

# **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

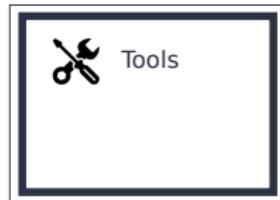
Lehrstuhl Bioinformatik  
University of Freiburg

30.06.2017

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- ▶ 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

# Tools

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

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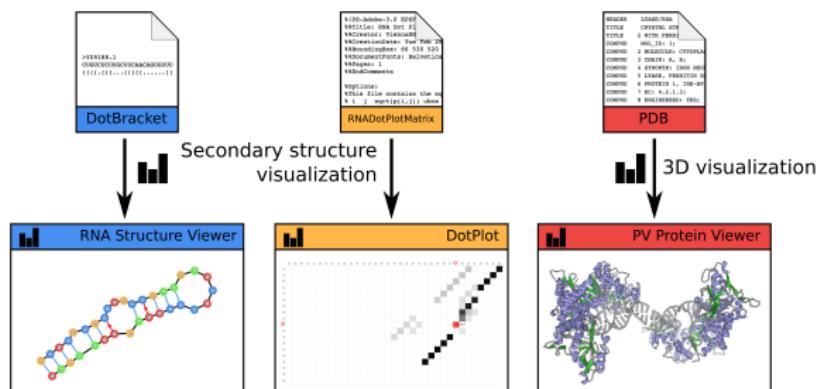
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- Classical *RNA* bioinformatics (INFERNAL, ViennaRNA, ...)
- *RNA*-seq analysis (FuMa, PARalyzer, ...)
- Integrated *RNA* visualization



# Workflows

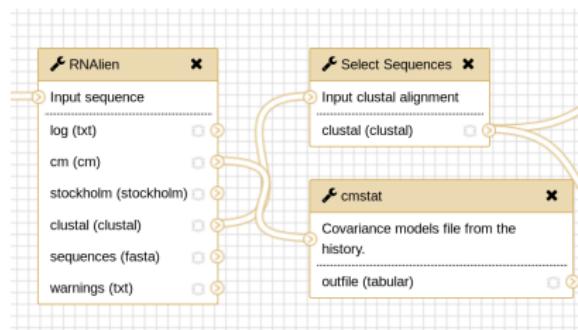
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- ▶ Based on tools as building blocks

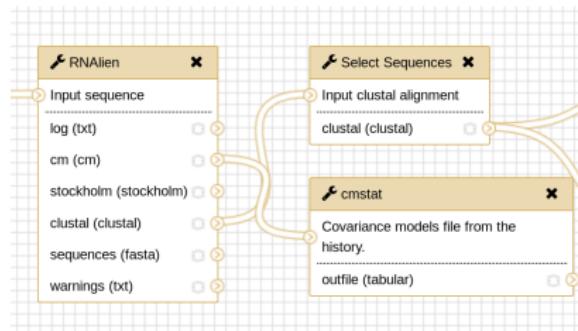
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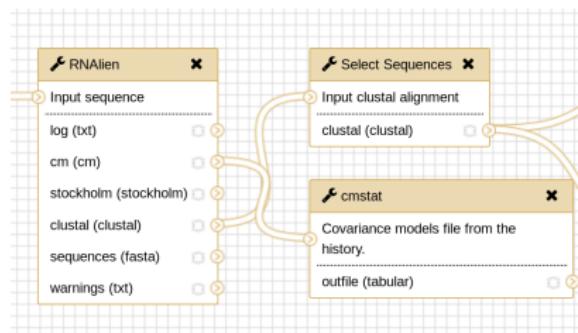
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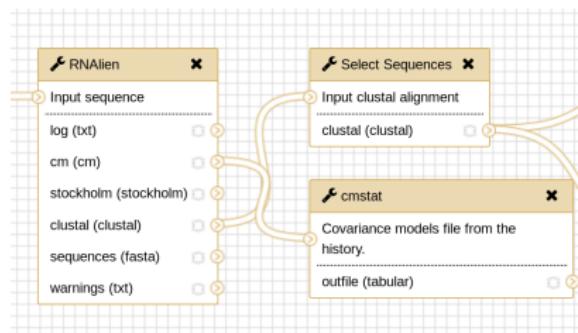
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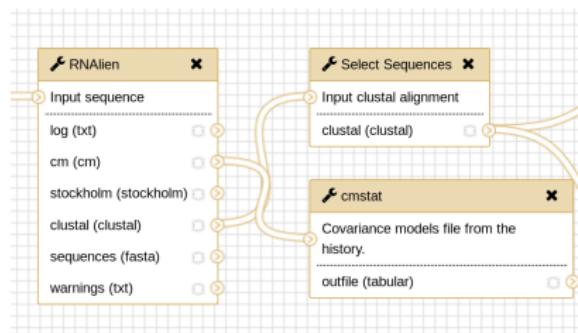
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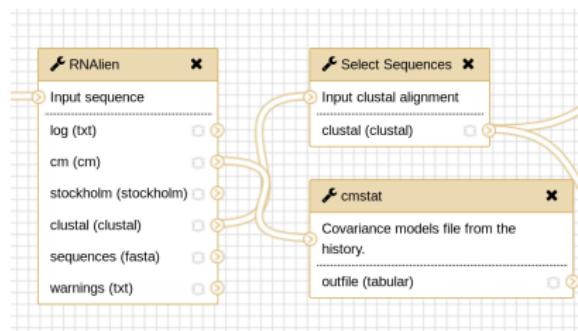
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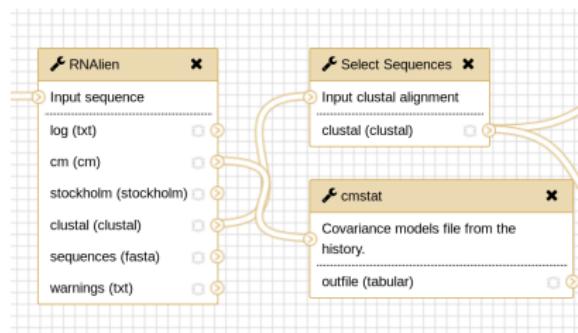
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  - ▶ C/D-box scan

