

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

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and the RNA Workbench Team

Lehrstuhl Bioinformatik  
University of Freiburg

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# Goals of the RNA Workbench



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- ▶ Community - authors and users
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- ▶ Easy and stable dissemination via Galaxy

# Tools

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

# Tools

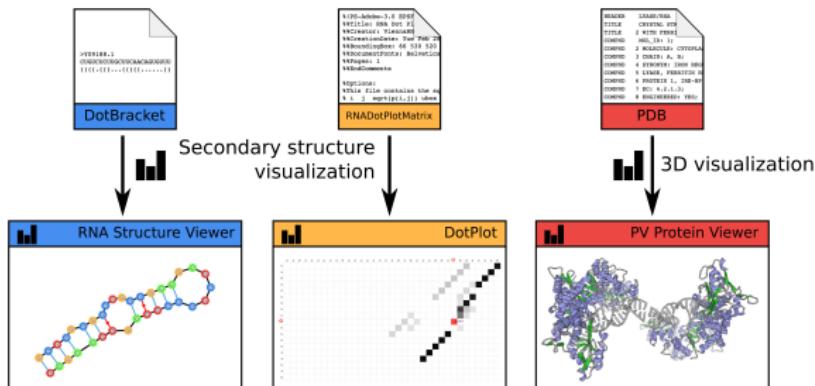
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# Tools

