Improvements in the detection power of algorithms for analyzing next-generation sequencing based bulked segregant analysis data via estimating thresholds at the genomic region level

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Abstract

Next-generation sequencing based bulked segregant analysis (BSA-Seq) has been widely used in identifying genomic regions associated with a trait of interest. However, the most popular algorithms for BSA-Seq data analysis have relatively low detection power, and high sequencing depths are required for the detection of genomic regions linked to the trait. Here we estimated the thresholds of the popular algorithms at the genomic region level and increased the detection power of these algorithms by at least 5 folds, which should drastically reduce the sequencing cost of BSA-Seq studies.

Introduction

Bulked segregant analysis (BSA) was developed for rapidly identifying genetic markers linked to a trait of interest (Michelmore *et al.*, 1991; Giovannoni *et al.*, 1991). For a particular trait, a certain number of individuals of a segregating population are selected to make two bulks or pools that have contrasting phenotypes of the trait. Equal amounts of DNA are pooled from each individual within a group. The pooled DNA samples are then examined via different methods to identify bulk and parent-specific genetic markers. Collectively, the genomic region(s) controlling the trait should be different while the other unlinked regions should be the same or very similar between the bulks. Thus the bulk and parent-specific markers should be associated with the trait. Initially, the bulks were genotyped using technologies such as restriction fragment length polymorphism (RFLP) and amplified fragment length polymorphism (AFLP) (Asnaghi *et al.*, 2004; Cai *et al.*, 2003; Hartl *et al.*, 2011; Zhang *et al.*, 2013; Michelmore *et al.*, 1991; Giovannoni *et al.*, 1991). This approach relies on the absence/presence of trait-associated DNA fragments in the gel, and it works well for traits controlled by a single qualitative gene. Recently, next-generation sequencing has been used for genotyping the bulks (BSA-Seq) (Gu *et al.*, 2017; Imerovski *et al.*, 2019; Klein *et al.*, 2018; Trick *et al.*, 2012; Arikit *et al.*, 2019; Cao *et al.*, 2021; Chen *et al.*, 2018; Clevenger *et al.*, 2018; Das *et al.*, 2015; Daware *et al.*, 2016; Takagi *et al.*, 2013; Magwene *et al.*, 2011). Genome-wide structural variants (SV) such as single nucleotide polymorphisms (SNP) and small insertions/deletions (InDel) can be easily identified via this approach, and SVs associated with different traits, including single gene-controlled traits, qualitative traits controlled by multiple genes with or without epistatic effects, and quantitative traits, can be easily detected with various algorithms.

An SV in a BSA-Seq dataset can be biallelic, triallelic, or tetraallelic. Biallelic SVs are the most abundant if the parents for generating the population are highly homozygous, and only this type of SVs are used in most BSA-Seq analysis algorithms. For a biallelic SV locus, one of its alleles is termed the reference allele (REF), while the other is referred to as the alternative allele (ALT). When the parental genome sequences are available, the SV alleles from one of the parents are

REF alleles, while the SV allele from the other parent are ALT alleles. Because each bulk contains many individuals, the vast majority of SV loci in a bulk contain both REF and ALT alleles. For each SV, the number of reads of REF/ALT alleles is termed allele depth (AD). Because of the phenotypic selection via bulking, for trait-associated SVs, their ALT allele should be enriched in one bulk while their REF allele should be enriched in the other. However, for SVs unassociated with the trait, both of their ALT and REF alleles would be randomly segregated in both bulks and enriched in neither. Hence these four AD values (REF/ALT reads from each bulk) can be used to assess how likely an SV is associated with the trait.

