DNACloud: A Tool for Storing Big Data on DNA

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Abstract—The term Big Data is usually used to describe huge amount of data that is generated by humans from digital media such as cameras, internet, phones, sensors etc. By building advanced analytics on the top of big data, one can predict many things about the user such as behavior, interest etc. However before one can use the data, one has to address many issues for big data storage. Two main issues are the need of large storage devices and the cost associated with it. Synthetic DNA storage seems to be an appropriate solution to address these issues of the big data. Recently in 2013, Goldman and his colleagues from European Bioinformatics Institute demonstrated the use of the DNA as storage medium with capacity of storing 1 peta byte of information on one gram of DNA and retrieved the data successfully with low error rate [1]. This significant step shows a promise for synthetic DNA storage as a useful technology for the future data storage. Motivated by this, we have developed a software called DNACloud which makes it easy to store the data on DNA. In this work, we present detailed description of the software.

Keywords—DNA storage, Biostorage, DNA Computing, DNA codes, Huffman Coding, Software, Open source, DNA hard disk, Error correction, Synthetic DNA, Organic data storage.

I. INTRODUCTION

Storage has been a fundamental requirement for the humans. In the modern era of computing and communication, huge amount of data is being generated and there is a pressing need for dense storage medium which is cost effective. Table 1 shows the typical amount of the data generated and the kind of storage device it will require to store such a data. It is predicted that by 2015, the amount of data generated by NSA (National Security Agency) will be so large that it may need 1000 billion tera bytes of hard disk space worth $1,000 trillion [2]. At present, the world is producing 1 exabyte of data per day and soon devices, machines and sensors of Internet of Things (IoT) will generate data in the order of bronobytes, where 1 bronobyte is 10^27 bytes, [3] for which a dense storage medium is needed. From the past 30 years, the blue print of life viz. DNA has been used as storage medium. Unlike existing storage device, DNA requires no maintenance and can be stored without electricity in cold and dark place. One of the venture to use the DNA as artistic material and convert the graphic image to the language of genetic code was initiated by Joe Davis in the work Microvenus [4]. In 1999, Synthetic gene that was created by Kac by translating a sentence from the biblical book of Genesis into Morse Code, and converting the Morse code into DNA base pairs according to a conversion principle [5]. In the 20th century, many researchers have translated English text, mathematical equations [6], latin text [7] and simple musical notations [8] to DNA using different DNA coding principles [9] [10] [11]. All the above mentioned efforts were successful on a small scale giving birth to the idea of data storage on DNA. But the most prolific work was done in 2012 by Church, et al. [12] of Harvard University. They encoded successfully entire book of Regenesis: How Synthetic Biology Will Reinvent Nature and Ourselves [13] including 53, 426 words, 11 JPG images and a JavaScript program into DNA using 1 bit per base encoding. The main draw back of their method was that it had high error rate [12]. In the subsequent year, in 2013, this limitation was overcomed by the Goldman and his group. They implemented a modified approach that includes error correction and scaled DNA based data storage [11]. Based on this method of DNA data storage [11], in this work we present the software called DNACloud which converts the data file to DNA sequences and vice versa. The reader is referred to excellent short reviews of synthetic DNA storage [14], [15] to get an overview of this new area.

This paper is organized as follows. Section 2 includes algorithms used for encoding and decoding data into DNA. Section 3 provides an overview of Graphical User Interface (GUI). Section 4 describes detailed GUI while Section 5 has remarks on limitations and assumptions in the software. Section 6 concludes with challenges in the area of synthetic hard drive and last section provides a link for downloading the software and related material.

II. ALGORITHMS FOR ENCODING AND DECODING DATA FILES

While implementing the methods of [11], we modified the algorithms little bit so that they are memory efficient. For encoding, algorithm [1] generates DNA string from given data file which is further divided into DNA chunks of lengths 117 using algorithm [2]. For decoding, algorithm [3] takes the DNA file containing DNA chunks of length 117 and produces DNA string which is further decoded to get the original data file using algorithm [4]. In order to describe these algorithms we define a term index info and also give remarks for algorithms [3] and [4].

Definition 1. (Index Info): Index info is base 3 string of length 15 which has format (ID: no of chunk : parity of the chunk), where ID has length 2, no of chunks has length 12 and parity of chunk has length 1. Later on, every chunk is also appended with ‘G’ or ‘C’ and prepended with ‘A’ or ‘T’.

