

Justification of the paper.

This work is based on the union of 4 people: 2 computer researchers and 2 researchers in the area of Bioinformatics. Through a previous review on bioinformatics research, we realized that the increase in software development for genomics and other branches in recent years has been enormous and we are aware that it is very difficult to identify software tools manually. As part of the solution, we began to work on an ambitious project in which was the research axis, how many software tools for bioinformatics and its branches exist? This led us to develop a tool that implements an effective method that allows us to know the current state of the technological tools of a specific area of the bioinformatics area. In the document presented, we apply the method together with the VigHub tool to carry out the systematic review of software projects related to genomics and its processes. The results of the document allowed us to know the results of interest for developers and researchers, among which are the most used programming languages, the classification of projects by categories and uses over time and, finally, the most important according to the use. Our idea is that the results serve to make the right decisions in research or software development of new inventions to benefit the area of bioinformatics. To conclude, it is important to mention that the method can be used to find the current software status of any other branch of bioinformatics, but this method is not intended to replace the traditional way of realizing the state-of-the-art (revision in bibliographical sources, conferences, books, among others), but rather aims to contribute to the state-of-the-art technique (revision of the current state of software tools in a specific field). We are currently working to implement a model with new data sources to obtain a more complete current state of the software tools.

Regards,

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