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In silico variant aware potential off-target site identification for genome editing applications

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Genome editing at specific target sites is common across fields, with CRISPR-Cas system being the most widely used tool due to its versatility, simplicity, and broad applications. However, the off-target effect can hinder the accuracy of CRISPR-Cas genome editing by causing unintended DNA alterations due to a mismatch between the guide RNA and target sequence. Therefore, it is required to identify all potential off-target sites before conducting genome alteration procedures as it can result in detrimental effects when it comes to clinical applications. The use of a reference genome alone to accurately identify potential off-target sites has drawbacks because the reference genome may not capture the full genetic diversity within a species. Here we propose a new pipeline to address this problem based on our previous approach Cas-OFFinder, a computational tool for identifying potential off-target sites, by considering not only a reference genome but also individual genetic variants. The tool is easily accessible via a renovated web interface, transitioning from the old interface at CRISPR RGEN Tools (rgenome.net) based on cutting-edge web technologies to enhance the user experience.

Keywords: CRISPR-Cas system, off-target effect, genetic variant, web tool, genome editing