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



# Workflows

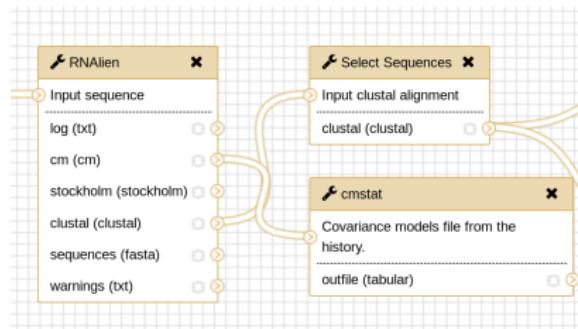
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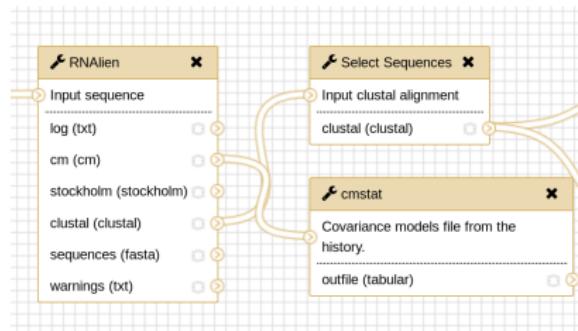
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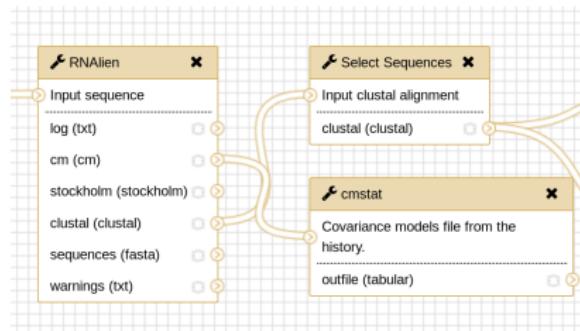
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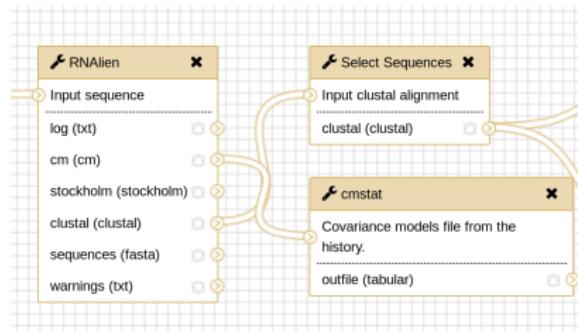
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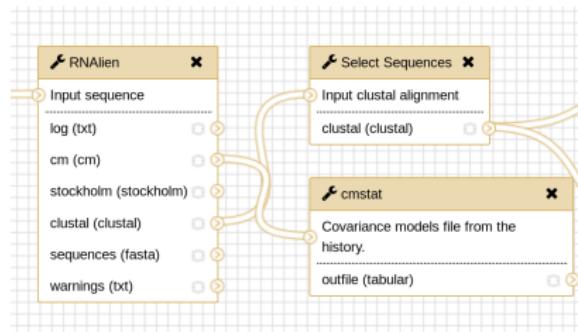
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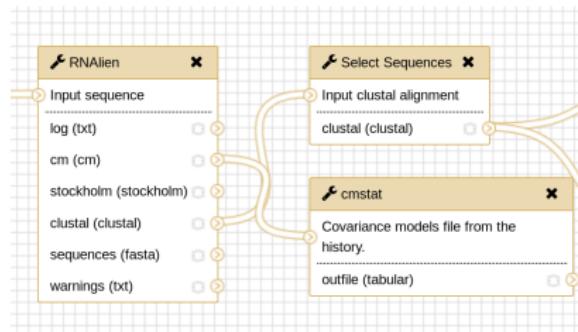
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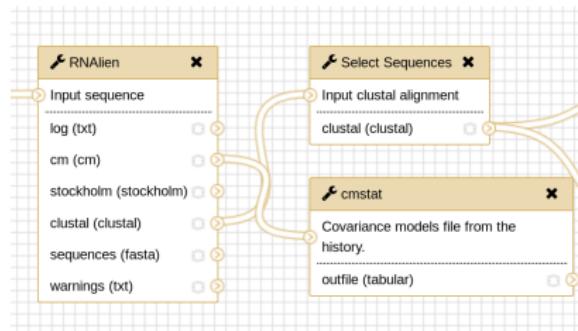
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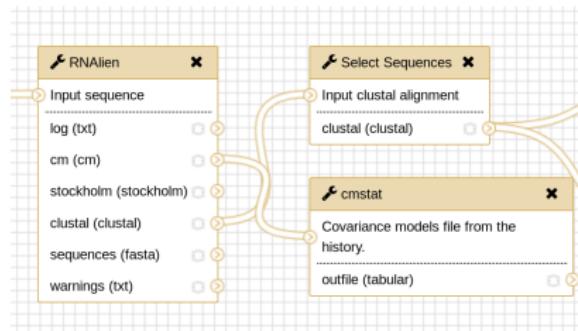
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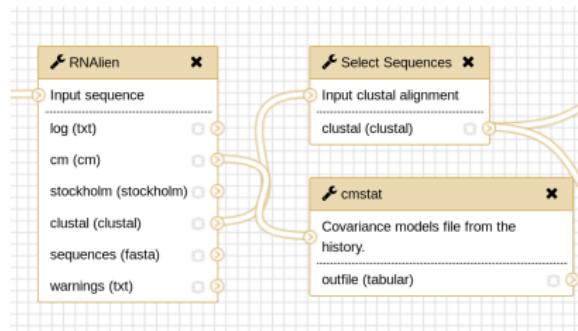
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- ▶ Test for functional structure via conservation

