nextflow

Nextflow Introduction

ScRNAseq in the Cloud: Pipelines to Insights 2024

Workflows

Using computers to collect, store, analyze, and disseminate data and information

Large files

> 100 GB for one raw human genome...

Many languages

Bash, Python, R, PERL...

Complex interactions

Networks of software and their dependencies...

Nextflow

Nextflow is a language, a runtime, and a community

Reproducible

Integration with code management tools, with versioned releases.

Portable

Docker, Singularity, Conda, works with most compute environments.

Scalable

5 samples on your laptop, 5k on an HPC or 5 million in the cloud.

Reproducibility

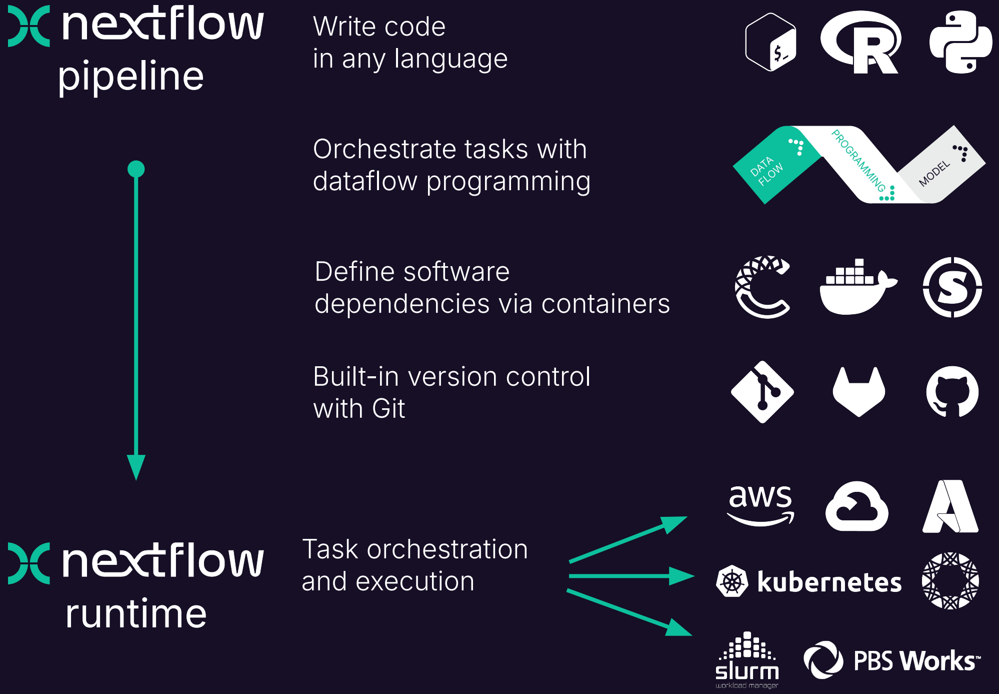
Hidden reproducibility issues are like an iceberg

> First, we tried to re-run the analysis with the code and data provided by the authors.
>
> Second, we rewrote the whole method in a Python package...

Experimenting with reproducibility:
a case study of robustness in bioinformatics
Kim et al., GigaScience (2018).
https://doi.org/10.1093/gigascience/giy077

