

# Program

	Wednesday 12th October, 2022	Thursday 13th October, 2022	Friday 14th October, 2022
10:00 AM		Session 2: Talks 10:00-11:30 AM	Session 7: Talks 10:00-11:15 AM
11:00 AM		Coffee break 11:30 AM-11:45 PM	Coffee break 11:15-11:30 AM
12:00 PM		Session 3: Talks 11:45-1:15 PM	Session 8: Talks 11:30-1:30 PM
1:00 PM		Lunch 1:15-2:15 PM	
2:00 PM	Summit arrivals and registration 2:00-5:00 PM	Session 4: Talks 2:15-3:45 PM	
3:00 PM		Poster session 3:45-4:15 PM	
4:00 PM		Session 5: Talks 4:15-5:30 PM	
5:00 PM		Coffee break 5:30-5:45 PM	
5:00 PM	Summit welcome 5:00-5:30 PM		
6:00 PM	Session 1: Talks 5:30-7:00 PM	Session 6: Talks 5:45-7:00 PM	
7:00 PM	Summit social 7:00-8:30 PM	Summit dinner 7:00-10:00 PM	
8:00 PM			
9:00 PM			
10:00 PM			

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## Wednesday 12th October, 2022

- 2:00 PM **Summit arrivals and registration**  
Torre Glòries, Avinguda Diagonal, 211, 08018 Barcelona, Spain
- 5:00 PM **Summit welcome**  
Evan Floden, Seqera Labs
- 5:30 PM **Session 1: Talks**  
**Designing mechanisms into Bactopia to support its users and contribute back to the community**  
Robert Petit, Wyoming Public Health Laboratory  
**nf-core: Community updates**  
Phil Ewels, Seqera Labs  
**Automated production engine to decode the tree of life**  
Priyanka Surana, Wellcome Sanger Institute  
**Using cloud can speed up your time to science. Why every scientist (and citizen) should care.**  
Brendan Bouffler, Amazon Web Services
- 7:00 PM **Summit social**  
Drinks, cocktails and networking

## Thursday 13th October, 2022

- 10:00 AM **Session 2: Talks**  
**Keynote: What could be next(flow): Workflows as augmented execution contexts to improve provenance tracking and interoperability**  
Robert Patro, University of Maryland  
**nf-core/airrflow: A pipeline to analyze Adaptive Immune Receptor Repertoires (AIRRs)**  
Gisela Gabernet, Quantitative Biology Center, University of Tübingen  
**Unlocking automated bioinformatics for large scale healthcare**  
Tony Zeljkovic, Curative  
**Pipeline economics on Cloud**  
Hatem Nawar, Google
- 11:30 AM **Coffee break**
- 11:45 AM **Session 3: Talks**  
**nf-core/modules: Re-usable, unit tested DSL2 wrapper scripts for the Nextflow community**  
Harshil Patel, Seqera Labs  
**nf-core/sarek: A workflow for germline, tumor-only, and somatic analysis of NGS data**  
Friederike Hanssen, Quantitative Biology Center, University of Tübingen  
**Price/performance of different cloud storage options for Nextflow workflows**  
Angel Pizarro, Amazon Web Services  
**Nextflow + Quilt: Label, query and visualize pipeline data**  
Aneesh Karve, Quilt Data
- 1:15 PM **Lunch**
- 2:15 PM **Session 4: Talks**  
**Nextflow and the future of containers**  
Paolo Di Tommaso, Seqera Labs  
**Pipeline parameter validation with the nf-core JSON schema**  
Júlia Mir Pedrol, Quantitative Biology Center, University of Tübingen  
**New pipeline resources for reproducible analysis**  
Cédric Notredame, Center for Genomic Regulation
- 3:45 PM **Poster session**

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4:15 PM

## Session 5: Talks

**EPI2ME Labs and democratising Nanopore sequence analysis**

Stephen Rudd, Oxford Nanopore

**Large scale image processing with Nextflow**

Konrad Rokicki, Janelia Research Campus

**nf-core/rnafusion: Implementing RNA-fusion detection in routine cancer diagnostics**

Annick Renevey, Clinical Genomics Unit, SciLifeLab

**From sharing our journeys to empowering the community: Nextflow & beyond**

Saba Saba Nafees, Chan Zuckerberg Biohub

5:30 PM

Coffee break

5:45 PM

## Session 6: Talks

**Deep dive into Nextflow on Azure**

Venkat Malladi, Microsoft

**Bringing GxP compliance to Nextflow workflows**

Yih-Chii Hwang, DNAnexus

**Nextflow Tower in the data analysis life cycle**

Evan Floden, Seqera Labs

7:00 PM

Summit dinner

Dinner and networking

## Friday 14th October, 2022

10:00 AM

## Session 7: Talks

**Nextflow, Kubernetes, and DRAGENs, Oh My!**

Mike Smoot, Illumina

**A workflow to generate a variant catalogue from whole genome sequences**

Solenne Correard, Centre for Molecular Medicine and Therapeutics, University of British Columbia

**jUNCtion: Let investigators turn their data into results**

Alan Hoyle, UNC Lineberger Comprehensive Cancer Center

**Options for leveling up your Nextflow workflows on AWS Batch**

Matt Vaughn, Amazon Web Services

11:15 AM

Coffee break

11:30 AM

## Session 8: Talks

**The Spinning Jenny: A Nextflow pipeline for an Agent Based Model of the First Industrial Revolution**

Nicola Visonà, Università degli Studi di Macerata

**Applying and deploying AlphaFold at scale to decode the human gut microbiome proteome**

Francesco Strozzi, Enterome

**From zero to Nextflow, bringing Nanorate (NanoSeq) into a workflow**

Raul Alcantara Aragon, Wellcome Sanger Institute

**Automated bioinformatics infrastructure for large scale SARS-Cov-2 genomic surveillance at QIB**

Thanh Le Viet, Quadram Institute Bioscience

**Workflow automation: Using the Aviti benchtop sequencing system and Nextflow Tower**

Bryan Lajoie, Element Biosciences

**nf-core hackathon report**

Phil Ewels, Seqera Labs

**Summit wrap up and farewell**

Evan Floden, Seqera Labs

1:30 PM

Summit departures