

Accessible and scalable pipelines for fast and easy (foodborne) pathogen detection and tracking

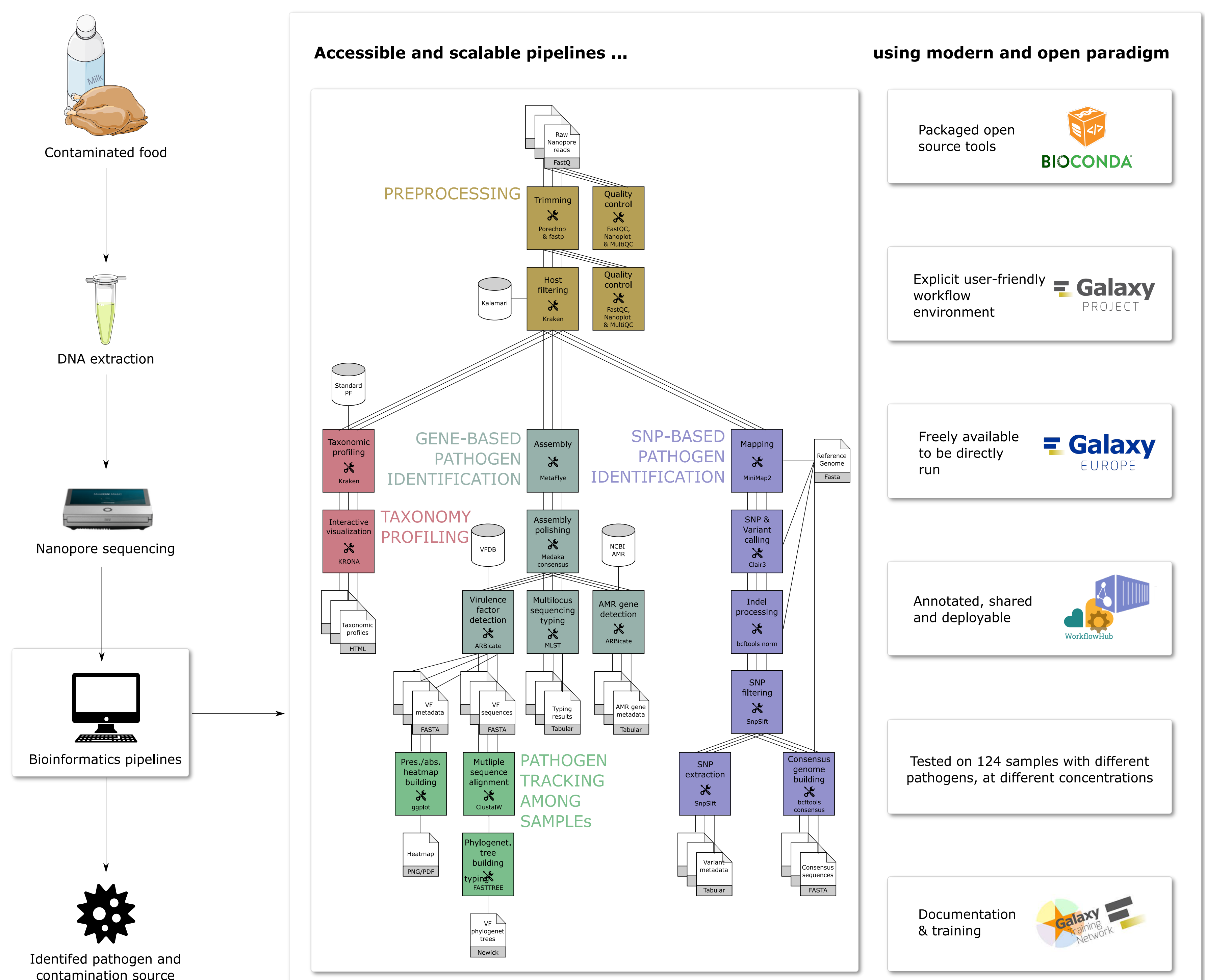
Engy Nasr, Anna Henger, Tobias Schindler, Paul Zierep, Björn Grüning, Bérénice Batut

Context

Food contamination by pathogens affects around **600 million people a year** and impacts socioeconomic development at different levels. During the investigation of a foodborne outbreak, a microbiological analysis of the potentially responsible food vehicle is performed in order to detect the responsible pathogens and identify the contamination source. **Traditional methods** require the isolation of the targeted pathogen, which is **time-consuming**, not always straightforward, nor successful. The **metagenomics** approach could solve this issue, by giving an overview of the genomic composition in the sample, including the food source itself, the microbial community, and any possible pathogens. It is **not based on prior DNA isolation**, nor limited to specific genes and it is **more accurate**. Metagenomics combined with **Oxford Nanopore sequencing** makes the identification of pathogens **quicker, easier, more accessible, and more practical**. But processing such data stay complex because of the **lack of accessible, easy-to-use, and openly available pipelines**.

