One of the most common forms of complex computing takes place in a biological lens. Back in the early 2000’s one of the most ambitious computational feats was the Human Genome Project. Although the project was launched and funded in 1994 it was not considered complete until April 13, 2004. In modern times, the same kind of computation can be done in a fraction of the time, but it does not mean we are not computing more complicated systems. The article I am looking at is discussing how cellular features can be improved with machine learning tactics (<https://www.analyticsindiamag.com/how-cellular-features-improve-ml-accuracy-in-phenotyping/>). This article explores the visualization of microscopic scale objects such as cells.

Although machine learning has been instrumental in automating the gathering and forecasting of data, it fails to utilize the information from calls and tissues. Machine learning only looks at the properties (or features) within the data and does not actually properly analyze cellular features that determine or influence the features have on the wholistic person.

Phenotyping is the process of predicting how biological characteristics are determined by the genetic makeup and environment. Phenotyping has applications in anatomy and histology, or any other kind of biomedical research. One of the largest challenges is creating an algorithm that takes into account both intrinsic and extrinsic factors on molecular levels.

In the case covered in the article, researchers integrated supervised machine learning to extract the environmental variables and test how ‘cellular neighborhood’ affect phenotyping. Random forest, naïve bayes, sequential minimal optimization and multilayer perceptron are all machine learning algorithms used in this study. Researches then looked at two types of data—breast cancer cells treated with two different treatment drugs (MCF-7 Dataset) and the images of tissue sections of cancerous urinary bladders (UCB Dataset).

For the experiments, the scientists used image pre-processing and cellular segmentation methods. And interface is used to allow the operators to segment regions into different classifiers. Once these classifications are created then analysis using the machine learning algorithms are implemented on single cells.