Tripal File Documentation

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TRIPAL FILE EXTENSION MODULE

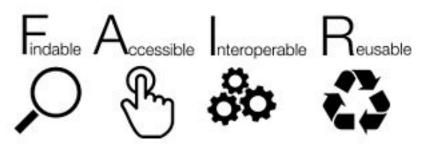
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CHAPTER

OVERVIEW

Warning: The Tripal file module is compatible only with Tripal v3.6 or higher.

The Tripal File module supports association of data files with content in a Chado database and for integration of those associations with content types on a Tripal website.



These associations are meant to support FAIR data principles by integrating with Tripal content web services such that:

- Files are findable and accessible via Tripal's content web services.
- Metadata about files use globally unique controlled vocabularies. These metadata can be assigned as properties of each file.
- License and usage details can be assigned to each file.

This module provides two new content types for Tripal sites: File and License.

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CHAPTER

INSTALLATION

2.1 Step 1: Module Installation

The Tripal File module is available as a full Drupal module. Therefore, it can be installed following the typical Drupal module installation either via the GUI or via Drush. We'll do so here using a Drush command:

drush pm-enable tripal_file

If you do not have the module already downloaded and available in the *sites/all/modules* folder of your Drupal site, then you will be asked if you would like to download and then enable the module.

The module will create two new content types: *File* and *License*. It will also create a variety of tables in your Chado database for associating files to base records. Upon installation you should see the following:

\$ drush pm-enable tripal_file

The following extensions will be enabled: tripal_file	
Do you really want to continue? (y/n) : y	
INFO (TRIPAL_ENTITIES): Done.	
INFO (TRIPAL_ENTITIES): Done.	C - 1-7
tripal_file was enabled successfully.	[ok]
Custom table, 'file', created successfully.	[status]
Custom table, 'license', created successfully.	[status]
Custom table, 'file_contact', created successfully.	[status]
Custom table, 'fileloc', created successfully.	[status]
Custom table, 'fileprop', created successfully.	[status]
Custom table, 'fileloc', already exists. Table structure not changed, but	[status]
definition array has been saved.	
Custom table, 'file_license', created successfully.	[status]
Custom table, 'analysis_file', created successfully.	[status]
Custom table, 'assay_file', created successfully.	[status]
Custom table, 'biomaterial_file', created successfully.	[status]
Custom table, 'cv_file', created successfully.	[status]
Custom table, 'eimage_file', created successfully.	[status]
Custom table, 'feature_file', created successfully.	[status]
Custom table, 'featuremap_file', created successfully.	[status]
Custom table, 'library_file', created successfully.	[status]
Custom table, 'nd_protocol_file', created successfully.	[status]
Custom table, 'organism_file', created successfully.	[status]
Custom table, 'phylotree_file', created successfully.	[status]
Custom table, 'project_file', created successfully.	[status]

(continues on next page)

(continued from previous page)

Custom table, 'pub_file', created successfully.	[status]
Custom table, 'stock_file', created successfully.	[status]
Custom table, 'stockcollection_file', created successfully.	[status]
Custom table, 'study_file', created successfully.	[status]
NOTICE: Added the EDAM ontology. Please navigate to Tripal >> Data L	oaders >>[status]
Chado Vocabularies >> OBO Vocabulary Loader and submit a job to impo	rt the
EDAM VOCADULALY.	

2.2 Step 2: Install the EDAM Vocabulary

The EDAM vocabulary is needed for the File module because it provides many of the file types (e.g. FASTA, GFF3, VCF, etc). Any file that is managed by the Tripal File module requires a file type.

The EDAM vocabulary details are automatically added by the Tripal File module, but you will need to install the vocaulary. To do this navigate to the Administration > Tripal > Data Loaders > Chado Vocabularies > OBO Vocabulary Loader page via the administrative menu. Select the EDAM vocabulary from the Ontology OBO File Reference drop down and click the Import OBO File.

2.3 Step 3: Set Permissions

Now that the Tripal File module is installed, we must set permissions so that users can view and or create File and License content types. To set permissions, navigate to **People** page and click the **Permissions** tab in the top right. Look for permissions that begin with prefix *File*: and *License*: and set the according to your needs.

