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Citation for published version:

Digital Object Identifier (DOI):
10.3389/fgene.2014.00005

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Publisher's PDF, also known as Version of record

Published In:
Frontiers in genetics

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Assessment of insert sizes and adapter content in fastq data from NexteraXT libraries

Frances S. Turner*

ARK-Genomics, Genetics and Genomics, Roslin Institute, University of Edinburgh, Easter Bush, UK

INTRODUCTION

The Illumina NexteraXT transposon protocol is a cost effective way to generate paired end libraries. Transposonases are used to fragment DNA to be sequenced and add adapter sequences in a single step (known as tagmentation). The DNA between adapter sequences is the insert. The length of this sequence is known as the insert size. Primers are used to check the sequence of the adapter, and remove adapter sequence from the reads. This protocol does not require a reference genome or prior knowledge of the sequence to be trimmed. The detection of such read pairs may indicate the need to trim adapter sequences. As these read pairs are less useful than those with longer inserts, the number of read pairs with an insert size greater than the length of a single read may provide a better indication of the amount of useable data, rather than the total number of read pairs.

A measurement of the numbers of read pairs with an insert size of less than the length of a single read is a useful step in the quality control of fastq data from NexteraXT libraries (or any other library in which the presence of small insert sizes is suspected). The detection of such read pairs may indicate potential problems with the library preparation. The proportion of read pairs with short inserts that can be found in a dataset before the laboratory may need to be alerted, or the data may be considered inadequate for the planned analysis, will depend on the individual circumstances of the experiment. The proportion of fragments with small inserts that may be expected in a library will vary according to the exact details of the library preparation. The extent to which a certain proportion of read pairs with short inserts will impact on the data analysis will depend upon the total number of read pairs generated, and the aims of the analysis. Guidelines regarding the level of short inserts in a dataset that may be considered problematic are beyond the scope of this paper.

The presence of these short inserts in a library may be reflected in a number of possible quality control metrics. Programs such as USEARCH (Edgar, 2010) can be used to scan for specified adapter sequences. K-mer plots produced by FastQC (Andrews, 2010) show the relative enrichment of k-mers along the reverse complement of the adapter attached to read 2, and vice versa.
Turner Quality control of NexteraXT data

Several approaches exist for measuring insert sizes, with short insert sizes being of particular interest. The approach taken here is relatively simple and can be carried out without the need for a reference genome, although this is not a requirement. It relies on the presence of adapter sequences at the end of the fragments, which serve as a marker for the end of the insert size.

Protocol

1. Fastq dataset from NexteraXT libraries
2. Adapter sequence trimming
3. Mapping of reads to a reference genome
4. Measurement of insert size

By mapping read pairs to a reference genome, the insert size can be reliably measured. For reads that do not overlap, the insert size is equal to the length of the contig produced by FLASH. For overlapping reads, the insert size is the length of the contig minus the length of the adapter sequence.

Equation:

\[ i = (r_1 + r_2) - c \]

Where \( i \) is the insert size, \( r_1 \) is the length of read 1, \( r_2 \) is the length of read 2, and \( c \) is the length of the contig produced by FLASH.

Results

Measurements of insert size obtained by mapping reads to a reference genome (CoPERS) and by trying to overlap the reads using FLASH (Magoˇc and Salzberg, 2011) were compared. The insert size was measured for a subset of reads where the insert size was less than the length of both reads, but more than the length of a single read. The two methods showed few differences, with most discrepancies occurring for reads with insert sizes between the lengths of a single read and the length of both reads.

For 92% of reads, the difference between the measurements was less than 250 bp. However, for 9% of reads, the difference was greater than 250 bp, with some reads having insert sizes greater than the length of both reads. For these reads, FLASH was able to overlap the reads, whereas CoPERS was not.

In conclusion, the approach described here allows for the reliable measurement of insert sizes, even for reads that do not overlap. This is particularly useful for detecting small insert sizes, without the need for a reference genome.

