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## De novo long reads assembly using integer linear programming

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UNIVERSITÉ DE RENNES 1  
UFR SCIENCES DE LA VIE  
ET DE L'ENVIRONNEMENT

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*De novo* LONG READS ASSEMBLY  
USING INTEGER LINEAR PROGRAMING

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BIOINFORMATIC MASTER 1  
- INTERNSHIP REPORT -

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2019 april 23 — 2019 july 31



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*Professeur Epaix*

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# Introduction

## 1.1 The *de novo* assembly

**The long reads assembly advantage against repetitions in genomes** In order to sequence a genome, it has to be cut in several sequences - called reads, with a reasonable length. Indeed, as assembly is based on similarity between two reads, it is important to know if this similarity does make sense or if it is an artefact due to too small sequences. Artefacts can be obtained because of repetitions in the genome - large repetitions imply more similarity artefacts. For bacteria genome, short repeated sequences are more abundant [1] due to evolution [2] but in the human genome repetitions are longer and in high frequency [3]. So using long reads permits to decrease the number of assembly errors due to artefacts, as they are more likely to contain the entire repetition - and especially an extremity which allows the differentiation of two same repetitions.

**The long reads sequencing technology errors issue** For the moment, short reads assembly seems to be more used than long reads assembly. Indeed, while Illumina technology uses short reads and has a little error rate - with some substitutions, long reads sequencing technology as the Oxford Nanopore technology has approximately ten times more error with indel error type [4]. Also, the cost is two times higher according to the same source.

**The current long reads assemblers** For citing a couple of long reads assemblers, wtdbg2 [5] uses *De Bruijn Graph* just like SPAdes [6], but combines normal k-mers and homopolymer-compressed k-mers to find read overlaps. Very fast, it should be more interesting using it for larger eukaryote genomes because of limited resources it requires [7].



## 1.2 The linear optimization: a mathematical exact approach

While previously cited assemblers use *De Bruijn Graph* and heuristics, linear optimization permits to find an exact solution. Linear means that all the equations in the mathematical model are written as linear variables combination. As an example:

$$\sum_{i=1}^n C_i * x_i \leq B, \text{ where } x_i \text{ are variables, } C_i \text{ and } B \text{ constants, and } n \text{ integers.}$$

In a linear model, there is an objective function representing the aim of the mathematical solver: *maximize* or *minimize* the value of a linear expression. Then, there are linear constraints directing the objective function to a wanted solution. The set of possibilities is reduced by these constraints and the permissible solutions are in the new subset.

As this project is based on mixed integer linear programming (MILP), the wanted variables for the solution are integer types, and finding the solution can be slow. The solving method is *Branch and Bound* [8]: it explores the tree of possibilities with using lower and upper bounds - compared with the current value of an admissible solution, in order to find the optimal solution or eliminate nodes - so reducing the tree exploration.

Choosing an exact approach with finding optimal solution should reduce assembly errors, added to sequencing errors. But this approach can be more time consuming than using heuristics.

## 1.3 The LOREAS program: the first step of a long read assembler

Two steps composed the proposed assembly method: first, a main structure of the genome has to be found with ordering long reads, then a consensus sequence has to be done. The programmed pipeline named LOREAS during this internship executes the first step : it permits to obtain an order of long reads using MILP on overlaps graph - described in section 2.2, paragraph 3.

# Material and methods

## 2.1 Material and tools

**Bacteria genomes** The following table contains the genomes used by LOREAS program in this study. All genomes were extracted from NCBI:

<b>Bacteria name</b>	<b>NCBI database ID</b>	<b>Genome size (in bp)</b>
Acinetobacter baumannii (Abau)	NZ_CP009257.1	4,335,793
Bacillus sp. 1NLA3E (B1NL)	NC_021171.1	4,815,602
Escherichia coli (Ecol)	NZ_CP032667.1	4,639,694
Helicobacter pylori (Hpyl)	NC_000915.1	1,667,867
Mycobacterium bovis (Mbov)	NC_002945.4	4,349,904
Prochlorococcus sp. MIT 0604 (Pmit)	NZ_CP007753.1	1,780,061
Salmonella enterica (Sent)	NC_003198.1	4,809,037
Staphylococcus aureus (Saur)	NC_007795.1	2,821,361
Streptococcus thermophilus (Sthe)	FR875178.1	1,929,905
Yersinia pestis (Ypes)	NC_003143.1	4,653,728

Table 2.1: The first column contains the name of bacteria used by LOREAS, while the second and the third columns report their NCBI ID and their size respectively.

**DEEPSIMULATOR 1.5 [9] - an Oxford Nanopore long reads generator** DEEPSIMULATOR is an open source software which generates - thanks to machine learning, long reads from a reference genome with error generation close to Oxford Nanopore sequencing errors.

**MINIMAP2 2.17 [10] for long reads alignment** MINIMAP2 is a long reads aligner. It can make the mapping of long reads against a reference or make the overlap alignment of long reads against long reads. The advantage of MINIMAP2 is the possibility of choosing the long reads sequencing origin - as Oxford Nanopore does or PacBio.

**AMPL 3.5.0 [11] optimization mathematical implementation language** AMPL is a mathematical commercial language. All the integer linear problems were written in this language.

**GUROBI 8.1.0 [12] solver to solve the implemented problems in AMPL** GUROBI is a solver which solves MILP.

**METIS 5.1.0 [13] - a graph partitioner** METIS is a partitioner of undirected graphs.

**Programation with Python 3.6.8 [14] and Linux Bash 4.4.19 [15]** All the programs were written in Python 3.6.8 version language. Also, the program uses the Python packages NetworkX 2.3 [16] for graph manipulation, matplotlib 3.1.1 [17] for graphic generation and NumPy 1.17.0 [18]. The scripts for the commands of the project and for the full pipeline were programed in Bash 4.4.19.

