GHGA THE GERMAN HUMAN GENOME-PHENOME ARCHIVE

WORKFLOWS

Providing standardised, comparable, and reproducible omics workflows for the research community.
https://www.ghga.de/resources/data-analysis

Curating Best Practice

Working closely with the nf-core community, we build on existing workflows to curate best practise pipelines.

Available Workflows

... include variant calling methods, long-read and rare disease sequencing analysis.

Upcoming Workflows

... include tools for RNA-sequencing quantification, benchmarking, single cell sequencing and diagnostic tools.

PRESENT

In the GHGA Metadata Catalog stage our workflows are openly available and run independently, locally by the users – without GHGA's direct intervention.

FUTURE

In later stages, we will provide processing capabilities to users via our compute nodes (GHGA Atlas) or in a cloud compute environment (GHGA Cloud).

Subscribe to our newsletter to learn about new available workflows.