Exercise 2: Pysam - CGC Interactive analysis

- Create an `AlignmentFile` object for "merged-tumor.bam" from Public files gallery
  - Take the first read from the `AlignmentFile`
  - Inspect the fields in the `AlignedSegment`
  - Inspect the flag field
- Check out the <u>flag for some reads</u>
- Calculate:
  - How many unmapped reads are in the file?
  - Total number of reads
  - Number of reads with mapping quality 0
  - Average mapping quality for all the reads
  - Average mapping quality if reads with 0 mapp quality are filtered out
- Send the link to Github repo with Jupyter Notebook of executed analysis to pedjao@etf.bg.ac.rs, together with name and number of index, the mail subject should be "GI2023_DZ2". Deadline: 26th of March, 23:59