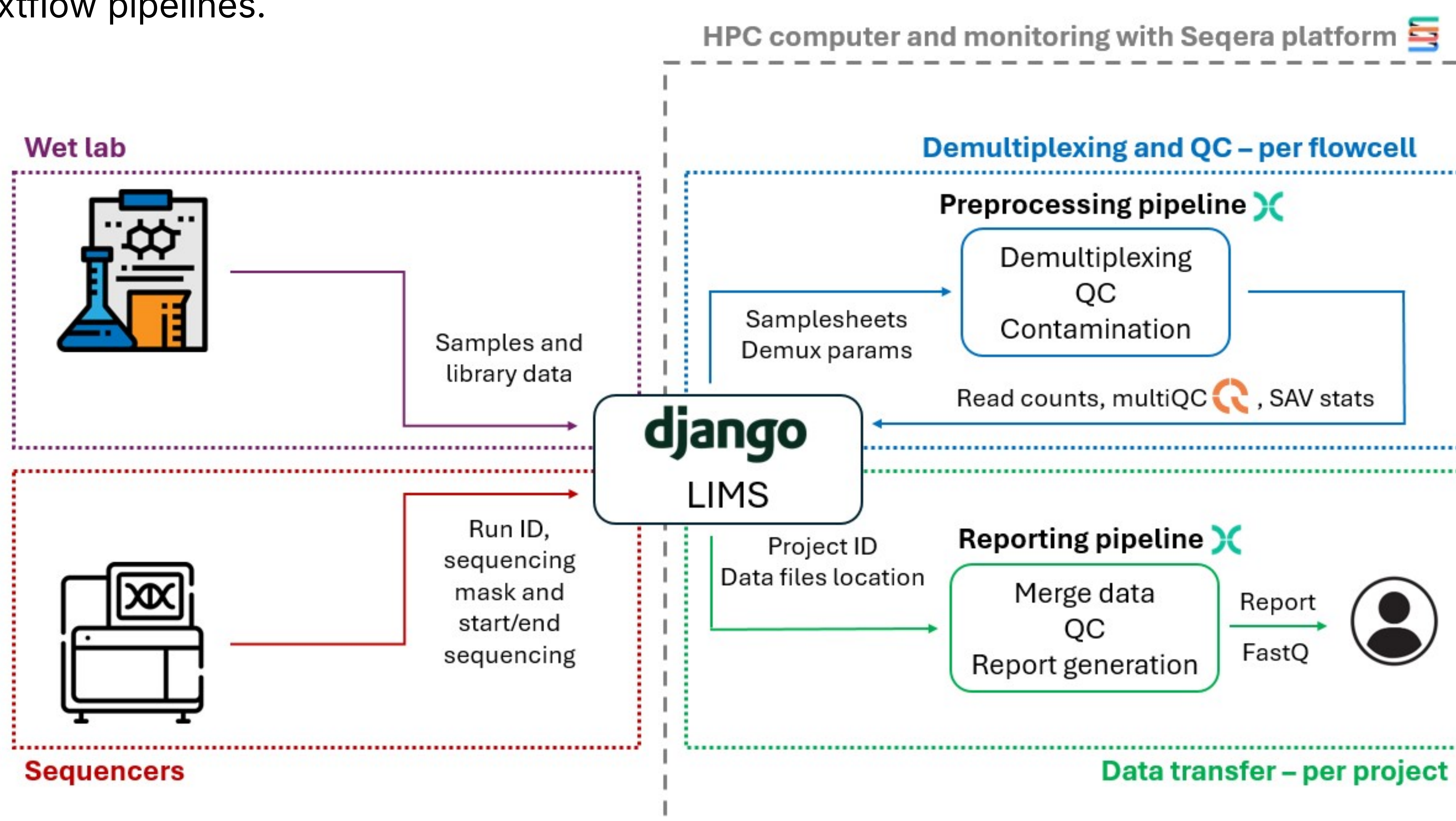


Automating Data Management and Analyses in Sequencing Facilities using a Django-Based LIMS and Nextflow

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Introduction and overview of the workflow:

The increasing complexity and volume of data generated in sequencing facilities necessitate robust solutions for data management and analysis. We present an integrated approach to automating data processing, analysis and management by combining an in-house developed Django-based Laboratory Information Management System (LIMS) and a custom API with two Nextflow pipelines.



Results:

1. The Nextflow pipelines **automate** the demultiplexing, quality control and, data transfer, without command line expertise as they are launched through the **LIMS interface** and monitored with the Seqera platform.
2. Communication between the pipelines and LIMS is facilitated through custom **API** and **in-house Python scripts**.
3. The use of containers, HPC computing, and Nextflow enhances the **scalability** and **portability** of the workflow.

Conclusions:

The implementation of these procedures allowed **seamless data flow**, while ensuring its reproducibility and reducing manual errors.

This approach, which combines the use of Nextflow pipelines, a LIMS system with its respective API and custom Python scripts, provides a comprehensive solution for sequencing facilities, streamlining both **data management and computational processes**.