An integrative computational pathology approach to classify prostate cancer. Combining phenotypical, genomic and tumor microenvironment figures using deep learning.

In 2017, prostate cancer was the second most common cancer in men after lung cancer. Conventionally, it is diagnosed evaluating tissue biopsies and classified according to the Gleason grading system. Novel molecular classifications of prostate cancer have been proposed, however their clinical use is limited due to a number of reasons including their lack of localization information.

The main goal of this work is to implement an automatic tissue classification that takes into account the phenotype, the micro environment and a genomic signature predictive of recurrence to improve the existing grading system.

Modern techniques to classify images keep getting broader and accurate, in particular with the introduction of Convolutional Neural Networks. This approach is clearly different from the traditional classification as it lets the network decide which features are of major discriminative importance.

Therefore, instead of using a classic fully connected layer, we will integrate heterogeneous inputs, at different levels. To avoid normalization mismatches between the data from the phenotype and genomic signature, we introduce them via different layers. The images will serve as an input in the first layer, while the gene expression from the omics and micro environments data will be input in the last layer.

Using that approach, we can classify the image, with respect to the survival rate as to the risk of recurrence, the gold standard of any cancer. Therefore, our method is able to generate an augmented score, enabling a more accurate and personalized diagnosis.