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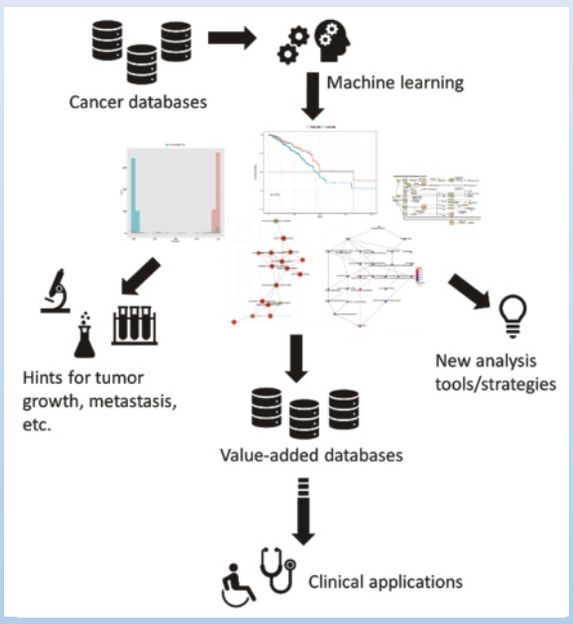
研究興趣

本實驗室研究主題為利用開放癌症基因體資料庫開發預測癌症預後、治療藥物相關之預測工具或相關資料庫。已經有許多癌症疾病相關的定序資料在公開資料庫中，藉由這些資料我們找到了與癌症後期發展相關的生物特徵，近期論文成果包括在2019年二月於*Sci Rep*發表了的TACCO，是個整合型資料庫，提供了TCGA中的25種癌症中的1.差異表現RNA及微小RNA、2.上述差異表現RNA所參與之反應路徑分析、3.可預測癌症分群預測模組、4.可預測癌症預後的預測模組。在2019年七月發表於*The oncologist*的口腔癌研究論文，在這篇論文中我們發現了在口腔鱗狀上皮癌的病人癌組織樣本中MLLT3這個基因的拷貝數在口腔癌病人中常常是增加並伴隨著MLLT3這個基因的表現量上升，進一步的臨床資料分析更發現MLLT3的拷貝數量增加與口腔癌的侵襲性強弱呈現正相關，並且也與病人的整體存活率呈現負相關。



除了癌症研究之外，本實驗室亦參與在許多利用高通量分析技術的合作計畫，藉由開發或利用現有之生物資訊工具協助醫師或研究學者分析並解讀資料。合作計畫近期發表包括在2019年三月發表於Analytica Chimica Acta的論文，我們藉由分析口腔鱗狀上皮癌樣本中的代謝體找出可能具有作為生物標誌潛力的代謝體，分析這些代謝體相關反應路徑的轉錄體資料更發現可以藉由這些轉錄體的基因表現量解釋代謝物量的改變。在2019年五月發表於*Molecular therapy Nucleic acids*的論文，我們利用了微陣列晶片分析結果發現了在A型流感病毒感染宿主細胞後，宿主細胞會被刺激表現miR-1290這一個微小RNA，而這個微小RNA對下游基因的調控則會最終結果則是導致增加A型流感病毒量(virus titer)。

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Research Interests

My research interest is to utilize data from public genomic databases in prediction of cancer prognosis or patient stratification for precision medicine. We used the vast amounts of sequenced data from cancer databases to identify biomarkers or signatures. In addition to cancer research, my lab also actively cooperates with many clinicians and biologists in projects solving biological problems or issues in clinical researches with high throughput technologies and bioinformatic approaches.

Our recent works include:

- We constructed a cancer transcriptome database, TACCO, (http://tacco.life.nctu.edu.tw) is an integrated database providing (1) differentially expressed miRNA/mRNA in tumors, (2) pathways enriched with the differentially expressed genes or targets of the differentially expressed miRNAs, (3) prediction models for cancer classification and (4) prognosis signatures for cancers with various machine learning algorithms. (*Scientific Reports*, February 2019)

- We found that the copy number of MLLT3 is frequently amplified in oral cavity squamous cell carcinoma. The amplification is associated with higher expression level of MLLT3 and poorer overall survival. We also found reduced cell intensiveness and cell migration in MLLT3 knockdown cell line. (*The oncologist*, July 2019)

- Identification of potential metabolites as biomarker in oral cavity squamous cell carcinoma. (*Analytica Chimica Acta*, May 2019)

- With high throughput microarray, we found the host miRNA, miR-1290 is induced after Influenza A Virus infection and the target gene vimentin was downregulated which results in retaining virus ribonucleoprotein in the nucleus and increase of viral titer. (*Molecular therapy Nucleic acids*, March 2019)