Galaxy Tool Generator Documentation

Ming Chen, Bradford Condon

Nov 16, 2018

Contents:

CHAPTER 1

Quick Start Guide

This repository builds a Docker image that can be used to quickly launch the GTG web application for Galaxy tool development.

To get necessary docker images:

```
docker pull mingchen0919/gtgdocker
docker pull bgruening/galaxy-stable:17.09
```

Warning: This documentation is under active construction and should be completed by November 17th 2018, so please check back then if you can't find what you need.

1.1 Launch GTG

```
wget https://raw.githubusercontent.com/MingChen0919/gtgdocker/master/launch_dev_env.sh
sh launch_dev_env.sh
```

This script will launch a docker container running the GTG app and another container running a Galaxy instance. Login to the Galaxy instance with username **admin** and password **admin** so that you can install tools from tool shed.

CHAPTER 2

User's Guide

2.1 Launching GTG

2.1.1 Docker

` wget https://raw.githubusercontent.com/MingChen0919/gtgdocker/master/launch_dev_env.sh sh launch_dev_env.sh `

This script will launch a docker container running the GTG app and another container running a Galaxy instance. Login to the Galaxy instance with username **admin** and password **admin** so that you can install tools from tool shed.

After running this script, you should see the following directories in your current directory:

` gtg_dev_dir/ ├── database ├── galaxy_tool_repository └── shed_tools `

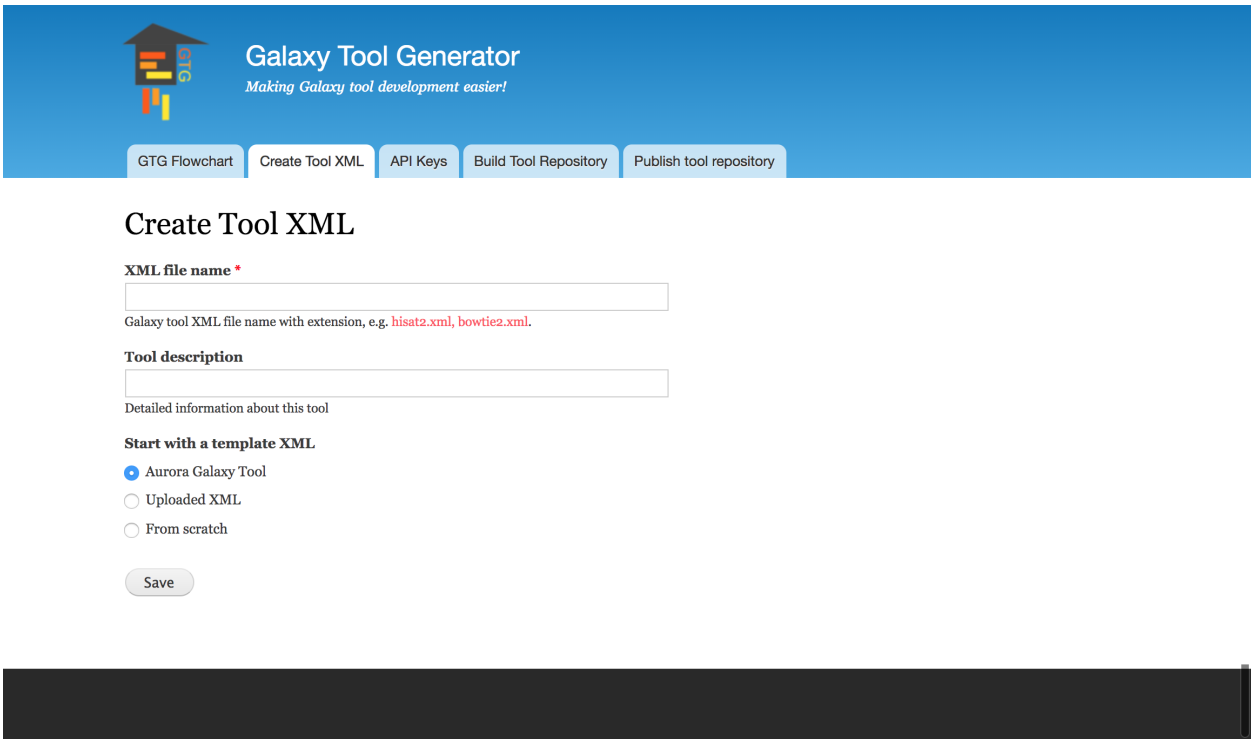
2.1.2 Drupal Site

If you want to add the galaxy tool generator to an existing Drupal site. . . .

2.2 Build Tool XML

GTG provides three ways to build a Galaxy XML file:

- Aurora Galaxy Tool: this option starts with an template file for developing an Aurora Galaxy Tool.
- Uploaded XML: starts with an uploaded XML.
- From scratch: builds XML from scratch.

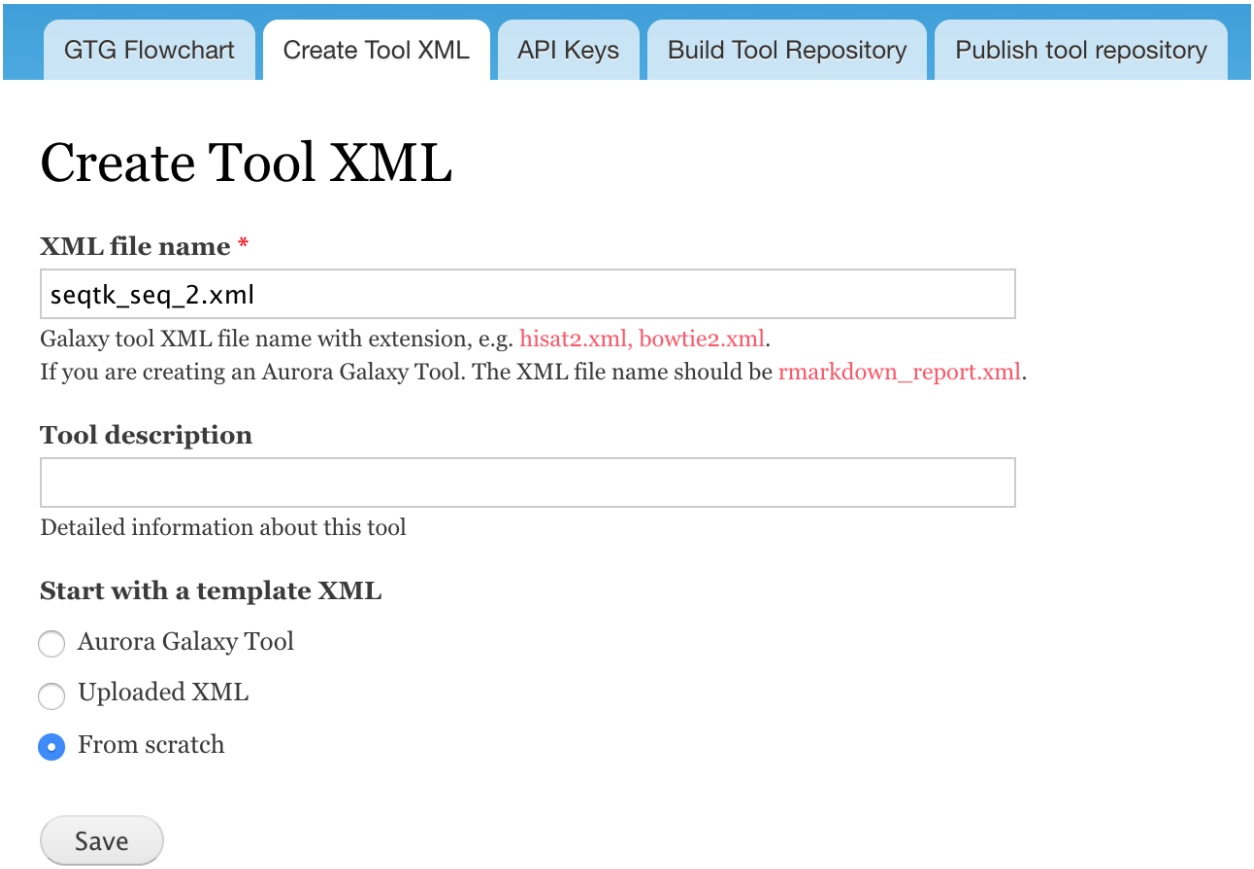


2.2.1 Start from scratch

For comparison with another software for Galaxy tool development planemo <https://planemo.readthedocs.io/en/latest/> '_, I am going to use 'an example from the planemo use cases. In this example we are going to use GTG to build this seqtk_seq_2.xml file.

