Eco-Flow

Bridging communities

connecting nf-core, BioFAIR and now WorkflowHub to the ecology & evo-bio world

Christopher Wyatt Centre for Biodiversity & Environment Research · UCL

WorkflowHub community meeting · 8 July 2026

THE GAP

Reproducible workflows haven't reached ecology & evo-bio

Technical barriers

- Non-model organisms with diverse, messy genomes
- Heterogeneous experimental designs — no standard protocols
- Tools built for model organisms & clinical genomics first

Cultural barriers

- Limited software training; researchers are self-taught
- Publication incentives reward papers, not maintained pipelines
- No tradition of sharing analysis workflows

Structural barriers

- Small, siloed groups, that leave frequently
- Limited funding for software development & maintenance
- Fragmented ecology community across disciplines


Agri-Ecologists

THE GAP

Reproducible workflows haven't reached ecology & evo-bio

Technical barriers

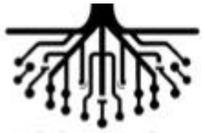
- Non-model organisms with diverse, messy genomes
- Heterogeneous experimental designs — no standard protocols
- Tools built for model organisms & clinical genomics first

Cultural barriers

- Limited software training; researchers are self-taught
- Publication incentives reward papers, not maintained pipelines
- No tradition of sharing analysis workflows

Structural barriers

- Small, siloed groups, that leave frequently.
- Limited funding for software development & maintenance
- Fragmented ecology community across disciplines

Informaticians


So there's a bridge to build — from the workflow world to the field-biology world.

WHAT WE DO

Eco-Flow: reproducible bioinformatics for eco/evo

Pipelines — nf-core standard, built by request for or with

Training — hands-on workshops for biologists

Mentorship — bringing ECRs into reproducible science

Hackathons — collaborative nf-core development

Infrastructure — HPC configs, ready to run

Support — Advice, debugging, review, discussion

Chris Wyatt

Fernando Duarte Frutos

Seirian Sumner

PIPELINES

genomeqc

Genome and annotation quality comparisons

pollen metabarcoding

Amplicon metabarcoding for biodiversity surveys

excon

Gene-family expansion / contraction — CAFE5 + OrthoFinder

WHAT WE DO

Eco-Flow: reproducible bioinformatics for eco/evo

- **Pipelines** — nf-core standard, built by request for or with
- **Training** — hands-on workshops for biologists
- **Mentorship** — bringing ECRs into reproducible science
- **Hackathons** — collaborative nf-core development
- **Infrastructure** — HPC configs, ready to run
- **Support** — Advice, debugging, review, discussion

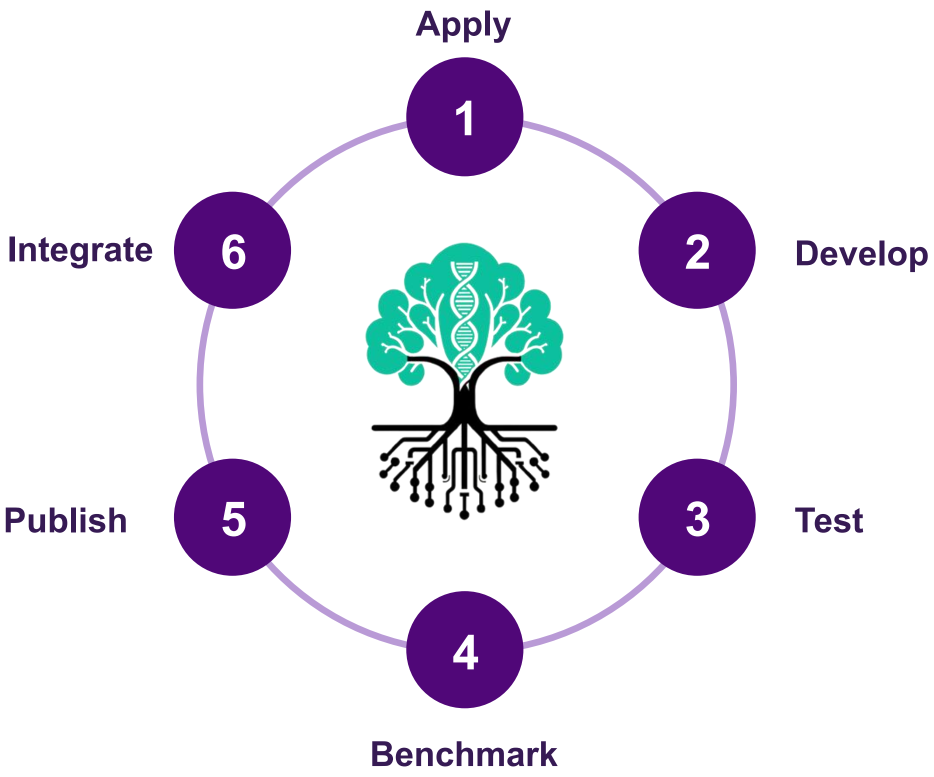
Chris Wyatt

Fernando Duarte Frutos

Seirian Sumner

OUR PROCESS

How we work with end users



1. Apply
2. Develop
3. Test
4. Benchmark
5. Publish
6. Integrate

Open from the start

🔒 Private → 📚 Open

Where we can!