Remark 2. (For * in Algorithm [3]) The decoding is always not possible since the format of .dna file is [‘chunk1’, ‘chunk2’,...,‘chunk_n’]. Now while reading x chunks...
**TABLE I. HOW BIG IS THE BIG DATA?**

| Data Unit    | Size          | How big it is                                                                 | On what it can be stored [2]                                                                 | Remarks [16]                                                                 |
|--------------|---------------|-----------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------|
| Tera Byte (TB) | 1000 GB       | 200000 Photos                                                              | 1 TB Hard Disk                                                                             | 400 Terabytes: National Climactic Data Center (NOAA database)                |
| Peta Byte (PB) | 1000 PB       | 3 years of EOS data (NASA’s Earth Observing System)                         | 16 Backblaze storage pads in two datacenter                                                | 200 Petabytes: All printed material.                                         |
| Exa Byte (EB)  | 1000 PB       | 2 Exabytes: Total volume of information generated in 1999                  | A city Block of 4 storey datacentre                                                         | 5 Exabytes: All words ever spoken by humans.                                  |
| Zetta Byte (ZB) | 1000 EB       | 1.9 Zettabytes of information sent through broadcast technology like T.V and GPS. [17] | 20 percent of Manhattan, New York                                                          | 5 Zettabyte is equal to 3.14 Zettabytes is of traffic annually over the internet in 2016 [19] |
| Yotta Byte (YB) | 1000 YB       | 1 YB is the total Volume of government data the NSA (National Security Agency) | State of Delaware and Rhode Island with million Data centre [19]                           | 5 Zettabyte is equal to government data the NSA (National Security Agency)    |

**Algorithm 1 Algorithm for generating DNA string**

**Require:** File size and chunk size

**Ensure:** DNA string for the file

1. **if** file size < chunk size **then**
   - Do not divide file into chunks
2. **else**
   - Divide file into chunks where no of chunks = file size / chunk size + 1
3. **end if**

4. **if** no of chunks > 1 **then**
   - Read bytes string from chunk one
   - Convert the string to ascii values list
   - Convert the ascii values list to base 3 string
   - Convert base 3 string to DNA bases and store the last base of the DNA string
4. **end for**

5. **for** chunk number 1 to total number of chunks - 1 **do**
   - Read the bytes string for the chunk
   - Convert the bytes string to ascii values list
   - Convert the ascii value list to base 3 string
   - Convert base 3 string to DNA bases using pervious chunk’s last base
   - Concatenate this new DNA string with original one
   - Store the last base of the DNA string
5. **end for**

6. **if** file size < chunk size **then**
   - Do not divide file into chunks
7. **else**
   - Divide file into chunks where no of chunks = file size / chunk size + 1
6. **end if**

**Algorithm 2 Algorithm for generating DNA chunks**

**Require:** DNA string for the file obtained in algorithm 1

**Ensure:** DNA chunks of length 117

1. **if** file size < chunk size **then**
   - Do not divide file into chunks
2. **else**
   - Divide file into chunks where no of chunks = file size / chunk size + 1
3. **end if**

4. **if** no of chunks > 1 **then**
   - Read DNA string for the chunk one
   - Divide the string into chunks of length 100 and add index info in these chunk
   - Store last 75 DNA bases of the DNA string read
4. **end for**

5. **for** chunk number 1 to total number of chunks - 1 **do**
   - Read DNA string in the chunk
   - Append the read DNA string to last stored temporary DNA string of 75 bases
   - Again divide the string into chunks of length 100, add index info and store its last 75 DNA bases
   - Concatenate the list of chunks to original list of chunks
5. **end for**

6. **if** file size < chunk size **then**
   - Read entire file and divide the string into chunks of length 100 and add index info in these chunks (trivial case)
7. **else**
   - if no. of chunks = 1 **then**
     - Read entire file and divide the string into chunks of length 100 and add index info in these chunks (trivial case)
    **end if**
8. **end if**

This entire list obtained is stored in .dnac file

**Remark 3.** (For ** in Algorithm 4) The decoding here also is not always possible since huffman values are either of length 5 or length 6. So we keep on removing the last byte from the read string and try decoding again and again unless decoded.
Algorithm 3  Algorithm for regenerating DNA string from DNA chunks

Require: .dnac file containing DNA chunks of length 117 obtained from algorithm 2

