

Msc Bioinformatics thesis

Study of Division of Labor in Pseudomonas through single-cell RNA-seq

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Master 2 in Bioinformatics

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Internship conducted at Ecobio UMR 6553 CNRS-University of Rennes



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Abstract

Study of *Pseudomonas brassicacearum* gene expression variation in environmental constraints, towards the validation of Division Of Labor.

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Keywords :

Single-cell RNA-seq, *Pseudomonas brassicacearum*, Division Of Labor, (4-5 keywords) bacterial population, metabolism, specialization, root colonization

Acknowledgements

I would like to thank ... Ecobio ANR Divide

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technical work; analysis and interpretation of research data; drafting significant parts of the work or critically revising it to contribute to the interpretation.

List of Abbreviations

| Abbreviation | Definition |
|--------------|----------------------------------|
| AI | Artificial Intelligence |
| ANR | Agence Nationale de la Recherche |
| DNA | Deoxyribonucleic Acid |
| DOL | Division Of Labor |
| NGS | Next Generation Sequencing |
| RNA | Ribonucleic Acid |
| RNA-seq | RNA sequencing |
| scRNA-seq | single-cell RNA sequencing |

List of Symbols

| Symbol | Definition |
|----------|------------|
| α | Alpha |
| β | Beta |
| γ | Gamma |

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Chapter 1

Introduction

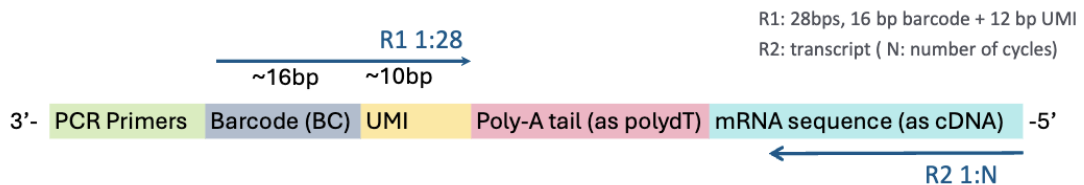


Figure 1.1: image d'un elephant

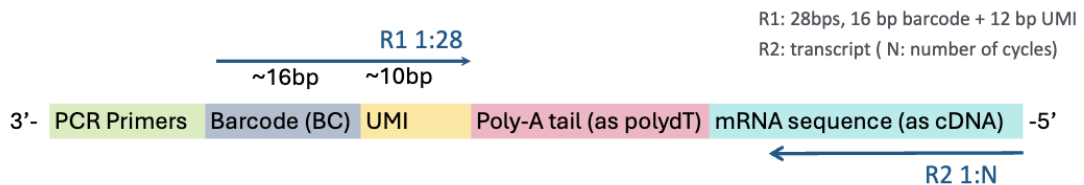


Figure 1.2: image d'un elephant

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1.1 Litterature review

deddfefde^{1,2} Internship description

The survival of organisms in evolving environments is driven by their fitness. The cost-benefit ratio of traits is constantly balanced and gives rise to different populational evolutionary strategies. To succeed, organisms will have to compete, cooperate and/or specialize as a result of how fit their

traits are considering their biotic and abiotic environment. Bacteria are unicellular organisms with therefore little option to specialize and give up certain traits production to limit their metabolic costs, unlike multicellular organisms that present many different forms of specialized cells in one single organism. However, [[auxotrophic bacteria]] (i.e bacteria lacking genes coding for a molecule essential for their survival) have been studied (Morris et al., 2012).³

Auxotroph bacteria can take advantage of leaky functions of helper's organisms to fulfill their needs in specific compounds (Morris et al., 2014, Estrela et al., 2016).^{4,5} With a reduced genetic material, the beneficiary organism fitness is improved, at the risk of being dependent on the helpers presence in their environment. The conditions in which patterns of such [[division of labor (DOL)]] arise are still obscure, but its advantages for bacterial population are clear: DOL allows to diminish the cost associated to certain functions and the possibility of cohabitation of various mutants/specialized cells within the population to respond as a whole to environmental constraints, and thrive. New technologies allow us to access within-species diversity and study the possible metabolic specialization between cells. Single-cell -omics have been developed for this purpose in human health and are now applied to microbial systems. However, analyzing such datasets still requires custom pipelines to respond to the specificity of bacterial biology and technical challenges.

The goal of this internship is to explore [[scRNA-seq]] (single-cell RNA-seq) datasets of [[*Pseudomonas brassicacearum*]], a root colonizer. The student will analyse samples datasets from various nutritional conditions to determine if DOL can be detected within this species as a strategy for efficient root colonization. The intern will have to implement transcriptomic data analyses from ultra-high throughput sequence run(s). Thus the main aim of the intern will be to set up bioinformatic workflow(s) from existing tools to produce interpretable results.

