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**EDUCATION****George Washington University| Bioinformatics (Master)****AUG 2018–MAY 2020**

Course Keynote:

**GPA: 3.61**

Major: Bioinformatics, Next Generation Sequencing, Big data, Biochemistry, Medical Genome

Tools: Database, Python, Linux, R, NGS analysis

**China Agricultural University| Biological Science (Bachelor)****SEP 2013–JUL 2017**

Course Keynote:

**GPA:3.24**

Major: Biochemistry, Molecular Biology, Biology of Microorganisms, Microbial Genetics

Tools: Bioinformatics, Document Retrieval, C Programming Languages

Lab: Biology of Microorganisms Experiment, Biochemistry Laboratory, Cell Biology Laboratory

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**RESEARCH EXPERIENCE****Improve the pipeline and algorithm for the SPLIT-seq analysis****Advisor: Wei Li| Children's National Hospital****DEC 2019–Still Attending**

- Collaborated with Teng Fei's Lab, Northeastern University in China, to improve the current pipeline for the SPLIT-seq analysis.
- Developed the algorithm and made it more suitable for the data structure of SPLIT-seq.

**Building an Epigenome-TFs-Transcriptome Network on Mouse ESCs CROP-seq Dataset****Advisor: Wei Li| Children's National Hospital****JUN 2019–Still Attending**

- Collaborated with Jin Zhang's Lab, Zhejiang University in China, to applied Single-cell CRISPR screening on mouse ESCs with naïve and primed state.
- Applied scMAGeCK on the dataset to identify the strong epigenetic factors whose knockout could still maintain self-renewal ability without 2i/LIF.
- Used the trajectory analysis to validate the function of potential epigenetic factors that affect the differentiation.

**Developed Novel Bioinformatics Methodology for Single-Cell CRISPR Screening****Advisor: Wei Li| Children's National Hospital****DEC 2018–DEC 2019**

- Used the Robust Rank Aggregation (RRA) and the linear regression (LR) based approach to detect regulatory relationship of gene expressions from cells with perturbations in the Single-Cell level.
- Developed scMAGeCK. Validation by applying it on the public CROP-seq dataset such as breast epithelial cells (MCF10A), unstimulated and stimulated primary human T Cell and myelogenous leukemia cells (K562) for further analysis.

**Performed Next Generation Sequencing Analysis Using Existing Bioinformatics Tools (Full Time)****Advisor: Wei Li| Children's National Hospital****MAY 2019–AUG 2019**

- Used current pipeline (10x genomics, Seurat, Monocle, Scanpy, etc.) combined with scMAGeCK, to analyze Single-Cell CRISPR screening data.
- Fulfilling bioinformatics analysis requests from the collaborators.

**Gene Function of Electron Transport in *Paenibacillus polymyxa* WLX78****Advisor: Sanfeng Chen | China Agricultural University****JUL 2016–AUG 2017**

- Reconstructed of plasmid vector of PET28b with synthetic gene, then introduced to *E. coli*.
- Screened successfully introduced strains and cultured.
- The synthetic plasmid was introduced into *Saccharomyces cerevisiae* by electroporation.
- Protein induction, extraction, isolation, validation.

**Associated with Nitrogen-fixation, Expression of *nif* Genes from *S. cerevisiae* Genome****Advisor: Sanfeng Chen | China Agricultural University****FEB 2017–JUN 2017**

- Used gene-editing methods to engineer N<sub>2</sub>-fixing cereals, integrating *nif* genes into the genome of *Saccharomyces cerevisiae*.
- Used galactose as the sole carbon source triggers bidirectional promoter GAL1-10p with galactose regulation to express *nifS*, *nifU* genes in the anoxic growth conditions.
- Purified ferritin from *S. cerevisiae*.

**Microbes on Plant Pathogenic Bacteria****NOV 2014–APR 2015****Advisor: Sanfeng Chen | China Agricultural University**

- Cultured *Paenibacillus polymyxa* with common plant pathogens covering *Piricularia oryza*, *Giberella zeae* et al, on the same substrate.
- Identified the antifungal activity of strains for different plant pathogenic fungi.

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**PUBLICATIONS**

1. Yang, L., Zhu, Y., Yu, H. *et al.* scMAGeCK links genotypes with multiple phenotypes in single-cell CRISPR screens. *Genome Biol* **21**, 19 (2020). <https://doi.org/10.1186/s13059-020-1928-4>
2. Chen, S., Yang, L. & Li, W. CRISPR Screening “Big Data” Informs Novel Therapeutic Solutions. *Cris. J.* (2019). doi:10.1089/crispr.2019.29062.sch

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**RELEVANT EXPERIENCE****Peer-review:** ISBRA Conference**Attendance at conferences:** RECOMB

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**SKILLS**

- Bioinformatics Skills: R, Linux, Python, NGS analysis, BLAST, Chimera
- Experimental Skills: DNA and RNA Extraction, PCR, Western Blot, SDS-PAGE