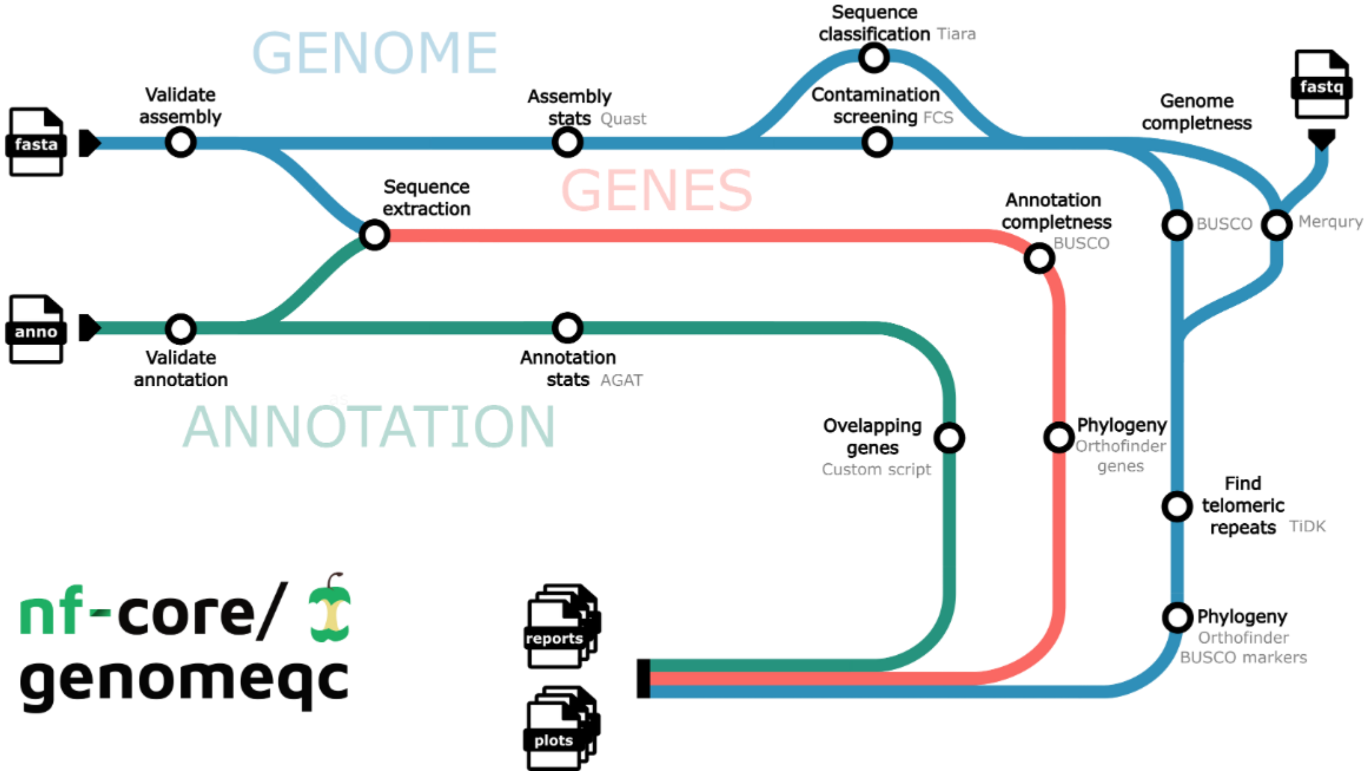
★ Star us on GitHub

FLAGSHIP PIPELINE

nf-core/genomeqc

Compare the quality of multiple genomes and their annotations — in a single Nextflow run.

- Runs on FASTA/GFF files or NCBI accessions
- Assembly QC — BUSCO, Merqury, QUAST, tidk, contamination screening
- Annotation QC — AGAT stats and gene overlaps
- Orthology & phylogeny with OrthoFinder, plus an interactive Shiny report



