Ping Luo

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Status: Permanent Resident

Research Experience

Postdoctoral Fellow (algorithm design) at Dr. Trevor Pugh's lab   Nov 2019 - present
in Princess Margaret Cancer Centre

Early diagnose cancer based on cell-free DNA

- I designed a bootstrapping-based algorithm to identify high-quality cancer-specific markers from the blood cell-free DNA sequencing data, which could be used to non-invasively early diagnose cancers for patients with hereditary cancer syndromes (>90% lifetime risk to develop various types of cancers). Machine learning models trained with these markers achieved high prediction performance (>0.90 sensitivity).
- Our study (Wong & Luo et al., 2023, under revision at *Cancer Discovery*) is the first one that uses multi-view plasma sequencing data to predict cancers for patients with hereditary cancer syndromes. Our multimodal prediction yielded an impressive 31.66% to 55.8% improvement in accuracy compared to individual sequencing analyses.
- The pipeline I designed for predicting cancers were applied to 4 collaborative projects including 6 types of cancers and gained satisfactory performance (mean AUC>0.90). Collaborative skills were obtained through working with oncologists, pathologists, and pediatricians.

Study the tumor microenvironment with single cell data

- I co-led a team that conducted a comprehensive evaluation of 26 cell type prediction algorithms on 8 cancer datasets and provided benchmarking and recommendations for annotating cells in the tumor microenvironment. This study resulted in a co-first author publication (Christensen & Luo et al.) in *Briefings in Bioinformatics*.

- I collaboratively designed algorithms to study the tumor microenvironment of patient with bone marrow cancer and identified mechanisms related to longer survival. The manuscript was recently accepted by *Nature Communications*.

Doctoral student in University of Saskatchewan   Sep 2015 - Sep 2019

Predict disease-associated genes with artificial intelligence

- I Improved the accuracy of disease gene prediction by designing deep learning-based algorithms to integrate multi-omics data. The designed methods extracted cross-modality features, resulting in an enhancement of 10% to 20% in terms of AUC and AUPR compared to existing algorithms.

- I published 6 lead-author manuscripts in esteem journals such as *Bioinformatics*.

Master student in Beijing Institute of Technology   Sep 2013 - Jun 2015
Develop a micro-stereotactic system for Deep Brain Stimulation

- I designed a software tool that could build personalized 3D printed frames based on patients' MRI and CT images, which significantly reduce the cost of Deep Brain Stimulation surgery.

Teaching Experience

Teaching Assistant at the Bioinformatics.ca   Jul 2023

- Amazon Web Services (AWS) and Unix Basics (1 day)

  Taught students connect their laptops to AWS through personalized assistance.
  Provided guidance on Unix commands, established a strong foundation for
  subsequent workshops and skill development.

- Single cell RNA-seq Analysis (2 days)

  Facilitated students' success in single-cell analysis labs by providing hands-on assistance in resolving errors and delivering explanations for the functions and packages employed.

Guest Lecturer at Thomson River University   May 2021

- Introduction to Bioinformatics

- level: graduate, time: 60 min, size: 9 students

  I was invited to give a talk on the methods used in single cell analysis and prepared a 30-slide presentation with frequent breaks for students to ask questions. Students showed great enthusiasm in machine learning models and their application on single cell analysis.

Teaching Assistant at University of Saskatchewan   2017 - 2019

- General Engineering 124 & 125 (GE124 & GE125)

- level: undergraduate, time: 3 h lab, 2 h marking (weekly), size: ~100 students

  In the lab, I helped students apply the principles of statics to solve practical problems, which involved friction, trusses, machines, etc. Students needed to take a quiz in each lab, and I was responsible for marking the quiz and explaining the problems at the beginning of the next lab. I obtained positive feedback from students in GE124 and was invited to work in GE125.

