Characterizing Metagenomes Using K-mer Abundance

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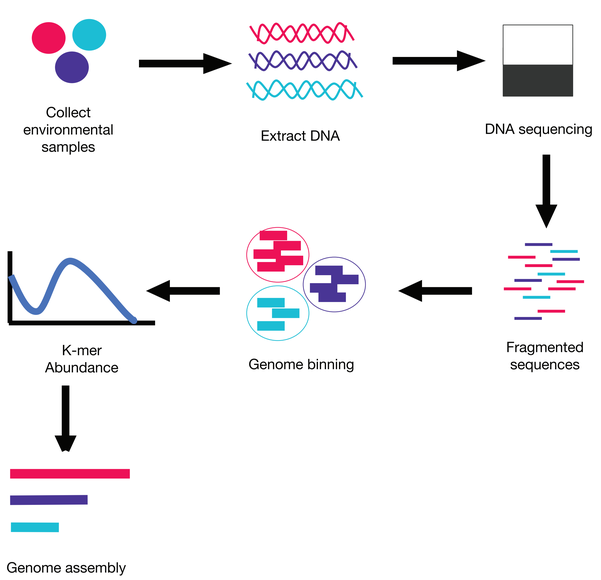
Introduction

Metagenomic methods allow us to understand microbial communities found in environmental samples.

Methods use short sequences of length k for efficient counting. Where k-mers are all substrings of length k in a sequence. Counting k-mers is a preliminary step in bioinformatics applications to assess the data before performing assembly.

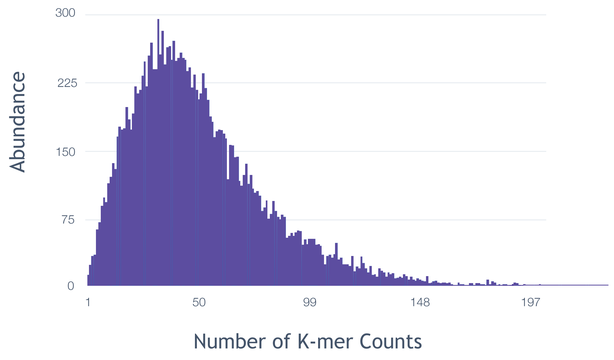
Abundance histograms can be generated from counting all k-mers in a sequence. Generating histograms can be used to estimate genome size, coverage, and estimate an important parameter for assembly.



Future Direction

- Estimate the best k value parameter for each genome present in metagenomic data
- Test the k values by perfoming assembly.

Generating Abundance Histograms



7-mers	K-mer Count
AGATTAG	1
GGAATAC	1
TAAGATC	12
AGTACGT	6
GATGACA	2

K-mer Count	Abundance
1	12
2	23
3	33
4	34
5	62

Figure 1. Abundance of an Algae Genome

DNA sequences are fragmented into k-mers and stored with a value of counts. Abundance refers to the number of k-mers that have the same number of counts in a sequence.

Effect of K-mer Size

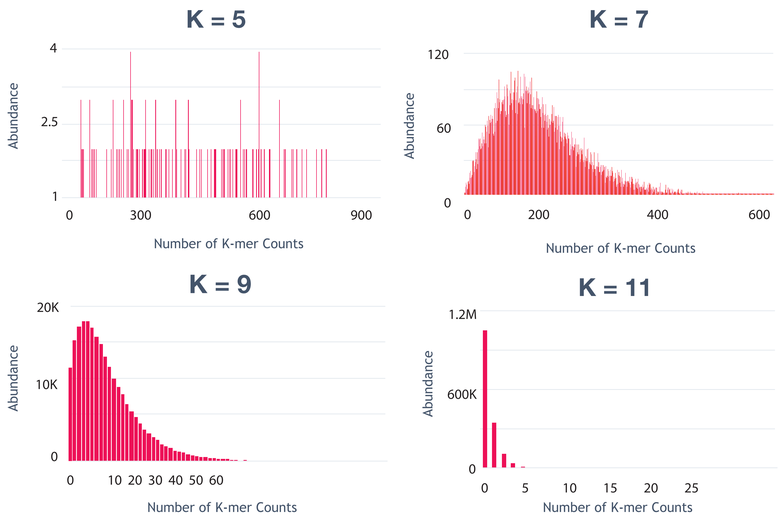


Figure 3. Effect of K = 5, 7, 9, 11

Choosing a k-mer size affects the quality of sequence assembly. Shorter k-mers will be more repetitive in a sequence and contain less information, but increase chance of overlaps. Longer k-mers are less repetitive in a sequence and contain more information, but decrease chance of overlaps.

Metagenome Abundance

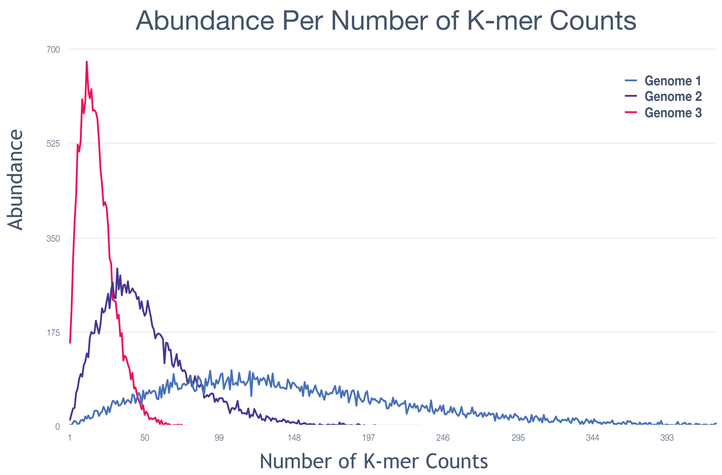


Figure 2. K-mer Abundance Profiles of 3 Different Genomes

K-mer abundance of three different algae genomes binned by MetaBAT. Here each distribution is represented by 7-mers. Ideally, each genome will require a different k-value depending on the abundance of each specie.

De Brujin Graph Assembly

Read AGATACAT

K-mers AGA, GAT, ATA, TAC, ACA, CAT, ATA, TAC

De Brujin Graph

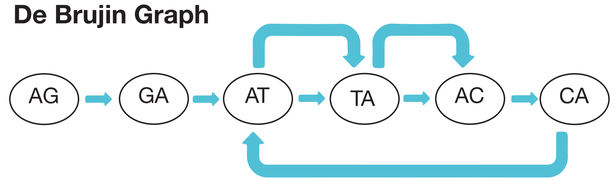


Figure 4. De Bruijn Graph Assembly with K = 3

Sequences are fragmented into k-mers, and overlaps represented by (k-1) are nodes in the graph. The arrows are directed edges which are used to reconstruct the the original genome.