BAP – Bacterial Analysis Pipeline

CoP Bioinformatics

2 May 2024

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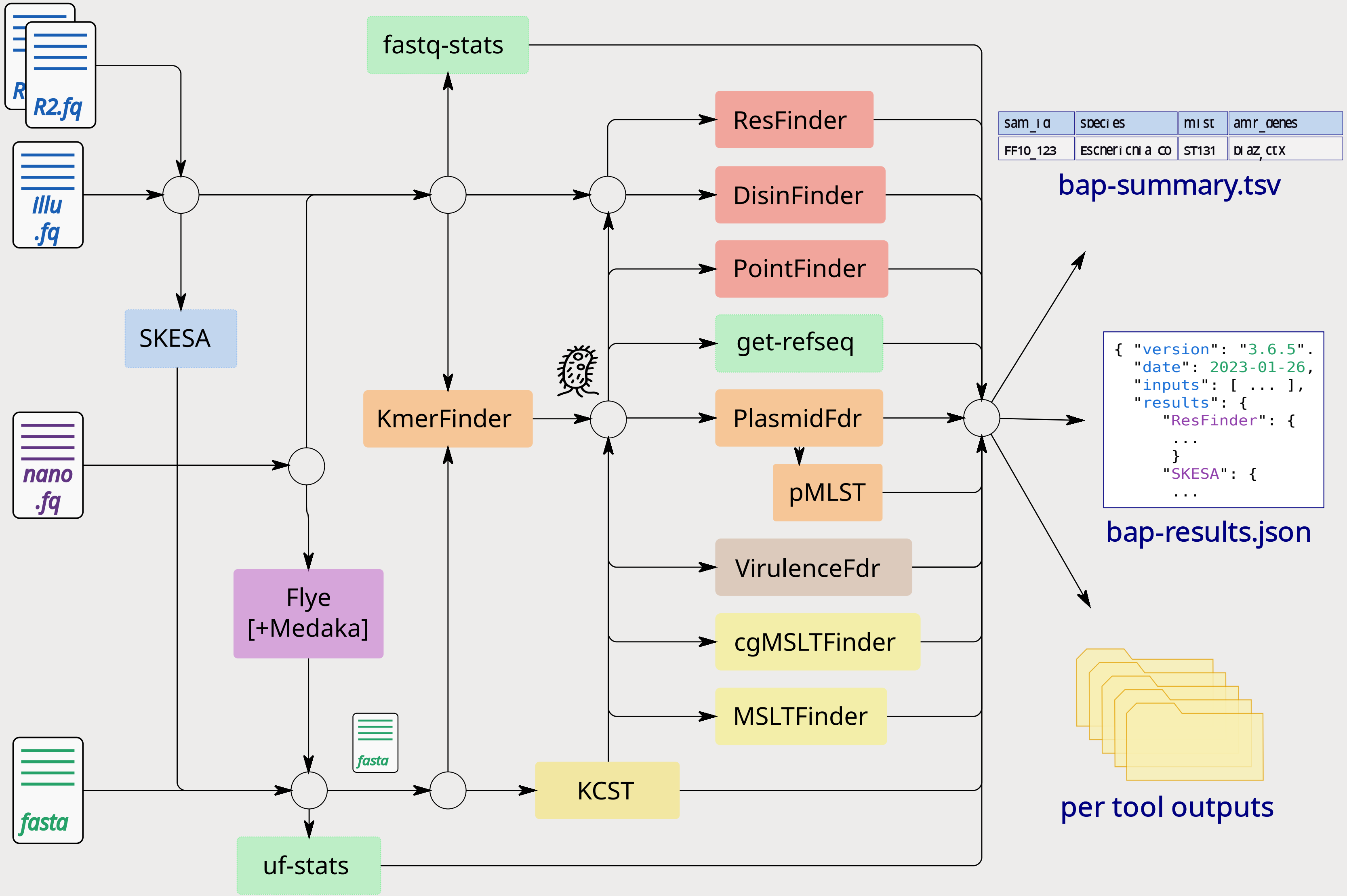
The “BAP”

- CGE Bacterial Analysis Pipeline
  - https://github.com/zwets/cge-bap
- History
  - 2013/14 KCRI starts WGS: collaboration with DTU
  - Sequencing *and* bioinformatics analysis at KCRI (Moshi, Tanzania)
  - DTU CGE services & databases “ported” from Computerome to Laptop (workstation)
  - Online CGE services: BAP project at DTU
    - Run all services in one go
    - Run multiple samples in batch
  - KCRI CGE BAP started from the “CGE BAP Backend” (Docker)

CGE BAP 3.7.0 (“The BAP”)



