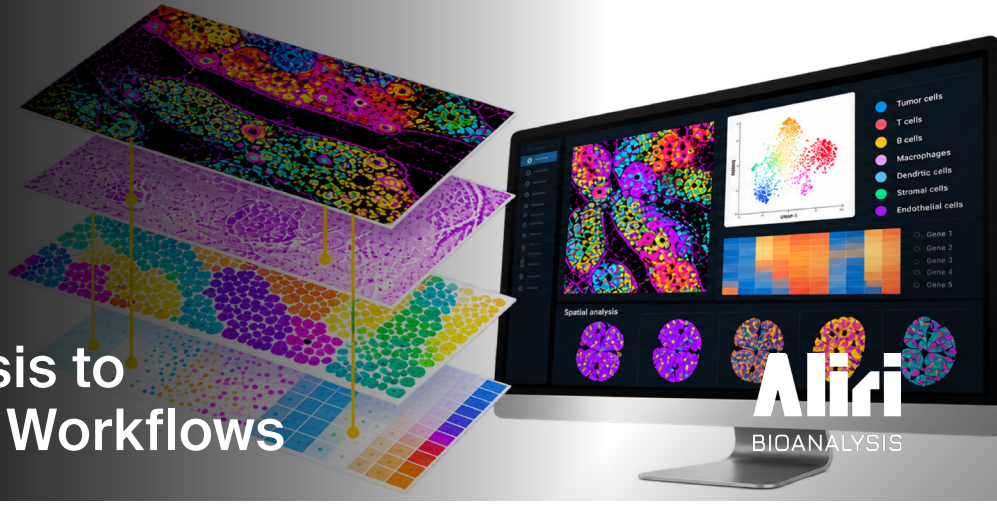
CASE STUDY



From Manual Analysis to Scalable Biomarker Workflows

How Aliri is automating analytical pipelines for reproducibility, traceability and scale

The Objective

Move repetitive computational analysis from manually coordinated scripts toward standardized, automated and production-ready workflows that can scale with increasing study size and analytical complexity.

The Challenge

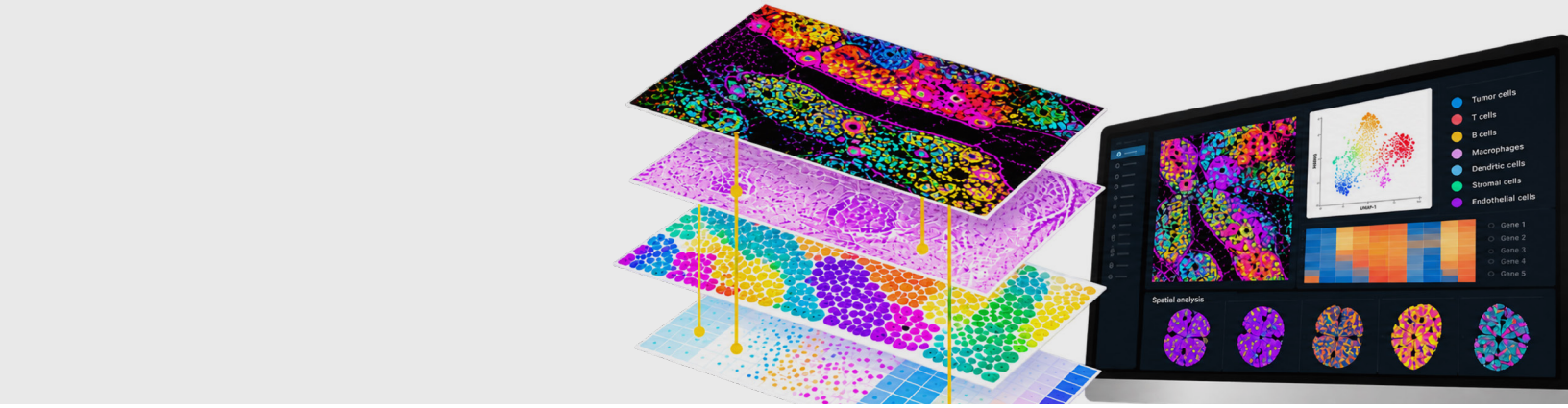
As biomarker studies increase in size and analytical complexity, high-performing analytical methods must also be executed consistently, reproducibly and efficiently across increasing numbers of samples and studies.