0. Initialize an XML

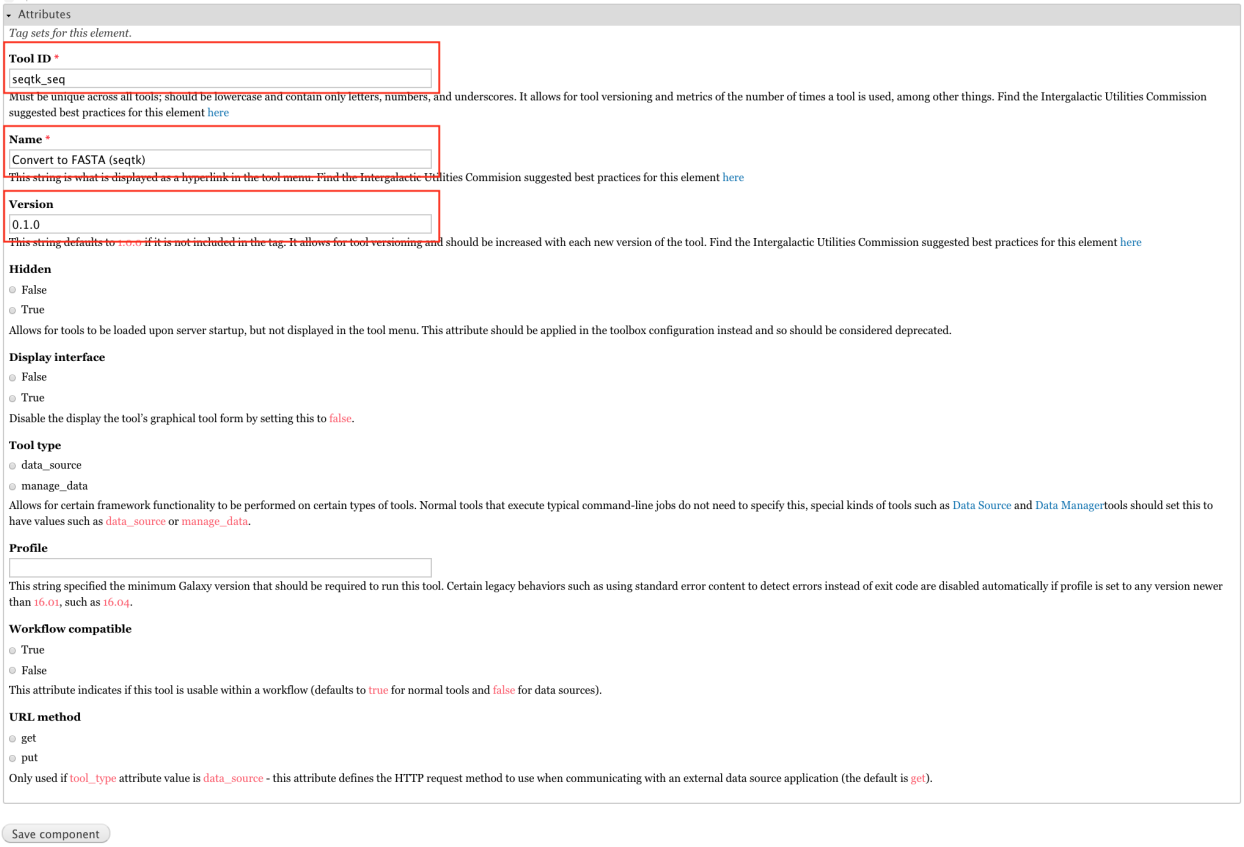
- Click **Create Tool XML**
- Enter *seqtk_seq_2.xml* into **XML file name**
- Select **From scratch** and click **Save**



1. Create tool component, which is the root component.

```
` <tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0"> `
```

Edit tool component attributes



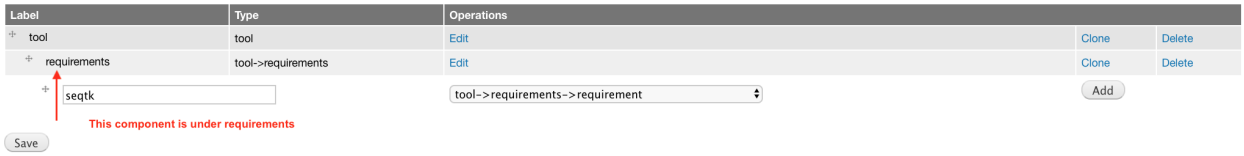
2. Create tool->requirements component.

```
<requirements>
        <requirement type="package" version="1.2">seqtk</requirement>
</requirements>
```

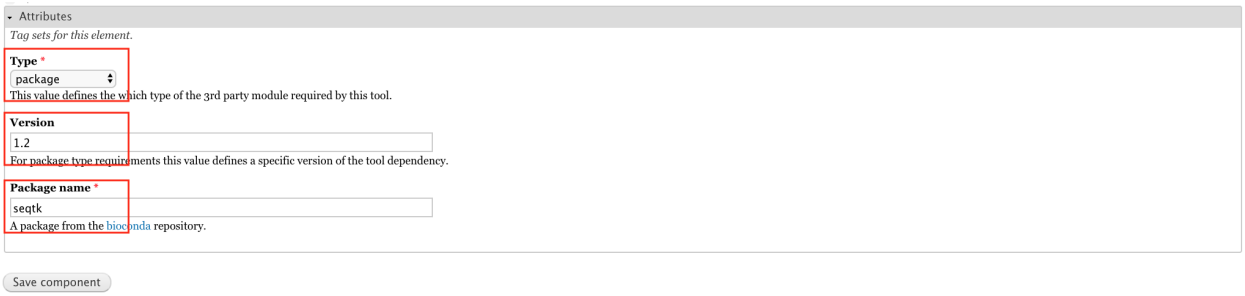
Add **tool->requirements** component

Edit **tool->requirements** component attributes. However, this component does not have any attributes.

Add **tool->requirements->requirement** component



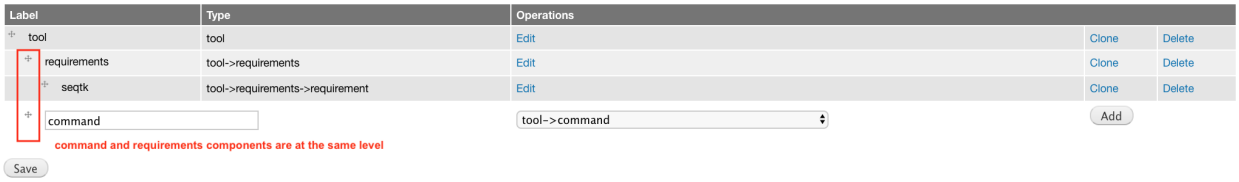
Edit **tool->requirements->requirement** component attributes.



