**MULTI-OMICS DATA IN THE PREDICTION OF KIDNEY CANCER SUBGROUPS**

**ANNOTATION**

[1] Wu J, Jin S, Gu W, Wan F, Zhang H, Shi G, Qu Y and Ye D (2019) Construction and Validation of a 9-Gene Signature for Predicting Prognosis in Stage III Clear Cell Renal Cell Carcinoma. Front. Oncol. 9:152. doi: 10.3389/fonc.2019.00152

[2] This article introduces a better approach to predicti the status of stage III Renal Cell Carcinoma patients. [3] Common differently expressed genes from 14 pairs of stage III tumor,normal tissue (mRNA expression data ( GSE53757 )) and 16 pairs of mRNA expression data ( TCGA ) were used to train a model.C-index and time-dependent ROC were used as the testing data. [4] This article considered about the common Kidney Cancer subgroups. [5] It used a multi-omics data approach and a machine learning method known as Lasso Cox regression analysis for data analysis. [6] They stated that The accuracy of the model may reduce with different subgroups. [7] This classifier was able to classify stage III RCC patients as low and high-risk categories with what accuracy?. [8] This article is related to our data analyzing approach (multi-omics) with a machine learning model.