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

**ANNOTATION 4**

(1) Lovino, M., Bontempo, G., Cirrincione, G., Ficarra, E. (2020). “**Multi-omics Classification on Kidney Samples Exploiting Uncertainty-Aware Models**”. In: Huang, DS., Jo, KH. (eds) Intelligent Computing Theories and Application. ICIC 2020. Lecture Notes in Computer Science (), vol 12464. Springer, Cham. <https://doi.org/10.1007/978-3-030-60802-6_4>

(2) In this paper, they proposed a method consisting of a tree-based multi-layer perceptron (MLP), which estimates the class-membership probabilities for classification. (3) The authors downloaded data from Genomic Data Commons (GDC) database for kidney tumor subtypes, selected samples for which all mRNA, miRNA and methylation data are available. Some stomach samples (do not belong to the kidney classes) were obtained from GDC for test the model. They proposed a tree MLP classifier and it was compared with support vector machine (SVM), random forest (RF) classifier, standard MLP and Bayesian neural network (BNN) classifiers to give relevance to all the omics and also to label as *Unknown* those samples for which the classifier is uncertain in its prediction. (4) Their research focused on creating automatic tools to integrate different omics information, which may favor clinical practice. (5) The article is useful to our research topic, as authors used SVM and RF for the same problem and those showed high classification rates. (6) The main limitation of this article is the standard consensus is given by the absence of a measure to check the relevance of each individual omics in the classification. (7) Authors indicated that tree MLP architecture is reliable for classification on the individual omics exploiting uncertainty-aware models. (8) This research is on the same domain and gave an idea about *Unknown* sample’s affect in multi omics.