

```

#!/usr/bin/env nextflow

/*
 * pipeline input parameters
 */

params.inDir = "fastaFiles"

Channel
.fromPath( "${params.inDir}/*.fa" )
.ifEmpty { error "Cannot find any input sequence files matching: *.fa" }
.set { fastaFiles }

/*
 * Get sequence lengths
 */
process getLengths{

input:
    file aFile from fastaFiles

output:
    file 'lengths.txt' into lengths

script:
    """
    awk -F "\\n" '!/^>/ {print length ($0) } /^>/ { printf "%s\\t", $0}' ${aFile}
    > lengths.txt
    """
}

//Collect all the files into a single file
lengths
.collectFile(name: file("seqLengths.txt"))
.set{lengths2}

/*
 * Use the lengths to create a density plot in R
 */
process plotLength{

input:
    file seqLengths from lengths2

output:
    file "lenDist.pdf" into plot

script:
    """
    #!/usr/bin/env Rscript
    lengths <- read.table("${seqLengths}", sep = "\\t", header = F)
    pdf("lenDist.pdf")

```

```
plot(density(lengths[,2]), xlab = "Sequence length (nts)")
dev.off()
"""
}

//Collect the file so it is created in our working directory
plot
.collectFile(name: file("lenDistribution.pdf"))
```