DNA COMPUTING: ACOMPLETE OVERVIEW

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Abstract

DNA computing is a nascent technology that seeks to capitalize on the enormous informational capacity of DNA, biological molecules that can store huge amounts of information and are able to perform operations similar to computers through the deployment of enzymes, biological catalysts that act like software to execute desired operations i.e. Computers made of genes' building blocks. Because of their speed, miniaturization and Data Storage potential DNA computers are being considered as a replacement for silicon-based computers. Current DNA computer disquisition has formerly proven that DNA computers are suitable of working complex fine equations and storing enormous amounts of data.

Keywords: *DNA Computing, DNA Computing techniques, Operations on DNA for Computing, Applications of DNA Computing, DNA Computing as future technology.*

1. INTRODUCTION

One of the most significant features of DNA is its ability to replicate or copy itself. The double helix structure of DNA allows each strand to act as a template for creating a duplicate sequence of bases. As a result, every DNA sequence has a complementary sequence. For example, the complement of sequences (attacgtcg) is s' (taatgcagc), and these two sequences can combine or hybridize to form double-stranded DNA. This complementarity makes DNA a unique structure for computation and can be utilized in various ways, such as error correction.

DNA can experience errors due to several factors, including mistakes by DNA enzymes, thermal energy, and UV energy. When an error occurs in one of the strands of double-stranded DNA, repair enzymes can use the complement strand as a reference to restore the correct sequence. This property makes double-stranded DNA similar to a RAID 1 array, where data is mirrored on two drives, allowing data recovery from the second drive if errors

occur on the first. In biological science, this process is critical during cell division as each new cell requires an exact copy of the DNA present in the old cell.

DNA computing is not visually apparent as it appears as a clear water solution in a test tube, without any mechanical device. A trillion bio-molecular devices can fit into a single drop of water. Instead of being displayed on a computer screen, the results are analyzed using a technique that allows scientists to observe the length of the DNA output molecule. To make the output visible to the naked eye, human manipulation is required. This is why DNA computers are often referred to as "computers in a drop of water." The DNA strands have the ability to generate billions of potential solutions simultaneously, making them suitable for solving "fuzzy logic" problems that have multiple potential solutions, unlike binary computers that are limited to either/or logic.

2. LITERATURE REVIEW

DNA computing is a rapidly evolving field that has been gaining attention in recent years due to its potential applications in various fields such as data storage, cryptography, and bioinformatics. The concept of DNA computing was first introduced by Adleman in 1994, where he solved a mathematical problem using DNA molecules as computational elements. Since then, researchers have been exploring different ways of utilizing DNA for computation.

One of the main advantages of DNA computing is its massive parallelism. DNA molecules can exist in vast numbers, and each molecule can be viewed as a tiny computer capable of performing simple operations. This makes DNA computing suitable for solving problems that require massive parallel processing, such as searching and optimization problems.

However, there are also significant challenges associated with DNA computing. One of the main challenges is the issue of error correction. DNA is prone to errors due to mutations and degradation, which can lead to incorrect results. Researchers are exploring different methods of error correction, such as redundancy and error-correcting codes.

Another challenge is the issue of scalability. As the size of the problem increases, more DNA molecules are required, which can lead to issues of cost and efficiency. Researchers are exploring different ways of scaling up DNA computing, such as using microfluidic devices for DNA manipulation.

Overall, DNA computing is a promising field with significant potential applications.

However, there are still many challenges that need to be addressed before it can be widely adopted. Further research is needed to explore different approaches to DNA computing and to address the challenges associated with it.

3. CLASSIFICATION OF PROBLEM

a) Finite State Problem

To develop bio-molecular computation as a competitive technology to silicon-based computing, it is necessary to achieve fast execution of basic operations, including arithmetic and boolean operations, in a massively parallel manner. Guarnieri and Bancroft developed an addition algorithm based on DNA that utilized successive primer extension reactions to perform binary addition with carries and boolean logic. The algorithm was demonstrated using recombinant DNA and showed the feasibility of the approach through a simple biochemical example. However, it had limitations such as the inability to take advantage of massive parallel processing capabilities and the lack of repetitive operations due to distinct input and output encodings. Other proposed methods for basic operations such as arithmetic allow chaining of output to input, enabling repetitive operations and massive parallel processing. Rubin demonstrated an experimental implementation of such a method for chained integer arithmetic.[1]

b) Combinational Problems

DNA computing has shown promising results in solving complex computational problems such as the Hamilton path problem (HPP) and the satisfiability problem (SAT). One of the advantages of DNA-based computing is its massive parallelism, which has the potential to yield significant speedups over conventional electronic computers for search problems.[1]

