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A SIGNIFICANCE OF COMPUTATIONAL TECHNIQUES IN HLA TYPING FOR STEM CELL TRANSPLANTATION

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Abstract: Stem cells have the remarkable potential to develop into many different cell types in the body during early life and growth. In addition, in many tissues they serve as a sort of internal repair system, dividing essentially without limit to replenish other cells as long as the person or animal is still alive. When a stem cell divides, each new cell has the potential either to remain a stem cell or become another type of cell with a more specialized function, such as a muscle cell, a red blood cell, or a brain cell. Transplantation is the important process in the medical field where healthy stem cells can be transplanted to the donors who in need of those. The difficulty in stem cell transplantation is finding the donors. HLA typing is the process for finding the unrelated donors for stem cell transplantation. Research on stem cells continues to advance knowledge about how an organism develops from a single cell and how healthy cells replace damaged cells in adult organisms. Stem cell research is one of the most fascinating areas of contemporary biology, but, as with many expanding fields of scientific inquiry, research on stem cells raises scientific questions as rapidly as it generates new discoveries. Data mining is one such field which helps can be incorporated in the various activities of the medical field, thus making it beneficial. The database is used to search for similar genes which in turn help in the process of HLA typing.

Keywords: Stem cells, HLA Typing, Genes, Transplantation.

I. INTRODUCTION

Human leukocyte antigen (HLA) typing is used to match with a donor for transplantation of Stem cells. This is not the same as Blood typing. HLA is a protein or marker found on most cells in the human body. HLA matching is important because a close HLA match

- Increases the likelihood of a successful transplant.
- Improves engraftment—when the donated cells start to grow and make new blood cells in recipient's body.
- Reduces the risk of complications after transplant, especially graft-versus-host disease (GVHD). GVHD is a potentially serious complication. GVHD occurs when the immune cells, which are part of the donated marrow or cord blood, attack the recipient's body.

The primary use for human leukocyte antigen (HLA) testing is to match organ and tissue transplant recipients with compatible donors. It identifies the major HLA genes a person has inherited and the corresponding antigens (proteins) that are present on the surface of their cells. HLA matching is the most important factor but not the only factor that can affect the chances of having a successful transplant.

- The number of blood-forming cells needs to be suitable for the size of the patient. Larger patients need more blood-forming cells. Cord blood units have fewer cells than adult donors. Sometimes, more than one cord blood unit is needed for a patient.
- Different donor characteristics have an impact on a transplant's success. These include the donor's:
    - Age
    - Gender
    - Blood type
    - Body size
    - The number of times a female donor has been pregnant

If more than one well-matched adult donor is found for the recipient, these factors mainly to be consider is the donor's Infection history, it can also affect transplant outcomes and choice of a donor. Transplant centers may face a greater challenge finding a match for some patients because some HLA types are less common. HLA types are inherited, so the best chance of finding a suitable donor may be with someone of a similar racial or ethnic background. Some people have very diverse tissue types that reduce the chances of finding suitably matching donors. The Matching focuses on adding potential donors and cord blood units from diverse backgrounds to the registry so that all patients in need of a transplant can receive one.

II. RELATED WORK

Human leukocyte antigen (HLA) [1] region is the most polymorphic in the human genome, which located on the chromosome 6p21 encodes more than 200 genes.HLA loci are known to influence susceptibility to numerous diseases including complex autoimmune and inflammator diseases, type 1 diabetes, cancers; infectious diseases including malaria, tuberculosis, and AIDS; rejection of hematopoietic stem cell or organ transplants.Next-generation sequencing (NGS) technologies introduced for whole genome sequencing and for quantitation of viral variants or genetic mutations in tumor tissues. Its significant feature is that a large amount of clonal sequences could be generated in a single sequencing run. The significant improvement in NGS make it has great potential to overcome traditional sequencing-based typing, resulted in revolutionary changes in HLA typing. New technologies substantially improve the allele resolution for genotyping and lead to a better understanding of HLA disease association.

