

## PathoGFAIR: collection of Galaxy FAIR workflows for pathogen detection and samples comparison

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#### ▶ To cite this version:

Engy Nasr, Anna Henger, Bjoern Gruening, Paul Zierep, Bérénice Batut. PathoGFAIR: collection of Galaxy FAIR workflows for pathogen detection and samples comparison. GCC 2024 - Galaxy Community Conference, Jun 2024, Brno, Czech Republic. 10.7490/f1000research.1119769.1 . hal-04644577

HAL Id: hal-04644577

https://hal.science/hal-04644577

Submitted on 11 Jul 2024

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# PathoGFAIR

Collection of Galaxy FAIR Workflows for Pathogen Detection & Samples Comparison

Presented by: **Engy Nasr** from the University of Freiburg

on behalf of all authors: Anna Henger, Björn Grüning, Paul Zierep and Bérénice Batut



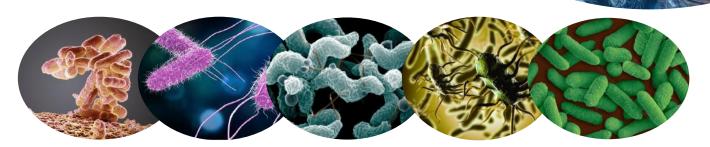


#### Food Contamination: A Global Health Threat

Food pathogen: A harmful microbe in food that can cause illness, including

bacteria, viruses, parasites and fungi

Affects 600 million people a year, casing illness and even death



## Pathogen Detection Challenges

#### Traditional Methods

PCR (Polymerase Chain Reaction) Limited to a specific small DNA region



WGS (Whole Genome Sequencing) Requires prior DNA isolation of a

targeted pathogen

Needs of prior knowledge of DNA

Time consuming

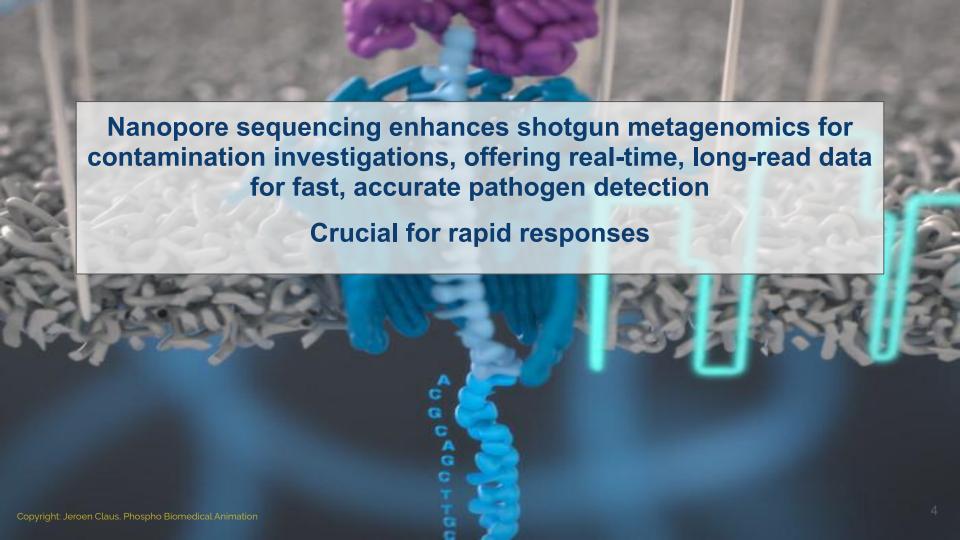
### **Shotgun Metagenomics Approach: A Breakthrough**

Analyzes all genetic material present in a complex sample, such as microbial communities in environmental or clinical samples.

**Detects and identifies pathogens & studies** interactions and functions between microbes.



Copyright: Sanford doddlab



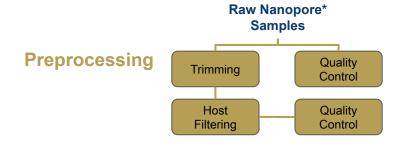
## Limitations of Other Pathogen Detection Approaches

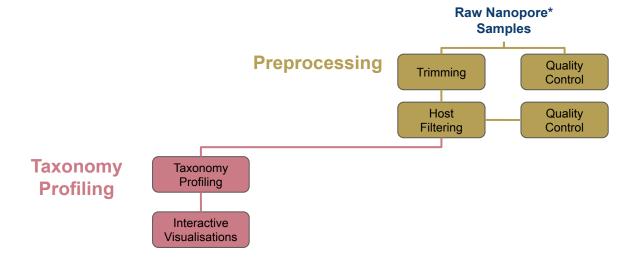
Lack of available, accessible, free or easy-to-use pipelines, e.g. OneCodex, SURPI, and Sunbeam

