

Crossmapper

Based on in-silico read simulation and back-mapping to the original genomes of sequenced organisms, Crossmapper allows the users to assess the rate of incorrect unique and multimapped reads to non-corresponding genomes and thus helps to optimize the sequencing parameters such as the read length, paired/single-end, mapping parameters, etc., prior of performing the actual sequencing experiment.
Barcelona Supercomputing Center - Centro Nacional de Supercomputación

Source URL (retrieved on 22 Dic 2024 - 07:45): <https://www.bsc.es/es/research-and-development/software-and-apps/software-list/crossmapper>