



MASTER PROJECT

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# Point cloud compression for DNA based storage

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*Author:*  
Romain GRAUX

*Supervisors:*  
Dr. Touradj EBRAHIMI  
Davi LAZZAROTTO

# Chapter 1

## Introduction

Each year, we produce more data than the previous one. All those datas are stored in multiple datacenters spread all over the world. Those datacenters require a lot of energy to maintain bits of information in spinning disks, tapes, capacities, transistors, ...

The Independent reported in 2016 that data centers will consume three times as much energy as they are currently using over the course of the next decade. [1]

It becomes naturally important to find more eco-friendly ways to store data.

## Chapter 2

# Problem defintion

In this work, we will try to build an end-to-end point cloud compression model for quatarnary based entropy coding.

We will first discover the state of the art of compression models for point cloud that leads to the best bitrates for various point clouds and then adapt it to output **A**, **C**, **G** and **T** symbols instead of the classical 0 and 1 binary base.

Then we will have to study the state of the art of DNA based storage and how we can store our long sequence of **A**, **C**, **G** and **T** in the most efficient way to minimise the cost of storing those datas while trying to recover the compressed point cloud in the most XXXX way. For this last part, we will have to study the influence of each parameters to store the DNA strand as small chunks in a solution. At the end, we will have to propose the best parameters to store a DNA strand for a certain period of time.

And finally, we will have to provide the reconstruct model to go from the compressed version to the point cloud as closed as possible from the original one.

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# Chapter 3

## State of the art

### 3.1 DNA based storage

As we produce more data every year, we need to find a way to store it efficiently. Currently, we store our data in big data center consuming a lot of energy to keep these informations in electronic devices, **Find the consumption of data centers**

It would be a good idea to find a way to store our data in a more efficient and ecological way. For storing information, hard drives don't hold a candle to DNA. Our genetic code packs billions of gigabytes into a single gram. A mere milligram of the molecule could encode the complete text of every book in the Library of Congress and have plenty of room to spare. [2]

But it can not be applied to all data types, for example, it is not possible yet to replace an USB stick by a DNA based USB stick and expecting the same experience. The information retrieval latency and high cost of the DNA sequencer and other instruments "currently makes this impractical for general use," says Daniel Gibson, a synthetic biologist at the J. Craig Venter Institute in Rockville, Maryland, "but the field is moving fast and the technology will soon be cheaper, faster, and smaller." Gibson led the team that created the first completely synthetic genome, which included a "watermark" of extra data encoded into the DNA. [2]

This does not mean that there are no applications for DNA based storage. DNA based storage can be used for long term media preservation archives (so called cold media storage) which are infrequently accessed and thus do not need low information retrieval latency.

#### 3.1.1 Constraints

Unfortunately, nucleic acids have biological constraints and can not be assembled in any order like it is the case for binary digits. The DNA strands have to be created in a way that the double helix binds well together and is not immediately desctructed. We must therefore respect the biological constraints to build strong strands that can last for a certain period of time.

In this part, we are going to go through some of the constraints that we have to respect to build a DNA strand and be able to recover it when sequencing it. Unfortunately, the list of constraints is not exhaustive and in the real life, each arangement of nucleic acids has an impact on the strength of a strand, therefore we can only simulate the longevity of a strand thanks to the actual discoveries but not strictly respect the biological constraints.

All constraints could be reduced to limitations regarding GC content, long strands of a single nucleotide (so-called homopolymers), several repeated subsequences in a strand and motifs with biological relevance. In the next sections, we are going to divide the constraints into each step of the process, the explanation for each constraint comes directly from [3].

#### Synthesis

For example, to synthesis synthetic DNA, *in silico* designed constructs have to be split into smaller fragments [usually 200–3000 base pairs (bp)] [4]. The fragments are then splitted into several oligonucleotides (so-called oligos) [usually 40-100 bp] that are individually synthetized. Once synthetized, all oligos are merged back together with either ligase or polymerase-based methods. One of the constraints on the GC content comes from the fact that depending on the synthetis method and the overall GC content of a fragment, the GC content of each oligo

has to be within a specific range. In oligos with high GC content, neighboring guanines tend to form an increased amount of hydrogen bonds, leading to inter/intra-strand folding [5]. To assemble oligos into larger fragments, the melting temperature (and thus the GC content) should only deviate slightly between oligos. To adhere to this restriction, the designed DNA fragments should be homogenous with respect to GC content. Homopolymers further increase the synthesis complexity, leading to fragments that are only synthesizable by using modified oligos and more sophisticated assembly methods, resulting in increased synthesis costs.