Adleman's experiment is a landmark demonstration of data processing and communication on the level of biological molecules. He set up the first DNA computer to solve the TSP or HPP, which is a simple instance of the directed traveling salesmen problem.

Lipton proposed a solution to the SAT problem using DNA computing, which can solve an n-variable m-clause SAT problem in m steps. The algorithm he proposed is highly space-efficient and error-tolerant compared to conventional brute-force searching and can be scaled-up to solve large and hard SAT problems. The heart of Lipton's method is a process he calls extraction, which removes DNA strands that do not satisfy a given clause. For example,

to solve a two-variable SAT problem, the algorithm extracts all DNA strands corresponding to the first variable and then extracts all DNA strands corresponding to the second variable to obtain a partial solution. These partial solutions are then extended step by step satisfying one clause in one step there by solving the entire problem and finding a complete solution in steps using the ligation process.

Overall, DNA computing has shown great potential in solving complex computational problems using massively parallel processing. However, it still faces challenges such as scalability and error correction. Nonetheless, with ongoing research and development, DNA computing may become a useful tool for solving a wide range of computational problems.[2]

CLASSES OF DNA COMPUTING TECHNIQUES OF PROBLEM

3.1 Intramolecular

To the intramolecular DNA computing operates by means of intramolecular conformational transitions. The transitions are controlled by the sequence of the DNA molecule and the environmental conditions, such as temperature and salt concentration. In intramolecular DNA computing, the computation is performed within a single DNA molecule, without the need for external components or reagents. This makes it a promising approach for developing molecular computing devices that can operate in small spaces, such as inside cells or microfluidic devices. Intramolecular DNA computing has been used for a variety of applications, including logic gates, signal processing, and pattern recognition. For example, Hagiya's state machine DNA was able to recognize and classify different RNA sequences based on their secondary structure. Intramolecular DNA computing is a rapidly evolving field, and ongoing research aims to explore new applications and improve the efficiency and reliability of intramolecular DNA computing devices.[2]

3.2 Intermolecular

It is obtained by sequencing the successful paths. In intermolecular DNA computing, the DNA strands used for computation are separate and interact only when hybridized. This allows for a more flexible and scalable approach to DNA computing, as different DNA strands can be designed and synthesized separately and then combined as needed for the computation. Intermolecular DNA computing has also been used in the solution of other combinatorial problems such as the SAT problem and the graph coloring problem. The

hybridization step can be achieved by various methods such as microarrays, solution-phase hybridization, or even in vivo hybridization with engineered bacteria. Intermolecular DNA computing has the potential to provide significant speedups over traditional electronic computers for certain types of problems, especially those involving large-scale parallelism.[2][3]

3.3 Supermolecular

In supramolecular DNA computing, the DNA molecules are programmed to self-assemble into larger structures to perform computations. This approach takes inspiration from the self-assembly process that occurs in nature, such as the complex structure of the ribosome. The goal of supramolecular DNA computing is to create nanometer-sized elements by assembling small molecular building blocks. This approach has potential applications in drug delivery and as sensors for detection purposes. The interactions between low-molecular weight substances and DNA are also being explored for medicinal treatments. Supramolecular DNA computing has the advantage of being highly parallel, and the ability to perform computations in a highly confined space, which can be useful for applications in nanotechnology. However, it is still a relatively new area of research, and much work is needed to develop efficient and scalable methods for performing complex computations.[3]

4. DNA OPERATIONS FOR COMPUTING

4.1 Watson-Crick Based Pairing

The Watson-Crick base pairing is critical for the stability and replication of DNA. It ensures that the two strands of DNA are complementary and allows for accurate replication of genetic information during cell division. In addition to the Watson-Crick base pairing, DNA also has a unique 3-dimensional structure that is critical for its function. The double helix structure of DNA (as shown in figure 1) is stabilized by interactions between the bases on each strand, as well as interactions between the sugar-phosphate backbones. The major and minor grooves that result from the helical structure of DNA play important roles in the recognition of DNA by proteins and other molecules. The ability to manipulate and engineer DNA has led to a wide range of applications in fields such as medicine, biotechnology, and genetic engineering.[5][6]

