INDEX

Alteria	
Abstract	020
CHAPTER 1: INTRODUCTION	
1.1 Next generation sequencing technologies	2
1.2 Next generation sequencing applications	6
1.3 Metagenomics and the human microbiome	10
1.4 Role of the human gut microbiome	11
CHAPTER 2: THE HUMAN GUT MICROBIOME IN COMMON DISEASES OF THE HUMAN (GUT
2.1 Inflammatory bowel disease	14
2.2 Celiac disease	15
2.3 Crohn's disease	17
2.4 Influence of gut microbiome in common human g	ut diseases 19
CHAPTER 3:	
BIOINFORMATICS APPROACHES AND	TOOLS
FOR METAGENOMICS ANALYSIS	

3.1 Classification of metagenomics sequencing methods	23	5.3.5. Diversity analysis: Alpha and Beta diversity
3.2 Metagenomics shotgun sequencing analysis	25	5.3.6 Statistical analysis
3.3 Amplicon-based metagenomics analysis	27:4	
3.3.1 16S rRNAs detection, clustering and identification	29	CHAPTER 6:
3.3.2 Taxonomic and phylogenetic assignment	34	RESULTS
3.3.3 Basic input and expected analysis output	37	
3.3.4 Diversity analysis	39	6.1 Sequencing results
3.3.5 Statistical analysis	48	6.2 Taxonomic classification
		6.2.1 16S rRNA bacteria profile
CHAPTER 4: AIM OF THE PROJECT AND MOTIVATION	52	6.2.2 ITS fungal profile in celiac disease study
	32	6.3 Diversity analysis
CHAPTER 5:		6.3.1 Alpha diversity analysis in Crohn's disease study
MATERIALS AND METHODS	55	6.3.2 Alpha diversity analysis in celiac disease study
5.1 Patients and sampling collection	54	6.3.3 Beta diversity analysis in celiac disease study
5.2 16S and ITS rRNAs amplification and sequencing	56	
5.3 Bioinformatics analysis	57	
5.3.1 Quality filtering, primers detection and demultiplexing	57	CHAPTER 7: DISCUSSION
5.3.2 Pick Operational Taxonomic Units (OTUs) and pick a		
representative sequence from each OTU	58	7.1 The altered gut microbiome in a Crohn's disease
5.3.3 Assigning taxonomic identity to OTU using a reference		patient is normalized after nutritional therapy
database	58	parters to normalized arter narrational alerapy
5.3.4 Aligning OTU sequences, filtering the alignment and	03	
building a phylogenetic tree	59	

7.2 Celiac disease may be associated wi	th alterations
in the gut microbiome	98
CHAPTER 8:	
CONCLUSIONS	103
BIBLIOGRAPHY	106