Welcome!

The easiest way to **navigate** this slide deck is by hitting `[space]` on your keyboard.

You can also navigate with arrow keys, but be careful because some slides can be nested inside of each other (vertically).
TOOL SHED
Sharing Galaxy tools
1. What is a Tool Shed?
= Galaxy App Store
= Galaxy App Store

- Galaxy tools
- Recipes for installing and compiling tools,
- Data Managers,
- Custom datatypes,
- Exported workflows.
Galaxy Tool Shed = Galaxy App Store

- For Galaxy administrators, facilitates:
  - installing/updating tools

- For tool developers, facilitates:
  - sharing of Galaxy utilities
  - versioning
Available Tool Sheds

- Galaxy community Tool Shed -> Main Tool Shed
- Galaxy community test Tool Shed -> Sandbox for testing
- List of public Tool Sheds
- IFB Tool Shed
### Tool Shed interface

![Galaxy Tool Shed](image)

#### Repositories by Category

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
<th>Repositories</th>
</tr>
</thead>
<tbody>
<tr>
<td>Assembly</td>
<td>Tools for working with assemblies</td>
<td>81</td>
</tr>
<tr>
<td>CHIP-seq</td>
<td>Tools for analyzing and manipulating CHIP-seq data.</td>
<td>41</td>
</tr>
<tr>
<td>Combinatorial Selections</td>
<td>Tools for combinatorial selection</td>
<td>6</td>
</tr>
<tr>
<td>Computational chemistry</td>
<td>Tools for use in computational chemistry</td>
<td>27</td>
</tr>
<tr>
<td>Constructive Solid Geometry</td>
<td>Tools for constructing and analyzing 3-dimensional shapes and their properties</td>
<td>11</td>
</tr>
<tr>
<td>Convert Formats</td>
<td>Tools for converting data formats</td>
<td>68</td>
</tr>
<tr>
<td>Data Export</td>
<td>Tools for exporting data to various destinations</td>
<td>1</td>
</tr>
</tbody>
</table>

**Tool categories**: Assembly, CHIP-seq, Combinatorial Selections, Computational chemistry, Constructive Solid Geometry, Convert Formats, Data Export

**Description of the category**: Tools for working with assemblies, Tools for analyzing and manipulating CHIP-seq data, Tools for combinatorial selection, Tools for use in computational chemistry, Tools for constructing and analyzing 3-dimensional shapes and their properties, Tools for converting data formats, Tools for exporting data to various destinations

**Nb of repositories per category**: 81, 41, 6, 27, 11, 68, 1
Example of tool
2. Installing tools from a Tool Shed
Connect your Galaxy to a Tool Shed

- Connect your Galaxy to a Tool Shed in config/tool_sheds_conf.xml:

```xml
<tool_sheds>
  <tool_shed name="Galaxy main tool shed" url="https://toolshed.g2.bx.psu/>
</tool_sheds>
```
Connect your Galaxy to a Tool Shed

- Set dependencies resolution
  - in `config/galaxy.ini`:
    ```
    conda_prefix = <tool_dependency_dir>/.conda/
    conda_auto_install = True
    conda_auto_init = False
    tool_dependency_dir = ../tool_dependencies
    ```
  - in `config/dependency_resolvers_conf.xml` (be careful order matters):
    ```
    <dependency_resolvers>
    <conda />
    <conda_versionless="true" />
    <tool_shed_packages />
    <galaxy_packages />
    <galaxy_packages_versionless="true" />
    </dependency_resolvers>
    ```

- Restart Galaxy
Install a tool from the Tool Shed

• Go to the admin interface and click on "Search Tool Shed" 