Stem cells [2] are the basic building blocks of the body. All the cells in the body are not stem cells; this is a special type of cell, which can rejuvenate themselves with a more specific function, such as blood cells, brain cells, heart muscle or bone. The several sources of stem cells are : Embryonic stem cell, Adult stem cell, Induced pluripotent stem cells, Perinatal stem cells. Transplantation of stem cells helps to save the life of patients. When these cells are shared between unrelated people this will bring drastic changes in the medical field. It will be achieved by connecting all the donor registries for matching, bone marrow worldwide registry is already sustaining for storing these data. The different methods of transplantation are :Autologus , Autogenic , Syngenic ,Allogenic. Allogeneic transplantation there is a need for high chance of donor matching perfectly, because donors are unrelated persons and their stem cells have to be matched with the recipients.The HLA matchmaker is the computer based algorithm to determine donor recipient HLA compatibility. This algorithm is for assessing donor-recipient compatibility that are shared by HLA antigens, so called CREG (Cross reactive antigen groups).Methods for HLA typing are described including serological methods, molecular techniques of Sequence Specific Priming (SSP), Sequence Specific Oligonucleotide Probing (SSOP). These methods are used to decrease the rate of rejection with less side effect and complications.The HLA matching is the only way to match the allogeneic stem cells. In HLA there are two main alleles class I and II, in class I the antigens or genes are HLA-A, -B, -C and minor alleles or genes are HLA-E, HLA-F and HLA-G and in class II the antigens or genes are HLA -DR, -DM, -DOA, -DOB, -DQ and -DP. HLA is inherited as a "Set" of the three HLA groups, A, B, DR. This set is known as a "Haplotype".

Mining the gene expression data [3] for predicting the gene functioning for the possibility of cancerous behavior. This paper proposes innovative incremental fuzzy rules for fuzzy mining algorithm. The algorithm effectively uncover hidden patterns for accurate identification of gene function anomalies related to cancer allowing prompt and accurate detection in early stage and determine if a cell or tissue can go cancerous.

Hematopoietic stem cell transplants (HSCT) [4] are used to correct defects that occur in blood cells by supplanting the patient's hematopoietic stem cells with those derived from donors, so that new healthy blood cells can develop to replace the existing defective blood cells. Over a million hematopoietic stem cell transplants (HSCTs) have been performed around the world for treatment of a range of cancers and hematological indications.

Healthcare organization [5] today are capable of generating and collecting large amounts of data. This increase in volume of data requires automatic way for these data to be extracted and analyzed when needed. Millions of people would like to store cell specimens, for use in all sorts of contingencies. Stem cell research plays a key role in regenerative medicine. Stem cells are the basic building blocks of the body. All the cells in the body are not stem cells; this is a special type of cell, which can regenerate themselves with a more specific function, such as blood cells, brain cells, heart muscle or bone. No other cell in the body has the natural ability to generate new cell types. Stem cell sources need to be identified in human body. The stem cell mostly lives in embryos, bone marrow, regular adult cells reprogrammed into induces pluripotent cells and amniotic fluid.

III. PROPOSED WORK

The algorithm is used to classify the HLA genes into two classes namely class I and class II. This can be done with the help of considering the MHC description which is nothing but the Major Histocompatibility complex which helps in maintaining the immunity in a human being. By using the MHC as a condition we can classify the chromosome 6 genes into two classes. Then it is needed to create a diverse dataset which consists of all the other genes present which comprise of the various protein data. All this classified data is used to create a proper database for the immune data for future use.

Database creation and Database cleaning: The first step of creating any database is to collect proper and useful data and process that data. This includes the ELT process, where the data is cleaned and loaded and transformed into suitable form. This can be further explained by saying that the data is purified by removing the unwanted data and the formats are changed, so that they're all even and then this data is given for the classification process.

Implementation of genetic algorithm: The genetic algorithm is implemented by feeding into the mining tool like Weka or Rapid miner and then this is applied to the training dataset which is then classified into the two classes. The algorithm is thus used to filter the data on the basis of their type.

Classification of chromosome6 genes: The classification of the chromosome 6 genes is done by using a mining tool. In this tool we feed the algorithm that we created and this is applied to the training dataset which is acquired from the database. The data is classified into two classes namely class I and class II and the data which doesn't come under neither is under the diverse data.

Suitable Database for HLA Matching: The classified data tables are used to create a database which is used to check the immunity of any human more easily. This thus simplifies the process as the immunity genes are now gathered to one place and this database helps in achieving that.

Report Generation: Finally the reports are created by using the mining tools. These reports depict the relations and they make it easier to understand the relations between the genes much better.

IV. CONCLUSION

The future work will be increasing the data so that if any gene is identified it can be added. The Database mainly used to identify the unrelated donors for finding the suitable match byusing the techniques of HLA Typing. The attributes essentially needed for HLA Matching is huge in Medical history, those have to be considered completely for further classification in mining algorithms.

V. REFERENCES

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