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- ▶ Test for functional structure via conservation

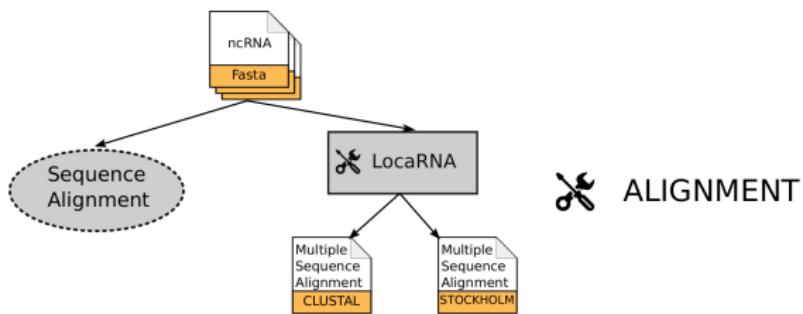
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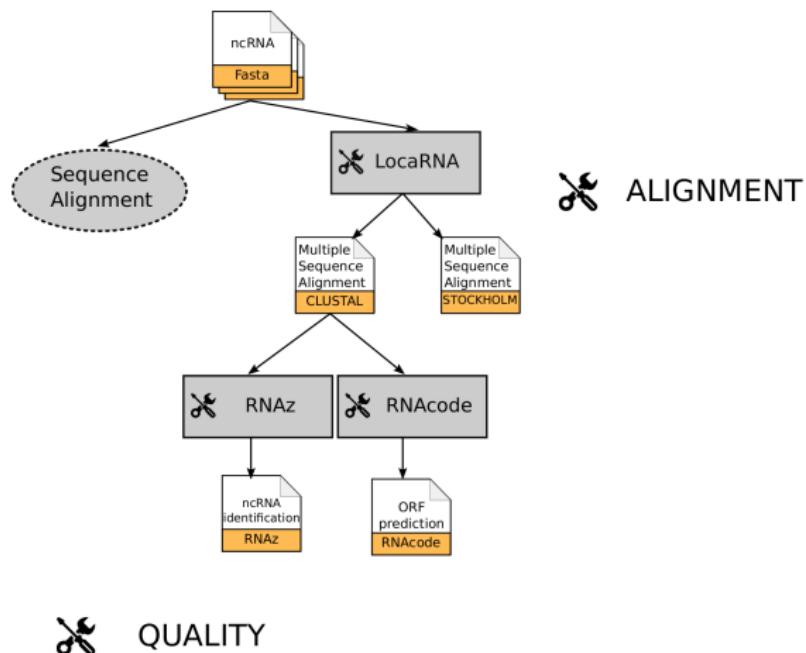
