# Developing and sharing reproducible bioinformatics pipelines: best practices

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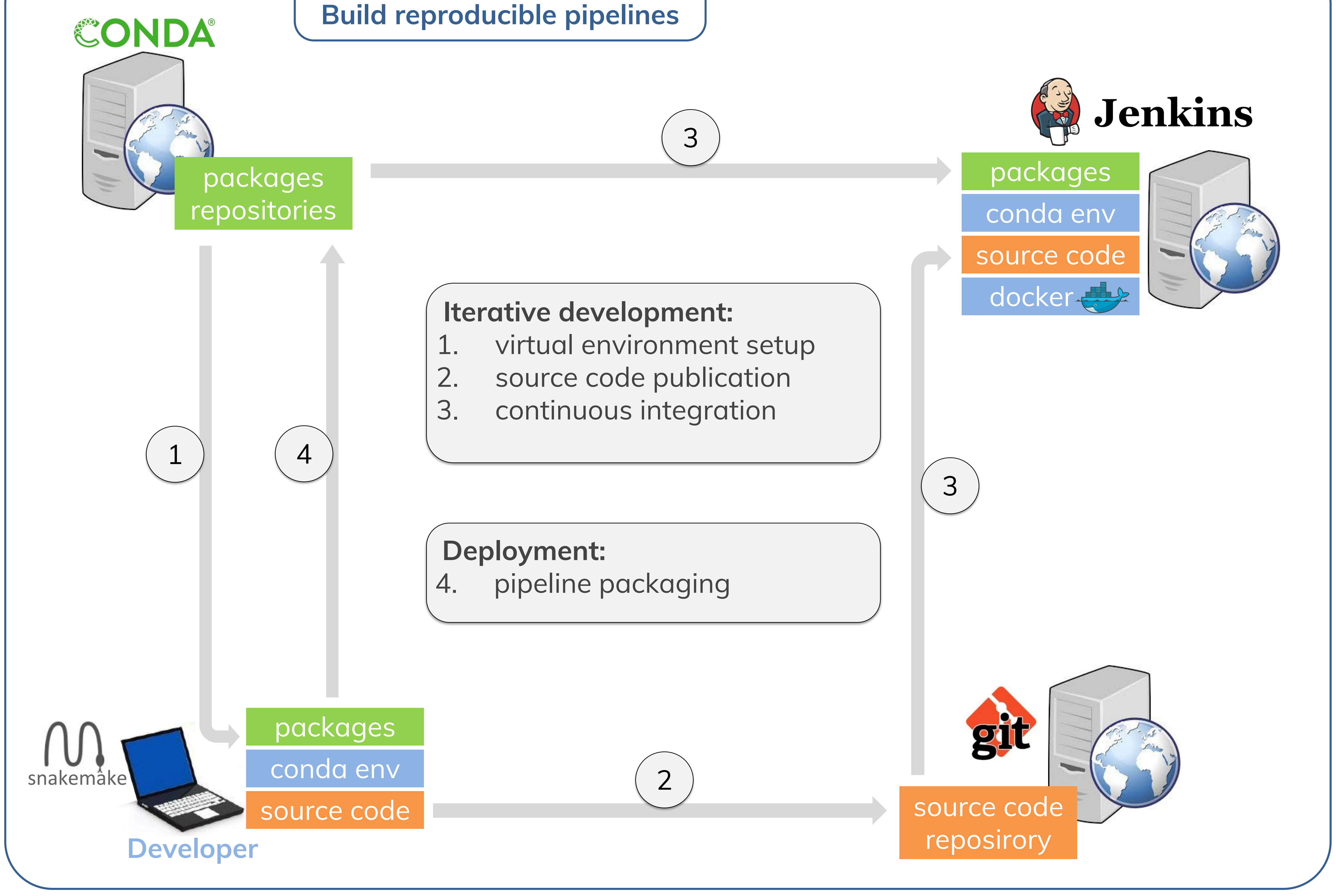
## Introduction

Life-sciences are nowadays conducted in multi-disciplinary and multi-centric studies. In this context, the same software components must be deployed in multiple environments for reproducibility and scalability issues. In addition, data analysis pipelines are usually composed of multiple components, continuously evolving, which leads to maintenance and long-term support challenges. To promote FAIR (Findable – Accessible – Interoperable – Reusable) principles, providing controlled software environments becomes mandatory. We propose a set of best practices taking advantage of proven or promising tools: **Git, Conda, SnakeMake, Jenkins and Docker.**

