



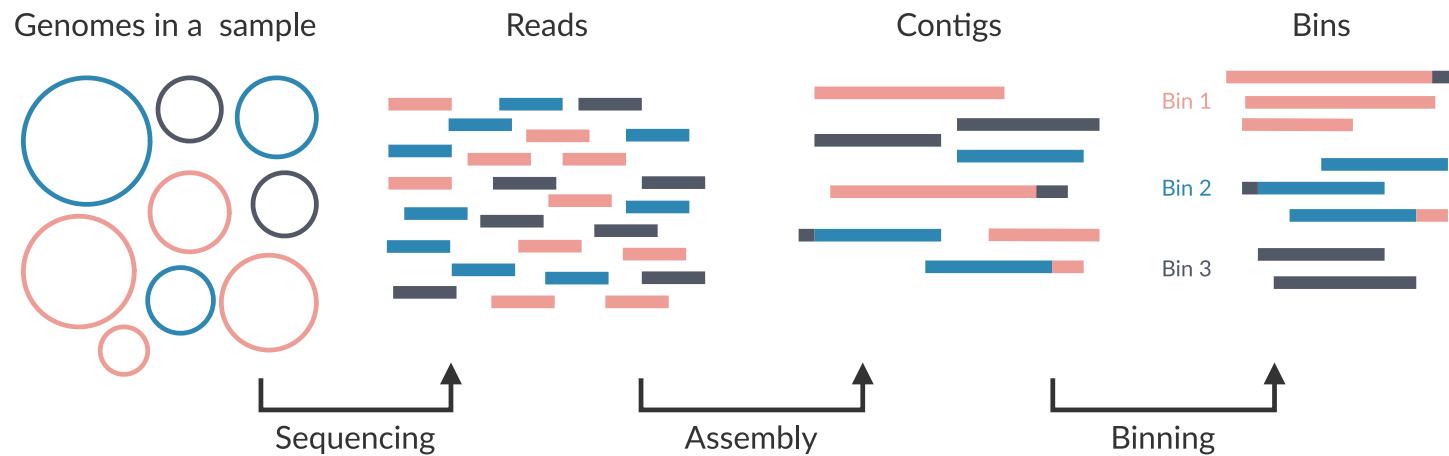
nf-core 
mag v5

Diego Alvarez S. |  [dialvarezs](#)

Universidad de Magallanes

28.10.2025

Metagenome Assembly & Binning



History & Maintainers

Timeline

 v1.0 - Dec 2019

Purple Corgi

Hadrien Gourlé

 v2.0 - Jun 2021

Silver Swan

Sabrina Krakau

 v3.0 - May 2024

Magenta Magpie

James A. Fellows Yates

 v4.0 - May 2025

Blue Huemul

James A. Fellows Yates

 v5.0 - Sep 2025

Green Squirrel

James A. Fellows Yates

Current maintainers



James A. Fellows Yates

@jfy133



Jim Downie

@prototaxites



Daniel Straub

@d4straub



Adam Rosenbaum

@muabnezor



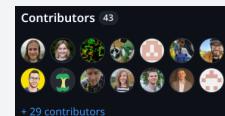
Diego Alvarez S.

@dialvarezs

Thanks! 🙏

Past maintainers

Hadrien Gourlé, Sabrina Krakau,
Maxime Borry



+ many other contributors

What's New?

Long read assembly

Using Flye and/or MetaMDBG

New tools

Binners: CONCOCT

Bin QC: CheckM, CheckM2

Viral/eukaryotic MAGs: geNomad, Tiara, MetaEuk

Depth normalisation: BBNorm

Updated tools / databases

Basically everything!

Deprecated

RAW read taxonomic profiling

→ Use nf-core/taxprofiler instead

What's New?