A few algorithms have been developed to identify trait-associated genomic regions based on BSA-Seq data. The allele frequency method (QTL-seq) is the most widely used for such a purpose (Takagi *et al.*, 2013). It calculates the REF or ALT allele frequencies (AF) of an SV in both bulks with the four AD values and uses the allele frequency difference (ΔAF) between bulks to assess the likelihood the SV locus is associated with the trait; obviously, a high absolute value of the ΔAF suggests that the SV is more likely associated with the trait. The G-statistic method uses G-test to calculate the G-statistic value of an SV with the four AD values and uses the calculated value to judge how likely the SV is associated with the trait, a high G-statistic value suggests that the SV is more likely associated with the trait (Magwene *et al.*, 2011). We have previously developed the significant structural variant method for BSA-Seq data analysis (Zhang and Panthee, 2020, 2022). In this method, an SV is assessed with Fisher's exact test using its AD values of both bulks. An SV with a low p-value of Fisher's exact test tends to have a high absolute ΔAF and G-statistic values and is more likely linked to the trait. An SV is considered significant if the p-value of Fisher's exact test is lower than a specific type I error rate, e.g., $\alpha=0.01$, and non-significant otherwise. Since SVs normally are not evenly distributed across chromosomes, we use the ratio of the significant SVs (sSV) to the total SVs (totalSV) within a genomic region to judge if this region is associated with the trait of interest in our method. A genomic region with a high sSV/totalSV ratio is more likely associated with the trait. The sSV/totalSV ratio is a parameter at the genomic region level, whereas both the allele frequency and the G-statistic value are parameters at the SV level, which is the key difference between the significant structural variant method and the standard allele frequency and G-statistic methods, and the root cause of our method's higher statistical power in the detection of the genomic region-trait associations.

The G-statistic and allele frequency methods (they are referred to as the standard methods hereafter) were developed in 2011 and 2013, respectively, much earlier than the significant structural variant method. As such, these methods became the established norm for BSA-Seq analysis in many laboratories. Although our method has higher detection power, the standard methods are still widely used in recent publications. Due to the prevalence of their use, it is necessary to improve the detection power of the standard methods if possible. In this study, we estimated the threshold of the standard methods at the genomic region level, which increases the detection power of these methods to a level similar to that of the significant structural variant method.

Materials and Methods

The rice sequencing data used in this study were generated by (Lahari *et al.*, 2019). In that study, the size of the F_2 population was 178, and the size of both the resistant and the susceptible bulk were 23 plants each. The parents of this population are LD24 and VialoneNano. Illumina MiSeq

Sequencing System and MiSeq v3 chemistry were used for sequencing the DNA samples of both the parents and the bulks. The accession numbers of the sequences of LD24, VialoneNano, the resistant bulk, and the susceptible bulk are ERR2696318, ERR2696319, ERR269632, and ERR2696322, respectively.

Most methods used in this study had been described previously (Zhang and Panthee, 2020, 2022), minor modifications are described as below.

SV calling

The rice BSA-Seq sequencing data were downloaded from the European Nucleotide Archive (ENA) using the Linux program wget, and the rice reference sequence (Release 47) was downloaded from https://plants.ensembl.org/Oryza_sativa/Info/Index. Sequencing data preprocessing and structural variant calling were performed using fastp, samtools, BWA-MEM, and GATK4 (Li *et al.*, 2009; Li, 2011, 2013; McKenna *et al.*, 2010; S. Chen *et al.*, 2018) as described previously (Zhang and Panthee, 2020, 2022). The SV calling-generated .vcf files were converted to .tsv files using the GATK4 utility VariantsToTable, which served as input files for our Python script.

Workflow of the Python scripts

The SV dataset generated via SV calling was processed with our Python script to identify significant SV-trait associations. A single script contains all three algorithms and the code is available on http://github.com/dblhlc. The workflow of the scripts is as follows:

1. Convert the .tsv/.csv input file(s) generated via SV calling to a pandas DataFrame (size-mutable and potentially heterogeneous two-dimensional tabular data structure with labeled rows and columns) (McKinney 2010; Reback *et al.* 2021).
2. Filter SVs on the pandas DataFrame. Details of SV filtering can be found in our previous publication (Zhang and Panthee, 2022).
3. Perform Fisher's exact test to obtain the p-value, calculate the ΔAF value, or perform G-test to obtain the G-statistic value of each SV in the filtered pandas DataFrame using its four AD values (AD_{ref1} and AD_{alt1} of bulk 1 and AD_{ref2} and AD_{alt2} of bulk 2). The p-values of Fisher's exact tests, the ΔAF values, and the G-statistic values of all SNPs on each chromosome are smoothed by applying a Savitzky-Golay filter (Savitzky and Golay, 1964).
4. Estimate the ΔAF and the G-statistic thresholds of each SV in the filtered pandas DataFrame via simulation. A Savitzky-Golay filter (Savitzky and Golay, 1964) is applied to these values at the chromosome level as well to smooth the threshold curves. The thresholds will be used to identify the significant peaks/valleys in the plots generated in the next step in the old approach.
5. Estimate genome-wide thresholds for all three BSA-Seq algorithms.
6. Use the sliding window algorithm to plot the sSV/totalSV ratios, the ΔAF values, or the G-statistic values against their genomic positions.
7. Identify potential significant peaks/valleys using the genome-wide thresholds.
8. Calculate the thresholds of sliding windows with a potential significant peak/valley to verify if the potential peaks/valleys are really significant.

