

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

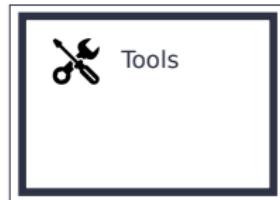
Lehrstuhl Bioinformatik
University of Freiburg

30.06.2017

Goals of the RNA Workbench



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- ▶ Comprehensive set of *RNA*-bioinformatics tools

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- ▶ Comprehensive set of *RNA*-bioinformatics tools
- ▶ Community - authors and users
- ▶ Set of predefined workflows and associated descriptions/training material
- ▶ Easy and stable dissemination via Galaxy

Tools

- More than **50** *RNA* bioinformatics tools

Tools

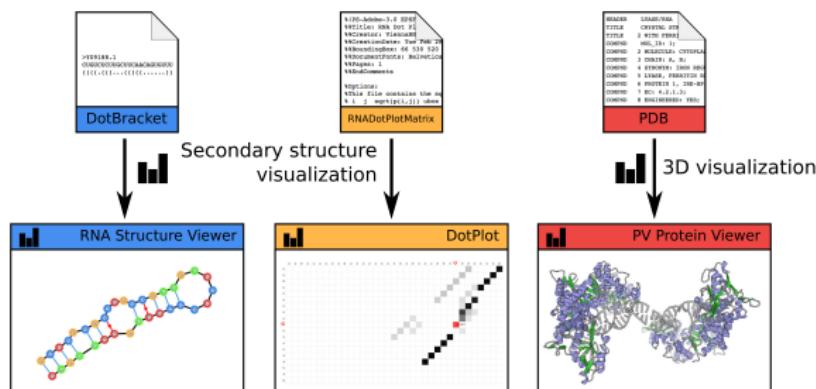
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- ▶ Classical *RNA* bioinformatics (INFERNAL, ViennaRNA, ...)

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- More than **50** RNA bioinformatics tools
- Classical *RNA* bioinformatics (INFERNAL, ViennaRNA, ..)
- *RNA*-seq analysis (FuMa, PARalyzer, ..)
- Integrated *RNA* visualization



Workflows

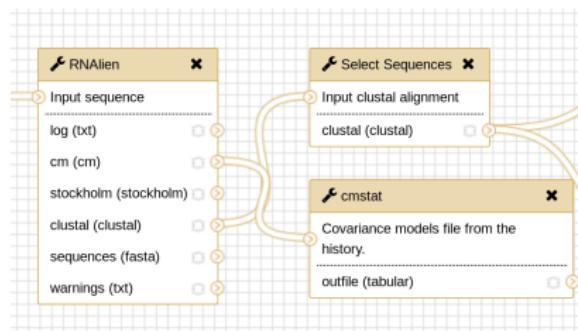
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Workflows

- ▶ Standardized analysis procedures
- ▶ Based on tools as building blocks

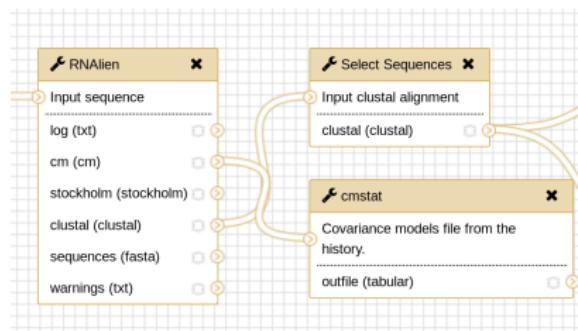
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- ▶ Can be developed, adapted and shared
(ToolShed/myexperiment.org)