Traditional workflows based on manually coordinated Bash, R or Python scripts can be effective for small or isolated projects. At production scale, however, operators must coordinate software dependencies, parallel execution, intermediate files, failures and computational resources. This increases hands-on effort and the risk of inconsistent processing, limited traceability and unnecessary recalculation.

The Aliri approach

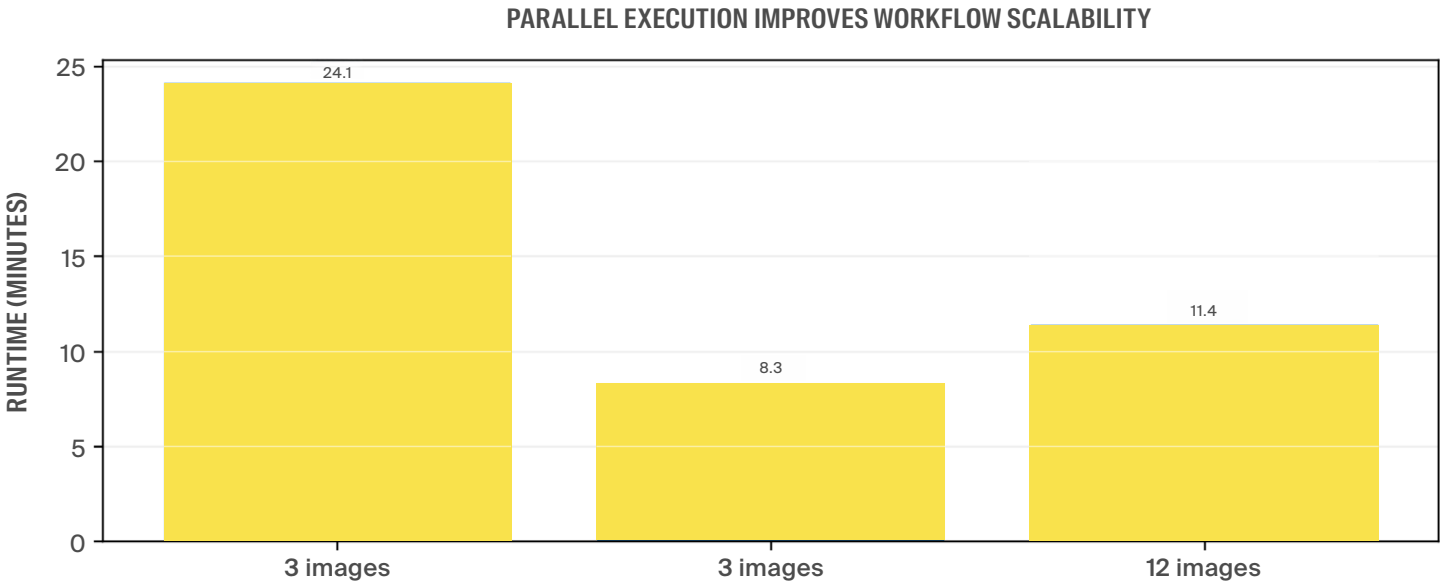
Aliri is implementing workflow orchestration using Nextflow to automate and standardize key steps of analytical pipelines. Nextflow does not replace the underlying analytical tools; it coordinates them within a controlled workflow so that the same analytical process can be executed consistently and at scale.

1	2	3	4	5
Standardize	**Automate**	**Parallelize**	**Recover**	**Trace**
Software environments	Workflow execution	Independent tasks	After failures	each analysis



Use case: Automated image processing

A representative image-processing workflow was automated to evaluate the impact of workflow orchestration and parallel execution on scalability. Images were converted from .ndpi to pyramidal OME-TIFF on the same computer using sequential and parallel execution strategies.



