

## **nf-core as the standard for BovReg reference pipelines**

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The BovReg project aims to produce a set of bioinformatics reference pipelines that will become a long-lasting resource for the annotation of the functional genome of cattle. To achieve this goal, BovReg reference pipelines should stick to the best current computational standards. In short, these standards should enable the deployment of the pipeline in different environments (from the cloud to HPC clusters), the traceability and reproducibility of its results and the interoperability between the produced results.

Here, we will describe how nf-core provides a perfect framework to develop pipelines that follow high computational standards. The nf-core community collects bioinformatics pipelines implemented with the Nextflow workflow manager. These pipelines should follow best computational practices and thus meet a series of requirements and recommendations that guarantee reproducibility, interoperability and a unified minimal functionality. In the BovReg project, we agreed early on that our reference pipelines should also meet these standards. Remarkably, some nf-core pipelines already cover certain BovReg analysis aspects and can directly be used. For other nf-core pipelines, the need for added novel functionalities was identified within BovReg and implemented. Finally, in the few cases where no nf-core pipelines were found suitable, novel pipelines are being implemented by BovReg partners and standardized to adhere to the nf-core computational standard and eventually become part of the nf-core collection.