

UNIVERSITÀ DEGLI STUDI DI SALERNO
DOTTORATO IN MANAGEMENT & INFORMATION TECHNOLOGY



CURRICULUM: INFORMATION SECURITY & INNOVATION SYSTEMS

COORDINATORE: Ch.mo. Prof. Antonelli Valerio

Ciclo XVII N.S.

Novel tools for reproducible
Next Generation Sequencing data analysis and integration

Relatori

Ch.mo. Prof. Tagliaferri Roberto

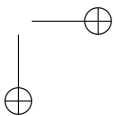
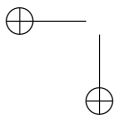
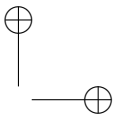
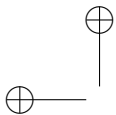
Ch.mo. Prof. Angelini Claudia

Candidato

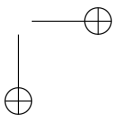
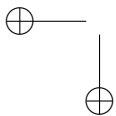
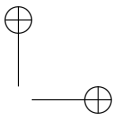
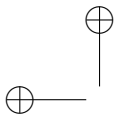
Righelli Dario

Matr. 8800800010

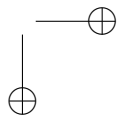
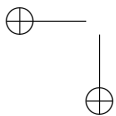
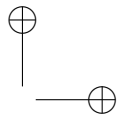
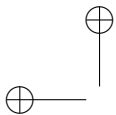
ANNO ACCADEMICO 2017/2018



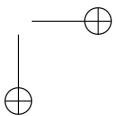
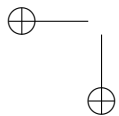
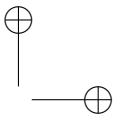
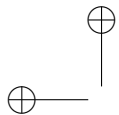
How to reach a goal?
Without haste but without rest
Goethe



Add acknowledgements here



Write your abstract here



Contents

Acknowledgements	5
Abstract	7
1 Introduction	11
1.1 Biological Background	11
1.2 Sequencing Techniques	11
1.2.1 RNA-Seq	11
1.2.2 ChIP-Seq	12
1.2.3 Atac-Seq	12
1.2.4 Other Sequencing Techniques	12
1.3 Data Analysis	12
1.3.1 RNA-Seq Methods	12
1.3.2 ChIP-Seq Methods	12
1.3.3 Atac-Seq Methods	12
1.4 Integration	12
1.4.1 Low Level Integration	12
1.4.2 High Level Integration	12
1.5 Reproducible Computational Research	12

2	Methods	13
2.1	TiCoRSe - Time Course RNA-Seq data analysis	13
2.2	DEScan2 - Differential Enriched Scan 2	13
2.3	IntegrHO - Integration of High-Throughput Omics data	13
3	Results	15
3.1	TiCoRSe - Time Course RNA-Seq data analysis	15
3.2	DEScan2 - Differential Enriched Scan 2	15
3.3	IntegrHO - Integration of High-Throughput Omics data	15
4	Future Works	17
5	Conclusions	19
	Appendices	21
6	Bibliography	23
	List of Figures	25
	List of Tables	27

Chapter 1

Introduction

1.1 Biological Background

1.2 Sequencing Techniques

1.2.1 RNA-Seq

proviamo a scrivere qualcosa

1.2.2 ChIP-Seq

1.2.3 Atac-Seq

1.2.4 Other Sequencing Techniques

1.3 Data Analysis

1.3.1 RNA-Seq Methods

1.3.2 ChIP-Seq Methods

1.3.3 Atac-Seq Methods

1.4 Integration

1.4.1 Low Level Integration

1.4.2 High Level Integration

1.5 Reproducible Computational Research

Chapter 2

Methods

- 2.1 TiCoRSe - Time Course RNA-Seq data analysis
- 2.2 DEScan2 - Differential Enriched Scan 2
- 2.3 IntegrHO - Integration of High-Throughput Omics data

Chapter 3

Results

- 3.1 TiCoRSe - Time Course RNA-Seq data analysis
- 3.2 DEScan2 - Differential Enriched Scan 2
- 3.3 IntegrHO - Integration of High-Throughput Omics data

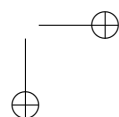
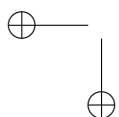
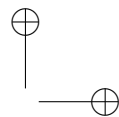
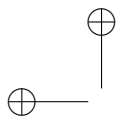
Chapter 4

Future Works

Chapter 5

Conclusions

Appendices



Chapter 6

Bibliography

1. Wang, Z., Gerstein, M. & Snyder, M. RNA-Seq: a revolutionary tool for transcriptomics. *Nature reviews. Genetics* **10**, 57–63. ISSN: 1471-0064 (2009).

List of Figures

List of Tables