MOPS2

20 November 2025

EUROPEAN FOOD SAFETY AUTHORITY

AGENDA

- Genetic modification characterisation – from theory to code
- Testing – pipelines changes and UAT
- Main feedback received
- Next steps

GM CHARACTERISATION


Adopted: 24 September 2025
DOI: 10.2903/j.efsa.2025.9705
efsa JOURNAL
GUIDANCE

Guidance on the characterisation of microorganisms in support of the risk assessment of products used in the food chain

- Characterisation of genetic modification by comparison WGS data of the GMM with the **non-GM reference strain** (e.g. parental strain)
- **Mandatory** for bacteria, viruses, yeasts and filamentous fungi, recommended for microalgae and other protists
- Any **gene of concern** should be clearly indicated
- Details are given in **EFSA WGS Statement 2024**


Adopted: 28 June 2024
DOI: 10.2903/j.efsa.2024.8912
efsa JOURNAL
STATEMENT

EFSA statement on the requirements for whole genome sequence analysis of microorganisms intentionally used in the food chain

European Food Safety Authority (EFSA)

GM CHARACTERISATION

- Based on the alignment between the GMM and the reference strain, **any genetic modifications** (i.e. intended and unintended) should be reported.
- The focus of the unintended modifications is on **genes of concern**
- The alignments between the GMM and the reference strain should be provided
- A **map or graphic presentation** should be provided with all insertions, deletions and substitutions found in the genome (chromosome(s) and extra-chromosomal genetic elements) of the GMM.
- For each inserted, modified or deleted open reading frame(ORF) the amino acid sequence, function and metabolic role should be provided.

Adopted: 28 June 2024

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efsa JOURNAL

STATEMENT

EFSA statement on the requirements for whole genome sequence analysis of microorganisms intentionally used in the food chain

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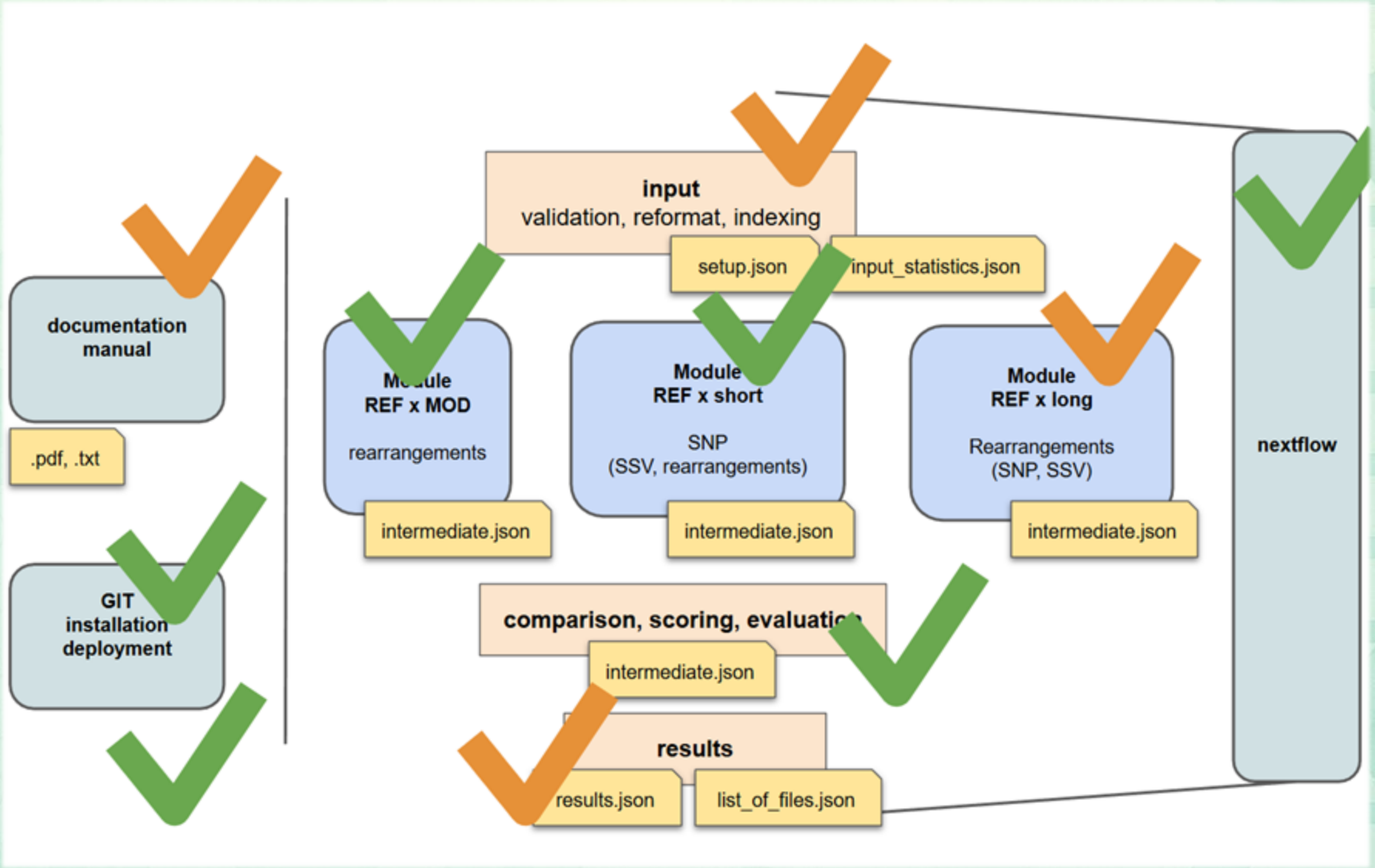
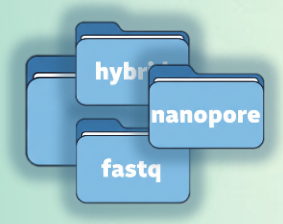
GM CHARACTERISATION