Nextflow

Nextflow is a language, a runtime, and a community



nextflow pipeline

Write code in any language

Orchestrate tasks with dataflow programming

Define software dependencies via containers

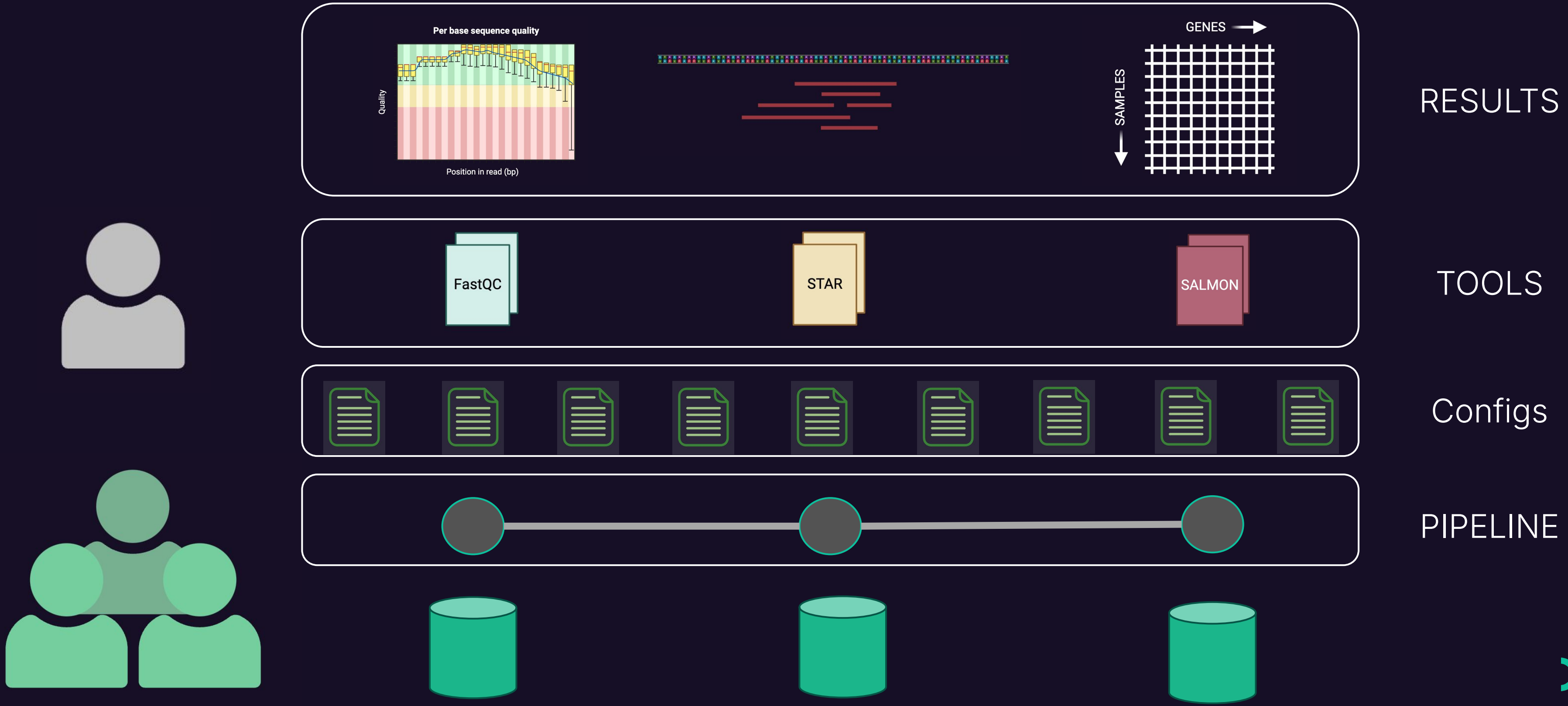
Built-in version control with Git

nextflow runtime

Task orchestration and execution

Nextflow

Nextflow is a language, a runtime, and a community



RESULTS

TOOLS

Configs

PIPELINE

nf-core

A community effort to collect a curated set of analysis pipelines built using Nextflow

