

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

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

Lehrstuhl Bioinformatik
University of Freiburg

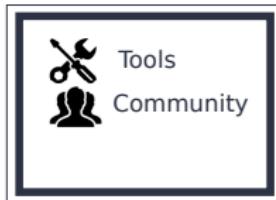
30.06.2017

Goals of the RNA Workbench



- ▶ Comprehensive set of *RNA*-bioinformatics tools

Goals of the RNA Workbench



- ▶ Comprehensive set of *RNA*-bioinformatics tools
- ▶ Community - authors and users

Goals of the RNA Workbench



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

Goals of the RNA Workbench



- ▶ 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 in Docker

Tools

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

Tools

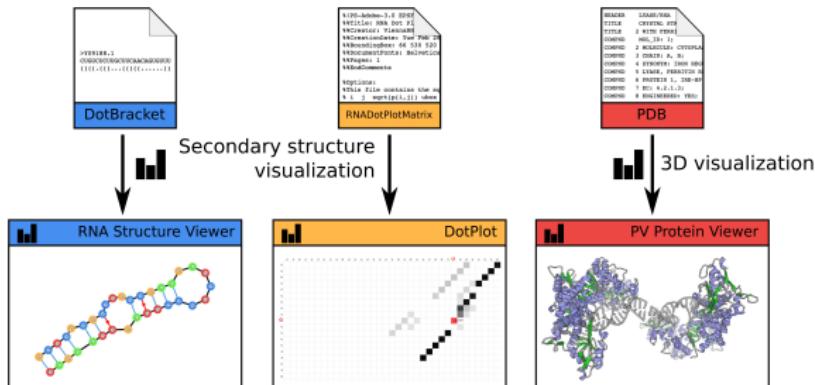
- ▶ More than **50** *RNA* bioinformatics tools
- ▶ Classical *RNA* bioinformatics (INFERNAL, ViennaRNA, ...)

Tools

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

Tools

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



Workflows

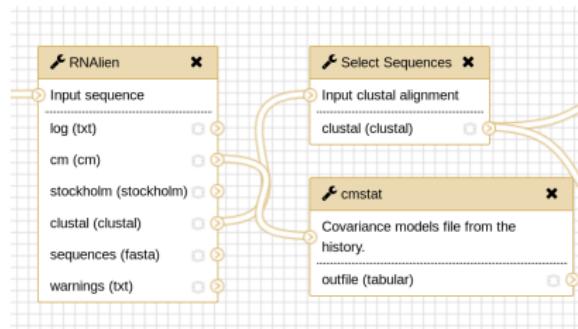
- ▶ Standardized analysis procedures

Workflows

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

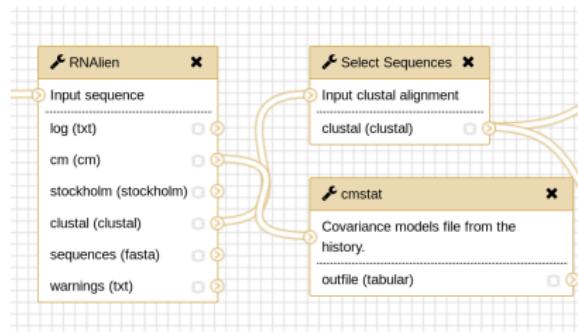
Workflows

- ▶ Standardized analysis procedures
- ▶ Based on tools as building blocks
- ▶ Can be developed, adapted and shared
(ToolShed/myexperiment.org)



Workflows

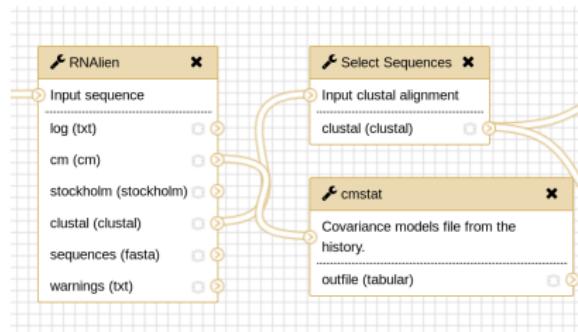
- ▶ Standardized analysis procedures
- ▶ Based on tools as building blocks
- ▶ Can be developed, adapted and shared
(ToolShed/myexperiment.org)



