

The RNA Workbench - reproducible, transparent, and accessible RNA research

Florian Eggenhofer, Björn Grüning, Bérénice Batut, Jörg Fallmann, Andrea Bagnacani, Peter F. Stadler, Rolf Backofen
and the RNA Workbench Team

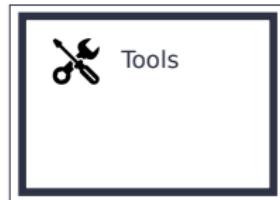
Lehrstuhl Bioinformatik
University of Freiburg

30.06.2017

Goals of the RNA Workbench



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- ▶ Comprehensive set of *RNA*-bioinformatics tools

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- ▶ Community - authors and users

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- ▶ Community - authors and users
- ▶ Set of predefined workflows and associated descriptions/training material
- ▶ Easy and stable dissemination via Galaxy and Docker

Tools

- More than 50 *RNA* bioinformatics tools

Tools

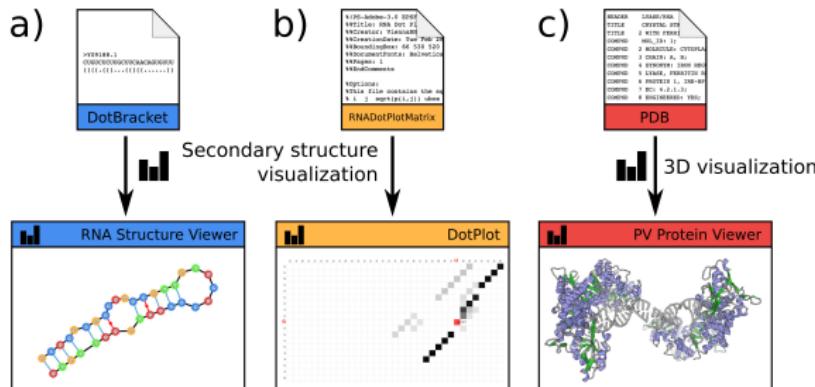
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- *RNA*-seq analysis (FuMa, Paralizer, ...)
- Included *RNA* visualization



Workflows

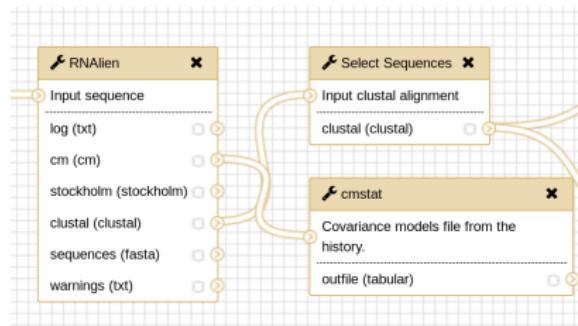
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Workflows

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- ▶ Based on tools as building blocks

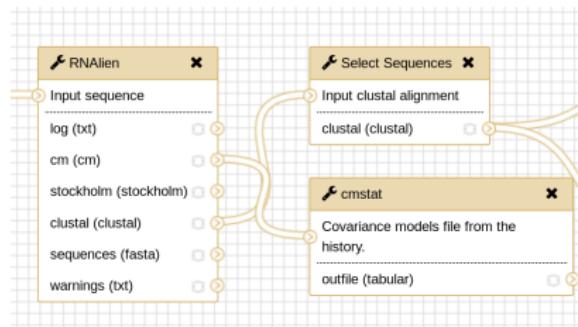
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- ▶ Can be designed and shared ([ToolShed/myexperiment.org](#))