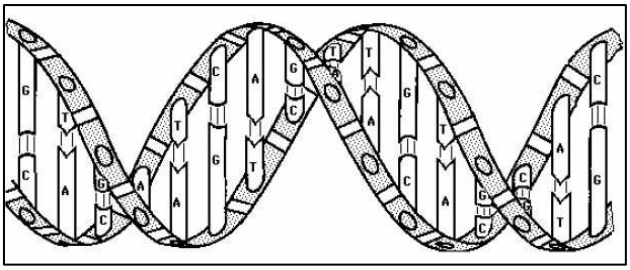

Figure1:Helical Structure pairing of DNA

4.2 Hybridization and Denaturation

In uni-molecular hybridization, a single-stranded DNA molecule can fold upon itself and form a double-stranded hairpin structure, where a complementary sequence in one region of the molecule base-pairs with another complementary sequence in a different region of the same molecule. This process is also referred to as self-hybridization or intramolecular hybridization. The hairpin structure is formed due to the base pairing between complementary sequences, resulting in a stem and loop structure, as shown in figure 2. This type of hybridization is commonly used in DNA computing, as it allows for the design of compact and efficient DNA circuits that can be implemented using a single strand of DNA. The hairpin structure can be opened by a specific trigger, such as a complementary DNA strand or a change in temperature, to release the information stored in the stem region or a low salt buffer solution, which can cause the hydrogen bonds to break and lead to strand separation. The melting temperature (Tm) is the temperature at which half of the DNA molecules are in their native double-stranded form and half are in their denatured single-stranded form. The Tm depends on the length and base composition of the DNA sequence, as well as the concentration of salt in the solution. The Tm can be used to optimize hybridization conditions for specific DNA sequences, such as in PCR or hybridization-based assays. Overall, hybridization and melting of DNA strands are essential processes in DNA computing and molecular biology applications.

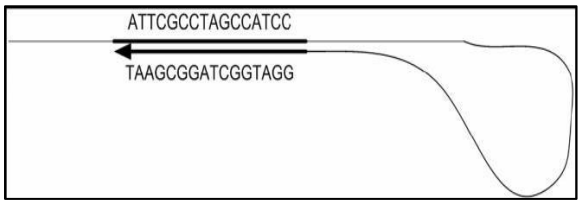

Figure 2: Hairpin Formation of DNA

4.3 Ligetion

Ligation is an important step in many DNA manipulation techniques, including DNA cloning and DNA sequencing. In DNA cloning, ligation is used to join the DNA fragment of interest

with a vector, such as a plasmid, to create a recombinant DNA molecule. In DNA sequencing, ligation is used to join small pieces of DNA together to create a longer DNA fragment for analysis.

The enzyme T4 DNA ligase is commonly used in ligation reactions. This enzyme catalyzes the formation of a phosphodiester bond between adjacent nucleotides, joining two DNA fragments together. In addition to T4 DNA ligase, other DNA ligases, such as E. coli DNA ligase and thermostableligases, can also be used for ligation reactions.

During the ligation reaction, the DNA fragments to be joined are mixed with the ligase enzyme and ATP or NAD+.[5] The ligase enzyme recognizes and binds to the cohesive ends of the DNA fragments, bringing them into close proximity for ligation to occur. Once the fragments are ligated together, the resulting DNA molecule can be transformed into a host cell for further analysis or manipulation.