12k+
Slack
users

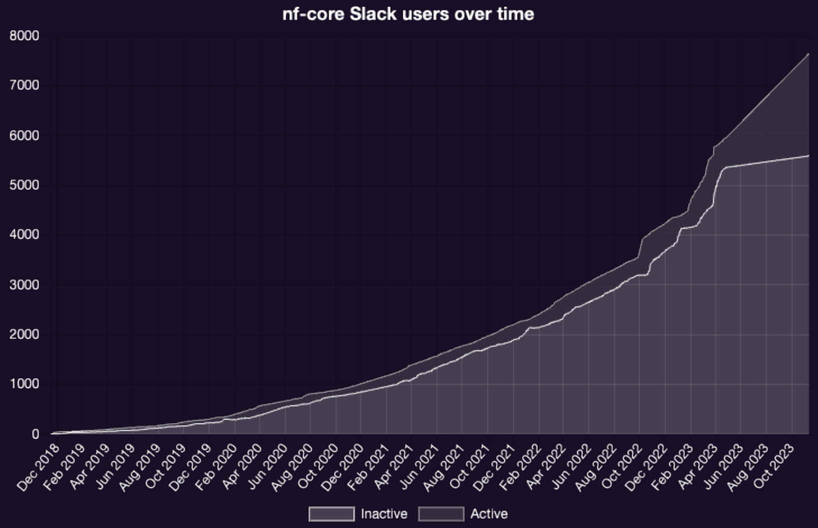
2k+
GitHub
contributors

120+
Pipelines

40k
GitHub
commits

16k+
Pull
requests

7k+
GitHub
issues


nf-core Slack users over time

nf-core principles

Principles that guide the nf-core community

Cooperation

Develop with the community

Standards

Use a common template

Collaboration

No duplicate pipelines within nf-core

Helper Tools

Tools built for everyone

Compatibility

Tools work for any Nextflow pipeline

Components

Collaborate on component-level

nf-core components

Pick and choose which component you need

Pipelines

>95 pipelines and a base template

Subworkflows

>55 subworkflows

Modules

>1150 modules

Linting

Choose conventions to test for consistency

Schema

Validation, channels and user interface

Tooling

Development and deployment

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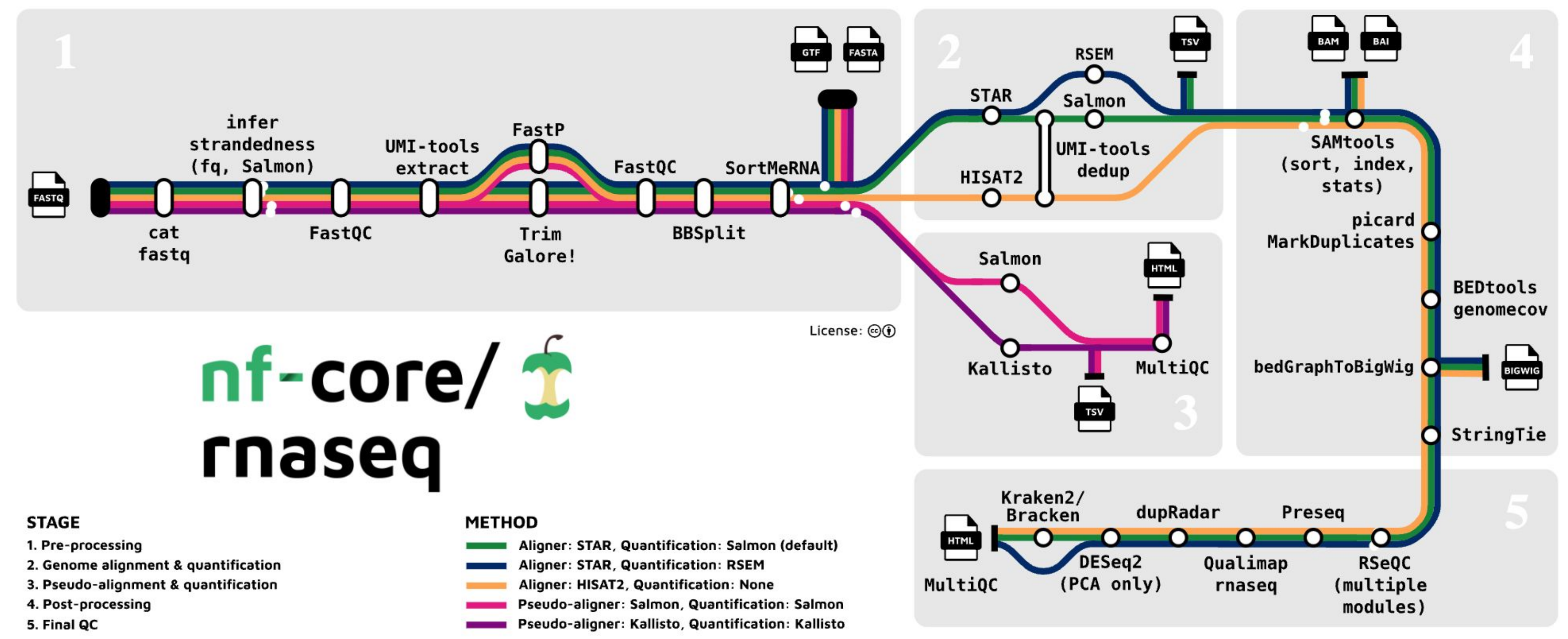
Managing modern workflows is complicated



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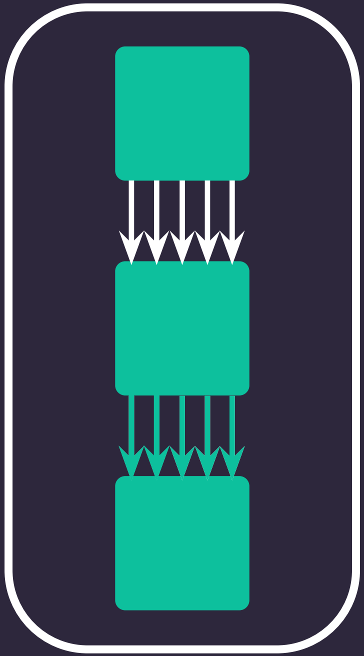
A reactive workflow framework and a programming DSL