**GEPHI 0.9.2 [19]** GEPHI 0.9.2 is an open free tool for visualizing graphs.

**Run material** The programs were executed on a personal laptop, on UBUNTU 18.10 OS. The laptop had 16 GB of RAM, a processor Intel i5 7th generation with 2.50GHz of CPU and a NVIDIA GeForce GTX 1050 as GPU.

## 2.2 Methods

**Long reads generation with DEEPSIMULATOR** Long reads from bacteria genomes cited above were generated with DEEPSIMULATOR, using the Oxford Nanopore Technology official basecaller Albacore. The depth sequencing was set to 30X. In order to obtain the coordinates of long reads on the genome, MINIMAP2 was used for mapping long reads on the reference genome with the option *map-ont*. In the sequel, these coordinates are called *mapping coordinates*.

**Reads all vs all alignment with MINIMAP2 and filter wanted overlap types** All reads are aligned versus all the others. The alignments have to be filtered according the following overlap definition: an alignment between two long reads is considered as an overlap if the suffix of the first read overlaps with the prefix of the second read.

Because of sequencing issue, it is necessary to define a threshold, denoted  $x_{thr}$  which permits flexibility on the read suffix-prefix definition.

However, if an alignment between two sequences, with respect to the threshold  $x_{thr}$ , represents a read subsequence of the other, then this alignment is eliminated.

Let define in figure (2.1a) some alignment areas for reads  $u$  and  $v$  - aligned by MINIMAP2, in order to mathematically filter alignments:

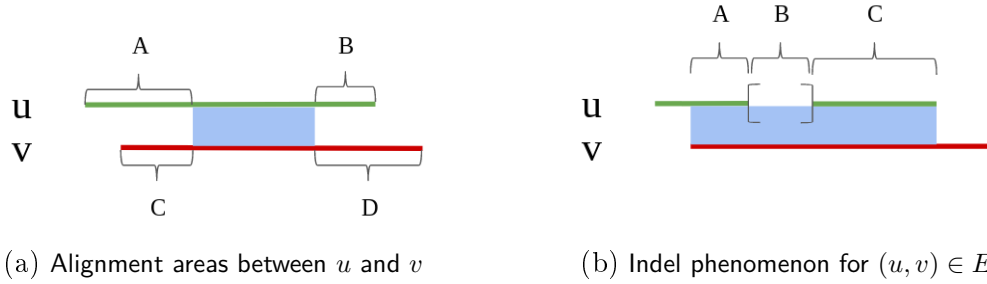


Figure 2.1:  $u$  and  $v$  are two reads aligned each other by MINIMAP2. In (2.1a): the alignment area - so the nucleotide similarity between  $u$  and  $v$ , is represented by the blue color; A, B, C and D are integers and represent the length of areas whose  $u$  and  $v$  nucleotides sequences were not considered as similar by the alignment software. In (2.1b): the square brackets represent the consequence of an indel on read  $u$  - it can be a deletion on  $u$ , or an insertion on  $v$  if the overlap between  $u$  and  $v$  is biologically true. A, B and C are now lengths of sub-overlapping where B is the length of the indel.

We assume, according figure (2.1a), that  $u$  overlaps  $v$  if, and only if:

$$(u, v) \in E \iff \begin{cases} C < x_{thr} \\ B < x_{thr} \\ C < A \\ B < D \end{cases} \quad \text{where } E \text{ is the set of overlaps}$$

During the sequencing step, some reads could have extra parts or at the opposite did not have nucleotide sequences from the real sequencing DNA fragment. Extra parts and deleted parts are respectively called *insertion* and *deletion*. More globally, both represent *indel* errors.

In order to take in account potential indel errors in a long reads alignment, we filter on the difference between the two read alignment lengths. Consider other areas for representing indel phenomenon with the figure (2.1b). The overlap  $(u, v) \in E$  is accepted -

according figure (2.1b), if and only if:

$$B \leq \frac{\frac{2 \times A + 2 \times C + B}{2}}{10}$$

When the MINIMAP2 alignments were filtered respecting the overlap definition and the indel threshold, let define the overlap length of the overlap  $(u, v) \in E$   $\lambda_{uv} = A + B + C$ . Furthermore, let define  $g_{uv}$  the length of the global indel for the overlap  $(u, v) \in E$  as follow:

$$g_{uv} = \begin{cases} 0 & \text{if the indel is on } u \\ B & \text{else} \end{cases}$$

Then, all the overlaps are considered on their overlap length by a global threshold - denoted by  $\lambda_{min}$ , when  $\lambda_{uv} > \lambda_{min}$ .

**Creation of the overlaps graph** Towards to order the reads, graph modelisation is used. The overlaps graph  $G$  is defined as follow:  $G = (V, l, E, \lambda)$  where  $V$  is the set of vertices *i.e.* the set of long reads  $v$  of size  $l_v$ , and  $E$  the set of edges *i.e.* the set of couples  $(u, v) \in V^2$ , weighted by  $\lambda_{uv}$ . In the overlaps modelisation, the graph  $G$  is directed, *i.e.* for  $u \in V$  and  $v \in V$ , *if*  $(u, v) \in E$ ,  $(v, u)$  is not necessary in  $E$ .