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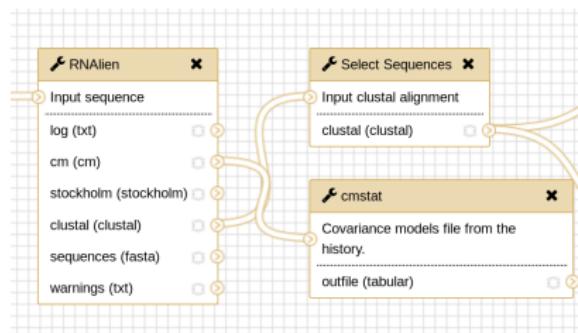
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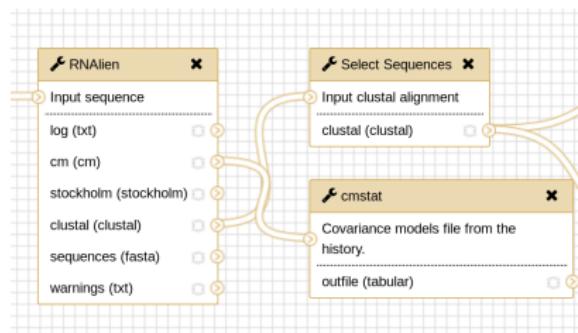
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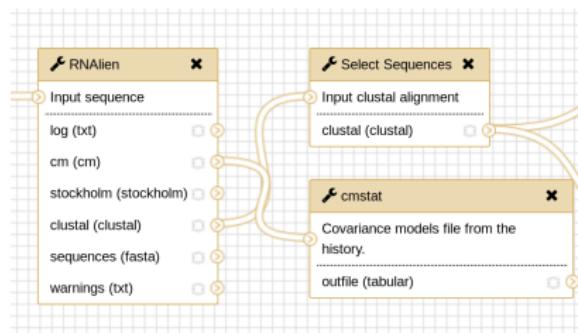
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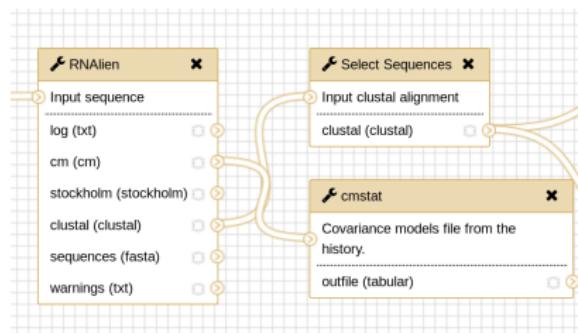
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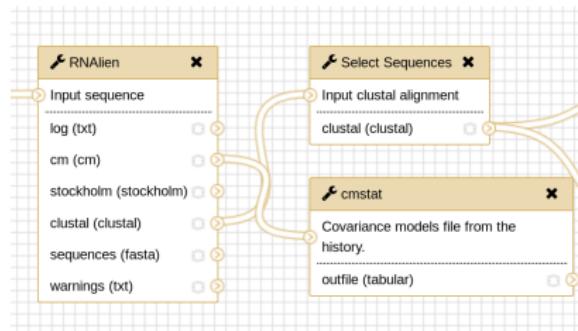
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 - ▶ C/D-box scan