★ Star us on GitHub

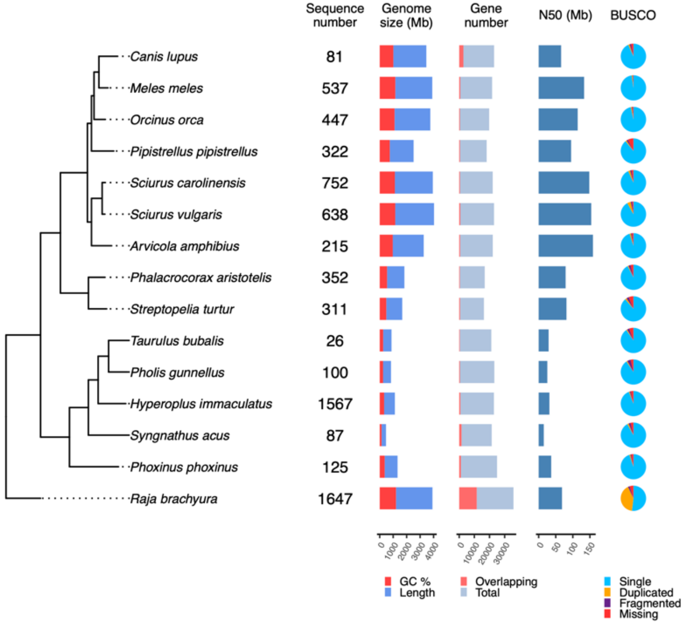
Fernando Duarte Frutos

PIPELINE OUTPUT

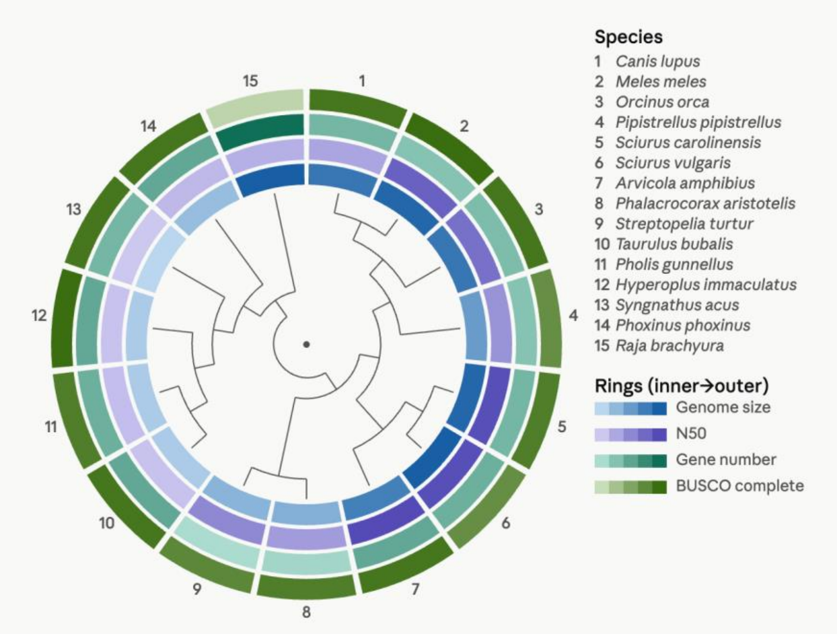
nf-core/genomeqc

Outputs a phylogeny (OrthoFinder) with BUSCO completeness, TEs, ideograms and quality stats per genome.

AVAILABLE NOW



COMING SOON



FUNDING

Funded to make bioscience analysis FAIR

BBSRC

Biotechnology and Biological Sciences Research Council

Our primary funder, via UKRI. Grant BB/X018768/1 supports Eco-Flow's pipeline development. Bioinformatics and Biological Resources Fund (24BBR)

BioFAIR

BioFAIR fellowship programme, promoting/funding the work that Eco-Flow does. Hackathons and pipelines too.

Seqera

Creators of Nextflow, helped support our grant, and provided financial help to progress the project.

FAIR = Findable · Accessible · Interoperable · Reusable

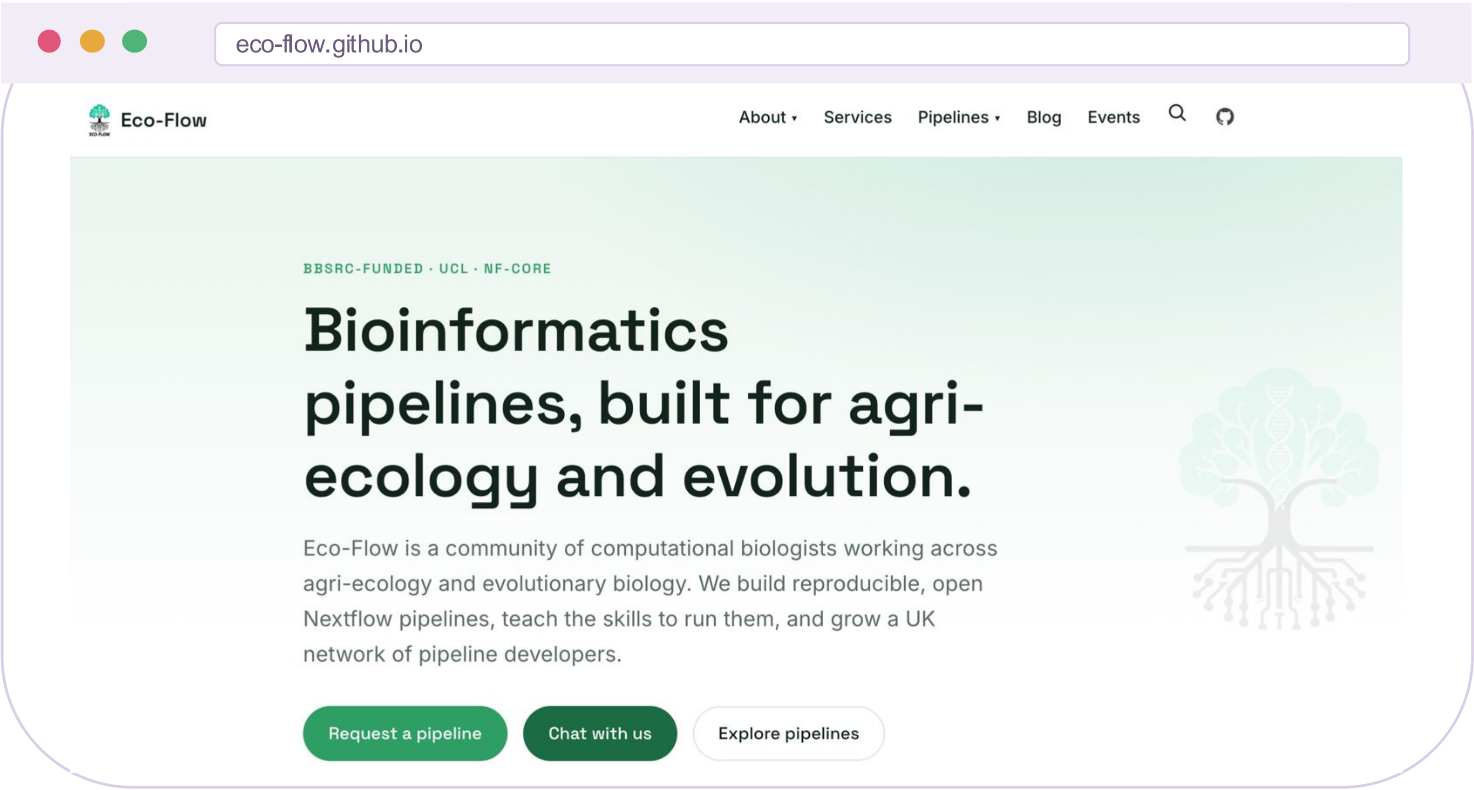
NOW LIVE

Our new website is live

What’s on the site

- Browse and request pipelines
- Blog, events and training resources
- Docs, configs and GitHub in one place