+300%

Increase in workload
3 → 12 images

+37.6%

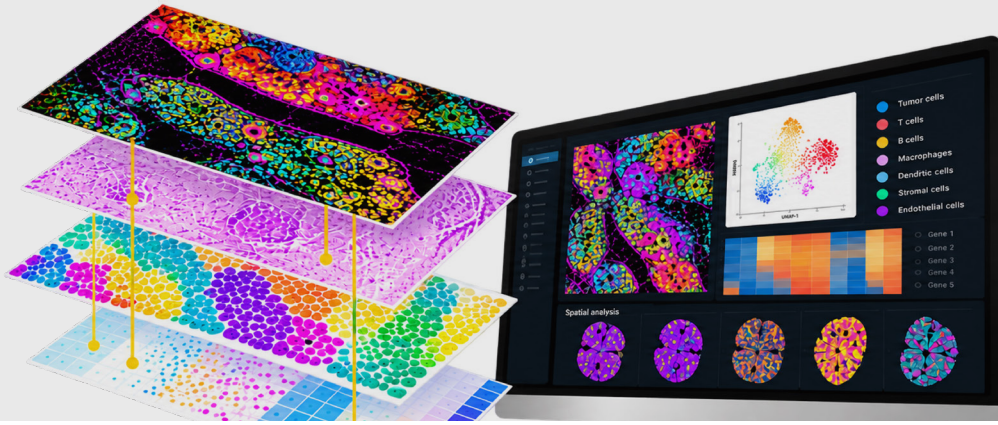
Increase in runtime with
parallel execution

What the result shows

Parallel execution substantially reduced total processing time compared with sequential execution. Increasing the number of images from 3 to 12 (+300%) resulted in only a 37.6% increase in runtime in the tested configuration. With a larger workload, the workflow made better use of the available computing capacity.

Scalability, not just speed

The objective is not to make an individual analytical tool intrinsically faster. Workflow orchestration allows independent samples and analytical steps to run concurrently, improving total throughput as study size increases.



Reproducibility and resilience by design

The value of workflow automation extends beyond runtime. For a production analytical environment, reproducibility, failure recovery and traceability are equally important.

REPRODUCIBILITY

Software environments are defined with the workflow using containers or Conda environments. This reduces environment drift and supportts consistent execution across computing environments.

RESILIENCE

Nextflow records completed tasks. Following an interruption or correction, the workflow can resume from successful steps and rerun only tasks that failed or were affected by a change.

TRACEABILITY

Execution logs, trace files, timelines and reports connect each task to its inputs, outputs, status, duration and resource consumption.

PORTABILITY

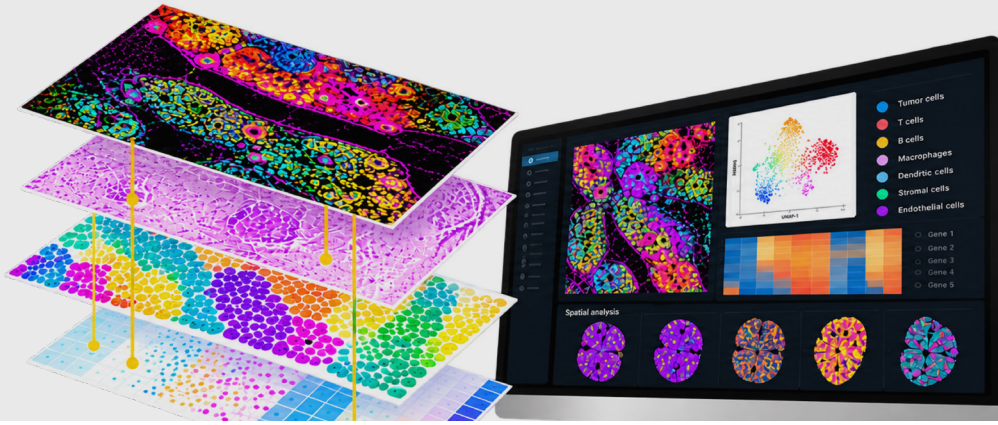
The same workflow logic can be deployed across a workstation, HPC cluster or cloud environment without redesigning the analytical process.

