

Due October 11, 2016

1. Write an R function that takes ShortReadQ reads, trims low quality bases from these reads, and removes the reads that after trimming are shorter than the minimum length. . In addition to the reads, the function takes three parameters: *minimum quality*, *first base* and *minimum length*. (10 points)
2. Generate a random sample of 10000 reads from the dataset that you used in the lab. Then apply the function you created in Question 1 to generate a new dataset such that the minimum quality score is 20 and the minimum sequence length is 30. Then use *table* (*width()*) functions to summarize the remaining sequences in the new dataset. (10 bonus points)