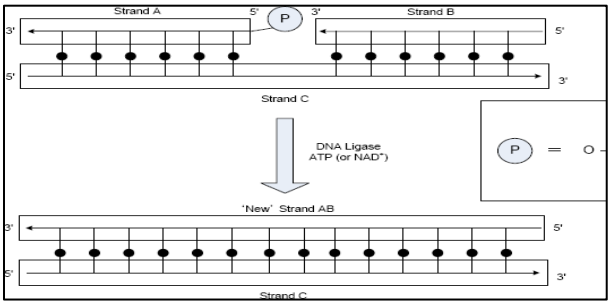

Figure 3: Ligetion

4.4 Polymerization

DNA polymerase can only add nucleotides in a 5' to 3' direction, so the primer strand that is annealed to the template must have a free 3' OH group to which the polymerase can add nucleotides. The polymerase reads the template strand in the 3' to 5' direction and adds nucleotides to the 3' end of the primer strand in the complementary 5' to 3' direction. The incoming dNTPs are incorporated into the growing strand through the formation of a phosphodiester bond between the 3' OH group of the last nucleotide in the growing strand and the 5' phosphate group of the incoming dNTP. The energy required for this reaction comes from the hydrolysis of the phosphate groups on the incoming dNTPs.[4]

4.5 Polymerase Chain Reaction (PCR)

PCR is a powerful tool in molecular biology that allows the amplification of a specific DNA sequence. It relies on the use of DNA polymerase, primers, and repeated cycles of heating and cooling to separate the DNA strands, anneal primers, and extend the new DNA strands.

In the first step of PCR, the DNA sample is denatured by heating it to 95°C, which separates the double-stranded DNA into single strands. In the second step, the temperature is lowered to around 55°C to allow the primers to anneal to their complementary sequences on the single-stranded DNA template. The third step involves raising the temperature to 72-74°C, which is the optimal temperature for DNA polymerase to extend the primers and synthesize a new DNA strand.

After each cycle of PCR, the number of copies of the target DNA sequence is doubled, resulting in an exponential increase in the amount of DNA. PCR is used in many applications, such as genetic testing, forensics, and medical diagnostics, and has revolutionized the field of molecular biology.[3][4]

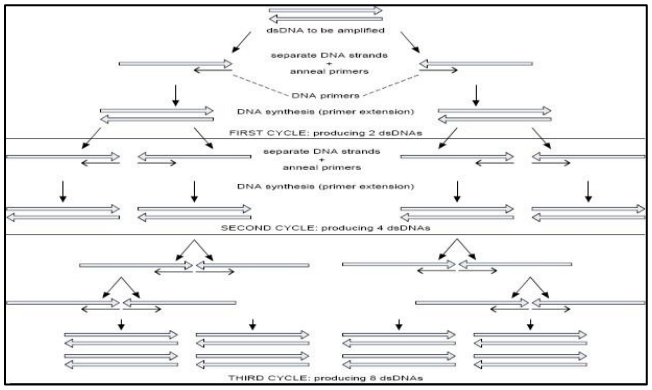

Figure 4: Polymerization in Action

4.6 Result Visualization: Gel Electrolysis

Gel electrophoresis is indeed a useful technique for visualizing the results of DNA computing experiments. By labeling specific strands of DNA with fluorescent or radioactive markers, it is possible to track the movement of these strands through the gel and determine their lengths. This information can be used to verify the successful completion of certain operations, such as PCR or ligation, or to detect the presence of specific strands in a mixture. Gel electrophoresis can also be combined with other techniques, such as hybridization or enzymatic digestion, to create more complex computational processes. Overall, gel electrophoresis plays an important role in the experimental verification of DNA computing algorithms.[3][5]

4.7 DNA Extraction

One common method for DNA extraction is using a column-based purification kit. This involves passing the DNA-containing solution through a column that binds the DNA, while

other impurities are washed away. The DNA is then eluted from the column with a low-salt buffer or water.

Another method is phenol-chloroform extraction. This involves mixing the DNA-containing solution with phenol and chloroform, which separates the DNA from proteins and other impurities. The DNA is then separated by centrifugation, and the aqueous layer containing the DNA is removed and further purified.

A third method is ethanol precipitation. In this method, salt is added to the DNA-containing solution to make it more polar, and then ethanol is added to precipitate the DNA. The DNA is then washed with ethanol and dried before being dissolved in a buffer for further use.

These methods are often used in combination to obtain pure and high-quality DNA for downstream applications such as PCR, sequencing, and cloning.