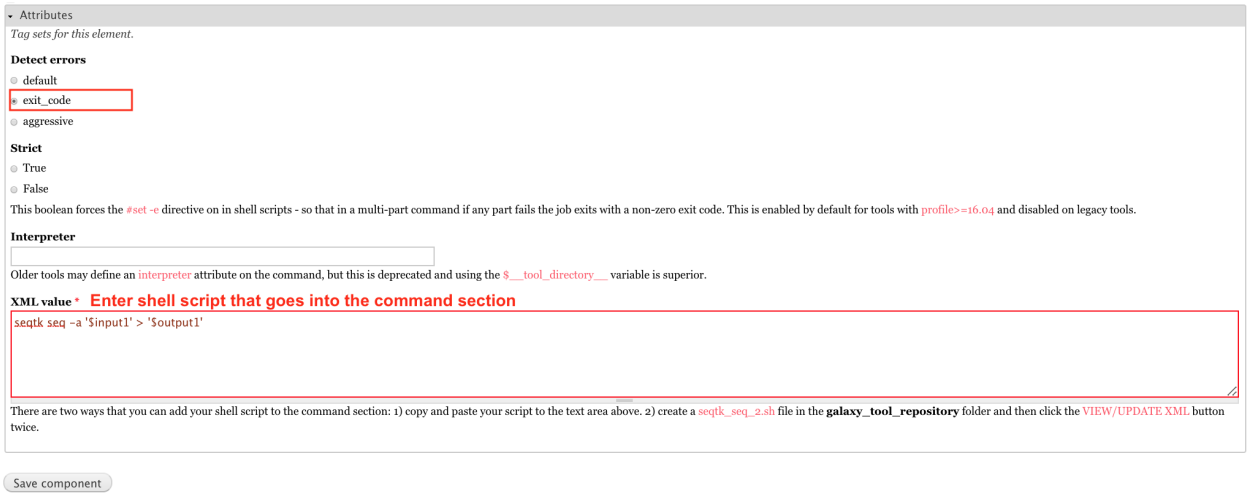
3. Create tool->command component

```
<command detect_errors="exit_code"><![CDATA[
    seqtk seq -a '$input1' > '$output1'
]]></command>
```

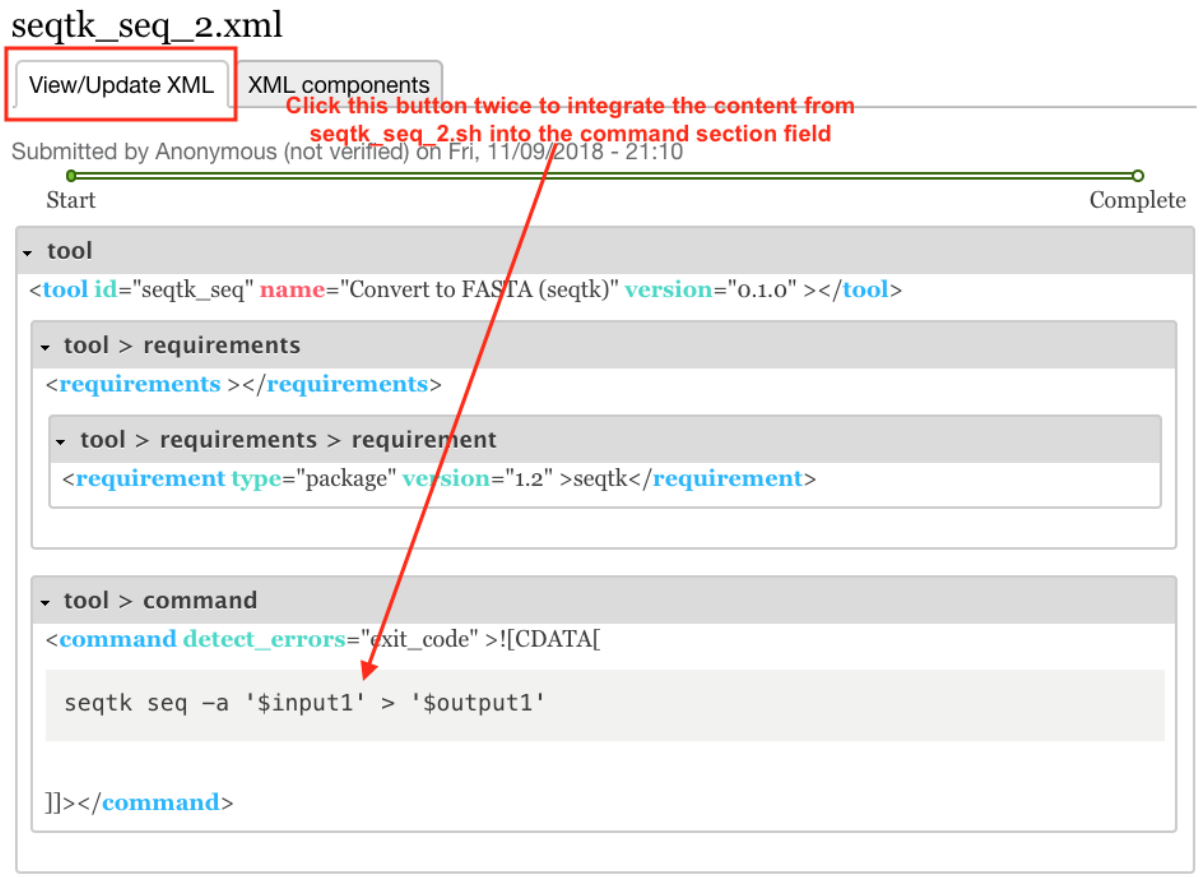
Add **tool->command** component



Edit **tool->command** component attributes.



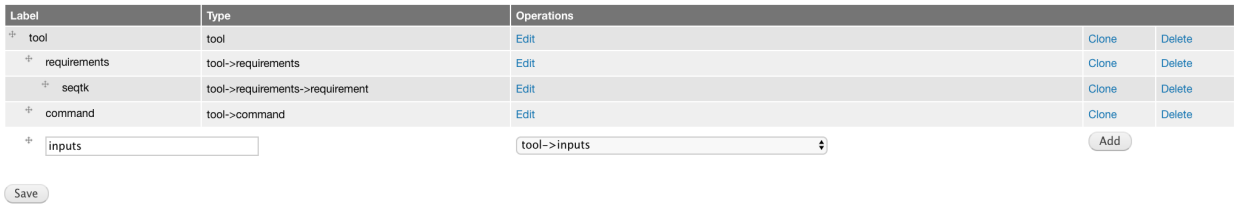
The **XML value** field in the above web form is used to collect the shell script for the command section. However, there is an easier way to input shell script into the tool XML file. Go to the **gtg_dev_dir/galaxy_tool_repository** and create a `.sh` file. Put the shell script into this file, the content will be automatically integrated into the web form field when the XML webform page is being viewed (see the image below). The `.sh` file should have exact the same base name as the XML file. For example, in this example, the XML file is `seqtk_seq_2.xml`, then the `.sh` file should be `seqtk_seq_2.xml`.



4. Create tool->inputs component

```
  <inputs>
    <param type="data" name="input1" format="fastq" />
</inputs>
```

Add **tool->inputs** component



Edit **tool->inputs** component attributes

In this example, we don't need to edit any attributes for this component.

Attributes

Tag sets for this element.

Action

URL used by data source tools.

Check values

- True
- False

Set to false to disable parameter checking in data source tools.

Method

- get
- put

Data source HTTP action (e.g. get or put) to use.

Target

UI link target to use for data source tools (e.g. _top).

Nginx upload

- True
- False

This boolean indicates if this is an upload tool or not.

Save component

Add **tool->inputs->param(type: data)** component

Label	Type	Operations		
tool	tool	Edit	Clone	Delete
requirements	tool->requirements	Edit	Clone	Delete
seqtk	tool->requirements->requirement	Edit	Clone	Delete
command	tool->command	Edit	Clone	Delete
inputs	tool->inputs	Edit	Clone	Delete
input_data	tool->inputs->param(type: data)	Add		

Save

Edit **tool->inputs->param(type: data)** component attributes

Attributes

Tag sets for this element.

Name *

input1

Name for this element. This name is used as the Cheetah variable containing the user-supplied parameter name in command and configfile elements. The name should not contain pipes or periods (e.g. .). Some "reserved" names are REDIRECT_URL, DATA_URL, GALAXY_URL.

