

nf-core/ seqinspector

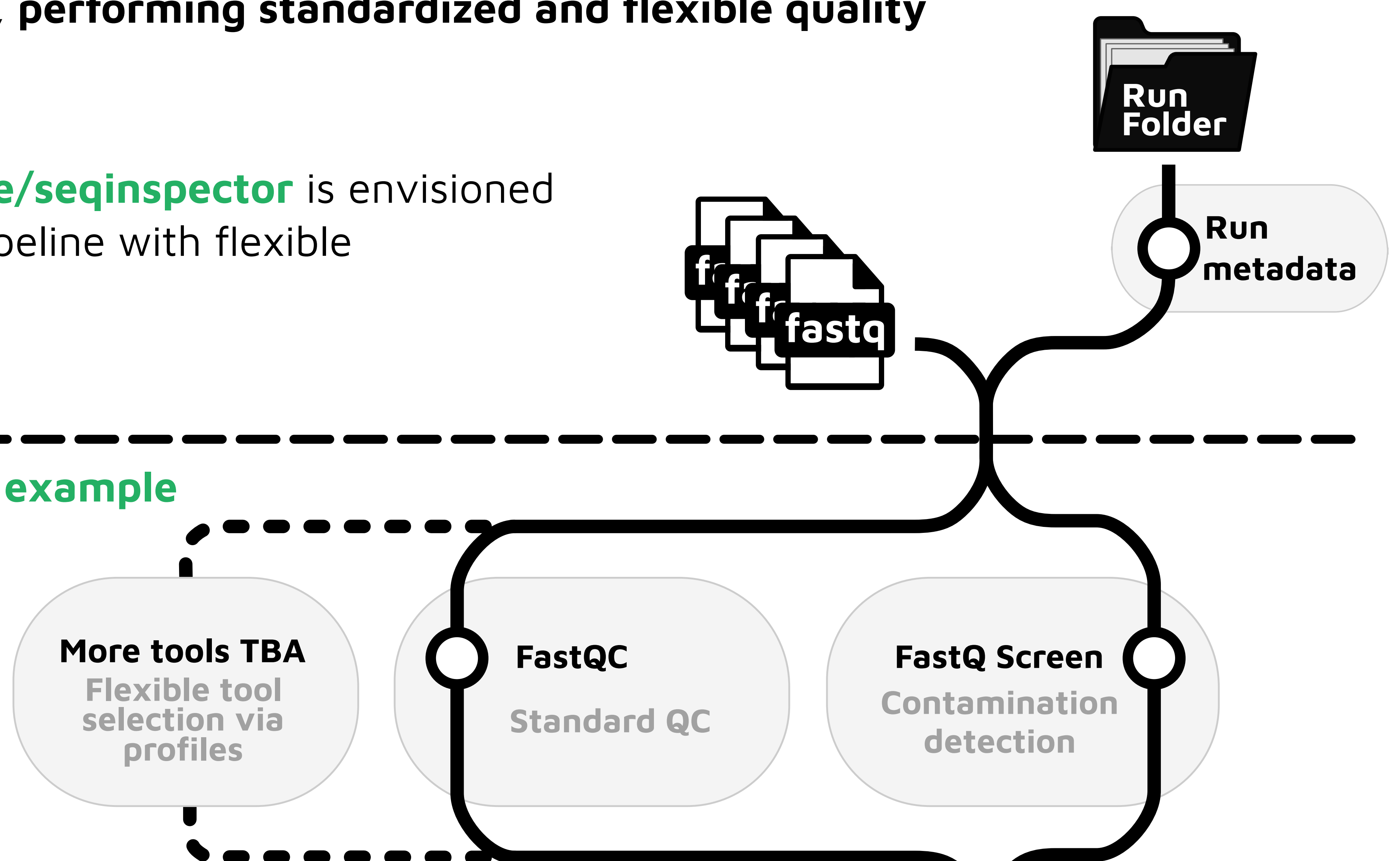
a basic QC pipeline for sequencing core facilities

It is in the interest of every sequencing facility to provide high quality data to their users from a range of different sequencing instruments. In order to monitor sequencing quality, performing standardized and flexible quality control is essential.

The Nextflow pipeline **nf-core/seqinspector** is envisioned as a unified quality control pipeline with flexible aggregation of QC results.