- ▶ Currently six workflows in the *RNA* workbench

Workflows

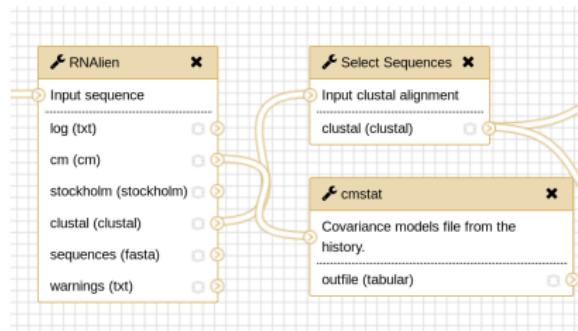
- ▶ Standardized analysis procedures
- ▶ Based on tools as building blocks
- ▶ Can be developed, adapted and shared
(ToolShed/myexperiment.org)



- ▶ Currently six workflows in the *RNA* workbench
 - ▶ ncRNA analysis

Workflows

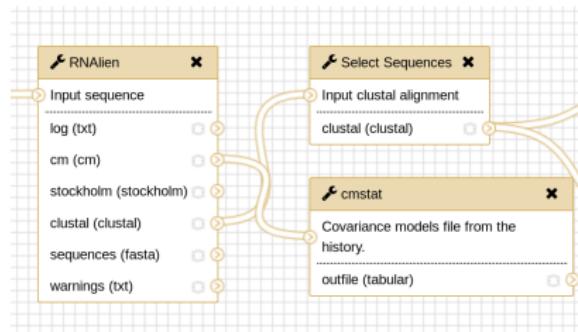
- ▶ Standardized analysis procedures
- ▶ Based on tools as building blocks
- ▶ Can be developed, adapted and shared
(ToolShed/myexperiment.org)



- ▶ Currently six workflows in the *RNA* workbench
 - ▶ *ncRNA* analysis
 - ▶ *RNA* model construction

Workflows

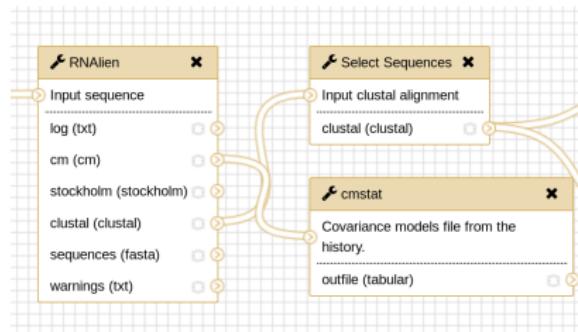
- ▶ Standardized analysis procedures
- ▶ Based on tools as building blocks
- ▶ Can be developed, adapted and shared
(ToolShed/myexperiment.org)



- ▶ Currently six workflows in the *RNA* workbench
 - ▶ ncRNA analysis
 - ▶ RNA model construction
 - ▶ RNA-seq analysis

Workflows

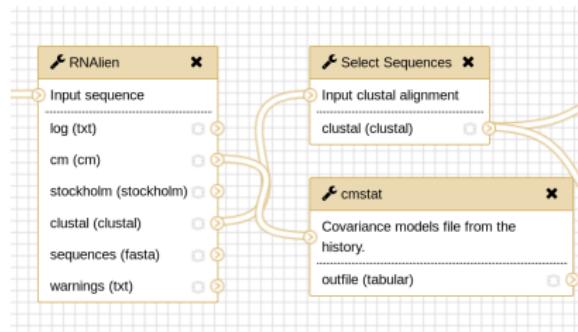
- ▶ Standardized analysis procedures
- ▶ Based on tools as building blocks
- ▶ Can be developed, adapted and shared
(ToolShed/myexperiment.org)



- ▶ Currently six workflows in the *RNA* workbench
 - ▶ ncRNA analysis
 - ▶ RNA model construction
 - ▶ RNA-seq analysis
 - ▶ Two workflows for CLIP analysis

Workflows

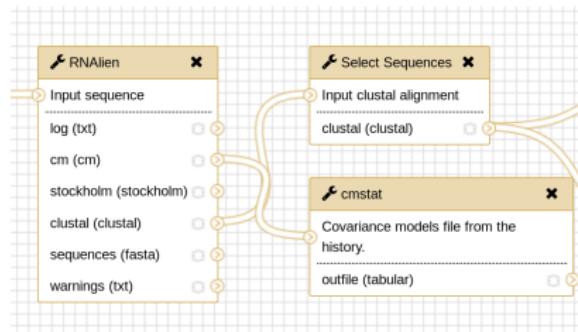
- ▶ Standardized analysis procedures
- ▶ Based on tools as building blocks
- ▶ Can be developed, adapted and shared
(ToolShed/myexperiment.org)



