

Predicting the Fate of Stem Cells with Software

Pathak Darshita S

Computer Engineering,
V.V.P.Engineering College, Rajkot
dsp.pathak@gmail.com

Abstract—This Abstract is a revolution in the field of computer engineering tie-up with biotechnical engineering for developing software which founds the base of stem cell, futures diseases and inherited symptom.

I. INTRODUCTION

This research is about developing the software which interacts through the hardware given to the computer as an input uses inbuilt software provided to the algorithm and logic to it and gives us proper result of it. DNA is the heart part of stem cell which also plays an interactive part during software implementation.

Using advanced computer vision technology to detect subtle cell movements that are impossible to discern with the human eye. But, by allowing the isolation of cells with specific capabilities, this discovery could one day lead to effective methods for growing stem cells on large scale for therapeutic use.

II. APPROACH TOWARDS STEM CELLS

A. Initial Stage

"If you have many cells in a culture, they all look the same. But our new method senses all sorts of tiny differences in the shapes and movements of the cells, and uses these cues to predict what kind of cells it will divide into no of cells. "By doing computer research with stem cell," We believe this method will be beneficial for one day taking cells from a patient, and then growing large amounts of the kind of cells that patient is in need of. This could enable many new and exciting types of medical treatments using stem cells."

Quantitative approaches are essential for the advancement of strategies to manipulate stem cells or their derivatives for therapeutic applications. Predictive models of stem cell systems would provide the means to pose and validate non-intuitive hypotheses and could thus serve as an important tool for discerning underlying regulatory mechanisms governing stem cell fate decisions. In this paper we review the development of computational models that attempt to describe mammalian adult and embryonic stem (ES) cell responses. Early stochastic models that relied exclusively on statistical distributions to describe the in vitro or in vivo output of stem cells are being revised to incorporate the contributions of exogenous and endogenous parameters on specific stem cell fate processes.

B. Method of Working

A single hematopoietic stem cell (HSC) can generate a clone, consisting of daughter HSCs and differentiated progeny, which can sustain the hematopoietic system of multiple hosts for a long time. At the same time, this massive expansion potential must be restrained to prevent abnormal, leukemic proliferation. We used an interdisciplinary approach, combining transplantation assays with mathematical and computational methods, to systematically analyze the proliferative potential of individual HSCs. We show that all HSC clones examined have an intrinsically limited life span. Daughter HSCs within a clone behaved synchronously in transplantation assays and eventually exhausted at the same time. These results indicate that each HSC is programmed to have a finite life span. This program and the memory of the life span of the mother HSC are inherited by all daughter HSCs. In contrast, there was extensive heterogeneity in life spans between individual HSC clones, ranging from 10 to almost 60 mo. We used model-based machine learning to develop a mathematical model that efficiently predicts the life spans of individual HSC clones on the basis of a few initial measurements of donor type cells in blood. Computer simulations predict that the probability of self-renewal decays with a logistic kinetic over the life spans of a normal HSC clone. Other decay functions lead to either graft failure or leukemic proliferation. We propose that dynamical fate probabilities are a crucial condition that leads to self-limiting clonal proliferation.

C. Methodology for Coding

In the initial part of programming the algorithm is first developed and based on the time parameter the DNA is detected by the slide made with the molecules of the human cells. Then the software will detect the part of the stem cell from the DNA. The Software will find the stem as per we have implemented the coding into the software. This software will find the appropriate stem cell according to the code AGCT-DNA code.

According to this parameter the human being are found in the category of living things means either the mammals and non-mammals. As per this the identification of the stem cell will be covered in the code.

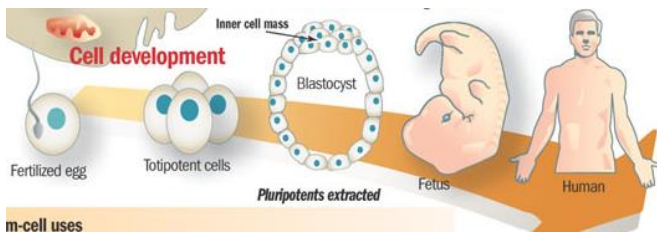


Figure 1. Fundamental Chain Of Human Birth

III. DNA

The human beings are identified their DNA cells which come from their inherited human being. This proves come from their inherited human being. This proves you that you that you are range from that group of people

