

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

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and the RNA Workbench Team

Lehrstuhl Bioinformatik
University of Freiburg

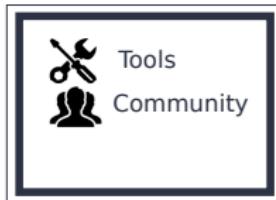
30.06.2017

Goals of the RNA Workbench



- ▶ Comprehensive set of *RNA*-bioinformatics tools

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

Tools

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

Tools

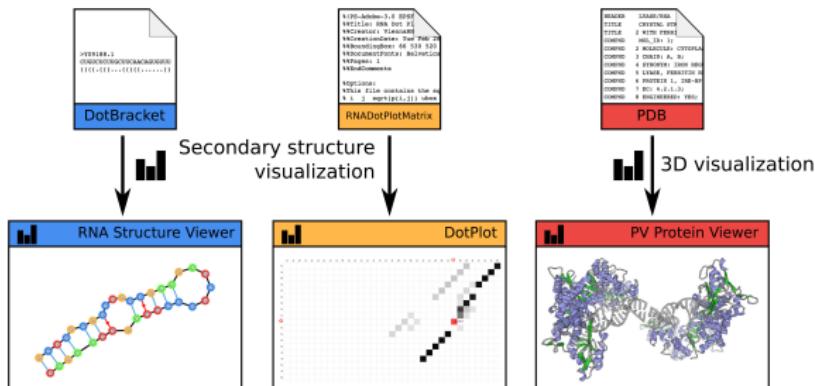
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- More than **50** RNA bioinformatics tools
- Classical *RNA* bioinformatics (INFERNAL, ViennaRNA, ..)
- *RNA-seq* analysis (FuMa, PARalyzer, Star, DEseq, ..)
- Integrated *RNA* visualization



Workflows

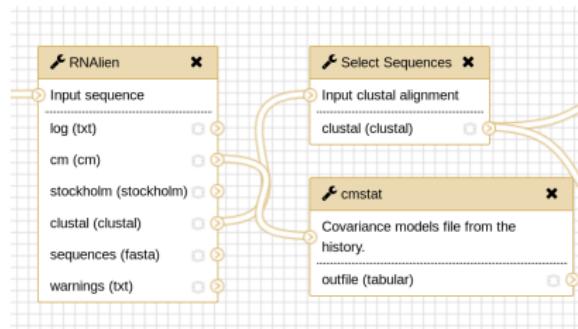
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- ▶ Based on tools as building blocks

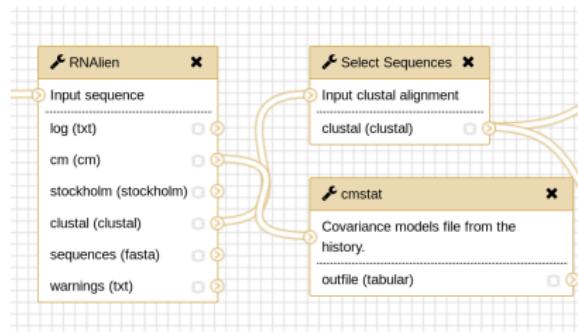
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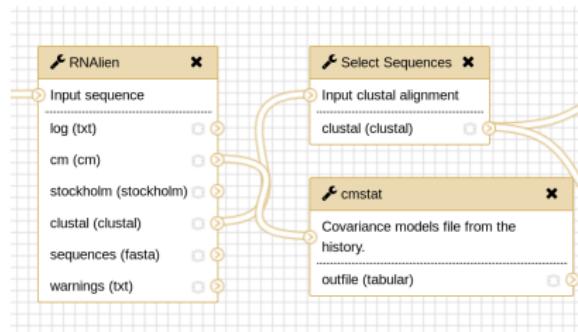
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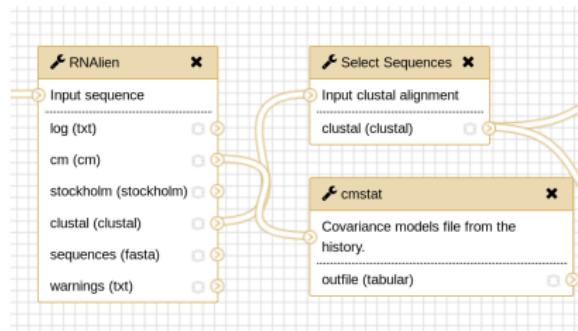
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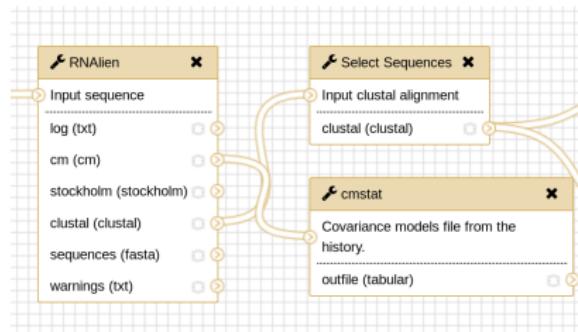
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 - ▶ *RNA* model construction

