Name: Ulvi Bajarani

Student ID: 20539914

The name of presenter: Dr. Dongchul Kim

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1) "In this context, it is more appropriate to separately evaluate sensitivity (that is, the fraction of enhancers detected) and precision (that is, the percentage of predicted enhancers that are truly enhancers). The balanced classifier described above has a high precision (>99.9%) but a very low sensitivity of 0.5%." [[Source](https://www.nature.com/articles/nrg3920" \l "df25)]

How do classifiers:

a) identify a positive example?;

b) identify the correctness of positive example?;

2) "The first method we propose, IMLARF, consists of three steps. Figure 2a describes the overview of the proposed method. First, a symmetric edge weight matrix M is calculated by mutual information assuming that, if two genes have a higher mutual dependency, they are more likely to be in the regulation relationship." [[Source](https://bmcmedgenomics.biomedcentral.com/articles/10.1186/s12920-016-0202-9/figures/2)]

How about the situation where more than two parameters (genes) have either the same or near mutual dependencies (for example. 0.74 and 0.75: in this case, creating the matrix might lead to erroneous results). In other words, how such problems are solved in machine learning?