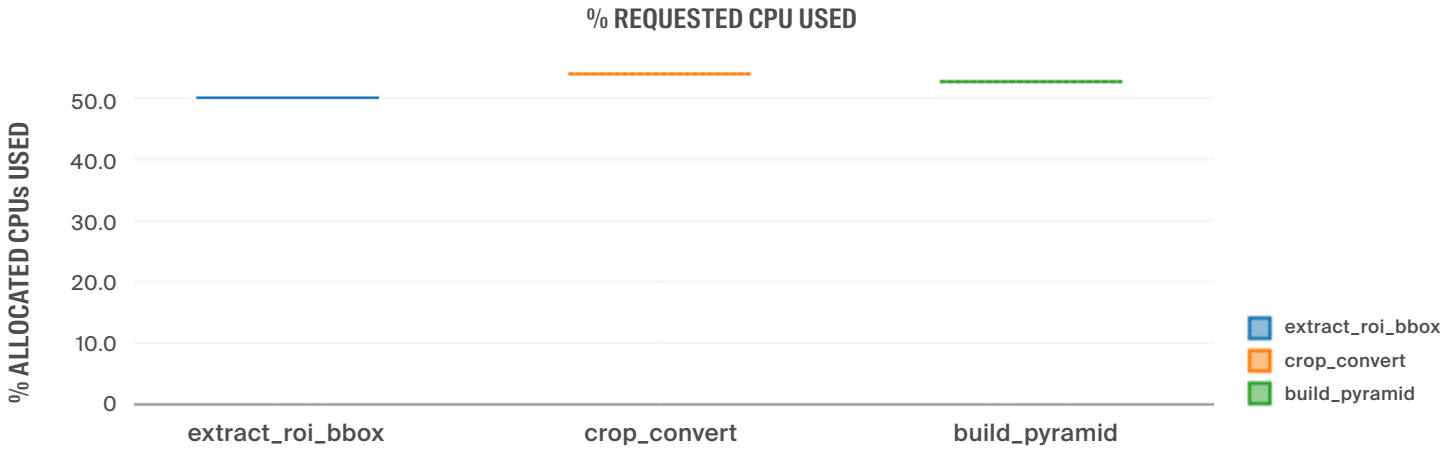
Example — failure recovery

In the tested image-processing pipeline, resuming the workflow took approximately 5 seconds. A manual recovery would require the operator to determine which steps completed successfully, identify the point of failure and restart the appropriate steps, increasing recovery time and the opportunity for human error.

Data-driven resource optimization for greater scalability

Beyond automating execution, the workflow records CPU and memory use for each processing step. These traceable metrics help identify underused capacity and bottlenecks, informing future resource allocation and supporting greater throughput as study volumes grow.





In the tested configuration, monitored processes used approximately 50% of their allocated CPU capacity. This reveals an opportunity to tune future runs and potentially process more tasks concurrently on the same infrastructure. The client value is more efficient use of computing resources and a data-driven path to scalable, traceable biomarker analysis.

From automation to operational value

The final, optimized methods delivered strong, reproducible linearity across every matrix tested:

Less Manual Intervention	Consistent Execution	Faster Cohort Processing	Improved Traceability	Scalable Biomarker Analysis

For Aliri, workflow automation is part of a broader strategy to industrialize complex biomarker analysis without compromising scientific rigor. By moving repetitive computational processes into standardized and traceable workflows, analytical teams can spend less time coordinating execution and troubleshooting individual runs and more time on data quality, biological interpretation and scientific decision-making.

BUILDING THE AUTOMATED BIOMARKER LABORATORY

Automation is not simply about processing data faster. At Aliri, it is about building analytical workflows that are reproducible, traceable, resilient and scalable by design. This use case illustrates our broader strategy of combining scientific expertise, automation and data science to scale advanced biomarker analysis.

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