Argument

If the parameter reflects just one command line argument of a certain tool, this tag should be set to that particular argument. It is rendered in parenthesis after the help section, and it will create the name attribute from the argument attribute by stripping the dashes (e.g. if argument="--sensitive" then name="sensitive" is implicit).

Label

The attribute value will be displayed on the tool page as the label of the form field (label="Sort Query").

Help

Short bit of text, rendered on the tool form just below the associated field to provide information about the field. Find the Intergalactic Utilities Commision suggested best practices for this element here.

Optional

- False
- True

If false, parameter must have a value. Defaults to "false".

Refresh on change

- False
- True

Force a reload of the tool panel when the value of this parameter changes to allow code file processing. See deprecation-like notice for code blocks.

Format

fasta

Only if type attribute value is data or data_collection - the list of supported data formats is contained in the /config/datatypes_conf.xml.sample file. Use the file extension.

Multiple

- True
- False

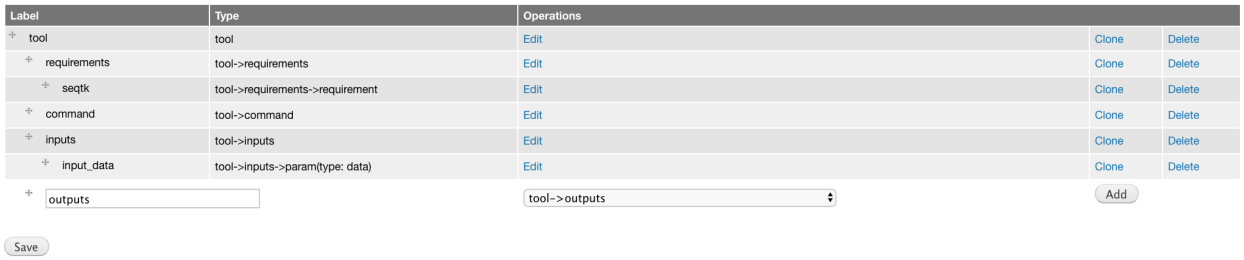
Allow multiple valus to be selected. Valid with data and select parameters.

Save component

5. Create tool->outputs component

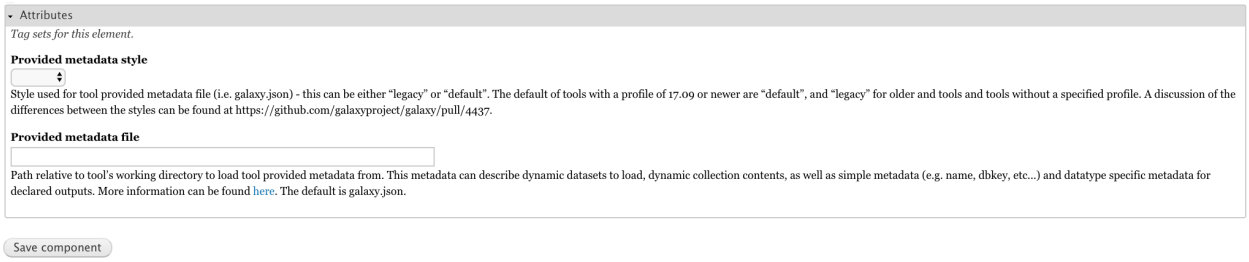
```
<outputs>
    <data name="output1" format="fasta" />
</outputs>
```

Add **tool->outputs** component



Edit **tool->outputs** component attributes

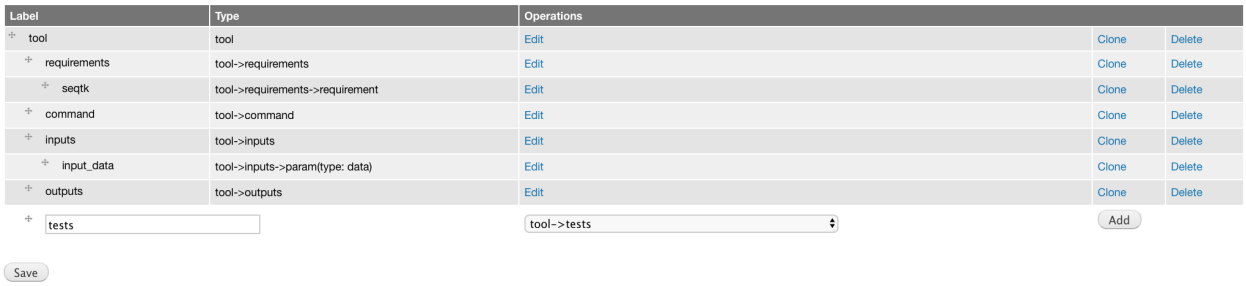
In this example, we don't need to edit any attributes for this component.



6. Create tool->tests component

```
  <tests>
    <test>
        <param name="input1" value="2.fastq"/>
        <output name="output1" file="2.fasta"/>
    </test>
</tests>
```

Add **tool->tests** component



Edit **tool->tests** component attributes

This component does not have attributes

Attributes

Tag sets for this element.

Save component

Add **tool->tests->test** component

Label	Type	Operations		
tool	tool	Edit	Clone	Delete
requirements	tool->requirements	Edit	Clone	Delete
seqtk	tool->requirements->requirement	Edit	Clone	Delete
command	tool->command	Edit	Clone	Delete
inputs	tool->inputs	Edit	Clone	Delete
input_data	tool->inputs->param(type: data)	Edit	Clone	Delete
outputs	tool->outputs	Edit	Clone	Delete
tests	tool->tests	Edit	Clone	Delete
test	tool->tests->test		Add	

Save

Edit **tool->tests->test** component attributes

This component does not have attributes

Attributes

Tag sets for this element.

Save component

Add **tool->tests->test->param** component

Label	Type	Operations		
tool	tool	Edit	Clone	Delete
requirements	tool->requirements	Edit	Clone	Delete
seqtk	tool->requirements->requirement	Edit	Clone	Delete
command	tool->command	Edit	Clone	Delete
inputs	tool->inputs	Edit	Clone	Delete
input_data	tool->inputs->param(type: data)	Edit	Clone	Delete
outputs	tool->outputs	Edit	Clone	Delete
tests	tool->tests	Edit	Clone	Delete
test	tool->tests->test	Edit	Clone	Delete
input1	tool->tests->test->param		Add	

Save

Edit **tool->tests->test->param** component attributes

Attributes

Tag sets for this element.

Name *

2.fastq

This value must match the name of the associated input parameter (param).

Value

File type

This attribute name should be included only with parameters of type data for the tool. If this attribute name is not included, the functional test framework will attempt to determine the data type for the input dataset using the data type sniffers.

dbkey

Specifies a dbkey value for the referenced input dataset. This is only valid if the corresponding parameter is of type data.

Save component

Add **tool->tests->test-output** component

Label	Type	Operations		
tool	tool	Edit	Clone	Delete
requirements	tool->requirements	Edit	Clone	Delete
seqtk	tool->requirements->requirement	Edit	Clone	Delete
command	tool->command	Edit	Clone	Delete
inputs	tool->inputs	Edit	Clone	Delete
input_data	tool->inputs->param(type: data)	Edit	Clone	Delete
outputs	tool->outputs	Edit	Clone	Delete
tests	tool->tests	Edit	Clone	Delete
test	tool->tests->test	Edit	Clone	Delete
input1	tool->tests->test->param	Edit	Clone	Delete
output1		tool->tests->test->output	Add	

Save

Edit **tool->tests->test-output** component attributes

Attributes

Tag sets for this element.

Name

output1

This value is the same as the value of the name attribute of the data tag set contained within the tool's outputs tag set.

File

2.fasta

If specified, this value is the name of the output file stored in the target test-data directory which will be used to compare the results of executing the tool via the functional test framework.

ftype

If specified, this value will be checked against the corresponding output's data type. If these do not match, the test will fail.

Sort

true

false

This flag causes the lines of the output to be sorted before they are compared to the expected output. This could be useful for non-deterministic output.