PERMISSION	ANONYMOUS USER	AUTHENTICATED USER	ADMINISTRATOR
File: View Content Allow the user to view File content			<
<i>File</i> : Create Content Allow the user to create <i>File</i> content <i>Warning: Give to trusted roles only; this permission has security implications.</i>			Z
File: Edit Content Allow the user to edit File content Warning: Give to trusted roles only; this permission has security implications.			
<i>File</i> : Unpublish Content Allow the user to unpublish <i>File</i> content. Unpublishing of content removes it from visibility on the site but does not delete the record in the underlying database.			
<i>File</i> : Delete Content Allow the user to delete <i>File</i> content. When content is deleted it is first unpublished and then deleted from the database. <i>Warning: Give to trusted roles only; this permission has security implications.</i>			
License: View Content Allow the user to view License content			
<i>License</i> : Create Content Allow the user to create <i>License</i> content <i>Warning: Give to trusted roles only; this permission has security implications.</i>			
<i>License</i> : Edit Content Allow the user to edit <i>License</i> content <i>Warning: Give to trusted roles only; this permission has security implications.</i>			✓
<i>License</i> : Unpublish Content Allow the user to unpublish <i>License</i> content. Unpublishing of content removes it from visibility on the site but does not delete the record in the underlying database.			
<i>License</i> : Delete Content Allow the user to delete <i>License</i> content. When content is deleted it is first unpublished and then deleted from the database. <i>Warning: Give to trusted roles only; this permission has security implications</i> .			

Warning: You should not give the anonymous user any permissions other than 'view' permission.

CHAPTER

THREE

USAGE

3.1 Adding a License

To ensure data files offered by your Tripal site meet FAIR data principles, all files must be associated with a license. Therefore, before adding files, you must first create new **License** content types. You can create as many **License** files as needed for the data on your site.

To create a new license page, navigate to Admin > Add Tripal Content Types and scroll to the bottom of the page where the **Other** category is found. There you will see the **License** content type. Click the link to create a new license page.

lome » Add Tripal Content	
lame *	<u>i</u>
	a
 Web page addresses and e-mail addresses 	
Text format Filtered HTML V	More information about text formats 🕜
Web page addresses and e-mail addresses t	turn into links automatically.
	<cite> <blockquote> <code> <dl> <dt> <dd></dd></dt></dl></code></blockquote></cite>

To create your license page you can:

- 1. Option 1: Fully define the license by giving it a name and provide the full description
- 2. Option 2: Summarize the license by giving a name, providing a brief summary (or no summary) and providing the URL to the full license online.

Note: It is best practice to provide a human readable summary of the user's rights in the Summary field and to provide

a link to the full legal text of the license via the URI field.

3.1.1 Example Licenses

A few example licenses are provided below along with the values that may be appropriate for the License page fields.

3.1.1.1 Public Domain Data

Data that is public, where no on retains rights to it. Therefore, it needs a license page even though "public domain" is not an actual license. You can use the following values when creating a public domain license page:

Field	Value
Name	Public Domain
Summary	The data has no known copyrights or restrictions and can be be freely used by anyone.

3.1.1.2 CC0 1.0 Universal (CC0 1.0)

The text for the summary below came from https://creativecommons.org/publicdomain/zero/1.0/.

Field	Value
Name	CC0 1.0 Universal (CC0 1.0)
Summary	 The person who associated a work with this deed has dedicated the work to the public domain by waiving all of his or her rights to the work worldwide under copyright law, including all related and neighboring rights, to the extent allowed by law. You can copy, modify, distribute and perform the work, even for commercial purposes, all without asking permission. In no way are the patent or trademark rights of any person affected by CCO, nor are the rights that other persons may have in the work or in how the work is used, such as publicity or privacy rights. Unless expressly stated otherwise, the person who associated a work with this deed makes no warranties about the work, to the fullest extent permitted by applicable law. When using or citing the work, you should not imply endorsement by the author or the affirmer.
URI	https://creativecommons.org/publicdomain/zero/1.0/ legalcode

3.1.1.3 Attribution 4.0 International (CC BY 4.0)

The text for the summary below came from https://creativecommons.org/licenses/by/4.0/.