- ▶ Currently six workflows in the *RNA* workbench
 - ▶ ncRNA analysis
 - ▶ RNA model construction
 - ▶ RNA-seq analysis
 - ▶ Two workflows for CLIP analysis
 - ▶ C/D-box scan

Workflows

- ▶ Standardized analysis procedures
- ▶ Based on tools as building blocks
- ▶ Can be developed, adapted and shared
(ToolShed/myexperiment.org)



- ▶ Currently six workflows in the *RNA* workbench
 - ▶ *ncRNA* analysis
 - ▶ *RNA* model construction
 - ▶ *RNA*-seq analysis
 - ▶ Two workflows for CLIP analysis
 - ▶ C/D-box scan

Workflow - Analysis of non-coding RNAs

- ▶ Test for functional structure via conservation

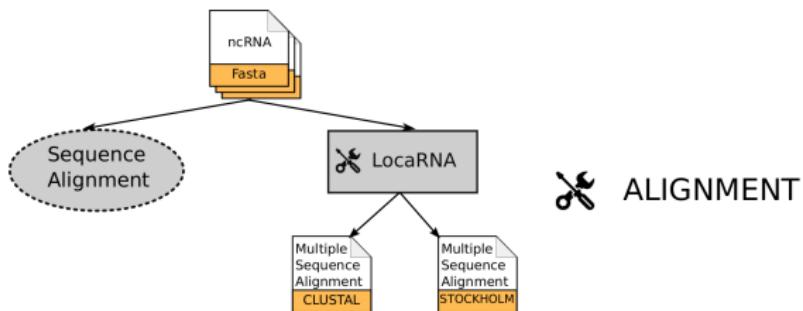
Workflow - Analysis of non-coding RNAs