🚀 Just Released!

v5.1.0 - *Platinum Pudu*



New binner

COMEBin



Documentation

Usage of

*_percentidentity



Bug fixes

metaSPAdes CPUs config,
LR assembly mode and
more

Codebase Improvements

From v3.0 to v5.0



1,106

commits



626

files changed



-23

local modules (migrated to nf-core ones)



50,417

additions



10,678

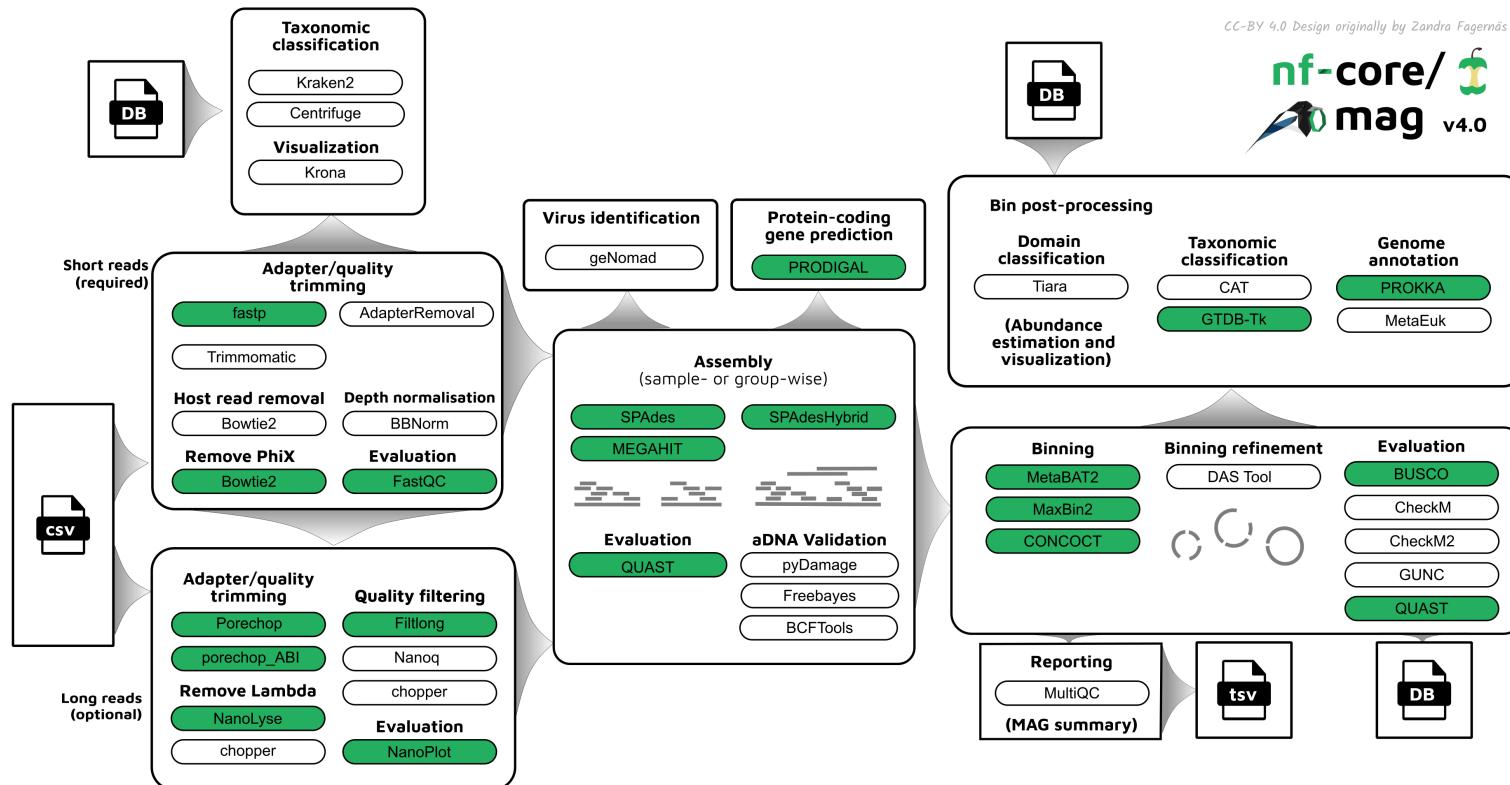
deletions



11

new subworkflows

Previous Workflow (v4.0)



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Longread only PR by @muabnezor

- Complete rebuild of the pre-processing and assembly subworkflows
- New tools specific for long reads
- New parameters

- ~100 commits
- ~5000 new lines
- ~6 months of development
- 200+ comments

Longread only functionality #718

Merged muabnezor merged 96 commits into [nf-core:dev](#) from [muabnezor:longread_only](#) on Jun 6