Sliding window settings

The sliding windows algorithm was used to mitigate noise generated by random errors introduced in bulking and sequencing. For all three methods, the size of the sliding windows is 2 Mb and the incremental step is 10 kb.

Simulate allele depth values under the null hypothesis

If a biallelic SV is not associated with the trait, the probability of its ALT allele in the bulks is 0.5 for an F_2 population and 0.25/0.75 for a backcross population, and its AD_{alt} should follow the binomial distribution. Based on that, we used the above probability and the sequencing depth (AD_{ref}+AD_{alt}, number of trials) of an SV to simulate the allele depths of its REF/ALT alleles in a bulk. The simulated $smAD_{ref1}$/$smAD_{alt1}$ of bulk 1 and $smAD_{REF2}$/$smAD_{ALT2}$ of bulk 2 are used for threshold estimation below.

Calculation of ΔAF/G-statistic and estimation of their thresholds

Calculation of the G-statistic value and the ΔAF value of each SV in the dataset and estimation of its thresholds were performed as described previously (Zhang and Panthee, 2020, 2022). In brief, equation 1 is used for ΔAF calculation while equation 2 is used for G-statistic calculation. In equation 2, *O* indicates the AD value of an SV (AD_{REF1}, AD_{ALT1}, AD_{REF2}, or AD_{ALT2}), *E* is the expected AD value under the null hypothesis (the SV is not linked to the trait) and is calculated as in the original G-statistic method (Magwene *et al.*, 2011), and *ln* denotes the natural logarithm. Most sliding windows contain many SVs. The ΔAF/G-statistic value of a sliding window is the average value of all SVs in it.

$$\Delta AF = \frac{AD_{alt2}}{Ad_{ref2}+AD_{alt2}} - \frac{AD_{alt1}}{AD_{ref1}+AD_{alt1}} \qquad (1)$$

$$G = 2\sum_{i} O_i \times ln(O_i/E_i) \qquad (2)$$

ΔAF/G-statistic threshold estimation for each SV in the dataset is performed by simulation. For each SV, its ΔAF or G-statistic value is calculated using the simulated AD values in both bulks with equation 1 or equation 2. This process is repeated 10,000 times, the threshold for the allele frequency method is the 99% confidence interval of the 10,000 ΔAF values, and the threshold for the G-statistic method is the 99.5th percentile of the 10,000 G-statistic values. As in the real dataset, the threshold of a sliding window is the average value of all SNPs in it.

Identification of significant SVs

For each SV in the dataset, Fisher's exact test was performed using its four AD values. An SV with its p-value less than α=0.01 is defined as a significant SV. Calculating the sSV/totalSV ratio of a genomic region is straightforward.

Genome-wide and sliding window specific threshold estimation

Calculating a threshold for all sliding windows of the SV dataset would take a very long time. To overcome this obstacle, we first calculate a genome-wide threshold and use it to identify

potential significant peaks/valleys, then sliding window thresholds of these peaks are calculated via simulation to verify if these peaks/valleys sliding windows are really significant.

Genome-wide threshold: The number of SVs that are the same as the average number of SVs per sliding window are randomly selected from the entire dataset. For each SV in this sample, the four simulated AD values are used to obtain the p-value via Fisher's exact test and to calculate the ΔAF/G-statistic values. An SV with its p-value less than $\alpha=0.05$ is considered an sSV ($\alpha=0.01$ is used for the real dataset to reduce the chance of false positives). Then the ΔAF, G-statistic, and sSV/totalSV ratio of the sample (treated it as a genomic region) are calculated as above. This process (starting from sampling SNPs) is repeated 10,000 times. The 99% confidence interval of the simulated 10,000 ΔAF values is used as a significant threshold for the allele frequency method, and the 99.5^{th} percentile of these 10,000 simulated G-statistic values or sSV/totalSV ratios is used as the significance threshold for the significant structural variant or G-statistic methods for detection of potential significant peaks.

