devesh@DESKTOP-J4SSHPI:~\$ sudo apt update

[sudo] password for devesh:

See "man sudo_root" for details.

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Usage: seqtk <command> <arguments>

Version: 1.4-r122

Command: seq common transformation of FASTA/Q
size report the number sequences and bases
comp get the nucleotide composition of FASTA/Q

sample subsample sequences subseq extract subsequences from FASTA/0

fqchk fastq QC (base/quality summary)
mergepe interleave two PE FASTA/Q files

split split one file into multiple smaller files

trimfq trim FASTQ using the Phred algorithm

hety regional heterozygosity

gc identify high- or low-GC regions

mutfa point mutate FASTA at specified positions

mergefa merge two FASTA/Q files

famask apply a X-coded FASTA to a source FASTA dropse drop unpaired from interleaved PE FASTA/Q

rename rename sequence names

randbase choose a random base from hets

cutN cut sequence at long N gap get the gap locations

listhet extract the position of each het hpc homopolyer-compressed sequence

telo identify telomere repeats in asm or long reads

```
devesh@DESKTOP-J4SSHPI:/mnt/c/Users/Dell/Desktop/internships/barc dataset$ segtk sample -s100 SRR15718926_2.
fastq 0.1 > SRR15718926_2_subsampled.fastq
devesh@DESKTOP-J4SSHPI:/mnt/c/Users/Dell/Desktop/internships/barc dataset$ segtk sample -s100 SRR15718926_2.
fastq 0.1 > SRR15718926_2_subsampled.fastq
devesh@DESKTOP-J4SSHPI:/mnt/c/Users/Dell/Desktop/internships/barc dataset$ grep -c "^+$" SRR15718926_2.fastq
9739476
devesh@DESKTOP-J4SSHPI:/mnt/c/Users/Dell/Desktop/internships/barc dataset$ grep -c "^+$" SRR15718926_2_subsa
mpled.fastq
975478
devesh@DESKTOP-J4SSHPI:/mnt/c/Users/Dell/Desktop/internships/barc dataset$
```