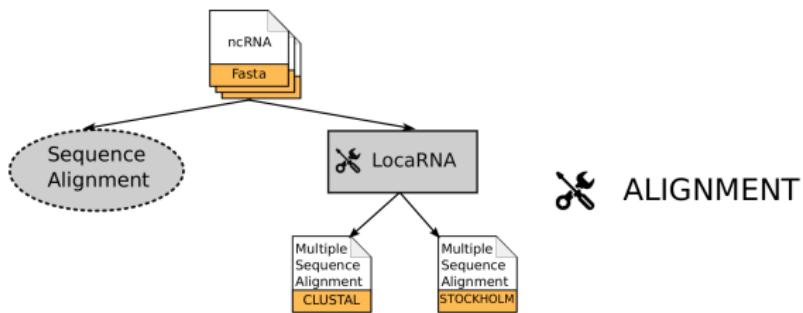
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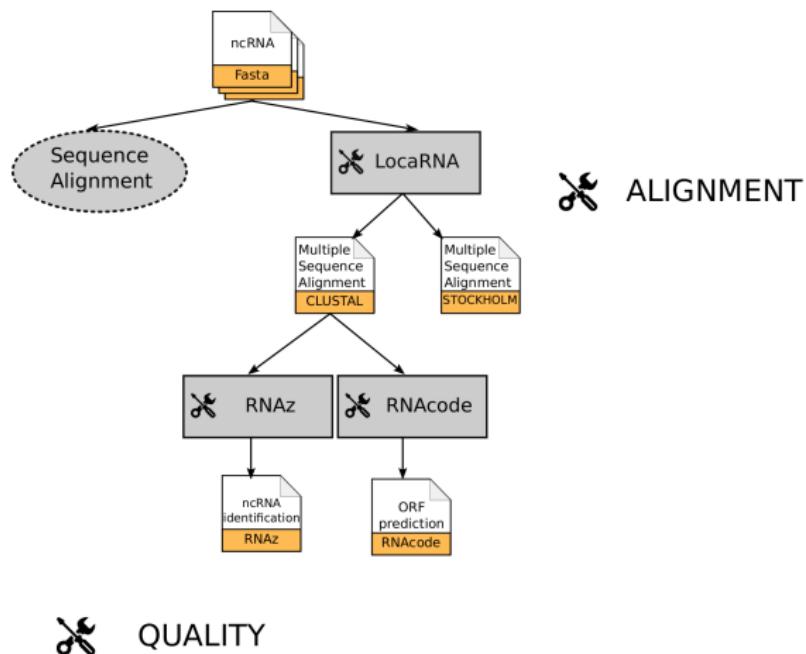
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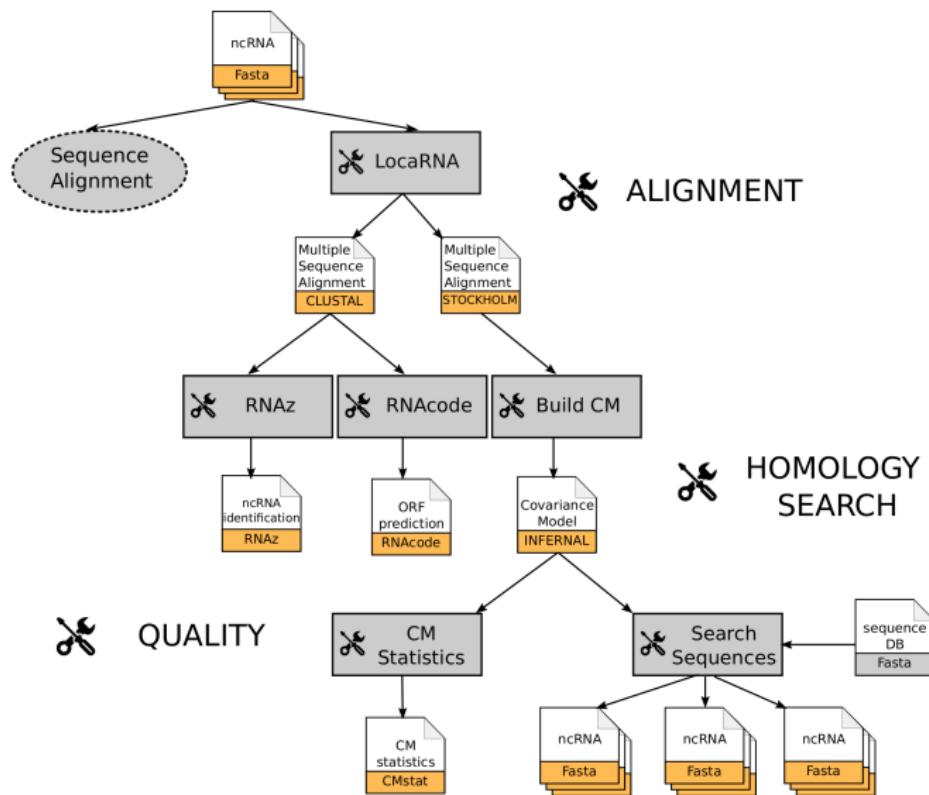
