

Nextflow: reproducible and portable bioinformatics data analyses

24 – 26 September 2019

Course description:

The “Nextflow: reproducible and portable bioinformatics data analyses” workshop will be held at International Agency for Research on Cancer (IARC) on 24-26 September 2019 and will provide a global overview about [Nextflow technology](#), starting from basic through to advanced concepts, Nextflow workflows and reproducibility concepts.

The workshop is intended for PhD students, post-docs and researchers who are seeking to improve their skills in data analysis using Nextflow technology.

Combining lectures from the creators and lead developers of Nextflow, computer-based practical sessions and interactive discussions, the workshop will provide a platform for discussion of the key questions and challenges in this field of reproducible and portable data analysis, from launching Nextflow pipelines to writing Nextflow pipeline scripts.

The first half-day of the workshop will be facilitated by Matthieu Foll, Bioinformatics Scientist from IARC with the aim of sharing experience between participants.

The second and third days of the workshop will be facilitated by Paolo Di Tommaso and Evan Floden, the creators and lead developers of Nextflow from [Seqera Labs](#), a spin-off of the Center for Genomic Regulation (CRG).

Participants ideally must have basic knowledge of the Linux operating system and also shell programming concepts.

Key dates:

- Application deadline: 26 July 2019
- Notification of decision to participants: 5 August 2019
- Deadline for confirmation of participation: 9 September 2019
- Workshop dates: 24-25-26 September 2019

Application and Registration process:

- **Application process:**

Click on the following link to apply to the workshop by **26 July 2019**

<https://www.surveygizmo.com/s3/5075096/2019-09-Nextflow-reproducible-and-portable-bioinformatics-data-analyses-External-application>

Should you encounter any problems in filling out and/or submitting the application form, please contact learning@iarc.fr.

Thanks to Cancéropôle Lyon Auvergne Rhône-Alpes (CLARA) the application process is open to all PhD students, post-docs, researchers and other scientific specialists working in the Auvergne-Rhône-Alpes region.

- **Registration fee**

Cancéropôle Lyon Auvergne Rhône-Alpes (CLARA) is partially subsidizing the registration fee for the **first 10 confirmed participants**. The full registration fee amounts to €300 for each participant. For the first 10 confirmed participants, CLARA will fund €150 and each participant will fund the difference of **€150**. All other confirmed participants will need to fund the full registration fee of €300 each.

The fee includes teaching materials, certificate, training fee and coffee/tea breaks during the two and a half day course. One laptop for each participant, a repository with all necessary material and software will be provided as well as an AWS cloud environment to carry out the activities during the practical sessions. The registration fee does not include travel to and from the venue nor any accommodation or meal costs during the workshop.

- **Payment process:**

Selected applicants will be notified by e-mail and will be asked to confirm their participation by 9 September 2019 at the latest. The payment instructions will be communicated to all successful applicants by email.

Nextflow: reproducible and portable bioinformatics data-analyses

24 – 26 September 2019

 2,5 days	 Paolo Di Tommaso and Evan Floden, Seqera Labs Matthieu Foll, Bioinformatics Scientist, GEN/GCS
Venue	IARC 150 cours Albert Thomas, Lyon 69008; Princess Takamatsu Hall
Introduction	Nextflow is a widely used open source workflow system for running high throughput genomic applications across cloud and clusters. With over 15,000 downloads per month, it is fast becoming the de-facto technology platform for running genomics pipelines.
Target audience	PhD students, post-docs and researchers would like to learn about the Nextflow technology, starting from basic to advanced concepts, Nextflow workflows and reproducibility concepts
Aim of workshop	Acquire proficiency with Nextflow workflows and reproducibility concepts. Enable participants to develop and deploy their own workflows.
Learning objectives	After completing the two and a half day workshop, participants will be able to: <ul style="list-style-type: none"> - launch Nextflow pipelines, - configure and deploy on specific infrastructure - write their own Nextflow pipeline script.
Main topics	<p>Day 1 (half day): presentations from participants.</p> <ul style="list-style-type: none"> • The objective of this half day workshop is to facilitate the exchange of experience between participants • Participants of the workshop are encouraged to submit an abstract to present their use case of Nextflow in the context of their particular work environment or to describe how they are currently tackling the problem of reproducible analyses, why/how they are planning to use Nextflow <p>Day 2:</p> <ul style="list-style-type: none"> • Overview of Nextflow workflow system • Nextflow language syntax and data structures • Dataflow variables and channel semantics • Nextflow operators • Nextflow processes • Simple pipeline implementation • Pipeline sharing & best practices for reproducibility <p>Day 3:</p> <ul style="list-style-type: none"> • Nextflow configuration and profiles • Managing dependencies with containers • Executors & deployment scenarios • Error recovery & strategies for error handling • Workflow and runtime metadata and events • Common implementation patterns • Implementation of a variant calling pipeline
Learning methods	Lecture, practical application on computer, demonstration, interactive discussion, questions and answers.
Language of workshop	English
Prerequisite	Participants ideally have basic knowledge of the Linux operating system and also shell programming concepts.