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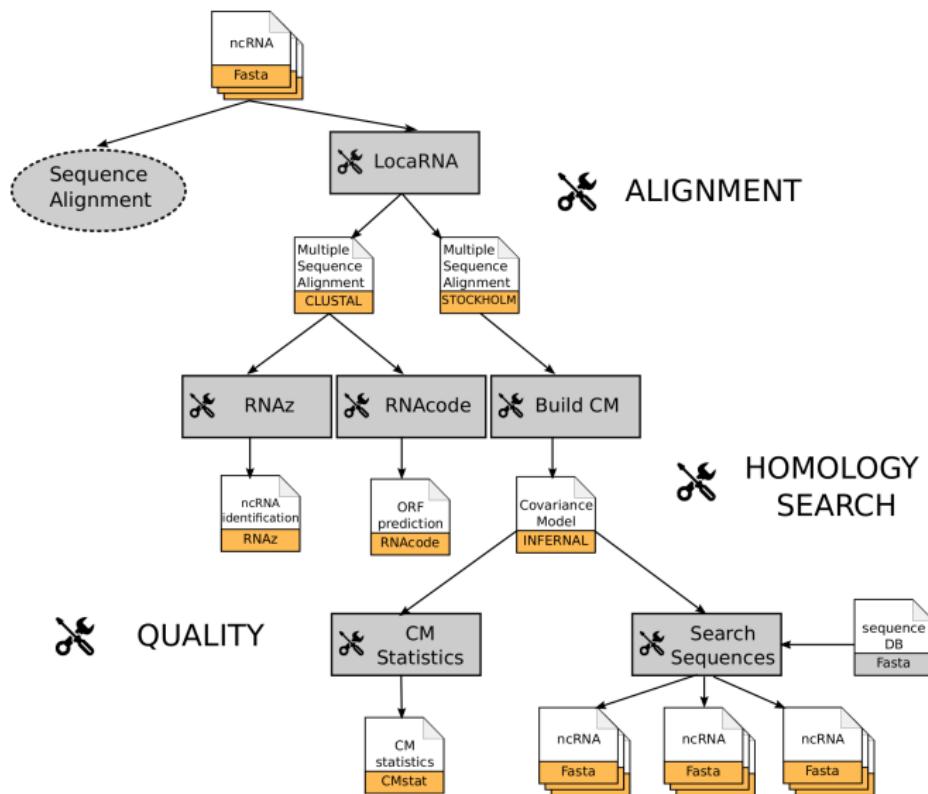
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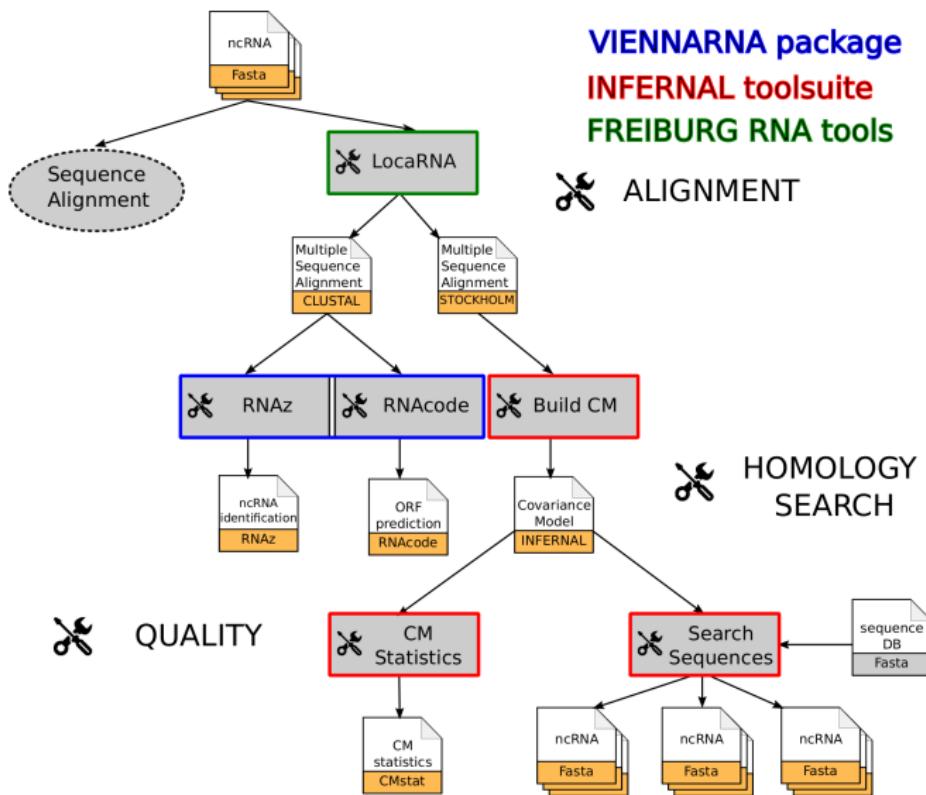
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