Field	Value
Name	Attribution 4.0 International (CC BY 4.0)
Summary	 You are free to: Share: copy and redistribute the material in any medium or format Adapt: remix, transform and build upon the material for any purpose, even commercially. The licensor cannot revoke these freedoms as long as you follow the following license terms: Attribution You must give appropriate credit, provide a link to the license, and indicate if changes were made. You may do so in any reasonable manner, but not in any way that suggests the licensor endorses you or your use. No additional restrictions You may not apply legal terms or technological measures that legally restrict others from doing anything the license permits
	Notices:
	 You do not have to comply with the license for elements of the material in the public domain or where your use is permitted by an applicable exception or limitation. No warranties are given. The license may not give you all of the permissions necessary for your intended use. For example, other rights such as publicity, privacy, or moral rights may limit how you use the material.
URI	https://creativecommons.org/licenses/by/4.0/legalcode

3.2 Adding a File

To demonstrate adding a file, we will provide an example using the genome files that are provided in the Tripal User's Guide in the section titled Setup of an Example Site. Those instructions direct the reader to create an **Analysis** page to represent the whole genome assembly of the *Citrus sinensis* v1.0 genome. We will associate the files to that analysis. If you have followed along with the Tripal User's Guide you will already have those files uploaded.

If you have not followed the Tripal User's Guide but would like to follow along here, you must follow these instructions to create an Analysis page. And obtain the files here:

- Citrus sinensis-orange1.1g015632m.g.gff3
- Citrus sinensis-scaffold00001.fasta
- Citrus sinensis-orange1.1g015632m.g.fasta

To create a new file page, navigate to Admin > Add Tripal Content Types and scroll to the bottom of the page where the **Other** category is found. There you will see the **File** content type. Click the link to create a new file page. The following page appears.

le ⊛	
Iome » Add Tripal Content	
lame *	
Description	
O Source X □ □ □ □ □ □ + → → Q □ □ ○ □ □ = □ ○ Ω X □	
Format - B I U S X x X I I I I I I I I I I I I I I I I I	
witch to plain text editor	
Text format Filtered HTML V	Ν
 Web page addresses and e-mail addresses turn into links automatically. Allowed HTML taos: <a> <cite> <blockguote> <code> <u > <o > <d > <dt> <dd><</dd></dt></d > </o ></u ></code></blockguote></cite>	
this page you can:	

- 1. Provide a **name** (required) and **description** for the file.
- 2. Indicate a file **type** (required).
- 3. Indicate the file source (or contact person) who was rights to the data.
- 4. Indicate the file **location** (either locally or via remote URL).
- 5. And set the **license** (required).

First, we will create the whole genome FASTA file page. Enter the following in the File page fields:

Field	Value
Name	Citrus sinesis Whole Genome Assembly v1.0
Description	The whole genome assembly, v1.0, of <i>Citrus sinensis</i> .
Туре	FASTA
File Source	Leave blank or provide any contact you may have already
Location	Citrus sinensis-scaffold00001.fasta
File License	Select whatever license you may have already added

If you already have the file uploaded to Tripal then it will automatically appear in the Tripal Managed File section:

DOWN	ILOAD *
	Remote URL
.t.	If the file is not managed by Drupal or Tripal then enter the full URL to the file. Use this field if the file is shared publicly on this same web server but not i
+++	Tripal Managed File
	Citrus_sinensis-scaffold00001.fasta
	Please select a file.
	Remote URL
	If the file is not managed by Drupal or Tripal then enter the full URL to the file. Use this field if the file is shared publicly on this same web server but not i
÷‡•	Tripal Managed File
	Select a File 🗸
	Please select a file.
The do	ownload location of the file.

Otherwise you can provide a remote URL for the file. If you have files on your site that are not managed by Tripal, you can use a URL here that points to the full path on your site. In both of these cases file size and md5 checksum cannot be automatically generated. Alternatively, you can use a public:// prefix for local files, in which case the file size and md5 checksum can be automatically included. As an example, you might upload a file to your local filesystem in the directory *sites/default/files/bulk_data/* and then you could specify a Remote URL of *public://bulk_data/Citrus_sinensisscaffold00001.fasta*

Note: A file can have more than one download location, and you can combine both local and remote files.

Note: Providing a file source or "contact" is optional, but is recommended. Every file with a license should indicate, via the "file source" field, who retains the license rights (if applicable).

