YIDAN PAN

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EDUCATION

Rice University — Houston, TX
Doctor of Philosophy, Systems, Synthetic, and Physical Biology (SSPB) — *May 2020*
Thesis: Profiling Genome Editing Outcomes for Biological Studies and Disease Treatment

Southern University of Science and Technology — Shenzhen, China
Bachelor of Science, Biology — *Jan. 2015*

WORK EXPERIENCE

Assoc. Scientist, Post Doc Fellow — Boston, MA
Merck Sharp & Dohme Corp. — *Nov. 2020 - Present*

· Interpret high-throughput single-cell RNA-seq (scRNA-seq) data and perform deconvolution analysis in bulk tumor profiles for better understanding of complex tumor-immune interactions and novel hypotheses for resistance mechanisms to oncology treatment.

Research Associate, Postdoctoral Fellow — Houston, TX
Rice University — *Jun. 2020 – Nov. 2020*

· Develop pipelines for the rational design of genome editing tools, minimizing potential off-target effects, and performing safety assessments based on the altered DNA sequences.

Graduate Research Assistant — Houston, TX
Rice University — *Jan. 2016 – May 2020*

· Perform analysis for personalized CRISPR-Cas9 off-target effect and mutagenesis pattern profiling.
· Utilize multiplexed CRISPR-Cas9 system to introduce mutation and measure perturbation level for moderate-throughput fine-mapping casual genome variants.

Undergraduate Research Assistant — Houston, TX
Rice University — *Jul. 2014 – Aug. 2015*

· Perform analysis on influenza B evolution and predict influenza B vaccine effectiveness.

RESEARCH EXPERIENCE

Biomarker discovery for novel targets in tumor stroma — Boston, MA
Supervisor: Dr. Andrey Loboda — *Nov. 2020 – Present*

· Created analytical framework for integrating bulk RNA-seq and scRNA-seq data of tumor microenvironment
· Analyzed stroma subsets for biomarker identification; Performed tumor-specific association and survival analysis for prioritizing biomarkers

Off-Target Analysis for Personalized CRISPR-Cas9 gRNA Designs — Houston, TX
Supervisor: Dr. Gang Bao — *May 2017 – Nov. 2020*

· Performed experimental genome-wide off-target screening in 5 individual lymphoblastoid cell lines, which proved that individual variants could alter CRISPR-Cas9 targeting profiles

- Developed bioinformatics tool for variant aware off-target screening and annotation-based ranking
- Compared the performance of existing CRISPR-Cas9 off-target scoring algorithms and proposed a novel deep-learning algorithm for CRISPR/Cas9 off-target risk assessment

Consequences Profiling of CRISPR-Cas9 Mediated Genome Editing Houston, TX
Supervisor: Dr. Gang Bao *May 2019 – Nov. 2020*

- Developed Illumina short read platform based assay (LongAmp-seq) to profile on-target CRISPR-Cas9 mutagenesis patterns, which revealed up to 31% large deletions that were previously missing from the gold standard amplicon short-range Next-Generation Sequencing(NGS)
- Established pipeline for high-throughput profiling of editing consequences, including symmetric and asymmetric large deletions, insertions and chromosomal rearrangements
- Explored bioinformatics options to overcome the potential bias and errors from PCR and sequencing to achieve quantification

Genome Editing based Fine-Mapping within eQTL Credible Intervals Houston, TX
Supervisor: Dr. Gang Bao. In collaboration with Dr. Gregory Gibson *Dec. 2016 – May 2020*

- Combined multiplex CRISPR-Cas9 genome editing with single cell RNAseq to measure perturbation in transcript abundance for fine-mapping causal genomic variants with moderate throughput, which successfully identified two causal SNPs by screening 67 targets in parallel
- Performed genome editing and cell line preparation in low throughput (single-cell clone) and moderate throughput (lenti-virus library), with experimental and computational validation in editing efficiencies and transcript abundance variations

Unbiased Genome-Wide Off-Target Site Detection Assay Houston, TX
Supervisor: Dr. Gang Bao *Jan. 2016 – Jun. 2018*

- Established assays for unbiased in-cellular genome-wide CRISPR off-target site detection, which had over 30-fold signal enrichment for on-target sites
- Explored the potential of using chromatin immunoprecipitation(ChIP) and click-chemistry for the labeling of CIRSPR/Cas9 off-target sites and examined options for signal enrichment and background removal

Prediction of Influenza B Vaccine Effectiveness from Sequence Data Houston, TX
Supervisor: Dr. Michael W. Deem *Jul. 2014 – Aug. 2015*

- Refined the antigenic determinant model of the influenza B virus based on its evolution from 1960 to 2014 for better annual flu vaccine design
- Established an estimate of flu B vaccine effectiveness against a range of viral strains based on antigenic distance, which outperformed the gold standard HI assay based on 1979-2014 epidemiology data

PUBLICATIONS

Journal Articles

Pan, Y., Tian, R., Lee, C., Bao, G., and Gibson, G. (2020). Fine-mapping within eQTL Credible Intervals by Expression CROP-seq. *Biology Methods and Protocols*.