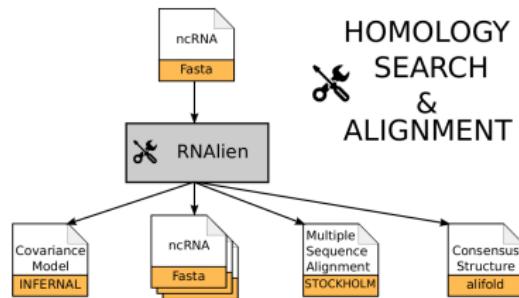
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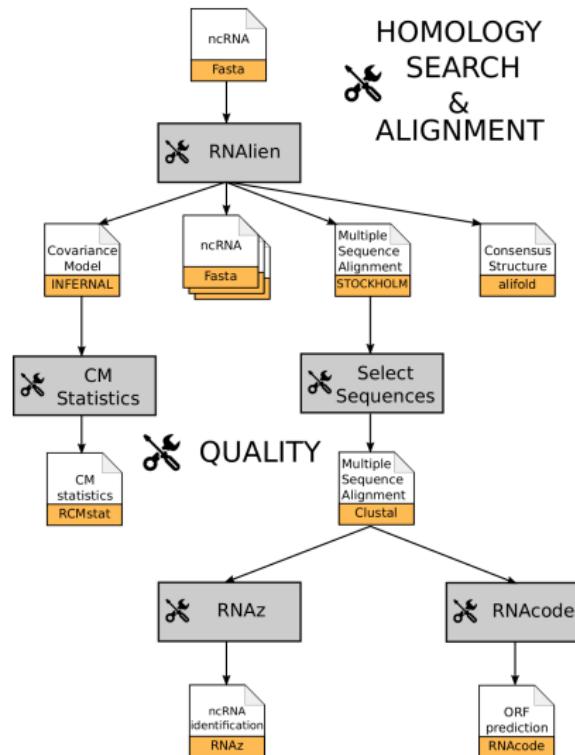
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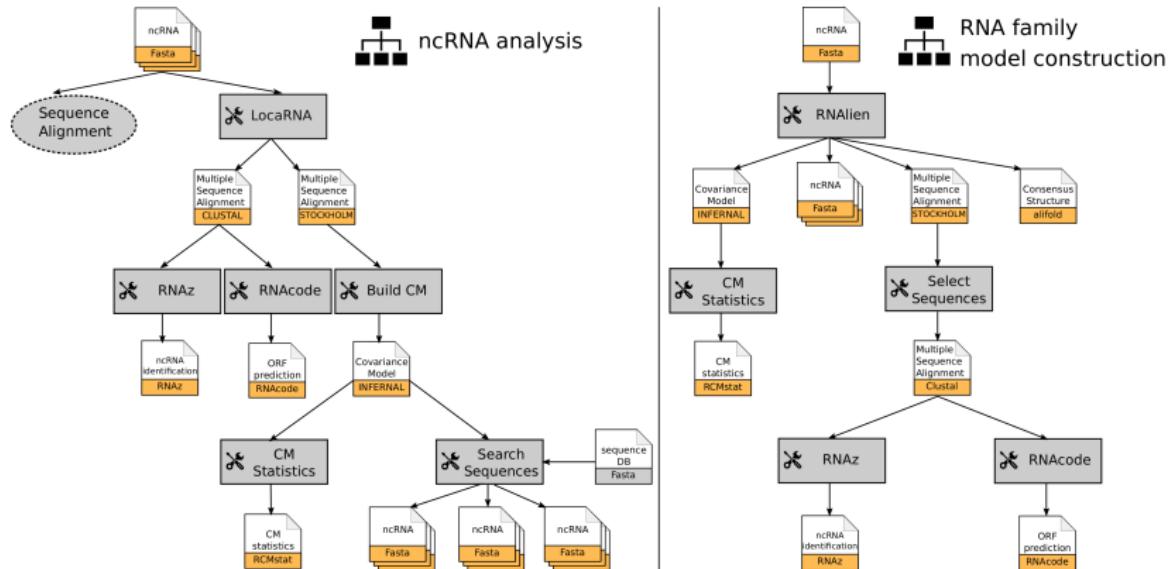