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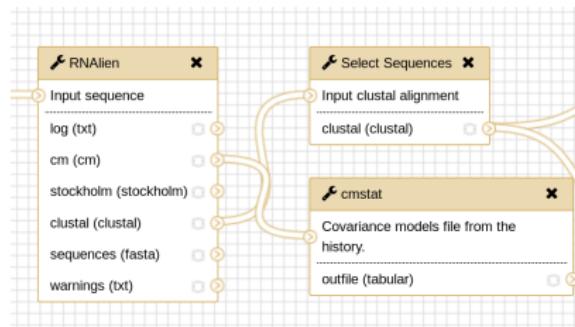
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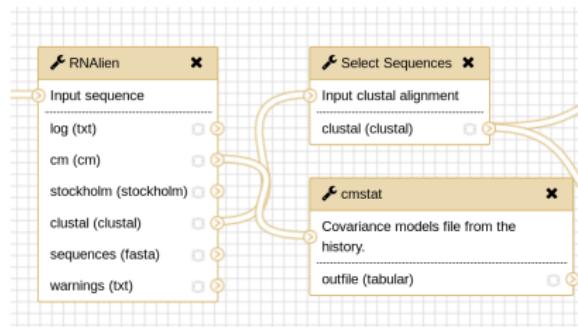
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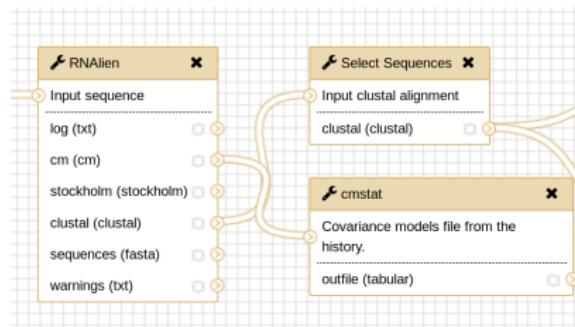
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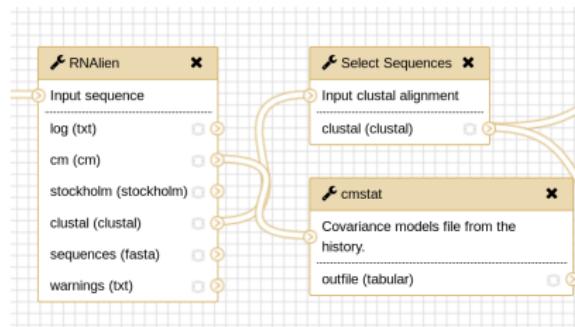
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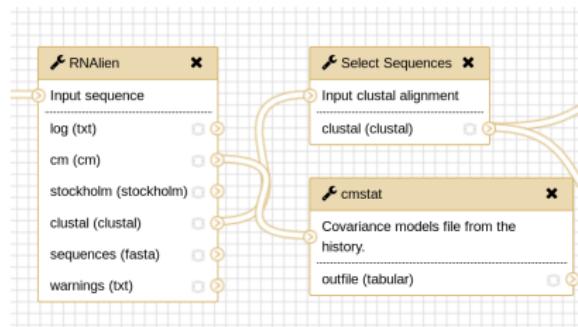
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 - ▶ C/D-box scan