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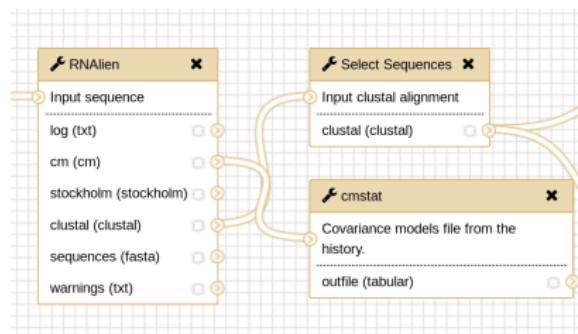
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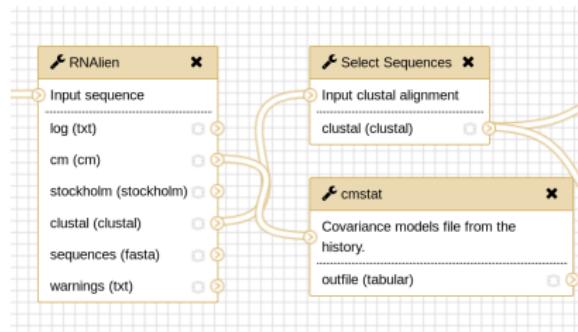
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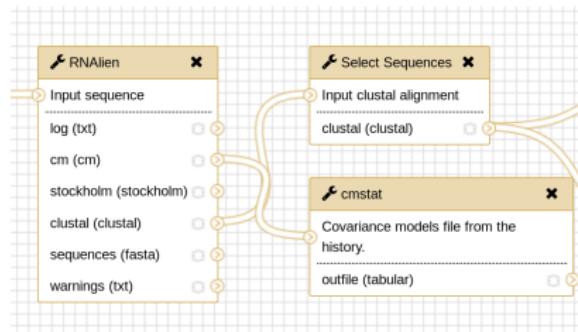
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Workflow - Analysis of non-coding RNAs