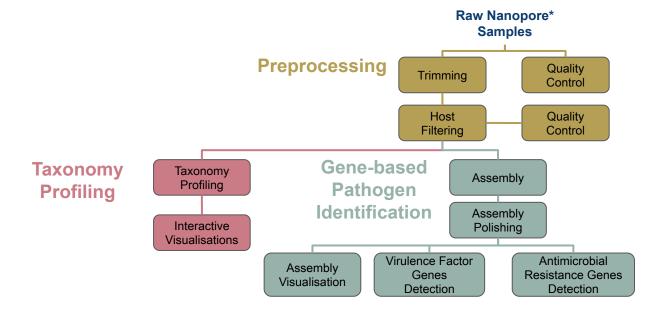
So we introduce PathoGFAIR

a very cool and awesome series of <u>Galaxy-based 5 FAIR</u> workflows for <u>Pathogen Detection</u>

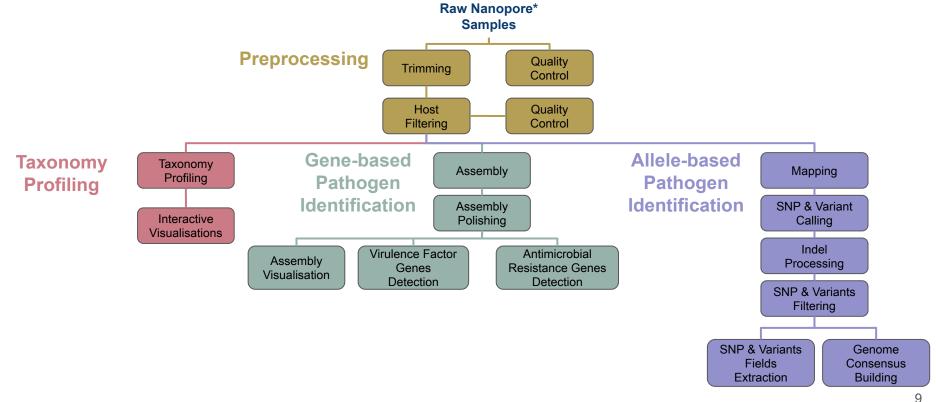




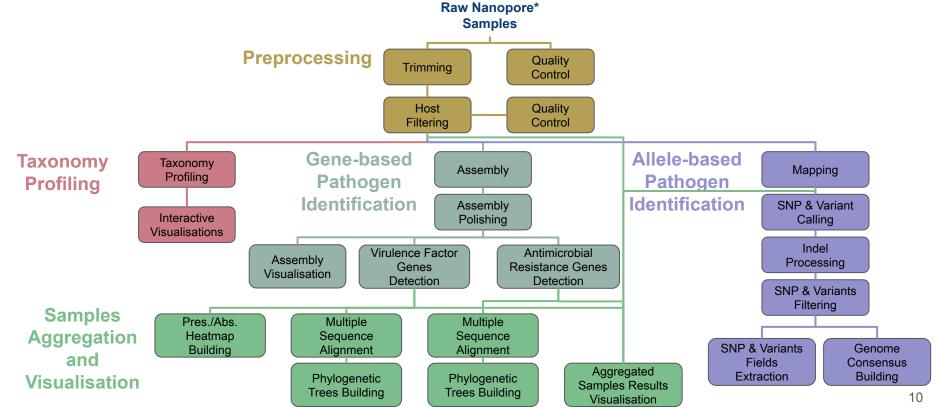




<sup>8</sup> 



Eåsily adaptable to any other type of sequencing technique



<sup>\*</sup> Easily adaptable to any other type of sequencing technique

Web Interface

PathoGFAIR workflows are deployable on all Galaxy servers, which have a wonderful user friendly web interface





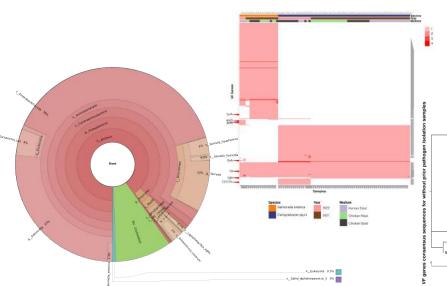
PathoGFAIR is very easy to use, it requires **zero** computer science background, with a simple one mouse click, all analyses, results, visualisations and reports are out