### **PCR: Polymerase Chain Reaction**

The amplification of DNA using polymerase chain reaction (PCR) is indispensable for biological science. From DNA synthesis over cloning to DNA sequencing, PCR is used in a wide range of applications. One important factor of a successful PCR is the base composition of the amplification substrate. High melting temperatures due to high GC content of the DNA fragments hinder the separation of strands during the denaturation phase of the PCR. This reduces the yield of the PCR process, since the polymerase cannot efficiently synthesize the growing strand in the presence of previously existing hydrogen bonds. Stretches of repetitive DNA or high GC content can lead to the formation of secondary structures, hindering the elongation of the growing strand. Repetitive regions, as well as homopolymers, can also lead to polymerase slippage, a process in which polymerase briefly loses the connection to the template strand and reconnects at a different position with similar nucleotides content [6].

### **Storage**

Further restrictions on the composition of the DNA construct are due to the cloning process: the GC content should be close to the GC percentage of the host genome and motifs used for the cloning process have to be avoided during the design of the DNA construct

### **Sequencing**

The base composition of a DNA fragment is also an important factor for the successful retrieval of genetic information using DNA sequencing technologies. Illumina sequencing, Oxford Nanopore and PacBio sequencing technologies are biased toward DNA with an intermediate GC content, leading to reduced coverage of regions with strongly deviating GC content [7]. Illumina and Nanopore sequencers also show an increased error rate in the presence of homopolymers [7]. Depending on the sequencing method used, the resulting data show increased substitution rates for specific DNA patterns: for PacBio data, common substitution patterns are  $CG \rightarrow CA$  and  $CG \rightarrow TG$ , Nanopore data contain an increased amount of  $TAG \rightarrow TGG$  and  $TAC \rightarrow TGC$  substitutions [8] and a common substitution pattern in Illumina data is  $GGG \rightarrow GGT$  [9].

#### **3.1.2 Requirements**

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#### **3.1.3 MESA: Mosla Error Simulator**

In order to simulate without going through an expensive and long process that is DNA synthesis and sequencing, we are going to use a simulator that takes into account a large majority of biological constraints. This simulator has been introduced [3] in March 2020 and is a web application for the assessment of DNA fragments in terms of guanine-cytosine (GC) content, homopolymer occurrences and length, repeating subsequences and undesirable sequence motifs. Furthermore, MESA contains a mutation simulator, using either the error probabilities of the assessment calculation, literature-based or user-defined error rates and error spectra. MESA is fully customizable using an easy-to-use web interface, without requiring programming experience. All functionality of MESA is also contained in a REST API, enabling the

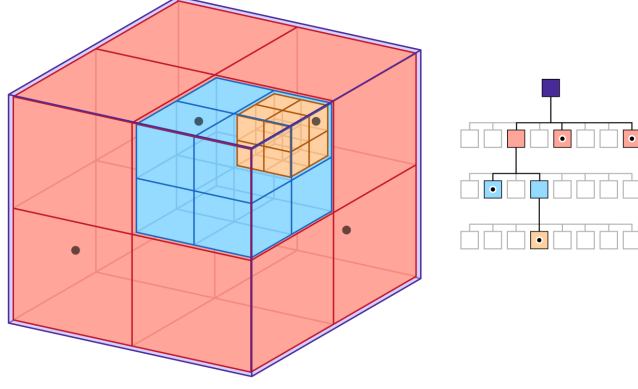


Figure 3.1: Octree representation of a point cloud

incorporation of MESA evaluations into custom workflows for high-throughput evaluation and error simulation of DNA.

As we have seen in the previous section, DNA has a lot of constraints during the synthesis, storage, PCR and sequencing step; With this simulator it is now possible to have a feedback of the strength of a particular DNA strand and thus help us to move towards the best DNA coding to ensure good information retrieval in the end.

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### 3.2 JPEG DNA codec

### 3.3 Point cloud compression

Numerous methods have been proposed to compress point clouds in the literature. They are usually based on different structures than a classical list of coordinates. Octrees, for example, have been widely used for this purpose [10]. The octree representation consists of diving recursively the three dimensional space as nodes of a tree as shown on Figure 3.1.

Compression algorithms using learning based autoencoders architectures have also demonstrated good performance. While some take as input point coordinates [11], others take as input voxelized versions of the point clouds. Voxelized point clouds consist of occupancy grid of regular spaced points so that several points are merged together in a single voxel. A voxel is similar to a three dimensional pixel. These three dimensional grids can be then used as input for a *3D convolutional layer*.

The current state of the art for point cloud compression that we will use in this project is a model called "Latent Space Slicing For Enhanced Entropy Modeling in Learning-Based Point Cloud Geometry Compression" and that has been developed by Nicolas Frank, Davi Lazzarotto and Touradj Ebrahimi at the MMSPG laboratory (EPFL).

#### 3.3.1 Model architecture

This model is shown on Figure 3.2 and consists in a 3D autoencoder architecture with latent entropy coding. The input of the model is an occupancy cubic grid with  $k \times k \times k$  voxels represented by 1 when occupied and 0 otherwise.