Sliding window threshold: Estimating a sliding window specific threshold is very similar to estimating the genome-wide threshold; the only difference is that we do not need to sample SVs from the genome. Instead, the SVs and their associated AD values in each bulk in the sliding window are used for simulation, and the rest is the same as above.

Results and discussions

Appropriate threshold estimation of BSA-Seq data analysis

If an SV or a genomic region is not associated with a trait, its ΔAF, G-statistic, and sSV/totalSV values should be close to zero (base value). Otherwise, due to allele enrichment/depletion, the values of these parameters for an SV or a genomic region will deviate from the base value significantly, and thus peaks/valleys will be formed in the trait-associated genomic regions in the BSA-Seq curve. However, chance variation (random error) can be introduced during bulking and sequencing, which can lead to sequencing depth variations across the genome and result in the formation of false peaks/valleys. The genuine peaks/valleys should have higher absolute values than those of the false peaks/valleys. An appropriate threshold is needed to distinguish these two types of peaks/valleys.

Thresholds should be estimated at an appropriate level. If we try to associate an SV with a trait, the thresholds should be estimated at the SV level. In contrast, if we try to associate a genomic region with a trait, the thresholds should be estimated at the genomic region level. We can associate an SV to a trait with an extremely large population, large bulk sizes, and high sequencing coverage. Large populations ensure the occurrence of recombination events between the trait-controlling gene and its flanking sequences, a large bulk size ensures the inclusion of such recombination events in the bulks for genotyping, and high sequencing coverage allows us to differentiate the trait-controlling SVs from the flanking ones and identify the trait-associated SV with sufficient statistical significance. However, doing so is probably not feasible because of the labor requirement and high costs. Therefore, it is more realistic to associate a genomic region(s) to a trait. In this case, instead of estimating the threshold at the SV level, it is more appropriate to estimate it at the genomic region level.

Thresholds are estimated in different ways in different algorithms. The most widely used allele frequency method calculates the confidence interval of each SV in a dataset via simulation and uses the mean of the confidence intervals of all SVs in a genomic region to judge if this region is significant (Takagi *et al.*, 2013). The way to estimate thresholds in the original G-statistic method is even more conservative (Magwene *et al.*, 2011; Zhang and Panthee, 2020; Mansfeld and Grumet, 2018). The sSV/totalSV ratio used in our significant structural variant method is a parameter at the genomic region level, its threshold is estimated at the genomic region level, and our method has at least five times higher detection power than the standard methods (Zhang and Panthee, 2020). The threshold would be greatly overestimated if we calculate the threshold of each SV in a genomic region and use their mean as the threshold of the genomic region. Doing so would assume that the allele frequencies of all SVs in the genomic region are at the extreme ends of the allele frequency distribution and very different from the probability of the REF/ALT alleles, which is against the null hypothesis, and thus leads to a very conservative threshold value. In contrast, when we simulate the AD values of all SVs in a genomic region, most SVs in this region will have their allele frequencies close to the REF/ALT probability and only a very small portion of the SVs have their allele frequencies at the extreme ends of the allele frequency distribution, thus it is likely that the thresholds will be significantly decreased at the genomic region level and the detection powers of the standard methods will be increased significantly.

Estimate the thresholds of the standard methods at the sliding window level

We modified our code to estimate the thresholds of the standard methods at the sliding window (a genomic region of a certain length) level and analyzed the rice nematode resistance data (Lahari *et al.*, 2019) with both the original and modified scripts. Previously we used α=0.01 to identify sSVs in the real dataset and used α=0.1 to identify sSVs in the simulated dataset. In this way we obtained higher thresholds and lowered the chance of false positives. Here we used α=0.01 to identify sSVs in both real and simulated dataset to level the play field for the detection power comparison among the different algorithms. Only the major peak on chromosome 11 was identified as significant using the old standard methods. However, in addition to this major peak, many minor peaks on chromosomes 1, 3, 4, 5, 6, 7, 8, 9, 10, 11, and 12 become significant as well when the thresholds are estimated at sliding window level (Figure 1), which means that the detection power of the standard methods is increased by at least 5 folds (Zhang and Panthee, 2020, 2022). The average sliding window threshold of the G-statistic is 9.00585070076413, and the average sliding window confidence interval of the allele frequency method is -0.68221874129103-0.683282282173592 using the old approach. Whereas these values are 1.2492238068569297 and -0.00979694695809328 to 0.009111848721497237, respectively, using the new approach, very close to their base values. The genome-wide threshold of the significant structural method is 0.004921092821992194. Using the new approach, the threshold value is drastically lower and the confidence interval is drastically narrow, thus the detection power of the standard methods is dramatically increased.

