BIOGRAPHICAL SKETCH

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NAME: **Xianlu (Laura) Peng**

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

POSITION TITLE: **Research Assistant Professor**

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
Nanjing University of Aeronautics and Astronautics, Nanjing, China	BA	06/2012	Biomedical Engineering
The Chinese University of Hong Kong, Hong Kong, China	PhD	07/2016	Chemical Pathology
The University of North Carolina at Chapel Hill, Chapel Hill, NC, US	Postdoctoral Training	04/2020	Cancer Genomics

A. Personal Statement

I am a computational biologist with my research focused on addressing biomedical problems through bioinformatics approaches. During my PhD training, I have been involved in multiple research projects in distinct topics and gained hands-on experiences of mining omics data for biological and medical answers. I played a leading role in the project of studying enhancer regulation in myogenesis and established the analysis pipelines for the lab (Peng, Nucleic Acids Research). In another project, I studied the cell-free fetal DNA in maternal plasma and developed a framework for accurate quantification of this parameter using shallow-depth DNAseq data (Jiang and Peng, npj Genomic Medicine).

I joined Dr. Jen Jen Yeh's lab at University of North Carolina as a postdoctoral research associate to pursue my interest in cancer genomics. To gain better insight of the molecular underpinning of differential patient outcome and drug response in pancreatic cancer, I have been focusing on analyzing multiple layers of data using established, as well as novel computational methods. I have developed computational framework for the deconvolution of bulk tumor samples into biological compartments and successfully associated clinical implications for these compartments in pancreatic cancer (Peng, Nature Communications). I was also involved in the development of a clinically feasible pancreatic cancer subtypes classifier, which is predictive for patient survival and treatment response (Rashid and Peng, Clinical Cancer Research). In addition, I have been working on the identification of novel therapeutic targets in pancreatic cancer, as well as the evaluation of chemotherapy responses. By analyzing mass spectrometry and RNAseq data in patient tumors and patient-derived xenograft models, I have identified subtype-specific kinase signatures and drug targets for patients.

Currently, I am advancing my analytical techniques and understandings toward cancer genomics in the position of Research Assistant Professor. I have a broad interest in using computational methods to address clinical questions in different cancers. One of the studies as an extension of current projects is to determine the robust subtypes of the microenvironment in pancreatic cancer. In this aim, I have been using single-cell RNAseq to better delineate cell types and gene profiles, as well as developing and optimizing analysis methods. As the principal investigator on another epigenetics project, I seek to identify novel drug targets through the analysis of enhancer networks using the patient-derived xenograft models. My preliminary analysis on publicly available datasets has demonstrated the shift of enhancer landscapes in tumor compared to normal samples. Therefore, the re-shaped enhancers driving aberrant gene activation in tumors may be evaluated as novel drug targets for tailoring therapeutics. I am also interested in studying the molecular disparities underpinning the differential pathologic stage and mortality rate of Black or African American compared to other races in gastric cancer.

Apart from working on my own projects, I have extensive collaborative projects with collaborators on campus, as well as in other institutions, such as Memorial Sloan Kettering Cancer Center, Harvard University, University of Iowa, University of Rochester and University of California at San Francisco.

As a senior scientist in the lab, I have supervised 2 rotation Ph.D. students and 6 research assistants since 2017. I have been providing project design suggestions, analysis ideas and coding tutors to them. In addition, I closely work with other lab members when their projects need bioinformatics analysis or advice.