- ▶ Test for functional structure via conservation

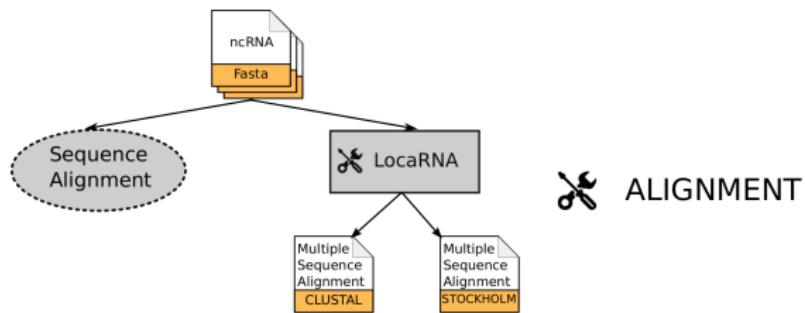
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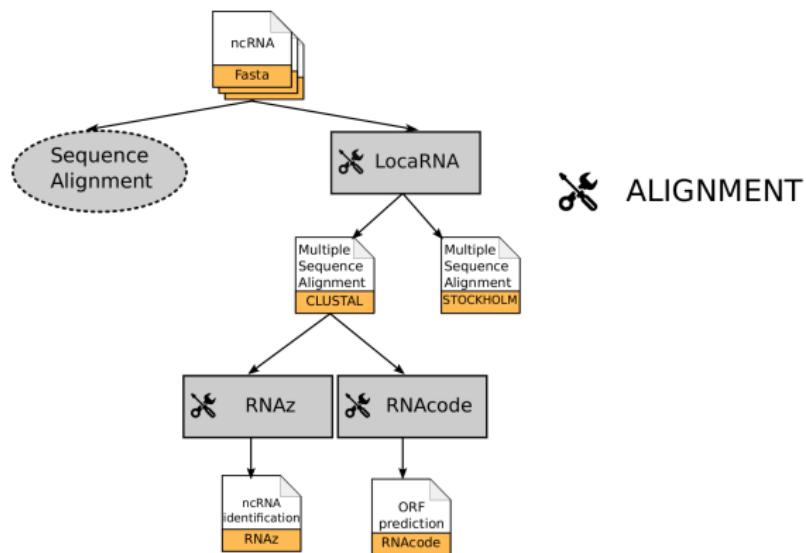
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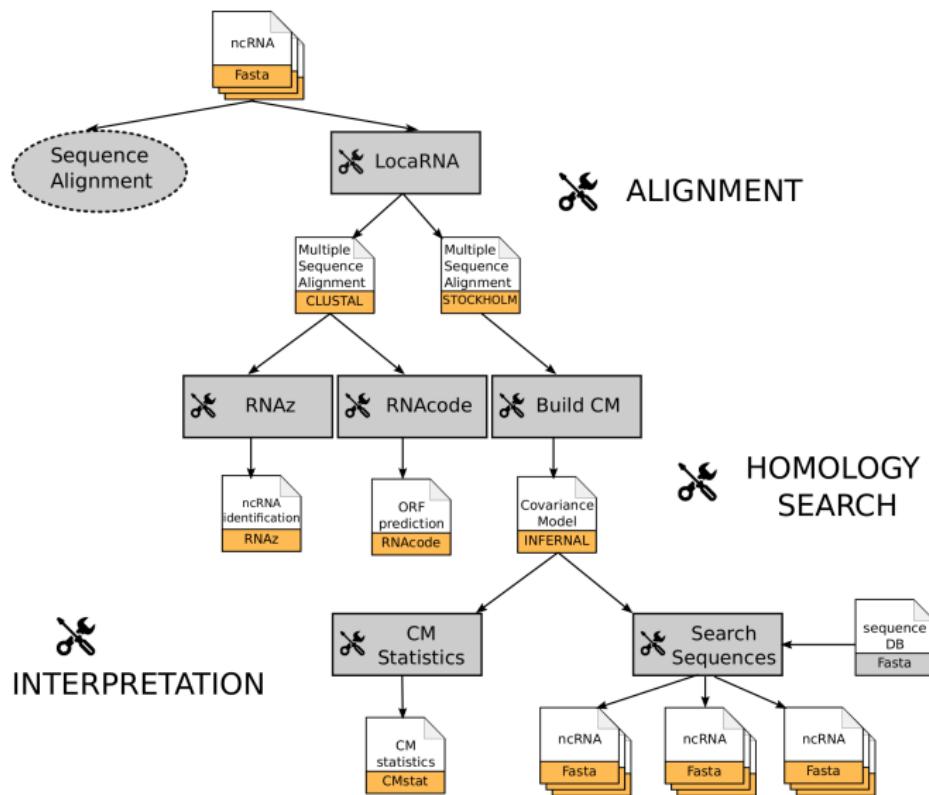
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✂ INTERPRETATION