When estimating thresholds at the genomic region level, the G-statistic method has the lowest detection while the allele frequency method has the highest detection power, and the significant structural variant method has detection power between those of the above methods. However, all the additional significant peaks/valleys detected via the allele frequency or the significant structural variant methods are extremely minor. Although the way we obtain the new thresholds is statistically sound, it is very likely the very minor peaks/valleys do not contribute much to the

trait phenotype; moreover, lower thresholds may increase the chance of false positives. It is possible that some very minor genuine peaks/valleys might be missed, slightly increasing the threshold can decrease the chance of false positives, which should be practically beneficial. We used α=0.01 for the identification of the significant structural variants in both the real and simulated data here. If we use α=0.05 as described in the Methods section or α=0.1 as we did previously for the identification of the significant SVs in simulated data, and use α=0.01 for the identification of the significant SVs in real data, the threshold of the significant structural variant method could be significantly higher. The ΔAF value of an SV will fluctuate closely around zero under null hypothesis (it is not associated with the trait); in a genomic region, positive values and negative values would cancel each other when calculating the ΔAF mean, leading to the threshold value very close to zero. Thus, we will use the absolute ΔAF of each SV in a genomic region to calculate the ΔAF of this region. If the 99.5th percentile of these 10000 ΔAF values is *a*, the confidence interval will be between -*a* and *a*. These approaches will be used to estimate the thresholds of the allele frequency and significant structural variant (α=0.05) methods for sections below.