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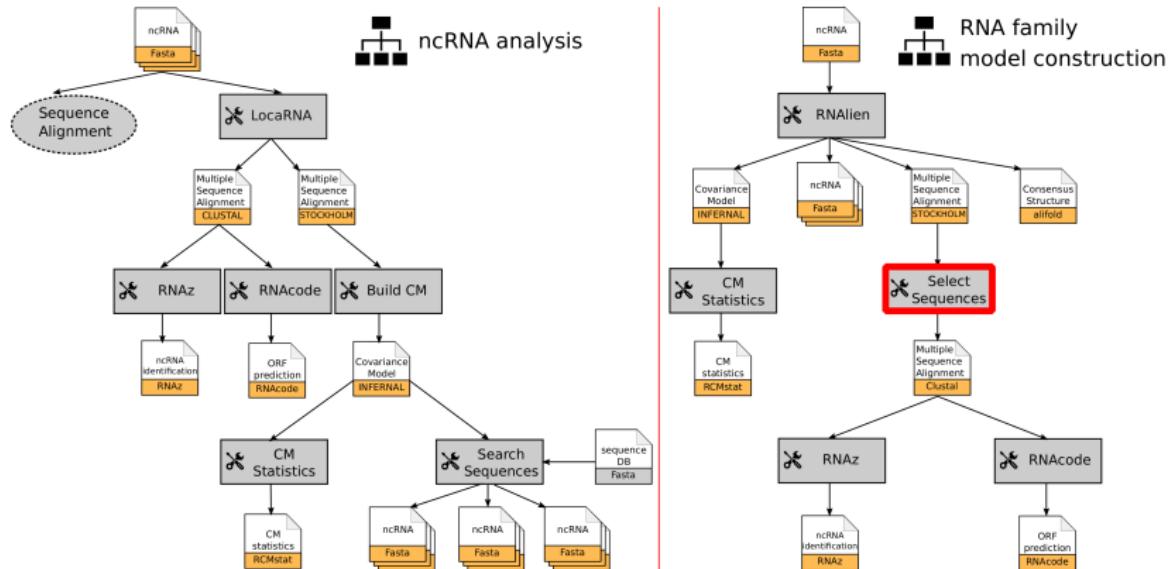
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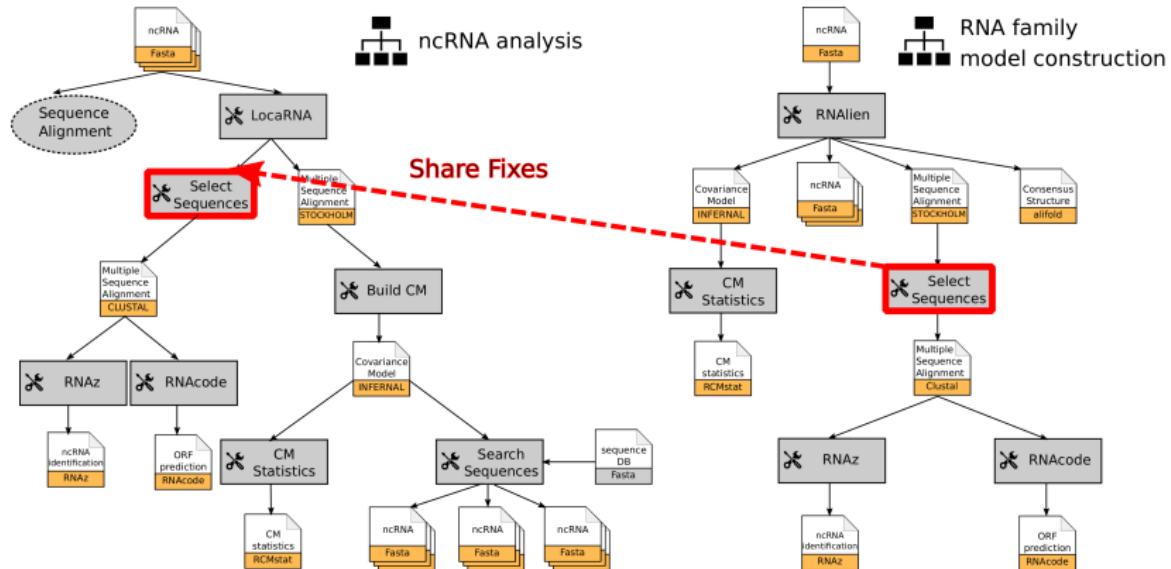
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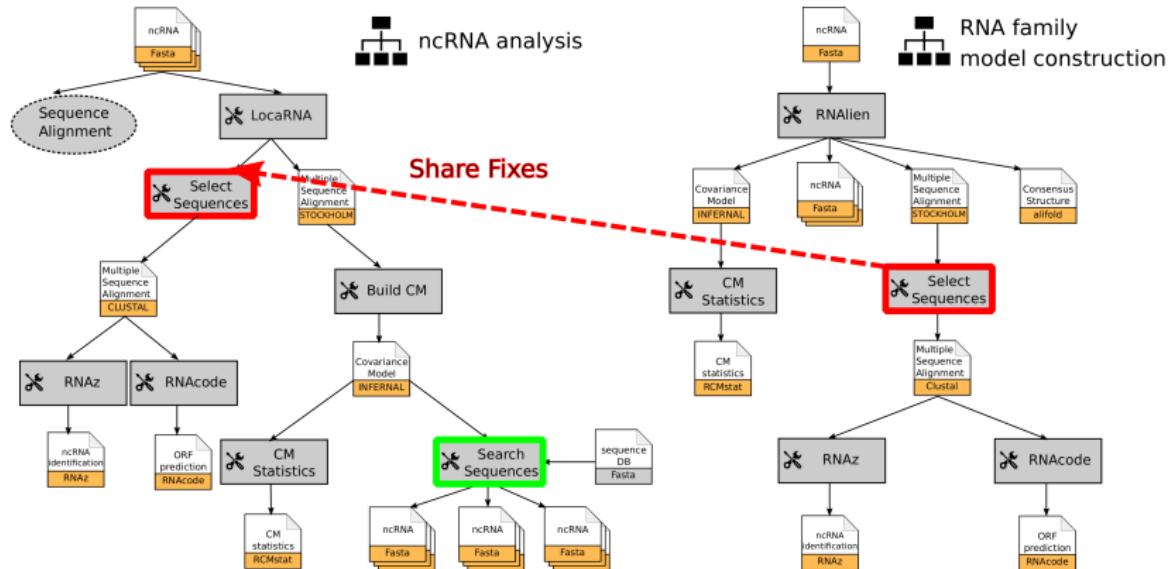