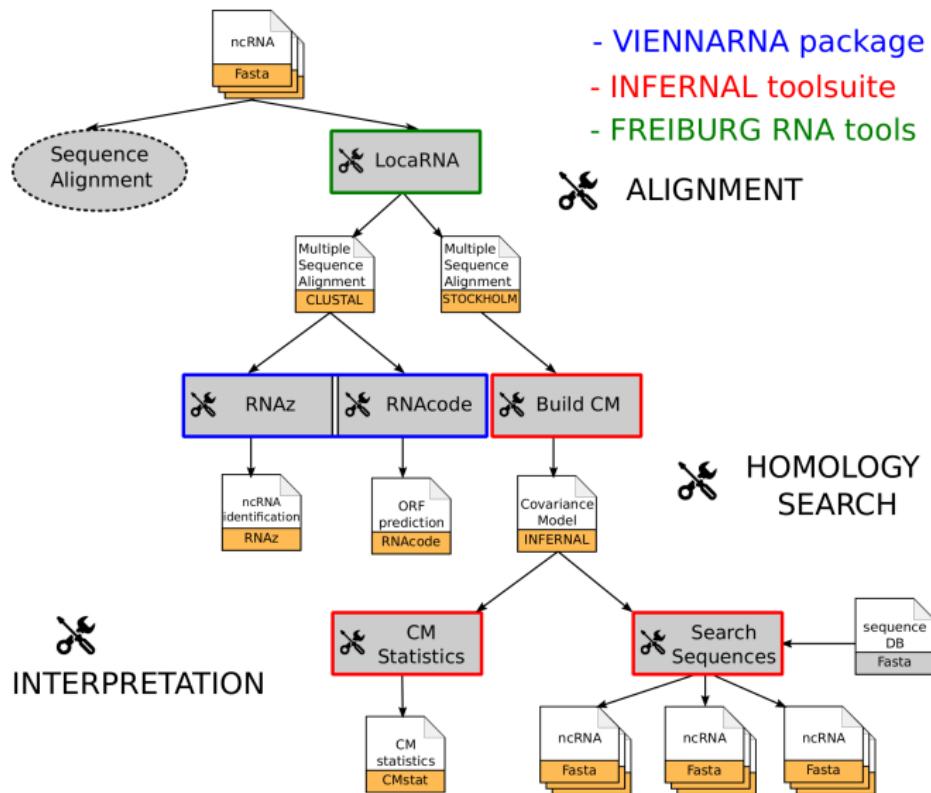
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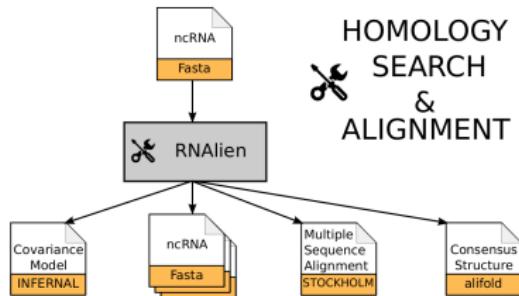
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