The first block (Analysis transform) of the model is composed of 3 *3D convolutional layers* and 2 *convolutional residual blocks* arranged staggered which produces a latent representation  $y$  of shape  $l \times l \times l \times d$  with  $d$  being the latent dimension.

This latent representation is then fed into an Hyper-Analysis transform block yielding  $z$ . This hyperprior is passed to the bitstream as side information after quantization, and is used to model the entropy of the quantized latent features  $\hat{y}$  after going through the hyper-synthesis.

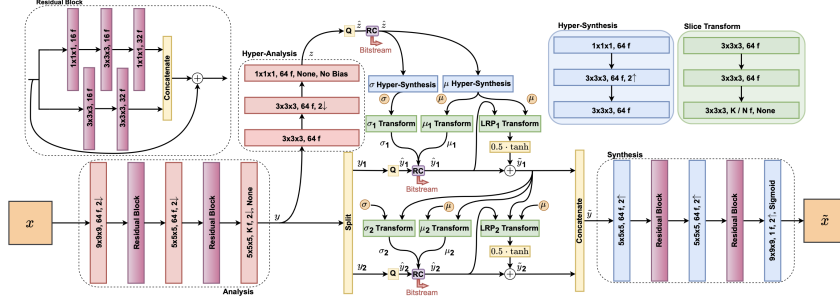


Figure 3.2: The "Latent Space Slicing For Enhanced Entropy Modeling in Learning-Based Point Cloud Geometry Compression" architecture with 2 slices.

While in other solutions for learning-based point cloud compression the hyperprior would be the only variable used to estimate the scale and mean of  $\hat{y}$ , they use previously decoded channels for entropy modeling.

The latent representation  $y$  is sliced along the channel dimension into  $N$  non-overlapping and equally sized tensors  $y_i$  with  $i \in \{1, \dots, N\}$ .

Once the latent representation  $y$  is sliced, they compute the entropy parameters  $(\mu_i, \sigma_i)$  for each slice  $y_i$  from the global entropy parameters  $(\mu, \sigma)$  and the previously decoded latent representation slices  $\tilde{y}_j \forall j \in \{0, \dots, i-1\}$ .

The final latent representation reconstruction  $\tilde{y}_i$  is produced from  $\hat{y}_i$  after going through a latent residual prediction (LRP) transform that predicts the quantization error  $y_i - \hat{y}_i$  in order to take into account this error from the global entropy parameters  $(\mu, \sigma)$ , the current  $\hat{y}_i$  and previously decoded latent representation slices  $\tilde{y}_j \forall j \in \{0, \dots, i\}$ . A  $\tanh$  non-linearity scaled by a factor 0.5 is applied to the output of the transform to keep the output of the LRP within the range of quantization error. The predicted residuals are then added to  $\hat{y}_i$ , generating  $\tilde{y}_i$ . These slices are then concatenated along the channel dimension before going through the synthesis transform. This last learned block finally generates the output block  $\tilde{x}$  containing a probability estimation for the occupancy of each voxel in the grid.

They trained the model from end-to-end between the input occupancy grid and output probability occupancy grid as a rate-distortion minimization problem represented by the loss function expressed as  $\mathcal{L} = R + \lambda D$ . The trade-off parameter  $\lambda$  is used to balance the importance of compression rate against reconstruction quality. The distortion is computed from a focal loss (FL) which can be expressed as:

$$\text{FL}(x, \tilde{x}) = -x\alpha(1 - \tilde{x})^\gamma \log(\tilde{x}) - (1 - x)(1 - \alpha)\tilde{x}^\gamma \log(1 - \tilde{x})$$

with  $\alpha$  and  $\gamma$  being configurable hyperparameters. This focal loss is a so-called binary weighted focal crossentropy loss.

The last step to recover the actual binary occupancy grid from the output probability occupancy grid  $\tilde{x}$  is to apply a threshold  $t$  and round every value above  $t$  to 1 and 0 otherwise. While a naive approach would be to set this threshold  $t$  to 0.5, they decided to find the best threshold  $t \in [0, 1]$  such that it minimizes the point-to-point MSE [12] between the original and reconstructed rounded block.

This technique was introduced by [13] and has proven to enhance reconstruction quality without significantly impacting the bitrate as it is only required to add a threshold  $t \in [0, 100]$  in the final bitstream.

## Chapter 4

# Implementation

### 4.1 DNA latent representation

In this section, we will plug all parts together in order to implement a latent representation of DNA. With these pieces of DNA strands, we will be able to synthesis and encapsulate them in a real medium to preserve them.

The first step in order to achieve this is to extract the features of the point clouds with the analysis transform of the model presented previously.



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