

## Towards automating workflow analyses in Galaxy

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### Introduction

The Galaxy community is promoting RNA-Seq protocols and best practices through the reuse of existing tools, and the consolidation of a Training Network to provide guidance to researchers through example datasets, tutorials, and interactive tours. However, the more tools and techniques are showcased, the more complex the options for tool chaining and parametrization become.

### Objectives

- Assist researchers in carrying out their analyses
- Integrate the Galaxy framework with an interactive recommendation system leveraging on community consolidated best practices as well as EDAM annotated tools
- Promote the adoption of well established pipelines
- Allow room for experimental tools
- Consolidate protocols and reproducibility

### Materials and Methods

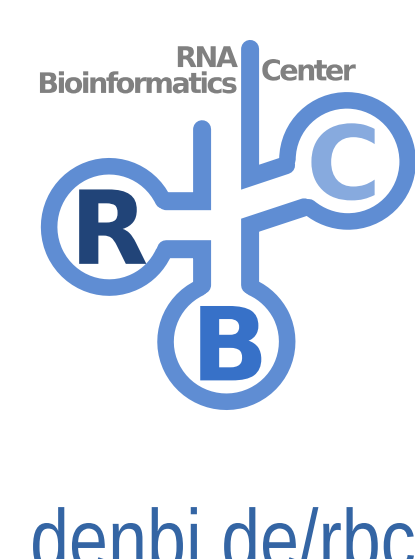
Tool chaining and parametrization through Galaxy's interactive tours



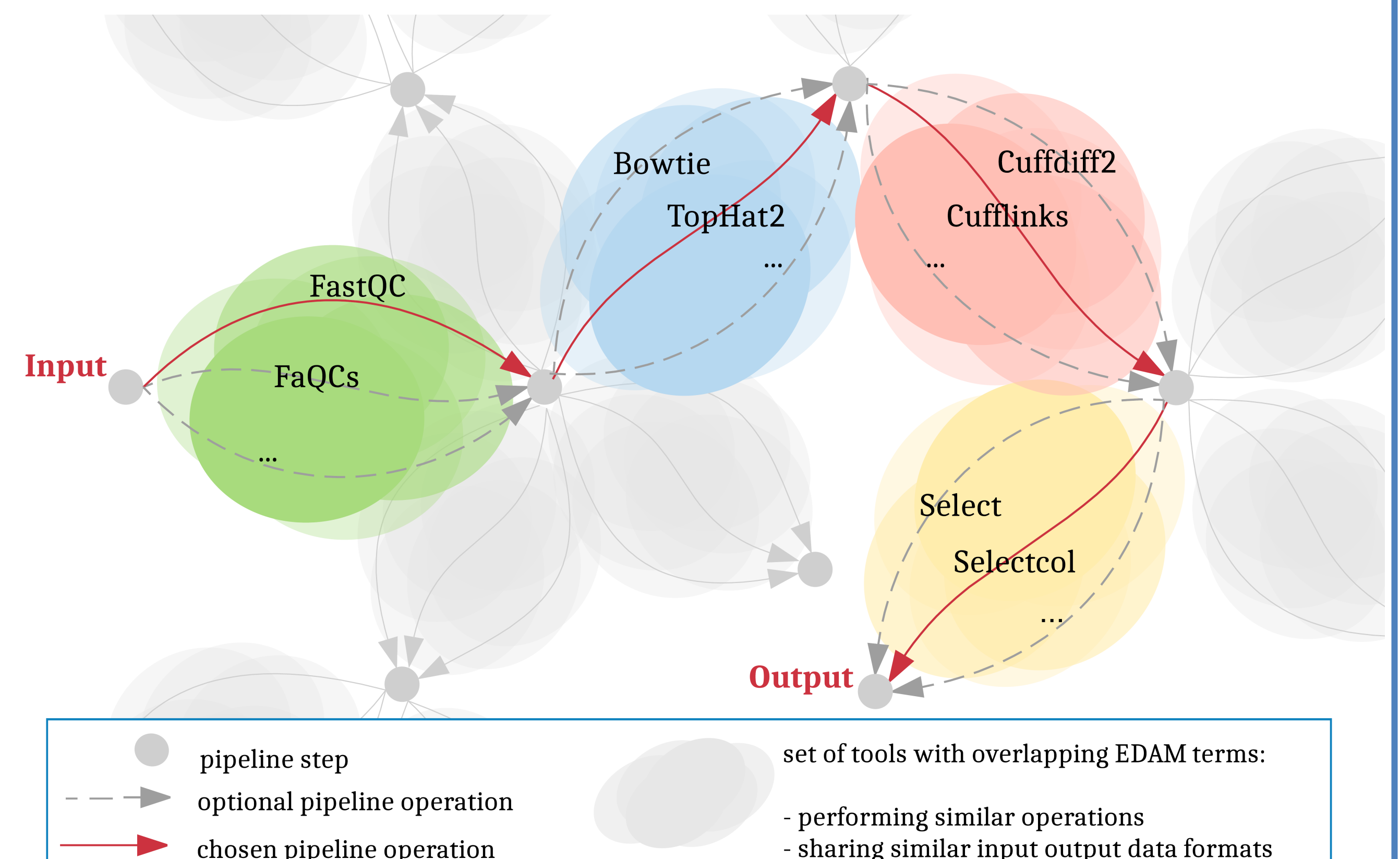
Tool operations and input / output formats through Elixir's bio.tools



