Adding Phred Quality Scores to Sequence

Task Name: join-quality

Adds Phread quality scores to a sequence and saves the result to the output FASTQ file.

Parameters:

in — input sequence file. [String, Required]

quality — input Phred quality scores file. [String, Required]

out — output FASTQ file. [String, Required]

Example:

```
ugene join-quality --in=e_coli.fa --quality=e_coli.qual --out=res.fastq
```