Workflow - Analysis of non-coding RNAs

- ▶ Test for functional structure via conservation

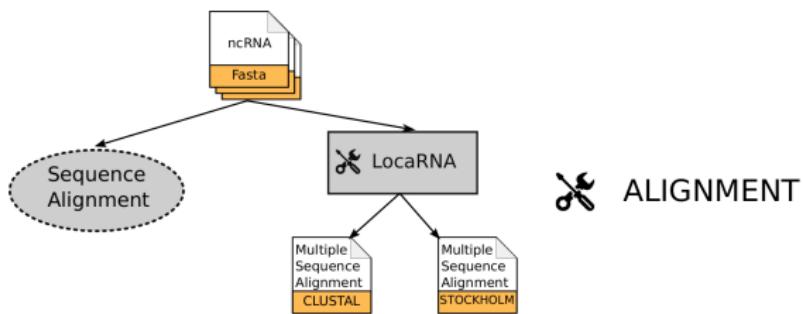
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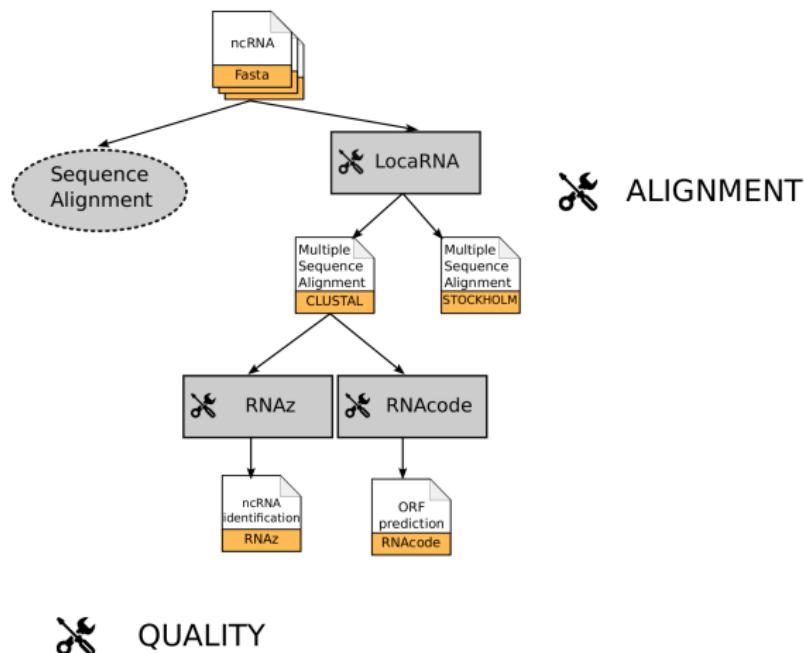