Visit eco-flow.github.io



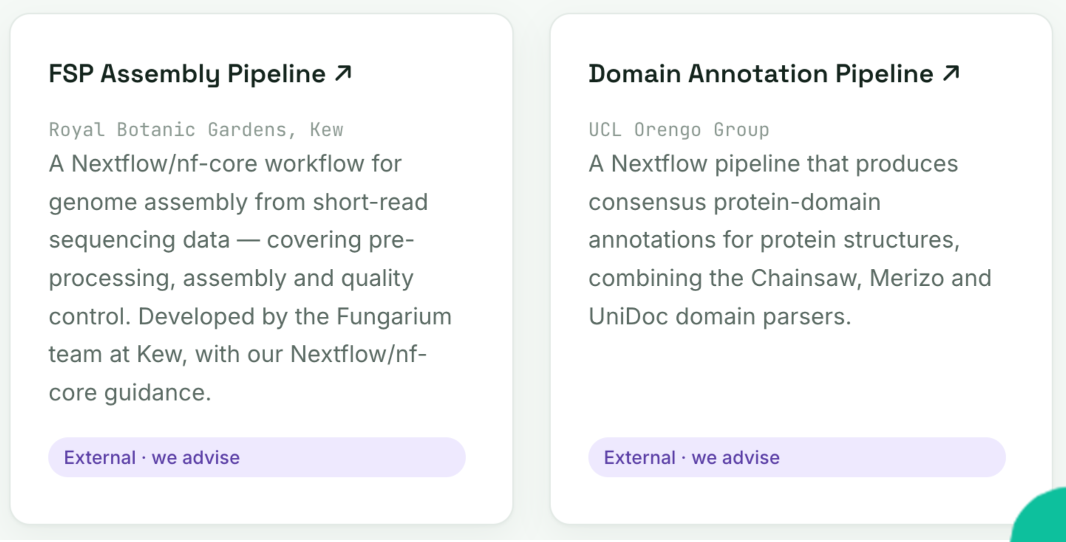
BBSRC-FUNDED · UCL · NF-CORE

Bioinformatics pipelines, built for agri-ecology and evolution.

Eco-Flow is a community of computational biologists working across agri-ecology and evolutionary biology. We build reproducible, open Nextflow pipelines, teach the skills to run them, and grow a UK network of pipeline developers.

THE ECOSYSTEM

How the pieces fit together



FSP Assembly Pipeline ↗

`Royal Botanic Gardens, Kew`

A Nextflow/nf-core workflow for genome assembly from short-read sequencing data — covering pre-processing, assembly and quality control. Developed by the Fungarium team at Kew, with our Nextflow/nf-core guidance.

