Comparative analysis of **Fastqc** using **Nextflow vs Bash script**

1. **Bash script**

{ CODE BLOCK

```bash
#!/bin/bash

# Define input and output directories
INPUT_DIR="/home/Desktop/Prcatise/Nexflow_prac/my_pipelines/fastq_files"
OUTPUT_DIR="/home/Desktop/Prcatise/Nexflow_prac/my_pipelines/fastq_files/output_bash_fastqc"

# Create the output directory if it doesn't exist
mkdir -p "$OUTPUT_DIR"

# Loop through all .fastq.gz files in the input directory
for file in "$INPUT_DIR"/*.fastq.gz
do
        echo "Running FastQC on $file..."
        fastqc "$file" --outdir "$OUTPUT_DIR"
done

echo "All FastQC analyses completed!"
}
```

```
Approx 55% complete for SRR33317478.fastq.gz
Approx 60% complete for SRR33317478.fastq.gz
Approx 65% complete for SRR33317478.fastq.gz
Approx 70% complete for SRR33317478.fastq.gz
Approx 75% complete for SRR33317478.fastq.gz
Approx 80% complete for SRR33317478.fastq.gz
Approx 85% complete for SRR33317478.fastq.gz
Approx 90% complete for SRR33317478.fastq.gz
Approx 95% complete for SRR33317478.fastq.gz
Analysis complete for SRR33317478.fastq.gz
All FastQC analyses completed!
[ble: elapsed 42.864s (CPU 117.5%)] bash fastqc_bash.sh
```

Bash takes 42 seconds to complete analysis

2. Nextflow script

```
[CODE BLOCK

#!/usr/bin/env nextflow

params.reads =
'/home/Desktop/Prcatise/Nexflow_prac/my_pipelines/fastq_files/*.fastq.gz'
params.outdir =
'/home/Desktop/Prcatise/Nexflow_prac/my_pipelines/fastq_files/output_fastqc'

process FastQC {
    publishDir params.outdir, mode: 'copy'

    input:
    path read_file

    output:
    path "*.html"
    path "*.zip"

    script:
    """
    fastqc $read_file
    """
}

workflow {
    Channel
    .fromPath(params.reads)
    .set { read_files }

    FastQC(read_files)
}
]
```
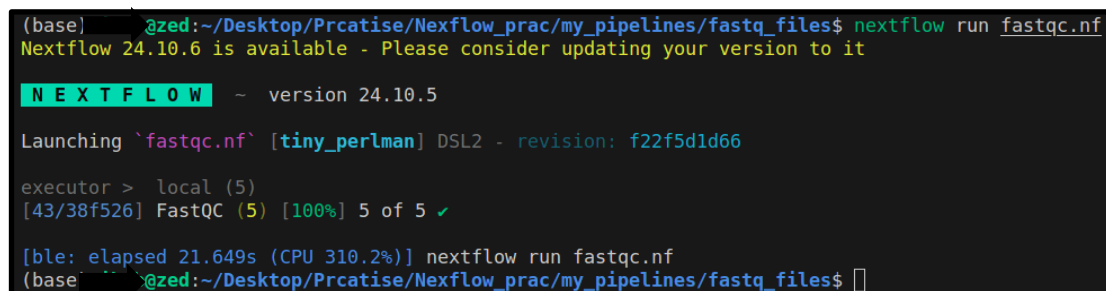
```
(base)      @zed:~/Desktop/Prcatise/Nexflow_prac/my_pipelines/fastq_files$ nextflow run fastqc.nf
Nextflow 24.10.6 is available - Please consider updating your version to it

 N E X T F L O W   ~  version 24.10.5

Launching `fastqc.nf` [tiny_perlman] DSL2 - revision: f22f5d1d66

executor >  local (5)
[43/38f526] FastQC (5) [100%] 5 of 5 ✔

[ble: elapsed 21.649s (CPU 310.2%)] nextflow run fastqc.nf
(base      @zed:~/Desktop/Prcatise/Nexflow_prac/my_pipelines/fastq_files$ []
```

Nexflow take only 21 seconds to finish task