KAI LI

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WORK EXPERIENCE

Baylor College of Medicine   Dec 2018 - Present
Bioinformatics Programmer Breast Center   Houston

- NeoFlow project: took responsibility to develop and mantian this proteogemonics data analysis pepline based on NextFlow.
- Clinical Proteomic Tumor Analysis Consortium (CPTAC) projects: applied NeoFlow to predicate neoantigens and find RNA or protein evidences. Untill now, NoeFlow was applied on five cancer projects in CPTAC.
- Eveluation of different quality control methods for variant peptide identification in proteogenomics: took in charge of data analysis and data interpretation. The recommended strategy was implemented in NeoFlow to support proteogenomics-based neoantigen prioritization, enabling more sensitive discovery of putative neoantigens.
- DeepRescore project: took responsibility of data analysis, data interpretation and workflow development. To improve peptide identification in immunopeptidomics, two deep learning-derived features as indicators of PSM quality were combined them with other previously used features for PSM rescoring in DeepRescore. DeepRescore increased both the sensitivity and quality of MHC-binding peptide and neoantigen identifications compared to existing methods.

BGI-Shenzhen   Jun 2017 - Oct 2018
Bioinformatician Bioinformatics platform, MS department   Shenzhen

- PDV project: took in charge of coding of this software using Java. The goal of this project was to develop an integrated proteomics data viewer. The functions including database searching results visualization, denovo sequencing results visualization, proteogenomics files (proBAM and proBED) visualization, public database data visualization and MS/MS data visualization. In addition, it also provides a GUI to proteoQC for data quality analysis. PDV is platform-independent and can be used through both GUI and command line modes.
- PDV applications: generated spectra annotation figures using PDV for several projects, including published paper (PMID: 29222161) and unpublished projects.

BGI-Shenzhen   Mar 2016 - May 2017
Bioinformatician (Internship) Bioinformatics platform, MS department   Shenzhen

- SWATH-expert project: took in charge of developing a GUI tool for XIC extraction and visualization for large scale SWATH dataset using Java language. It was a part of SWATH-expert which is a new tool for SWATH data analysis. This was a collaboration with Dr. Tiannan Guo from the laboratory of Dr. Ruedi Aebersold in ETH Zurich.
- Explored applications of the cutting-edge deep learning in proteomics data analysis. Predicated the peptide phosphorylation sites by convolutional neural networks (CNNs) based on MXNet.
- Learned to use Nextflow to build pipeline for RNA-Seq and Exon-Seq data analysis.

EDUCATION

Qingdao University (QDU)   Sep 2013 - Jun 2017
Biotechnology (Genomics and Bioinformatics) Bachelor

- GPA: 3.3 / 4.0
- Courses: Molecular Biology, Genomics and Bioinformatics, Python Programming, Data Mining, Data Structure and Algorithm Basics, Database System, Operating System, Digital Image Processing, Bioinformatics Algorithm etc.

BGI College   Mar 2016 - May 2017

- Courses: Statistic Applied in Bioinformatics, New Technology of Genomics, Bioinformatics Technology

Missouri State University (MSU) Springfield MO U.S.   Sep 2015 - Dec 2015

- Courses: Microbiology, Cellular Biology, Biology experiments training

HONORS & AWARDS

Outstanding graduate student of Shandong Province (5%)	June.2017
Third class scholarship in BGI College (7/71).	2016 - 2017
Model Student of Academic Records in QDU (1/19)	2015 - 2016
1st prize of China High School Biology Olympiad (Shandong Province division 3‰)	2011

LEADERSHIP EXPERIENCE

Art Work   Oct 2015
Leader of China exhibition area   Springfield MO U.S.

- Art Work was an official exhibition in the downtown in Springfield MO. Led a team of 15 members and took one week to collect materials, design and decorate the exhibition area and attracted more than 500 local visitors.

PUBLICATIONS

- **Kai Li**, Antrix Jain, Anna Malovannaya, Bo Wen*, Bing Zhang*. DeepRescore: leveraging deep learning to improve peptide identification in immunopeptidomics (under revision).
- Wen, B., **Li, K.**, Zhang, Y., & Zhang, B. (2020). Cancer neoantigen prioritization through sensitive and reliable proteogenomics analysis. *Nature communications*, *11*(1), 1-14.
- **Li, K.**, Vaudel, M., Zhang, B., Ren, Y., & Wen, B. (2019). PDV: an integrative proteomics data viewer. *Bioinformatics*, *35*(7), 1249-1251.
- Full publication list in page 2.

MISCELLANEOUS

- **Skills:** Java, Linux, R, Python, AWS
- **Languages:** Chinese (Native), English (TOEFL: 91)
- **Conference:** Speaker on ASMS(American Society for Mass Spectrometry) 2020 Reboot
- **Activities:** AWSome Day for AWS training (Student), BGI Life Periodic Plan (Principal of dasypodidae)