Parallelism

Reentrancy
(Resume partial runs)

Reproducibility

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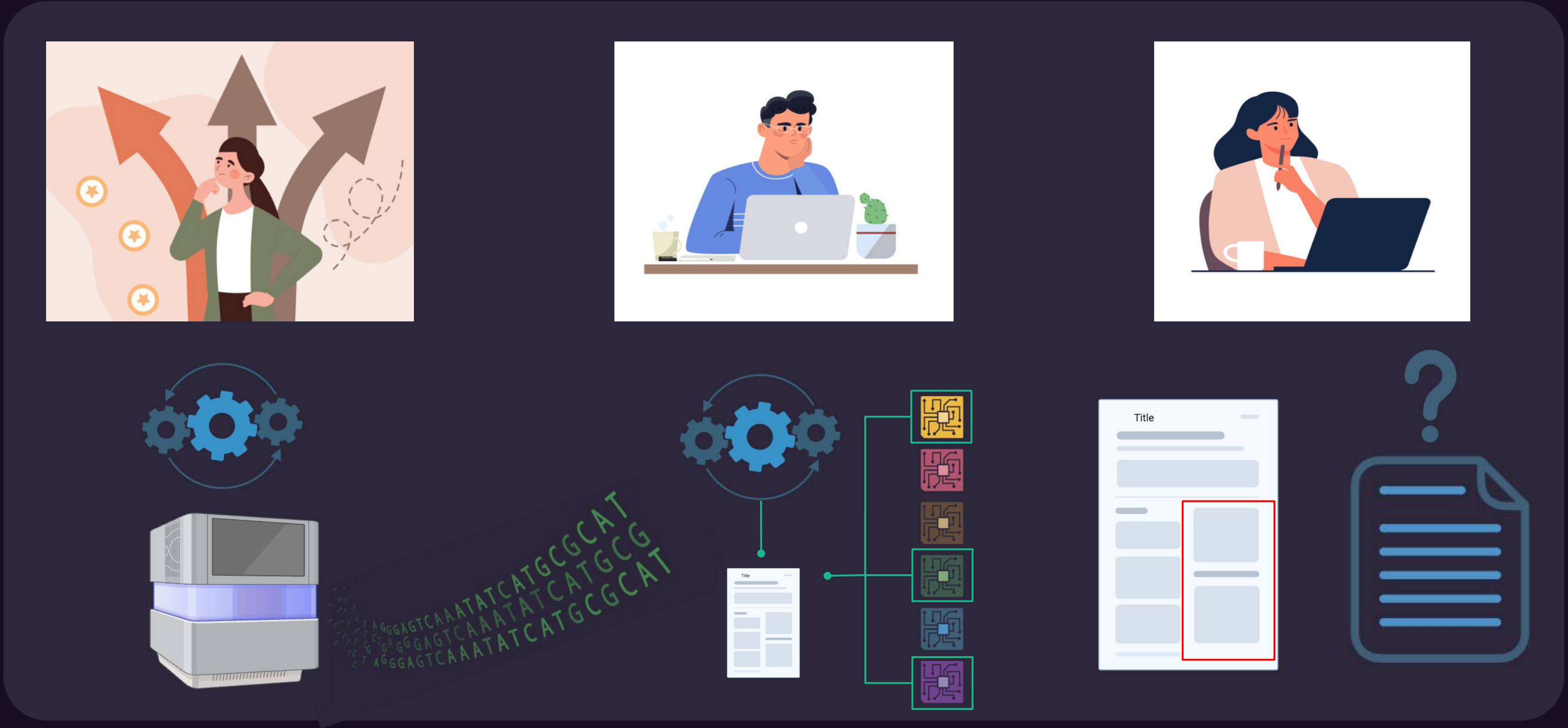
Use Case Studies - Reproducibility