Using probes made of complementary DNA: To perform an extraction in practice, Lipton proposed using probes made of complementary DNA. If, for example, a strand of the sequence gggta is to be extracted out, Lipton would make its complementary sequence cccat and attach copies of it to magnetic particles. When these probes were poured into the test tube, they would latch onto the DNA strands which are represented by the sequence gggta. Then, with a magnet, Lipton would extract the magnetic particles together with the probes and long DNA strands. In another test tube he would peel off the probes to leave the required DNA strands.[2][3]

Using complementary strands within solution: Adleman and his team have developed a powerful technique for DNA extraction that is useful for partial matching and further computations, which is commonly used in digital computations. They start with numerous identical strands of DNA, each of which is thousands of bases long. These "memory strands" represent long strings of 0s. To add a 1 in specific positions, Adleman uses "stickers" which are short strands of DNA complementary to the memory strands in those positions and stick there naturally.[2]

Adleman's sticker method is comparable to Lipton's technique but has additional capabilities. Adleman can change his memory strands during the computation by adding stickers to every strand in the test tube at the same place on each strand. This ability is similar to that of silicon computers and enables Adleman to update his calculations. The sticker computer also eliminates the need for enzymes since none of the calculation steps involve copying strands, cutting strands, or linking two strands end to end.

Using complementary strands on Surface: Anne Condon and her colleagues at the University of Wisconsin proposed a technique that involves attaching DNA strands to a surface and manipulating them there instead of in a liquid solution. This method aims to prevent the loss of DNA molecules that may occur during extraction steps. However, unlike Lipton and Adleman's techniques, the Wisconsin team's method is more limited in terms of computing operations since they cannot extract the DNA strands.[3][4]

Arrangement of strands in 2-D bricks: Erik Winfree at Caltech has moved away from using individual DNA strands and instead utilizes two-dimensional "bricks" made up of multiple DNA strands to form structures with four corners. These bricks are designed to fit together similar to how DNA strands do in Adleman's work, but the self-assembly occurs in two dimensions instead of one. The bricks assemble themselves into an inverted triangle, starting with one in the first row, two in the second, and so on. The final answer can be determined from the sequence of the last row of bricks once the triangle is complete. Winfree is also exploring the use of three-dimensional structures, such as pyramids.[3]

4.8 Operations in Parallel

In living cells, various enzymes modify DNA through a biochemical process. Enzymes are small protein machines that process DNA based on nature's design, performing a wide range of operational functions that manipulate DNA at the molecular level. Some enzymes cut DNA, while others paste it back together. Other enzymes act as copiers or repair units. Molecular biology, biochemistry, and biotechnology have developed techniques that allow these cellular functions to be replicated in the test tube. With this cellular machinery, along with some synthetic chemistry, scientists can perform computations using a palette of operations. Similar to how a CPU has a basic set of operations like addition, bit-shifting, and logical operators (and, or, not nor), DNA has cutting, copying, pasting, repairing, and many other operations. In the test tube, enzymes can work on multiple DNA molecules simultaneously rather than sequentially, as many copies of the enzyme can work in parallel. This is the key strength of DNA computing, as it can operate in a massively parallel manner.[2][4]

5. CHALLENGES TO DNA COMPUTING

The challenges facing DNA computing include the need to represent all data in terms of DNA sequences and the lack of practical protocols for input and output of data into memory.

Additionally, an understanding of the information capacity of hybridization interactions in large collections of DNA sequences is necessary to ensure proper information flow. Controlling DNA operations to produce desired results is also a complex task, and appropriate physical models to guide design and experimentation are yet to be developed.

6 APPLICATIONS OF DNA COMPUTING

6.1 Solving NP-complete and hard computational problems

After the pioneering work of Adleman and Lipton, much of the research in DNA computing has focused on solving NP-complete and other hard computational problems. These problems are characterized by the absence of a known polynomial time solution using conventional computer algorithms, with the time required to solve them increasing at an exponential rate as the complexity of the problem increases. Examples of such problems include HPP and SAT, which have already been discussed.[7]

Aside from technical challenges, DNA computing has also been applied to real-life problems, including business planning and management science. Many optimization problems faced by managers fall within the domain of NP-complete, and are currently solved using heuristic methods and approximations. Examples include scheduling, routing, and optimal use of raw materials, which have already been solved using DNA computation, either theoretically or experimentally. However, the current limitations of laboratory technology preclude the use of DNA computation as a method of solving real-time problems. As such, classical DNA computing is best suited for problems where the calculation of optimal solutions can be performed over a period of days, weeks, or months. Applications include long-term production planning in areas such as chip design and manufacturing, as well as optimizing airline and bus routes for planning purposes.