External · we advise

Domain Annotation Pipeline ↗

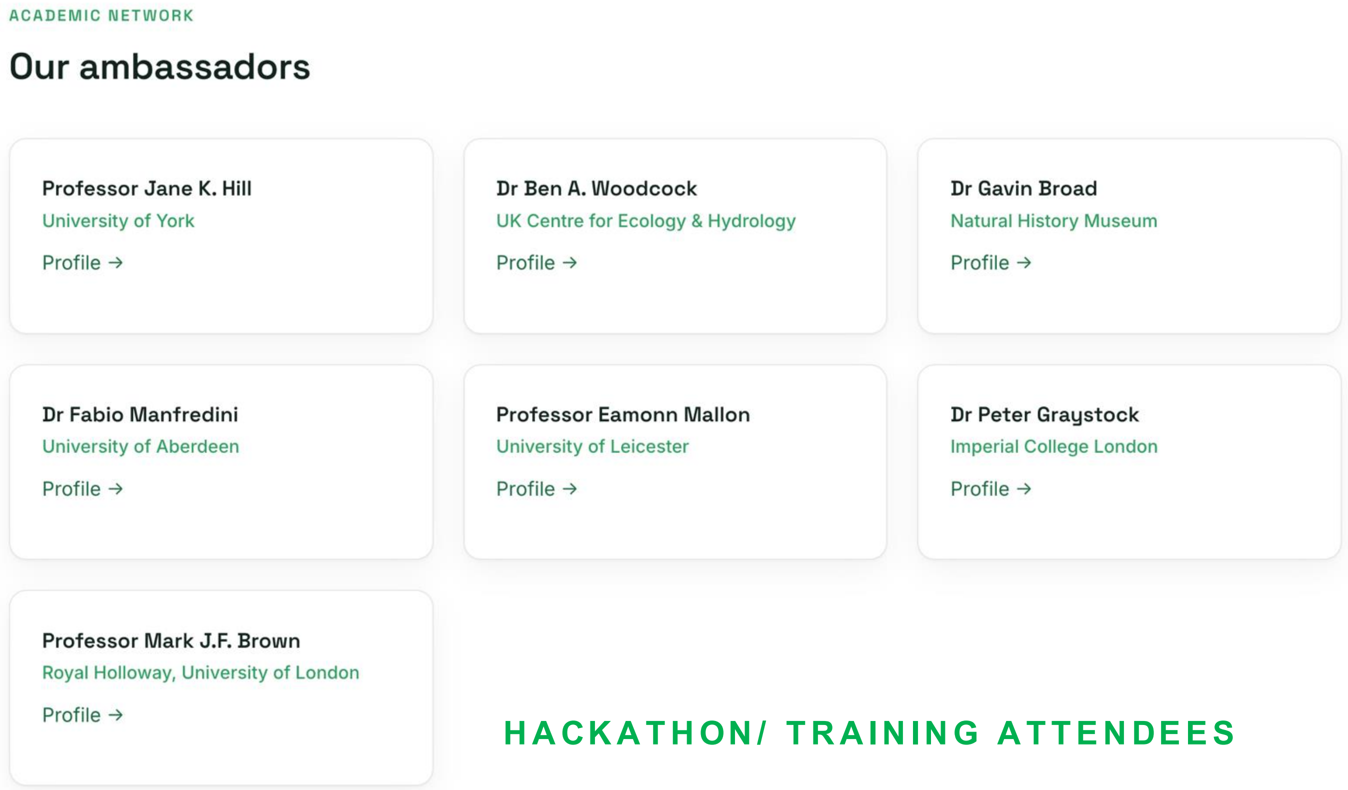
`UCL Orengo Group`

A Nextflow pipeline that produces consensus protein-domain annotations for protein structures, combining the Chainsaw, Merizo and UniDoc domain parsers.

External · we advise

COLLABORATIVE PARTNERS

ECOLOGY EXPERTS



ACADEMIC NETWORK

Our ambassadors

Professor Jane K. Hill
University of York
Profile →

Dr Ben A. Woodcock
UK Centre for Ecology & Hydrology
Profile →

Dr Gavin Broad
Natural History Museum
Profile →

Dr Fabio Manfredini
University of Aberdeen
Profile →

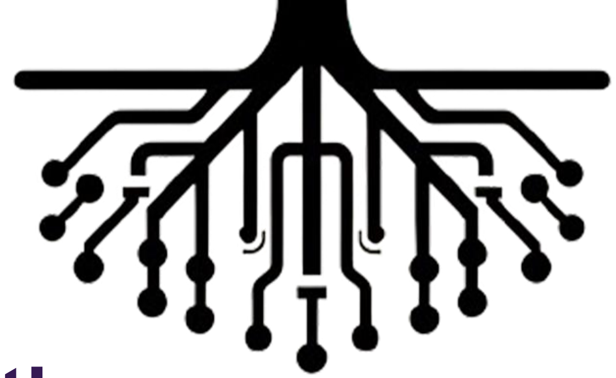
Professor Eamonn Mallon
University of Leicester
Profile →

Dr Peter Graystock
Imperial College London
Profile →

Professor Mark J.F. Brown
Royal Holloway, University of London
Profile →

HACKATHON/ TRAINING ATTENDEES

Our community of agri-eco-evo biologists



THE TECHNICAL SIDE

How the pieces fit together

nf-core

BioFAIR

WorkflowHub

Three thriving communities — Eco-Flow pulls them into a field that hasn't yet adopted them.

THE CORE

nf-core is at the heart of Eco-flow

STRICT TEMPLATES

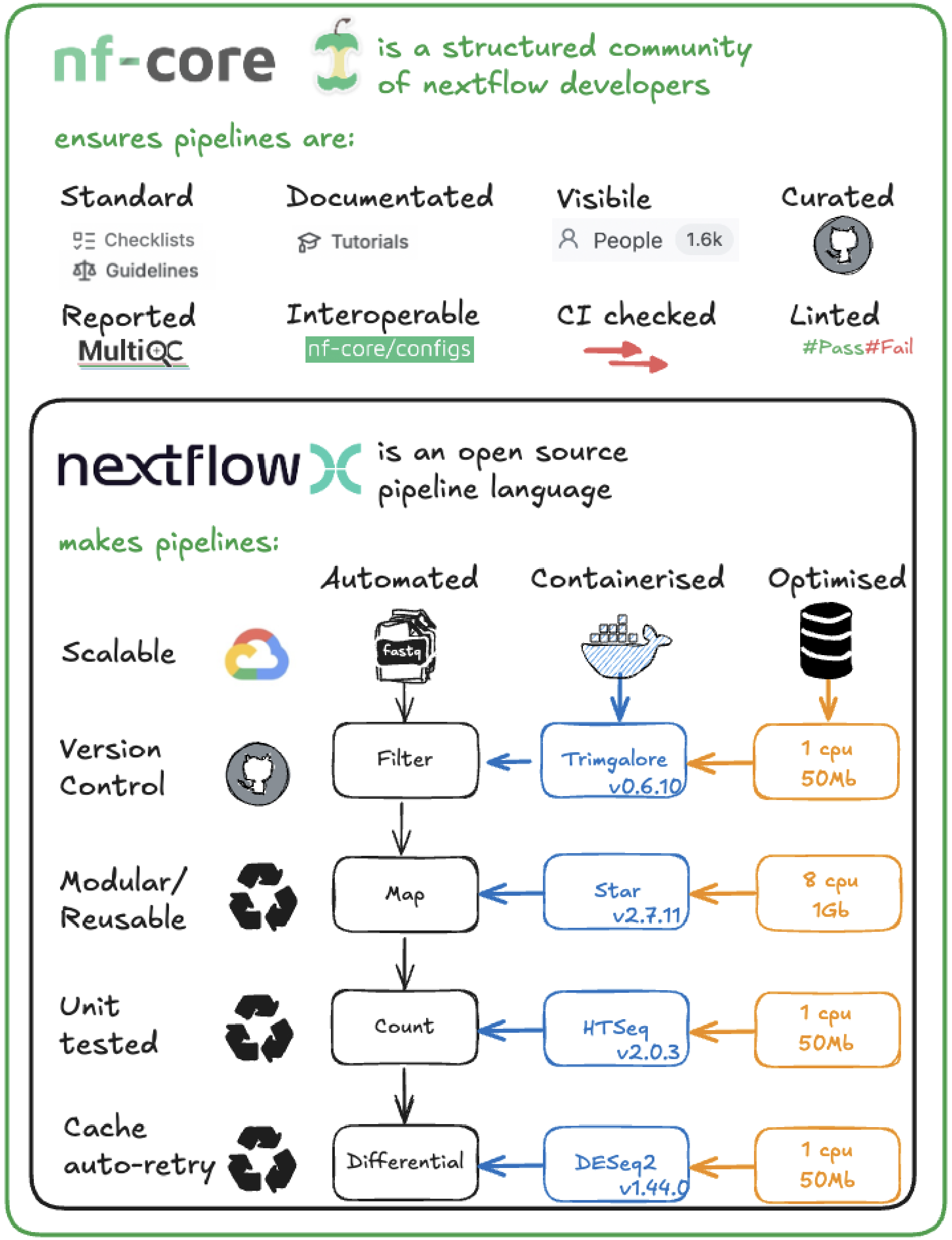
Takes nf-core's template to build FAIR pipelines by default