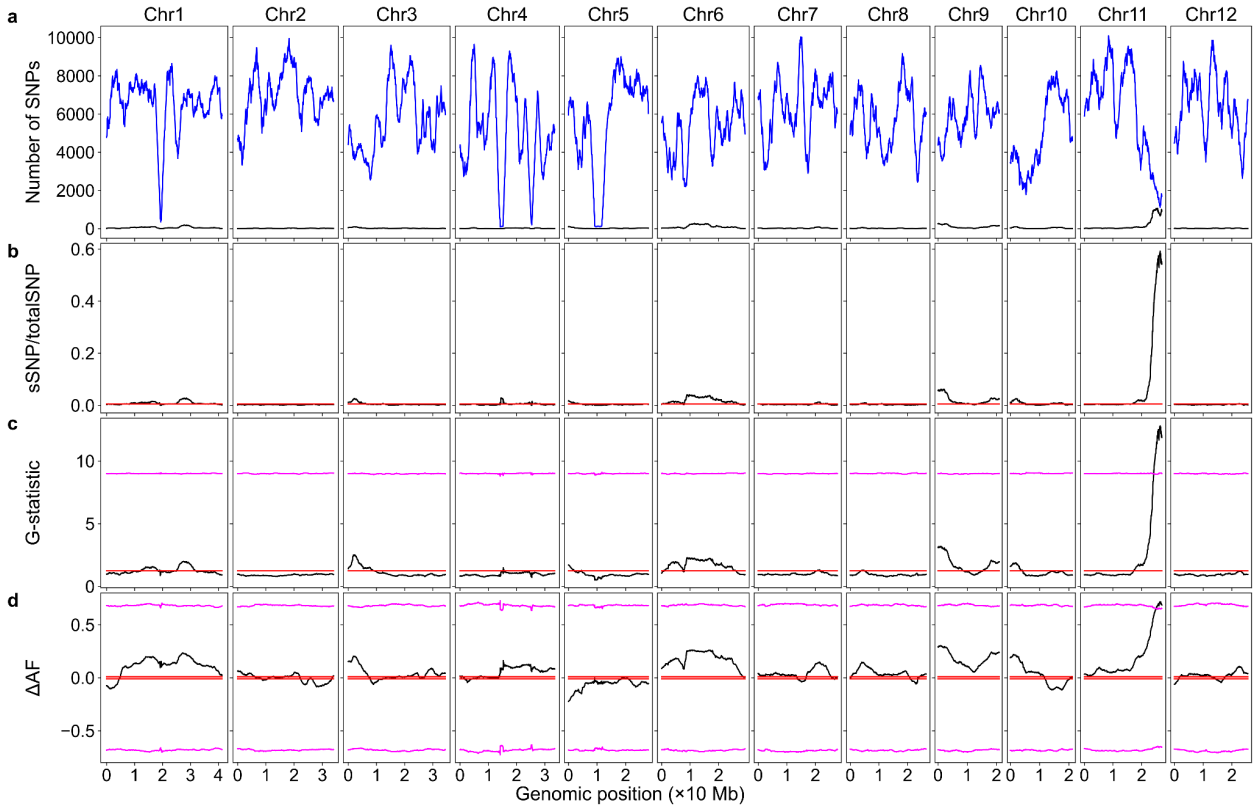

Figure 1. BSA-Seq data analysis using both the parental and bulk genome sequences in rice. The red lines/curves are genome-wide thresholds, while the magenta lines/curves are the thresholds estimated at the SV level. The black curves represent the number of sSNPs (A), sV/totalSV ratios (B), G-statistic values (C), or ΔAF values (D). (A) Genomic distributions of sSVs and total SVs. Blue curves: total SVs. (B) Genomic distributions of sSV/totalSV ratios. (C) Genomic distributions of G-statistic values. (D) Genomic distributions of ΔAF values.

The sliding window with the major peak on chromosome 11 contains 1139 SNPs; the average sequence depths of these SNPs are 7.6540 and 8.7471, respectively, in bulks 1 and 2, and the

corresponding standard deviations are 3.0440 and 2.8205. The threshold of its G-statistic was decreased from 9.0472 to 1.2930, and the confidence interval of its allele frequency difference (ΔAF) method was narrowed down from -0.6500-0.6496 to -0.2229-0.2229. To test the precision of the new threshold estimation approach, we repeated the process 500 times and generated 500 threshold values of the sliding window containing the major peak on chromosome 11 for all three methods. These threshold/confidence interval values are extremely consistent, and the coefficient of variance (CV) values of the 500 values are less than 0.01 for the standard methods and 1.16% for the significant structural method. But the range of the 500 thresholds of the latter is very narrow, the min is 0.0360 and the max is 0.0369 (Table 1).

Table 1. Statistical summary of the 500 thresholds of different algorithms

	sSNP/totalSNP	G-statistic	ΔAF
Min	0.0359964881474978	1.2858852296992	0.22229617283634
Max	0.0368744512730465	1.30044138260958	0.223570624666076
Mean	0.036314503950834	1.29299772054259	0.222924623486806
SD	0.000422208343043444	0.00247340791486133	0.000239143546550072
CV	0.011626438395388	0.00191292519357527	0.00107275518877001

Sliding window sizes are negatively correlated with thresholds

We used the genome-wide threshold for identifying potential significant peaks/valleys, and used sliding window-specific thresholds for verifying if such peaks/valleys are really significant. We randomly sampled the number of SVs equal to the average SVs per sliding window from the entire dataset for estimating genome-wide threshold, such samples can be treated as special sliding windows; the sizes of sliding windows are the same, but the sequencing depths may vary among the samples because they contain different sets of SVs (Please see the methods section for details). For real sliding windows, both their number of SVs and the average sequencing depths could be different among sliding windows. These two parameters may affect threshold estimation, and we tested how they affect threshold estimation at the sliding window level using simulated data.

We first tested how sliding window sizes affect threshold estimation at the sliding window level. Sliding window sizes of 1000, 2000, 3000, and 4000 were tested with average sequencing depth of 15. We simulated sequencing depths with cv=0.4 (based on the rice nematode resistance date). The sequencing depth and the REF/ALT reads of each SNP are simulated as described in the sequencing simulation section. Figure 2 shows the distribution of 10,000 values of sSV/totalSV, G-statistic, and allele frequency of a sliding window. With a fixed average sequencing depth (15), a larger window size resulted in smaller threshold values for all the methods. The means of these 10000 values are very similar between different window sizes. However, the standard deviation becomes smaller with a larger window size. Thus, a larger sliding window has less threshold value when the average sequencing depth is fixed.

