YINGYING YU

(347)888-0284 | yyu109@jhmi.edu | Baltimore, Maryland

EDUCATION

Johns Hopkins University, Bloomberg School of Public Health

Master of Health Science, GPA: 4.0/4.0

• Major in Epidemiology, cancer track

Baltimore, MD

Expected May. 2024

New York University, College of Arts and Science

Bachelor of Arts, magna cum laude, GPA: 3.87/4.00

• Major in Biology, minor in Chemistry

• Honors: Dean's List for the Academic Years 2018, 2019, and 2020

New York, NY Seq. 2018 – Jan. 2022

RELATED EXPERIENCE

Johns Hopkins University

Thesis research

Baltimore, Maryland

Ongoing

• Investigating the effect of breastfeeding and parity on the breast cancer recurrence and mortality across various subtypes, utilizing data from the Breast and Ovarian Surveillance Service (BOSS) Cohort.

National Cancer Institute, Rouf Banday lab

Summer research fellow

Bethesda, Maryland

- Jun. 2023 Aug. 2023
- Conducted a genome-wide analysis of transcriptomes between untreated and interferon-treated HT-1376 bladder cancer cell line, and identified 30 novel isoforms exclusively present in IFN-treated samples.
- Developed and implemented an advanced RNA-Seq analysis pipeline using R packages DESeq2, edgeR, ASpli, software IGV, spliceV, and Enricht to investigate novel alternative splicing patterns in genes.
- Delivered research findings through a poster presentation at the NIH Summer Poster Day, and shared insights with fellow summer interns and the broader NIH community.

NYU Shanghai, JS Kang lab

Shanghai, China

Undergraduate researcher

Aug. 2021 – Dec. 2021

- Constructed plasmids containing target inserts of five distinct histone H2A.FV truncations and designed specific primers for these primers.
- Investigated the potential interaction mode between histone H2A.FV and the chromosomal segregation-related protein INCENP; utilized Co-Immunoprecipitation techniques in HeLa cell lines for analysis.
- Conducted over-expression on wild-type H2A.FV and three mutant variants; compared mitotic defects by immunofluorescence and micronuclei counting to quantify differences in cellular response.

Shanghai Luming Biological Technology

Shanghai, China

Bioinformatics Analyst Intern

Feb. 2021 – Jun. 2021

- Processed raw mass spectroscopy data using software Progenesis QI.
- Analyzed processed data quantitatively and qualitatively for potential marker metabolites using R.
- Generated 122 analysis reports and related graphs according to customer's needs using R.

SKILLS

Programming skills: R, Python, Unix, SQL, Version control, Power Query, Progenesis QI. Language: Fluent in Mandarin, Cantonese, and English.