Chapter 2

Materials and Methods

2.1 Materials

Chapter 3

Results

3.1 Overview

This chapter presents the findings of our single-cell RNA-seq analysis of *Pseudomonas*, focusing on the division of labor within bacterial populations.

3.2 Single-cell RNA-seq Analysis

3.2.1 Data Quality and Preprocessing

3.2.2 Cell Type Identification

3.2.3 Differential Expression Analysis

3.2.4 Division of Labor Patterns

3.3 Functional Analysis

3.3.1 Pathway Enrichment

3.3.2 Gene Set Analysis

3.3.3 Regulatory Network Analysis

3.4 Integration with Previous Studies

3.5 Summary of Key Findings

Chapter 4

Discussion

4.1 Interpretation of Key Findings

4.1.1 Division of Labor Mechanisms

4.1.2 Biological Significance

4.1.3 Technical Considerations

4.2 Comparison with Existing Literature

4.2.1 Similarities with Previous Studies

4.2.2 Novel Insights

4.2.3 Discrepancies and Their Implications

4.3 Methodological Strengths and Limitations

4.3.1 Technical Advantages

4.3.2 Potential Limitations

4.3.3 Future Methodological Improvements

4.4 Biological Implications

4.4.1 Ecological Significance

4.4.2 Evolutionary Perspectives

4.4.3 Potential Applications

4.5 Future Research Directions

4.5.1 Open Questions

4.5.2 Suggested Follow-up Studies

4.5.3 Technical Improvements

4.6 Conclusion

Chapter 5

Conclusion and Future Work

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5.1.1 Key Discoveries

5.1.2 Methodological Contributions

5.1.3 Biological Insights

5.2 Impact on the Field

5.2.1 Contribution to Single-cell RNA-seq Methodology

5.2.2 Contribution to Pseudomonas Research

5.2.3 Broader Implications for Microbial Ecology

5.3 Future Research Directions

5.3.1 Technical Improvements

5.3.2 Biological Questions to Address

5.3.3 Potential Applications

5.4 Final Remarks

5.5 References

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Appendix A

Vous pouvez insérer ici des tableaux supplémentaires ou des sorties d’analyses.

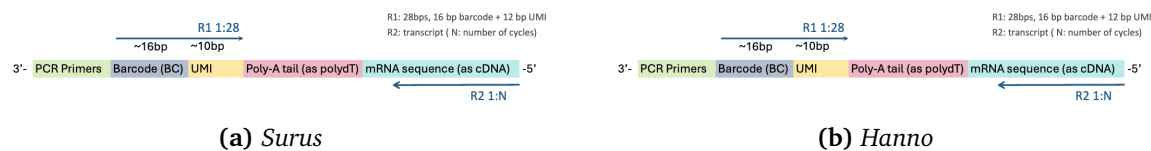


Figure A.1: Famous Elephants

Table A.1: Titre du tableau

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Appendix B

Annexe B: erferfrefref



Figure B.1: *Figure A*

Appendix C

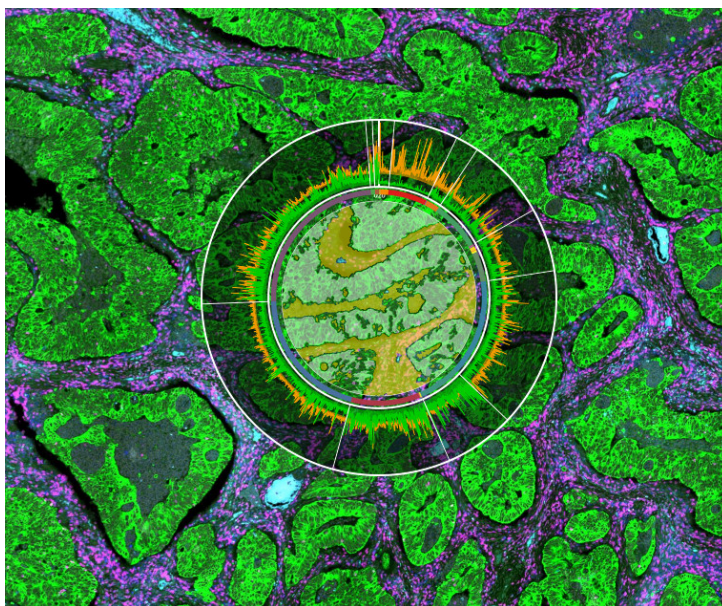
Annexe C: codcefe

Table C.1: *Tableau représentant les résultats des expériences*



Master's Thesis in Bioinformatics

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This thesis was conducted in the framework of the Master's program in Bioinformatics at the University of Rennes. The research presented here contributes to the field of computational biology and bioinformatics.

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