Value

An alias for file

md5

If specified, the target output's MD5 hash should match the value specified here. For large static files it may be inconvenient to upload the entry file and this can be used instead.

checksum

If specified, the target output's checksum should match the value specified here. This value should have the form hash_type:hash_value (e.g. sha1:8156d7ca0f46ed7abac98f82e36cfaddb2aca041). For large static files it may be inconvenient to upload the entiry file and this can be used instead.

Compare

diff

7. Create tool->help component

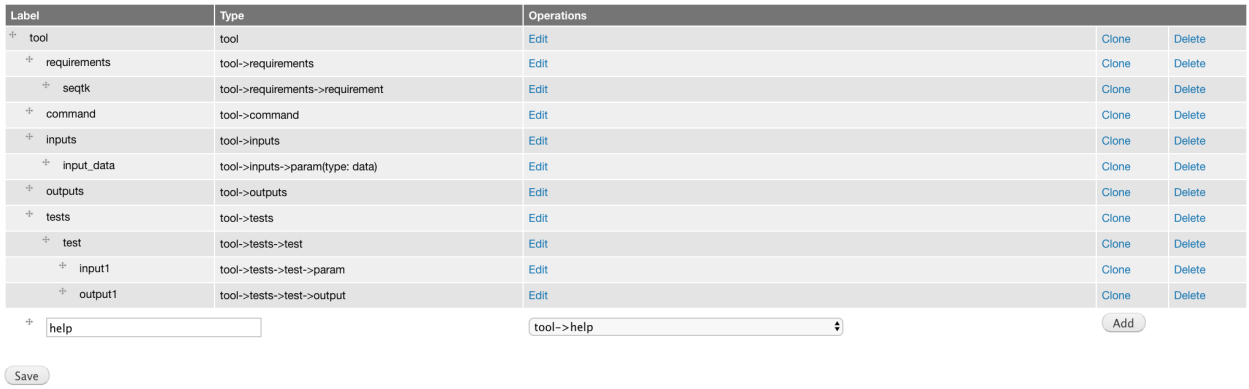
```
<help><![CDATA[

Usage:   seqtk seq [options] <in.fq>|<in.fa>
Options: -q INT    mask bases with quality lower than INT [0]
         -X INT    mask bases with quality higher than INT [255]
         -n CHAR   masked bases converted to CHAR; 0 for lowercase [0]
         -l INT    number of residues per line; 0 for 2^32-1 [0]
         -Q INT    quality shift: ASCII-INT gives base quality [33]
         -s INT    random seed (effective with -f) [11]
         -f FLOAT  sample FLOAT fraction of sequences [1]
         -M FILE   mask regions in BED or name list FILE [null]
         -L INT    drop sequences with length shorter than INT [0]
         -c        mask complement region (effective with -M)
         -r        reverse complement
         -A        force FASTA output (discard quality)
         -C        drop comments at the header lines
         -N        drop sequences containing ambiguous bases
         -1        output the 2n-1 reads only
         -2        output the 2n reads only
```

(continues on next page)

(continued from previous page)

```
        -V        shift quality by '(-Q) - 33'
        -U        convert all bases to uppercases
        -S        strip of white spaces in sequences
    ]]></help>
```

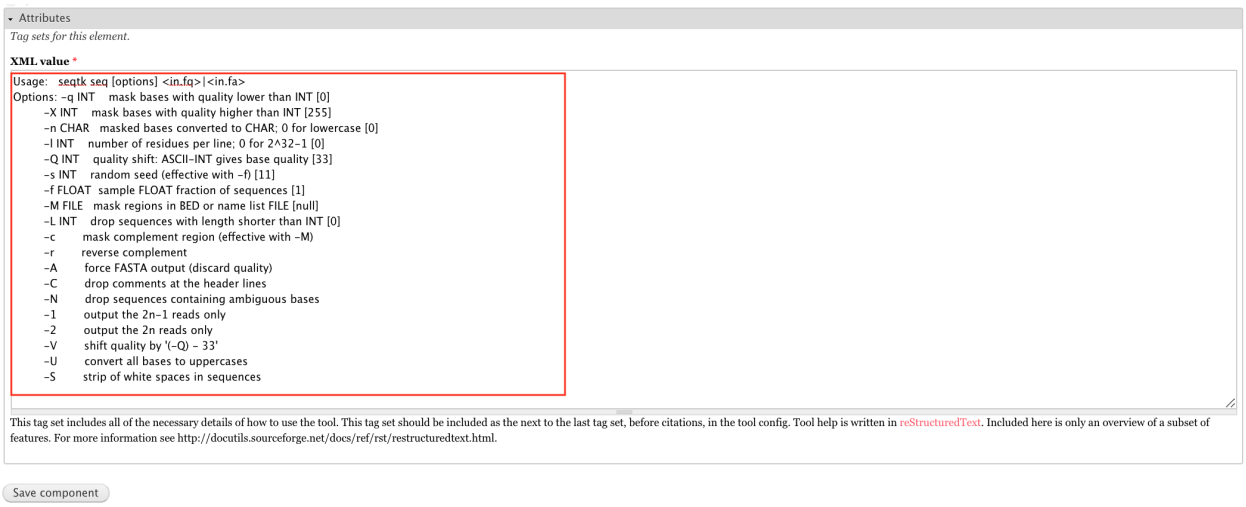
Add **tool->help** component



Label	Type	Operations		
tool	tool	Edit	Clone	Delete
requirements	tool->requirements	Edit	Clone	Delete
seqtk	tool->requirements->requirement	Edit	Clone	Delete
command	tool->command	Edit	Clone	Delete
inputs	tool->inputs	Edit	Clone	Delete
input_data	tool->inputs->param(type: data)	Edit	Clone	Delete
outputs	tool->outputs	Edit	Clone	Delete
tests	tool->tests	Edit	Clone	Delete
test	tool->tests->test	Edit	Clone	Delete
input1	tool->tests->test->param	Edit	Clone	Delete
output1	tool->tests->test->output	Edit	Clone	Delete
help		tool->help	Add	

Save

Edit **tool->help** component attributes



Attributes

Tag sets for this element.

XML value *

```
Usage:   seqtk seq [options] <in.fq>|<in.fa>
Options: -q INT    mask bases with quality lower than INT [0]
         -X INT    mask bases with quality higher than INT [255]
         -n CHAR   masked bases converted to CHAR; 0 for lowercase [0]
         -l INT    number of residues per line; 0 for 2^32-1 [0]
         -Q INT    quality shift: ASCII-INT gives base quality [33]
         -s INT    random seed (effective with -f) [11]
         -f FLOAT  sample FLOAT fraction of sequences [1]
         -M FILE   mask regions in BED or name list FILE [null]
         -L INT    drop sequences with length shorter than INT [0]
         -c        mask complement region (effective with -M)
         -r        reverse complement
         -A        force FASTA output (discard quality)
         -C        drop comments at the header lines
         -N        drop sequences containing ambiguous bases
         -1        output the 2n-1 reads only
         -2        output the 2n reads only
         -V        shift quality by '(-Q) - 33'
         -U        convert all bases to uppercases
         -S        strip of white spaces in sequences
```

This tag set includes all of the necessary details of how to use the tool. This tag set should be included as the next to the last tag set, before citations, in the tool config. Tool help is written in reStructuredText. Included here is only an overview of a subset of features. For more information see http://docutils.sourceforge.net/docs/ref/rst/restructuredtext.html.

