



# nf-core mentorship: From wet lab to DSL2

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## Background

Being a life scientist, it has been a roller coaster ride to learn about genomic analysis and apply them on my sequencing data. With little knowledge of computers, programming and genomics, I struggled to carry out analyses on my own. I had heard about Nextflow but never tried it and this mentorship program gave me an opportunity to get to learn and apply it to my research questions.

## Nextflow favourable features

- Basic knowledge of any scripting language is enough to get started
- Parallel tasking makes work quicker
- Resume function helps to avoid re-processing the same steps
- Troubleshooting is easier as all executions are saved in a specific space

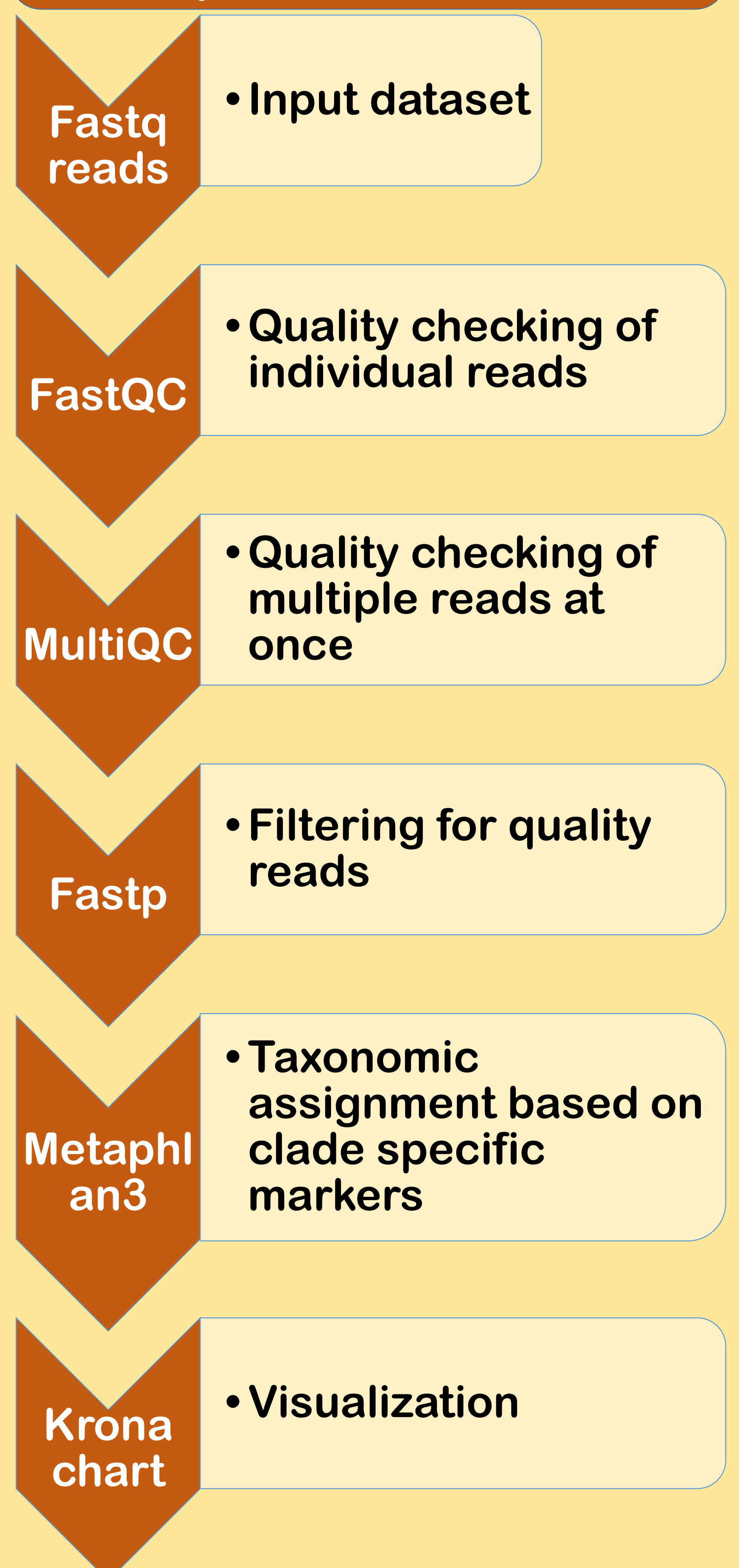
## Challenges

- Though pre-formed modules are available, DSL2 is more complex than DSL1.
- Slow internet connection in Nepal
- Inaccessible cloud computing infrastructure
- Windows OS system troubleshooting difficult

## Conclusion

During this fellowship, I learned the bash script, Groovy language basics, nextflow pipeline development, pipeline testing using test data, troubleshooting, cloud computing basics, result visualization, sharing pipelines on GitHub and many more.

## Pipeline developed: Metaphlankrona



## References

- First pipeline in DSL1: [https://github.com/maxibor/nextflow-mentoring/tree/main/first\\_pipeline](https://github.com/maxibor/nextflow-mentoring/tree/main/first_pipeline)
- Second pipeline in DSL1 : [https://github.com/maxibor/nextflow-mentoring/tree/main/second\\_pipeline](https://github.com/maxibor/nextflow-mentoring/tree/main/second_pipeline)
- Second pipeline converted to DSL2: <https://github.com/suchitrathapa/metaphlankrona>