

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	
6:00 PM	Summit welcome 5:00-5:30 PM	Session 6: Talks 5:45-7:00 PM	
7:00 PM	Session 1: Talks 5:30-7:00 PM		
8:00 PM	Summit social 7:00-8:30 PM	Summit dinner 7:00-10:00 PM	
9:00 PM			
10:00 PM			

Program

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
Add versioning, verifiability, and visualization to your pipeline with one link
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

Program

3:45 PM	Poster session
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 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 Edmund Miller, Element Biosciences nf-core hackathon report Phil Ewels, Seqera Labs Summit wrap up and farewell Evan Floden, Seqera Labs
1:30 PM	Summit departures