

How-to incorporate NEXT-RNAi into Galaxy environment

This is a how-to guide for implementing the NEXT-RNAi program into your local Galaxy environment.

Background

About Galaxy

Galaxy is a framework, developed by [Galaxy Team](#), for integrating computational tools. It allows nearly any tool that can be run from the command line to be wrapped in a structured, well defined interface.

On top of these tools, Galaxy provides an accessible environment for interactive analysis that transparently tracks the details of analyses, a workflow system for convenient reuse, data management, sharing, publishing, and more.

You can find more information about Galaxy [here](#). [Wiki](#) documentation is also available.

About NEXT-RNAi

NEXT-RNAi is a software for the design and evaluation of genome-wide RNAi libraries and performs all steps from the prediction of specific and efficient RNAi target sites to the visualization of designed reagents in their genomic context. The software enables the design and evaluation of siRNAs and long dsRNAs and was implemented in an organism-independent manner allowing designs for all sequenced and annotated genomes. It requires minimal input such as the desired target sequences and an off-target database.

Full documentation can be found [here](#).

Prerequisites:

1. Galaxy environment. Installation guide from the Galaxy wiki site is available [here](#).
2. NEXT-RNAi program. You can download the software [here](#). Installation of NEXT-RNAi into your local environment is described at [this wiki page](#)
3. Galaxy configuration files for NEXT-RNAi. Download the Galaxy [configuration bundle](#) for NEXT-RNAi which includes:
 - a XML configuration file: `nextrna.xml`
 - a perl wrapper: `nextrna_wrapper.pl`
 - location files:
 - `nextrna_gbrowse.loc`
 - `nextrna_genomes.loc`
 - `nextrna_transcripts.loc`

You can find a short introduction to location files in Galaxy [here](#).

Install NEXT-RNAi in Galaxy Environment

Before you start, please read this [short tutorial](#) on how to add a tool into Galaxy in general.

For adding NEXT-RNAi into Galaxy take the following steps:

1. Put the tool definition file **nextrna.xml** and the wrapper **nextrna_wrapper.pl** into Galaxy's **tools** directory. You can create a subdirectory like `own_tool/` in **tools** and put the two files there.
2. Modify the **nextrna.xml** file according to your environment, i.e. change the paths of the programs required by NEXT-RNAi. The default path in `nextrna.xml` is always `/software/bin/`; replace it with the path in your system for each program.
3. Modify the wrapper **nextrna_wrapper.pl**. Find the line `perl /software/bin/nextrna.pl/` in the **nextrna_wrapper.pl** script and replace it with the path to the NEXT-RNAi program `nextrna.pl` located on your system
4. Put the location files into the **tool-data** directory located in the root directory of the Galaxy distribution.
5. Make Galaxy aware of NEXT-RNAi. Add these lines to the **tool_conf.xml** file located in the root directory of the Galaxy distribution:

```
<section name="NextRNAi" id="nextrnai">
<tool file="b110_tools/nextrnai.xml" />
</section>
```

where "b110_tools/nextrnai.xml" (the path to nextrnai.xml) has to be adjusted according to your installation in step 1.

Note. There are three location files:

1. **nextrnai_transcripts.loc** for transcripts bowtie index files. See -d option of [NEXT-RNAi documentation](#).
 2. **nextrnai_genomes.loc**: for genome bowtie index file. See GENOME BOWTIE of [NEXT-RNAi documentation](#).
 3. **nextrnai_gbrowser.loc**: for genome browser. See GBROWSEBASE of [NEXT-RNAi documentation](#).
- Please define the location files according to your system. File 1 is important, whereas files 2 and 3 are rather optional.

Screenshots

If you successfully installed Galaxy, you should be able to see an interface similar to the following:



Contact

Please contact [b110-it](#) if you have any suggestion or find a bug.

References

Thomas Horn, Thomas Sandmann and Michael Boutros. Design and evaluation of genome-wide libraries for RNAi screens. *Genome Biol.* 2010 Jun 15;11(6):R61. [Link to manuscript](#)

Goecks, J, Nekrutenko, A, Taylor, J and The Galaxy Team. Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. *Genome Biol.* 2010 Aug 25;11(8):R86.

Blankenberg D, Von Kuster G, Coraor N, Ananda G, Lazarus R, Mangan M, Nekrutenko A, Taylor J. "Galaxy: a web-based genome analysis tool for experimentalists". *Current Protocols in Molecular Biology.* 2010 Jan; Chapter 19:Unit 19.10.1-21.