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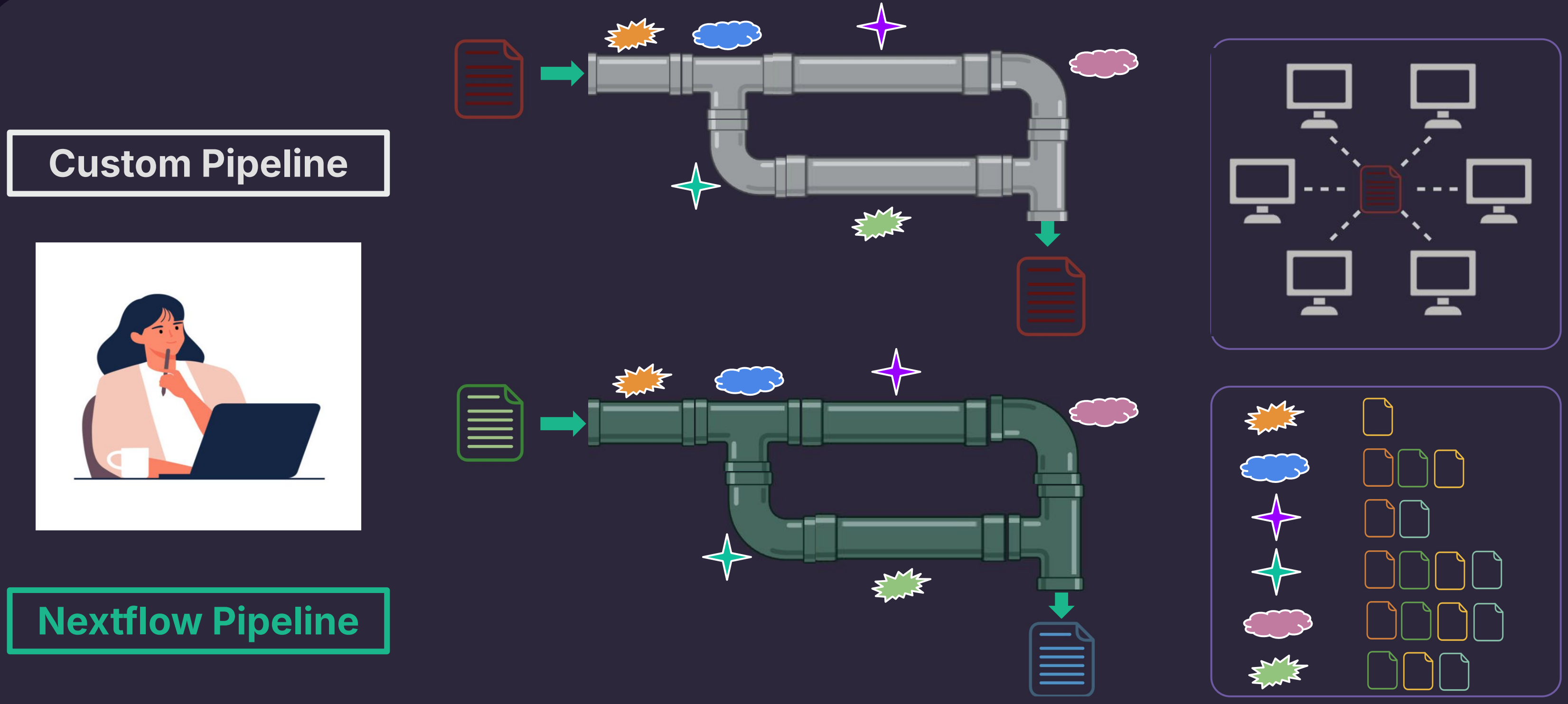
Use Case Studies - Reentrancy

