



Developing reproducible bioinformatics workflows with Nextflow

**Workshop
23rd/24th January 2020
Limited to 30 participants
Cost 210 Euros/pp**

**University of Liège
GIGA institute
Leon Fredericq auditorium**

**Trainers:
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Contact and inscription:

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Program

Day One, basic concepts :

1. Overview of Nextflow workflow system
2. Nextflow language syntax and data structures
3. Dataflow variables and channel semantics
4. Nextflow operators and processes
5. Simple pipeline implementation
6. Modules and DSL2
7. Pipeline sharing and best practice for reproducibility

Day Two, advanced concepts :

1. Nextflow configuration and profiles
2. Managing dependencies with containers
3. Executors and deployment scenarios
4. Error recovery and strategies for error handling
5. Workflow and runtime metadata
6. Common implementation patterns
7. Implementation of a variant calling pipeline

Informations to participants

Prerequisites :

1. Unix laptop
2. First experience with bioinformatics pipelines

Participants should be able to create and run their pipelines with Nextflow after this workshop.