PhD Proposal

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Introduction

Computational pangenomics is a new emerging research field in computational biology based on the idea that we need to move from the traditional view of a reference genome as a *linear sequence* to the one where we consider the *genetic variations* or *variants*, in a large collection of individual genomes. This new reference, which was firstly introduced in 2005 for dealing with the comparison of genes in bacterial species, is called a *pangenome*. Pangenomics is becoming increasingly essential in the field of biology and personalized medicine, mainly thanks to **genome-wide association studies (*GWAS*)**, which need to analyze a large collection of individual genomes. Moreover, these studies also require such data to be indexed, queried and analyzed. Just to give some examples, from a Computer Science point of view, the *homo sapiens reference genome (GRCh38.p14)* consists of ~ 3.1 characters *Gb* and contains $\sim 59,265$ genes, as reported by NCBI. Biological studies based on the *1000 Genome Project* have pointed out that there are over 88 million variants between those human genomes. Among these variants, 84.7 million are **Single Nucleotide Polymorphisms (*SNPs*)**, 3.6 million are **short insertions/deletions (*indel*)** and 60000 are **structural variants**, involving more than 50 nucleotides. Moreover, it is necessary to consider that the final goal is the sequencing of at least 100 thousand individuals, in the next few years, also thanks to the latest developments in sequencing technologies, (**Next Generation Sequencing (*NGS*)** and **third-generation sequencing**). Therefore, it is clear that dealing with this amount of data is challenging for the current state-of-the-art algorithms. The problem of *pattern matching* is one of the most fundamental topics in the field of algorithmics and bioinformatics, where the input is a long text (a genome) and a short pattern (a read) and the output is the list of all occurrences of the pattern as a substring of the text. We can notice that such problem has practical and efficient linear-time solutions if there is proper indexing of the text. The interest in such problems is due to the need to align sequences or to search for specific patterns within a database of *DNA* sequences. In this context, a large number of data structures and algorithms have been designed. Among these, one of the most used is the **Burrows-Wheeler transform (*BWT*)**, introduced in 1994 to compress texts, on which the *FM-index* is based. The use of such algorithms is essential in speeding up alignment algorithms such as **BLAST**, one of the most widely used aligners and implementation of one of the most cited theoretical studies in the field of bioinformatics. This aligner is based on the *seed-and-extend paradigm*, where pattern matching occurrences, the so-called *seed*, are chosen to be the starting point of the alignment. Then, from the seed, the algorithm proceeds to extend the match to compute the alignment, increasing the efficiency of the algorithm compared, for example, to those based on dynamic programming. The key point, talking about *BWT*, is the ability to compress large texts and query the compressed texts themselves, allowing alignment even in very large databases such as those used by *BLAST*.

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As introduced, in the last few years the researchers are focusing on the study of the *pangenome*, which is a compact representation of multiple genomes, encoding the variations of a multitude of individual genomes from the same species. From a computational point of view, *pangenome* is often represented as a *pangenome graph* but also as a *collection of haplotypes* [1], for which space complexity can be optimised thanks to *succinct data structures*. By *pangenome*, it has been possible to take into account the high variability in population genomes, in addition to the specificity of a single genome, allowing even more the use of computational techniques for a *personalized approach to medicine*, an approach that will become increasingly important even in near future.

The main focus of this proposal is improving the current pattern matching algorithms and data structures state of the art to represent and query biological sequences, with a focus on space complexity. In fact, the design of data structures and algorithms to handle large collections of data will fill the current gap that exists between the exponential growth of genomic data and the available state of the art algorithms to manage such data. Theese research fields will have an impact on the ability of molecular biologists to analyze the current amount of data to extract important genomic information from *pangenome graphs*.

State of the art

Now I present a brief overview of the main algorithms, data structures and tools that are the state of the art of computational pangenomics.

