Sequence analysis

ACCUSA2: multi-purpose SNV calling enhanced by probabilistic integration of quality scores

Michael Piechotta and Christoph Dieterich*

Bioinformatics in Quantitative Biology, The Berlin Institute for Medical Systems Biology at the Max Delbrück Center for Molecular Medicine, Robert-Rössle-Strasse 10, 13125 Berlin-Buch, Germany

ABSTRACT
Summary: Direct comparisons of assembled short-read stacks are one way to identify single-nucleotide variants. Single-nucleotide variant detection is especially challenging across samples with different read depths (e.g. RNA-Seq) and high-background levels (e.g. selection experiments). We present ACCUSA2 to identify variant positions where nucleotide frequency spectra differ between two samples. To this end, ACCUSA2 integrates quality scores for base calling and read mapping into a common framework. Our benchmarks demonstrate that ACCUSA2 is superior to a state-of-the-art SNV caller when sample read depths and reliably detects subtle differences among sample nucleotide frequency spectra. Additionally, we show that ACCUSA2 is fast and robust against base quality score deviations.

Availability: ACCUSA2 is available free of charge to academic users and may be obtained from https://bbc.mdc-berlin.de/software.

Contact: christoph.dieterich@mdc-berlin.de

Supplementary information: Supplementary data are available at Bioinformatics online.

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The introduction of next-generation sequencing platforms has paved the way to a new understanding of biological systems. Currently, available sequencing set-ups deliver billions of short reads in one run. This unprecedented sequencing depth is ideally suited for variant detection, e.g. SNP detection in DNA or RNA samples. For example, the variant caller in the samtools package (Li, 2011) infers genotypes by comparing a sequencing sample to a reference sequence. Our solution is more general, as it compares BCs and associated quality scores (QSs) from short reads/C223 compared with one another.

Where nucleotide frequency spectra differ considerably. In our experiments (BCs) and associated quality scores (QSs) from short reads/C223 compared with one another.

Our proposed method ACCUSA2 performs cross-sample comparisons to identify variant sites based on as few previous assumptions as possible and tests whether the underlying hypothesis of equal nucleotide frequencies in the two compared samples can be rejected.

In brief, we model the observed nucleotide frequencies $\Phi$ of each sample $i \in [A, B]$ by a Dirichlet distribution $\text{Dir}(\alpha') : \alpha = (\alpha_A, \alpha_C, \alpha_G, \alpha_T)$ where the BC QSs and mapping QSs are integrated as priors. ACCUSA2 performs a head-to-head comparison of two BAM files. To this end, pairwise read stacks are built for every reference position that passes a user-defined minimal read coverage and quality threshold. First, we transform and combine the base quality $Q_{\text{BC}}$ and mapping quality $Q_{\text{MAP}}$ for each BC in the current pileup to a probability vector $p = (p(A), p(C), p(G), p(T))$ by transforming the Phred quality scores to error probabilities (see Supplementary Material for details).

$$Q_{\text{BC}}^{\text{Phred}} = -10 \log_{10} P(\text{wrong BC})$$

$$Q_{\text{MAP}}^{\text{Phred}} = -10 \log_{10} P(\text{wrong mapping})$$

In a second step, we compile a $n \times 4$ probability matrix $M'$ over individual base probability vectors $p'$ from each read in the pileup ($n$ equals read coverage). Matrix column averages are used to parameterize $\text{Dir}(\alpha')$. We use a log-odds (LOD) score $Z$ that is

*To whom correspondence should be addressed.
defined as the ratio of likelihoods of $\text{Dir}(\Phi^i; \alpha^i)$ to rank our SNV calls. This score becomes zero if $\alpha^A = \alpha^B$:

$$Z = \log_{10} \frac{\text{Dir}(\Phi^A; \alpha^A) \cdot \text{Dir}(\Phi^B; \alpha^B)}{\text{Dir}(\Phi^A; \alpha^B) \cdot \text{Dir}(\Phi^B; \alpha^A)} \quad (3)$$

We implemented our approach in a JAVA program called ACCUSA2 and contrasted it with SAMtools/BCFtools (Li, 2011) on simulated datasets DNA-seq and RNA-seq. Briefly, we used the MAQ simulation tools and the Flux simulator (Griebel et al., 2012) to build our benchmark read datasets from the reference sequence of Caenorhabditis elegans. Our benchmark is designed to contrast two samples of either DNA (a) or RNA short reads (b). We account for the different read properties by using MAQ for benchmark (a) and the Flux simulator for benchmark (b). Our benchmark implements a read mixing scenario (i.e. one sample contains only reads that originate from a reference sequence and another sample contains reads from a diverged sequence and mutation-less reads) in combination with a scan over different input read coverages. In both benchmarks, each of the two input samples was sequenced to a different read depth (see Supplementary Material for details). We explore different read mixing ratios (amount of mutated versus unmutated reads) for the second sample (10–90%).

We compared our method with the SAMtools/BCFtools pipeline. Figure 1 shows the performance of both methods in benchmark (a) without quality score recalibration. ACCUSA2 performs better in situations where read coverages differ between samples, and SNVs of interest might only be lowly represented. Higher robustness of ACCUSA2 against QS deviations enables applications where variant positions are a priori unknown, and recalibration can not be easily performed. Future versions of ACCUSA2 will target specialized applications such as RNA editing event analysis, selection experiments, bulk segregant analysis, and novel assays for mapping of RNA–protein interactions (e.g. PAR-CLIP).

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**REFERENCES**