Ongoing and recently completed projects that I would like to highlight include:

3R01CA199064-03S1A1
Yeh (PI)
09/01/2016 – 07/31/2026
Tumor subtypes and therapy response in pancreatic cancer

U24CA211000-04
Raphael (contact PI), Yeh (MPI)
09/15/2016 – 08/31/2021
Pathway and Network Integration of Cancer Genomics and Clinical Data

UNC Lineberger Comprehensive Cancer Center (LCCC) Clinical/Translational Research Award
Peng (PI)
07/01/2021 – 06/30/2022
Interrogation of epigenetic disparities in minority population for precision medicine in gastric cancer

Junior Faculty Development Awards, University of North Carolina at Chapel Hill
Peng (PI)
01/01/2021 – 12/31/2021
Interrogation of epigenetic disparities in minority population for precision medicine in gastric cancer

NC TraCS Institute Pilot Grant Award
Peng (PI)
04/01/2022 - 03/31/2023
Investigate the intercellular dynamics of pancreatic ductal adenocarcinoma by spatial transcriptomics

B. Positions and Honors

Positions

05/2020-	Research Assistant Professor, Pharmacology Department, University of North Carolina, Chapel Hill, NC
02/2017-04/2020	Postdoctoral Research Associate, Lineberger Comprehensive Cancer Center, University of North Carolina, Chapel Hill, NC
08/2012-01/2017	Research Assistant, Chemical Pathology, The Chinese University of Hong Kong, Hong Kong, China

Honors

2012-2016	Postgraduate Studentship, The Chinese University of Hong Kong
2012	Honor for Excellent Student, Nanjing University of Aeronautics and Astronautics
2010	First Prize in National English Contest for College Students, China
2009	Scholarship for Outstanding Performance in CET-4 English Test, Nanjing University of Aeronautics and Astronautics

Patents

De novo compartment deconvolution and weight estimation of tumor tissue samples (DECODER); U.S. Application 453 Provisional Filed

C. Contributions to Science

1. I have used bioinformatics approaches and developed computational tools to understand the molecular profiles and cellular heterogeneity in cancers. My work deconvolving bulk tumor samples has led to the

development of a computational framework, DECODER, which is applicable to multiple cancer types and data types. DECODER has accurately captured biologically relevant cellular compartments in pancreatic cancer, which showed meaningful clinical implications. The quantification feature for cellular compartment of this tool may found applications in treatment evaluation and tumor-of-origin identification. In another work, I have shown the difference of treatment response and survival of two subtypes in pancreatic cancer. A classifier, PurIST, was developed to accurately call subtypes for pancreatic cancer patients using sample types and platform types that are highly feasible in the clinical setting.

a) **Peng XL**, Moffitt RA, Torphy RJ, Volmar KE, Yeh JJ. De novo compartment deconvolution and weight estimation of tumor samples using DECODER. *Nat Commun*. 2019 Oct 18;10(1):4729. PMC6802116
b) Rashid NU[#], **Peng XL**[#], Jin C, Volmar KE, Kawalerski R, Belt BA, Panni RZ, Nywening TM, Herrera SG, Moore KJ, Hennessey S, Morrison AB, Nayyar A, Chang AE, Schmidt B, Kim HJ, Linehan DC, Moffitt RA, Yeh JJ. Purity Independent Subtyping of Tumors (PurIST), a platform and sample type independent single sample classifier for treatment decision making in pancreatic cancer. *Clin Cancer Res*. 2020 Jan 1; 26(1): 82-92. PMC6942634. [#]**co-first authors**

2. I have analyzed the active kinome in patient-derived xenografts tumors to improve the development of targeted therapy. For pancreatic cancer where kinase mutations are uncommon, determination of kinome-wide kinase activation profiles will be key to tailoring the use of kinase inhibitors for effective therapy.

a) Lipner MB, **Peng XL**, Jin C, Gao Y, East MP, Rashid N, Moffitt RA, Herrera SG, Morrison AB, Golitz BT, Vaziri C, Graves LM, Johnson G, Yeh JJ. Irreversible JNK1-JUN inhibition by JNK-IN-8 sensitizes pancreatic cancer to 5-FU/FOLFOX chemotherapy. *JCI Insight*. 2020 Apr 23; 5(8): e129905. PMC7205424

