Analysis of PHRED Score using Python

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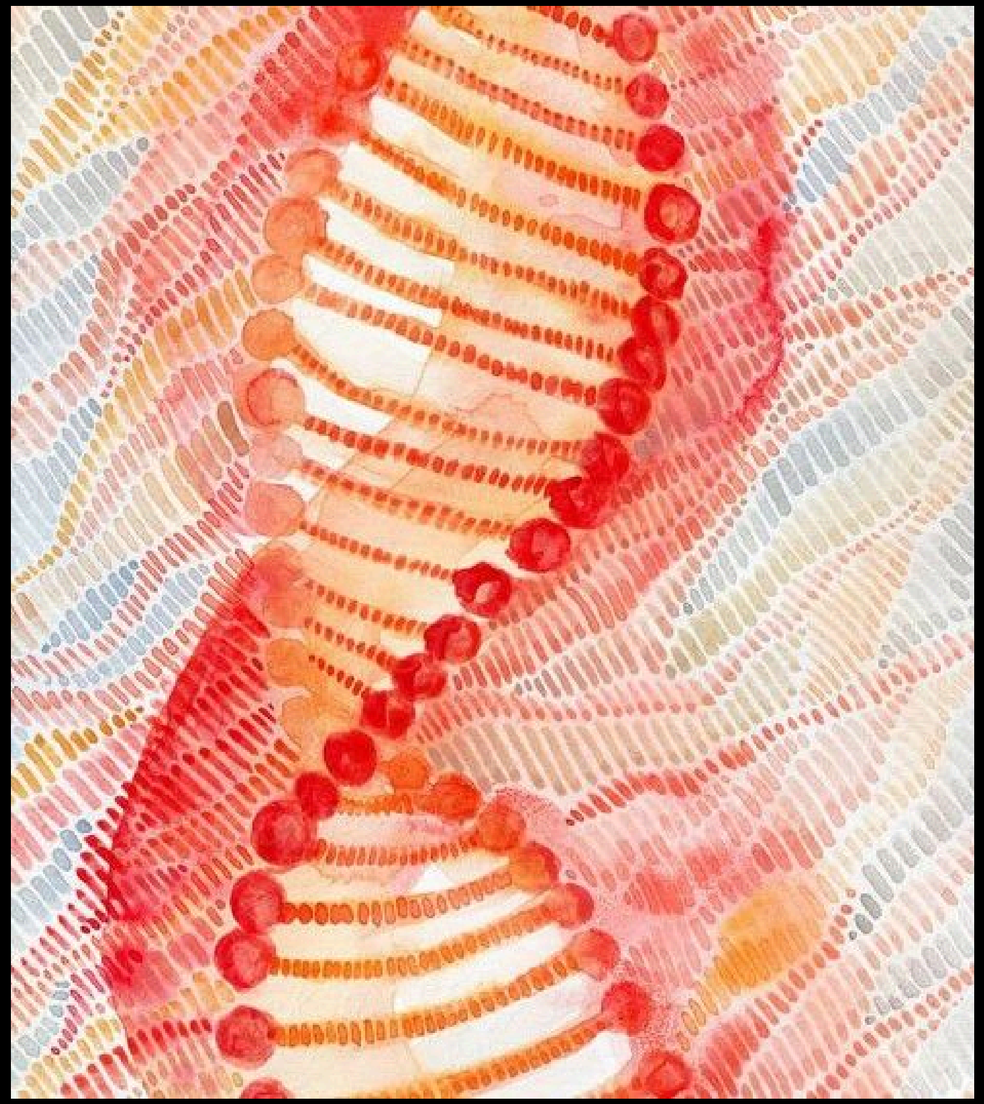
OBJECTIVES

- Implement a Python-based method to identify low-quality reads
- Output results in a structured format (CSV)
- Understand Phred quality scores in sequencing data
- Highlight their importance in bioinformatics