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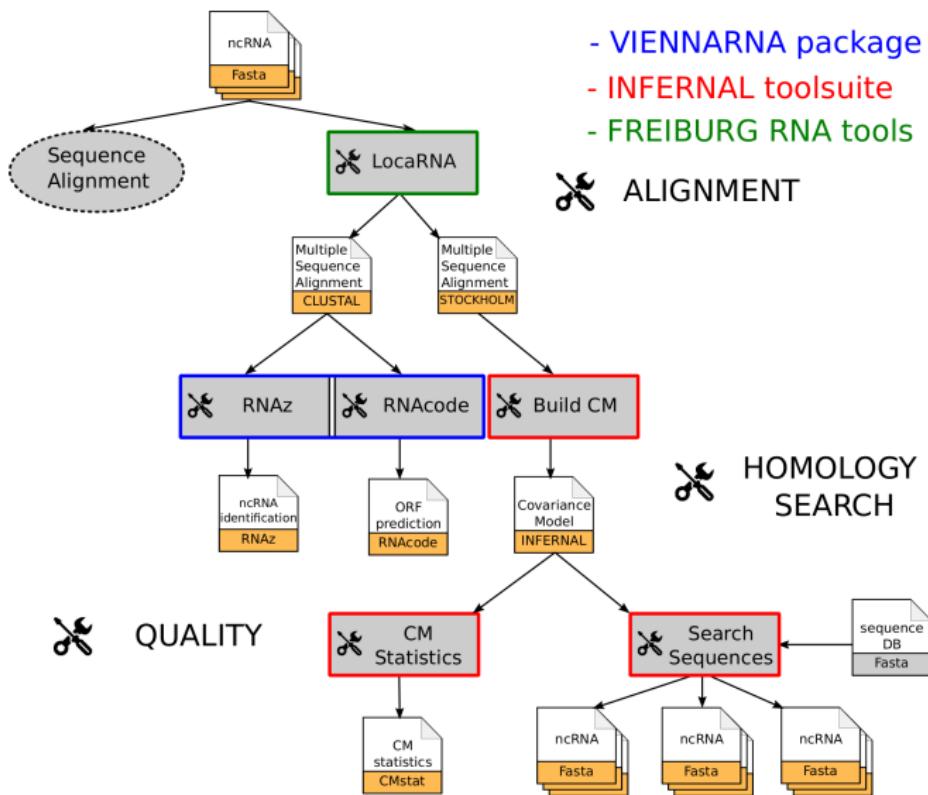
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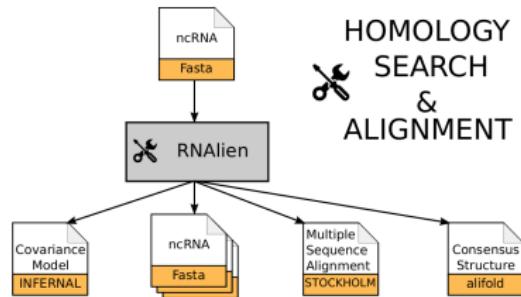
