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Combining Edge and Cloud Computing for Low-Power, Cost-Effective Metagenomics Analysis

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Abstract

Metagenomic studies are becoming increasingly widespread, yielding important insights into microbial communities covering diverse environments from terrestrial to aquatic ecosystems. This also because genome sequencing is likely to become a routinely and ubiquitous analysis in a near future thanks to a new generation of portable devices, such as the Oxford Nanopore Min-ION. The main issue is however represented by the huge amount of data produced by these devices, whose management is actually challenging considering the resources required for an efficient data transfer and processing. In this paper we discuss these aspects, and in particular how it is possible to couple Edge and Cloud computing in order to manage the full analysis pipeline. In general, a proper scheduling of the computational services between the data center and smart devices equipped with low-power processors represents an effective solution.

Keywords: Metagenomics; Environmental genomics; Edge computing; Cloud computing; Internet of Things; Internet of Living Things

1. Introduction

Genome sequencing is one of the most effective analysis technique to monitor both the human body, in physiological settings and pathological conditions, as well as the bacterial communities of different environments. Developed in the 1970s with a cost of hundred million dollars, its impressive

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