Part 1 Demultiplexing | BIO 622

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Part 1

1.

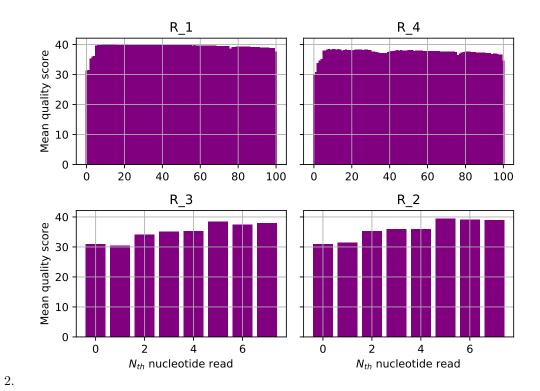| Filename	Read
$1294_S1_L008_R1_001.fastq.gz$	Read 1
$1294_S1_L008_R2_001.fastq.gz$	Index 1
$1294_S1_L008_R3_001.fastq.gz$	Index 2
$1294_S1_L008_R4_001.fastq.gz$	Read 2

2.

Figure 1: Distribution of average quality score R1

Due to the first two biologcal reads – for both R1 and R2 – are quite low $\approx< 36$, I would set the cutoff for 37, to make sure we are getting high quality biolocial reads.

To find the total number of N's within the two index reads, I used the following bash command

zcat emp_files/1294_S1_L008_R[2-3]* | awk 'NR%4==2' | grep N | wc -l > countN_Index.txt