Apply primary QC tools, for example

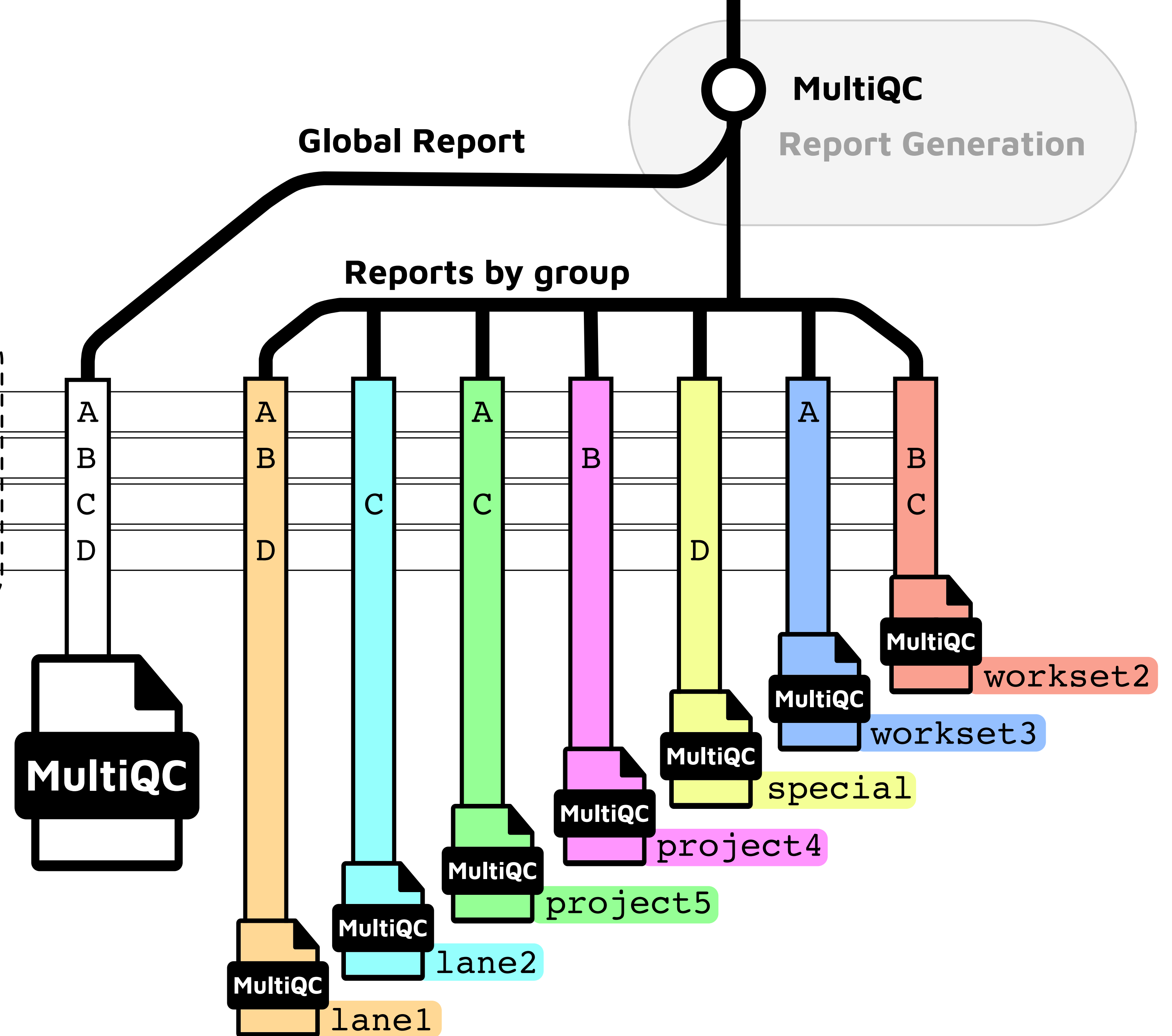
- quality
- duplication level
- complexity
- adapter content
- biological contaminants



Aggregate into MultiQC reports

Tags can be added to the samplesheet to aggregate the MultiQC reports of any subset of samples

| sample | tags |
|--------|-----------------------------|
| A | project5 : workset3 : lane1 |
| B | lane1 : project4 : workset2 |
| C | workset2 : lane2 : project5 |
| D | lane1 : special |



Co-authors

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