After creation, the file page appears:

View Edit	Reload		
<u>Summary</u> File Source	Summary		×
License Location	Resource Type	File	
	Name	Citrus sinesis Whole Genome Assembly v1.0	
	Description	The whole genome assembly, v1.0, of <i>Citrus sinensis</i> .	
	File Type	FASTA format	
	License		×
	Name At	tribution 4.0 International (CC BY 4.0)	
	License Yo Summary	 are free to: Share: copy and redistribute the material in any medium or format 	

Citrus sinesis Whole Genome Assembly v1.0

3.3 Adding File Metadata

3.3.1 Manually Adding Metadata

You can add additional metadata to a file by adding new fields to the file content type. To do this, navigate to Admin > Structure > Tripal Content Types and click the manage fields link in the File row. Scroll to the section titled Add new field. The field Type and field widget should be Chado Property:

LABEL	MACHINE NAME	FIELD TYPE	WIDGET	OPERATIONS
🕂 Download	schemaitemlocation	File Location	File Location	edit delete
🕂 License	schemalicense	License	License	edit delete
+ References	sioreferences_file	References	References	edit delete
+++ Add new field)	Chado Property Type of data to store.	Chado Pro Form elemen	perty ✔ t to edit the data.

Name the property according as needed. Suppose we wanted to add a **genus** and **species** property to each file as metadata. We would add each one by first providing the name and clicking the **Save** button at the bottom. Next, Tripal provides a page for more details. Here the most important setting is the **Controlled Vocabulary Term**. To ensure data meets FAIR standards all metadata must be associated with a controlled vocabulary term. Here, we can search for and

select the term **genus** and click the **save settings** button. We can repeat this step for the **species**. Once completed we should see two new fields associated with our File content type.

LABEL	MACHINE NAME file_contact	FIELD TYPE Contacts	WIDGET	OPER/	ATIONS delete	TERM contact (local:contact)	SUPPORTED BY * CHADO
+ Download	schemaitemlocation	File Location	File Location	edit	delete	itemLocation (schema:itemLocation)	CHADO
+ License	schemalicense	License	License	edit	delete	license (schema:license)	CHADO
+ References	sioreferences_file	References	References	edit	delete	references (SIO:000631)	CHADO
🕂 Genus	field_genus	Chado Property	Chado Property	edit	delete	genus (TAXRANK:0000005)	CHADO
+ Species	field_species	Chado Property	Chado Property	edit	delete	species (TAXRANK:000006)	CHADO

We now have two new fields that can be used for metadata but we must make those visible on the page when data is present for them. You can follow the instructions for Configuring Page Layout in the Tripal User's Guide to place these new metadata fields where you want on the page. For this example, we will pace them in the **Summary** section of the page layout.

If we return to the any File page and edit it then we will now have a new metadata field for storing the genus.

File License *	
Attribution 4.0 International (CC B	Y 4.0) 🗸
Please select a license that properly	describes to the user their rights, priviledge and or usage permissions for this file.
Genus	
Citrus	
Specles sinensis	
Authoring information	Authored by
Publishing options	admin
Published	Leave blank for Anonymous.
	Authored on
	2021-03-01 20:50:12 -0800
	Format: 2021-03-01 20:50:12 -0800. The date format is YYYY-MM-DD and -0800 is the time zone

Now when we view the page we can see the genus and species metdata for the file

View Edit	Reload	e Genoi	ne Assembly v1.0	
Download File Source	Summary			×
License <u>Summary</u>	Resource Type	File		
<u>Summary</u>	Name	Citrus sines	s Whole Genome Assembly v1.0	
	Description	The whole g	enome assembly, v1.0, of Citrus sinensis.	
	File Type	FASTA form	at	
	Genus	Citrus		
	Species	sinensis		
	Download			×
	Available at	Size	MD5	
	Tripal v3 Dev	6.03MB	85934c1cc36308d829dc73e4eb9dcea3	

..... . .

3.3.2 Adding Metadata in Bulk

Because there is no common file format for providing metadata the best way to add metadata in bulk is to use the Tripal Bulk Loader, a module that comes built-in to Tripal v3. You can find a tutorial for learning to use the bulk loader at the Bulk Loader tutorial of the Tripal User's Guide.

Use of the bulk loader requires a good understanding of Chado, its database tables, their constraints and relationships. If you are comfortable with Chado, you can use the Tripal bulk loader to add metadata about files using a tab-delimited file. To do so you need to

- 1. Identify controlled vocabulary (CV) terms for each metadata value.
- 2. Ensure that those CV terms are already in Tripal and if not, you need to add them.
- 3. Create a tab-delimited file that contains the file name used in Tripal and as many columns of metadata values as desired.
- 4. Create a bulk loader template to recognize the file and import it.

The following provides the schema for the file and fileprop tables that were added to Chado by the Tripal File module. The **fileprop** table is where you will add metadata values.