Workflow - Analysis of non-coding RNAs

- ▶ Test for functional structure via conservation

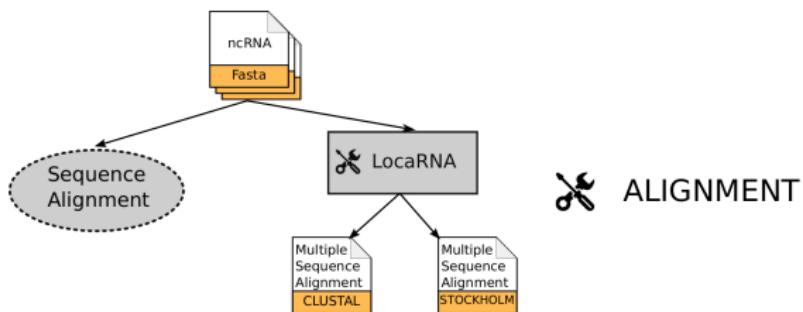
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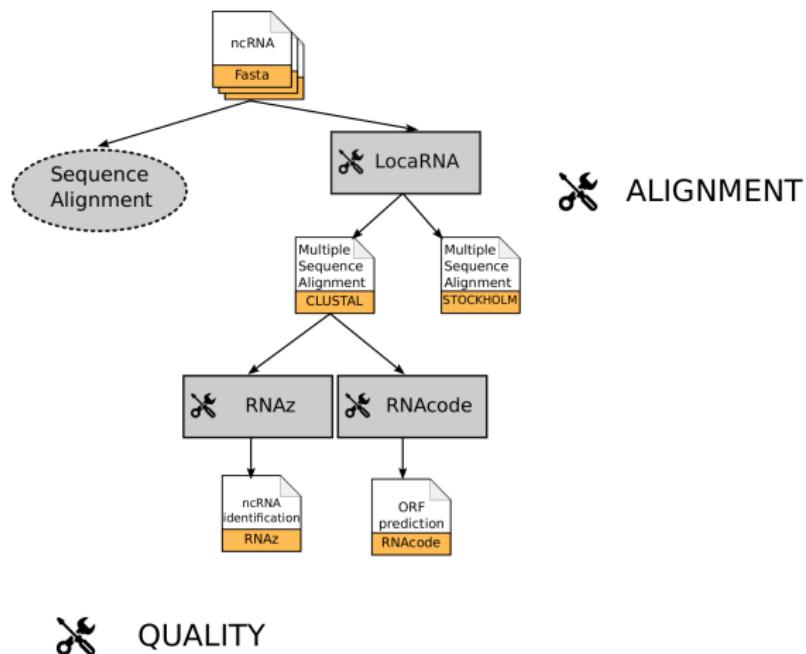
