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Nota di contenuto	Intro -- 1 Introduction -- 2 Biological background -- 2.1 Ribonucleic acid (RNA) -- 2.2 Small RNA -- 2.3 Sequencing -- 2.4 Microbiology -- 2.5 Neurodegenerative diseases -- 2.6 Pathogens in neurological diseases -- 3 Bioinformatics background -- 3.1 Data sources -- 3.2 Metadata and biological ontologies -- 3.3 Read alignment -- 3.4 Comparative analysis -- 3.5 Metagenomic analysis -- 3.6 Integrated analysis pipelines -- 4 Computer science background -- 4.1 Web development -- 4.2 Data science and machine learning -- 5 Small RNA Expression Atlas (SEA) -- 5.1 Background -- 5.2 System architecture -- 5.3 Implementation -- 5.4 System behavior -- 5.5 Results -- 6 Biological discoveries through SEA -- 6.1 Tissue specificity of small RNA -- 6.2 User data and Parkinson's disease -- 6.3 Pathogens in neurodegenerative diseases -- 6.4 Sex specificity of small RNA in human body -- 6.5 Discussion -- 7 Pathogen detection in RNA-seq data -- 7.1 Background -- 7.2 Identification algorithm -- 7.3 Performance measures -- 7.4 Evaluation -- 8 Path(ogen)s to disease -- 8.1 Analysis pipeline -- 8.2 Burkholderia stabilis in frontotemporal dementia -- 8.3 Discussion -- 9 Conclusion -- Bibliography -- A SEA JSON communication objects -- B Pathonoia algorithms -- C Detailed analysis results.