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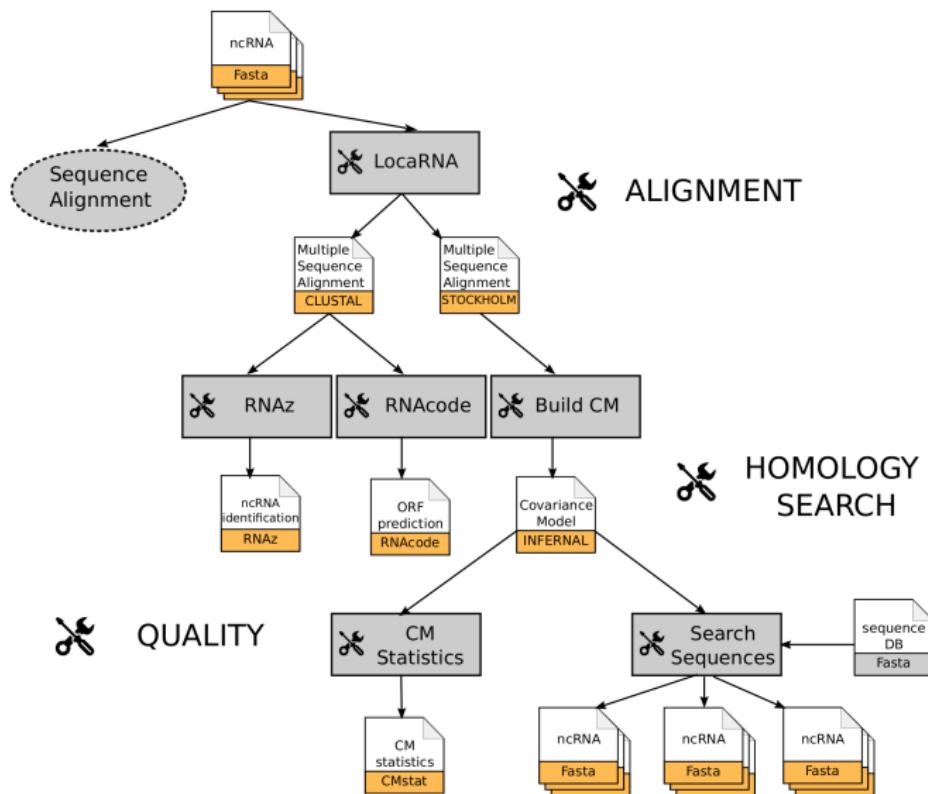
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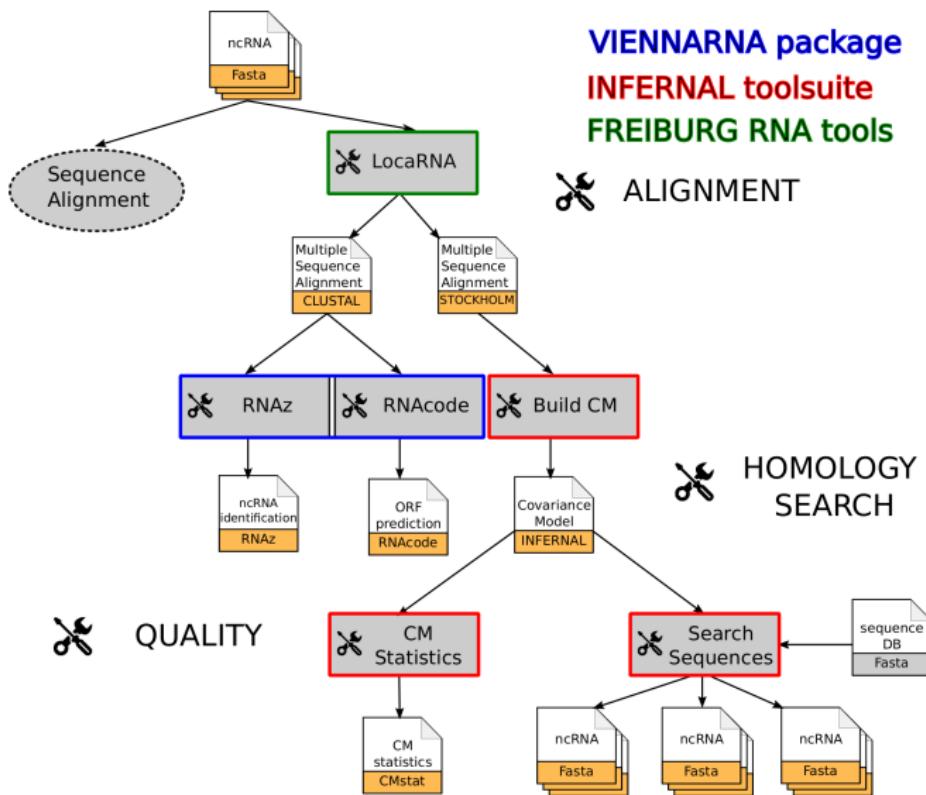
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