Sequencing depths are reversely correlated with thresholds for the standard methods, but positively correlated with thresholds for the significant variant methods

Next, we tested how sequencing depths affect threshold estimation. Sequencing depth of 5, 10, 15, and 20 were tested. Again sequencing depths were simulated with CV=0.4. We used the sliding window size of 6000 to test the effects of sequencing depth on threshold estimation. As shown in Figure 3, increasing sequencing depth slightly increases the threshold of the significant structural variant method but decreases the thresholds of the other methods. These results suggest that increasing sequencing depth can increase the detection power of the standard methods; however, it does not mean that doing so will decrease the detection power of the significant structural variant method. The number of sSVs increases more with higher sequencing depths in trait-associated genomic regions in real datasets because of the way p-values are calculated in Fisher's exact test, and thus increasing sequencing depth increases the detection power of the significant structural variant method as well (Zhang and Panthee, 2020, 2022).

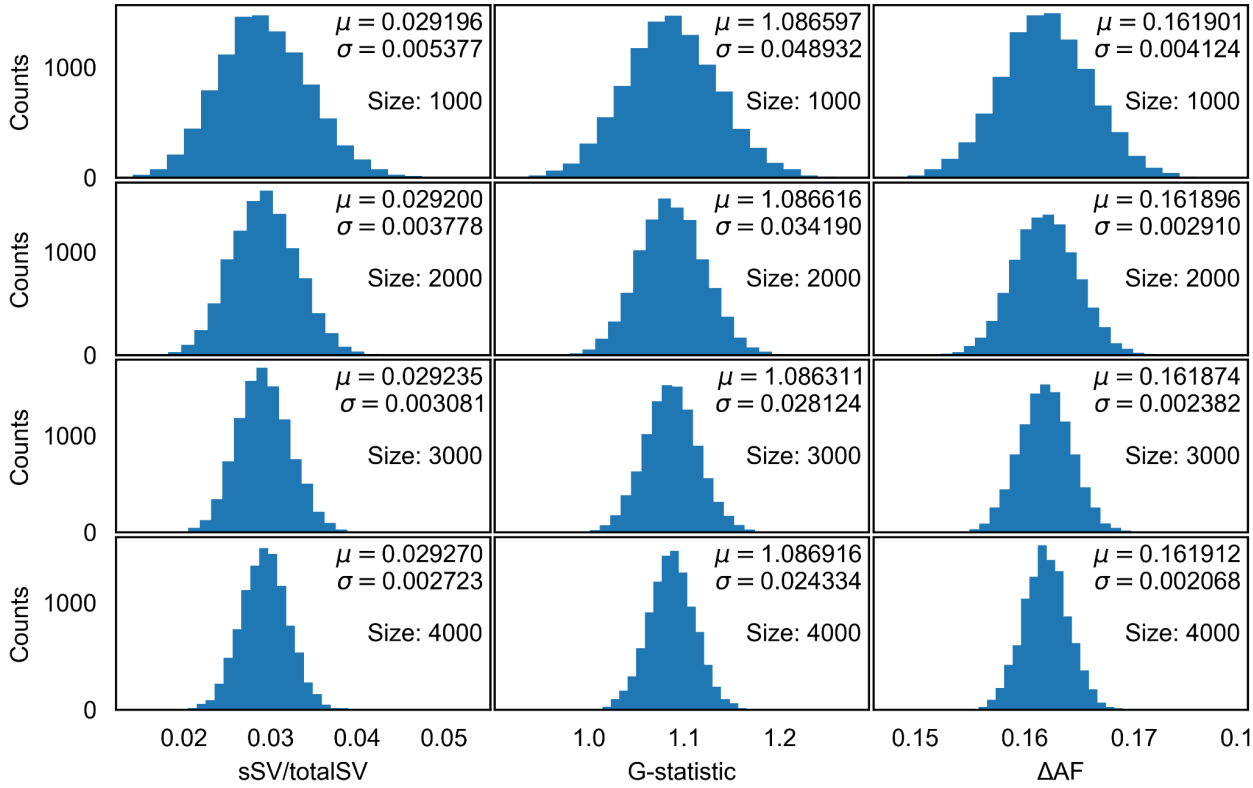

Figure 2. Distribution of 10000 values of sSV/totalSV, G-statistic, and ΔAF obtained via simulation under the null hypothesis (all SNPs are not associated with the trait). Conditions: sequencing depth = 15; the coefficient of variation (sequencing depth) is 0.4, the number of SNPs per sliding window - 1000, 2000, 3000, and 4000 (from top to bottom).

