

UMI error correct documentation

Run the pipeline from start using the following command: `run_umierrorcorrect.py`

Output directory

Specify the path to the output directory. If it doesn't exist it will be created.

```
run_umierrorcorrect.py -o output_directory
```

Input files

- `-r1` Path to the read1.fastq.gz input file
- `-r2` Path to the read2.fastq.gz input file (if applicable)