Ensure: DNA string for the chunks

1: if file size < chunk size then
   Do not divide file into chunks
else
   Divide file into chunks where no of chunks = file size / chunk size + 1
end if
2: if no of chunks > 1 then
   Decode the given chunks read to correspond to DNA string if possible*
   while not decoded do
      Remove last base from buffer of .dnac file and try decoding again
      Store this base at the end of prepend string if a bit is removed
   end while
3: for chunk number 1 to total number of chunks - 1 do
   Prepend last stored string to buffer read if prepend string is not null
   while not decoded do
      Remove last base from buffer of .dnac file and try decoding again
      Store this base at the end of prepend string if a bit is removed
   end while
   write the DNA string obtained to original file
end for
4: Prepend last stored string to buffer read if prepend string is not null, decode it and append it to original DNA string
else
   if no. of chunks = 1 then
      Trivial case so read entire file at once and convert it to DNA string
   end if
end if

III. Graphical User Interface (GUI) Overview

DNACloud has been primarily developed to facilitate the storage of data on DNA. The software converts any type of data (text, image, audio or video etc.) into DNA strings and enables it to store on DNA and helps to retrieve the data stored on DNA. The GUI of DNACloud is developed to enable this feature. Along with the encoding and decoding facility, DNACloud provides the user various estimations related to the data storage on DNA as shown in Figure 1. There are three basic modules of the software as discussed in Sections A, B and C.

A. DNA Encoder (File to DNA)

To store data on DNA, one has to find ways for encoding the given data into DNA sequence. There are many encoding techniques available to convert the data into DNA sequences by using DNA codes [20]. One of the most efficient source coding technique called Huffman codes is well known for data compression [21]. The DNA encoding by Huffman is uniquely decodable. In this software, similar Huffman encoding is implemented [1]. For error correction, the overlapping codes [1] are implemented and data is retrieved from DNA with reduced error rates. The encoding module takes the data file of any format (.text, .png, .jpg, .mp3, .mkv etc.) as an input. The DNA sequence encoded is divided into fixed length of DNA chunks and the part of the DNA chunks were overlapped implementing four fold redundancy for error correction. The

Algorithm 4  Algorithm for regenerating original file from DNA chunks

Require: DNA string obtained from algorithm 3

Ensure: Original computer file

1: if file size < chunk size then
   Do not divide file into chunks
else
   Divide file into chunks where no of chunks = file size / chunk size + 1
end if
2: if no of chunks > 1 then
   Read DNA string for the chunk 1
   Convert the DNA string to base 3 string
   Convert the base 3 string to list of Huffman values if possible**
   while not decoded do
      Remove last base and try decoding again
      Add removed base to ‘prepend string’
   end while
   Convert the huffman list to corresponding ascii list
   Convert ascii list to string of bytes and write to file
3: for chunk number 1 to total number of chunks - 1 do
   Read DNA string for the chunk and prepend ‘prepend string’ to it if not null
   Convert the DNA string to list of Huffman values if possible
   while not decoded do
      Remove last base and try decoding again
      Add removed base to ‘prepend string’ (after clearing)
   end while
   Convert Huffman list to corresponding ascii list
   Convert the ascii list to string of bytes and write to file
end for
4: Read last chunk, convert this to base 3 string, to corresponding Huffman list, to corresponding ascii list, to string of bytes and write this bytes to file
else
   if no. of chunks = 1 then
      Trivial case process entire file at once and convert it to base 3 then to Huffman list which in turn is converted to ascii list and then to stream of bytes which are then written to a file
   end if
end if
original file is converted to Huffman base 3 code (0,1,2) with code length of 5 which is transformed to triplet codon to DNA code according to the conversion principle as substituting each trit (triplet) with one of the three nucleotide different from the preceding one. If G is the preceding, then A or T or C will be placed, this ensures that no homo polymers are generated to reduce the sequencing error. For these code, if any DNA chunk or base was deleted, then it can be regenerated by reading that overlapped code sequence. This module saves the encoded file with extension “fileformatextension.dnac”. E.g. an image file will be encoded and saved as “.png.dnac”.

B. DNA Decoder (DNA to File)

To retrieve the data stored on DNA, data has to be decoded from DNA. The reverse step of encoding is followed for decoding. The data stored in DNA can be retrieved by excluding the index bits and converting base 3 Huffman DNA codes back to original data. This module takes the DNA sequence as input and gives original data stored as output. The output of the sequencer can be used as input for this module. It takes “.dnac” file as input.

C. Storage Estimator

This module gives various statistics and biochemical properties of DNA for the encoded file. These estimated values are helpful while doing the experiments for storing data in DNA. Estimator has two main sections.