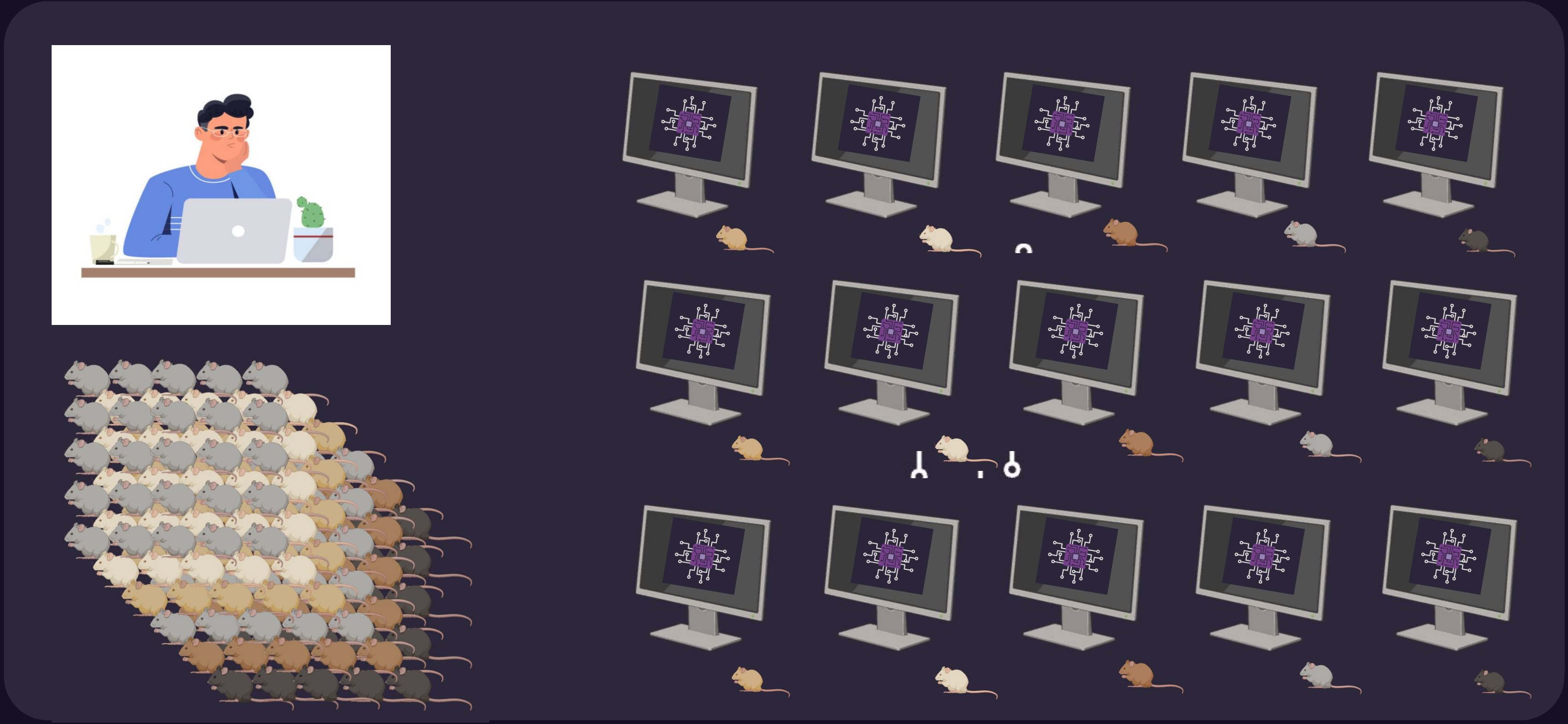


Custom Pipeline

Nextflow Pipeline

Nextflow

Use Case Studies - Parallelism



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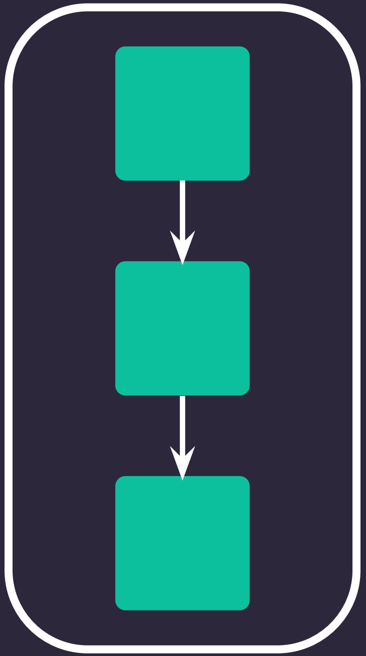