CoPERS (Liu et al., 2012) and PANDASeq (Masella et al., 2012) are available for detecting small insert sizes, without the need for a reference genome. However, this approach to measurement of insert size relies on both a reference genome sequence and accurate mapping of reads to the reference. Where discrepancies occur, they may be due to FLASH either failing to overlap reads or not detecting small insert sizes. The two methods show few differences where the insert size is less than the length of both reads, but more than the length of a single read. The two approaches give similar measurements of insert size.
IDENTIFICATION OF ADAPTER SEQUENCE

Just as using FLASH to overlap the reversed sequence of the reads can identify those likely to contain adapter, the same principle can be applied to identify the adapter sequence to be trimmed. The bases occurring after the $i$th position of a read (where $i$ is the insert size as calculated in Section “Measurement of Insert Size”) come from the oligonucleotide attached to the insert. After overlapping the reversed sequences of read pairs, and recording the lengths of the contigs formed by each pair, the section of each read calculated to be after the insert was extracted in fastq format. Examination of the extracted sequence confirmed that this matched the expected sequence. For read 1 this is the reverse complement of the Nextera transposase sequences attached to read 2, followed by the reverse complement of the index, then the PCR primers. Figure 7B shows a plot of nucleotide distribution at each base for sequences extracted from of read 1 for a single library. The first 67 bases show virtually no variability, as it is all adapter sequence. Where the insert size was very short and the read went...
possible to compare the performance of different adapter trimming algorithms based on estimated insert sizes. A number of tools are available to trim adapter sequences from reads. Some published tools include AlienTrimmer (Criscuolo and Brisse, 2013), cutadapt (Marcel, 2011), AdapterRemoval (Lindgreen, 2012), Btrim (Kong, 2011). A comparison of the performance of all available adapter trimming tools is beyond the scope of this paper. However, Cutadapt and AlienTrimmer performed well in a recent comparison of adapter trimming tools (Criscuolo and Brisse, 2013), and AlienTrimmer is designed to efficiently trim a number of possible sequences, so may be a good choice where there is some uncertainty regarding the adapter sequence to be trimmed. For these reasons AlienTrimmer and cutadapt were chosen for assessment of their performance on this dataset. AlienTrimmer searches sequences for all possible k-mers of a given adapter sequence, so its results can vary depending upon the size of k-mer used. The performance of AlienTrimmer with three different k-mer values was compared. The sensitivity and specificity of the two tools were measured. A true positive result was defined as a read for which mapping to the genome indicated an insert of <250 bases, and for which the adapter was trimmed to leave no more than five bases of putative adapter sequence. A false positive result was defined as a read trimmed at least five bases more than necessary, based on the predicted insert size. A true negative result was defined as a read with a predicted insert size of >250, which was not trimmed more than five bases. A false negative result was defined as a read with a predicted insert size of <250, that after trimming had more than five bases of putative adapter sequence. Sensitivity is defined as tp/(tp + fn), where tp is the number of true positives and fn is number of false negatives. Specificity is defined as tn/(tn + fp) where tn is the number of true negatives and fp is number of false positives. Results are shown in Table 1.

The low sensitivity of AlienTrimmer for this particular dataset seems to be at least partly due to its poor performance for reads that extended past the length of the fragment. Figure 8 shows how the specificity of cutadapt and AlienTrimmer (for k-mer = 10) change depending of the number of bases that need to be trimmed. Where less than around 70 bases need to be trimmed, the performance of AlienTrimmer was more comparable to the cutadapt. Where more than 70 bases need to be trimmed AlienTrimmer was not successful. In these cases the read continues beyond the length of the fragment.

**MATERIALS AND METHODS**

The dataset used here consists of 250 bp paired reads from E. coli sequenced on the MiSeq platform at ARK genomics. Demultiplexed fastq files were generated using CASAVA version 1.8. About 96 separate libraries were sequenced in one run. All analysis in this paper is performed using a dataset of 10,000 randomly chosen reads from each library. Libraries were prepared using standard dual index NexteraXT transposon protocol.

Read pairs were filtered by base quality. If after quality trimming using sickle (Najoshi, 2011) with a quality cutoff of 20, the combined length of both ends of the read would be less than 250 base pairs, the read pair was discarded. Read pairs where mapped to the K12_MG1655 genome using BWA (Li and Durbin, 2009) mem version 0.7.5 with default parameters.
FIGURE 7 | Plot showing the base composition of the sequence calculated to occur after the insert (B) compared to a plot of the expected sequence of the Nextera adapter (A).

Table 1 | Comparison of the specificity and sensitivity of two adapter trimming tools.