Save component

8. Create tool->citations component

```
<citations>
        <citation type="bibtex">
@misc{githubseqtk,
  author = {LastTODO, FirstTODO},
  year = {TODO},
  title = {seqtk},
  publisher = {GitHub},
  journal = {GitHub repository},
  url = {https://github.com/lh3/seqtk},
}</citation>
    </citations>
```

Add **tool->citations** component

Label	Type	Operations		
tool	tool	Edit	Clone	Delete
requirements	tool->requirements	Edit	Clone	Delete
seqtk	tool->requirements->requirement	Edit	Clone	Delete
command	tool->command	Edit	Clone	Delete
inputs	tool->inputs	Edit	Clone	Delete
input_data	tool->inputs->param(type: data)	Edit	Clone	Delete
outputs	tool->outputs	Edit	Clone	Delete
tests	tool->tests	Edit	Clone	Delete
test	tool->tests->test	Edit	Clone	Delete
input1	tool->tests->test->param	Edit	Clone	Delete
output1	tool->tests->test->output	Edit	Clone	Delete
help	tool->help	Edit	Clone	Delete
citations	tool->citations		Add	

Save

Edit **tool->citations** component attributes

This component does not have attributes

Attributes

Tag sets for this element.

Save component

Add **tool->citations->citation** component

Label	Type	Operations		
tool	tool	Edit	Clone	Delete
requirements	tool->requirements	Edit	Clone	Delete
seqtk	tool->requirements->requirement	Edit	Clone	Delete
command	tool->command	Edit	Clone	Delete
inputs	tool->inputs	Edit	Clone	Delete
input_data	tool->inputs->param(type: data)	Edit	Clone	Delete
outputs	tool->outputs	Edit	Clone	Delete
tests	tool->tests	Edit	Clone	Delete
test	tool->tests->test	Edit	Clone	Delete
input1	tool->tests->test->param	Edit	Clone	Delete
output1	tool->tests->test->output	Edit	Clone	Delete
help	tool->help	Edit	Clone	Delete
citations	tool->citations	Edit	Clone	Delete
citation githubseqtk	tool->citations->citation		Add	

Save

Edit **tool->citations->citation** component attributes

Attributes

Tag sets for this element.

Title

doi

bibtex

Type of citation - currently doi and bibtex are the only supported options.

Citation *

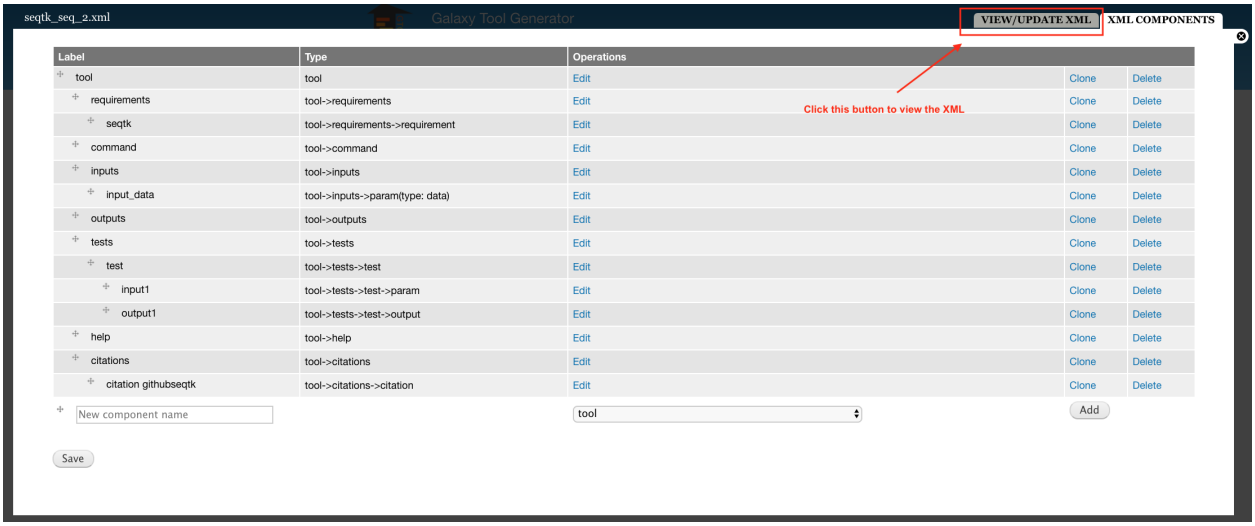
```
@misc{githubseqtk,
  author = {LastTODO, FirstTODO},
  year = {TODO},
  title = {seqtk},
  publisher = {GitHub},
  journal = {GitHub repository},
  url = {https://github.com/lh3/seqtk},
}
```

Citation in doi and bibtex format

Save component

9. View the complete XML file

Now you have created all the components for building the seqtk_seq_2.xml file, you can view the XML page to see how it look like on GTG. Of course, you can view the XML page any time you want. It doesn't have to be after you have added all the components.



Below is the XML page.

seqtk_seq_2.xml

View/Update XML | XML components

Submitted by Anonymous (not verified) on Fri, 11/09/2018 - 21:10

Start — Complete

tool

```
<tool id="seqtk_seq" name="Convert to FASTA (seqtk)" version="0.1.0" ></tool>
```

tool > requirements

```
<requirements ></requirements>
```

tool > requirements > requirement

```
<requirement type="package" version="1.2" >seqtk</requirement>
```

tool > command

```
<command detect_errors="exit_code" >![CDATA[

seqtk seq -a '$input1' > '$output1'

]]></command>
```

tool > inputs

```
<inputs ></inputs>
```

tool > inputs > param (type: data)

```
<param type="data" name="input1" optional="False" format="fasta" ></param>
```

tool > outputs

```
<outputs ></outputs>
```

tool > tests

```
<tests ></tests>
```

tool > tests > test

```
<test ></test>
```

tool > tests > test > param

```
<param name="2.fastq" ></param>
```

tool > tests > test > output

```
<output name="output1" file="2.fasta" compare="diff" ></output>
```

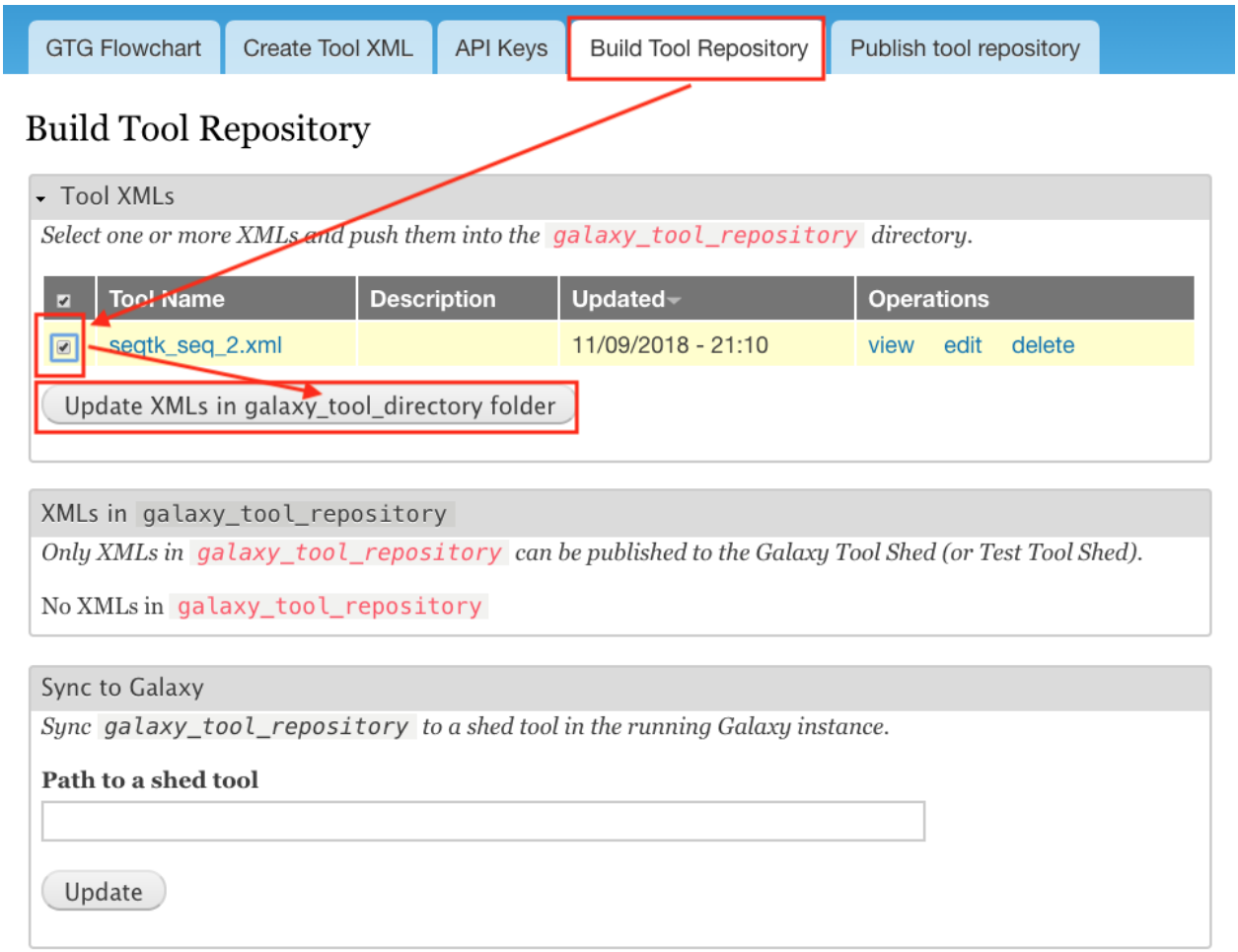
tool > help

```
<help >![CDATA[

Usage:   seqtk seq [options] |
```