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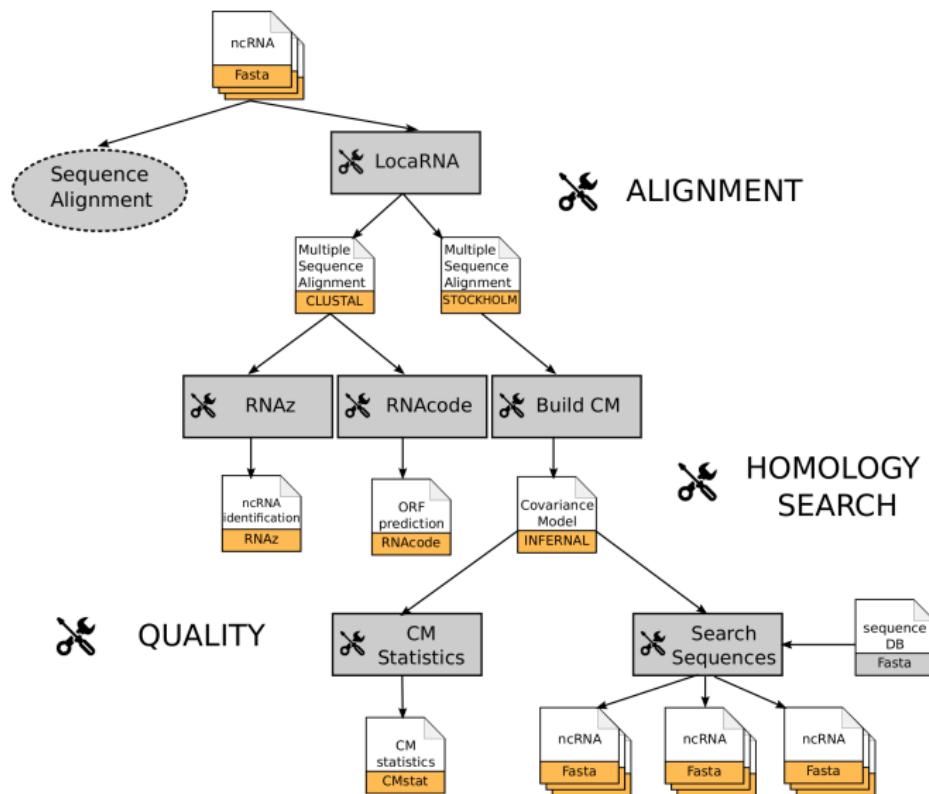
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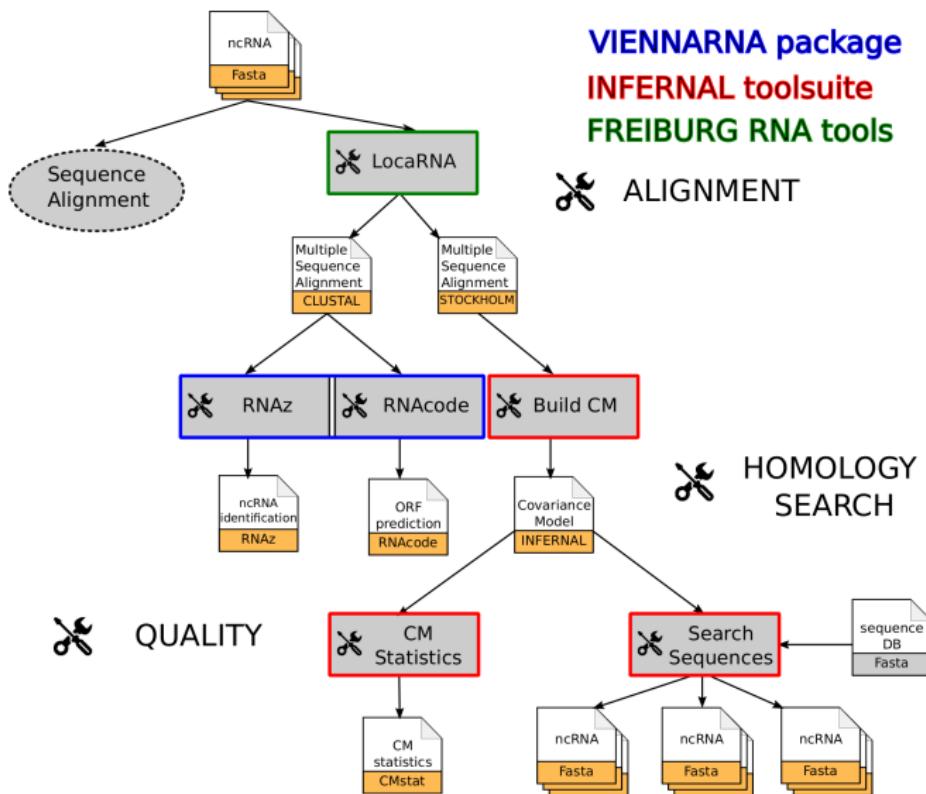
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Workflow - RNA family model construction

