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A Copy-Number Recalibration Method using Object Integration for Next Generation Sequencing Data

Both point mutations and copy number alterations are widespread characteristics of tumour. Whole genome sequencing is one of the most popular technologies to detect both of them. Many methods have been developed for calling copy-number alteration using reads counts and non-reference allele frequencies. The differences in normalization method and presumed statistical models result in different outcomes. An object integrated copy-number recalibration method is proposed to evaluate and improve copy-number calls. The performance of the proposed method is presented and compared with several copy-number callers including HMMcopy, TitanCNA and Control-FREEC.