Efficient and compact boolean data structures. If $\mathcal{X}$ is the optimal number of bits needed to store some data, a representation of this information is defined *succint* if it takes $\mathcal{X} + o(\mathcal{X})$ bits of space. A *bitvector*, of the most important *succint data structures*, is an array on n bits that allows two particular operations, called **rank** and **select**, in addition to the classic operations on boolean arrays, such as *random access* in *constant time*. More in detail, the *rank function* allows calculating how many occurrences of one are up to a certain index. Instead, the *select function* allows obtaining the index of every 1 present in the *bitvector*. Formally, given a bitvector B, such that $|B| = n$, and given an index i, such that $0 \leq i < n$, we can define $rank_B(i) = \sum_{k=0}^{k<i} B[k]$. Instead, about the select function, given an integer i, such that $0 < i \leq rank_B(n)$, we can define $select(i) = \min\{j \mid rank_B(j+1) = i\}$. From a theoretical point of view, these two operations can be supported in *constant time*, with the additional cost of $o(n)$ bits in memory. There are several implementations of the same (for example *plain bitvector, interleaved bitvector, sparse bivector*, etc...) within **SDSL (*Succint Data Structures Library*)**, one of the most important C++ library used in bioinformatics proposed by Gog et al. in 2014. Thanks to the various implementations, both the computational time of the two main operations and the additional bits needed vary, allowing a better choice of the best variant possible depending on the use case. Due to their compactness in memory, *bitvectors* are widely used in algorithms for the analysis of biological sequences.

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Run-length encoding and succinct data structures. Speaking of *pangenome*, linear indexing via *FM-index* is no longer the best solution as it does not handle the large repetitions there are in this new type of sequences. A simple but effective strategy to compress texts is based on encoding a **run** of consecutive identical characters as the pair (characters, length of the run). For example, the string `AAAAAA` is encoded as (`A`, 6). Clearly, such an encoding achieves a better compression ratio the more consecutive character we can find. In 2005 Mäniken and Navarro defined the **Run-Length encoded Burrows–Wheeler Transform (*RLBWT*)**. Given a text T, $RLBWT_T$ is a representation of BWT_T with a compact storage of consecutive equal characters, the so-called *runs*. With this new perspective, some recent papers — *MONI* [2] and *PHONI* [3] — present two practical indexing tools that are tailored for pangenomes. In these works, algorithms have changed from being linear over the length of the text, n, to be linear over the number of runs, r, so sub-linear over the length of the text. The new indexing method, introduced by Gagie et al., was called **r-index** and it corresponds to the *RLBWT* plus the *suffix array sampling* at the beginning and the end of every run.

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To better describe how *pattern matching* works in these papers, we need to introduce some definitions. First of all, the main purpose of these algorithms is to compute **Maximal Exact Matches (*MEMs*)** of a pattern in a text. Given a text T and a pattern P, a substring of the pattern $P[i : i+l-1]$, of length l, is a *MEM* of P in T if $P[i : i+l-1]$ is a substring of T but neither $P[i-1 : i+l-1]$ nor $P[i : i+l]$ are, that is the match cannot be extended in any direction. The authors state that computing *MEMs* is equivalent to computing **matching statistics (*MS*)**. Formally, the *MS* of a pattern P in respect to a text T is an array M of pairs position/length (pos/len), $|M| = |P|$, such that $T[M[i].pos : M[i].pos+M[i].len-1] = P[i : i+M[i].len]-1]$ and $P[i : i + M[i].len]$ does not occur in T. To compute *MS*, *random-access* over the text is required but it is also required that the text is stored in a compressed way. For this purpose, the authors get a compressed representation of the text, via a **straight-line program (*SLP*)**, that is based on a *grammar-compression* algorithm (by a *context-free grammar*). To compute *MS*, in *MONI*, the authors used the so-called **thresholds**, defined as the minimum **Longest Common Prefix (*LCP*)** value between two consecutive runs of the same character. This solution requires two sweeps over the *MS array* and *random access* over the *SLP*. The improvement in *PHONI* is due to the fact that it was decided to use **longest common extension (*LCE*) queries**, to compute *MS*, through a single sweep and reducing the number of accesses to the *SLP*. Formally, given two positions i and j in a text T, such that $|T| = n$, an *LCE query* compute the length of the longest common prefix between $T[i : n-1]$ and $T[j : n-1]$. So, *LCE* is the right equal common extension between two positions in the text. Summing up, after computing the *MS array*, as stated by Bannai et al., it is possible to obtain directly *MEMs*. Furthermore, using a particular function called φ (and its inverse φ^{-1}), based on the use of the **inverse suffix array (*ISA*)**, it has been possible to find all starting positions of all copies of P in T from starting position of the match extracted by *MS*, quickly calculating, given a position p in SA, the previous and next index stored in the suffix array. It is important to note that the use of *bitvectors*, to efficiently store and query *runs*, allows many improvements in memory usage. In fact, for example, according to Rossi et al., *BWA-MEM*, one of the most used *read aligners*, uses between 1.1 and 3.8 times more memory than *MONI*, having further improved results in *PHONI*.