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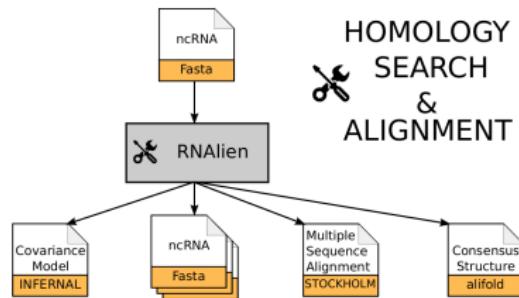
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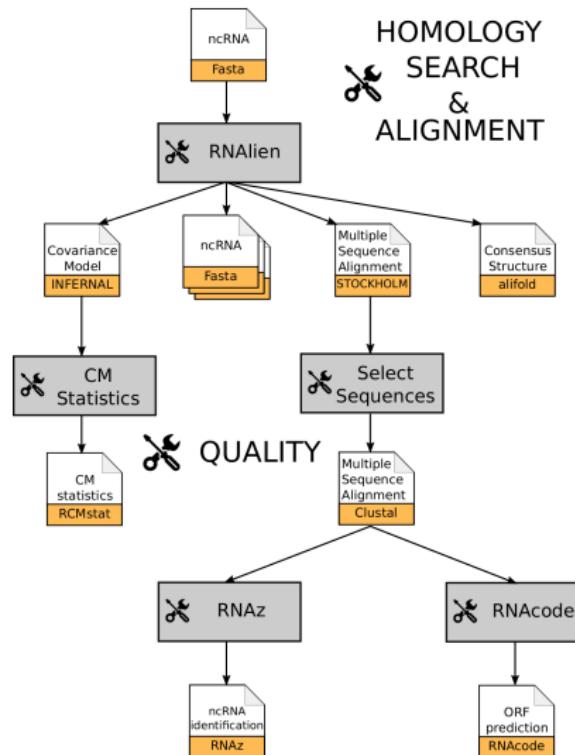
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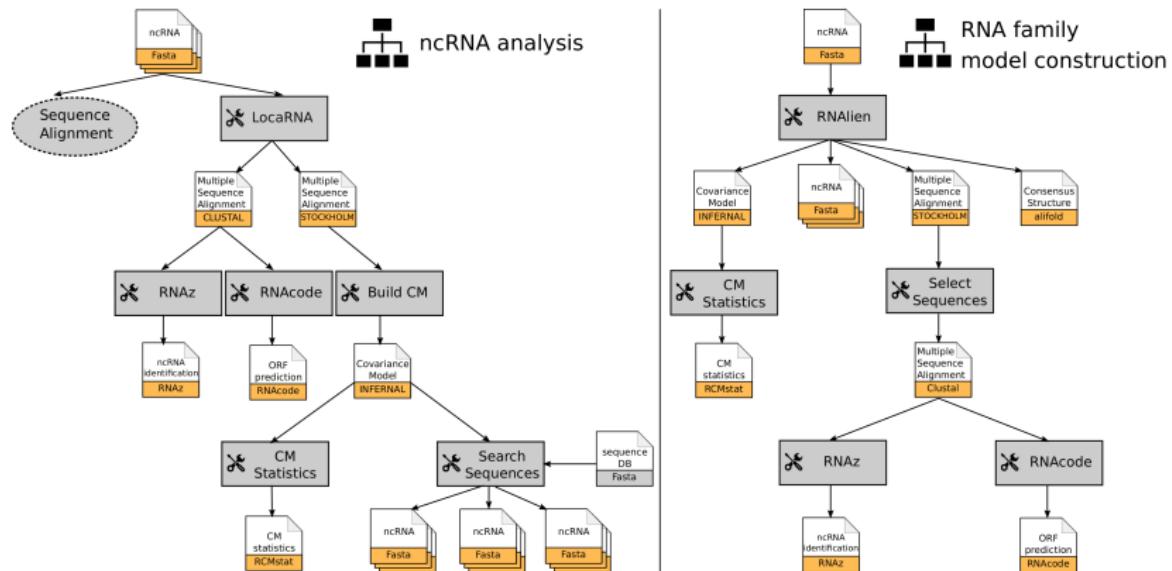


