FACULDADE DE ENGENHARIA DA UNIVERSIDADE DO PORTO

Information and Data Analysis System for Gene Expression

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TECHNICAL REPORT

Mestrado Integrado em Engenharia Informática e Computação

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Abstract

Resumo

Acknowledgements

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Abbreviations

cDNA	Complementary DNA
DNA	Deoxyribonucleic Acid
FEUP	Faculty of Engineering of the University of Porto*(Faculdade de Engenharia da Universidade do Porto)*
IBMC	Institute for Molecular and Cell Biology *(Instituto de Biologia Molecular e Celular)*
mRNA	Messenger RNA
RNA	Ribonucleic Acid
RNA-Seq	RNA Sequencing
tRNA	Transfer RNA
WTSS	Whole Transcriptome Shotgun Sequencing

Chapter 1

Introduction

This chapter aims at giving a general overview about the themes address by this thesis. We will address the context in which the thesis is inserted, as well as the motivation that led to its proposal. Furthermore there will be brief description of this thesis' main objectives and the methods that will be used to achieve those objectives.

1.1 Context and Motivation

1.2 Objectives

While defining the concrete objectives of this thesis it becomes relevant to separate them in two groups: strictly biology research related objectives and more general, software solution development objectives. Despite this division, both objectives are tightly interconnected, and each complements the other.

From a molecular biology standpoint, the main objective of this thesis will be to try to understand the mechanisms that regulate the speed of transcription for coding regions of the DNA. This information will be obtained using the RNA Sequencing method, that will be further discussed in Chapter 2. There are several intermediate objectives for this particular problems, as follows:

- Alignment of the given sequencing reads into a known reference genome. This is one of the first steps in the RNA Sequencing process and is effectively one of the most complex problems addressed by this thesis. Some of the tools used in this particular step of the process will be referenced in Section 2.2.2.

- Further analysis of the RNA Sequencing results using machine learning algorithms, applied to data mining. These techniques will be used in an effort to try to understand the already mentioned transcription mechanisms. This topic will be developed in Section 2.3.

The last objective of this thesis is the development of a software platform prototype. This prototype comes as a materialization of the work done along the previous objectives, combining the developed genetic data processing pipeline, with a web information system and with data mining tools. When completed, the prototype should allow for users to store, search and manipulate their genome sequencing data. This data can them be assembled using the tool pipeline developed for the analysis of our own experimental dataset. Lastly, the prototype should integrate data mining tools, that would allow users to reproduce the types of data analysis that were done in this thesis, on their own results.

This document, however, will not dwell in the details of the implementation of such a platform, but rather in the molecular biology section of the overall problem. This is largely due to the fact that the development of the web platform is highly dependent on the tools and methods that will be used for tackling the biology aspects of the problem and, as such, is likely to suffer significant alterations.

1.3 Document Outline

Besides the introduction chapter, this document is composed three additional chapters. These chapters have the following structure:

Chapter 2 introduces some basic Biology and RNA Sequencing concepts, that are essential to understand the problems with which this document deals. Furthermore, we describe the main techniques used for genome/transcriptome sequencing and assembly, their differences and applications and the tools and data formats typically used on those areas. Lastly, we give some insight about machine learning algorithms and how they will be applied to this work.

Chapter 3 presents the datasets that will be studied and used in this work, their origins and features. We will also refer the validation methods that will be used to access the quality of our results.

Chapter 4 outlines the main steps in the development of this thesis (and the respective software prototype). In the last part of this chapter we will attempt to provide a feasible schedule for this work's execution.

Chapter 2

Background

2.1 Introduction

2.2 Genome Assembly and RNA Sequencing

2.2.1 Assembly Methods

2.2.2 RNA Sequencing Tools

2.2.3 Common Data Formats

2.3 Machine Learning

2.4 Conclusions

Background

Chapter 3

Datasets and Validation

3.1 Datasets

3.2 Result Validation

3.3 Conclusions

Chapter 4

Work Plan

4.1 Development Phases

4.2 Schedule Planning

4.3 Conclusions

References