- ▶ Test for functional structure via conservation



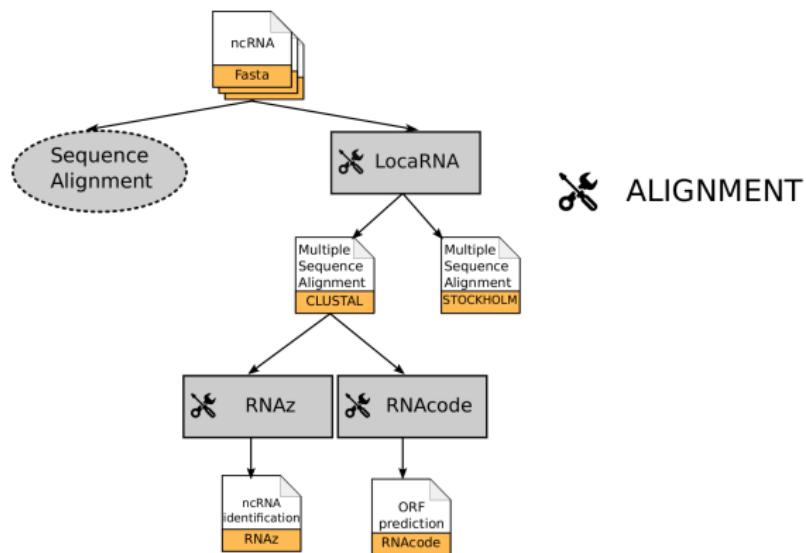
Workflow - Analysis of non-coding RNAs

- ▶ Test for functional structure via conservation



Workflow - Analysis of non-coding RNAs

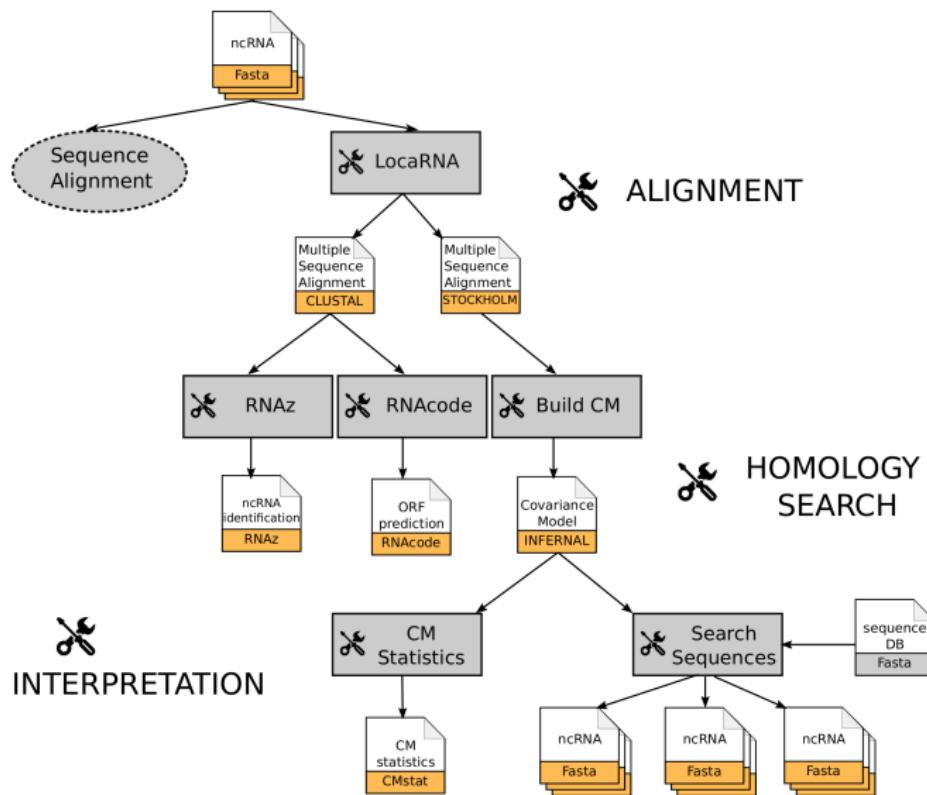
- ▶ Test for functional structure via conservation



✂ INTERPRETATION

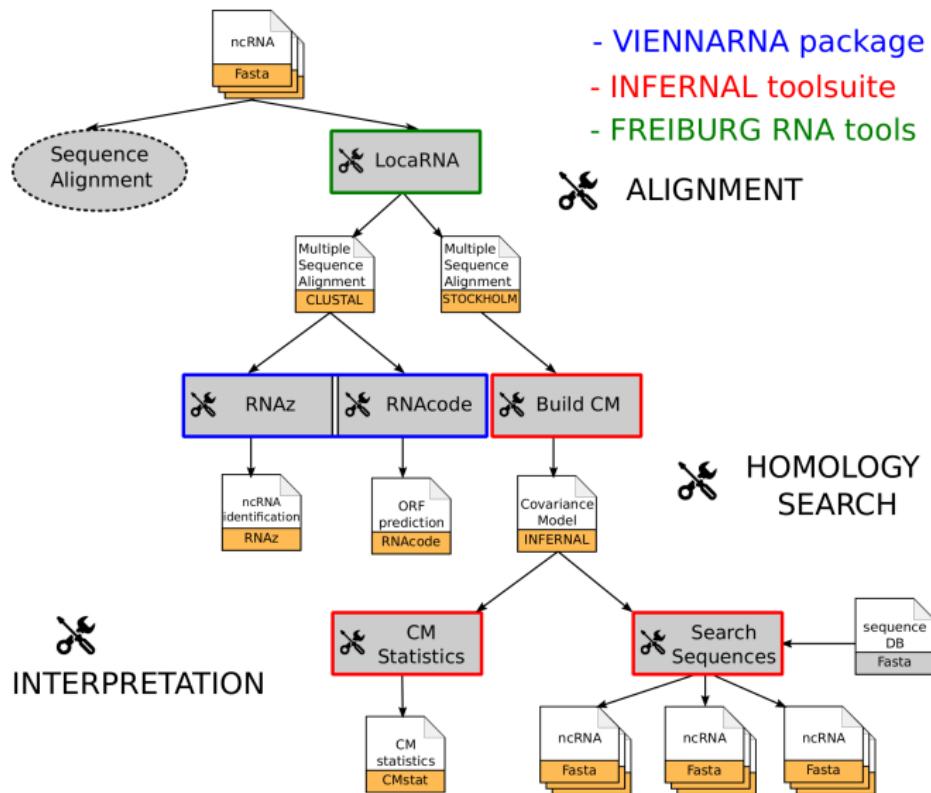
Workflow - Analysis of non-coding RNAs

- ▶ Test for functional structure via conservation



Workflow - Analysis of non-coding RNAs

- ▶ Test for functional structure via conservation



Workflow - RNA family model construction

- ▶ RNA family model construction

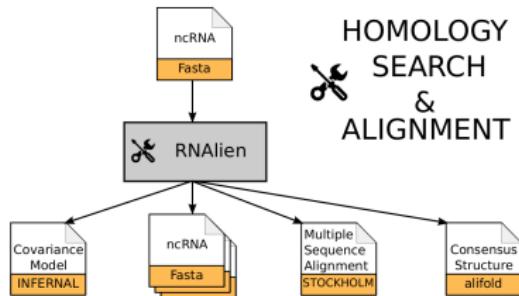
Workflow - RNA family model construction