So  $V$  is the set of long reads and  $E$  the set of overlaps. Depending of the local reads orientation - because the two complementary DNA strands are read in the opposite direction, the letters  $F$  and  $R$  - respectively for *Forward* and *Reverse* (which means the reverse complement of a read sequence), are ordered to nodes name. Let suppose the following overlap:

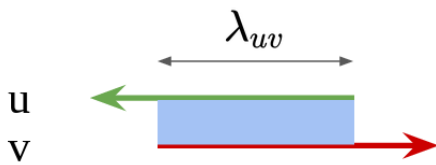
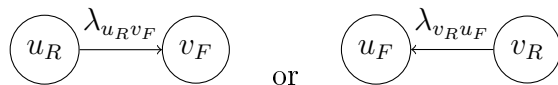


Figure 2.2:  $u$  and  $v$  are overlapping together:  $u$  in reverse orientation overlaps  $v$  in forward orientation is equivalent to say the reverse of  $v$  overlaps the forward of  $u$ .  $\lambda_{uv}$  is the length of the overlap (in blue). By convention,  $\lambda_{u_R v_F} = \lambda_{v_R u_F} = \lambda_{uv}$

It results in graph modelisation as:



As the overlap graph is oriented, an orientation of all the reads has to be chosen. An arbitrary read is chosen and an orientation is given for it (let take the *forward* orientation). Then, all its neighbors, *i.e.* all the reads overlapping with it, obtain an

orientation according to the overlap orientation. In the above example, if  $u$  is chosen  $F$ , then  $v$  has to be chosen  $R$ . When all the neighbors of the current read have an orientation, all the neighbors of a new oriented read have to get an orientation *etc.*

However, if a read  $w$  is discovered in both orientations then it and all the overlaps containing it are eliminated.

### **Finding the heaviest path in the overlap graph with mathematical programming**

**approach** Ordering the reads can be done by finding a path in the overlaps graph. We assume that a correct order of long reads is the heaviest path in the overlap graph *i.e.* finding a path that maximizes the number of overlaps under main constraints described below, using MILP:

- a long read can participate at most once - so it is either a starter, either an intermediate, either a terminal, or it does not participate in the path;
- there is only one starter read and only one terminal read;
- if the overlap  $(u, v) \in E$  -  $u$  and  $v$  two oriented reads, is chosen, the  $u$ 's right position and this of  $v$  must respect the overlap length  $\lambda_{uv}$ , the size of the reads and the gap  $g_{uv}$ .

All the mathematical model is described and interpreted in appendix C.1.

#### **2.2.1 Using graph partition for huge overlaps graph**

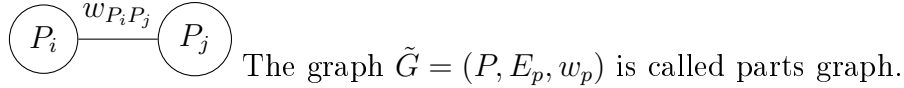
In LOREAS program, an overlaps graph  $G = (V, l, E, \lambda)$  is considered huge if  $\text{card}(E) > 2000$ . In this case, the graph  $G$  is partitioned in several parts.

**Partitioning  $G$  using METIS** METIS requires an undirected input graph. So temporarily,  $\forall (u, v) \in V^2, (u, v) \in E \implies (v, u) \in E$ . Long reads are partitioned in several parts using the length of reads (the size of a node) and the overlap lengths (the weight of an edge): these partitioning options are precised with the option  $\text{fmt} = 011$  in METIS input file. Each of these parts is required to be one connected component<sup>1</sup>. If this condition is not satisfied, the corresponding part is separated in several connected components.

---

<sup>1</sup>"In graph theory, [...] a connected component, of an undirected graph is a subgraph in which any two vertices are connected to each other by paths" *From Wikipedia, the free encyclopedia - Component (graph theory)*.

**Parts graph modelisation** Denote by  $P$  the set of parts obtained in this way. As explained above, any of them is one connected component. Any couple  $(P_i, P_j) \in P$  is connected by an edge of the size  $w_{P_i P_j}$  wich corresponds to the total number of cut overlaps between the reads in  $P_i$  and the reads in  $P_j$ :



**Finding the heaviest path in  $\tilde{G}$**  We want to know the order the parts have to be solved. This can be done by finding a path in the parts graph  $\tilde{G}$ , so MILP is used to find the heaviest path *i.e.* choosing the maximum of cut overlaps under main constraints described bellow:

- a part must participate in the path, so it is either a starter, either an intermediate, or a terminal;
- there is only one starter part and only one terminal part.

The entire mathematical model is described and interpreted in appendix C.2.

Once the heaviest path in  $\tilde{G}$  is found, each one of the parts  $P_i$  has to be solved, that is finding the heaviest path in the overlaps graph  $G_{P_i} = (V_{P_i}, E_{P_i}, \lambda)$ . So the first part in the path is solved, with taking care of the possibility to make the link with the second one, and this until the last part in the parts graph.

**Merging all the paths obtained in any of the parts** Once each part  $P_i$  of the parts in  $\tilde{G}$  is solved with finding its path  $path_i$ , all the paths are merged to obtain the final path  $path_f$ . Let us denote by  $V_f$  the set of reads in  $path_f$ , and by  $E_f$  the set of couple  $(u, v) \in V_f^2$ , where  $u$  and  $v$  are two consecutive reads in  $path_f$ .