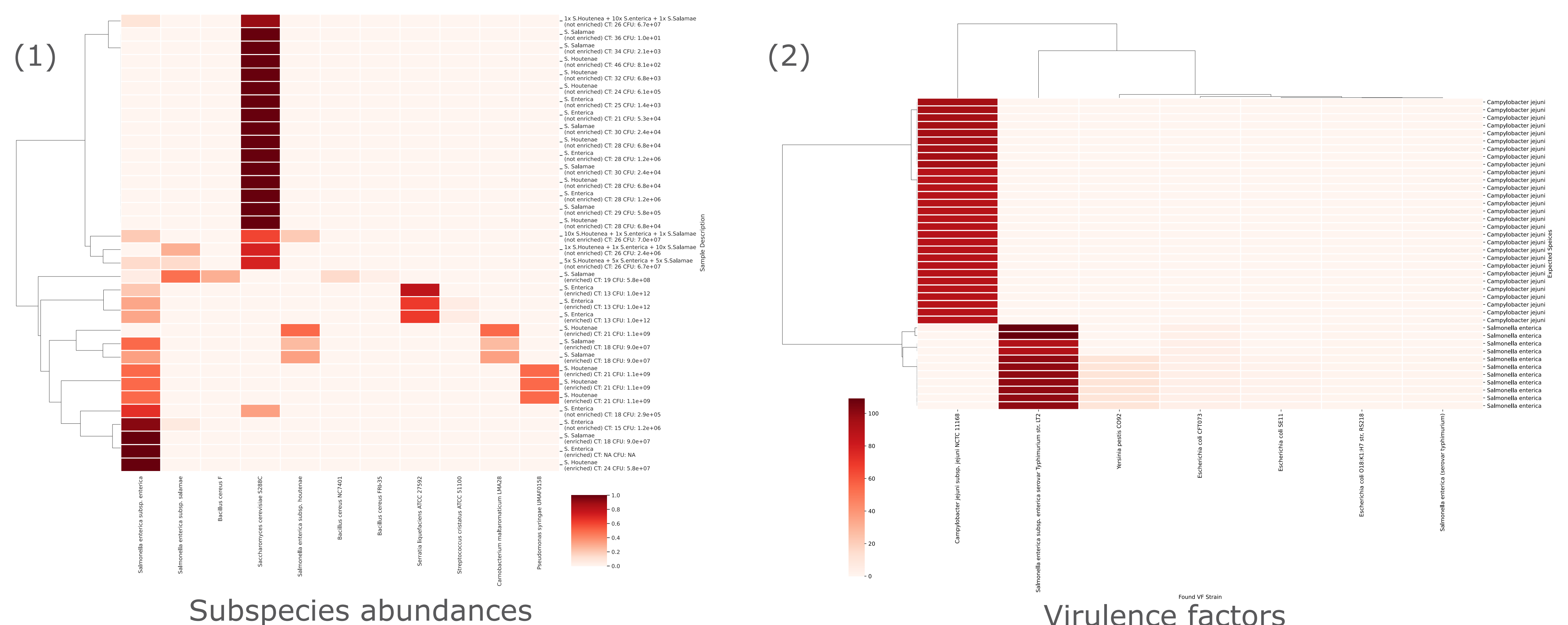
Accessible and scalable pipelines

To solve this issue, we have implemented a series of **FAIR Galaxy-based workflows**. These workflows integrate **state-of-the-art tools, visualization, and reports** to **detect** and **track** pathogens from any - not only food - metagenomics Oxford Nanopore sample.



Results

The workflows were **successfully tested** on (1) **spiked** food with different *Salmonella enterica* strains at different concentrations, and (2) samples collected from human & chicken stools, and meat in Palestine containing *Salmonella enterica* or *Campylobacter jejuni*.



Contact
berenice.batut@gmail.com

universität freiburg **Biolytix**

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