• Select a Tool Shed
Install a tool from the Tool Shed

- Search your tool

<table>
<thead>
<tr>
<th>Name</th>
<th>Synopsis</th>
<th>Type</th>
<th>Installable Revisions</th>
<th>Owner</th>
</tr>
</thead>
<tbody>
<tr>
<td>align_and_estimate_abundance</td>
<td>align_and_estimate_abundance.pl utility from trinityrnaseq package</td>
<td>Unrestricted</td>
<td>3 (2015-08-28)</td>
<td>anmoijh</td>
</tr>
<tr>
<td>package_trinity_2_0_6</td>
<td>Contains a tool dependency definition that downloads and compiles version 2.0.6 of Trinity</td>
<td>Tool dependency definition</td>
<td>0 (2015-11-20)</td>
<td>iuc</td>
</tr>
<tr>
<td>package_trinity_2_1_1</td>
<td>Contains a tool dependency definition that downloads and compiles version 2.1.1 of Trinity</td>
<td>Tool dependency definition</td>
<td>8 (2016-07-11)</td>
<td>iuc</td>
</tr>
<tr>
<td>package_trinity_2_2_0</td>
<td>Contains a tool dependency definition that downloads and compiles version 2.2.0 of Trinity</td>
<td>Tool dependency definition</td>
<td>0 (2016-07-27)</td>
<td>iuc</td>
</tr>
<tr>
<td>package_trinymrnaseq_2013_08_14</td>
<td>Contains a tool dependency definition that downloads and compiles version 2013_08_14 of trinity</td>
<td>Tool dependency definition</td>
<td>0 (2015-02-10)</td>
<td>jjohnson</td>
</tr>
<tr>
<td>package_trinymrnaseq_20140717</td>
<td>Contains a tool dependency definition that downloads and compiles version 20140717 of trinity</td>
<td>Tool dependency definition</td>
<td>9 (2015-09-03)</td>
<td>anmoijh</td>
</tr>
<tr>
<td>suite_trinity</td>
<td>Trinity tools to assemble transcript sequences from Illumina RNA-Seq data.</td>
<td>Repository suite definition</td>
<td>0 (2016-08-01)</td>
<td>iuc</td>
</tr>
<tr>
<td>trinity</td>
<td>Trinity (from the Trinity tool suite)</td>
<td>Unrestricted</td>
<td>10 (2016-08-01)</td>
<td>iuc</td>
</tr>
</tbody>
</table>
Install a tool from the Tool Shed

- Types of repository
  - Tool (orange): contains tools (tool wrappers)
  - Tool dependencies (red): contains only the file tool_dependencies.xml. !! tool_dependencies.xml file is no longer supported because of the use of conda! Required name: package_*
  - Tool suite (blue): contains only the file repository_dependencies.xml. Required name: suite_*
Install a tool from the Tool Shed

• Install the tool
Install a tool from the Tool Shed

- Install the tool

Reposotory README file - may contain important installation or license information

Confirm dependency installation

These dependencies can be automatically handled with the installed repository, providing significant benefits, and Galaxy includes various features to manage them.

Handle repository dependencies?

- Un-check to skip automatic installation of these additional repositories required by this repository.

When available, install tool shed managed dependencies?

- Un-check to skip automatic handling of these tool dependencies.

Tool dependencies - repository tool require handling of these dependencies

When available, install externally managed dependencies (e.g., conda) (Beta)

- Un-check to skip automatic installation of these dependencies.

Choose the tool panel section to contain the installed tools (optional)

Add new tool panel section:

Add a new tool panel section to contain the installed tools (optional).

Select existing tool panel section:

- Choose an existing section in your tool panel to contain the installed tools (optional).

Install

Clicking Install without selecting a tool panel section will load the installed tools into the tool panel outside of any sections.

- Selecting TS AND conda will make Galaxy to install both

- Recommended: use conda
Install a tool from the Tool Shed

- Check

<table>
<thead>
<tr>
<th>Monitor installing repositories</th>
</tr>
</thead>
<tbody>
<tr>
<td>Name</td>
</tr>
<tr>
<td>-------------------------------</td>
</tr>
<tr>
<td>Trinity</td>
</tr>
<tr>
<td>package_tiny.1.2.0</td>
</tr>
<tr>
<td>package_euroview.1.10.0</td>
</tr>
<tr>
<td>package.rqbc.3.2.1</td>
</tr>
<tr>
<td>package_tntcoref.2.11.1</td>
</tr>
<tr>
<td>package_hmogene.2.5.2</td>
</tr>
<tr>
<td>package_gnome.0.32.6</td>
</tr>
<tr>
<td>package_gnome.1.12.14</td>
</tr>
<tr>
<td>package_gnome.2.2.0</td>
</tr>
<tr>
<td>package_bioconductor lamein.2.20.10</td>
</tr>
<tr>
<td>package_bioconductor edgeR.3.14.0</td>
</tr>
</tbody>
</table>
Manage installed tools