- ▶ RNA family model construction



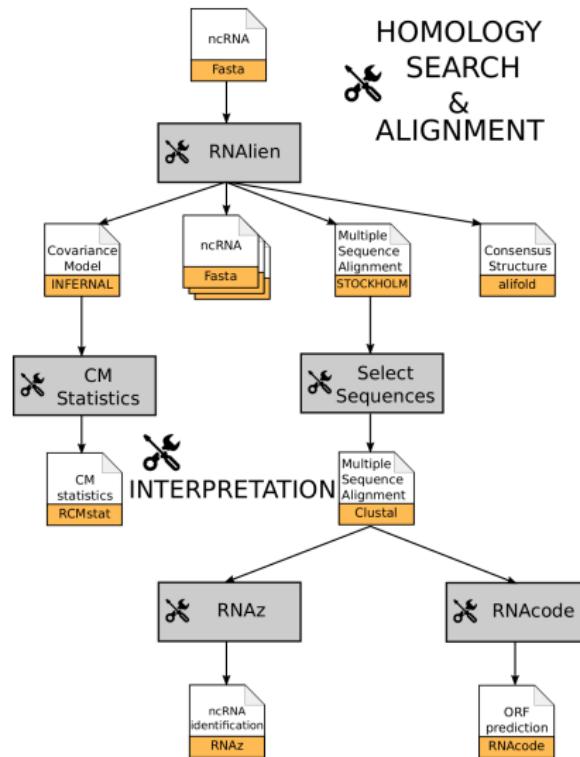
Workflow - RNA family model construction