sam_id	species	mlst	amr_genes
FF10_123	Escherichia coli	ST131	blaz, ctx

bap-summary.tsv

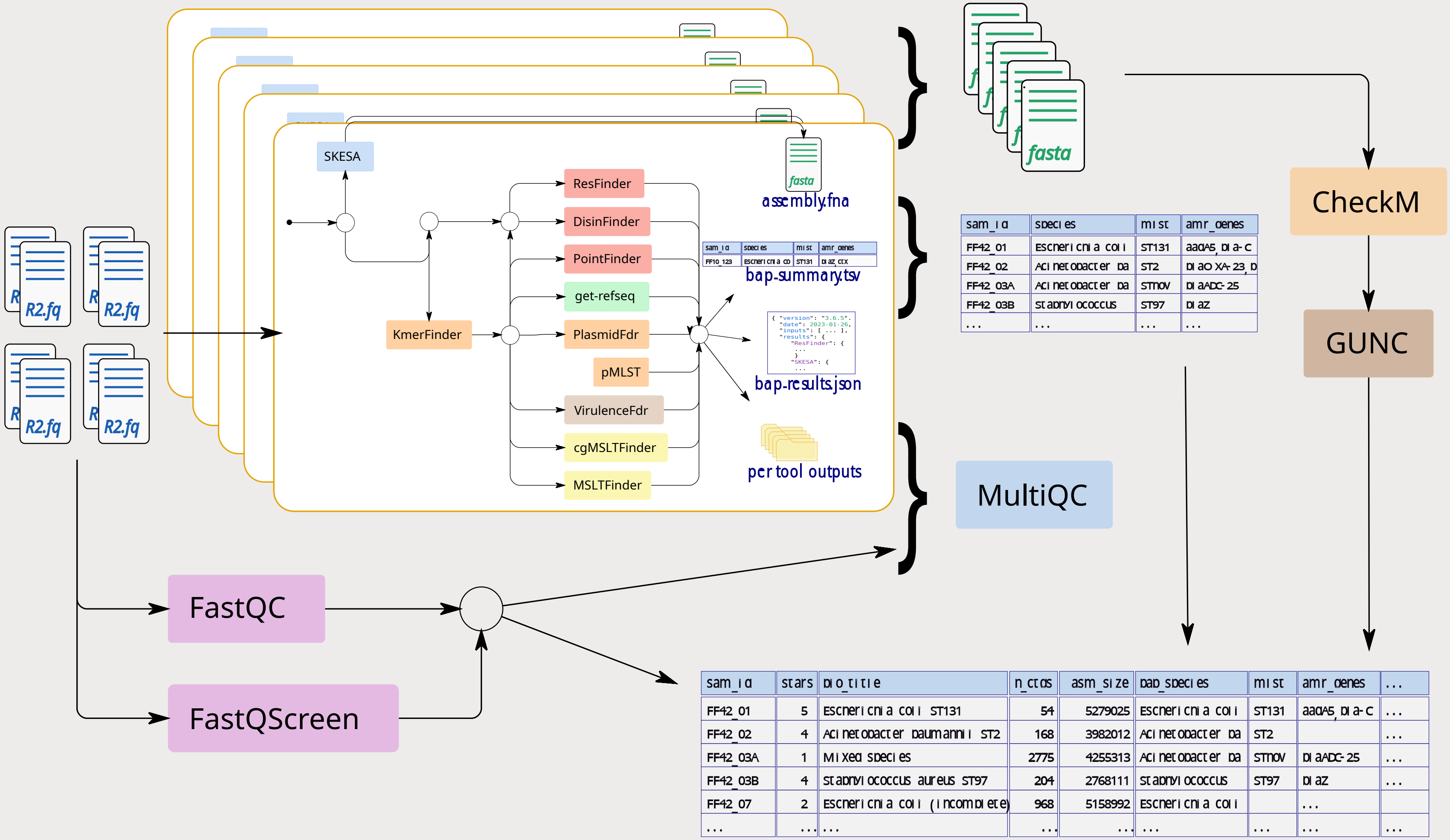
```
{ "version": "3.6.5".
  "date": 2023-01-26,
  "inputs": [ ... ],
  "results": {
     "ResFinder": {
      ...
      }
     "SKESA": {
      ...
```

bap-results.json

Bacterial Analysis Pipeline

- Standard workflow
  - Integrates the CGE Services
  - Default analyses & settings
  - Configurable “a la carte”
- One isolate at a time
  - Illumina or Nanopore reads
  - Genome assembly
- Open Source
  - github.com/zwets/cge-bap
- Moderate hardware
  - 32G laptop (Linux / MacOS)

The “Project BAP” workflow



sam_id	species	mlst	amr_genes
FF42_01	Escherichia coli	ST131	aadA5, bla-C
FF42_02	Acinetobacter ba	ST2	blaOXA-23, b
FF42_03A	Acinetobacter ba	STnov	blaADC-25
FF42_03B	Staphylococcus	ST97	blaZ
...	...	...	...

sam_id	stars	bio_title	n_ctgs	asm_size	bap_species	mlst	amr_genes	...
FF42_01	5	Escherichia coli ST131	54	5279025	Escherichia coli	ST131	aadA5, bla-C	...
FF42_02	4	Acinetobacter baumannii ST2	168	3982012	Acinetobacter ba	ST2		...
FF42_03A	1	Mixed species	2775	4255313	Acinetobacter ba	STnov	blaADC-25	...
FF42_03B	4	Staphylococcus aureus ST97	204	2768111	Staphylococcus	ST97	blaZ	...
FF42_07	2	Escherichia coli (incomplete)	968	5158992	Escherichia coli		...	
...	...	...	...	...	...	...	...	...

Project BAP

- “Batching the BAP”
  - Process all isolates of a project
  - Collate & aggregate
  - Bundle for customer
- Add QC, flag issues
  - Genome completeness
  - Contamination & Mixes
  - Quality rating: 0-5 star
  - “Label” assembly title
- Utilise HPC facilities
  - HTCondor job batching
  - HTCondor workflow control
  - Include heavyweight tools
  - The ‘genomics inventory’ (gi)

Concluding

- Stable workhorse for routine work
  - Minimal hands-on time, fully automated
  - Default settings, standard outputs
  - Keep up to date (centrally) with latest tools & databases
  - Can run on moderate hardware (current-day mid-range laptop)

But

  - World has moved on (esp internet connectivity!)
  - Not well suited for ONT work
  - All command-line, still need “bioinformatician support”

The
Fleming Fund
Regional Grants

Thank you

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COMMUNICABLE DISEASES
Division of the National Health Laboratory Service

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This programme is being funded by the UK Department of Health and Social Care.
The views expressed do not necessarily reflect the UK Government’s official policies.