- Admin > Manage installed tools

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
<th>Owner</th>
<th>Revision</th>
<th>Installation Status</th>
<th>Tool shed</th>
</tr>
</thead>
<tbody>
<tr>
<td>package_atta_3_10</td>
<td>Automatically Tuned Linear Algebra Software</td>
<td>uc</td>
<td>9bc017ec30b</td>
<td>Installed</td>
<td>toshesh.g2.bsc.edu</td>
</tr>
<tr>
<td>package_bowtie_1_1_2</td>
<td>Contains a tool dependency definition that downloads and compiles version 1.1.2 of bowtie2.</td>
<td>uc</td>
<td>d1c1d62e31b</td>
<td>Installed</td>
<td>toshesh.g2.bsc.edu</td>
</tr>
<tr>
<td>package_bowtie_2_2_6</td>
<td>Contains a tool dependency definition that downloads and compiles version 2.2.6 of bowtie2.</td>
<td>uc</td>
<td>97d7f4e73d6</td>
<td>Installed</td>
<td>toshesh.g2.bsc.edu</td>
</tr>
<tr>
<td>package_tophi_1_0</td>
<td>Contains a tool dependency definition that downloads and compiles version 1.0 of the topf library.</td>
<td>uc</td>
<td>a46c1723565</td>
<td>Installed</td>
<td>toshesh.g2.bsc.edu</td>
</tr>
<tr>
<td>package_ota_1_12_14</td>
<td>Contains a tool dependency definition to download and compile version 1.12.14 of the caro library.</td>
<td>uc</td>
<td>0b7f750b211</td>
<td>Installed</td>
<td>toshesh.g2.bsc.edu</td>
</tr>
<tr>
<td>package_make_3_2_3</td>
<td>CMake, the cross-platform, open-source build system.</td>
<td>uc</td>
<td>1e56068a25d</td>
<td>Installed</td>
<td>toshesh.g2.bsc.edu</td>
</tr>
<tr>
<td>package_deseq2_1_10_0</td>
<td>Contains a tool dependency definition that downloads and compiles version 1.10.0 of DESeq2.</td>
<td>uc</td>
<td>e4b13a7e30d</td>
<td>Installing tool dependencies</td>
<td>toshesh.g2.bsc.edu</td>
</tr>
</tbody>
</table>
Manage installed tools

- Click on the name of a tool
  - Manage and browse the repository
Tips: How to install workflows
How to install a workflow?

- Admin > Search Tool Shed
- Search the workflow

1. 

2. 

- Tools can come with the workflow if they are not yet installed
How to install a workflow?

- No workflow?
### How to install a workflow?

- **Click on the imported workflow**
How to install a workflow?

- Click on the workflow at the bottom of the “Contents of this repository” section
How to install a workflow?

- Repository Actions > Import workflow to Galaxy
How to install a workflow?

- Done!
3. Share your tool on a Tool Shed
3.1 Tool with dependencies
Tool with dependencies

tandem repeats finder

- test-data: 4.8 ko
- tandem_repeats_finder_wrapper.xml: 8.1 ko
- tandem_repeats_finder_wrapper.py: 4.2 ko

tandem_repeats_finder.tar.gz

Galaxy Tool Shed
Tool with dependencies

• Report the requirement in your wrapper in order to load environment with Conda
  tandem_repeats_finder_wrapper.xml

```xml
<requirements>
<requirement type="package" version="4.0">tandem_repeats_finder</requirement>
</requirements>
```
3.2 Tool suite: relationship between required repositories
Tool suite

Phylogeny pipeline

Fasta_to_phylip  Mafft  Trimal  Phylm

All wrappers in the same repository

Phylogeny pipeline

test-data
fasta_to_phylip_wrapper.xml  4,8ko  8,1ko
fasta_to_phylip.sh  4,2ko
mafft_wrapper.xml  8,1ko
phylm_wrapper.xml  4,2ko

phylogeny_pipeline.tar.gz
Tool suite

- One tool by repository
- How to link tools?
  - To install them together
Tool suite

- Repository dependencies
  - relationship between a dependent repository and one or more required repository (tools, datatypes, workflows,...)
  - -> One file

```xml
<?xml version="1.0"?>
<repositories description="Pipeline phylogeny">
<repository toolshed="http://testtoolshed.g2.bx.psu.edu"
    name="fasta_to_phylip" owner="gandres" changeset_revision="a895633"
<repository name="mafft" owner="gandres" />
<repository name="phylm" owner="gandres" />
[...]
</repositories>
```

- « toolshed » and « changeset_revision » are optional but they are completed during upload on the toolshed
Tool suite
Tool suite

```xml
<?xml version="1.0"?>
<repositories description="Pipeline phylogeny">
  <repository name="mafft" owner="gandres" />
</repositories>
```

```xml
<?xml version="1.0"?>
<repositories description="Pipeline phylogeny">
  <repository name="mafft" owner="gandres" toolshed="http://testtoolshed">
  </repository>
</repositories>
```
Tool suite

• New tool version
  ▪ Latest version is no longer
    changeset_revision="a895633568"
  ▪ Reload repository_dependencies.xml file in your
    repository
3.3 Workflow
Workflow

