Optimizing Computing Power in Predicting an Individual's Response to Certain Toxins

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I tried to determine if there was a chromosome that could best predict an individual's response to toxins so that my process could be shortened for future use. I started out with a spreadsheet containing individuals with known cytotoxicity levels, and individuals with unknown cytotoxicity levels. I also had a spreadsheet with all individuals and their single-nucleotide polymorphism (SNP) data for each chromosome. Finally, I had a list of individuals that greatly reacted, and a list of individuals that barely reacted for each toxin. I first performed a student t-test on the SNP data belonging to the high and low reacting individuals to select the biomarker SNP data. This file was further condensed to only include rows comparing an individual with a known cytotoxicity level to an individual with an unknown level. Next, an individual with an unknown level was paired with four individuals with known levels that yielded the highest coefficient of determination. I then either took an average or weighted averaged of the cytotoxicity levels belonging to the top four individuals, giving me my predicted cytotoxicity level. I then compared my predictions to the correct answers by taking the average of how much my predictions deviated from the correct answer for each chromosome. By comparing the averages, I was able to conclude that chromosome 20 predicted best. However, chromosome 3, 19, and X also predicted well, so I was hesitant to say that chromosome 20 was the clear winner. Next I want to see if the toxins had more to do with certain chromosomes and if that helped them predict better.

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