston, TX
- **Ningbo University** Sep. 2014 - Jul. 2018  
*Bachelor of Mathematics and Applied Mathematics*  
Ningbo, China
  - Ningbo University Scholarship (2015).
  - National First Award of The Mathematical Contest in Modeling (2016).
  - Team Honorable Mention in 2016 Mathematical Contest in Modeling (2016).
  - Excellent Paper Award in Shenzhen Mathematical Modeling Challenge (2016).
  - Zhengjiang State Scholarship (2017).

## TECHNICAL SKILLS

- **Languages:** Python, SQL, R, SAS, Matlab, C, Maple
- **Software:** Linux, GitHub, AWS,  $\text{\LaTeX}$
- **Research:** Bayesian Statistics, Machine Learning, Optimization, A/B Testing, Mixture Models
- **Packages:**
  - **ICeITH** model developer on GitHub (<https://github.com/pengyang0411/ICeITH>).
  - **MERIT** model developer on GitHub (<https://github.com/pengyang0411/MDR>).

## PUBLICATIONS

- [1]. **Yang, P.**, Yuan, Y. (2022). Design and Sample Size Determination for Multiple-dose Randomized Trials for Dose Optimization. Review in **Biometrics**.
- [2]. **Yang, P.**, Yuan, Y., Li, Z. (2022). A Novel Bayesian Model for Assessing Intratumor Heterogeneity of Tumor Infiltrating Leukocytes with Multi-region Gene Expression Sequencing. Review in **JASA (ACS)**.
- [3]. **Yang, P.**, Yuan, Y. (2022). A Bayesian Design to Adaptively Borrow Information by Incorporating Longitudinal Measurements. In preparation.
- [4]. Liu, S., Park, Y., **Yang, P.**, Mandrekar S., Yuan, Y. (2022). A Bayesian Adaptive Design for Avatar Driven Cancer Clinical Trials. In preparation.
- [5]. Cao, S., Wang, J. R., Ji, S., **Yang, P.**, Dai, Y., Guo, S., ... & Wang, W. (2022). Estimation of tumor cell total mRNA expression in 15 cancer types predicts disease progression. **Nature biotechnology**, 1-10.
- [6]. Bahrambeigi, V., Lee, J.J., Branchi, V., Henry, J.T., Rajapakshe, K.I., Stephens, B.M., Dhebat, S., Hurd, M.W., Sun, R., **Yang, P.** and Wang, W., 2022. Transcriptomic Profiling of Plasma Extracellular Vesicles Enables Reliable Annotation of the Cancer-specific Transcriptome and Molecular Subtype. *bioRxiv*.

## EXPERIENCE

- MD Anderson Cancer Center** Aug. 2019 - Present  
*Research Assistant*  
Houston, TX
- Experimental Design:** Determine the sample size of a multi-arm randomized clinical trial

- Proposed a generalized power function to identify the correct dose.
- Developed a maximum type I error function to control the overall type I error.
- Determined sample size and decision rules by balancing generalized power and type I error.
- Created user-friendly package MERIT in R to assist trial enrollment and decision-making

**A/B Testing:** *Draw treatment effect by information borrowing from historical data*

- Drew causal inference for experiment arms suffer from limited sample size by borrowing historical data.
- Achieved adaptive information borrowing by incorporating longitudinal biomarker data for similarity measure.
- Developed a Bayesian hierarchical model and optimized it by Metropolis-Hastings Random-Walk Sampling Algorithm.

**Mixture Model and Optimization:** *Evaluating the ITH with multi-region gene expression design*

- Proposed a Bayesian hierarchical model to leverage the cell type profiles as prior knowledge to decompose the mixture gene expression data while accounting for within-subject correlation.
- Developed a variational inference algorithm for optimization and significantly reduced computing time.
- Discovered the relation of proposed intratumor heterogeneity to survival outcomes that potentially serve for diagnosis.
- Achieved the best accuracy (correlation: 0.97; AUC: 0.85) and robustness benchmarked with other state-of-the-art methods.

**Clustering:** *Spatial clustering for cancer cell subclone identification on spatial transcriptomic data*

- Proposed a kernel-based dissimilarity measure that integrates high-dimensional spatial and transcriptomic profiles to identify cancer cell subclones by hierarchical and k-means clustering using R.
- Evaluated the sensitivity of weights between two kernels and came up with a better data normalization strategy.

**Variable Selection:** *Profile likelihood-based gene selection method*

- Developed a profile likelihood-based approach to rank the most informative genes and select the top of them to increase the identifiability of DeMixT likelihood using R and C.
- Conducted extensive simulations to assess the robustness of gene ranking performance over 4,000 patient samples in 16 different cancer types.

**Rice University**

Research Assistant

**Aug. 2018 - Present**

Houston, TX

**Casual Inference:** *Estimating causal effect by de-confounding mediators for Uber eats*

- Developed a simulation scheme for the causation of customers experiencing delay and their future engagement by incorporating potential mediators from a three-sided market.
- Implemented propensity score matching, inverse probability weighting, doubly robust regression, and instrumental variable approach to draw the correct causal effect.
- Proposed a strategy to benefit the company by distributing promo codes to neutralize the negative causal effect of customers experiencing a delay.

**Deep Learning:** *Satellite image segmentation*

- Performed data augmentation to enlarge the dataset and dimension reduction for outlier detection in Python.
- Adopted U-Net architecture for image segmentation and tuning hyper-parameters to achieve better convergence.
- Implemented bootstrap and dropout layers to reduce overfitting, and ensemble approach for better accuracy.

## EXTRACURRICULAR ACTIVITIES

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- Soccer, Billiards, Bouldering, Yo-Yo