- How to order tools?
Workflow

• In galaxy
Workflow

• You get a file: Galaxy-Workflow-NAME.ga
Workflow

- You have your file Galaxy-Workflow-NAME.ga
- How to automatically import all tools?
  - -> repository_dependencies.xml

```xml
<?xml version="1.0"?>
<repositories description="Phylogeny workflow">
<repository name="suite_phylogeny" owner="galaxy" />
</repositories>
```
Workflow
Workflow

- Everything must be on the same toolshed
Tips: what about tools working with *.loc files or new datatypes
Tools with *.loc files or new datatypes

- add them to the Tool Shed repository.
- *.loc files and datatypes files should be provided as *.sample file in a tool-data directory.
- tool-data/*.loc.sample files come along with tool_data_table_conf.xml.sample. Their content or the file themselves are put to the right location on tool set up.
Tools with .*loc files or new datatypes

- tool_data_table_conf.xml.sample

```xml
<tables>
  <!-- Locations of indexes in the Bowtie2 mapper format -->
  <table name="bowtie2_indices" comment_char="#">
    <columns>value, dbkey, name, path</columns>
    <file path="tool-data/bowtie2_indices.loc" />
  </table>
</tables>
```

On install, the content of the file and the right path to the .*loc file is added to

shed_tool_data_table_conf.xml
4. Publication with Planemo
Configuration

- Creates `.planemo.yml` file in your home directory

```yaml
## Planemo Global Configuration File.
## Everything in this file is completely optional - these values can all be
## configured via command line options for the corresponding commands.

## Specify a default galaxy_root for test and server commands here.
galaxy_root: /path/to/galaxy_root

## Username used with toolshed(s).
shed_username: "<TODO>"

sheds:
  toolshed:
    #key: "<TODO>"
    #email: "<TODO>"
    #password: "<TODO>"
  testtoolshed:
    #key: "<TODO>"
    #email: "<TODO>"
    #password: "<TODO>"
  local:
    #key: "<TODO>"
    #email: "<TODO>"
    #password: "<TODO>"
```
Configuration

planemo config_init

```yaml
## Planemo Global Configuration File.
## Everything in this file is completely optional - these values can all be
## configured via command line options for the corresponding commands.

## Specify a default galaxy_root for test and server commands here.
galaxy_root: /path/to/galaxy_root

## Username used with toolshed(s).
shed_username: "<TODO>"

sheds:

  toolshed:
    key: "ecj41p80g056545f2be3df671c638jlp"
    #email: "<TODO>"
    #password: "<TODO>"

  testtoolshed:
    key: "<TODO>"
    email: "gt@france-bioinformatique.fr"
    password: "secret"

local:

  #key: "<TODO>"
  #email: "<TODO>"
  #password: "<TODO>"
```
Creation

```
planemo shed_init --name="tandem_repeats_finder_2"
    --owner="gandres"
    --description="Tandem Repeats Finder description"
    --long_description="A long long description."
    --category="Sequence Analysis"
    [--remote_repository_url=<URL to .shed.yml on github]
    [--homepage_url=<Homepage for tool.>]
```

- Create .shed.yml file in the current repository (tool repository)
Planemo will determine the repository type based on these conventions
Creation

- Tools and tool suite .shed.yml:
  - implicitly define repositories for each individual tool in the directory and build a suite for those

```yaml
[...]
auto_tool_repositories:
  name_template: "{{ tool_id }}"
  description_template: "{{ tool_name }} (from the Trinity tool suite)"
suite:
  name: "suite_trinity"
  description: Trinity tools to assemble transcript sequences from Illumina RNA-Seq data.
```
Creation

$ planemo shed_lint --tools

Linting repository [...]/tandem_repeats_finder
Applying linter expansion... CHECK
.. INFO: Included files all found.
Applying linter tool_dependencies_xsd... CHECK
.. INFO: tool_dependencies.xml found and appears to be valid XML
Applying linter tool_dependencies_actions... CHECK
.. INFO:Parsed tool dependencies.
Applying linter repository_dependencies... CHECK
.. INFO: No repository_dependencies.xml, skipping.
Applying linter shed_yaml... CHECK
.. INFO: .shed.yml found and appears to be valid YAML.
Applying linter readme... CHECK
.. INFO: No README found skipping.
+Linting tool [...]/tandem_repeats_finder/tandem_repeats_finder_wrapper.xml
[...]
Creation

$ planemo shed_create --shed_target testtoolshed

Repository created
cd '[…]'/tandem_repeats_finder' && git rev-parse HEAD
Repository tandem_repeats_finder_2 updated successfully.