## Developers

**Build reproducible pipelines**

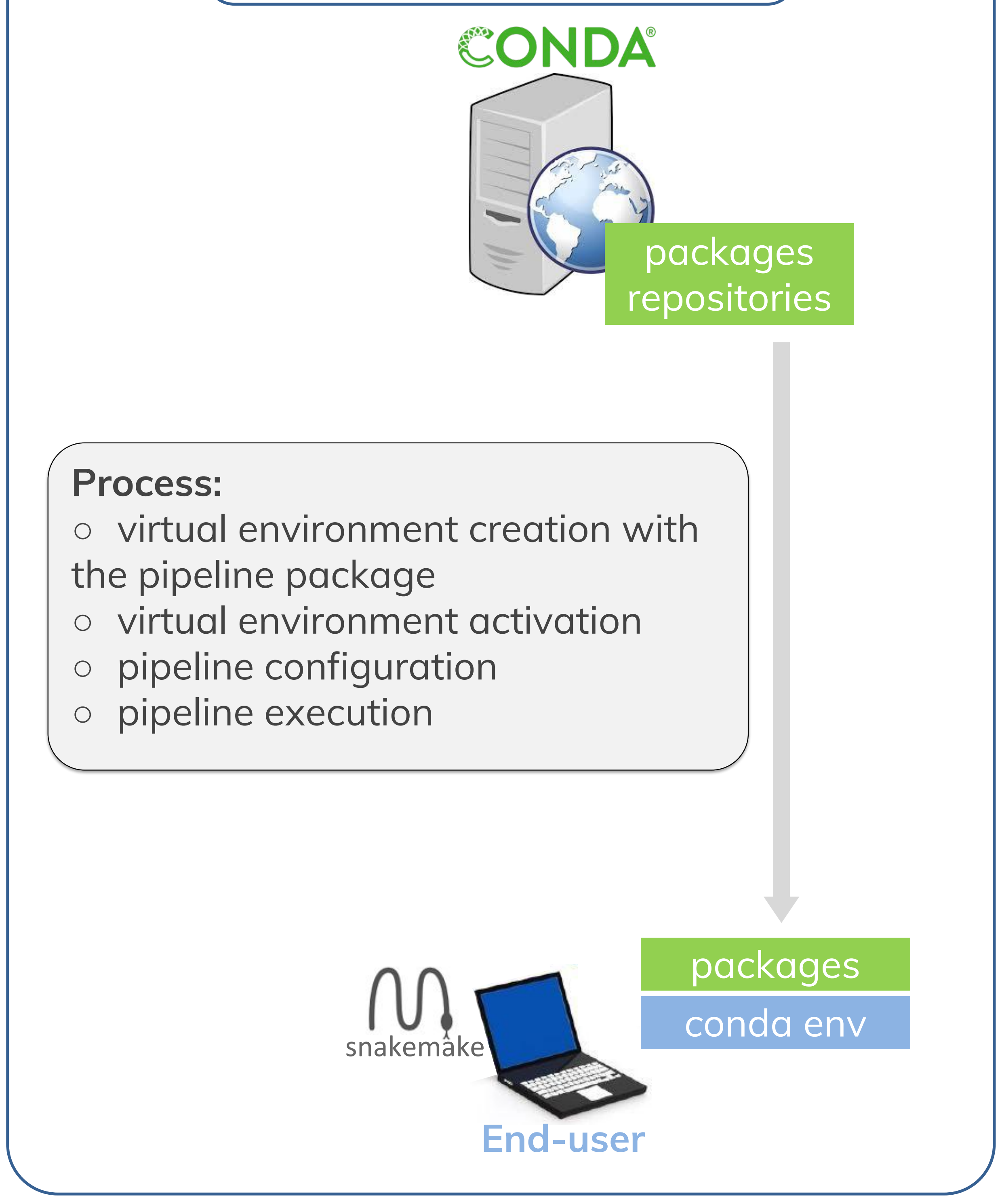


**Iterative development:**
1. virtual environment setup
2. source code publication
3. continuous integration

**Deployment:**
4. pipeline packaging

## End-users

**Deploy and launch pipelines**



**Process:**
- ○ virtual environment creation with the pipeline package
- ○ virtual environment activation
- ○ pipeline configuration
- ○ pipeline execution

## Results

**Achieved pipelines:**

☑ SingleCell RNASeq
☑ Exome variant calling

**In progress pipelines:**

□ DGESeq
□ Gene fusion detection
□ RNASeq variant calling
□ RNASeq Differential gene expression

**Web portal:**
http://bird_pipeline_registry.univ-nantes.io/PipelinesPortal

## Discussion

*Benefits:*

**F :** **Indexed** and **searchable** packages on https://anaconda.org

**A :** **Web-based** package management and installation
**Controlled deployment** on Linux containers / systems

**I :** **Virtual environments** to handle incompatible libraries
**Multi-platform**, **multi-language**: Snakemake + Conda

**R :** **Versioned** software environments to foster reproducibility

*Limitations:*

- ○ **Heavy data** resources required (reference genomes, etc.)
- ○ Some tools / libraries need to **be packaged** beforehand

## Conclusion

The best practices hereby proposed aim at promoting findable and accessible data analysis pipelines through web-based resources. This process allows to package and re-execute pipelines in the long run, and to adapt to continuously evolving environments. Our future works include two main directions: i) handling data resources as part of the pipeline distribution process (e.g. BioMaj), and ii) studying how to promote interoperability between multiple systems and infrastructures.

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