## 2.2.2 Results obtention and options used

The following table contains the final tests options for each bacteria:

Bacteria id	Abau	B1NL	Ecol	Hpyl	Mbov	Pmit	Sent	Saur	Sthe	Ypes
$\lambda_{min}$	5000	5000	5000	5000	7000	5000	5000	5000	5000	4000
$x_{thr}$	100	100	100	100	100	100	100	100	100	100

Table 2.2: Options used for obtaining LOREAS results. The  $\lambda_{min}$  represents the threshold of minimum overlap length;  $x_{thr}$  is the threshold described in section 2.2, paragraph 2. When the overlaps graphs have to be partitioned, the number of parts is the division quotient of the overlaps number by 2000.

# Results

## 3.1 Long reads generation and alignment filter

The following table summarizes the long reads generation with DEEPSIMULATOR, shows the effect on the number of MINIMAP2 alignments and on the number of reads after filtering according the overlap definition given in section 2.2, paragraph 2:

<b>Bacteria name</b>	<b>NR</b>	<b>RLM</b>	<b>NA</b>	<b>ALM</b>	<b>NCR</b>	<b>NCO</b>
A. baumannii	29,558	6,946	407,876	6,502	17,587	227,159
B. sp. 1NLA3E	32,833	6,920	559,411	9,424	19,539	253,711
E. coli	31,633	6,938	530,239	5,408	18,866	251,445
H. pylori	11,370	6,838	186,841	9,452	6,724	87,445
M. bovis	29,633	6,955	300,367	7,578	14,781	144,203
P. sp. MIT 0604	12,136	6,909	227,880	5,369	7,200	96,477
S. enterica	32,787	6,931	715,914	4,628	19,521	259,053
S. aureus	19,236	6,950	327,080	5,302	11,484	150,906
S. thermophilus	13,158	6,906	225,726	5,120	7,822	101,989
Y. pestis	31,726	6,929	688,471	6,324	20,814	302,795

Table 3.1: For each bacteria, the number of long generated reads (NR), the median of generated reads lengths (RLM), the number of MINIMAP2 alignments (NA), the median of MINIMAP2 alignments lengths (ALM), the number of considered overlaps (NCO) and the number of considered reads (NCR) are given.

## 3.2 Ordering results

In order to know if the final order was correct, local and global mapping coordinates variations were visualized. Indeed, if the global mapping coordinates variation was monotonous, then the order is correct. Two measures were used and compared: the global increasing variation (*GIV*) and the global decreasing variation (*GDV*) calculated as following:

$$GIV = \sum_{\substack{(u,v) \in E_f \\ c_v - c_u > 0}} (c_v - c_u) \quad GDV = \sum_{\substack{(u,v) \in E_f \\ c_v - c_u < 0}} |c_v - c_u|$$



where  $E_f$  is defined above in subsection 2.2.1, paragraph 4,  $c_u$  and  $c_v$  are respectively the mapping coordinate of reads  $u$  and  $v$  on the reference genome.

Also, let us denote by  $e_s$  the number of misplaced reads defined by:

$$e_s = \begin{cases} \sum_{\substack{(u,v) \in E_f \\ |c_v - c_u| > x_{thr}}} 1 & \text{if } GIV > GDV \\ \sum_{\substack{(u,v) \in E_f \\ (c_v - c_u) > x_{thr}}} 1 & \text{if } GIV < GDV \\ \min \left( \sum_{\substack{(u,v) \in E_f \\ |c_v - c_u| > x_{thr}}} 1, \sum_{\substack{(u,v) \in E_f \\ (c_v - c_u) > x_{thr}}} 1 \right) & \text{if } GIV = GDV \end{cases}$$

Where  $u$  is the predecessor of  $v$  in the final path  $path_f$ . Indeed, some variations were due to indel error type and not to an incorrect ordering.

Finally, let introduce the ratio  $RC = \frac{|GIV - GDV|}{size_{genome}}$ .

The following table summarizes the  $GIV$ ,  $GDV$ ,  $e_s$  and  $RC$  values for each tested genomes:

<b>Bacteria name</b>	<b><math>GIV</math> (in bp)</b>	<b><math>GDV</math> (in bp)</b>	<b><math>e_s</math></b>	<b><math>RC</math> (in %)</b>
A. baumannii	Unfeasible: impossibility of linking two parts			
B. sp. 1NLA3E	4,796,947	4	0	99.61
E. coli	20	4,632,003	0	99.83
H. pylori	4	1,656,989	0	99.35
M. bovis	2,385,520	0	0	54.84
P. sp. MIT 0604	Unfeasible: no paths could be found in the parts graph			
S. enterica	5,751,209	951,718	1	99.80
S. aureus	7	2,812,231	0	99.68
S. thermophilus	1,921,092	19	0	99.54
Y. pestis	4,647,944	37	0	99.87

Table 3.2: For each bacteria, global mapping coordinates variations  $GIV$  and  $GDV$ , the number of misplaced reads  $e_s$  and the ratio  $RC$  are written. In case of infeasibility *i.e.* if no solutions were given, the reason is described.

All the variations graphics are in appendix D, section D.1. A. baumannii and P. sp. MIT 0604 supplementary results are precised in appendix D, sections D.2 and D.3 respectively.

### 3.3 The execution time

In any of the cases, graphs - in order to visualize existing graph issue, and mapping coordinates variation graphics were build. The total real time takes in account the real execution time of graph-graphic building while non-visualization time does not:

<b>Bacteria name</b>	<b>Total time (in sec)</b>	<b>Non-visualization time (in sec)</b>
A. baumannii	254	> 120.708
B. sp. 1NLA3E	691	125.962
E. coli	676	145.940
H. pylori	185	40.883
M. bovis	302	119.911
P. sp. MIT 0604	63	> 42.633
S. enterica	663	128.258
S. aureus	346	73.213
S. thermophilus	219	47.918
Y. pestis	777	122.538

Table 3.3: Real execution times for each tested bacteria. The total time takes in account all the visualization needed for verifying the solution and the execution time of inputs creation while non-visualisation time is the sum of MINIMAP2, METIS, finding paths in parts graph and in all the overlaps graphs execution times.