6.2 Storage and associative memory

After Adleman and Lipton's initial work on DNA computing, research has continued to focus on solving NP-complete and other hard computational problems. These are problems where no polynomial time solution is known to exist using conventional computer algorithms. The complexity of these problems increases exponentially, making them intractable. DNA computing has been able to solve some of these problems, such as the HPP and SAT problems, which are in NP-complete.

In addition to solving technical problems, DNA computing has the potential to be used for content-addressable memory and to mirror the associative capabilities of the human brain. Baum proposed a method for building a large content-addressable memory using DNA, where data can be retrieved directly from storage by entering an input that closely resembles it. Baum's model involves assigning a specific DNA subsequence to each component value pair and building a fixed-length word from these subsequences. To retrieve the word closest to the input, marked complementary subsequences are introduced into the storage medium, and the molecule with the most matches to the input is chosen.[9] This technique could be further refined by appending words to only store attributes that an object has, rather than wasting space using '0's to represent attributes that an object does not have.

Baum also suggests that a memory could be constructed where only portions of the data are content-addressable and associative, with other information on an object stored in addresses relative to the associative portion of the entry. Such a DNA-based associative memory could have advantages over the human brain, as it could potentially store over 10^20 words in a large bath tub of DNA, without accounting for redundant molecules.[9]

6.3 DNA2DNA Applications

The use of DNA computation offers unique advantages over conventional computers in various areas. One such area is DNA2DNA computation, which involves performing operations on unknown pieces of DNA without first sequencing them. This is achieved by re-coding and amplifying unknown strands into a redundant form, which can then be operated on using techniques similar to those used in the sticker model of DNA computation. The potential applications of DNA2DNA computation include DNA sequencing and DNA fingerprinting.

DNA sequencing involves determining the order of nucleotide bases in a DNA oligonucleotide, which is useful in basic research and applied fields such as diagnostic and forensic research. DNA computing methods can improve the accuracy and efficiency of DNA sequencing by using techniques such as magnetic beads and optical scanners to read DNA directly into an electronic interface.[10][11][12]

DNA fingerprinting, on the other hand, utilizes repeating patterns in DNA to distinguish between living organisms. While this method does not provide individual fingerprints, it can determine whether two DNA samples are from the same person, related people, or non-related people. DNA fingerprinting is widely used in determining paternity and maternity,

criminal identification, forensics, and personal identification.[13]

DNA mutation and population screening is another area where DNA computing can be useful. Environmental factors and the process of separating and copying DNA strands can cause permanent changes in DNA sequence in a gene, which can result in genetic diseases. Screening a particular segment of the population can help detect these diseases during infancy or childhood, which is crucial for effective treatment. DNA computing can assist in conducting such screenings on a larger scale.[13][14]

6.4 Use in nanocomputing

DNA and nanotechnology can offer numerous benefits by utilizing the structure of DNA, which consists of a double-stranded molecule that can unzip and form branches that can self-assemble into valuable structures. Scientists can partially unzip the DNA molecule and use branches to join complementary sequences on other DNA strands to create complex structures.[15] Previous studies have shown the construction of various DNA nano mechanical devices that can exhibit different types of motions, such as open/close, extension/contraction, and motors/rotation through external changes such as the addition and removal of DNA fuel strands or changes in ionic composition. For instance, DNA walkers can be used to carry out computations and precisely transport nanoparticles of material.[8]

6.5 Intelligent systems based on DNA Computing

In 2004, Langdon and Buxton utilized genetic programming combined with a systematic objective function to evolve various non-linear functions of gene expression values. The objective was to reduce the thousands of data attributes, such as gene expression measurements, into a few predictive ones. Chen developed intelligent DNA memory to capture global information about a population of an organism, incorporating intelligent processing and reasoning capabilities into the test tube. The high storage capacity and parallelism of DNA are then used to draw inferences on the entire in vitro knowledge base.