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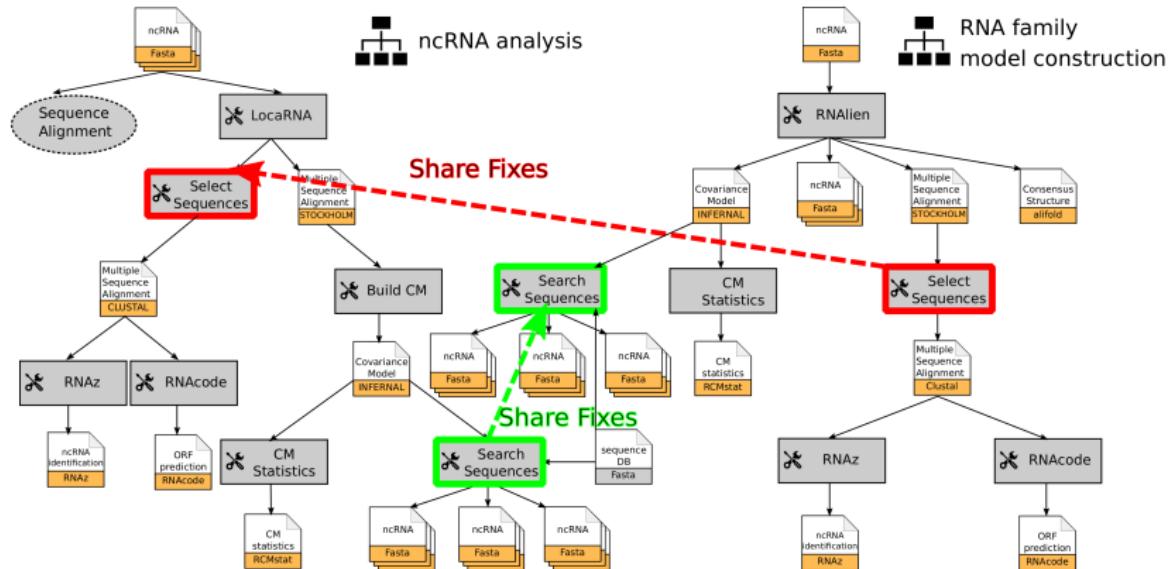
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- ▶ Authors keep tools updated

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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