Ping Luo

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Status: Permanent Resident

Research Interest

I'm interested in integrating multi-view biological data with cutting-edge deep learning models to facilitate the development of new cancer diagnosis and treatment strategies. In terms of diagnosis, I would focus on the analysis of cell free DNA and present a pan-cancer model that integrates multiple types of sequencing data obtained from the blood. As for cancer treatment, I am intrigued by the integration of single cell sequencing and T cell receptor sequencing data and will apply graphical model to predict T cell receptors (TCRs) that recognize tumor antigens, which will promote the development of new TCR-engineered T cell therapies.

Research Experience

Bioinformatics Specialist at Dr. Tak Mak's lab Sep 2023 - Present
in Princess Margaret Cancer Centre

Treatment design based on T cell receptor

- I apply machine learning models to analyze single cell RNA sequencing and TCR sequencing data to predict TCRs that recognize tumor antigens. Candidate TCRs validated in mouse model can be used to develop new TCR-T therapies.

Postdoctoral Fellow (algorithm design) at Dr. Trevor Pugh's lab Nov 2019 - Sep 2023
in Princess Margaret Cancer Centre

Early diagnose cancer based on cell-free DNA

- I designed an algorithm to non-invasively diagnose cancers for patients with hereditary cancer syndromes (high lifetime risk to develop various types of cancers). The algorithm identified high-quality cancer-specific markers known as differentially methylated regions (DMR) from the blood cell-free DNA, and machine learning models trained with these markers achieved high prediction performance (AUC>0.86). Our study (Wong & Luo et al., 2023, *Cancer Discovery*) is the first to use multi-view plasma sequencing data to predict cancers in patients with Li-Fraumeni syndromes. In addition, I am leading an innovative study focuses on advancing cancer diagnosis for patients with hereditary breast and ovarian cancer syndrome. A new algorithm is developed in this study to improve sensitivity and specificity. The manuscript is currently in preparation.
- I designed an ensemble model that used various types of fragment features learned from plasma whole genome sequencing data to predict cancers. The manuscript is under revision at *Nature Genetics*.
- The pipeline I designed for cancer prediction were applied to 4 collaborative cancer studies (>650 samples) and achieved satisfactory performance (mean AUC>0.95). I gained collaborative skills through working with oncologists, pathologists, and pediatricians.

Study the tumor microenvironment with single cell data

- I co-led a study that provided benchmarking and recommendations for annotating cells in the tumor microenvironment. In this study, I conducted a comprehensive evaluation of 26 cell type prediction algorithms on 8 cancer datasets and published a co-first author manuscript (Christensen & Luo et al.) in *Briefings in Bioinformatics*.
- I collaboratively designed algorithms to study the tumor microenvironment of patients with multiple myeloma (bone marrow cancer) and identified mechanisms related to longer survival. The manuscript (Coffey et al., 2023) is published in *Nature Communications*.

Doctoral student in University of Saskatchewan Sep 2015 - Sep 2019

Predict disease-associated genes with artificial intelligence

- I designed several algorithms to integrate multi-omics data and extracted cross-modality features to improve the accuracy of predicting disease-associated genes.

- My deep learning-based methods (Luo et al., 2019, *Bioinformatics* & 2019, *Frontiers in Genetics*) were the first two algorithms that applied these models to predict disease-associated genes and together have been cited over 120 times.

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 built personalized 3D printed frames based on patients' MRI and CT images to reduce the cost of Deep Brain Stimulation surgery.

Teaching Experience

Sessional Lecturer at Algoma University Fall - Winter 2023

- Introduction to Computer Science
- level: undergraduate, time: 3 hours (lecture), 1.5 hours (lab), weekly
  I instructed a total of 180 students, encompassing one lecture and five labs, fostering an interactive learning atmosphere that stimulated critical thinking, problem-solving, and proficient coding skills. Developed and administered course content, assignments, quizzes, and offered tailored feedback to enhance students' technical capabilities, with a focus on topics such as loop, recursion, and object-oriented programming. The average rating from students providing feedback for the labs I taught in the 2023 Fall term is 5 (strongly agree).

Teaching Assistant at Bioinformatics.ca Jul 2023

- Single cell RNA-seq Analysis
- level: graduate, time: 2 days, size: 30 students
  I Led single-cell analysis workshops, enhancing student proficiency in analysis pipelines and tool functions; achieved a 94% high satisfaction rate through effective hands-on assistance and clear, tailored explanations.

Guest Lecturer at Thomson River University May 2021

- Introduction to Bioinformatics
- level: graduate, time: 1 hour, size: 9 students
  I delivered a talk on single-cell analysis methods, engaging students through a comprehensive 30-slide presentation interspersed with interactive Q&A sessions, successfully sparking heightened enthusiasm in machine learning and single-cell analysis.

Teaching Assistant at University of Saskatchewan 2017 - 2019

- General Engineering 124 & 125 (GE124 & GE125)
- level: undergraduate, time: 5 hours (weekly), size: ~100 students
  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). Early cancer detection in Li-Fraumeni Syndrome with cell-free DNA. *Cancer Discovery*, https://doi.org/10.1158/2159-8290.CD-23-0456, 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. (2023). Immunophenotypic correlates of sustained MRD negativity in patients with multiple myeloma. *Nature Communications*, 14(1), 5335.

Wong, D., **Luo, P.**, ..., & Pugh, T. (2023). Cell-free DNA from germline TP53 mutation carriers reflect cancer-like fragmentation patterns. *Nature Genetics*, *Under revision*.

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. Co-first author.

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.