Genotyping variants problems and GWAS. Several computational problems, arising from computational biology, have led to the development of algorithms and data structures for analyzing specific sequence data, such as *haplotypes* and *genotypes*, in the **genotyping variants problem**. Briefly, we could define *haplotypes* as a combination of allelic variants, each one inherited from a parent. Instead, the *genotype* is combined information of the haplotypes. For example, humans have two haplotypes, being diploid, and the genotype is their combined information. Since 2005, the publication of **GWAS** has begun. The goal of this type of studies is to screen the *pangenome* looking for associations between genetic variants, for example, to study the outcomes of diseases. In this particular historical period, it is impossible not to mention viruses. In fact, by nature, viruses replicate a lot but often in a not perfect way, during infections. This produces many inexact clones, referred as **viral haplotypes**, which, taken together, form the **viral pangenome**. The identification of all these haplotypes is crucial both to the study of the spread of viruses and to the production of efficient drugs, in a context of high pharmacological resistance.
In 2014, Durbin proposed the **positional Burrows–Wheeler transform (*PBWT*)** to solve the problem of *pattern matching* on panels of haplotypes, with efficient compression. According to the author, the used memory by *PBWT* is nearly six times smaller than the raw data. In detail, he analyzed a biallelic-sites panel X, built on an alphabet $\Sigma \in \{0, 1\}$, with M haplotypes/individuals and N sites. This data structure is based on a *reversed-prefix ordering* at each column k that produces two different multidimensional arrays. The first one is the set of the **prefix arrays**, denoted by a, which contains the index of the haplotype m in the original panel, for each column k and each position i of a_k. More formally, we can say that $a_k[i] = m$ iff X_m is the i-th haplotype in the reversed-prefix ordering at column k. We can note x_m, such that $a_k[i] = m$, could be denoted by y_i^k. The second bidimensional array is the set of the **divergence arrays**, denoted by d, which indicates the index of the starting column of the longest common suffix, ending in column k, between a row and its previous one, at reversed-prefix ordering at column k. More formally, we can define $d_k[i] = h$ iff h is the smallest column index such that $y_i^k[h, k) = y_{i-1}^k[h, k)$. Thanks to these two bidimensional arrays, it is possible to compute all matches within X longer than a minimum length L, all set-maximal matches within X in linear time and all set-maximal matches, maximal in the width of the match, from a new sequence z to X in $\mathcal{O}(M^2N)$. Another interesting use of the *PBWT* is to extract common patterns in a set of haplotypes, computing the so-called *blocks* (maximal intervals of columns, not extendable in any direction, such that there is a subset of identical rows), for the identification of genomic regions that show, for example, signatures of natural selection. Since its development, there has been a growth in research based on it, both in terms of variants design, such as the **multiallelic PBWT** or the **dynamic PBWT** (where the static PBWT is generalized to a dynamic data structure via linked lists), and in terms of its use to study haplotype panels. An interesting paper is the one by Williams and Mumey, published in 2020, who studied *maximal perfect haplotype blocks* with the addition of a *missing data* management attempt, handled with the help of wildcards, using the *PBWT*. A very intriguing tool, talking about *GWAS*, is **IMPUTE5** [5], proposed by Rubinacci et al. in 2020. The main purpose of this software is to make *genotype imputation* to predict unobserved genotypes from a panel with millions of haplotypes, so it was necessary to use *PBWT*. Improving this data structure, it will be possible to help the *GWAS* on cancer and other disorders.
In conclusion, as haplotypes panel can be thought of as a particular case of *pangenome* (with fixed-length genomes) we can understand the importance of further improvements to this data structure in *computational pangenomics*, especially with regard to space complexity.