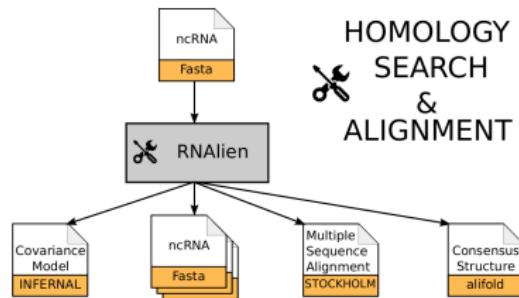
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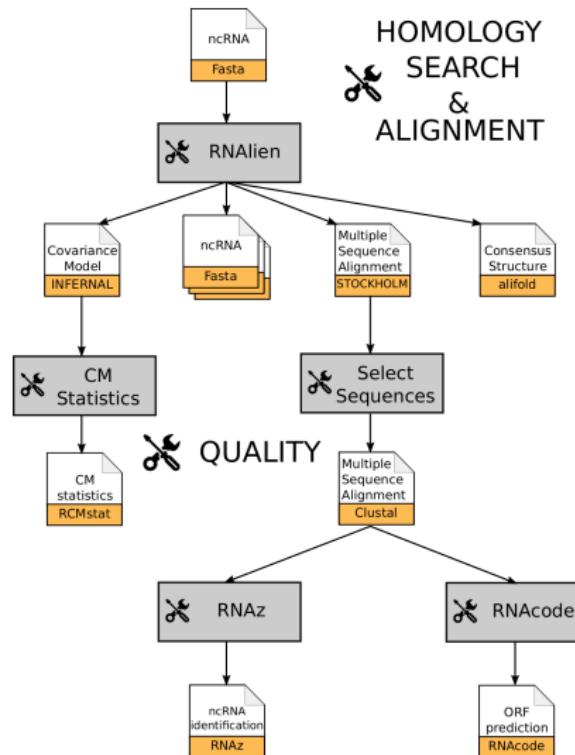
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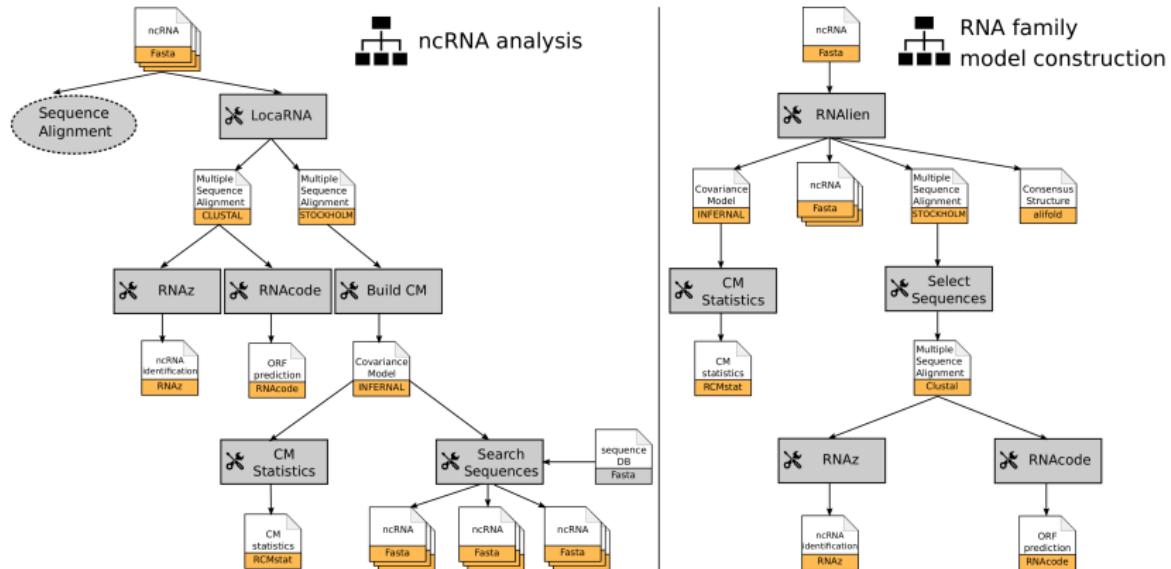