COMMUNITY BUILT

Pipelines public from day 1. Adapted as community need, with help.

KEEPS UP WITH DEVELOPING STANDARDS

Forces us to move with template changes



THE BIGGER SYSTEM

BioFAIR

What BioFAIR brings:

Community

UK research & developer network

User-stories paper

Real-world impact (in progress)

Hackathons

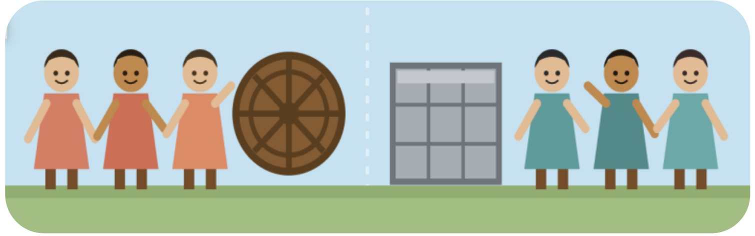
Funded events to co-build pipelines

BioFAIR podcast

Stories via the BioFAIR podcast

Funding

Time funded to build FAIR pipelines through the fellowship



Cross-domain network

Links to other fellows & labs

A GLOBAL, DIVERSE COMMUNITY

WorkflowHub: a registry to share, cite & publish

RO-Crate under the hood

Workflows packaged with metadata — FAIR by design.

DOIs & citability

A workflow becomes a citable research output.

Workflow-agnostic

Nextflow, Snakemake, Galaxy, CWL.

Wired into EOSC / FAIR

Discoverable in the wider European infrastructure.

Why I started using it: to make Eco-Flow pipelines more findable, citable and reusable beyond our existing groups.

MY EXPERIENCE

WorkflowHub in practice — what works

✓ **Citable outputs**

DOIs you can put in a paper and CV. Especially non-nf-core ones.

✓ **FAIR packaging done for you**

RO-Crate captures metadata you may not consider.

✓ **Tool-agnostic & central**

One home regardless of workflow language.

✓ **Forces the user to FAIR-ify**

Public hosting and checklist prompt user to best practices. Road to publication.

Activity

Views: 2374 **Downloads:** 720

Created: 26th Mar 2026 at 22:22
Last updated: 29th Jun 2026 at 13:23
Last updated by: Chris Wyatt

MY EXPERIENCE

…and what would make it better?

FAIR badges

Having a way to give credit to truly FAIR pipelines.

Social media / Web visibility

Showcasing new pipelines, to get end-users engaged.