We generated 500 thresholds for each treatment in Figures 2 and 3. As for the nematode dataset, these threshold values are extremely consistent, and the CV values for all the treatments are less than 0.01. Analysis of variation (ANOVA) and Tukey's Honest Significant Difference (HSD) tests revealed that the threshold difference between different sequencing depth/sliding window size level is significant at α=0.01.

The block regression mapping method is a variant of the allele frequency method with high detection power and it uses a different methodology to calculate a genome-wide threshold for the identification of significant peaks/valleys (Huang *et al.*, 2020). Our results suggest that it is not a

good idea to use a genome-wide threshold to judge if a peak/valley is significant, because SVs are not distributed evenly across a genome and sliding window sizes vary greatly in real datasets (Zhang and Panthee, 2020, 2022), and both parameters affect threshold estimation.

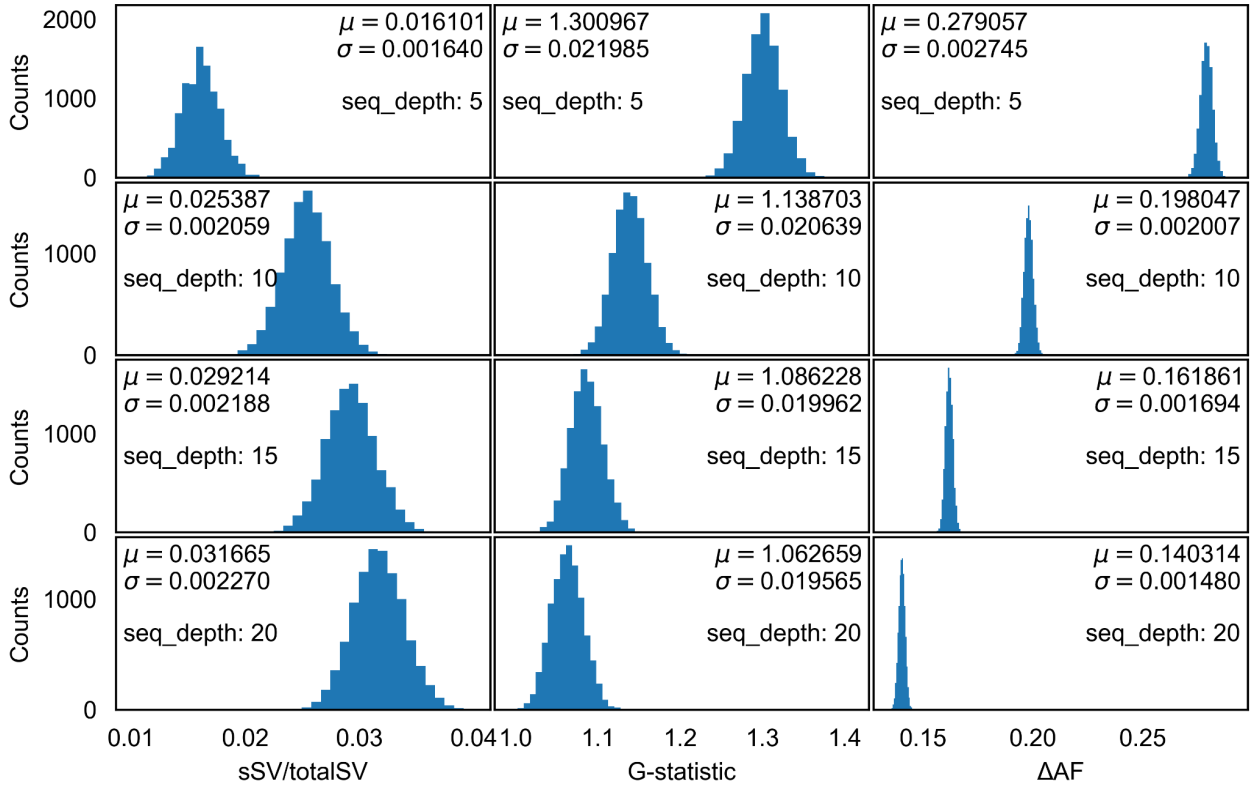

Figure 3. Distribution of 10000 values of sSV/totalSV, G-statistic, and ΔAF obtained via simulation under the null hypothesis (all SNPs are not associated with the trait). Conditions: the average sequencing depths are 5, 10, 15, and 20, from top to bottom; the coefficient of variation (sequencing depth) is 0.4; the number of SNPs per sliding window is 6000.

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