# Discussion

## 4.1 Expected filters behaviour

According to Table (3.1), for all the tested genomes, the number of considered overlaps was expected with regard to the value of ALM comparing to the threshold  $\lambda_{min}$  chosen. Surprisingly, for all the genomes, the number of filtered long reads is approximately the half of the original number.

## 4.2 Positive results for seven out of ten tested genomes

According Table (3.2) with figures (D.1a), (D.1b), (D.1c), (D.1d), (D.1f), (D.1g) and (D.1h), all ordered reads were correctly placed, in the case of genomes B. sp. 1NLA3E, E. coli, H. pylori, M. bovis, S. aureus, S. thermophilus and Y. pestis.

Furthermore, according to Table (2.1) and Table (3.2), for the same genomes except for M. bovis, the ratio  $RC$  are all greater than 99% - without taking in account the size of the first chosen read in the final path  $path_f$ , because of the mapping coordinate which is at the right end of the reads.

The ratio  $RC$  for M. bovis is due to the threshold  $\lambda_{min} = 7000$ . So it seems that the ends of the genomes were missing in the ordering.

## 4.3 LOREAS program is fast for bacteria genome

For all the genomes, the real execution time with taking care of graphs and results visualizations is low (less than 12 minutes) while mathematical optimization was used.

## 4.4 One misplaced read for *S. enterica*: a strong repetition consequence

The ratio  $\frac{\min(GIV,GDV)}{\max(GIV,GDV)}$  for *S. enterica* is equals to 16.55% and the huge value of *GDV* was due to the only one misplaced read - according to the definition of  $e_s$ . Indeed, the global monotonous of the function  $f(p_i) = mappingCoordinates$  - where  $p_i$  is the sequence of ordered reads that gives for  $i \in \mathbb{N}$  the  $i^{th}$  reads in the overlaps graph path, is affected by just this read, with respect to figure (D.1e).

## 4.5 Unfeasibility of finding a path in the overlaps graph in *A. baumannii*: a wrong path in the parts graph

LOREAS program raised a part linking error. Indeed, according to figures (D.2a) and (D.2b), the path in the parts graph was wrong. The impossibility of making a link can be explained by the fact that the parts graph was undirected while when the parts had to be solved sequentially, their overlaps graph was directed. In this case, the edge (11,10) in (D.2b) should not have been chosen. It was because the link between part 11 and part 10 is very strong, due to repeated regions. According to the model, choosing this edge and choosing this path maximizes the value of the objective function and made it greater than if the real path was chosen.

## 4.6 Unfeasibility of finding a path in the parts graph in *P. sp. MIT 0604* due to a cycle in the graph

With respect to figure (D.3a), the parts graph had a cycle, with origin the part 44. The figure (D.3b) shows the cause of this cycle: the part 44 had two distinct genome regions. The non-separation and the non-existence of two distinct connected components in the part 44 overlaps graph is due to strong repeated region. As only the part 44 made the link between 43 - 44 and between its two neighboring parts, a cycle is formed in the parts graph. As all the parts have to be chosen once - and only once, finding a path in the parts graph infeasible because of this cycle.

# Conclusion

LOREAS program gave very positive results for seven out of ten bacteria genomes in a reasonable execution time for a low simulated long reads sequencing depth. However, even using long reads sequencing, strong repeated regions continued to be source of errors.

As the verification of misplaced reads depends on the mapping coordinates on the reference genome, using MINIMAP2 for determining reads' coordinates with mapping reads on the reference genome is questionable: when a read has been mapped on two regions, the better region is chosen. However, with indel errors, it is not ensured that the sequenced read is a part of the better region - especially for repeated regions.

In order to prevent wrong path in the parts graph, we intend to make it directed by choosing an arbitrary read and orient it in order to giving a global orientation. The same algorithm as described in section 2.2, paragraph 3, can be used for this purpose.

Furthermore, to prevent cycle in the parts graph, merge all parts of the cycle with the cycle origin can be done. Another idea is to partition the cycle origin part.

Also, avoiding misplaced reads when solving the heaviest path in an overlaps graph can be realized using an *a posteriori* verification of non-created-inexistent-overlaps with the found ordering.

Another issue is the lost of genome extremities coverage when the threshold  $\lambda_{min}$  on the overlaps length is too stringent. To solve this, keeping the positive result of a higher threshold execution and add overlaps with a lower overlap length was envisaged. But currently, no working algorithm with positive result was created.

In this study, the second task - building a consensus sequence, was not realized. Making it will allow to add genome extremities with mapping the filtered reads on the pre-consensus sequence got with a higher  $\lambda_{min}$  threshold.

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# Host Presentation

## A.1 The Inria Rennes laboratory

The Inria Rennes is a computer science laboratory, associated with IRISA laboratory. The laboratory maintains collaborations with CENTRALESUPÉLEC, CNRS, ENS RENNES, IMT ATLANTIQUE, INSA RENNES, UNIVERSITÉ DE BRETAGNE SUD (UBS) and UNIVERSITÉ DE RENNES 1.