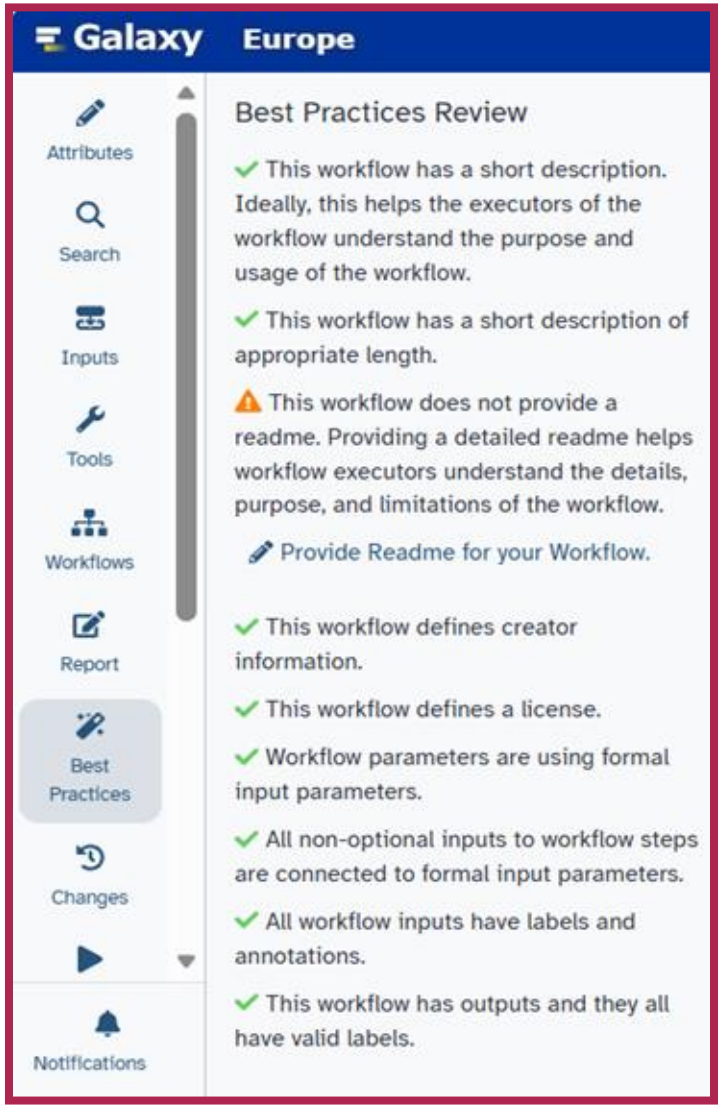
Sync with nf-core releases

Keeping WorkflowHub versions in step with new releases.

Promoting "the why"

Good entries take time; the payoff isn't always visible to a busy biologist.

+ Where do citations go? , are my download just bots?



Best Practices Review

✓ This workflow has a short description. Ideally, this helps the executors of the workflow understand the purpose and usage of the workflow.

✓ This workflow has a short description of appropriate length.

⚠ This workflow does not provide a readme. Providing a detailed readme helps workflow executors understand the details, purpose, and limitations of the workflow.

Provide Readme for your Workflow.

✓ This workflow defines creator information.

✓ This workflow defines a license.

✓ Workflow parameters are using formal input parameters.

✓ All non-optional inputs to workflow steps are connected to formal input parameters.

✓ All workflow inputs have labels and annotations.

✓ This workflow has outputs and they all have valid labels.

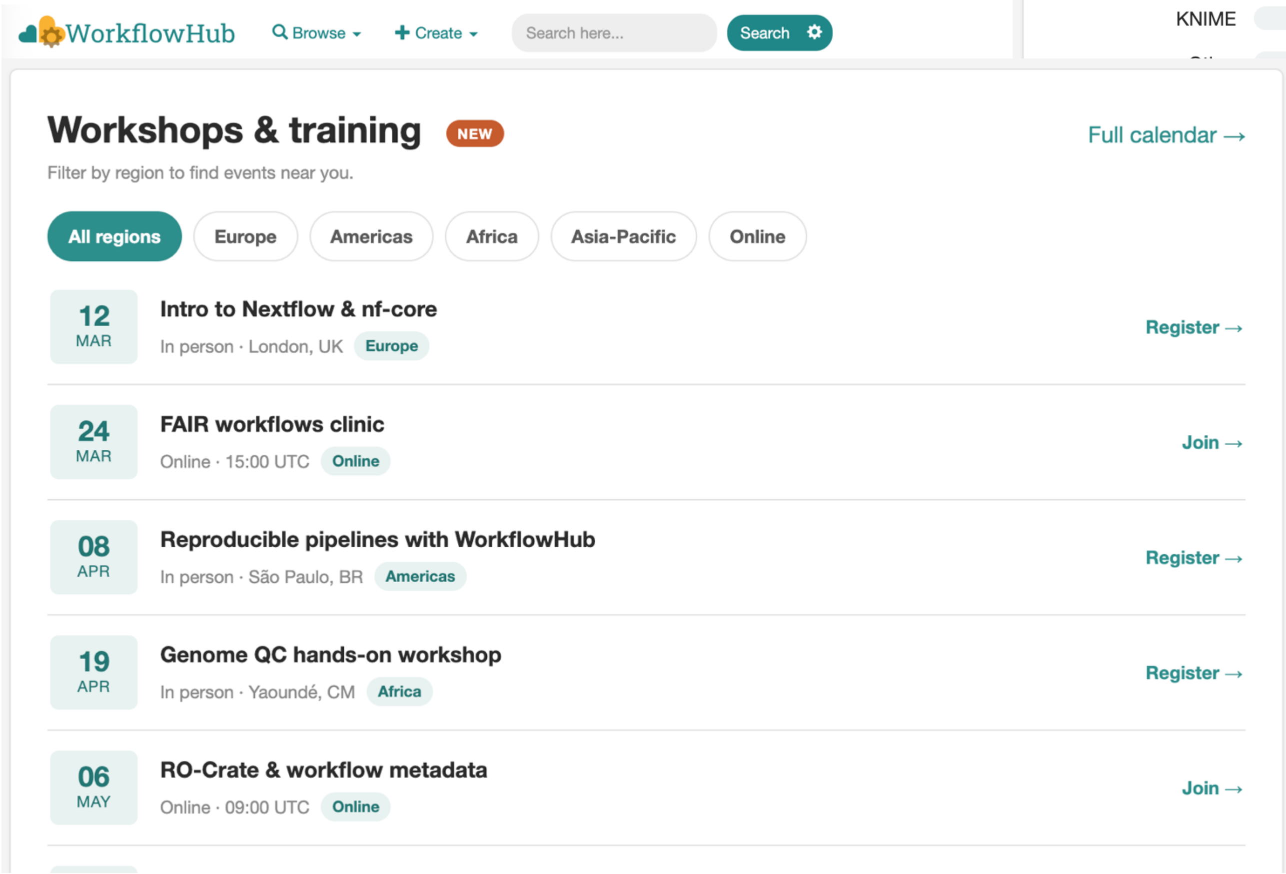
The general pipeline logic is as follows:

image

- Downloads genome and annotation files from N

MY EXPERIENCE · CONS

…and more human?



Workshops & training NEW

Full calendar →

Filter by region to find events near you.