PathoGFAIR provides **reports** highlighting all findings from the performed analyses, which includes multiple interactive and non-interactive

visualisations





PathoGFAIR is easily **adaptable** to any other type of sequencing technique, and **scalable** to thousands of datasets



PathoGFAIR has a training material on our awesome Galaxy Training Network (GTN),









PathoGFAIR has a training material on our awesome Galaxy Training Network (GTN), and a full documentation on PathoGFAIR

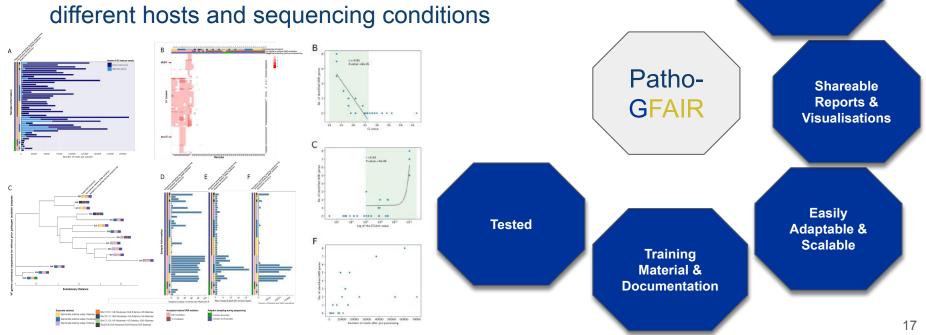
GitHub repository







PathoGFAIR has been tested successfully with 130 samples, with different pathogens, from different hosts and sequencing conditions



**Web Interface** 

**User Friendly** 

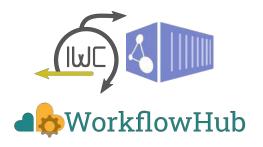
For more result details check our published bioarchive

All tools used in PathoGFAIR
workflows have available free
conda packages and are wrapped
in Galaxy tool wrappers

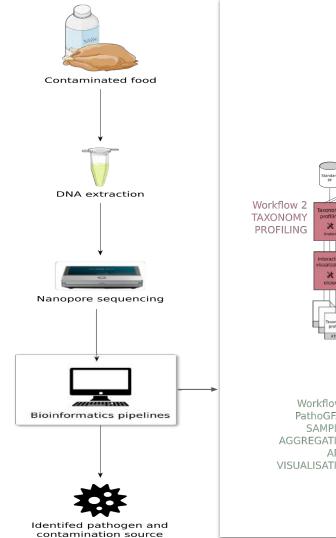


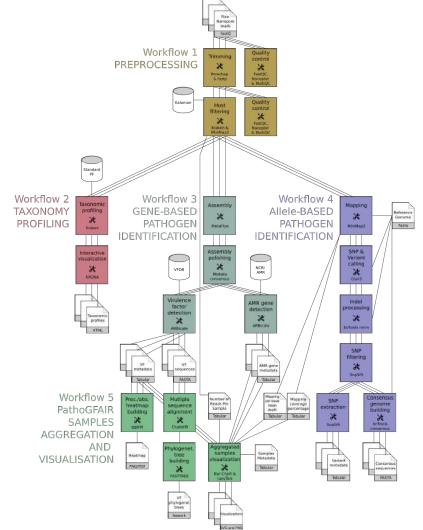


All 5 PathoGFAIR workflows are fully annotated, shared, and instantly deployable via the Intergalactic Workflow Commission (IWC), Dockstore and WorkflowHub









Packaged open source tools

BIOCONDA

Explicit user friendly workflow environment **= Galaxy** 

PROJECT

Freely available to be directly run

Galaxy

FUROPE

Annotated, shared and deployable



Training and Documentation



Tested successfully on 130 samples

#### Thank You ...

#### All authors







**Engy Nasr** 

Anna Henger Björn Grüning





Paul Zierep Bérénice Batut

# All Galaxy Freiburg Team specially







Wolfgang Maier

Mina Ansari

# EOSC-Life For Funding



#### Special thanks to





Peter van Heusden

Tobias Schindler



Marius van den Beek







Waiting for you all in the Pathogen Detection Training

Today at 13:00, Room: Congress hall B