## A.2 The GENSCALE team

The GENSCALE team is a bio-informatics research team. The team develops scalable methods, algorithm and software for processing genomic data. It is composed by researchers teachers, engineers, post-PhD, PhD students. Collaborations exist with international teams, for example with HIPCOGEN. I worked with RUMEN ANDONOV, a Rennes 1 researcher teacher, DOMINIQUE LAVENIER, the group leader and CNRS Research Director, and SEBASTIEN FRANÇOIS, the PhD student of MR ANDONOV.

## A.3 The LOS ALAMOS NATIONAL LABORATORY

During this internship, I had the luck to visiting the LOS ALAMOS NATIONAL LABORATORY, in New Mexico, USA. The laboratory has several departments in computer sciences. MR ANDONOV, MR LAVENIER and me visiting HRISTO DJIDJEV, for working on graph partitioning, and working on integer linear programming.

# Personal Review

During this internship, I had the great opportunity to discover the research world, and especially internationally thanks to working at LOS ALAMOS NATIONAL LABORATORY and participating in a 3-days conferences at SFAF MEETING in Santa Fe.

I really appreciated working with MR ANDONOV, MR LAVENIER and MR DJIDJEV. Indeed, sharing scientific ideas was very efficient and interesting.

I was really focused on my work during these three months and this was very instructive for building my scientific reasoning.

However, this reminded me that sleeping correctly is important to be concentrated and so as to remain psychologically stable.

I have learned a lot of things especially in programming optimisation with Python, in graph modelisation and in mathematical approaches.

This experience confirms my willingness to continue towards a thesis, and then engage in the world of scientific research.

All the program LOREAS is currently on a private GitHub repository.

# Supplementary methods

## C.1 The heaviest path in an overlaps graph

### Validity hypothesis

- There are at least two reads;
- There is only one connected component;
- There is no read subsequence of an other.

**The data** Let the overlaps graph  $G = (V, l, E, \lambda)$ , where  $V$  the set of vertices - the set of long reads of size  $l$ ,  $E$  the set of edges - the overlaps, and  $\lambda$  the associated weight - where  $\forall (u, v) \in E$ ,  $\lambda_{uv}$  is the  $(u, v)$  overlap length. Too, let define  $\forall v \in V$ ,  $l_v$  the length of read  $v$ ,  $\forall (u, v) \in E$ ,  $g_{uv}$  the  $(u, v)$  overlap gap defined in section 2.2, paragraph 2, and  $M = \sum_{v \in V} l_v$ .

Let define the set  $S \subseteq V$  - the set of long reads starter candidates, the set  $I \subset V$  - the set of long reads knowing for sure as intermediate or not participating reads, and the set  $T \subseteq V$  - the set of long reads terminal candidates.

This model uses the GAT formulation [20].

**The variables** Let define

$$\forall (u, v) \in E, X_{uv} = \begin{cases} 1 & \text{if the edge } (u, v) \text{ is participating in the path} \\ 0 & \text{else} \end{cases}$$

$\forall v \in V$ :

- $y_v \in \mathbb{N} \mid 0 \leq y_v \leq M$  the right position of read  $v$ ;

- $s_v \in [0, 1]^1$ , where  $s_v = 1$  if the read  $v$  is the first part in the final path, else  $s_v = 0$ ;
- $i_v \in [0, 1]^1$ , where  $i_v = 1$  if the read  $v$  is an intermediate part in the final path, else  $i_v = 0$ ;
- $t_v \in [0, 1]^1$ , where  $t_v = 1$  if the read  $v$  is the first part in the final path, else  $t_v = 0$ .

**The objective function** *maximize*  $\sum_{(u,v) \in E} X_{uv}$ : choosing the final path participating edges - the participating overlaps, with maximizing the number of overlaps.

### The constraints

•

$$\forall (u, v) \in E \begin{cases} y_v \geq y_u + (l_v - \lambda_{uv} + g_{uv}) * X_{uv} - (1 - X_{uv}) * M \\ y_v \leq y_u + (l_v - \lambda_{uv} + g_{uv}) * X_{uv} + (1 - X_{uv}) * M \end{cases}$$

If the overlap  $(u, v)$  is chosen, then the right positions of  $u$  and  $v$  must respect the overlaps characteristics;

- $\forall v \in V, y_v \geq s_v * l_v$ : initializes the value of  $y$  for the first chosen read;
- $\forall v \in V, s_v + i_v + t_v \leq 1$ : the read is starter, intermediate, terminal, or not participating in the final path;
- $\sum_{v \in V} s_v = 1$ : there is only one starter read;
- $\sum_{v \in V} t_v = 1$ : there is only one terminal read;
- $\forall v \in V, \sum_{(v,u) \in E} X_{vu} = s_v + i_v$ : a starter or an intermediate read has at least one successor in the final path;
- $\forall v \in V, \sum_{(u,v) \in E} X_{uv} = i_v + t_v$ : an intermediate or a terminal read has at least one predecessor in the final path;
- $\sum_{v \in S} s_v = 1$ : there is only one starter candidate which is starter;
- $\sum_{v \in I} s_v + t_v = 0$ : an intermediate candidate cannot be either a starter or a terminal;
- $\sum_{v \in T} t_v = 1$ : there is only one terminal candidate which is terminal;

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<sup>1</sup>According to [21], the variables are binary

- $\forall v \in V, i_v + t_v \leq |\{(u, v) \in E\}|$ : if there are no input edges, the read  $v$  cannot be intermediate or terminal;
- $\forall v \in V, s_v + i_v \leq |\{(v, u) \in E\}|$ : if there are no output edges, the read  $v$  cannot be starter or intermediate;

## C.2 The heaviest path in a parts graph

### Validity hypothesis

- There are at least two parts;
- There is only one connected component.