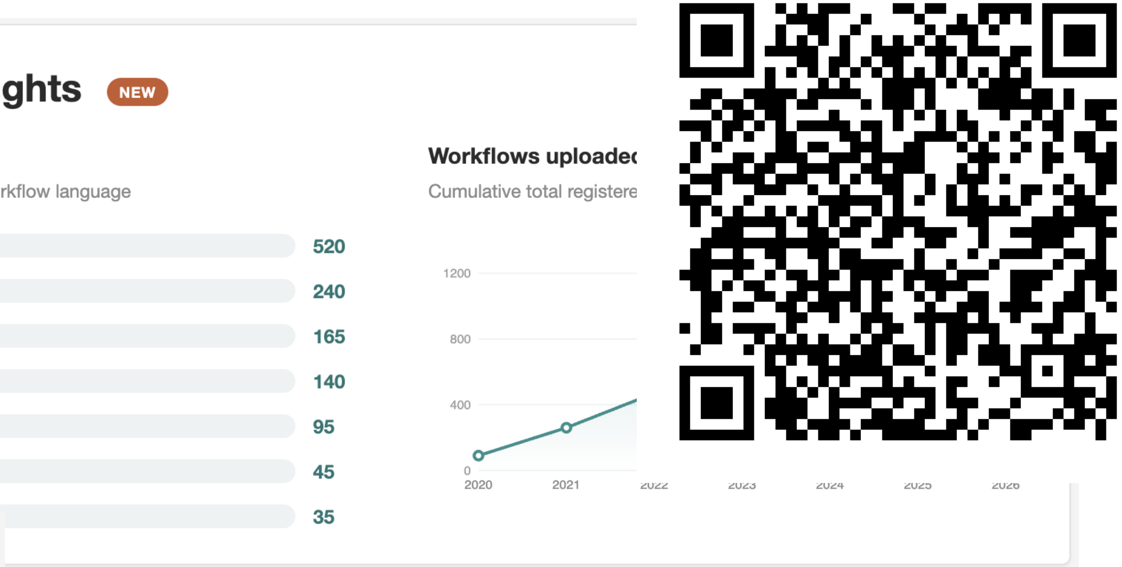
12 MAR — **Intro to Nextflow & nf-core** — In person · London, UK — Europe — Register →

24 MAR — **FAIR workflows clinic** — Online · 15:00 UTC — Online — Join →

08 APR — **Reproducible pipelines with WorkflowHub** — In person · São Paulo, BR — Americas — Register →

19 APR — **Genome QC hands-on workshop** — In person · Yaoundé, CM — Africa — Register →

06 MAY — **RO-Crate & workflow metadata** — Online · 09:00 UTC — Online — Join →



Registry insights NEW

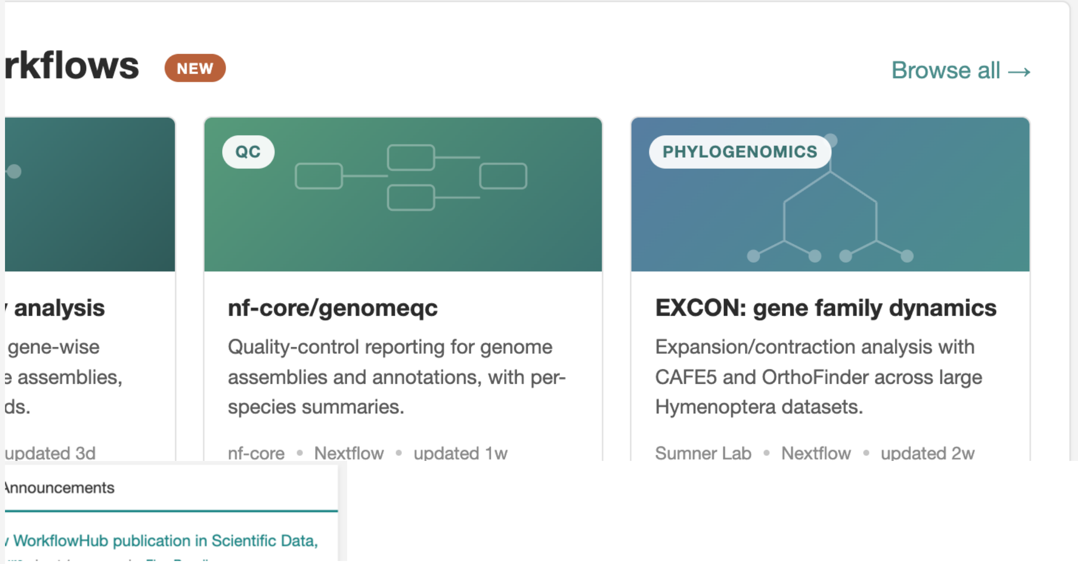
Workflows by type

Share of the registry, by workflow language

Galaxy	520
Nextflow	240
Snakemake	165
CWL	140
Jupyter	95
KNIME	45
	35

Workflows uploade

Cumulative total registere



rkflows NEW

Browse all →

analysis

gene-wise assemblies, ds.

updated 3d

nf-core/genomeqc

Quality-control reporting for genome assemblies and annotations, with per-species summaries.

nf-core • Nextflow • updated 1w

EXCON: gene family dynamics

Expansion/contraction analysis with CAFE5 and OrthoFinder across large Hymenoptera datasets.

Sumner Lab • Nextflow • updated 2w

Announcements

WorkflowHub publication in Scientific Data,

Thanks

Thanks to BioFAIR, nf-core & WorkflowHub communities, plus our Eco-Flow collaborators

eco-flow.github.io/

workflowhub.eu

nf-co.re

Chris Wyatt · CBER, Dept of GEE · UCL