Conversation 207 Commits 96 Checks 17 Files changed 85 +5,052 -350

muabnezor commented on Nov 28, 2024 • edited

This PR adds long-read only functionality to mag.
closes #662, #659, #275

PR checklist

- This comment contains a description of changes (with reason).
- If you've fixed a bug or added code that should be tested, add tests!
- If you've added a new tool - have you followed the pipeline conventions in the [contribution docs](#)
- If necessary, also make a PR on the nf-core/mag branch on the [nf-core/test-datasets](#) repository.
- Make sure your code lints (`nf-core pipelines lint`).
- Ensure the test suite passes (`nextflow run . -profile test,docker --outdir <OUTDIR>`).
- Check for unexpected warnings in debug mode (`nextflow run . -profile debug,test,docker --outdir <OUTDIR>`).
- Usage Documentation in `docs/usage.md` is updated.
- Output Documentation in `docs/output.md` is updated.
- `CHANGELOG.md` is updated.
- `README.md` is updated (including new tool citations and authors/contributors).

Reviewers: prototaxes, d4straub, erikrikarddaniel, diafarezs, jfy133

Assignees: No one—assign yourself

Labels: ready to review

Projects: None yet

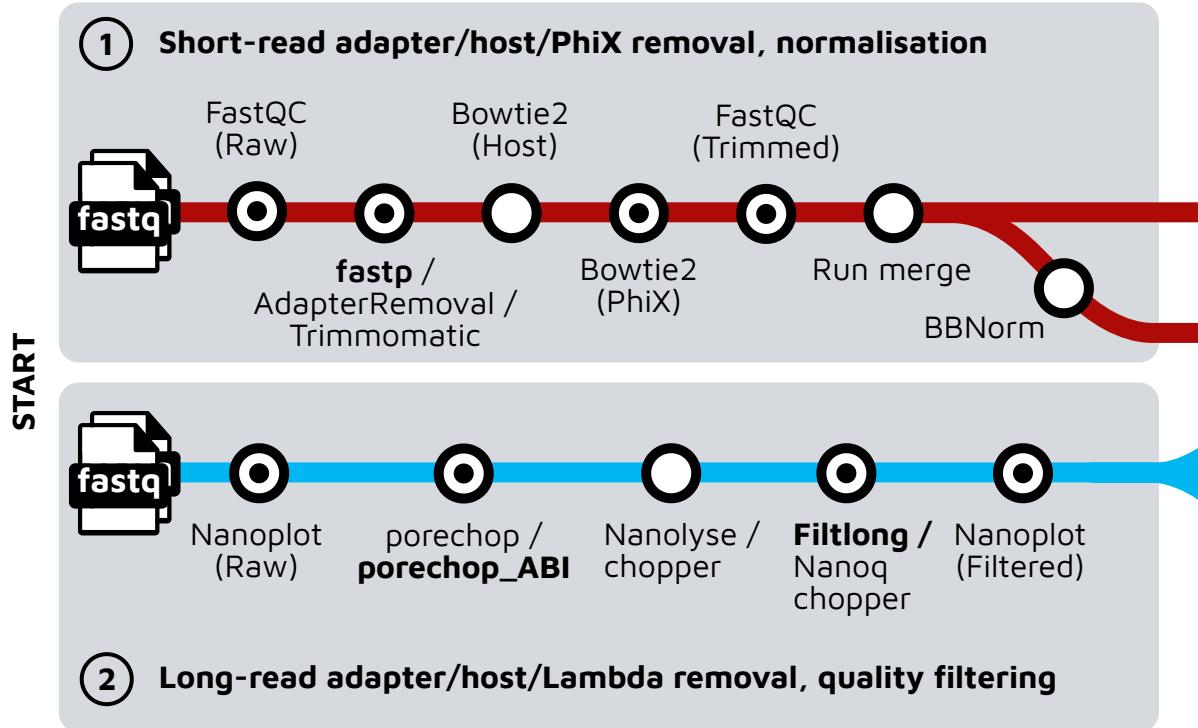
Milestone: No milestone

Development: Successfully merging this pull request may close these issues.