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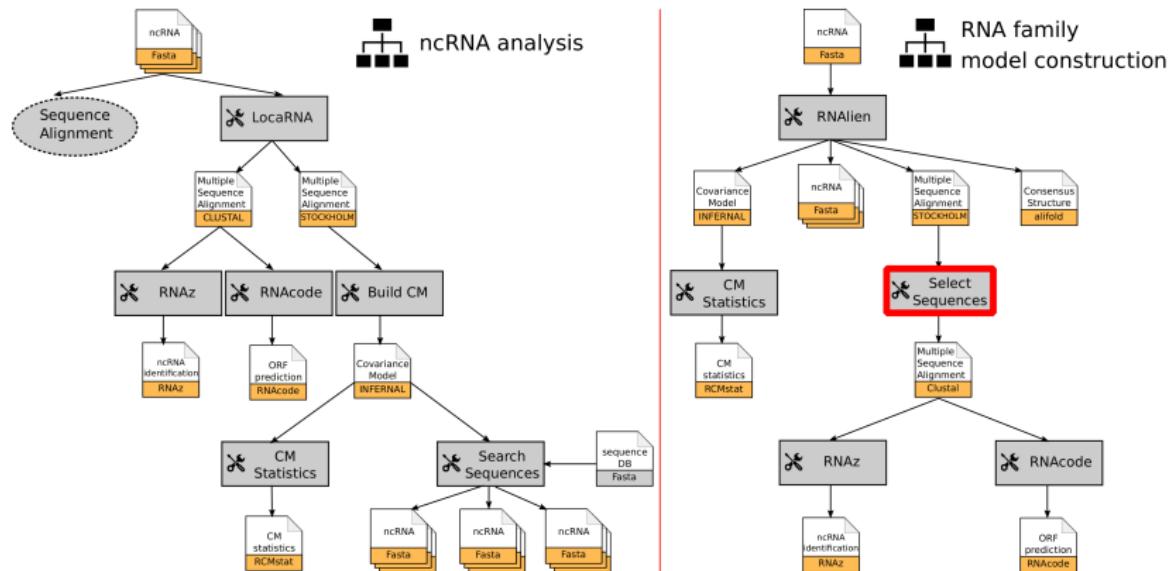
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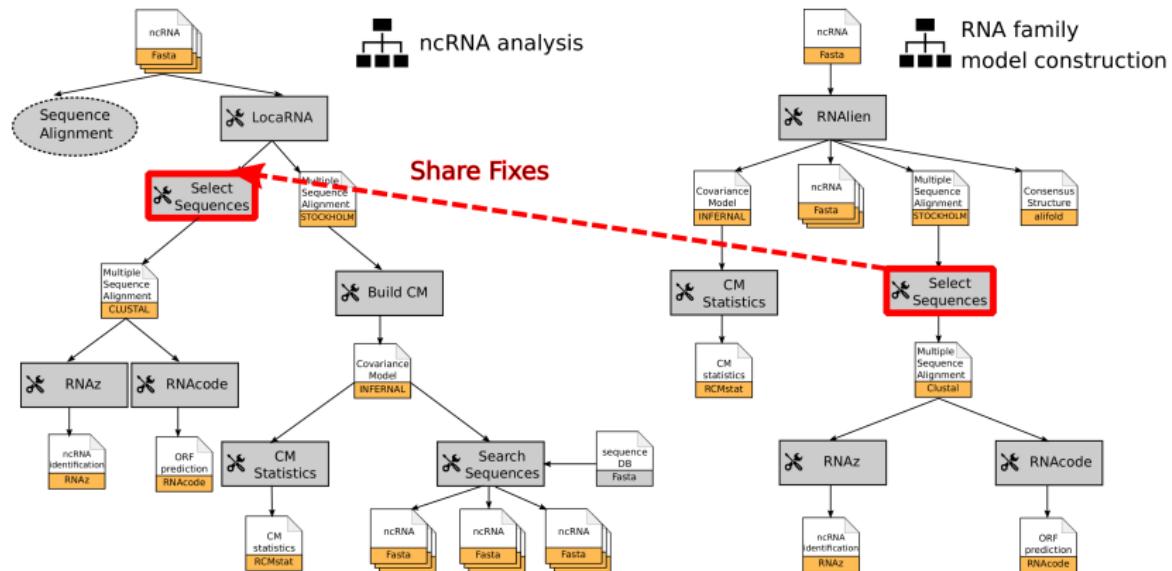
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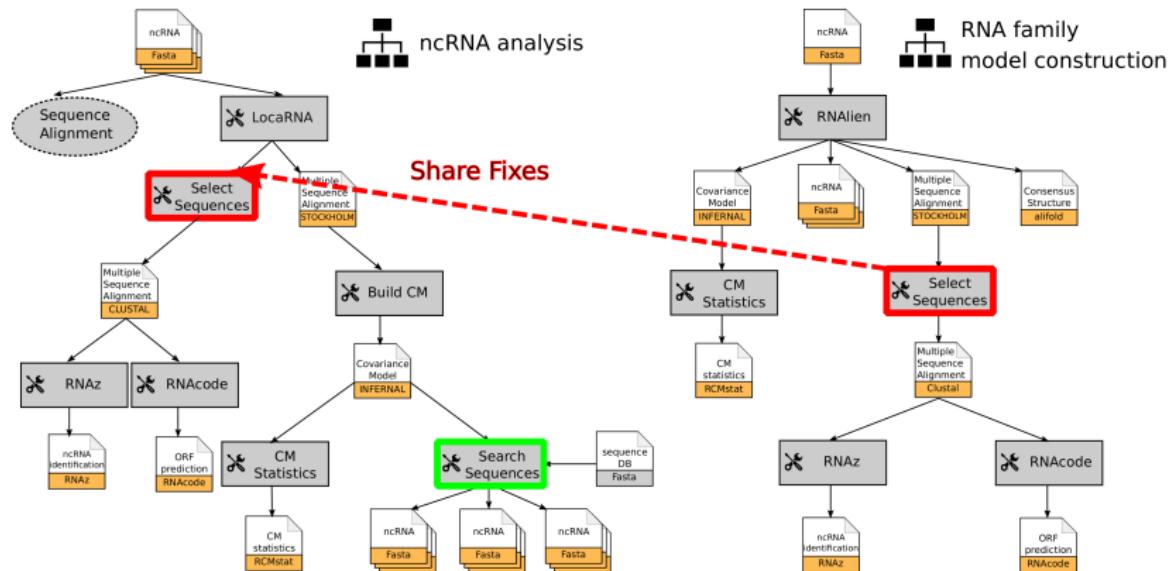
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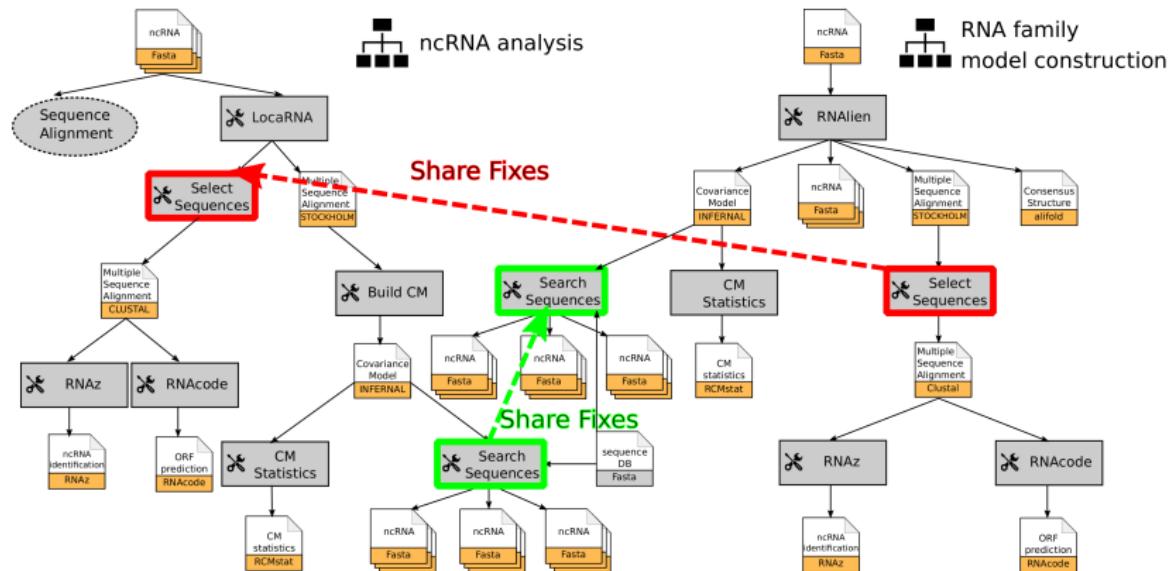
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Benefits from collaboration and integration

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Open participation, reward, and inclusion

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Using the workbench

- ▶ `docker run -d -p 8080:80 bgruening/galaxy-rna-workbench`

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- ▶ OSX and Windows using the graphical tool Kitematic

Acknowledgements & Thanks

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Wolfgang R. Hess, Olaf Wolkenhauer, Steve Hoffmann, Altuna Akalin,
Uwe Ohler, Peter F. Stadler, Rolf Backofen

Thank you for your attention!

RNA-seq analysis: trimming, mapping and read count

- ▶ Test for differential gene expression
- ▶ Quality control - Mapping & Annotation - Differential expression
- ▶ Template for customized workflows