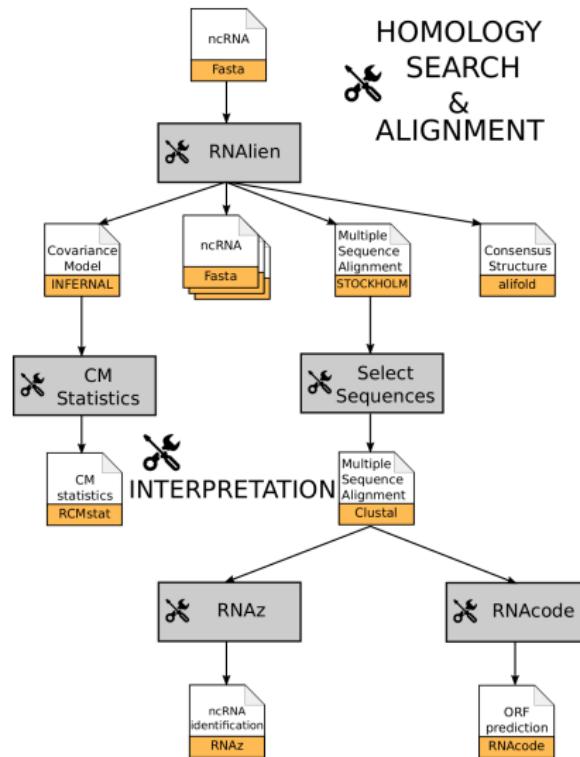
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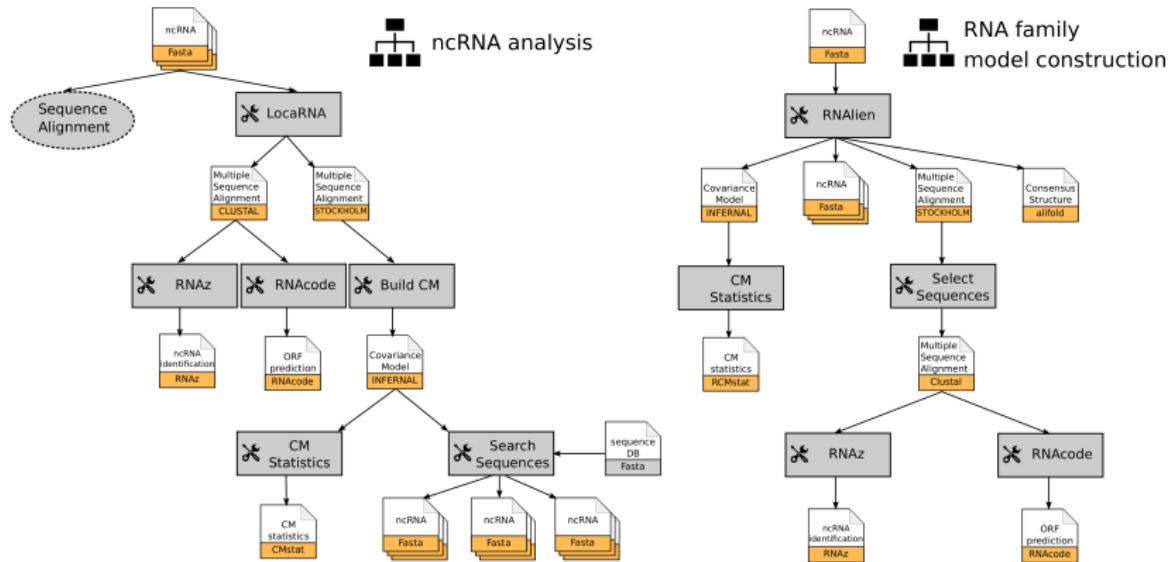