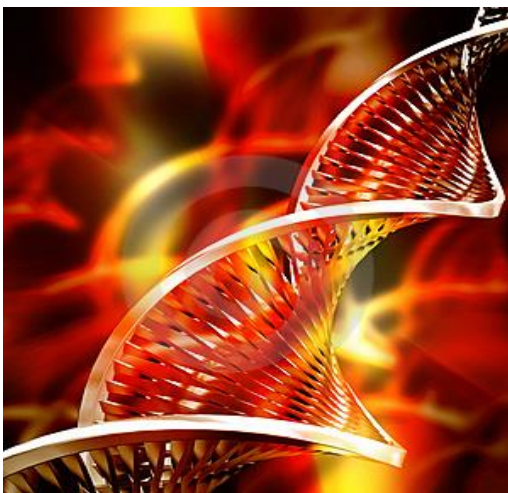
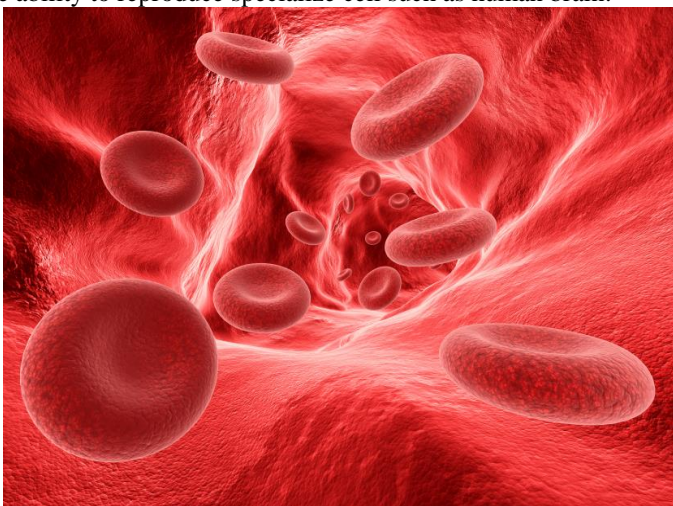


Figure 3: Cyclic Structure Of DNA

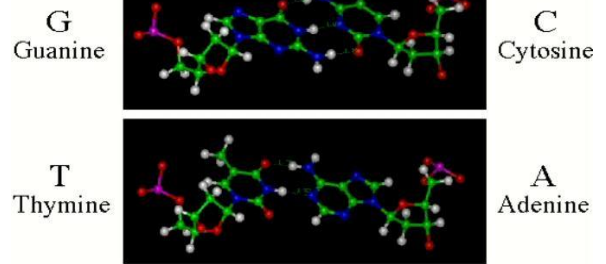
IV. STEM CELLS

Stem cell is the nucleus of DNA which shows the functionality of the particular part of the human body behavior. Stem cells the ability to reproduce specialize cell such as human brain.



V. IDENTIFICATION OF DNA AND STEM CELLS

Information Storage in DNA



- Information stored in DNA duplex as CG or AT base pairs
- Maximum information density of 2 bits per DNA base location

Figure 2 De-Cyclic Formation of DNA

The DNA is identified by the information stored in it. The multiplexing of the code is then combining in the different format such as the CAACGT and GTAAC etc.

Thus from the identification go through the Stem cell identification and produce a level of the code based on the biotechnical-methodology.

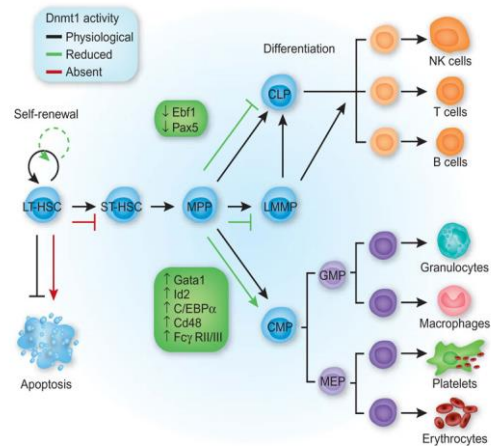
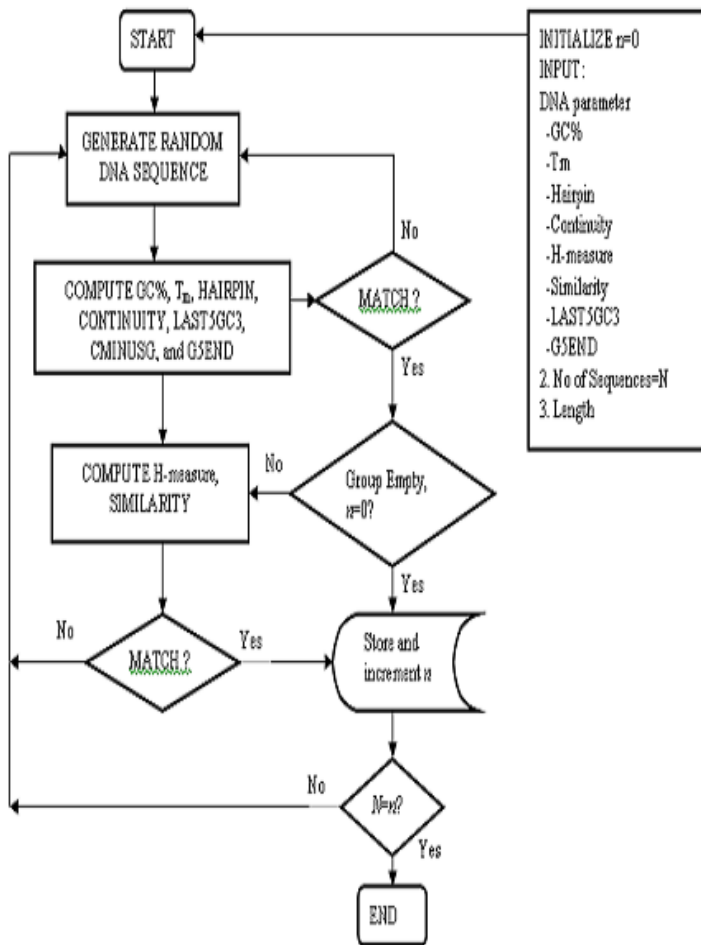