<table>
<thead>
<tr>
<th>Repository tandem_repeats_finder_2</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Name:</strong> tandem_repeats_finder_2</td>
</tr>
<tr>
<td><strong>Owner:</strong> gandres</td>
</tr>
<tr>
<td><strong>Synopsis:</strong> Tandem Repeats Finder description</td>
</tr>
<tr>
<td><strong>Detailed description:</strong></td>
</tr>
<tr>
<td>A long long description.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Content homepage:</th>
</tr>
</thead>
<tbody>
<tr>
<td>Development repository:</td>
</tr>
<tr>
<td>Sharable link to this repository: <a href="http://localhost:9009/view/gandres/tandem_repeats_finder_2/627f3110ba06">http://localhost:9009/view/gandres/tandem_repeats_finder_2/627f3110ba06</a></td>
</tr>
<tr>
<td>Clone this repository:</td>
</tr>
<tr>
<td>[hg clone <a href="http://gandres@localhost:9009/repos/gandres/tandem_repeats_finder_2/627f3110ba06">http://gandres@localhost:9009/repos/gandres/tandem_repeats_finder_2/627f3110ba06</a>](<a href="http://gandres@localhost:9009/repos/gandres/tandem_repeats_finder_2/627f3110ba06">http://gandres@localhost:9009/repos/gandres/tandem_repeats_finder_2/627f3110ba06</a>)</td>
</tr>
<tr>
<td>Repository type:</td>
</tr>
<tr>
<td>Unrestricted</td>
</tr>
<tr>
<td>Revision:</td>
</tr>
<tr>
<td>627f3110ba06</td>
</tr>
<tr>
<td>This revision can be installed:</td>
</tr>
<tr>
<td>True</td>
</tr>
</tbody>
</table>
Creation

$ planemo shed_create --shed_target testtoolshed

Repository created

cd '([...)/tandem_repeats_finder' && git rev-parse HEAD

Repository tandem_repeats_finder_2 updated successfully.

• Don't forget --shed_target. Default is main toolshed
Update

$ planemo shed_diff --shed_target testtoolshed

```bash
wget -q --recursive -0 -
'https://testtoolshed.g2.bx.psu.edu/repository/download?repository_id=6306156e4da9a8bf&changeset_revision=default&file_type=gz' | tar -xzf - -C/tmp/tool_shed_diff_DMc0R_/testtoolshed --strip-components 1
mkdir "/tmp/tool_shed_diff_DMc0R_/local"; tar -xzf "/tmp/tmp5ousfg" -C"/tmp/tool_shed_diff_DMc0R_/local"; rm -rf /tmp/tmp5ousfg

cd "/tmp/tool_shed_diff_DMc0R"; diff -r _local _testtoolshed

diff -r _local /tandem_repeats_finder.xml _testtoolshed/tandem_repeats_finder.xml

dl40

<param name="fileout_label2" type="text" value="Unused"
label="none" help="Output name for files" />
```

- Need to be updated
Update

```
$ planemo shed_update --check_diff --shed_target testtoolshed
```

- Tool updated
Update

$ planemo shed_update --check_diff --shed_target testtoolshed

• Tool updated
References

- ToolShed
- Install tools from the ToolShed
- Publish tools with Planemo
Hands-on
Start and configure your toolshed

- To start your toolshed (in galaxy home directory):
  - ./run_tool_shed.sh
- Toolshed available at:
  - http://localhost:9009
- Login under User tab:
  - galaxy/azerty
Publish your tool with Planemo

• Goal: Publish the seqtk_seq tool in your local toolshed with Planemo
Answers
Publish your tool with Planemo

- `planemo config_init`
  - create file `.planemo.yml` in your home directory

```yaml
[...] local:
#key: "<TODO>"
$email: "galaxy@localhost.fr"
#password: "azerty"
```
Publish your tool with Planemo

- `planemo shed_init --name=seqtk_seq --owner=galaxy --description="common transformation of FASTA/Q" --category="Fasta Manipulation"
- create file .shed.yml in your working dir:

```yaml
[categories: [Fasta Manipulation,Fastq Manipulation]
description: common transformation of FASTA/Q
name: seqtk_seq
owner: galaxy
```
Publish your tool with Planemo

- `planemo shed_lint`
  - Check Tool Shed repository for common issues.
- `planemo shed_create --shed_target local`
  - Create a repository in the toolshed and upload files

Modify your tool wrapper and then:

- `planemo shed_diff --shed_target local`
  - Diff between local repository and Tool Shed.
- `planemo shed_update --check_diff --shed_target local`
  - Update Tool Shed repository