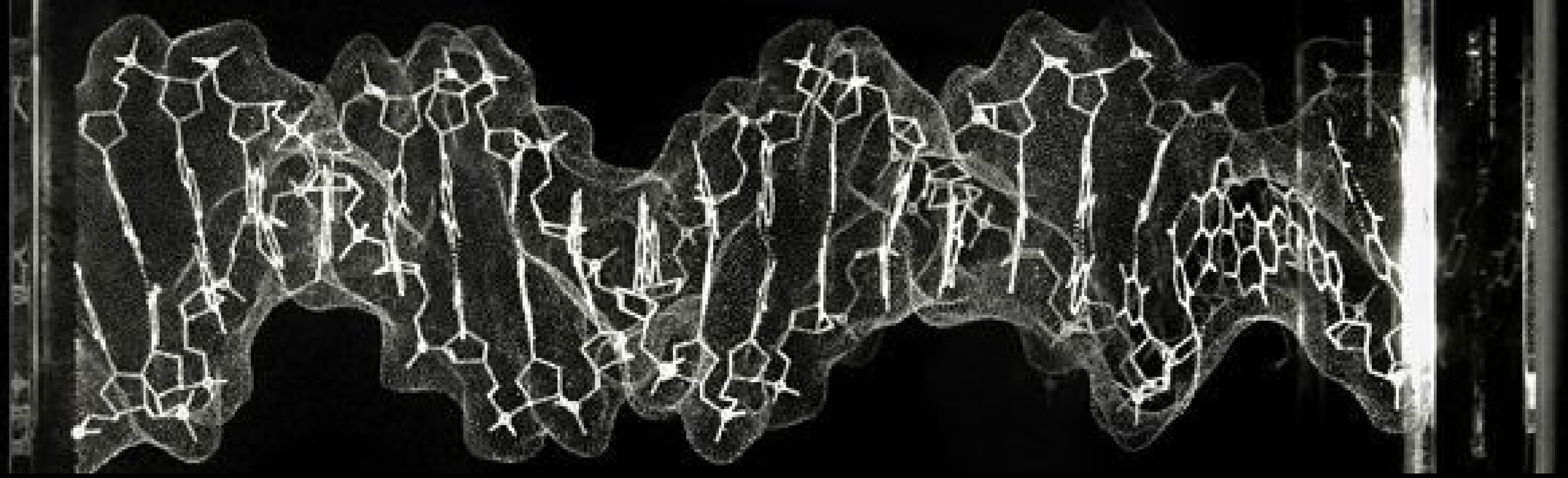
What is PHRED Score?

- A numerical value that represents the quality of each nucleotide base call in DNA sequencing
- Indicates the probability of an incorrect base call



Importance of PHRED score

- **Quality Control –** Filters out poor-quality bases/reads → ensures reliable data.
- **Better DNA Assembly –** Gives more weight to high-quality reads when combining sequences.
- **Accurate Variant Detection –** Reduces false positives in mutation analysis.
- **Universal Standard –** Used across all sequencing platforms, making results comparable.
- **Bioinformatics Pipelines –** Stored in FASTQ files → software uses scores for trimming, alignment, and analysis.
- **Reliable Genotyping –** Ensures confidence in calling genetic variants in populations and clinical studies



How is it Calculated?

- General formula:

$$Q = -10 \times \log_{10}(P)$$

Where:
Q = Phred Quality Score
P = Probability that the base call is incorrect

METHODOLOGY

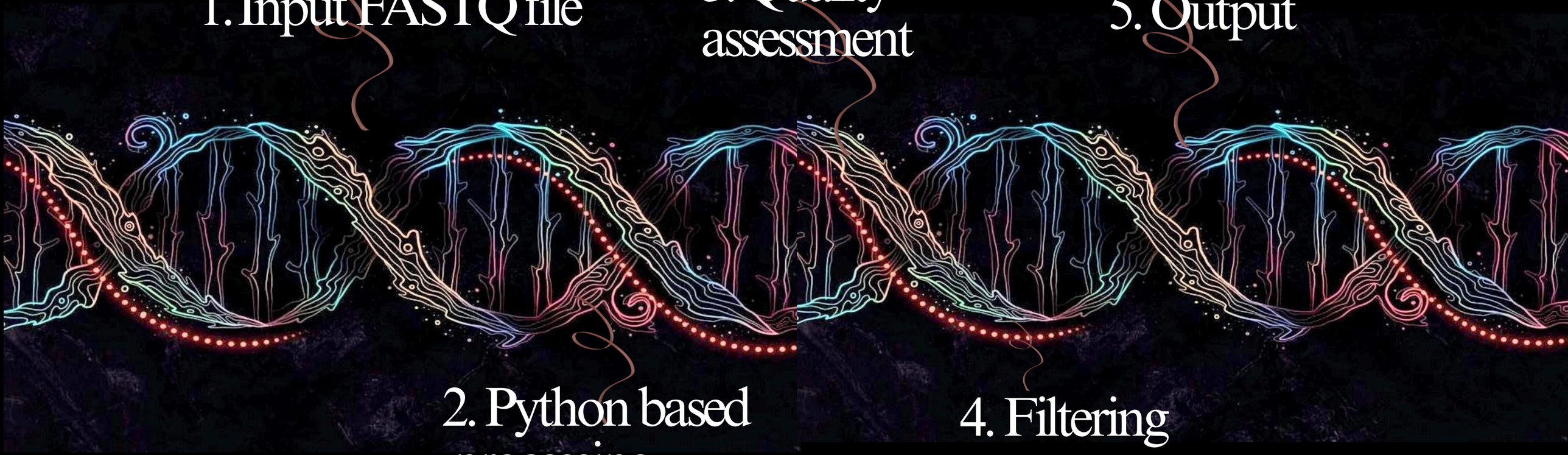
1. Input FASTQ file

2. Python based processing

3. Quality assessment

4. Filtering

5. Output



OUTPUT

The analysis produced a table of sequences that were identified as low-quality based on their mean Phred scores. Each record includes:

- Read ID: Unique identifier for each sequencing read.
- Sequence: The nucleotide sequence associated with that read.
- Mean Phred Score: Average quality score across the entire read.