Figure 4 Lipid Formation Of Stem Cells

VI. ALGORITHM FOR CODE

First of all, v1(a)v2(b)v3(c)v4(d) denotes a double-stranded DNA (dsDNA), which contains the base-pairs sub sequences, v1, v2, v3, and v4, respectively. Here, the subscripts in parenthesis (a,b,c,d) indicate the length of each respective base-pair subsequence. For instance, v1(20) indicates that the length of the double-stranded subsequence, v1 is 20 base-pairs (bp). When convenient, a dsDNA may also be represented without indicating segment lengths (e.g., v1v2v3v4). A reaction denoted by TaqMan(v0,vk,v1) indicates that real-time PCR is performed using forward primer v0, reverse primer v1, and TaqMan probe vk. Based on the proposed approach, there

are two possible reaction conditions regarding the relative locations of the TaqMan probe and reverse primer.



The first part of the approach, which is performed in vitro, consists of $\frac{(|V|-2) \cdot (|V|-2)}{2}$ real-time PCR reactions, each denoted by $TaqMan(v_0, v_k, v_l)$ for all k and l , such that $0 < k < |V|-2$, $1 < l < |V|-1$, and $k < l$. For this example instance, so that the DNA template is dsDNA $v_0v_2v_4v_1v_3v_5$, these 6 reactions, along with the output in terms of “YES” or “NO” are as follows:

- TaqMan(v_0, v_1, v_2) = NO (1)
- TaqMan(v_0, v_1, v_3) = YES (2)
- TaqMan(v_0, v_1, v_4) = NO (3)
- TaqMan(v_0, v_2, v_3) = YES (4)
- TaqMan(v_0, v_2, v_4) = YES (5)
- TaqMan(v_0, v_3, v_4) = NO (6)

```

Input: N[0...|V|-1]=2 // N[0, ?, ?, ?, ?, 5]
A [1...|V|-2] =|V| // A [1, 1, 1, 1]
for k=1 to |V|-3
  for l=k+1 to |V|-2
    if TaqMan(v0,vk,vl) = YES
      A[l] = A[l]+1
    else A[k] = A[k]+1
    endif
  endfor
endfor
N[ A[k] ] = k
    
```

```

endfor
N[ A[ |V|-2 ] ] = |V|-2
    
```

Sequence Design

- Melting temperature for primers should be between 58-60°C and melting temperature for probes should be 10°C higher
- Primers should be 15-30 bases in length GC content of primers and probes should ideally be 30-80%
- For primers: The run of identical nucleotides should be avoided. This is especially true for G, where runs of 4 or more Gs are not allowed. Further, the total number of G and C in the last five nucleotides at the 3’ end of the primer should not exceed 2 For probes, there should be more C than G, and not a G at the 5’ end.

Table 1 Algorithmic Results In Form Of ACTG

Table 1: The generated DNA sequences based on DNASequencesGenerator.