1) Memory Required

User can select the file to be encoded from the system and the following values of the file are estimated. This will help the user to decide how much memory of his system will be occupied for encoding and storing particular data file in DNA. These values are approximated.
   a) File size in bytes
   b) Size of DNA string
   c) Free Memory Required
   d) Amount of DNA Required

2) Biochemical Properties and Cost

This will estimate the biochemical properties of the DNA sequence used to store the data. Select ”.dnac” file from the system which contains the DNA sequences to estimate the properties. This will take salt concentration (mM) and cost per base as an input. It will estimate the GC content of DNA, melting temperature of the DNA and total cost to store the file in DNA. All the values are approximated. This facilitates the user to figure out the budget for the experiments depending on the total amount of DNA.

IV. DETAILED DESCRIPTION OF GUI

When the program is executed, a dialogue box is popped up for workspace where one can save his work. All the files generated will be automatically saved in this workspace. You can switch to other workspace. After this dialogue box user details are asked. It includes name, contact number and email address and file you are using as an input. This will save your details and Generate Barcode button will generate a barcode of it which can be used as unique identification by Biotech companies when performing the experiments. It is not mandatory but recommendable to fill the details else the box will remind you again and again. To Encode or decode the file select either of the options from File menu. Software includes options A to G in the menu.

A. Encode (File to DNA) Button

This option is available under the File menu which will convert any type of data to DNA strings. User can select the file to be converted into DNA string by clicking on Choose File button. Once the user selects the file to be encoded, the list of information for the encoded file will be displayed as below.

1) Length of DNA string
2) No of DNA oligonucleotides (chunks)
3) Length of each DNA oligonucleotide
4) File size in bytes

To save the encoded file, user can save the file with specific name on specific location by using Encode your File button. It will generate the file with extension ”.dnac” that has DNA string for the file selected. RESET button can clear the selected file then user can select new file. It is like clear button.

B. Decode (DNA to File) Button

This option is available under the file menu which will retrieve the data stored in DNA. User can select the DNA string from which data is to be retrieved in the text box against Please write DNA string option. User can also decode the encoded file from the system by option Select .dnac file. Once the file is selected, click on Decode option. To save the decoded file, give the name and save the file at specific location. This will
generate the original file that was encoded in DNA. **RESET button** can clear the selected file i.e., it is like a clear button.

### C. Storage Estimator

As mentioned above, it has two estimators. To estimate the memory required user can select the option from **File → Estimator → Memory Required**. This will take data file to be encoded as input and **Calculate** button will estimate the values as mentiond above. For second estimator, user can select **File → Estimator → Biochemical Properties** option. This will ask '.dna' file as an input and give the GC content and Melting temperature values and cost for total DNA. **Save button** will help to save estimated information.

### D. Export Button

This will help the user to export the file generated to different formats. DNA strings can be exported to file format that can be used as input for the synthesizer. File can be exported to file format that is required by the sequencer. These options are available in File menu. This will generate the feasible output of the DNA strings that is to be used by respective machines. To export the DNA file for the synthesizer to synthesize the DNA, use **Export DNA synthesizer File** option. To decode the file stored in DNA, use **Import DNA sequencer file** option to get the DNA sequences to be decoded. These options will be available in the next version of the software. The .dna file can be exported to PDF and latex file with all software output details in single PDF by using the option **Export .dna to PDF** and **Export to latex** respectively.

### E. Clear temp files

This will clear all your history of the software. It will remove all the temporary files generated by the software.

### F. Exit

Exit will help to quit the software.

### G. User details

This option is available in preferences menu. For the data security, user has to feed his details then the dialogue box to enter the password appear. Password can be reset with **Change Password** option in same menu. This helps the user to retrieve his files stored in DNA safely. The barcode generated can be used by biotech companies to tag the DNA on which the particular file is stored.

### V. Comparison of Data Storage on DNA

The software has limitation of encoding and decoding the file beyond certain file size. Table II compares the file size limit of different file types encoded by the software. At present, the maximum file size of 3486784400 bytes or 3.4 GB of DNA strings could be decoded by the software and any file of size 581130733.333 bytes or 554 MB can be encoded with DNACloud.

### VI. Conclusion

Considering the current rate of data explosion, DNA storage becomes an absolutely indispensable data storage medium because of its low maintenance cost, high data density, eco-friendliness and durability. However, the technological advancements are rudimentary, since still the cost for sequencing and synthesizing DNA is pretty high. But since the cost is decreasing every day, we expect that the research in encoding and decoding algorithms can avail common man with this technology within next few years. Thus, DNACloud can be considered as a potential tool to convert data files into DNA and vice versa. We are anticipating to enhance the capability of the software to encode large size data by implementing better encoding and decoding techniques and error correction methods.

### VII. Software Availability

The software source code, installers for Mac and Windows, user manual, product demo and other related materials can be downloaded from http://www.guptalab.org/dnacloud.

### VIII. Acknowledgement

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