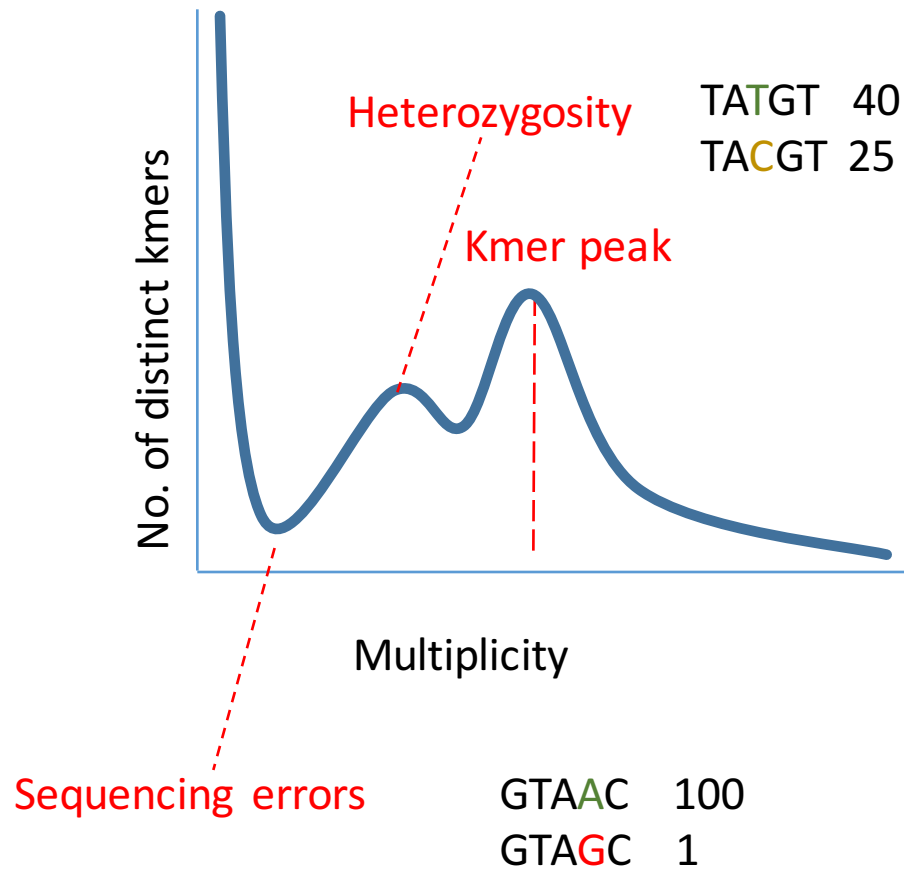


>Example_seq

ACTATGTCTGTAAGTGAAGTGTGTTGGAACGGTATAGGCGTGGCTGGTAAAAAACTACGT

jellyfish count -C -m 3 -s 5G -o output Example_seq.fasta
jellyfish histo -o output.histo output



Histogram

ACTAT	2
CTATG	3
TATGT	1
ATGTC	1
TGTCT	1
GTCTG	1
TCTGT	56
CTGTA	3
TGTAA	4
GTAAC	100
TAACT	120
AACTG	20
ACTGT	1
CTGTA	1
TGTAA	1
GTAAC	1
TAACT	1
AACTG	1

$$\text{Depth} = \frac{\text{Kmer peak} * \text{Avg read length}}{\text{Avg read length} - (K+1)}$$

$$\text{Genome size} = \frac{\text{total no of nucleotides}}{\text{Depth}}$$