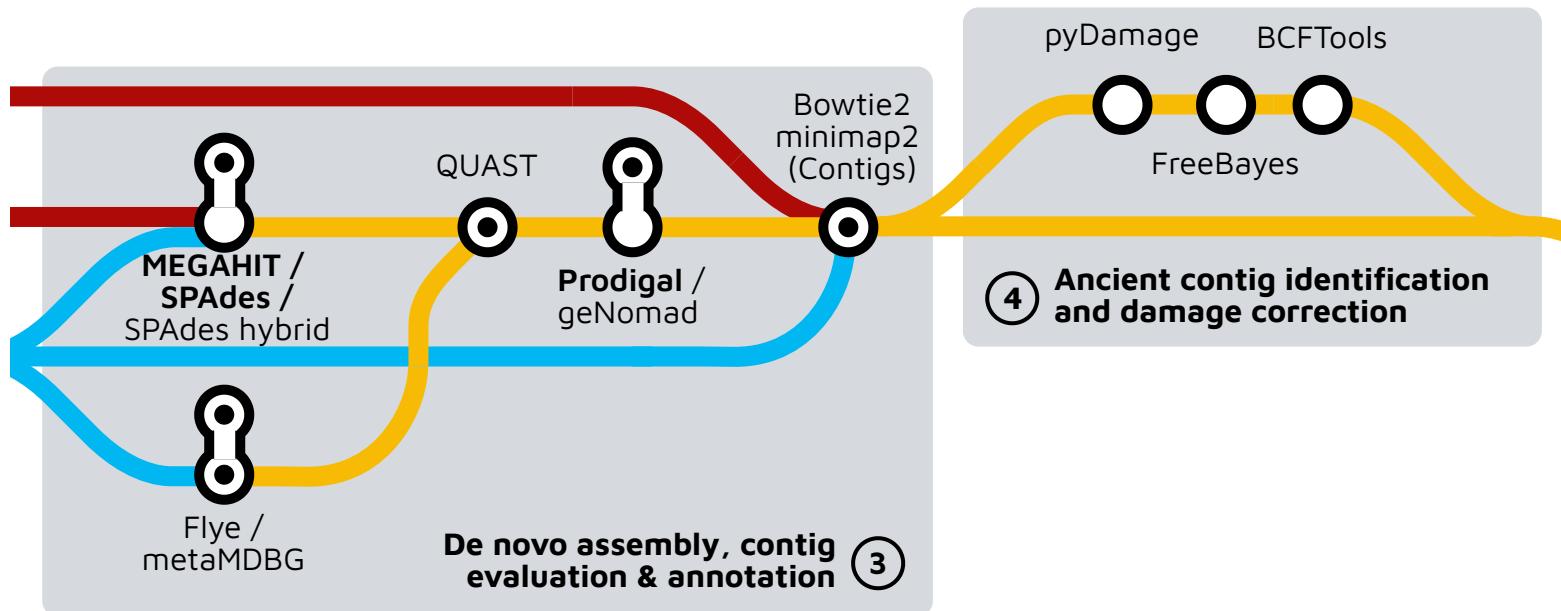
muabnezor added 12 commits 11 months ago

Current Workflow (v5.1)