- ▶ RNA family model construction

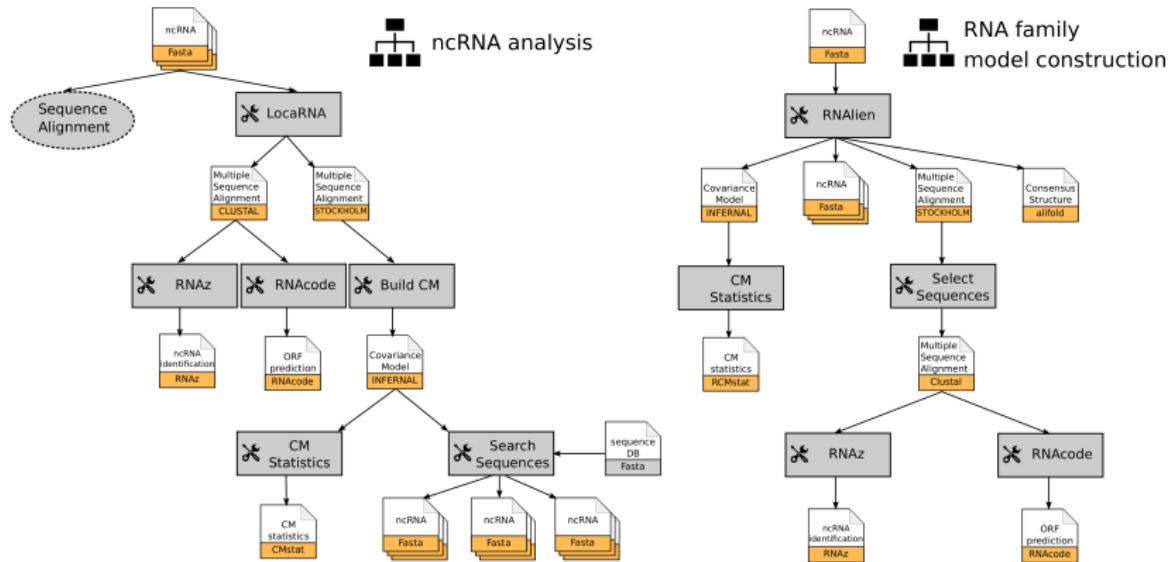


Workflow - RNA family model construction

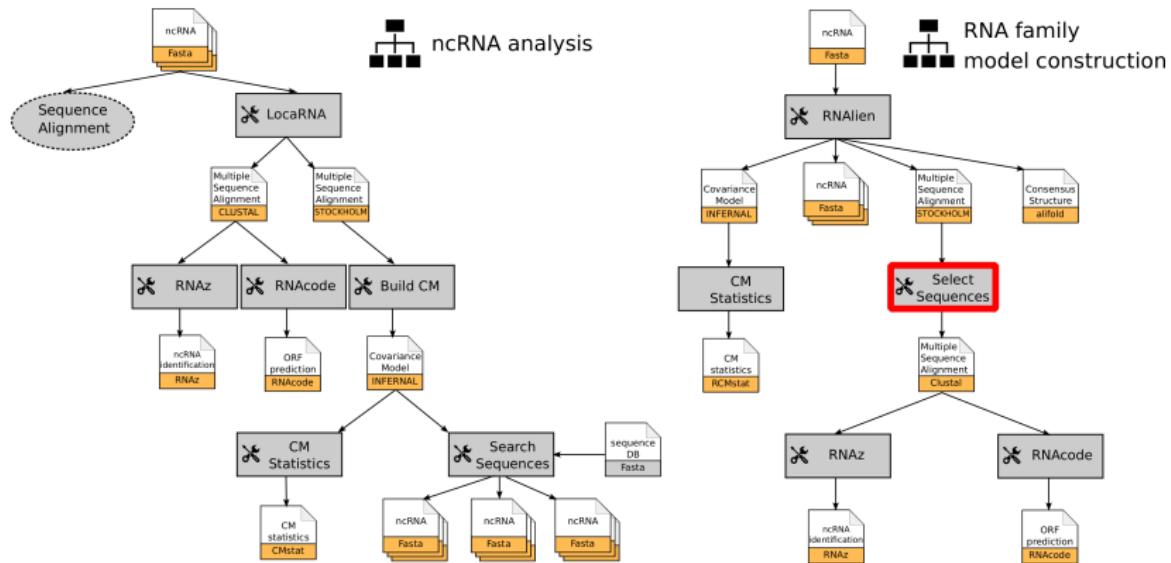
► RNA family model construction



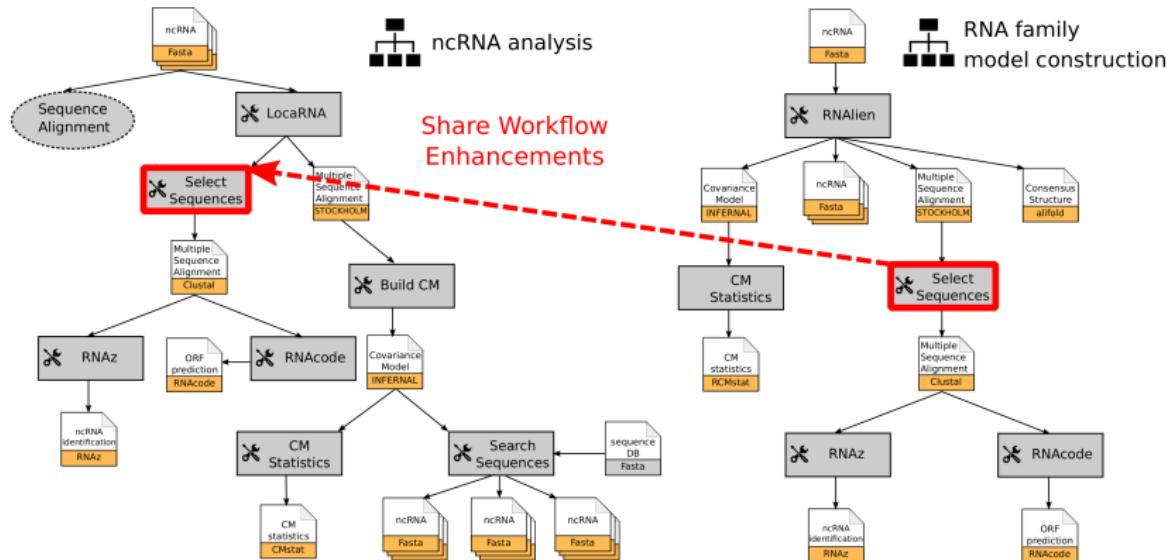
Collaborative development



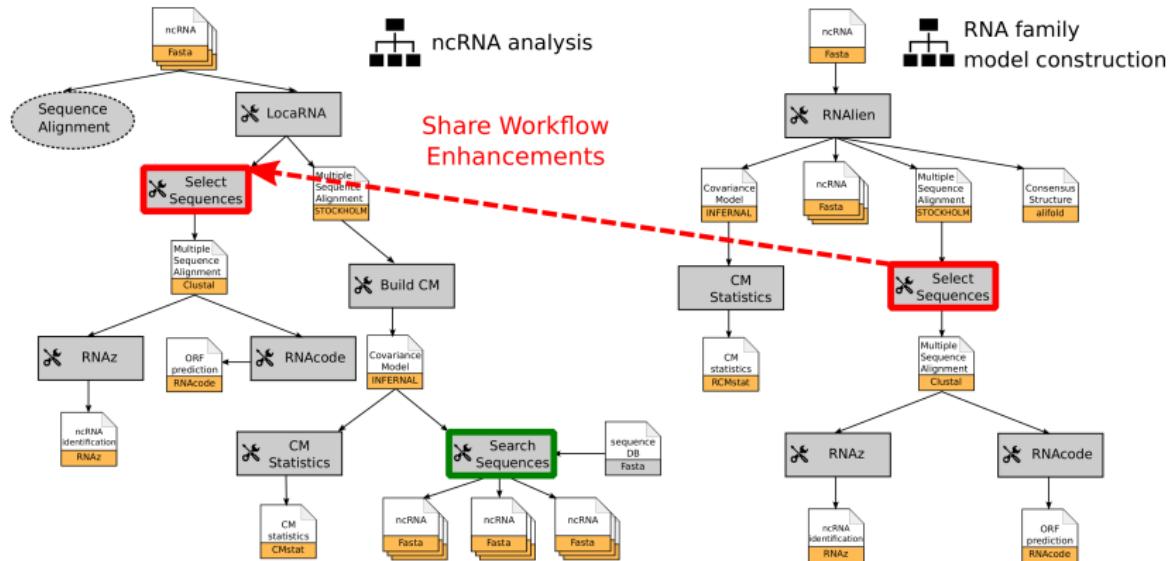
Collaborative development



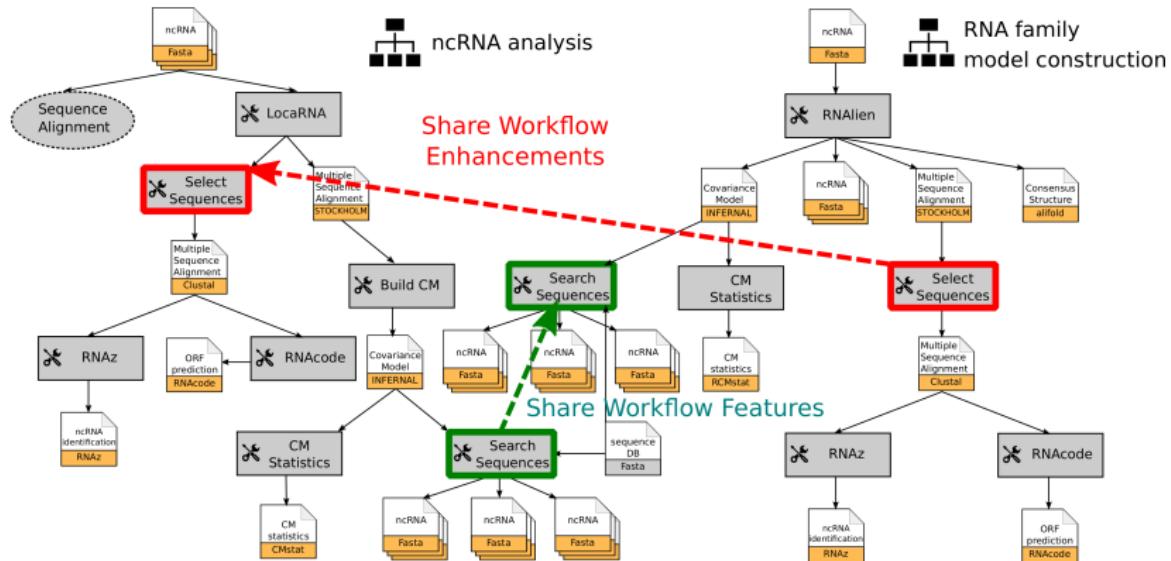
Collaborative development



Collaborative development



Collaborative development



Community

Workbench is a joint effort of the european *ncRNA* community

Community

Workbench is a joint effort of the european *ncRNA* community

- ▶ **12** contributors *RNA-workbench*

Community

Workbench is a joint effort of the european *ncRNA* community

- ▶ **12** contributors *RNA-workbench*
- ▶ **54** contributors *galaxytools*

Community

Workbench is a joint effort of the european *ncRNA* community

- ▶ **12** contributors *RNA-workbench*
- ▶ **54** contributors *galaxytools*

Benefits from collaboration and integration ?