3. I have performed integrative computational analyses to dissect how transcription program is regulated through the epigenetic program during muscle regeneration. My analyses on combined next-generation sequencing (NGS) datasets have led to the identification of novel enhancers and long non-coding RNAs (lincRNAs) playing key roles in the process. Moreover, the finding that individual enhancers cooperate as a functional unit to mediate target gene activation throughout the course of differentiation has added to the enhancer functional mechanisms in the field. The detailed methods of identifying *de novo* lincRNAs and preliminarily analyzing ChIPseq have been written as protocols in book chapters published by Springer.

a) **Peng XL**[#], So KK[#], He L[#], Zhao Y, Zhou J, Li Y, Yao M, Xu B, Zhang S, Yao H, Hu P, Sun H, Wang H. MyoD- and FoxO3-mediated hotspot interaction orchestrates super-enhancer activity during myogenic differentiation. *Nucleic Acids Res*. 2017 Sep 6;45(15):8785-8805. PMC5587775. [#]**co-first authors**
b) **Peng X**, Sun K, Zhou J, Sun H, Wang H. Bioinformatics for Novel Long Intergenic Noncoding RNA (lincRNA) Identification in Skeletal Muscle Cells. *Methods Mol Biol.* 2017;1556:355-362. PMID: 28247361
c) So KK, **Peng XL**, Sun H, Wang H. Whole Genome Chromatin IP-Sequencing (ChIP-Seq) in Skeletal Muscle Cells. *Methods Mol Biol*. 2017;1668:15-25. PMID: 28842899

4. I have dissected different layers of NGS data in the context of cell-free DNA (cfDNA), which has been increasingly recognized as “liquid biopsy” for a plenty of clinical applications, such as non-invasive prenatal testing and cancer screening. To avoid limitations in conventional estimation of fetal DNA fraction in prenatal diagnosis, I developed a bioinformatics algorithm based on linear regression to estimate the fetal DNA fraction by analyzing only maternal genotypes and shallow-depth sequencing of maternal plasma DNA, which is accurate and could be readily integrated into non-invasive prenatal testing.

a) Jiang P[#], **Peng X**[#], Su X, Sun K, Yu SCY, Chu WI, Leung TY, Sun H, Chiu RWK, Lo YMD, Chan KCA. FetalQuant[SD]: Accurate quantification of fetal DNA fraction by shallow-depth sequencing of maternal plasma DNA. *npj Genom Med*. 2016 May; 16013. PMC5685300. [#]**co-first authors**

b) **XL Peng**, P Jiang. Bioinformatics Approaches for Fetal DNA Fraction Estimation in Noninvasive Prenatal Testing. *Int J Mol Sci*. 2017 Feb; 18(2): 453. PMC5343987

5. To explore the potential of non-invasive detection for systemic lupus erythematosus (SLE), I have developed algorithms that statistically quantified the genomic and methylomic abnormalities in SLE patients. This study might open a new avenue for the diagnostic and monitoring of SLE and has identified SLE as a confounding factor in clinical non-invasive testing utilizing plasma DNA. Moreover, due to the frequent observation of DNA size aberrations in multiple diseases, I was then involved in investigating cfDNA fragmentation rationale by analyzing sequencing data in a DNase1 knockout mouse model. We found that this gene does not appear to play a major role in the process.

a) Chan RW, Jiang P, **Peng X**, Tam LS, Liao GJ, Li EK, Wong PC, Sun H, Chan KC, Chiu RWC, Lo YMD. Plasma DNA aberrations in systemic lupus erythematosus revealed by genomic and methylomic sequencing*. Proc Natl Acad Sci U S A.* 2014 Dec 9;111(49): E5302-11. PMC4267379

b) Cheng THT, Lui KO, **Peng XL**, Cheng SH, Jiang P, Chan KCA, Chiu RWK, Lo YMD. DNase1 does not appear to play a major role in the fragmentation of plasma DNA in a knockout mouse model. *Clin Chem*. 2018 Feb;64(2):406-408. PMID: 29097509

Complete List of Published Work:
https://pubmed.ncbi.nlm.nih.gov/?term=Xianlu+Peng