Build tool repository

You have just created the `seqtk_seq_2.xml` file in GTG. However, this file is not in the `gtg_dev_dir/galaxy_tool_repository` directory yet. We need to the XML file into it, and any other non-XML files if there is any.

Click the **Build Tool Repository** tab and select any XML files that you want to add to the `gtg_dev_dir/galaxy_tool_repository` directory. And then click the *Update XMLs in galaxy_tool_directory folder*. **This is also the button that you use to add an updated XML to the directory**.



You should be able to see the `seqtk_seq_2.xml` file in the `gtg_dev_dir` directory.

```
.
├── database
│   ├── citations
│   ├── compiled_templates
│   ├── files
│   ├── object_store_cache
│   ├── session_map.sqlite
│   └── whoosh_indexes
├── galaxy_tool_repository
│   └── seqtk_seq_2.xml
└── shed_tools
```

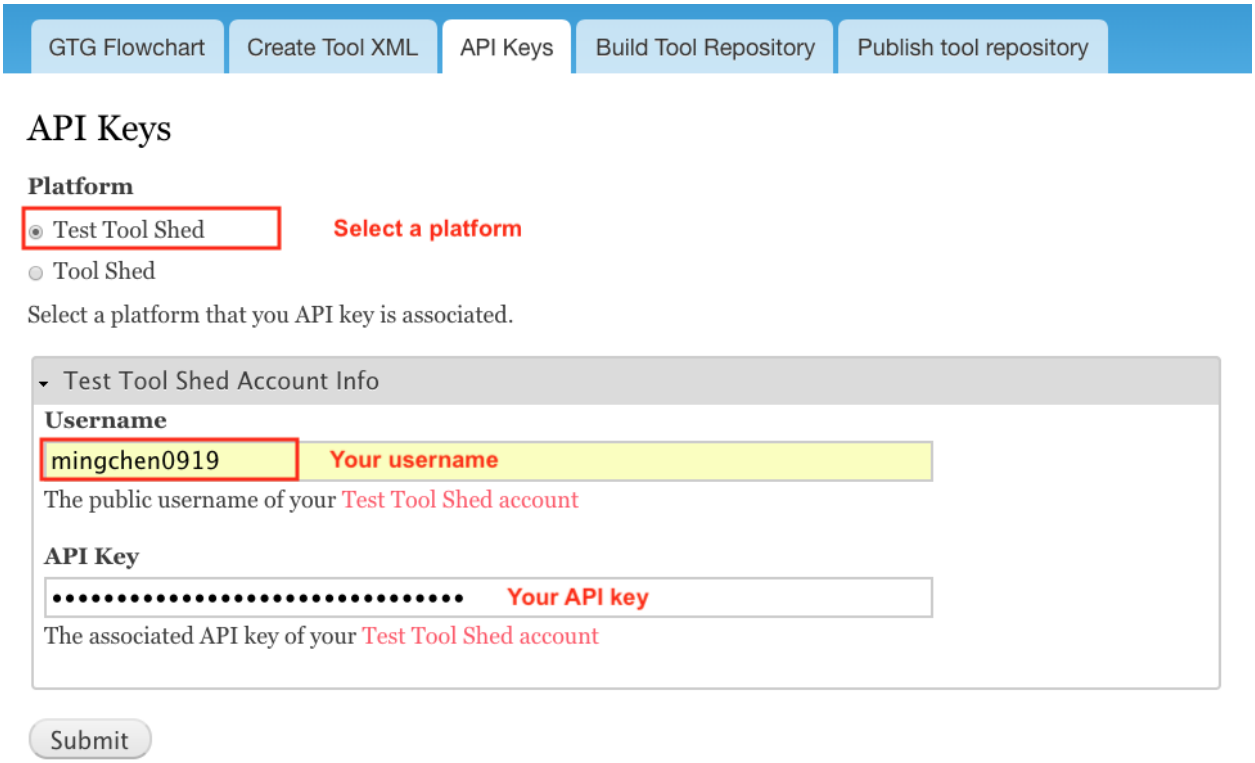
Add non-XML files

If this tool requires any other non-XML files (for example, test files, scripts, etc.), you can add them directory to the *gtg_dev_dir/galaxy_tool_repository* directory.

