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| 接收器房屋信封**Wei, Ning-Huang**  [louis840404@gmail.com](mailto:ddlockerwu@gmail.com) (+886) 970-549-951 Kaohsiung, Taiwan | |
| **Education** | |
| **National Yang Ming Chiao Tung University (NYCU)**  Master of Biomedical Information (Bioinformation group)  **National Central University (NCU)**  Bachelor of Life Science | **2017.09 – 2020.08**  **2013.09 – 2017.06** |
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| **Work experience** | |
| **Software Engineer, MPI CO., LTD.**   * Semiconductor equipment software development (wafer inspection function, machine control, and UI design). * Importing customer requirements and troubleshooting.   **Summer Internship, CRYOCORD Sdn Bhd.** | **2021.11 – Present**  **2020.09 – 2021.10** |
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| **Technical skills** | |
| **Programming languages:** Python, C#, .Net, C++, C, R, Git, Data visualization, ILSpy, DnSpy  **Certificates:** ITRI SECS/GEM Communication Technology, Coursera Deep Learning Specialization, TOEIC:790, | |
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| **OJT and Self-Directed Learning** | |  |
| **OJT In MPI**   * SkillTree OOP Workshop (using C#) * ITRI SEMI SECS/GEM Communication Technology Workshop   **Self-Directed Learning**   * Deep Learning – Coursera * Algorithm – self-study * Data Structure – self-study | |  |
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| **Project Achievements** | |  |
| **In MPI**   * **Offline Recipe Editor Tool (In progress)**   Design a tool that can modify recipe parameters without starting AOI software.  Benefits  1. It is expected to save at least 66% of the time to modify the recipe.  2. Support batch editing. | |  |
| **Thesis** | |  |
| **Clustering of immune hot/cold subgroups using the cell populations of tumor infiltrating lymphocytes in cholangiocarcinoma**  Cholangiocarcinoma is a malignant tumor arising from bile duct. The common treatments include surgical resection and chemotherapy, but the outcome is poor. In recent years, cancer immunotherapy has become a promising therapeutic approach for several types of cancers. However, in cholangiocarcinoma, the response rate for cancer immunotherapy is still low. Therefore, it is important to stratify the patients that can potentially respond to these therapies with effective biomarkers. One of the predictive biomarkers for cancer immunotherapy is tumor infiltrating lymphocytes. Here in this study, focused on tumor infiltrating lymphocytes, we would like to construct a simple classification model to identify hot tumors in cholangiocarcinoma. With the RNA-seq gene expression data downloaded from The Cancer Genome Atlas database, a transcriptomic marker-based method, MCP-counter, was used to quantify the population abundance of eight immune cells and two non-immune stromal cells in different samples. Subsequently, the abundances of these cells were then used to cluster the samples into hot or cold tumor subgroup by hierarchical clustering. Furthermore, a classification model was constructed based on principle component analysis. A simple two-gene model which includes MS4A1 (CD20) and CD79A was constructed for classification. The model was then validated using two independent datasets from Gene Expression Omnibus database (GSE107943 and GSE119336). The classification accuracy was 0.967 and 0.867, respectively. Together, we used a bioinformatics approach to construct a simple two-gene classification model to identify hot tumors in cholangiocarcinoma. We also found that B cells may be the dominant infiltrating lymphocytes for hot tumor identification and the identified hot tumors are significantly correlated with tertiary lymphoid structures, indicating that the two-gene model may be a potential predictive biomarker for cancer immunotherapy. Further experiments are needed to investigate if the samples identified as hot tumor by our two-gene model have better response to cancer immunotherapy. Hopefully, the constructed simple model can become validated immunotherapy biomarker that is suitable for clinical practice. | |  |

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| **Autobiography** |

I have graduated from National Central University with a bachelor’s degree in Life Science. In the first half of my college life, I usually do biology or chemistry experiments as other students in my class. In my senior grade, I signed up a course called “Big Data Analysis”, the purpose of this course is to teach students using programing to analyze genome sequencing data. I was highly interested in converting numerical data into easily understood graph and charts, thus I decided to apply for the Institute of BioMedical Informatic at National Yang Ming Chiao Tung University.

During the master’s degree, my main research the main project was to use programming languages (python and R) for data processing and analysis, then used machine learning methods to predict disease-prone groups. The research was also submitted to the Chinese Automatic Control Society (CACS) in October 2020.