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

**ANNOTATION 3**

[1] Eloise Withnell, Xiaoyu Zhang, Kai Sun, Yike Guo, XOmiVAE: an interpretable deep learning model for cancer classification using high-dimensional omics data, Briefings in Bioinformatics, Volume 22, Issue 6, November 2021, bbab315, https://doi.org/10.1093/bib/bbab315

[2] This article introduces a new mavhine learning architecture to increase the accuracy of the classification between different type of cancer. [3] This research aims to increase the accuracy of final observations, the required data was gathered from the UCSC Xena data portal, and a vanilla OmiVAE based interpretable deep learning model was used to analyze data. [4] This research targeted omics data of several cancer variants instead of one cancer with multiple groups. [5] It used an advanced deep learning model to analyze data, where we are targetting to use different machine learning models (Superset of Deep Learning) in our research. [6] This article focused on generalized behavior (Several Cancers) instead of specializing in Kidney cancer. [7] A VAE-based deep learning method is possible to explain the supervised task of the network and to obtain the most important genes of the prediction. [8] This article is related to our data analysis method as they also using omic data in the classification of cancer using machine learning models.