

Patient Stratification

Identifying patient subsets in breast cancer



THE AYASDI IMPACT

Ayasdi was able to analyze a thirteen year old data set from the Netherlands Cancer Institute (NKI) and discover missed insights about breast cancer patients. This data set consists of gene expression levels extracted from 272 tumors.

THE PROBLEM

Cancer research involves making sense of complex, high dimensional sets of patient data. Traditional analytical tools for analyzing this data often return simplistic results. The key to improving cancer treatment lies in identifying patient subgroups and exploring the subtle gene relationships that exist within these groups.

In order to extract information from these patient subgroups, we must understand the data from different dimensions. For example, it is not enough to identify that a subgroup of cancer patients have a single gene in common. Instead, it is necessary to know more about the correlations between genes in that subgroup.

THE SOLUTION

Figure 1 below shows the result of an Ayasdi analysis of the data. In this representation we see that there is an interesting shape of the data: a long trunk with two distinct flares. By delving deeper in to those two flares, Ayasdi found that they represented two distinct groups of patients who expressed a certain set of genes (including ESR1) and survived, versus those who had mixed levels of the gene and died.

Figure 2 shows a deeper analysis of the bottom flare in Figure 1. The coloring in this image is important because it shows either high levels of a certain gene (red) or a low level (blue). The separate groups of networks indicate that there are 7 separate groups of patient profiles that have varying levels of a cancer-causing gene. By grouping patient in this way, it becomes easier to delve into the genetic commonalities between members of those separated groups.

Figure 1

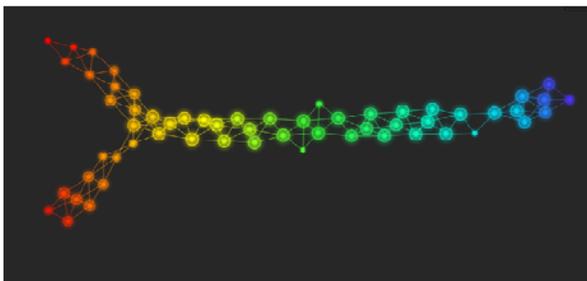


Figure 2