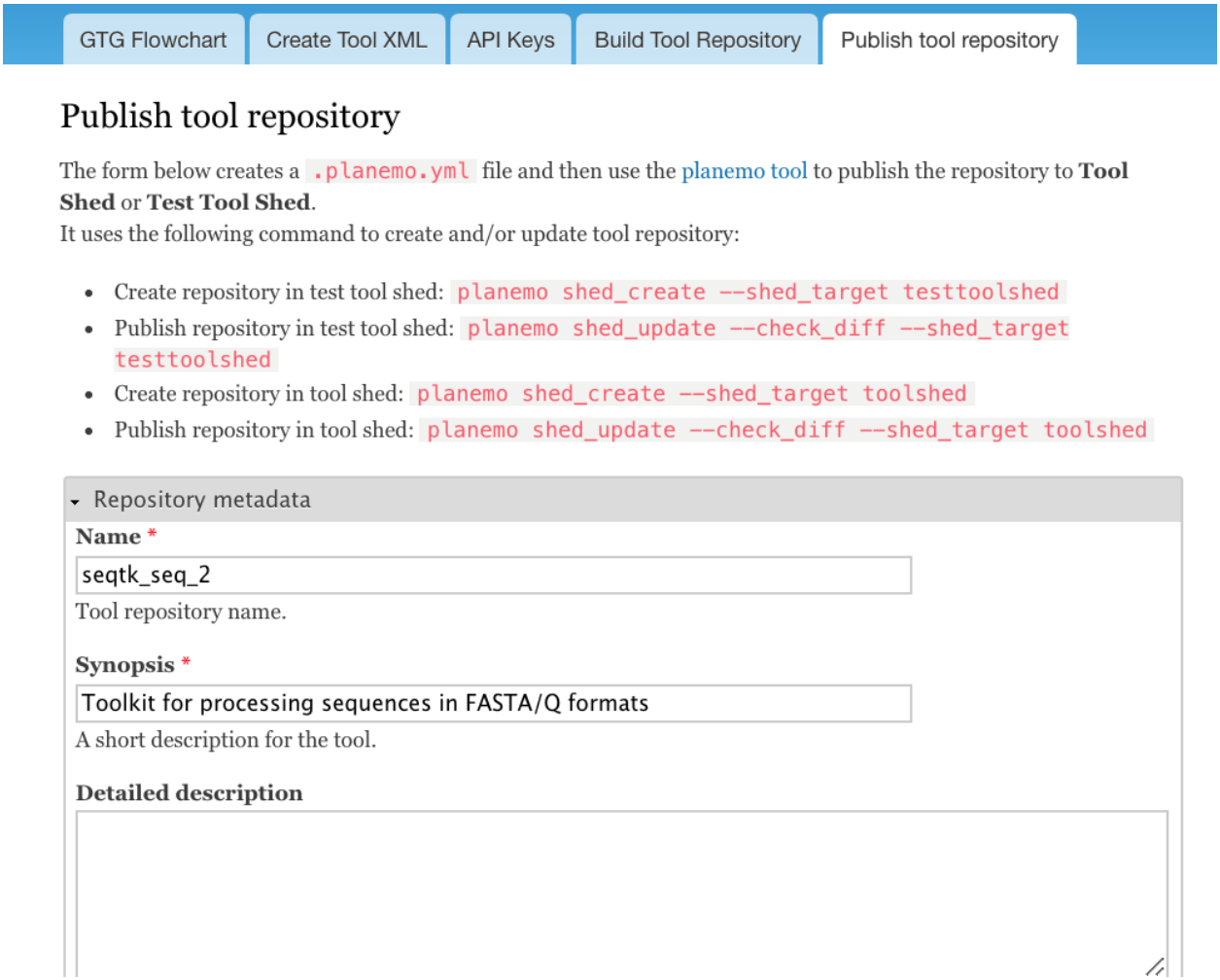
Publish tool to Test ToolShed

Once we have the XML file(s) and all other non-XML files in the *gtg_dev_dir/galaxy_tool_repository*, we can publish the tool to Test ToolShed or ToolShed with GTG.

First, we need to add the API key.



Then we can publish the tool through the interface below.



Install and test Tool in Galaxy

The next step would be to install and test the tool in the connected Galaxy instance. If the tool needs more work, you can use GTG to update the XML file.

The following interface is used to link the tool in GTG with the same tool installed in Galaxy so that the update will be automatically synced to Galaxy for testing.

Everytime you update XML file in Galaxy, you will need to restart Galaxy to integrate the updates. Below is the command to restart Galaxy.

```
docker exec -it gtg_galaxy sh -c 'supervisorctl restart galaxy:'
```

You expect to see the following stdout.

```
galaxy:galaxy_nodejs_proxy: stopped
galaxy:handler0: stopped
galaxy:handler1: stopped
galaxy:galaxy_web: stopped
galaxy:galaxy_nodejs_proxy: started
galaxy:galaxy_web: started
galaxy:handler0: started
galaxy:handler1: started
```

2.3 More examples

- [findSSRs tool](https://github.com/MingChen0919/gtgdocker/blob/master/example_tools/findSRRs/findSRRs.md): an example for developing [Aurora Galaxy Tools](https://github.com/statonlab/aurora-galaxy-tools).

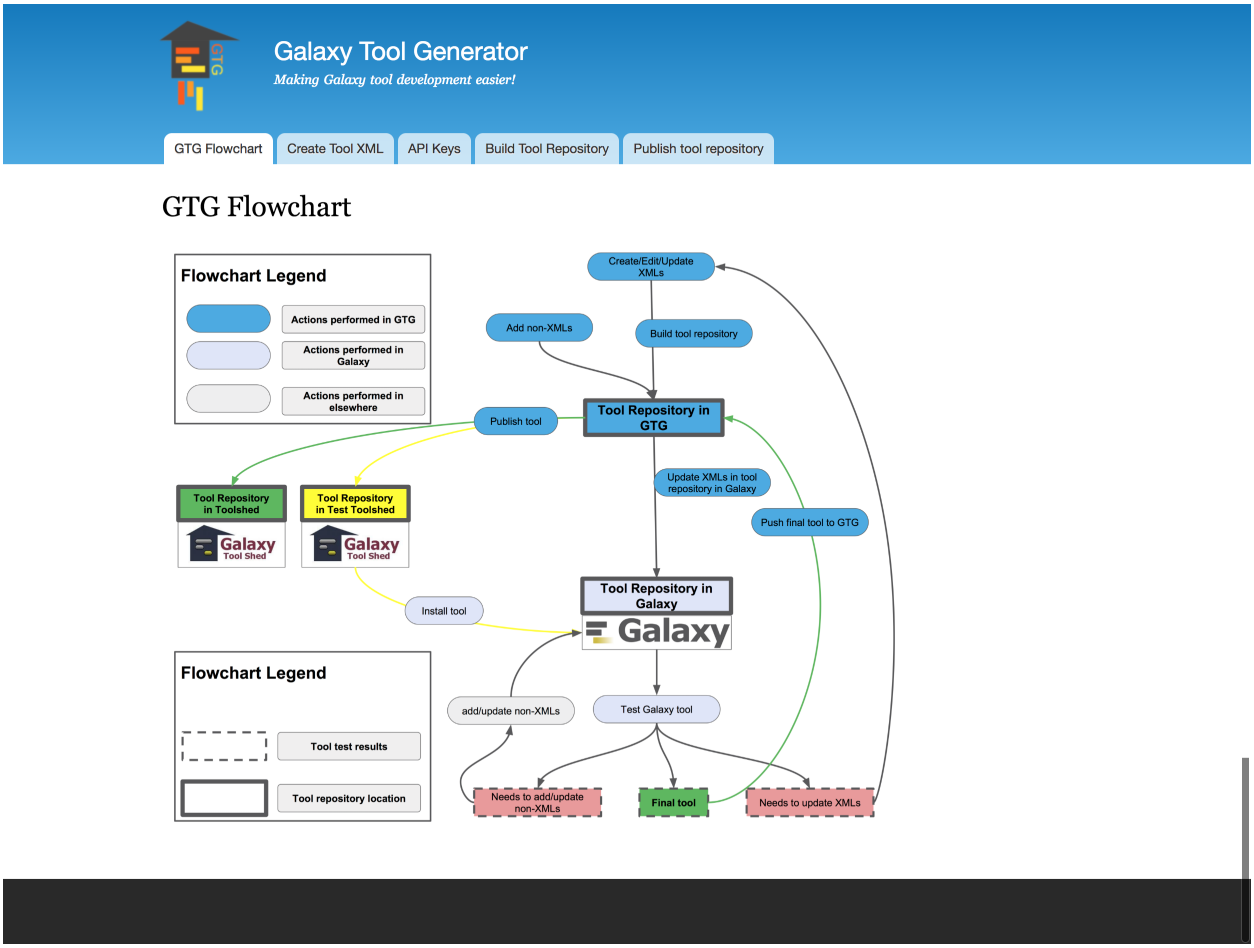
CHAPTER 3

Developer Guide

CHAPTER 4

What is Galaxy Tool Generator (GTG)?

GTG is a Drupal based web application which enables developing and publishing Galaxy tools through web interfaces. This web application consists of two Drupal modules: galaxy_tool_generator_ui and galaxy_tool_generator, and depends on the Drupal webform module.


Galaxy Tool Generator
Making Galaxy tool development easier!
GTG Flowchart
Create Tool XML
API Keys
Build Tool Repository
Publish tool repository
GTG Flowchart
Flowchart Legend
Actions performed in GTG
Actions performed in Galaxy
Actions performed in elsewhere
Create/Edit/Update XMLs
Add non-XMLs
Build tool repository
Publish tool
Tool Repository in GTG
Update XMLs in tool repository in Galaxy
Push final tool to GTG
Tool Repository in Toolshed
Tool Repository in Test Toolshed
Galaxy Tool Shed
Install tool
Tool Repository in Galaxy
Galaxy
Flowchart Legend
Tool test results
Tool repository location
add/update non-XMLs
Test Galaxy tool
Needs to add/update non-XMLs
Final tool
Needs to update XMLs