**The data** Let the parts graph  $G = (V, E, w)$ , where  $V$  the set of vertices - the set of parts,  $E$  the set of edges - the parts links, and  $w$  the associated weight - where  $\forall (u, v) \in E$ ,  $w_{uv}$  is the number of cut overlaps between part  $u$  and part  $v$ . Finally, let define  $M = \sum_{(u,v) \in E} w_{uv}$ . This model uses the GAT formulation [20].

**The variables** Let define

$$\forall (u, v) \in E, X_{uv} = \begin{cases} 1 & \text{if the edge } (u, v) \text{ is participating in the path} \\ 0 & \text{else} \end{cases}$$

$\forall v \in V$ :

- $y_v \in [0, |V| + 1]$  the position of part  $v$  in the final path;
- $s_v \in [0, 1]^1$ , where  $s_v = 1$  if the part  $v$  is the first part in the final path, else  $s_v = 0$ ;
- $i_v \in [0, 1]^1$ , where  $i_v = 1$  if the part  $v$  is an intermediate part in the final path, else  $i_v = 0$ ;
- $t_v \in [0, 1]^1$ , where  $t_v = 1$  if the part  $v$  is the last part in the final path, else  $t_v = 0$ .

**The objective function** *maximize*  $\sum_{(u,v) \in E} X_{uv} * w_{uv}$ : choosing the final path participating edges with maximizing the weight so the number of cut overlaps between parts.

## The constraints

- $\sum_{(u,v) \in E} X_{uv} = |V| - 1$ : all the parts participate in the final path;
- $\forall (u, v) \in E, y_v \geq (y_u + 1) * X_{uv} - (1 - X_{uv}) * M$ : a part participate only once;
- $\forall v \in V, y_v \geq s_v$ : initializes the value of  $y$  for the first chosen part;
- $\forall v \in V, s_v + i_v + t_v \leq 1$ : the part is starter, intermediate, or terminal;
- $\sum_{v \in V} s_v = 1$ : there is only one starter part;
- $\sum_{v \in V} t_v = 1$ : there is only one terminal part;
- $\forall v \in V, \sum_{(v,u) \in E} X_{vu} = s_v + i_v$ : a starter or an intermediate part has at least one successor in the final path;
- $\forall v \in V, \sum_{(u,v) \in E} X_{uv} = i_v + t_v$ : an intermediate or a terminal part has at least one predecessor in the final path;
- $\forall v \in V, i_v + t_v \leq |\{(u, v) \in E\}|$ : if there are no input edges, the part  $v$  cannot be intermediate or terminal;
- $\forall v \in V, s_v + i_v \leq |\{(v, u) \in E\}|$ : if there are no output edges, the part  $v$  cannot be starter or intermediate;

# Supplementary data

## D.1 Mapping coordinates variations results

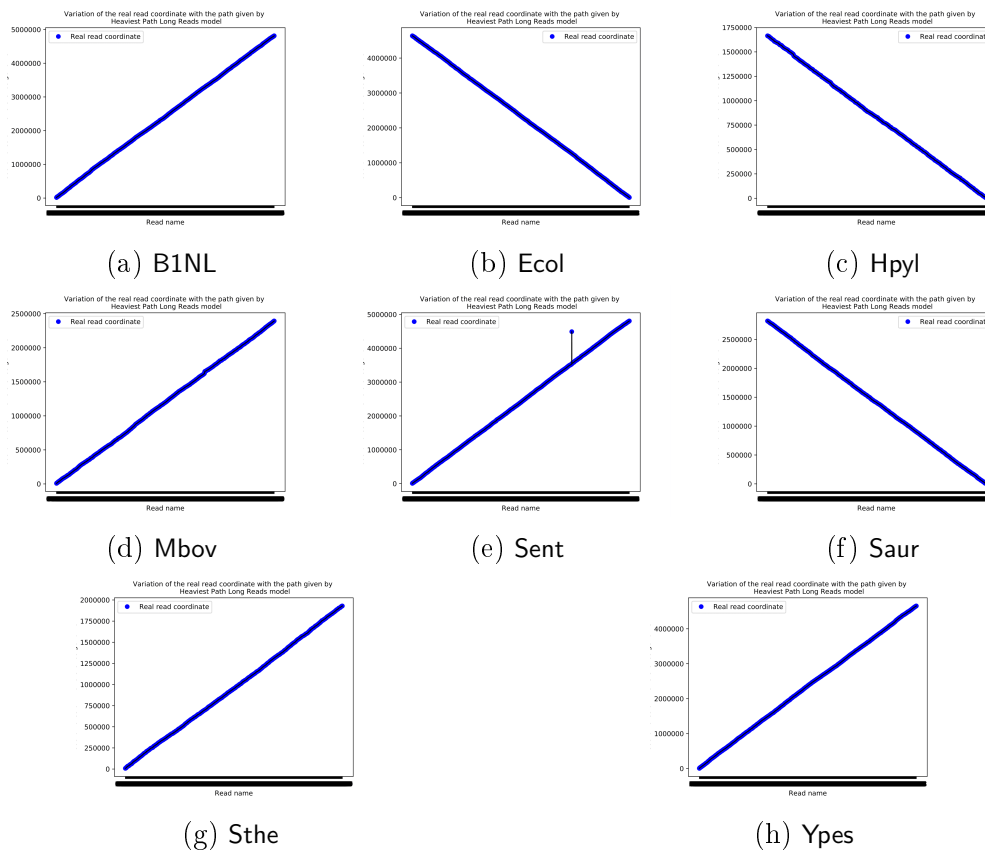
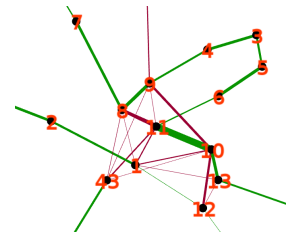


Figure D.1: Ordered reads mapping coordinates variation graphics. For all graphics, the x axis is the name of reads, in y axis there are the coordinates. (D.1a) *B. sp. 1NLA3E*; (D.1b) *E. coli*; (D.1c) *H. pylori*; (D.1d) *M. bovis*; (D.1e) *S. enterica*; (D.1f) *S. aureus*; (D.1g) *S. thermophilus*; (D.1h) *Y. pestis*.

