

# YINGYING YU

Tel: (347)888-0284 | Email: [yyu109@jhmi.edu](mailto:yyu109@jhmi.edu) | [Personal Website](#)

## EDUCATION

**Johns Hopkins University, Bloomberg School of Public Health**  
*Master of Health Science in Epidemiology, Cancer track*

*Seq 2022 – May, 2024 (Expected)*  
*Current GPA: 4.0/4.0*

**New York University, College of Arts and Science**  
*Bachelor of Arts in Biology, magna cum laude*

*Seq. 2018 – Jan. 2022*  
*GPA: 3.87/4.00*

## SKILLS

- **Data analysis:** R (*tidyverse*, *DESeq2*, *edgeR*, *ASpli*, *Shiny*...), Python (*pandas*, *numpy*, *sklearn*, *matplotlib*...), Stata, SAS
- **Data management:** SQL, Excel (vlookup, Power Query), version control (GitHub), Redcap

## RELATED EXPERIENCE

**Department of Epidemiology, Johns Hopkins University**  
*Research assistant for Prof. Kala Visvanathan*

Baltimore, Maryland  
*Aug. 2023 – Present*

- Conducted an in-depth analysis of the effects of breastfeeding on breast cancer mortality and recurrence by leveraging data from the Breast and Ovarian Surveillance Service (BOSS) Cohort and Maryland state registries.
- Executed comprehensive descriptive analyses to delineate baseline characteristics of participants in relation to the duration of breastfeeding in months, utilizing R programming with proficiency in the 'tidyverse' and 'table1' packages.
- Developing survival analysis by applying Cox proportional hazards regression models to estimate hazard ratios.

**National Cancer Institute, NIH**  
*Bioinformatics analyst for Dr. Rouf Banday*

Bethesda, Maryland  
*Jun. 2023 – Present*

- Directed a detailed genome-wide analysis of bladder cancer cells, uncovering 30 new isoforms in interferon-treated samples.
- Pioneered an RNA-Seq analysis pipeline to investigate unique alternative splicing patterns in cancer cells, utilizing R (*DESeq2*, *edgeR*, and *ASpli*), software IGV, and Linux software (*Samtools*, *STAR*, *spliceV*, and *Enrichr*).
- Showcased research outcomes at NIH Summer Poster Day and am currently extending the pipeline's application to larger datasets and additional cancers, including breast cancer, colorectal cancer, pancreatic cancer, and leukemia.

**BGI group**  
*Business development intern*

Shenzhen, China  
*Feb. 2022 – Jun. 2022*

- Coordinated the Million Microbiome from Human Project (MMHP). Proactively identified and reached out to 50 potential collaborators focusing on microbiome research within the European academic community.
- Assumed responsibility for collecting, analyzing, and summarizing 23 national genome projects in major Europe, with a focus on those participating in the European '1+ Million Genomes' Initiative (1+MG). Synthesized 23 reports for review.
- Executed a comparative analysis of major In-vitro diagnostics distributors in the Europe market by collecting product information, marketing tactics, and collaborations. Presented detailed findings to the senior team members.

**New York University Shanghai**  
*Research assistant for Prof. Jungseog Kang*

Shanghai, China  
*Aug. 2021 – Dec. 2021*

- Engineered plasmids featuring target inserts of five distinct histone H2A.FV truncations and designed specific primers.
- Investigated the potential interaction mode between histone H2A.FV and the chromosomal segregation-related protein INCENP by utilizing the technique of Co-Immunoprecipitation (CoIP) in HeLa cell lines for analysis.
- Conducted over-expression experiments on wild-type H2A.FV and three mutant variants, and compared mitotic defects by immunofluorescence and micronuclei counting to quantify differences in cellular response.

**Shanghai Luming Biological Technology**  
*Bioinformatics analyst intern*

Shanghai, China  
*Feb. 2021 – Jun. 2021*

- Processed raw liquid chromatography–mass spectrometry (LCMS) and gas chromatography–mass spectrometry (GCMS) data using Progenesis QI for baseline filtering, peak identification, integration, and normalization for more than 50 samples.
- Analyzed processed data for potential marker metabolites by quality control analysis, principle component analysis, fold change analysis, differential metabolite screening, correlation analysis, and pathway enrichment analysis using R.
- Generated 122 analysis reports using Rmarkdown. Translated 6 different analysis report templates from Chinese to English.