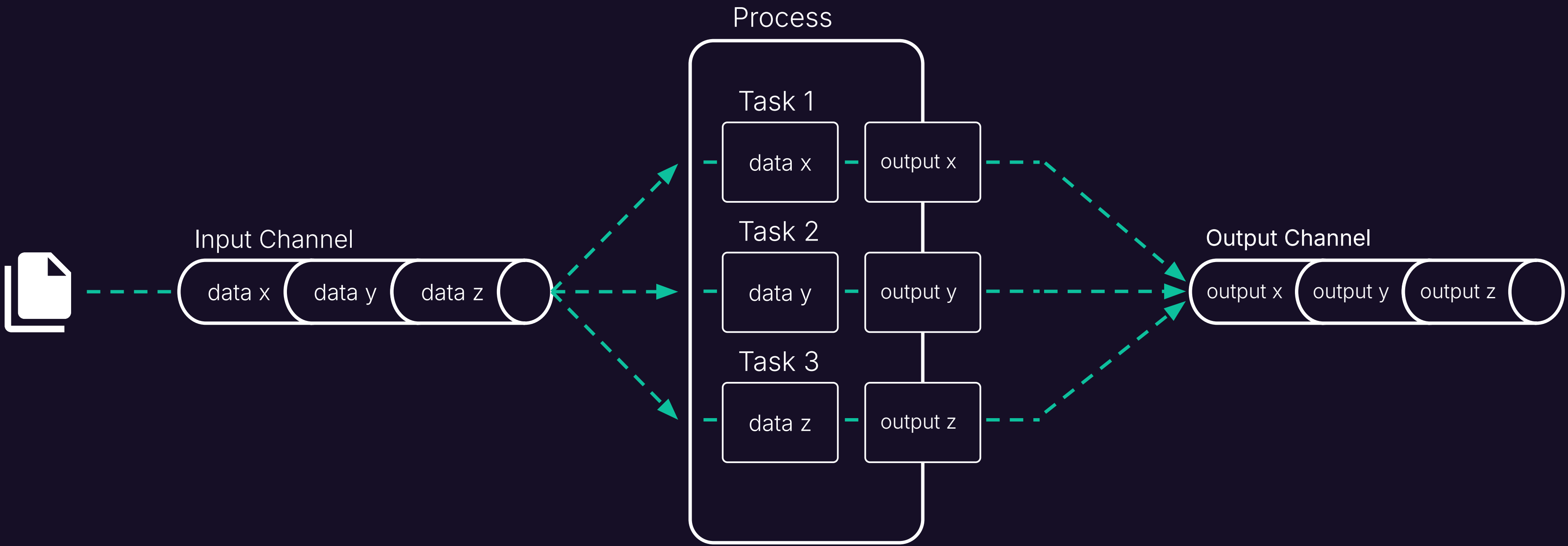
Processes

Channels

Workflow

Nextflow

A reactive workflow framework and a programming DSL



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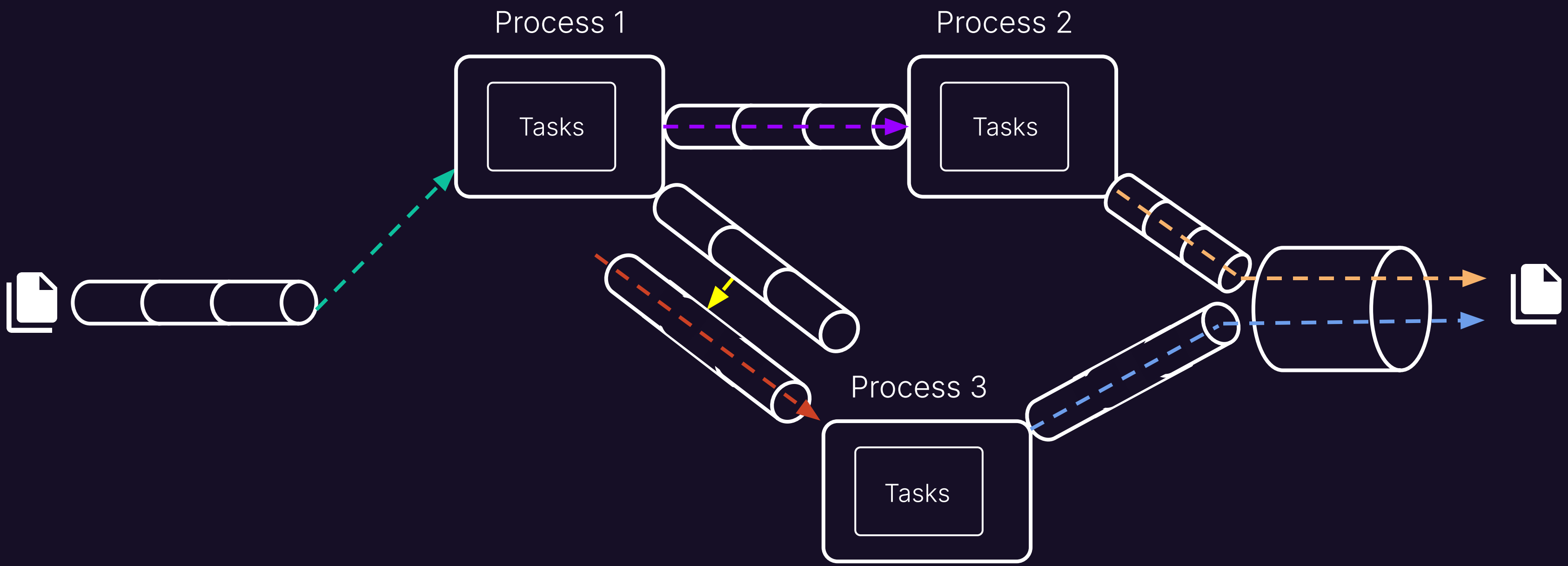
A reactive workflow framework and a programming DSL



