In the vast field of healthcare, there is immense potential for Artificial Intelligence (AI), to assist with clinical applications, such as to study the correlation between disease states and gene expression profiles. These profiles, obtained from multiple tissue samples, can help obtain further insight into the disease pathology by comparing genes expressed in normal vs diseased tissue. This technology can naturally apply to many disease pathologies. One such application has been researched within oncology to help determine the gene expression difference between normal (non-cancerous) tissues vs. cancerous tissues (Fakoor et al., 2013).

Quite a few machine learning (ML) classification techniques were initially utilized to recognize the difference (and therefore, conduct cancer diagnosis and classification accordingly), it wasn't an ideal approach due to the high dimensionality of the gene expression data (feature space) and low availability of samples for a given tumor (limited datasets) (Fakoor et al., 2013).

To combat the above issues, it was proposed to apply unsupervised feature learning and deep learning methods to create such cancer classifiers. Firstly, the Principal Component Analysis (PCA) algorithm was utilized to address the high dimensionality of the initial raw feature space. Then, a sparse autoencoder method was utilized to learn concise feature representation (from data that is not labeled for any one tumor and was instead combed data from different tumor cells sharing the same gene expression). The classifier is then constructed with the resulting features from all the different sets (Fakoor et al., 2013).

Deep Learning, even if the discussion is limited to oncology, will help forward research within the field immensely, which in turn will provide added clinical benefits to patients and clinicians alike. Applying the method described above (while comparing it to the baseline algorithms), the researchers discuss improvements in cancer classification problems while providing a general (and more scalable) approach to work with gene expression data (across various different types of cancer) (Fakoor et al., 2013).

References

Fakoor, R., Ladhak, F., Nazi, A. & Huber, M. (2013) Using deep learning to enhance cancer diagnosis and classification. *Proceedings of the international conference on machine learning* 28: 3937-3949. Available from: https://admis.tongji.edu.cn/_upload/article/files/a1/28/1a8d7ac94b05860e2d1fe6c3bf2a/dffeeaae-5d26-4e84-9b60-42bb4b47ee41.pdf [Accessed 18 April 2024].