Best practices and user-tracked data of RBC's Galaxy instance

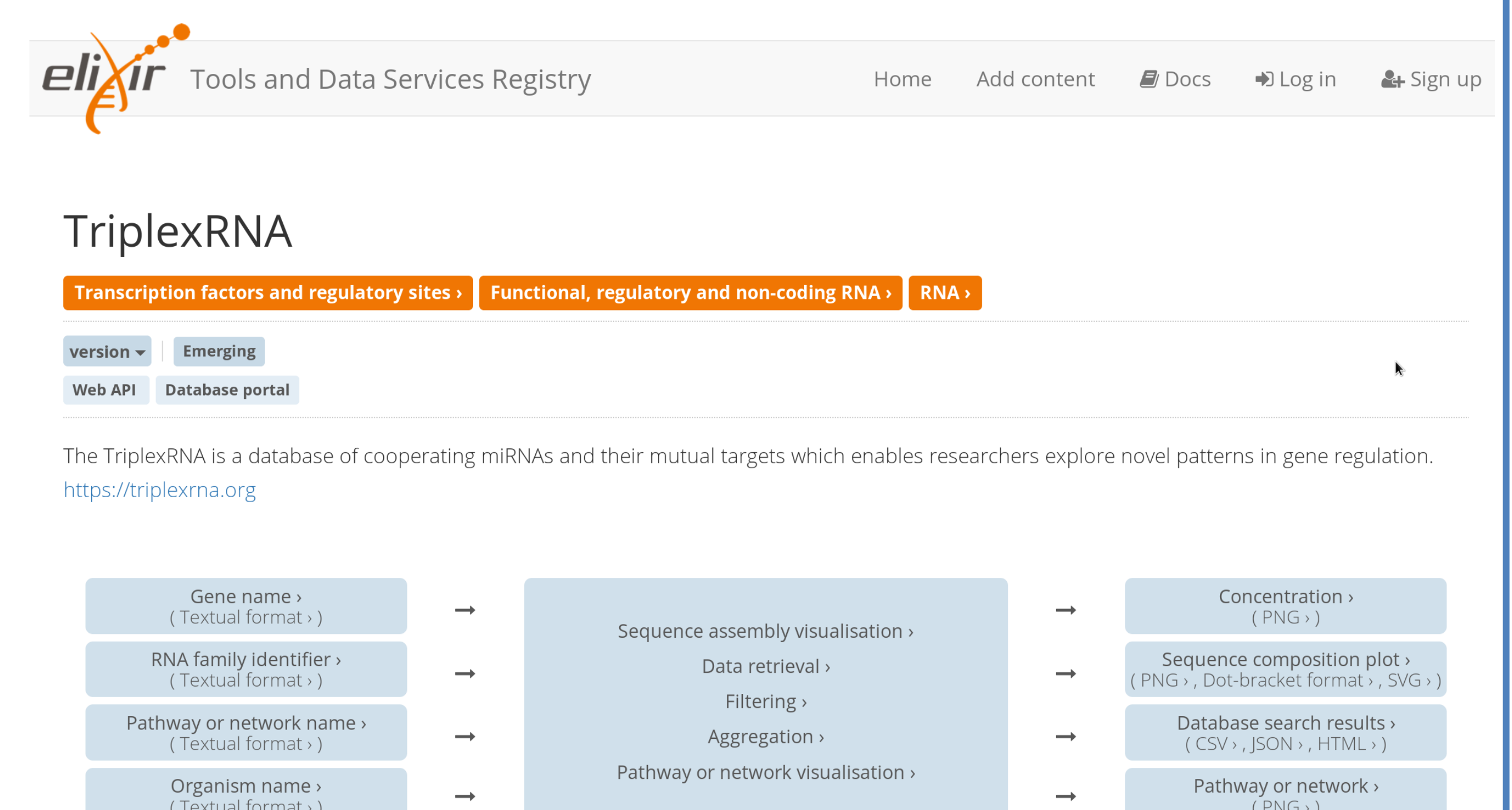


### Results and discussion



- Galaxy tools are grouped by function
- Each tool function bridges two different states of data
- Tools are chained on their input / output data formats
- Galaxy tours recommends pertinent tools step by step
- Users decide which tool to select and parametrize

### Conclusion



- A recommendation system enhances the visibility of each Galaxy tool, relieving the user from browsing tool categories, or sticking to the usual analysis tools
- Tool pertinence is inferred from manually curated EDAM annotations, therefore a tool's pertinence is as accurate as its bio.tools annotation

### References

Lott SC et al. Customized workflow development and data modularization concepts for RNA-Sequencing and metatranscriptome experiments. Journal of Biotechnology, 2017. [10.1016/j.jbiotec.2017.06.1203](https://doi.org/10.1016/j.jbiotec.2017.06.1203)



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