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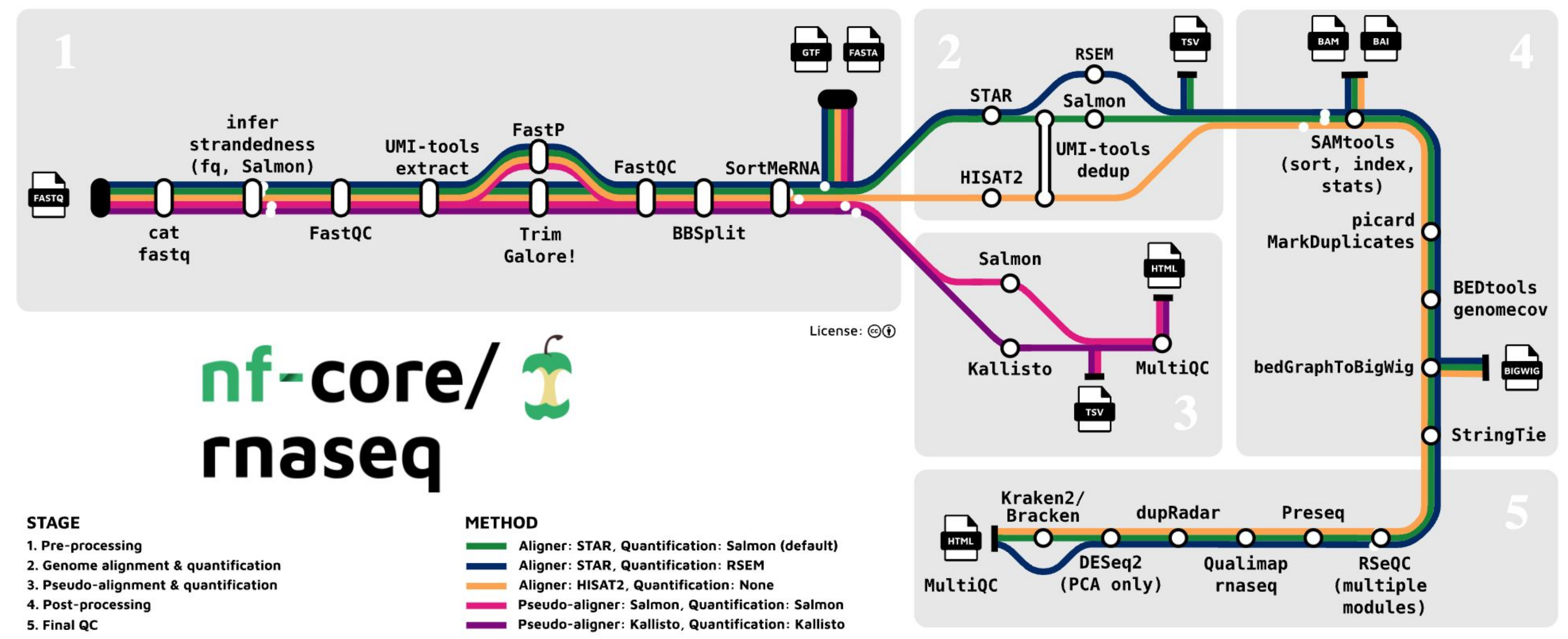
Managing modern workflows is easier with Nextflow



STAGE

1. Pre-processing
2. Genome alignment & quantification
3. Pseudo-alignment & quantification
4. Post-processing
5. Final QC

METHOD

🟩 Aligner: STAR, Quantification: Salmon (default)
🟦 Aligner: STAR, Quantification: RSEM
🟧 Aligner: HISAT2, Quantification: None
🟥 Pseudo-aligner: Salmon, Quantification: Salmon
🟪 Pseudo-aligner: Kallisto, Quantification: Kallisto