Sakakibara and Suyama introduced DNA chips with logical operations, known as intelligent DNA chips, which combined the DNA computing method for representing and evaluating Boolean functions with the DNA coded number (DCN) method to execute DNA chips with logical operations. The developed DNA chips are considered intelligent because they not only detected gene expression but also discovered logical formulae of gene expressions. This intelligent DNA could provide logical inferences for diagnoses based on detected gene expression patterns.[7]

7. PROMOTES TO DNA COMPUTING

The benefits of DNA computing are numerous and significant. First and foremost is its size, with the potential for DNA to hold an immense amount of information in a very small space. In fact, it has been estimated that DNA can hold more information in a cubic centimeter than a trillion CDs.

Another advantage is high parallelism, with every molecule in a DNA solution potentially acting as a small processor on a nano-scale, allowing for an enormous number of processors to operate simultaneously and produce simultaneous outputs. In an in vitro assay, for example, around 1018 processors could work in parallel.

DNA computing also has tremendous computational power, with future droplet-sized DNA computers predicted to have more computational power than today's most powerful supercomputers. Although the elementary operations in DNA computing may be slow compared to electronic computers, their parallelism allows for a potential number of operations per second of at least 1018, which is 100,000 times faster than the fastest supercomputers available today.

In addition to speed and computational power, DNA computing is also highly energy efficient, capable of performing 1019 operations per Joule, making it about a billion times more energy efficient than current electronic devices.

Finally, DNA computing has the ability to generate a complete set of solutions for problems that have a large number of possible solutions, which is unattainable with conventional computers. These benefits make DNA computing an exciting area of research with potential applications in a wide variety of fields.

8. ISSUES WITH DNA COMPUTING

One of the challenges in DNA computing is the potential for errors in the computation, which have been recognized from the beginning. As the size of the problem grows, errors can be introduced at various stages of the process, such as during the formation of DNA strands or due to sensitivity to chemical conditions like temperature and concentration. Additionally, scalability can be an issue as large volumes of DNA are required to solve significant problems, which can increase exponentially and require large codes for nucleotides, making encoding error-prone.

Another challenge is the need for human intervention at every step of the computation, including monitoring and controlling processes like hybridization, ligation, and extraction. Generating solutions and extracting results can also be inefficient for small problems, as DNA solutions need to be created for every element in the problem, and conversions may be required to interpret the results.

Despite these challenges, the potential benefits of DNA computing, such as high parallelism, computational power, energy efficiency, and the ability to generate complete solution sets for problems with a large number of possible solutions, make it an exciting area for continued research and development.

9. DNA COMPUTERS V/S QUANTUM COMPUTERS

A quantum computer is a device that directly utilizes distinctively quantum mechanical phenomena for computation, allowing for efficient solutions to complex problems. In contrast to quantum computing, DNA computing operates in natural environments and does not require electrical power. It is capable of embedded computing in microscopic environments and may eventually be used to construct self-organizing, partially electronic quantum computers due to its connection to molecular construction.[16][17]

10. DNA COMPUTERS V/S PARALLEL COMPUTERS AND NANO COMPUTERS

DNA computing is unique in providing massive parallelism for computation, which is not achievable by traditional parallel computing. While parallel computers have limitations in scalability and synchronization, DNA computers offer trillions of operations that can be performed simultaneously without traffic problems.

Nano computers, which are defined as computers with fundamental parts that are no larger than a few nanometers, are known for their small size. However, DNA computing can enable even more compact computers to be built. In fact, with DNA computing, more than 10 trillion DNA molecules can fit into a space no larger than a cubic centimeter, which is a revolutionary change in computer size.

11. CONCLUSION

The discovery of DNA in the 20th century has had a significant impact on fields such as medicine, agriculture, forensics, and paternity testing. Ongoing research in DNA continues to drive progress in these areas and new discoveries are likely in the future as funding and interest remain high.

Although DNA computing is still in its early stages and only a few centers around the world are working on it, it has the potential to revolutionize computing in various fields such as agriculture, weather forecasting, security code breaking, and developing DNA optical storage medium. Despite the challenges, with continued research and development, DNA computing has the potential to become an efficient and successful computing application in a wide variety of fields, and a promising technology for analyzing data and transmitting information in nanotechnology and other interesting applications.

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