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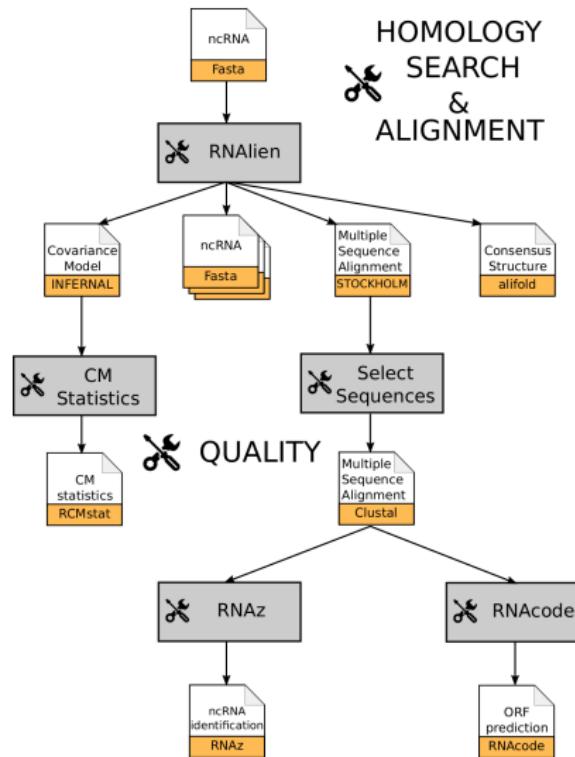
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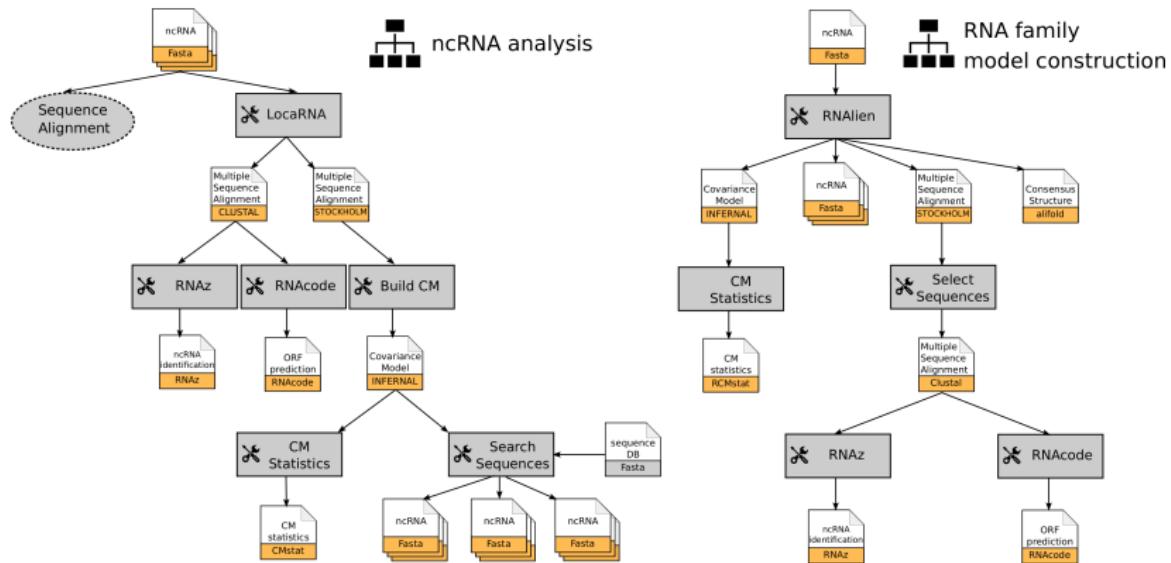


