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 affections and the disease, for this kind of data intensive problems, parallel computing is necessary. 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. In this project, I tend to create a high efficient parallel adaptive clustering algorithm to study the gut microbiome and hopefully lead to discovery of the bacteria 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 builded based on the task one, and reused as a start point for the model of the task two[8]. In this way, we could use a large dataset of a random open disease dataset to get a model for analyzing depression.

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 case, finding how microbiome work with human mental health is a crucial task needed to be solved.

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