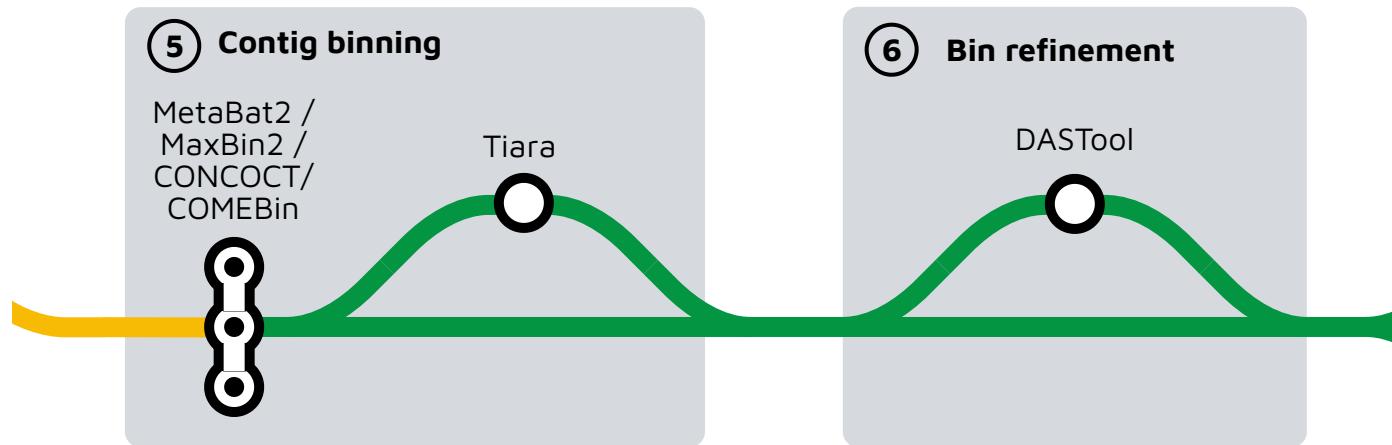
nf-core/mag v5.1 - Preprocessing



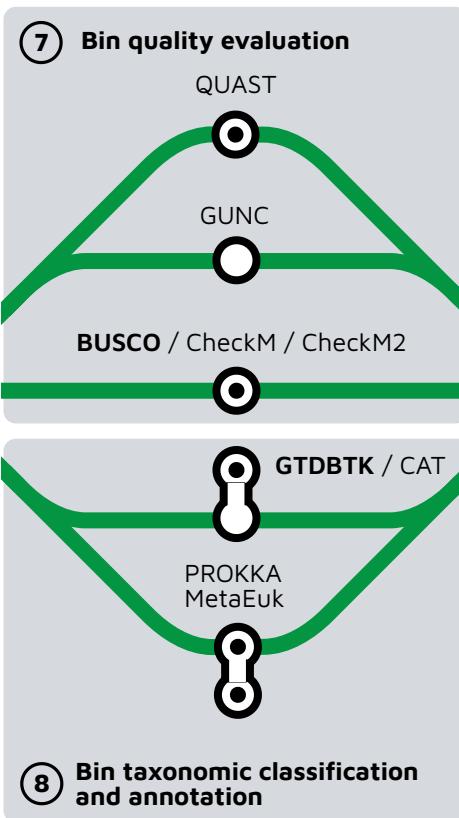
nf-core/mag v5.1 - Assembly and Annotation



nf-core/mag v5.1 - Binning and Refinement



nf-core/mag v5.1 - Bin QC and Taxonomy



How to run nf-core/mag v5.1.0?

```
nextflow run nf-core/mag -r 5.1.0 \
    -profile <docker/singularity/.../institute> \
    --input samplesheet.csv \
    --outdir results/
```

Mixed short + long read samplesheet

```
sample,group,short_reads_1,short_reads_2,long_reads,short_reads_platform,long_reads_platform
sample1,0,data/sample1_R1.fastq.gz,data/sample1_R2.fastq.gz,data/sample1.fastq.gz,ILLUMINA,OXFORD_NANOPORE
sample2,0,data/sample2_R1.fastq.gz,data/sample2_R2.fastq.gz,data/sample2.fastq.gz,ILLUMINA,OXFORD_NANOPORE
sample3,1,data/sample3_R1.fastq.gz,data/sample3_R2.fastq.gz,ILLUMINA,
```

Long read only, merging runs

```
sample,run,group,long_reads,long_reads_platform
sample1,1,0,data/sample1a.fastq.gz,OXFORD_NANOPORE
sample1,2,0,data/sample1b.fastq.gz,OXFORD_NANOPORE
sample2,0,0,data/sample2.fastq.gz,OXFORD_NANOPORE
sample3,1,0,data/sample3.fastq.gz,OXFORD_NANOPORE
```

What's Next?

Feature	Planned	In Progress	On Review
MetaBinner	✓	✓	✓
Bin QC by multiple tools	✓	✓	✓
BigMAG compatibility	✓	✓	
Hostile for decontamination	✓	✓	
nf-test snapshots (Hackaton!)	✓	✓	
CoverM for bin abundance	✓		



Thank you!

Questions? Suggestions? Issues?



GitHub

[nf-core/mag](https://github.com/nf-core/mag)



Slack

[#mag](#)



Documentation

nf-co.re/mag