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 lenght, paired/single-end, mapping parameters, etc., prior of performing the actual sequencing experiment. Barcelona Supercomputing Center - Centro Nacional de Supercomputación