Yung Hsing (Winston) Huang

Bioinformatics/Cancer Research Expert in 8⁺ ○

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Houston, TX

SUMMARY/OBJECTIVE

- 8+ years of academic and industrial research experience
- Equipped with molecular biology and bioinformatics knowledge
- Research expertise: translational research using bioinformatics approaches
- Strong background and experience in molecular biology techniques
- Lawful permanent resident in United States and a lawful citizen in Canada

WORK EXPERIENCE

Bioinformatician
Houston Methodist Research Institute | Houston, TX, USA | 02/2024 – Present

Spatial Omics Core, Houston Methodist Research Institute
- Data analyses for Spatial Omics Core of Houston Methodist Research Institute including bulk-RNA, single-cell RNA (10X Chromium), spatial transcriptomics (10X Xenium) and spatial proteomics (Akoya Phenocycler) data

Keith Syson Chan Lab, Department of Urology
I participate in the following projects as an in-lab bioinformatician by providing manpower in data mining, hypothesis validation, statistical analyses and exploratory data analysis:
- Heterogeneity of Cancer-associated fibroblasts (CAF) in non-muscle-invasive and muscle-invasive bladder cancer via bioinformatics approaches such as single-cell RNA sequencing and spatial transcriptomics RNA sequencing (Gao et al., *Science Advances,* 2025)
- Skewing of myelopoiesis in the bone marrow upon chemotherapy that affects local tumor microenvironment in bladder cancer (Wong et al., *Nature Communications*, under revision)
- Matrix-induced stress response of bladder cancer cells via the interaction with intratumoral collagens
- Neutrophil heterogeneity as a determining factor of the outcome after treatment with immune checkpoint blocker in bladder cancer
- The effect of T cell-mediated anti-cancer immunity upon high fat diet-induced obesity in bladder cancer
- Regulation of immunity by a subclass of endothelial cells within tumor microenvironment of bladder cancer
- Thrombosis in kidney clear cell carcinoma (in collaboration with Dr. Dharam Kaushik)
- Radiation vaccination clinical trial (in collaboration with Dr. Raj Satkunasivam)

Bioengineer
Systemic Bio by 3D Systems | Houston, TX, USA | 06/2022 – 11/2023
I worked for a subsidiary company of 3D Systems, Systemic Bio, which focused on development of organ/tumor-on-chip development for the purposes of preclinical drug efficacy/toxicity assessment. My main job functions included:
- Assay development and optimization for samples collected from 3D organ/tumor-on-chip systems including viability/cytotoxicity assays (LDH, Cell-Titer Glo, MTS, CCK8), histology assays (cryosessioning of 3D-printed hydrogels, IHC/H&E staining), analyte quantification assays (ELISA of soluble proteins, bile acids, enzyme activity colorimetric assays) and nucleic acid assays (qPCR, PicoGreen). Assessment of biocompatibility of organ/tumor-on-chip systems using primary human hepatocytes and immortalized human cell lines using various biomaterials, microfludic systems and hydrogel print patterns
- Establishment of pipelines for biological/biochemical assay data collection, analyses, visualization and interpretation Maintenance of core experimental equipment including Leica Cryostat, MiniAmp™ Plus Thermal Cycler, Nanodrop, QuanStudio 6, MACSQuant 10 Analyzer Flow Cytometer and Promega Glomax Plate Reader
- Participation of partnership million-scale funding projects using organ/tumor-on-chip for preclinical drug screening with two major pharmaceutical companies.

Postdoctoral Fellow
Houston Methodist Research Institute | Houston, TX, USA | 04/2019 – 05/2022
- Identified an innovative therapeutic target NHE6 for improved chemotherapy and antibody-based immunotherapy efficacy in multiple myeloma patients using Oncomine and GEO data
- Data mining of potential target genes/signaling pathways that contribute to obesity-mediated myeloma tumorigenesis using in-house RNAseq data (GSE132604)

- Discovered the impact of retinoic acid receptor (RARγ) and interferon β signaling pathway as a mechanism of carfilzomib resistance in multiple myeloma using in-house RNAseq data (GSE178340)
- Data mining of potential target genes/gene signaling pathways that are correlated with high-risk multiple myeloma using publicly available gene datasets on GEO.
- Patient survival analyses in myeloma patients segregated by gene expression level using publicly available GEO and Oncomine data
- Writing and preliminary data generation for a successfully funded CPRIT grant titled "Targeting NHE6 to improve clinical efficacy of daratumumab in myeloma" (Grant ID: RP220639)
- One manuscript titled "Inhibition of the NHE6-mediated endosome pathway improves therapeutic response in multiple myeloma" under revision (Nature Communication).

EDUCATION

Master of Science (M.Sc.) in Biomedical Informatics
University of Texas Health Science Center at Houston | Houston, TX, USA | Class of 2024
- Training on programming tools for biomedical informatics including MySQL, Python (pandas, numpy, matplotlib, seaborn, jupyter notebook etc), R (BiocManager and tidyverse), Google Colab, Tableau and Linux
- Practicum project (BMI 6000, Supervisor: Dr. Pora Kim):
  - Predict possible the breakpoints of KMT2A-AFF1 fusion proteins using the deep learning model FusionAI and FusionGDB2.0
  - Predict 3D protein structures of a fusion protein KMT2A-AFF1 using Alphafold2
  - Validate predicted structure using SAVES v6.0 and AlphaPickle
  - Prepare and identify potential active sites within a predicted protein structure for in silico drug binding screening using Schrodinger Maestro (Protein Preparation, SideMap, Grid and Glide)
  - Extract KMT2A-AFF1 breakpoint information from CCLE database using Linux
  - Perform RNAseq data alignment using STAR and Arriba to identify the presence of KMT2A-AFF1 fusion proteins in established AML/ALL cell lines
- Course project (BMI 5333 Systems Medicine: Principles and Practice): investigation on the genetic difference in black Americans compared to other ethnicities that could lead to worse survival and therapy response in myeloma patients using multiple myeloma research foundation (MMRF) database
- Course project (BMI 5330 Introduction to Bioinformatics): investigation on how obesity-related genomic defects could contribute to tumorigenesis using multiple bioinformatic databases including UCSC genome browser, dbSNP, ClinVAR, GEO, GWAS, 1000 Genome Project, TCGA, DAVID, BioGrid, OMIM etc

Doctor of Philosophy (Ph.D.) in Lab Medicine and Pathology
University of Alberta | Edmonton, AB, Canada | Class of 2019
- Development of a 3D cell culture model for therapy assessment and molecular analyses of primary myeloma cells and myeloma cell lines
- Development and preclinical assessment of anti-CD38-conjugated nanoparticles encapsulating STAT3 inhibitor as an innovative therapeutic agent for multiple myeloma

Bachelor of Science, Honours Degree (BSc.(Hon.)) in Biochemistry
University of British Columbia | Vancouver, BC, Canada | Class of 2013

PATENT

Pyroptosis-Associated Gene Signature (CASCADE) for Predicting Treatment Response in Bladder Cancer – Filed internally at Houston Methodist Research Institute # DISC2025014

RELEVANT CORE SKILLS

- Bioinformatics data processing and cleaning
- NGS analysis (bulk, scRNA, spatial omics)
- Bioinformatics databases (TCGA, GSE, etc)
- Version control and script management (GitHub)
- Pathway enrichment analyses (GO and KEGG, etc)
- Immune profile deconvolution analyses
- In silico simulation for drug discovery
- Data visualization and presentation
- Gene signature development
- Single-cell multiomics analyses
- Programming languages (Python and R)
- Linux for large-scale data manipulation