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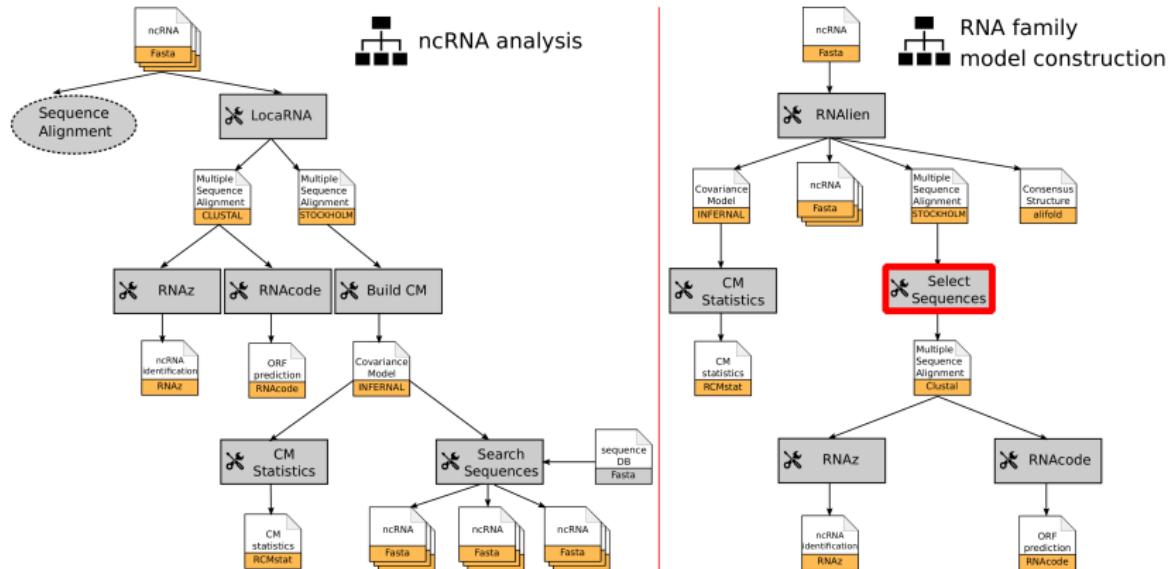
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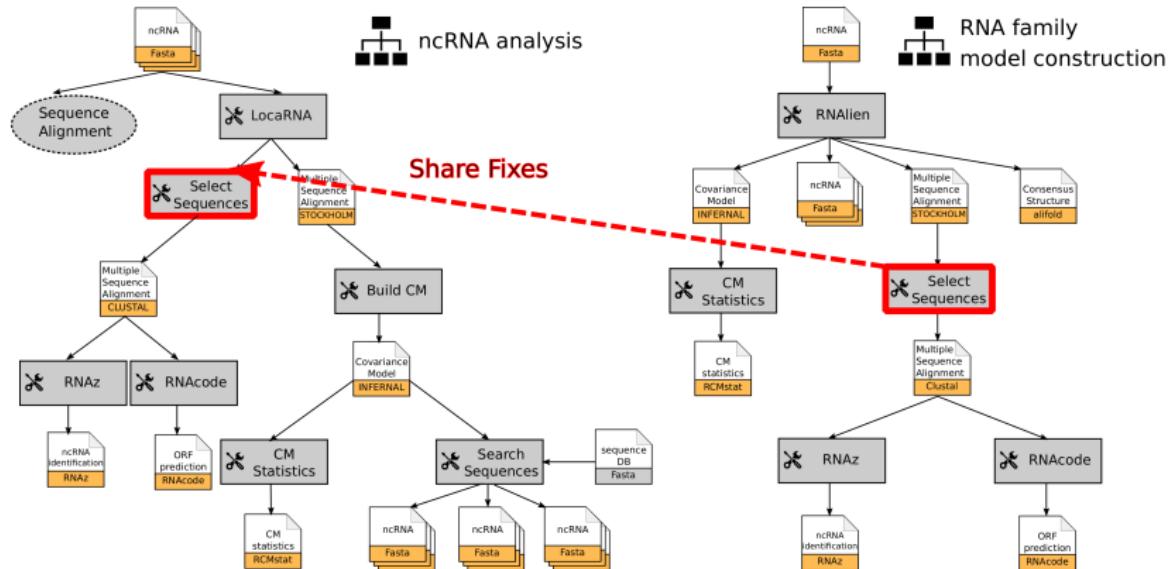
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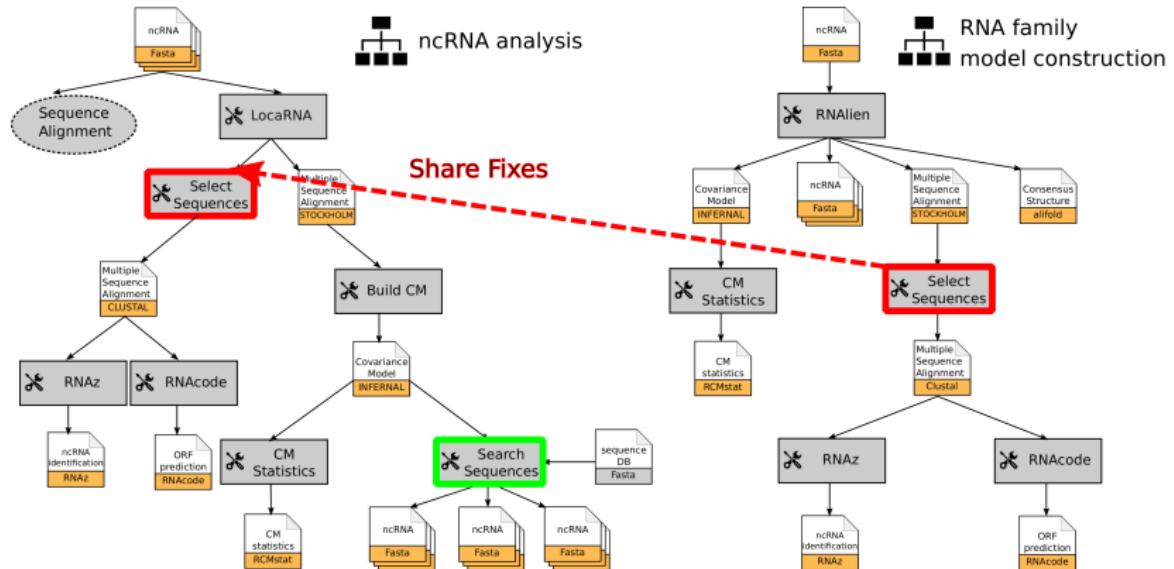
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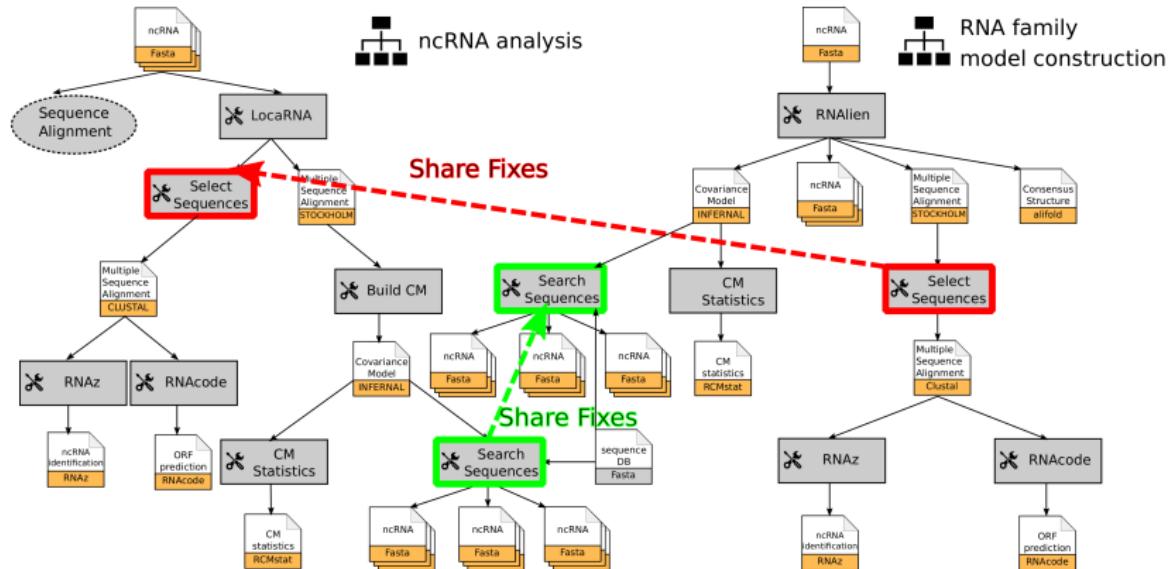
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54 contributors *Galaxy-tools*

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Open participation, reward, and inclusion

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- ▶ Training sessions (Introduction, HTS data and *RNA-seq* analyses)

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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

Björn A. Grüning, Jörg Fallmann, Dilmurat Yusuf, Sebastian Will,
Anika Erxleben, Torsten Houwaart, Bérénice Batut, Pavankumar Videm,
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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