Bao, X. R., **Pan, Y.**, Lee, C. M., Davis, T. H., and Bao, G. (2021). Tools for experimental and computational analyses of off-target editing by programmable nucleases. *Nature protocols 16*, 10–26.

Pavan, K., **Pan, Y.**, Vu, H.-A., Cao, M., Baraniuk, R. G., and Bao, G. (2021). The Need for Transfer Learning in CRISPR-Cas Off-Target Scoring. *bioRxiv*.

Tian, R., **Pan, Y.**, Etheridge, T. H., Deshmukh, H., Gulick, D., Gibson, G., Bao, G., and Lee, C. M. (2020). Pitfalls in Single Clone CRISPR-Cas9 Mutagenesis to Fine-map Regulatory Intervals. *Genes 11*, 504.

Park, S. H., Cao, M., **Pan, Y.**, Davis, T., Saxena, L., Deshmukh, H., Fu, Y., Todd, T., Sheehan, V., and Bao, G. (2022). Comprehensive analysis and accurate quantification of unintended large gene modifications induced by CRISPR/Cas9 gene editing. *Science Advance - In press.*

Sharma, R., Dever, D. P., Lee, C. M., Azizi, A., **Pan, Y.**, Camarena, J., Köhnke, T., Bao, G., Porteus, M. H., and Majeti, R. (2021). The TRACE-Seq method tracks recombination alleles and identifies clonal reconstitution dynamics of gene targeted human hematopoietic stem cells. *Nature Communications 12*, 1–12.

Pan, Y., and Deem, M. W. (2016). Prediction of influenza B vaccine effectiveness from sequence data. *Vaccine 34*, 4610–4617.

Conference Proceedings

Pan, Y., Lee, C., Deshmukh, H., and Bao, G. In *MOLECULAR THERAPY*, 2020; Vol. 28, pp 456–457.

Park, S. H., **Pan, Y.**, Davis, T., Deshmukh, H., and Bao, G. In *MOLECULAR THERAPY*, 2020; Vol. 28, pp 228–228.

Dever, D. P., Sharma, R., Lee, C. M., Aziz, A., Koehnke, T., Camarena, J., **Pan, Y.**, Zhao, F., Bao, G., Majeti, R., et al. In *MOLECULAR THERAPY*, 2019; Vol. 27, pp 5–5.

SELECTED PRESENTATIONS

Pan Y., Zhang C., Nebozhyn M., Loboda A, et al. "Integration of bulk and single cell RNA-seq data to characterize reproducible subtypes of fibroblasts across tumor types" Mechanisms and Models of Cancer – Aug. 2022, Poster presentation

Pan Y., Lee C. and Bao G. "Personalized off-target analysis of CRISPR-Cas9 gRNA designs using *in-silico* and experimental approaches." BIOE Innovation Symposium – Houston, TX, Oct. 2019, Podium presentation

Pan Y., Lee C. and Bao G. "*in-silico* design of CRISPR/Cas9 guide RNA for personalized medicine." BMES Annual Meeting - Phoenix, AZ, Oct. 2017, Podium Presentation

AWARD AND HONOR

Technical reviewer of book *Essential Statistics for Non − Stem Data Analysis*, 2020

Scholarship from the Summer Institute in Statistical Genetics of University of Washington, Jul. 2017

Best poster award in Precision Genome Editing Symposium, Houston, TX, Nov. 2016

RELEVANT SKILLS

Computation: Proficiency in MATLAB, R, Python and shell scripting. Experience in machine learning, deep learning and multi-omics data mining; NGS data processing including bulk RNA-seq and scRNA-seq, Nanopore and PacBio data; statistical modeling, data integration and biomarker discovery in Linux high performance computing environments.

Experiment: Oncology, Immunology, Cell and Molecular Biology techniques. Applications of CRISPR-Cas9 system, NGS library preparation and lenti-virus library production.