SmartDADA2 Report

Objective

When using 16S rRNA sequencing data there are three things that must be optimized when performing quality control on your reads:

1. Read length (as the longer the read the better the taxonimical classification)
2. Quality of the read (increasing the accuracy)
3. Number of reads (to ensure the most robust picture of the mirobial community)

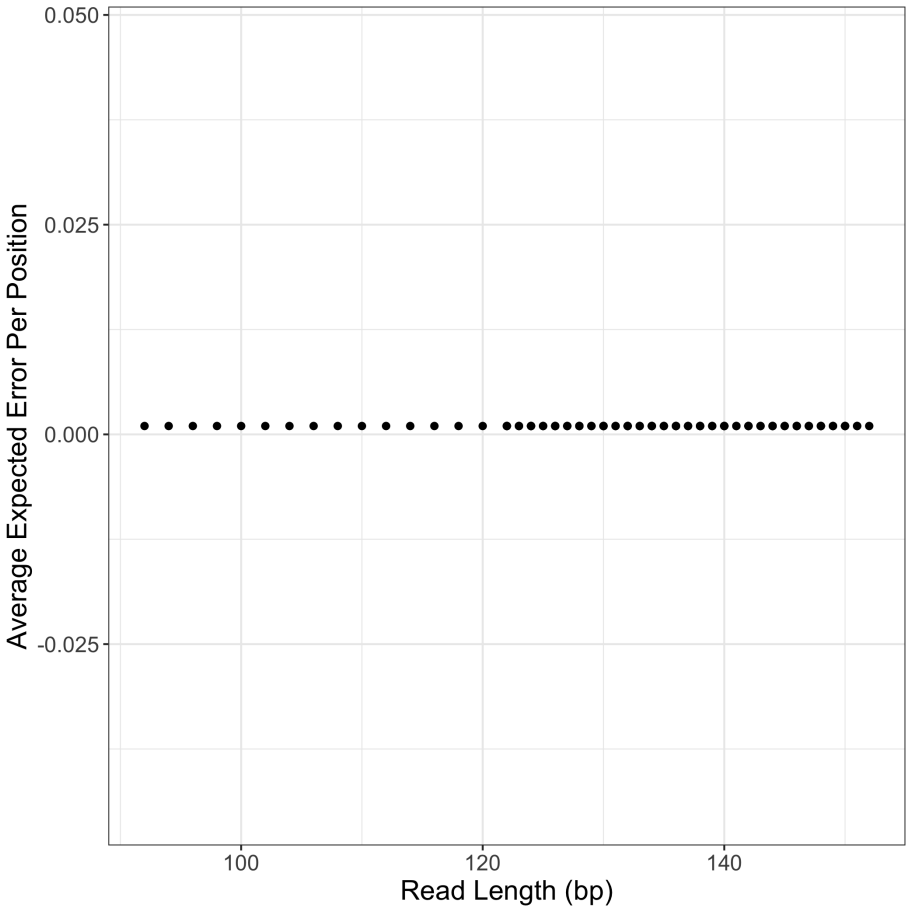
In order to maximize these factors this program has been designed to provide evidence for picking certain parameter values in the commonly used program DADA2 that is used to perform quality control in 16S rRNA seq processing pipelines.

Findings

Read Length and Quality

Here we plotted different sized reads by the average expected error per base. Each point is associated with a different set of left and right trim values.

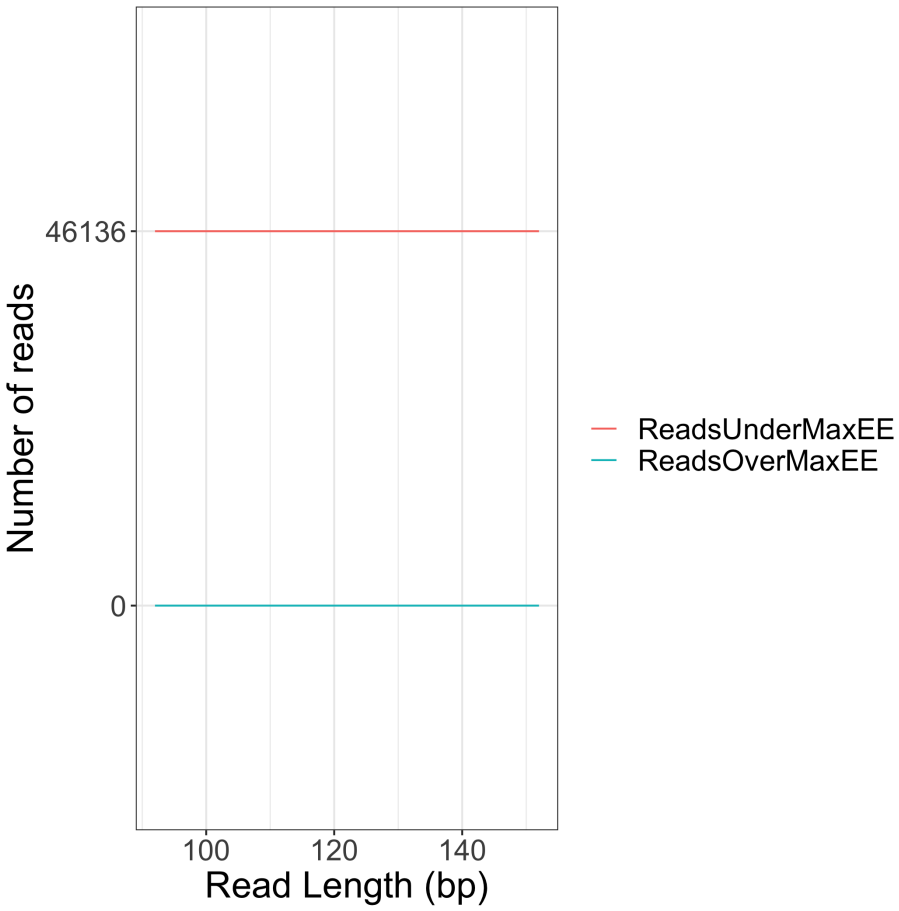
Note: It is important to understand that a read can be of the same length with different trimming values. For example, a read can be 100 bp long if trimmed from 0-100 or from 10-110.



Read Length by Maximum Expected Error

DADA2 has a parameter called maxEE which is the max number the sum of the expected error for a read should be. It defaults to 2.0, meaning that any read with an error higher than 2.0 will be discarded.

This plot is designed to show how many reads are above and below this threshold by different read sizes. This is in an effort to show whether increasing the max expected error might yield significantly more reads for downstream analyses.


46136
0
Number of reads
100
120
140
Read Length (bp)
ReadsUnderMaxEE
ReadsOverMaxEE