3.3.2.1 File Module Chado Tables

The file Table

The *file* table houses the base file record. The *name* field must be a unique value for each file and thus can be selected on for finding files.

Column	Туре	Null	Default Value	Constraint
file_id	integer	No	(auto)	Primary Key
name	text	No		Unique
type_id	integer	No		Foreign Key to cvterm
description	text	Yes		

The fileprop Table

The *fileprop* table holds the properties or metadata about files. The CV term is specified using the *type_id* column and the rank is incremented if multiple values of the same type are stored.

Column	Туре	Null	Default Value	Constraint
fileprop_id	integer	No	(auto)	Primary Key
file_id	integer	No		Foreign Key to file
type_id	integer	No		Foreign Key to cvterm
value	text	Yes		
rank	integer	No	0	

The fileloc Table

The *fileloc* table indicates where files can be downloaded. The *uri* column must contain the URI of the file. Even local files have a URI. For example a Drupal URI usually has a *public://* URI prefix. For example: `public://tripal/ users/1/Citrus_sinensis-scaffold0.fasta`. When a file has more than one location to download the can be ordered by setting the *rank* column. The Tripal file module automatically fills in the *size* and *md5checksum* values for local files. If you are adding file locations via the bulk loader you must provide these or the will not be available.

Column	Туре	Null	Default Value	Constraint
fileloc_id	integer	No	(auto)	Primary Key
file_id	integer	No		Foreign Key to file
uri	text	No		
rank	text	No	0	
md5checksum	integer	Yes		
size	char(1024)	Yes		

3.4 Associating a File with Other Content

Now that we have a file page we can associate that file with any other Tripal-based content. As stated earlier, we will follow the User's Guide example where an Analysis page for the *Citrus sinensis* whole genome page was already created. We will associate the whole genome FASTA file to the analysis page.

Before we can associate a file with an analysis, we must first add a new field for the file to the Analysis content type. Navigate to Admin > Structure > Tripal Content Types and click the manage fields link in the Analysis row.

Analysis ⊙_{ripal} v3 Dev

Home » Administration » Structure » Tripal Content Types » Analysis

+ Check for new fields

LABEL	MACHINE NAME	FIELD TYPE	WIDGET	OPEI
🕂 Resource Type	rdfstype	Content Type	Content Type	edit
+ URL redirects	redirect	Redirect module form elements		
🕂 Name	schemaname	Text	Text field	edit

Click the **Check for new fields** link. Unlike adding fields for Metadata, the Tripal File module can automatically add fields for files. You should see the following message after clicking the link:

Added field: sio___file

Once again we must tell Drupal where on the page to display this new field. Follow the instructions on the Configuring Page Layout of the Tripal User's guide to learn how to do this. For this example, we will use the Tripal Default Display option to automatically place the file field.

Note: You may be asking, why do I have to add the field then set the display? Why can't the module do it automatically? The reason is that Tripal supports full customization of every page by the site admin and the Tripal File module does not want to make any assumptions about when and where any fields will be displayed. So the site admin must add them manually.

Next, find the Analysis page via **Admin > Find Tripal Content**. If you followed the Tripal User's Guide it will be named "Whole Genome Assembly and Annotation of Citrus Sinensis (JGI)". But if do not have this page, any practice Analysis page will do. Edit the page and scroll to the new section titled **File**. You should see a drop down containing a list of available files.

Add another item

Select the file and click the Save button at the bottom. We now have a File item for the page.

Whole Genome Assembly and Annotation of Citrus Sinensis (JGI)

View Edit	Reload					
Summary Annotations	File					
<u>File</u> Publication	File Type					
Relationship	Citrus sinesis Whole Genome Assembly v1.0 FASTA format					
	Summary		×			
	Resource Type	Analysis				
	Name Whole Genome Assembly and Annotation of Citrus Sinensis (JGI)					
	Description Note: The following text comes from phytozome.org:					

Clicking the file link will take the user to the full file page where they can download the file, view the license information, and view metadata about the file.

3.5 Accessing Files via Web-Services

All information about files can be obtained via the built-in Tripal Content web services. You can learn about how to access Tripal web services via the Web Services page of the Tripal User's Guide. When web services are enabled you can:

- 1. Retrieve the list of files associated with any content.
- 2. Retrieve all information about a file, including its name, description, license, source, download locations and metadata.