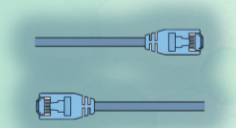
NOVEMBER MOPS PORTAL UAT: 3/11 TO 28/11

FOCUS ON THE PORTAL, NOT THE PIPELINE



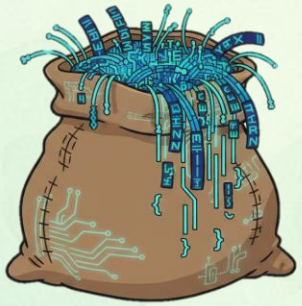
1) INSTRUCTIONS AND ADD PREEMPTIVE CHECKS TO ENSURE THE CORRECT COMBINATION OF FILES UPLOADED.

2) INSTRUCTIONS AND ADD PREEMPTIVE CHECKS TO ENSURE THE FORMAT AND NAME ARE CORRECT.



3) IMPROVE NETWORK SETTINGS TO SPEED UP THE UPLOAD OF LARGE FILES.

PIPELINE CHANGES FROM 1.0.83 TO 1.3.35



NEW BUNDLE COMING 1.3.35

1.Long-read files are now processed using FastpLong for improved quality control.

2.Submitted fungal samples are now placed in a phylogenetic tree using a maximum-likelihood approach.

3.The percentage of reference bacterial genomes of the input species containing the corresponding AMR gene is now presented. This value is calculated using the tool “Pipeline for the automated analysis of gene distribution in microbial species” (https://doi.org/10.5281/zenodo.12608405) and the reference genomes are retrieved from NCBI.

4.Report files (PDF and HTML) now include result tables for putative antimicrobial resistance genes and putative virulence factors. Additionally, secondary metabolite results generated by antiSMASH are directly incorporated as figures. Minor improvements and formatting enhancements are also applied.

5.Configuration files and related resources have been reorganised for improved clarity, consistency, and easier pipeline maintenance.

PIPELINE FEEDBACK

RISK ASSESSMENT

Feedback concerning bioinformatic analysis, methods, cutoffs etc.

IT

Feedback concerning ease of installation and execution of the pipeline outside EFSA, i.e. optimizations for portability.

RISK ASSESSMENT FEEDBACK (DONE)

1. Removing the analysis of AMR and virulence genes in the reference genome.

2. Remove some databases.

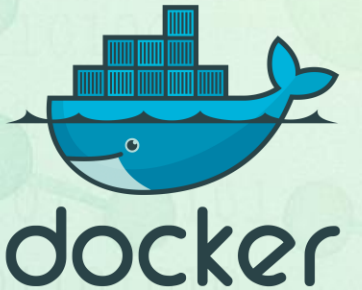
3. Enhanced reference databases with only type strains.

RISK ASSESSMENT FEEDBACK TO BE CONSIDERED

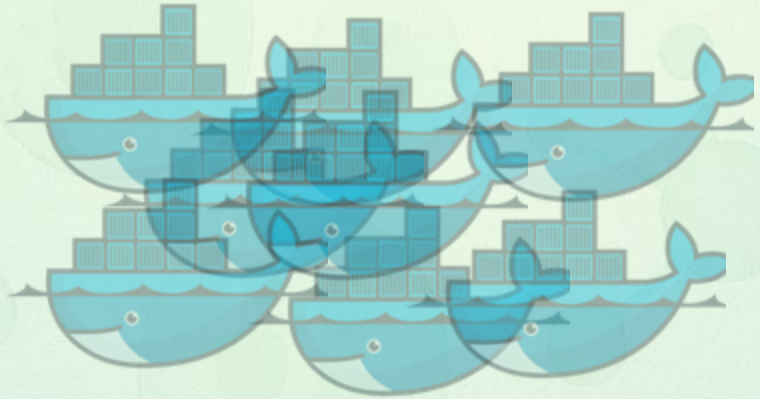
- To review some Cutoffs and threshold (QC, AMR, secondary metabolites, ANI threshold for yeast, others…).
- Bacteria assembly optimization: i.e. choosing different assemblers according to plasmids and sequencing type.
- Fungal assembly optimization: i.e. choosing different assemblers according to ploidy and sequencing type, polishing with short reads using polca + polypolish.
- Gene annotation results for fungal genomes were significantly inflated (we will review annotation altogether).
- Missing species for taxonomic identification (kraken database, ANI).
- Antismash reporting optimizations.
- Recommend a process added to map raw reads to reference genome to assess contamination and/or completeness where a reference is supplied. It is the most straight forward way.
- Include a dedicated plasmid summary in the report, listing detected plasmids with basic metadata (e.g. size, coverage, gene content).

IT FEEDBACK

Feedback concerning ease of installation and execution of the pipeline outside EFSA, i.e. optimizations for portability.



DOCKER VS APPTAINER



AMOUNT OF DOCKERS

EXTERNAL DATABASES

Misconception: NOT pipeline optimized for your IT.
Pipeline optimized for EFSA IT.

Next year: two “IT” versions of the pipeline, one for us, and an external version.


Thanks
for the attention