Read_ID	Sequence	Mean_Phred_Score
@SRR34999326.1 TBGYX:08006:1	CCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGGGGAACCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTATGGTTGTAAAGCACTTTTAAGCGAGGAGGAGGCTACTCTA(	30
@SRR34999326.2 TBGYX:08028:1	CCTACGGGGAGCAGCAGTCGGGATTTCCGGC	30
@SRR34999326.3 TBGYX:08031:1	CCTACGGGGAGGCAGCAGTGGGGGAATAATTGGGACAATTGGGGGGGAACCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTATGGTTGTAAAGCACGTTTAAGCGAGGAGGAGGC	30
@SRR34999326.4 TBGYX:08041:1	CCTACGGGGAGGCAGCAGTGGGGGAATATTTGCACAATGGGGGGAAACCCTGATGCAGCCATGCCGCGTGTGTGAAGAAAGGCCTTCGGGTTGTAAAGCACTTTCATGCGAGGAGGAAAGGT	30
@SRR34999326.5 TBGYX:07992:1	CCTACGGGAGGCAGCAGTGGGGGAATATTGGACAATGGGGGGGAACCCTGATCCAGCCATGCCGCGTTGTGTGAAGAAGGCCTTTTTGGTTGTAAAGCACTTTAAGCGAGGAGGAGGCGCTC	30
@SRR34999326.6 TBGYX:08025:1	CCTACGGGAGGCAGCAGTGGGGGAATATTGGACAATGGGGGGGAACCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTATGGTTGTAAAGCACTTTAAGCGAGGAGGAGGCTACTGA	30
@SRR34999326.7 TBGYX:08028:1	CCTACGGGGAGGCAGCAGTGGGGAATATTGGACAATGGGGGGGAACCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTATGGTTGTAAAGCACTTTAAGCGAGGAGGAGGCTACTGA	30
@SRR34999326.8 TBGYX:08029:1	CCCGGTACGGGACGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATTTAGGGAAGAACAAACG	30
@SRR34999326.9 TBGYX:08029:1	CCTACGGGAGGCAGCAGTGGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTCAGTAAGGAGGAAGCGTTGAGT	30
@SRR34999326.10 TBGYX:08017:	CCTACGGGAGGCAGCAGGCGCCGGTAAT	30
@SRR34999326.11 TBGYX:08023:	CCTACGGGAGGCAGCAGCCCGTACGTAT	30
@SRR34999326.12 TBGYX:08032:	CCTACGGGGAGGCAGCAGTGGGGGAATATTGGACAATGGGGGGGAACCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTGTGGTTTGTAAAGCACTTTTAAGCGAGGAGGAGGCTAC	30
@SRR34999326.13 TBGYX:08000:	CCTACGGGAGGCAGCAGTGGGGAATCTTTGCACAATGGGGCGGAAGCCTGATGCAGCGACGCCGCGTGAGGGATGACGGCCTTTCGGGTTTCGTAAACCTCTTTTTCGCCAGGGACGAAGC	30
@SRR34999326.14 TBGYX:08010:	CCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATGCCGCGTGGAGGTGGAAGGCCCACGGGTCGTCAACTTCTTTTTCTCGGAGAAGAAACAATGACC	30
@SRR34999326.15 TBGYX:08017:	CCTACGGGAGCAGCAGTGGGGAATATTGGACAATGGGGGGAACCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCGAGGAGGAGGCGCTCTAGGA	30
@SRR34999326.16 TBGYX:08021:	CCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATTAGGGAAGAACAACGTGTAAC	30
@SRR34999326.17 TBGYX:08029:	CCCTAAGGCAGCAGTGGGGAATATTGGACAATGGGGGGAACCCTGATCCAGCCATGCCGCGTTGTGTGAAAGAAGGCCTTTTGGTTTGTAAAAGCACTTTTAAGCGAGGAGGAGGCGCTCTAG	30
@SRR34999326.18 TBGYX:08024:	CCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGTCTGAAGAAGGCCTTCGGGTTGTAAAGGACTTTTGTCGGGGGAGGAATCCCCAGCC	30
@SRR34999326.19 TBGYX:08031:	CCCTCGGGGAGGCAGCAGTGGGGGGAATATTGGACAATGGGGGGAACCCCTGATCCAGCCATGCCGCGTGTGTGAAAAGAAGGCCTTATGGTTGTAAAAAGCACTTTAAGCGAGGAGGAGG	30
@SRR34999326.20 TBGYX:08032:	CCTACGGGGAGGCAGCAGTGGGGGAATATTTGCACAATGGGGGAAACCCTGATGCAGCCATGCCGCGTGTGTGAA	30
@SRR34999326.21 TBGYX:08014:	CCTACGGGGAGGCAGCAGTGGGGGAATATTGGACAATGGGGGGAACCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTTGTAAAAGCACTTTAAGCGAGGAGGAGGCGCTC	30
@SRR34999326.22 TBGYX:08032:	CCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGGGGAACCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTATGGTTGTAAAGCACTTTAAGCGAGGAGGAGGCTGACTGAC	30
@SRR34999326.23 TBGYX:08034:	CCTACGGGGAGGCAGCAGTGGGGAATATTGGACAATGGGGGGAACCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCGAGGAGGAGGCGCTCTAC	30
@SRR34999326.24 TBGYX:07995:	CCTACGGGGAGGCAGCAGTGGGGGAATATTGGACAATGGGGGGGAACCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTATGGTTGTAAAGCACGTTTTAAGCGAGGAGGAGGCTG	30
@SRR34999326.25 TBGYX:08018:	CCTACGGGGAGGCAGCAGTGGGGAATTTTTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGTCTGAAGAAGGCCTTCGGGTTGTAAAGGACTTTTTGTCGGGGGAGGAAATCCCC	30
@SRR34999326.26 TBGYX:08033:	CCTACGGGAGGCAGCAGTGGGGATTTTCCGCAATGGCGAAAGCCTGACGGAGCCAAT	30


Thank
You