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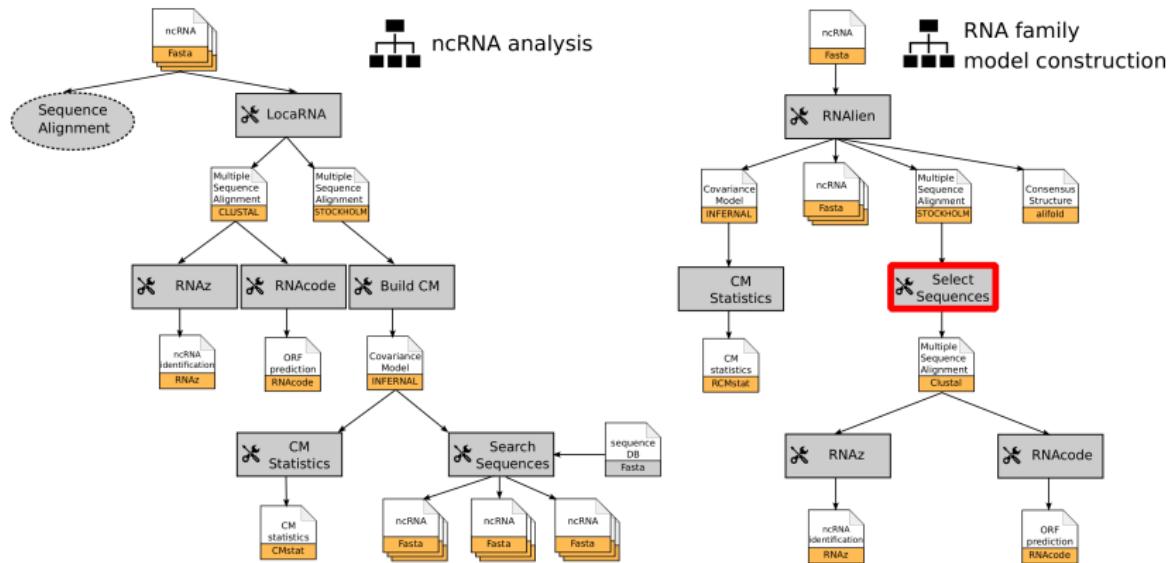
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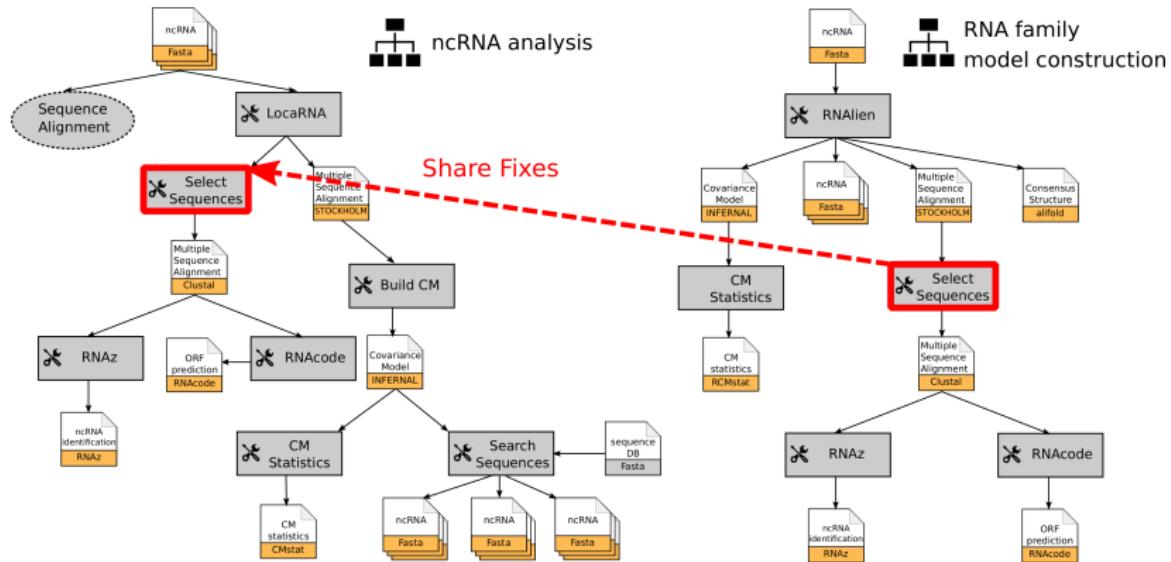
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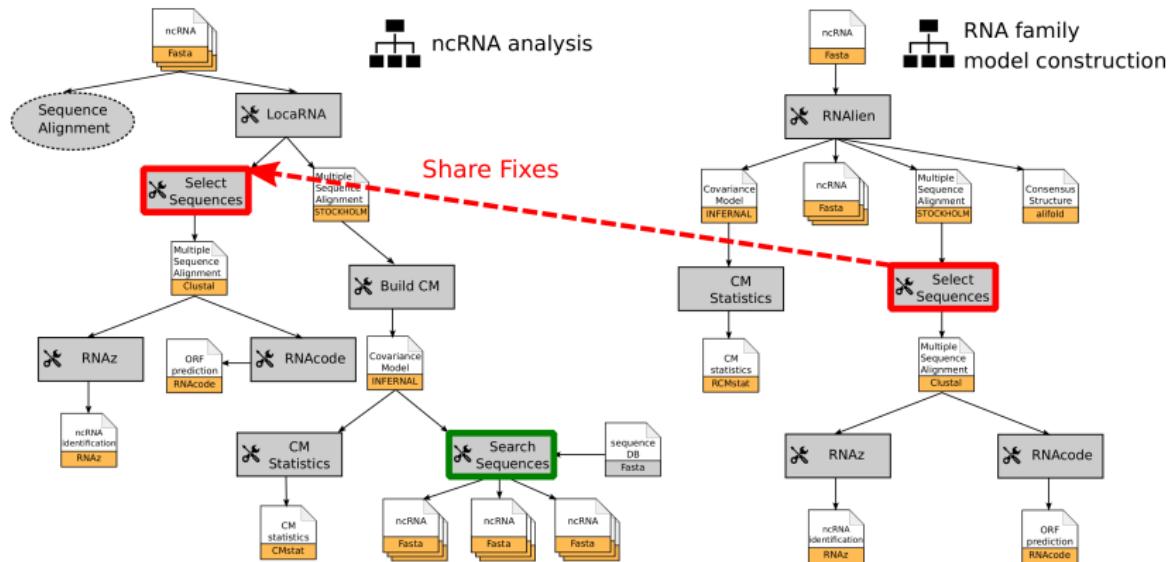
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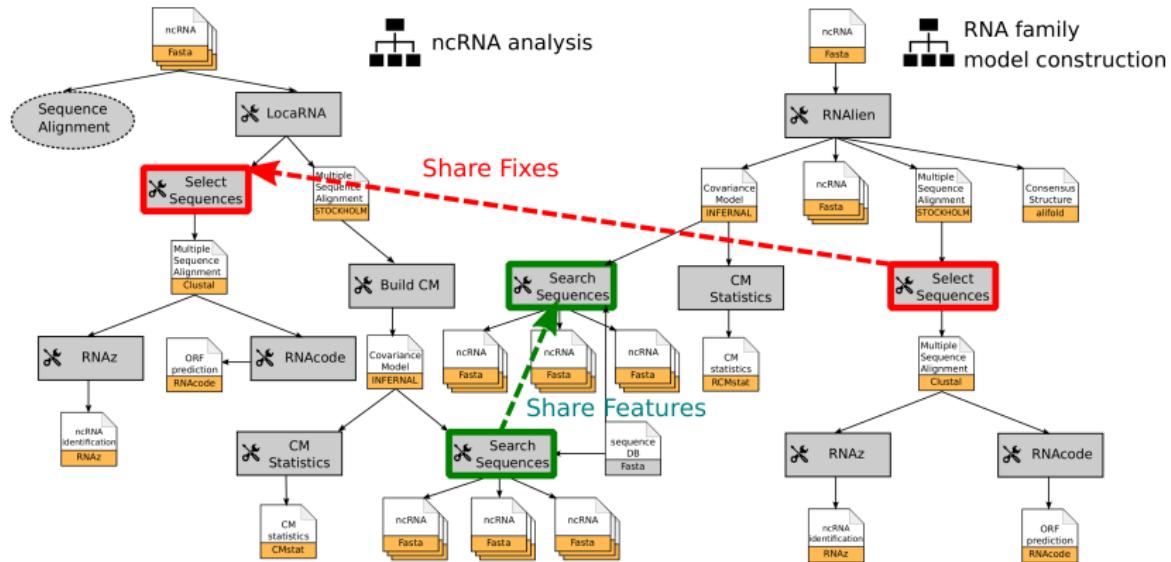
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Open **participation**, **reward**, and **inclusion**

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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,  
Andrea Bagnacani, Markus Wolfien, Steffen C. Lott, Youri Hoogstrate,  
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