Name DNA sequences (5’-3’)

v0 CCTTAGTAGTCATCCAGACC
v2 CGCGCACCTTCTTAATCTAC
v4 CCACTGGTTCTGCATGTAAC
v1 ATGCGCCAGCTTCTAACTAC
v3 TGGACAACCGCAGTTACTAC
v5 TCCACGCTGCACTGTAATAC
v0v2
GTAGATTAAGGGTCTGGATGACTACTAAGG
v2v4 GTAGTAACTGAAGGTGCGCG
v4v1 GTATTACAGTCGGTTGTCCA
v1v3 GTAGTTAGAAGCAGCGTGGA
v3v5
GTTACATGCAGAACCAGTGGGCTGGCGCAT

VII. RESULTING APPROACH

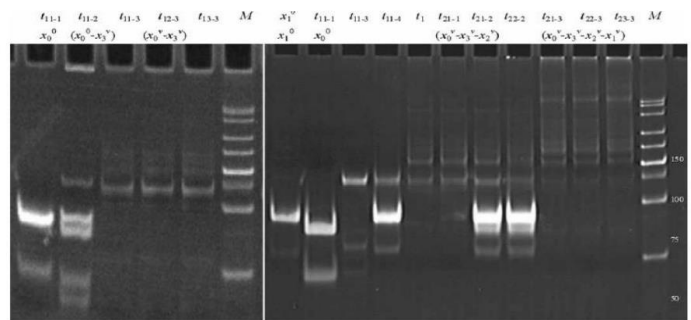


Figure 5 Results with Software Simulation

This Algorithm describes what steps is to be run during the result of the code. This code has the aspect of polymorphism so

it can be used in any programming language with the use of the text editor. Some termination of the operating system will not use this programming language code.

The software program uses mathematical techniques to track the movements of stem cells and predict what kinds of cells they will ultimately become based on those observations. Cohen and colleagues used the program to predict the fates of rat retinal progenitor cells (RPCs), which either duplicate or differentiate into a specific type of cell such as a photoreceptor.

“There were behavioral differences in cells based on what offspring they would eventually become,” Cohen told the Journal Sentinel. “Before they divided they produced subtle dynamic clues as to what they would ultimately produce.”

VIII. ACCURACY

According to the researchers, the program predicted with 99% accuracy whether the RPC would duplicate or create a specific cell type, and accurately determined the particular kind of cell a RPC would become 87% of the time.

APPLICATIONS

This developing code is used to identify mainly the inherited symptom of human being and classify the group of natural human relationships among the various people. The main applications would be in future to find out the human diseases such as cancer, brain tumor, diabetes and AIDS. The group of brain stem cell is shown in the figure if any type of damage will occur in it. It will identify that part of decay and the code will give that type of message to DNA and user will identify the diseases.

REFERENCES

- [1] Garzon M.,P.Neathery,R.Deaton, R.C.Murphy,S.E.Stevens Jr,1997.A new Metric for DNA Computing Prc.Genetic Program 472-478 <http://www.csse.uark.edu/~rdeaton/dna/papers/gp97code.pdf>
- [2] Wallac R.B.,J.Shaffer,RF Murphy,J Bonner 1979,Hybridization of synthetic oligodeoxybonucleatides to phi chi 174 DNA;the effect of single base pari mismatch. Nucleuc Acids Res,6: 3543 3558. <http://nar.oxfordjournals.org/cgi/content/abstract/6/11/35>
- [3] Mullis, Specific enzymtic amplification of DNA in vitro. The polymerae chain reaction. Cold spring Harb. Symo. Quant. <http://www.ncbi.nlm.nih.gov/pubmed/347723>
- [4] Walker, N. J. 2002. A technique whose time has come.Science 296: 557-559. DOI:10.1126/science.296.5567.557
- [5] Chen and Seeman 1991. Synthesisi from DNA of molecule with the connectivity of cube
- [6] Wetmue 1991, DNA probes. Application of principles of nucleic acid hybrdaization.Critical Rev. Biochem Molecular Bio
- [7] Tools Tutorials,Maintanence and Troubleshooting 2009,Applied Biosystems,<http://www.appliedbiosystems.com/support/apptech>
- [8] Tefvik M. 2002 Real Time PCR,<http://dorakmt.tripod.com/genetics/realtime.html>

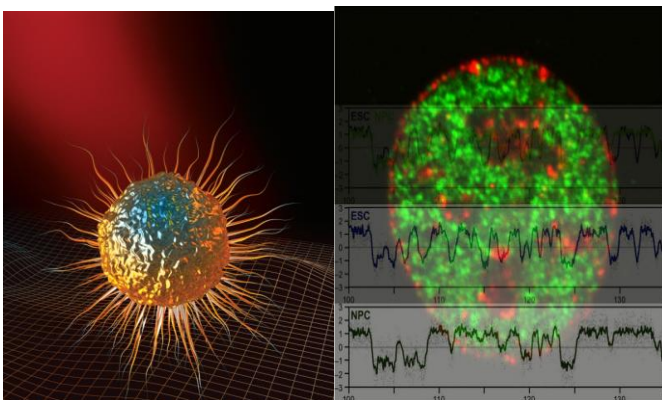


Figure 6 Comparison of O/p

CONCLUSION

The software program will be helpful to find much revolution in biotechnical department as well as in computer science also. This will help human being to identify what kind of relative parameters they have and also solve big troubles related diseases what human being have today.