The following screen shot provides an example of the JSON returned for the Analysis content to which we associated the genome file:

```
"@context": "http://localhost/sites/default/files/tripal/ws/context/content.v0 1.analysis.2.json",
   "@id": "http://localhost/web-services/content/v0.1/Analysis/2",
   "@type": "Analysis",
   "label": "Whole Genome Assembly and Annotation of Citrus Sinensis (JGI)",
   "ItemPage": "http://localhost/bio_data/2",
   "type": "Analysis",
   "name": "Whole Genome Assembly and Annotation of Citrus Sinensis (JGI)",
   "description": "<strong><em>Note: </em>The following text comes from phytozome.org:</strong>\r\n\r\n<u
   version (v.1) of the assembly is 319 Mb spread over 12,574 scaffolds. Half the genome is accounted for by 236 sc
   gene set (orange1.1) integrates 3.8 million ESTs with homology and ab initio-based gene predictions (see below).
   predicted, each with a primary transcript. An additional 20,771 alternative transcripts have been predicted, ger
   transcripts. 16,318 primary transcripts have EST support over at least 50% of their length. Two-fifths of the pr
   support over 100% of their length.\r\ncu>Sequencing Method</u><br />\r\nGenomic sequence was generate
   approach with 2Gb sequence coming from GS FLX Titanium; 2.4 Gb from FLX Standard; 440 Mb from Sanger paired-end
   libraries\r\n\r\n<u>Assembly Method</u><br />\r\nThe 25.5 million 454 reads and 623k Sanger sequence read
   effort by 454 Life Sciences, University of Florida and JGI. The assembly was generated by Brian Desany at 454 Li
   assembler.\r\n\r\n<u>Identification of Repeats</u><br />\r\nA de novo repeat library was made by running
   Hubley) on the genome to produce a library of repeat sequences. Sequences with Pfam domains associated with non-
   library of repeat sequences and the library was then used to mask 31% of the genome with RepeatMasker.
   />\r\nWe aligned the sweet orange EST sequences using Brian Haas's PASA pipeline which aligns ESTs to the best p
   filters hits to ensure proper splice boundaries.\r\n",
   "software": "Assembly and Annotation Performed by JGI",
   "version number": "Phytozome v9",
   "algorithm": null,
   "time executed": "2021-02-01 17:53:00",
   "source data": {
       "name": "JGI Citrus sinensis assembly/annotation v1.0 (154)",
      "version_number": null,
      "uri": "http://www.phytozome.net/citrus.php"
   3.
   "database_cross_reference": "http://localhost/web-services/content/v0.1/Analysis/2/database+cross+reference",
   "annotation": "http://localhost/web-services/content/v0.1/Analysis/2/annotation".
   "publication": "http://localhost/web-services/content/v0.1/Analysis/2/publication"
   "relationship": "http://localhost/web-services/content/v0.1/Analysis/2/relationship",
   "file": "http://localhost/web-services/content/v0.1/Analysis/2/file"
}
```

Note, the file key at the bottom of the JSON output? Following this URL provides information about the file. If more than one file is associated with the content then an array of files is provided.

Below is a screenshot of the JSON result for the file:

```
"@context": "http://localhost/sites/default/files/tripal/ws/context/content.v0 1.file.27.json",
 "@id": "http://localhost/web-services/content/v0.1/File/27",
 "@type": "file",
 "label": "Citrus sinesis Whole Genome Assembly v1.0",
 "ItemPage": "http://localhost/bio data/27",
  'type": "File",
 "name": "Citrus sinesis Whole Genome Assembly v1.0",
 "description": "The whole genome assembly, v1.0, of <em>Citrus sinensis</em>.\r\n",
 "additionaltype": "FASTA format",
 "contact": "http://localhost/web-services/content/v0.1/File/27/contact",
 "itemlocation": {
.....
     "@id": "http://localhost/web-services/content/v0.1/File/27/itemLocation",
     "@type": "Collection",
     "label": "Download",
     "totalItems": 1,
   v
    "member": [
      ∀ {
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    or format\r\n\t\r\n\t<strong>Adapt</strong>: remix, transform and build upon t
    \r\n\t\r\n\r\nThe licensor cannot revoke these freedoms as long as you follow t
    \r\n\r\n<u>\r\n\t<strong>Attribution</strong> You must give appropriate credit, pr
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    <strong>No additional restrictions</strong> You may not apply legal terms or technological measures
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