LITERATURE REVIEW: Parallel Computing on Depression Analysis

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1   Introduction

Parallel computing is a suitable answer to deal with enormous data and fit into the speedup requirement. The advantage of parallel computing is to use a collection of processors to attack multitasking on several cores simultaneously[5]. Especially, in the bioinformatics area, in order to approach the relationship between effection and the disease, for this kind of data intensive problems, parallel computing is necessary. But here also comes out another question, for those low resources diseases, is parallel computing still works perfectly?

Personally speaking, the depression disease interests me the most. Not only because an increasing number of people in the world are still suffering from it, but also more and more teens cannot help themselves to escape from this life-long problem. Depression is not the blues, or sadness or simply down, it is also a lasting overwhelming negative.

In this project, I tend to create a high efficient parallel adaptive transfer learning algorithm to study the heart attack and hopefully lead to discovery of the health category directly or indirectly causing depression.

2   Literature Review

The parallel adaptive clustering (PAC) algorithm has been presented to decrease the dataset dimensions. By using the clustering methods to define classes that could separate the irrelevant features and find the latent relationship between data rather than the predefined assumption[5]. However, the algorithm is based on the k-means clustering[7]. Most likely, the more information we have, the more precise models will get. In fact, under the doctor-patient protocols of hospitals, individual privacy, and kinds of social opinion. The training sets are smaller than expected. All the related papers mentioned below had amazing thoughts and controlled experiments, but still not able to have strong evidence to support their theories. Here comes the definition of transfer learning. The model will be built based on the task one, and reused as a start point for the model of the task two[8]. For example, we reused the network trained by distinguish cats and dogs to identify the pictures of chairs and desks. In this way, we could use a large dataset of a random open disease dataset to get a model for analyzing depression. In this way, the algorithms will be improved the standard

k-means clustering algorithm by applying Transfer Learning techniques on it, and do better classification from an unlabeled dataset.

For depression, a novel idea is based on the gut microbiome. As is well known, the human body is a set of microbial organisms[2]. The organs trans information by hormonal readiness to adjust to human health[3][1][4]. Having a clear thought between microbial organisms and human disease will lead to a new area from my perspective. I think there are so many unsolved puzzles because the human brain can't handle huge calculations, but computers can. Taking all variables into account, it is theoretically possible to predict the relationship between things to a certain extent.

The successful previous approach on Crohn's Disease inspired me about the same thing on depression. As for depression, we use antidepressants as the main treatment even though it has powerful side effects. More and more approaches show that microbes in the gut have something to do with this kind of mental disease, but the relationship between them is still unclear. However, probiotics as well as diet treatment are considered as potential choices for people who have depression [1][6].In this project, since I still could not find suitable dataset for this goal, I introduce the datasets of heart attack and depression diseases with normal health-related factors to build transfer learning network. Finding if any normal health indicators work with human mental health.

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