Education

Ph.D. in Biomedical Engineering   Sep 2015 - Sep 2019
University of Saskatchewan, Saskatoon, Canada
Thesis: "Identifying disease-associated genes based on artificial intelligence"
M.Eng. in Biomedical Engineering   Sep 2013 - Jun 2015
Beijing Institute of Technology, Beijing, China
Thesis: "An algorithm to create 3D-printed stereotactic
frames for Deep Brain Stimulation"
B.Eng. in Computer Science   Sep 2006 - Jun 2010
Hunan University, Changsha, China

Professional Association

Program Committee Member   2021 - present

IEEE International Conference on Bioinformatics and Biomedicine (BIBM)

Selected Publications

Journal

Wong, D. *****, **Luo, P. *** ..., & Pugh, T. (2023). Integrated analysis of cell-free DNA for the early detection of cancer in TP53-mutation carriers. *Cancer Discovery*, Under revision. Co-first author.

Christensen, E *****, **Luo, P. *** ..., & Shooshtari, P. (2023). Evaluation of single-cell RNAseq labelling algorithms using cancer datasets. *Briefings in Bioinformatics*, 24(1), bbac561. Co-first author.

Wong, D., **Luo, P.**, ..., & Pugh, T. (2023). Integrated, longitudinal analysis of cell-free DNA in uveal melanoma. *Cancer Research Communications*, 3(2), 267-280.

Coffey, D. G., Maura, F., Gonzalez-Kozlova, E., Diaz-Mejia, J., **Luo, P.**, ... & Landgren, O. (2022). Immunophenotypic correlates of sustained MRD negativity in patients with multiple myeloma. *Nature Communications*. Accepted.

Luo, P., Chen, B., Liao, B., & Wu, F. X. (2021). Predicting disease-associated genes: Computational methods, databases, and evaluations. *Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery*, 11(2), e1383.

Luo, P., Li, Y., Tian, L. P., and Wu, F. X. (2019). Enhancing the prediction of disease-gene associations with multimodal deep learning. *Bioinformatics*, 35(19), 3735-3742.

Luo, P., Ding, Y., Lei, X., and Wu, F. X. (2019). deepDriver: predicting cancer driver genes by convolutional neural networks. *Frontiers in Genetics*, 10, 13.

Luo, P., Xiao, Q., Wei, P. J., Liao, B., and Wu, F. X. (2019). Identifying disease-gene associations with graph-regularized manifold learning. *Frontiers in Genetics*, 10, 270.

Tian, L. P. *****, **Luo, P. ***, Wang, H., Zheng, H., and Wu, F. X. (2018). CASNMF: A converged algorithm for symmetrical nonnegative matrix factorization. *Neurocomputing*, 275, 2031-2040. <u>Co-first author</u>.

Luo, P., Tian, L. P., Ruan, J., and Wu, F. X. (2017). Disease gene prediction by integrating PPI networks, clinical RNA-Seq data and OMIM data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 16(1), 222-232.

Conference and Presentation

Luo, P. (Jun 2023), Integrated analysis of cell-free DNA for the early detection of cancer in TP53-mutation carriers, *Terry Fox retreat for Li-Fraumeni syndromes*, presentation, 20 minutes.

Luo, P. (Apr 2022), Tumor detection for LFS patients by cfMeDIP-seq, *Terry Fox meeting for Li-Fraumeni syndromes*, online, presentation, 1 hour.

Luo, P., Tian, L. P., Chen, B., Xiao, Q., and Wu, F. X. (June 2018). Predicting gene-disease associations with Manifold learning. In *14th International Symposium on Bioinformatics Research and Applications (ISBRA)*, (pp. 265-271), Beijing, regular paper.

Luo, P., Tian, L. P., Chen, B., Xiao, Q., and Wu, F. X. (April 2018). Predicting disease genes from clinical single sample-based PPI networks. In *International Conference on Bioinformatics and Biomedical Engineering (IWBBIO)*, (pp. 247-258), Granada, regular paper.

Luo, P., Tian, L. P., Ruan, J., and Wu, F. X. (December 2016). Identifying disease genes from PPI networks weighted by gene expression under different conditions. In *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, (pp. 1259-1264). Shenzhen, regular paper.

A complete list of publications is available at [Google Scholar](#).