<table>
<thead>
<tr>
<th></th>
<th>Sensitivity</th>
<th>Specificity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cutadapt</td>
<td>0.99</td>
<td>&gt;0.999</td>
</tr>
<tr>
<td>AlienTrimmer k=8</td>
<td>0.18</td>
<td>&gt;0.999</td>
</tr>
<tr>
<td>AlienTrimmer k=10</td>
<td>0.23</td>
<td>&gt;0.999</td>
</tr>
<tr>
<td>AlienTrimmer k=15</td>
<td>0.18</td>
<td>0.995</td>
</tr>
</tbody>
</table>

Reads were overlapped to form contigs using FLASH version 1.2.2 with the parameters –r 250 f 370 s 80. Default parameters are not suitable for reads of this length and range of insert size.

To test the two trimming tools, reads passing the quality filter were trimmed using cutadapt version 0.9.4 and AlienTrimmer version 0.3.2. AlienTrimmer was used with three different k-mer values (8, 10, and 15). The sequence provided to the two tools to be trimmed off read 1 was CTGTCTCTCTATACACATCTCCGAGCCCACGAGAC, which is the reverse complement of the Nextera transposase sequence attached to read 2 and the sequence to be trimmed of read 2 was CTGTCTCTCTATACACATCTGACGCTGCCGACGA which is the reverse complement of the Nextera transposase sequence attached to read 1 (Oligonucleotide sequence 2007–2012 Illumina, Inc. All rights reserved). The comparison of number of bases trimmed to insert size measured by mapping to the reference was based only on read pairs with high quality mappings. Reads with mapped with a mapping quality of less than 30, or that had split hits, were not included in the comparison.

DISCUSSION

Paired end reads with an insert size of less than the length of a single read contain less information than read pairs with longer insert sizes. If they occur at significant levels, the amount of usable sequence in a dataset will be reduced. Such reads will also contain adapter sequences, which may need to be trimmed as they can negatively impact on some types of analysis. The detection of these reads is therefore a necessary part of quality control.
control for any library likely to have small insert sizes. Such short inserts can be measured using FLASH (or a similar program) to overlap the reversed sequence of the paired reads. This allows for a very fast assessment of the number of read pairs in a dataset that have short inserts, without the need for a reference sequence. Read pairs, that FLASH is able to overlap in the reversed sequence should have adapter sequence at the ends. As the length of the insert can be calculated from the length of the individual reads and overlapped read, it is possible to calculate how far each read continued past the insert. It is also possible to confirm the sequence of the oligonucleotide the read covered after the insert. The sequence after the insert may need to be removed as it can affect analysis, in particular de novo assembly. If there is any uncertainty about the adapter sequence that needs to be trimmed, the sequence of a range of possible Illumina oligonucleotides could be provided to an adapter trimmer tool. AlienTrimmer is designed to be able run quickly, even given a long list of possible sequences to trim (Criscuolo and Brisse, 2013). However, the comparison of these tools in Section “Comparison of Insert Sizes to Length of Sequence Cut by Trimming Tools” suggests that AlienTrimmer failed to trim adapter from reads that continued past the adapter sequence. Therefore AlienTrimmer would not be a good choice for datasets with many such reads. Cutadapt did well even where the read continued past the adapter sequence. Cutadapt can also be provided with a long list of possible contaminant sequences (although this would cause it to run more slowly). Both tools (along with the wide range of other tools to detect and remove adapter sequence) need to be provided with a sequence to be trimmed (or a list of possible sequences to be trimmed). They would therefore fail if there is unexpected sequence occurring after the insert. Whilst the adapter sequence to be removed would generally be known, there may be some situations in which it is useful confirm this. In the context of data quality control a sequencing laboratory it would be useful to know if the sequence occurring after the insert is not the expected sequence, as this could indicate a problem with library construction. When working with data obtained from a public repository it may be difficult to obtain information regarding the adapters used.

This method to predict the position and sequence of the adapter to be trimmed cannot be applied to Nextera long mate pair (LMP) libraries. In these libraries the adapter sequence to be trimmed may occur anywhere in the read rather than at the 3′ end. Therefore the position of adapter in a read cannot be predicted from the length of counting formed when the 5′ ends of a read pair overlap. NextClip (Leggett et al., 2013) is a tool that can be used to detect and remove adapter sequences in LMP libraries.

CONCLUSION

The protocol described in this paper to detect and remove adapter sequences could in principle be applied to any small insert size Illumina paired end library, uses readily available tools, and does not require prior knowledge of the adapter sequence or access to a reference genome.

REFERENCES


Conflict of Interest Statement: The author declares that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Received: 03 December 2013; accepted: 06 January 2014; published online: 30 January 2014.

This article was submitted to Bioinformatics and Computational Biology, a section of the journal Frontiers in Genetics.

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