Abstract

There has been an exponential growth of affordable mobile phones and tablets with significant processing power and memory storage. Having revolutionized the business world, the mobile technology is gradually making inroads into the scientific computing and helping researchers work more efficiently and productively. Mobile apps (software for mobile devices) running scientific applications continue to grow in number, diversity and capability. However, none of the apps currently available provides a mobile interface to one of the most widely used service in bioinformatics for sequence alignment and analysis called Basic Local Alignment Search Tool or BLAST. To address this need, a mobile app – MobSBlast was developed and implemented for the Android platform based mobile devices. In MobSBlast, global sequence alignment is based on Needleman-Wunsch algorithm, which runs locally on the device, while the BLAST algorithm uses the RESTful services to match the user query with the sequence databases at European Bioinformatics Institute. Given the high usage of mobile devices, such bioinformatics app would raise productivity of researchers and facilitate the analysis of sequence data.

References
Mobile Application for Global Sequence Alignment and BLAST – MobSBlast


Index Terms

Computer Science
Information Sciences

Keywords

Bioinformatics  Global sequence alignment  Basic Local Alignment Search Tool (BLAST)  Android mobile application.