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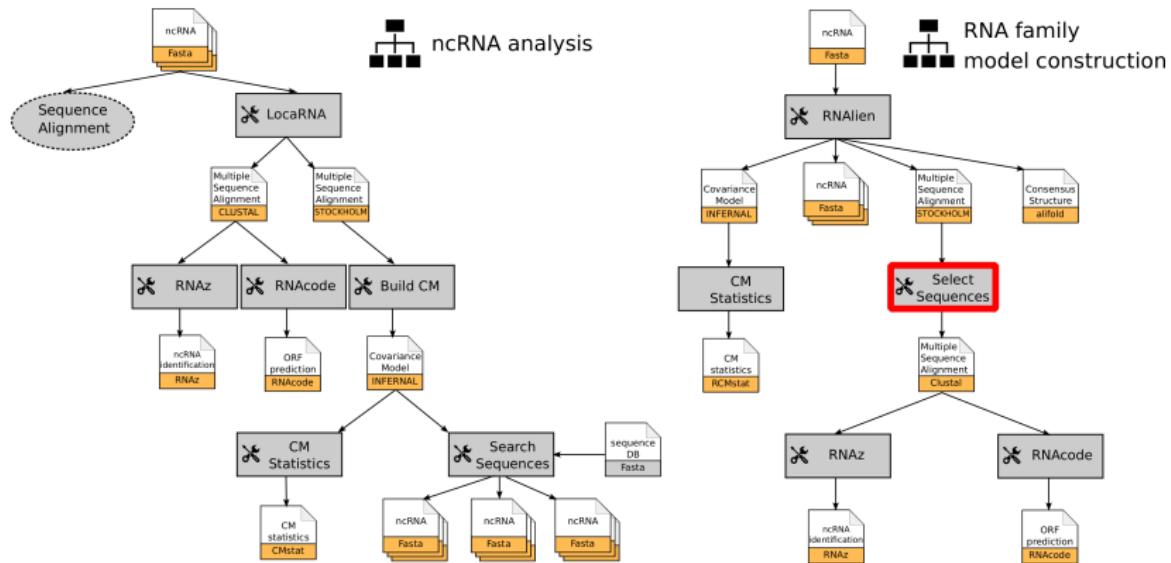
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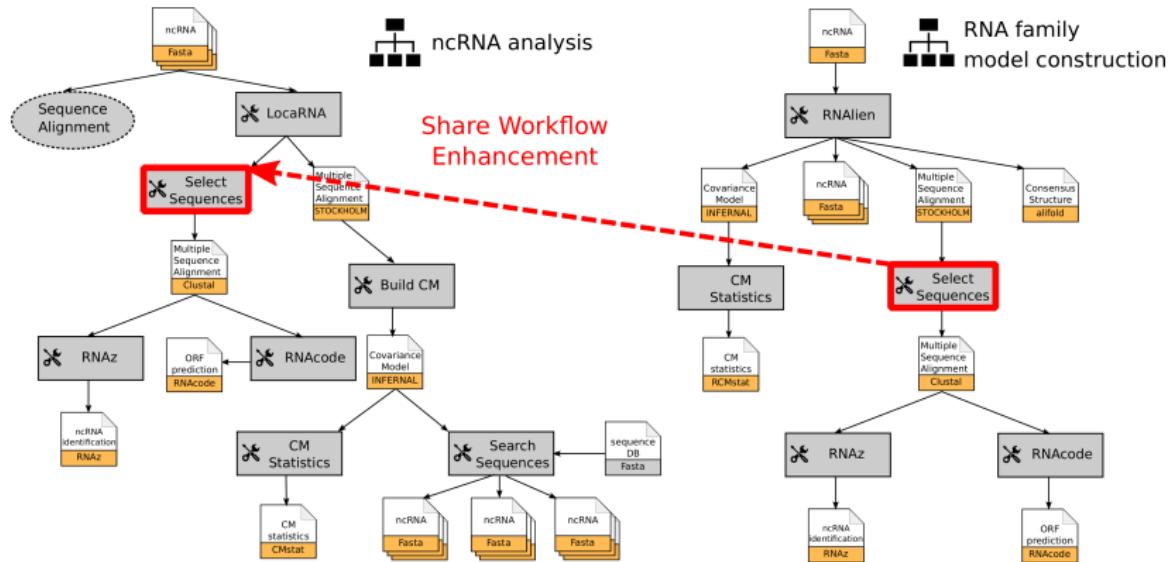
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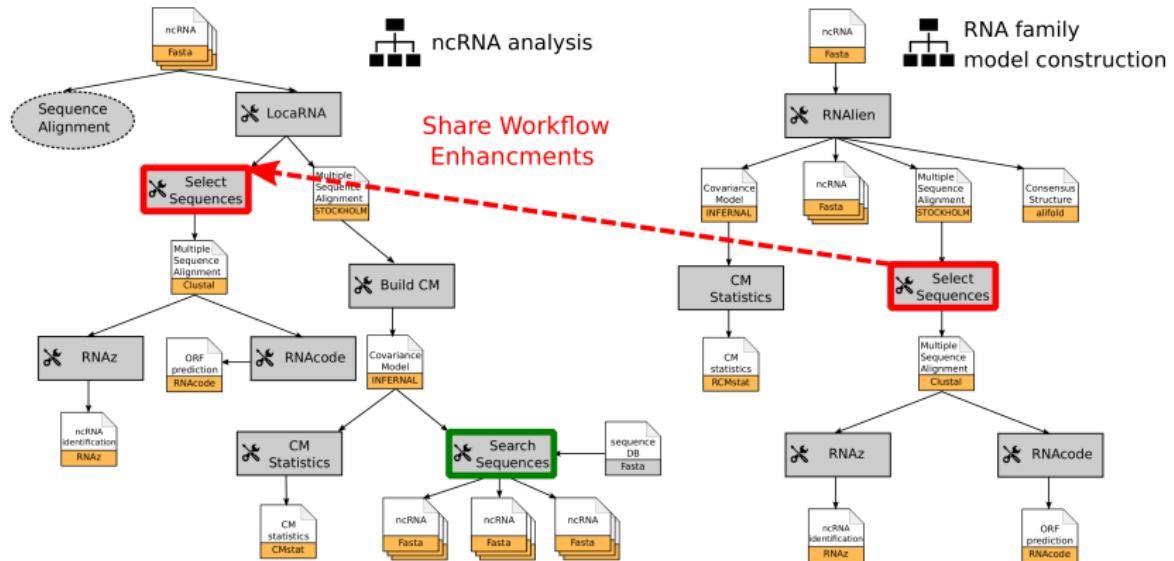
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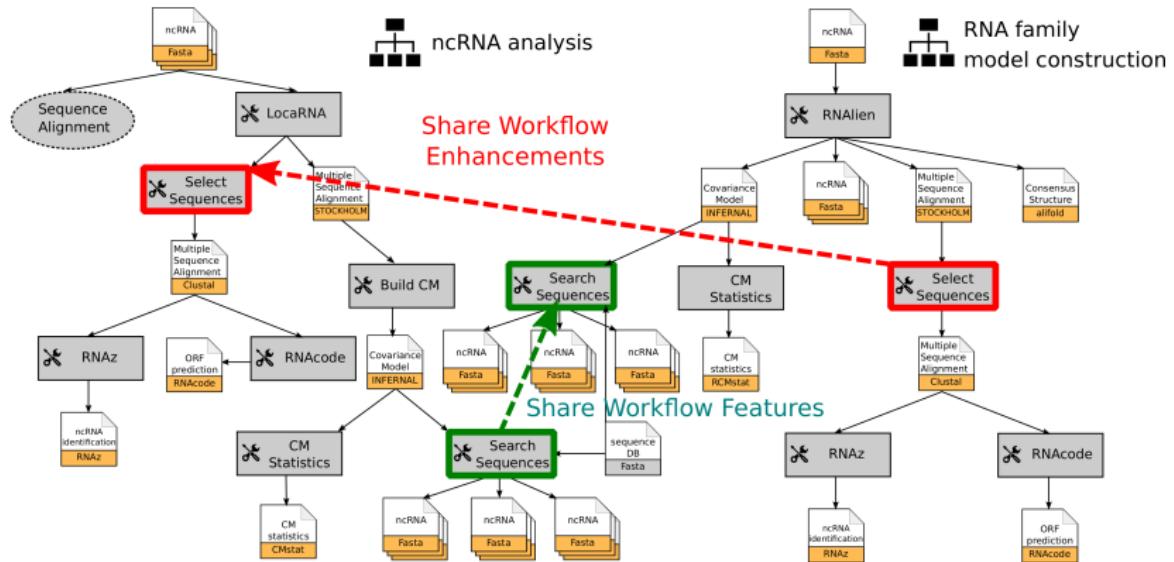
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Open participation, reward, and inclusion

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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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Uwe Ohler, Peter F. Stadler, Rolf Backofen

Thank you for your attention!

The RNA workbench: best practices for RNA
and high-throughput sequencing bioinformatics in Galaxy.
Nucleic Acids Res 2017 gkx409.
doi: 10.1093/nar/gkx409

RNA-seq analysis: trimming, mapping and read count

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