

عنوان مقاله:

Genius : A new Variant Discover Analysis Tool in the Python Programming Language on the Linux Platform

محل انتشار:

هشتمین همایش بیوانفورماتیک ایران (سال: 1397)

تعداد صفحات اصل مقاله: 1

نویسندگان:

حسن گیاهی - دانشگاه شیراز

فاطمه نوروزی - شیراز

اسماعیل ابراهیمی

حامد خراتی کوپایی

خلاصه مقاله:

The emergence of Next Generation Sequencing techniques has culminated in the development of a huge amount of data [1]. Using these data and interpreting them enhances our understanding of numerous biological processes [2]. Variant Discovery is one of the recent techniques in the field of Bioinformatics, which has been expanded by the emergence of New Generation Sequencing. This type of analysis leads to the recognition of genome nucleotide mutations, thus after identifying the changes that occurred in the genome it is capable to remedy the unwelcomed alterations through treatment [3]. In this paper, after detecting Variant Discovery analysis prerequisites, the best tools were chosen. Then the tools were combined to get the best results. The Genius tool written by using the Python programming language in the Linux environment can make Variant Discovery analysis much more easier, as well as fix the errors happened during the process performance. The capabilities of this software include data preparing (quality control, data trimming), data mapping and data variant detecting which in turn results in identification of single-nucleotide mutations in the Linux environment easily. The Genius tool has been uploaded to the Github database (<https://github.com/hassangiahi/easy-variant-calling>) and is publicly available

کلمات کلیدی:

variant Discovery, Genius, Next Generation Sequencing, SNP Discovery, Mutation

لینک ثابت مقاله در پایگاه سیویلیکا:

<https://civilica.com/doc/908707>