Community

Workbench is a joint effort of the european *ncRNA* community

- ▶ **12** contributors *RNA-workbench*
- ▶ **54** contributors *galaxytools*

Benefits from collaboration and integration ?

Tool authors

Community

Workbench is a joint effort of the european *ncRNA* community

- ▶ **12** contributors *RNA-workbench*
- ▶ **54** contributors *galaxytools*

Benefits from collaboration and integration ?

Tool authors

- ▶ Ensure correct application of tool

Community

Workbench is a joint effort of the european *ncRNA* community

- ▶ **12** contributors *RNA-workbench*
- ▶ **54** contributors *galaxytools*

Benefits from collaboration and integration ?

Tool authors

- ▶ Ensure correct application of tool
- ▶ Identify missing interfaces between tools

Community

Workbench is a joint effort of the european *ncRNA* community

- ▶ **12** contributors *RNA-workbench*
- ▶ **54** contributors *galaxytools*

Benefits from collaboration and integration ?

Tool authors

- ▶ Ensure correct application of tool
- ▶ Identify missing interfaces between tools
- ▶ New ideas for workflows

Community

Workbench is a joint effort of the european *ncRNA* community

- ▶ **12** contributors *RNA-workbench*
- ▶ **54** contributors *galaxytools*

Benefits from collaboration and integration ?

Tool authors

- ▶ Ensure correct application of tool
- ▶ Identify missing interfaces between tools
- ▶ New ideas for workflows

Galaxy developers

Community

Workbench is a joint effort of the european *ncRNA* community

- ▶ **12** contributors *RNA-workbench*
- ▶ **54** contributors *galaxytools*

Benefits from collaboration and integration ?

Tool authors

- ▶ Ensure correct application of tool
- ▶ Identify missing interfaces between tools
- ▶ New ideas for workflows

Galaxy developers

- ▶ Simpler workflow construction

Community

Workbench is a joint effort of the european *ncRNA* community

- ▶ **12** contributors *RNA-workbench*
- ▶ **54** contributors *galaxytools*

Benefits from collaboration and integration ?

Tool authors

- ▶ Ensure correct application of tool
- ▶ Identify missing interfaces between tools
- ▶ New ideas for workflows

Galaxy developers

- ▶ Simpler workflow construction
- ▶ Authors keep tools updated

Community

Workbench is a joint effort of the european *ncRNA* community

- ▶ **12** contributors *RNA-workbench*
- ▶ **54** contributors *galaxytools*

Benefits from collaboration and integration ?

Tool authors

- ▶ Ensure correct application of tool
- ▶ Identify missing interfaces between tools
- ▶ New ideas for workflows

Galaxy developers

- ▶ Simpler workflow construction
- ▶ Authors keep tools updated

Open participation, reward, and inclusion

Training & Usage

Training & Usage

Training

Training & Usage

Training

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

Training & Usage

Training

- ▶ Training sessions (Introduction, HTS data and *RNA-seq* analyses)
- ▶ <http://training.galaxyproject.org>

Training & Usage

Training

- ▶ Training sessions (Introduction, HTS data and *RNA-seq* analyses)
- ▶ <http://training.galaxyproject.org>
- ▶ Galaxy Interactive Tours

Training & Usage

Training

- ▶ Training sessions (Introduction, HTS data and *RNA-seq* analyses)
- ▶ <http://training.galaxyproject.org>
- ▶ Galaxy Interactive Tours

Using the workbench

Training & Usage

Training

- ▶ Training sessions (Introduction, HTS data and *RNA-seq* analyses)
- ▶ <http://training.galaxyproject.org>
- ▶ Galaxy Interactive Tours

Using the workbench

- ▶ `docker run galaxy-rna-workbench`

Training & Usage

Training

- ▶ Training sessions (Introduction, HTS data and *RNA-seq* analyses)
- ▶ <http://training.galaxyproject.org>
- ▶ Galaxy Interactive Tours

Using the workbench

- ▶ `docker run galaxy-rna-workbench`
- ▶ OSX and Windows using the graphical tool Kitematic

Acknowledgements & Thanks

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!

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