Research goals

For my master's thesis, I had to adapt the concept described for *RLBWT* in *MONI* and *PHONI*. Obviously, there are some limitations, as in Durbin's *PBWT*, such as studying only biallelic panels and ignoring the management of missing data, which are very frequent in real cases.
During my master's degree, I have deepened some theoretical issues related to algorithms, especially in bioinformatics, and some modelling and inference topics, related to computational systems biology. So, it is my interest to continue my studies with PhD to be able to deepen computer science potential in the biological context. In summary, the most important research goal of my PhD is designing and validating algorithms and data structures to deal with open problems in pangenomics, such as:

1. **Multiallelic data**. Thanks to the growth in the production of genotypic data, the number of multiallelic sites is expected to grow, as well as the number of individuals (even if there is only a 2% presence of triallelic sites, actually known in the human genome) Moreover, not only such sites could be more than expected but they are usually not considered by the majority of tools. The first step in this direction

was made by Naseri with the already cited *m-PBWT*. Talking about space complexity, the run-length encoded version of the stored arrays for the *FM-index* could allow the management of increasingly large data for the imputation phases. In this context, the aim is to implement a new version of the *RLPBWT* that can manage multiallelic data, adapting the current use of bitvectors to handle efficiently also the *LF-mapping* with more than two alleles.

2. **Missing data**. A second extension, that would be more complicated to design, is a *RLPBWT* version that admits the presence of missing data. Most algorithms and data structures mentioned above assume that they work on exact data. In reality, real data can contain errors or even gaps, both mainly due to the imperfections of sequencing technologies, although now they have high correctness rates. Unfortunately, this is still an open problem, even if most of the errors are corrected in a preliminary step (mostly by heuristic methods). Handling missing data is known to be *hard* because every gap could assume any possible value. Having said this, I should probably deal with *parametric* or *approximate algorithms*, based on research already developed in *BIAS*.
3. **Data structures and algorithms for the representation and indexing of pangenome graphs**. The above mentioned research goals are relevant in the context of a more general goal which is to deepen the study of data structures for representing the information of *pangenome graphs*. In fact, it is possible to interpret haplotype sequences as *pangenome graphs*, in a compact way via the **Graph BWT (*GBWT*)**, even if it is more a *multi-string BWT* than a classical graph. A first improvement would be space optimization. There are a lot of open problems regarding the use of *GBWT*, such as handling missing/erroneous data and representing complex and nested variants. Once I have tried to solve the problem of missing data for the *PBWT/RLPBWT*, I could think of an adaptation for the *GBWT* because it would be possible to analyze more precisely real data. I would also point out my interest in deepening all the other issues related to pattern matching, indexing structures and pangenome graphs, according to the *BIAS* laboratory's topics of interest. So far there has been talked of *bitvector-based* and *BWT-based indexing*. There are other data structures that would be interesting to study and extend, such as *wavelet tree*, another *succint data structure* used to compress texts. The design of new indexing structures, both for strings and graphs, could lead to very important results in the field of computational pangenomics, for example regarding the *string-graph alignment problem*.

The theoretical research requires an experimental verification, for this purpose some technologies that will be used during my PhD must be mentioned. During both my bachelor's and master's degree, I mainly focused on the use of the **C++ programming language**, thanks to the availability of efficient libraries, such as the already cited *SDSL*. However, in addition to *C++*, I had the opportunity to deepen **Python**, with libraries such as *biopython*, and **Rust**, with recently developed libraries such as *bio-rust* (even if still not complete from an algorithmic point of view). Always from an experimental point of view, there is currently a lack of libraries, in any programming language, dedicated to the study of *pangenome*, also with regard to benchmarking. It is therefore my interest to contribute to the development of such open-source libraries. Another point of interest is the analysis and the development of efficient algorithms based on parallel computing (also on *GPU*), that are increasingly in use in both *bioinformatics* and *computational systems biology*. To conclude this proposal, I also would point out the intention to remain in contact with various researchers, with whom I have already collaborated during my master thesis, including Christina Boucher (University of Florida) and Travis Gagie (Dalhousie University).

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