## D.2 *A. baumannii* supplementary figures



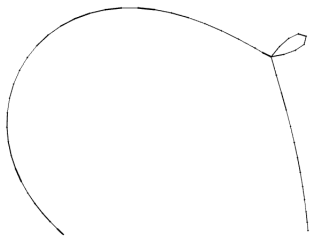
(a) Reads in parts mapped on reference



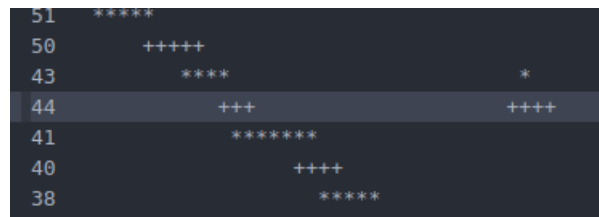
(b) Parts graph and the chosen path in green

Figure D.2: The cause of the error for *A. baumannii*: a wrong path in the parts graph. In (D.2a), the vertical axis represents the parts name which are sorted according to where the majority of their reads are on the reference genome, the horizontal axis represents where the longer reads of a part maps on the reference genome. In (D.2b) is represented the place of the parts graph where the path - in green, is wrong.

## D.3 *P. sp.* MIT 0604 supplementary figures



(a) Parts graph with the cycle, whose part 44 is the cycle origin



(b) Reads in parts mapped on reference

Figure D.3: The cause of the error for *P. sp.* MIT 0604: a cycle in the parts graph. In (D.3a) is represented the parts graph with a cycle. In (D.3b), the vertical axis represents the parts name which are sorted according to where the majority of their reads are on the reference genome, the horizontal axis represents where the longer reads of a part maps on the reference genome.





## ***De novo* long reads assembly using integer linear programming**

*In silico* studying a genome requires two steps: sequencing it with cloning and cutting the genome in several reads, and then, assembling the reads. It is well known that the number of sequencing errors is proportional to the reads' size. However, the use of long reads can be an advantage against genome repeated regions issues. *De novo* is an assembly method which does not use a reference. The purpose of the described here tool, named LOREAS, is to be a *de novo* assembler in two tasks: first, ordering the long reads, and then, obtaining a consensus sequence of the ordered reads. Currently, only the first task was realised. While other *de novo* long reads assemblers use heuristics and De Bruijn graphs, LOREAS is based on overlaps similarity between all the long reads. It uses integer linear programming, to find the heaviest path in a graph  $G = (V, E, \lambda)$ , where  $V$  is the vertices set corresponding to the long reads set,  $E$  the set of edges associated with the overlaps between long reads - weighted by  $\lambda$ : the overlap length. When this graph is too huge, the set of reads  $V$  is partitioned in several parts. Then, all the parts are solved sequentially. Here we present the solution concerning the first task related to ten bacteria genomes. Seven of them have been successfully solved for less than 12 minutes on a laptop.

*overlaps graph - mathematical programming - graph partitioning - exact algorithm - heaviest path problem*

## **Assemblage *de novo* de longues lectures par programmation linéaire**

Étudier *in silico* un génome nécessite deux principales tâches : le séquencer, en le clonant puis en le découpant en plusieurs lectures, puis assembler les lectures. Les erreurs de séquençage dépendent de la taille des lectures générées : le taux d'erreur pour les longues lectures est plus important que celui des courtes lectures. Toutefois, les longues lectures permettent de contrer les problèmes issus des régions génomiques répétées. L'assemblage *de novo* est une méthode qui n'a pas besoin de référence. Le programme présenté LOREAS, a pour but d'être un assembleur *de novo* en deux étapes : la première consiste à donner un ordonnancement des longues lectures, la deuxième, réaliser une séquence consensus des lectures ordonnancées. Pour le moment, seule la première étape fut réalisée. Alors que d'autres assembleurs *de novo* usent d'heuristiques et des graphes de De Bruijn, LOREAS est basé sur les similarités de chevauchements entre toutes les lectures. À cette fin, la programmation linéaire en nombres entiers permet de trouver le plus lourd chemin dans un graph  $G = (V, E, \lambda)$ , où  $V$  est l'ensemble des sommets qui sont les longues lectures,  $E$  l'ensemble des arcs représentant les chevauchements entre les longues lectures - pondérés par  $\lambda$ , la longueur de chevauchement. Si le graphe précédent est trop important, l'ensemble  $V$  est partitionné en parties distinctes, puis toutes les parties sont résolues séquentiellement. Dix génomes de bactéries simulés séquencés furent résolus pour la tâche d'ordonnancement des longues lectures. Il en résulte sept résultats positifs sur dix obtenus en moins de 12 minutes sur un ordinateur portable.

*graphe de chevauchements - programmation mathématique - partitionnement de graphes - algorithme exact - problème du plus lourd chemin*