

MetaHCR v1.0

Administrators Guide

This document is the administrators guide for the Metagenomics on Hydrocarbon Resources (MetaHCR) web application. All users should consult the accompanying Users Guide. The guide also contains a description of the data files used by the Upload functions of MetaHCR.

Note that the pages and examples in this Users Guide are based on the use of a public version of the MetaHCR database.

Overview


MetaHCR is a web application interface to a relational database that stores the inter-relationships amongst Hydrocarbon Resource Samples, their Single Gene and Metagenome Analyses and the Organisms found via these analyses. Ancillary tables provide metadata.

Administrators are users who have “super user” privileges. These privileges allow this user to:

- Create users and changing passwords.
- Create instances of all the tables utilized by MetaHCR.


Accessing MetaHCR and Logging On

Your system administrator will have given you a URL to use to access the web server that is hosting the MetaHCR application. Accessing this URL with a browser will result in the Home page being displayed:

**MetaHCR** Metagenomics on Hydrocarbon Resources

Register | Login
Database:

Home Browse Search Upload Admin



The MetaHCR Project

The area of molecular microbiology and metagenomics in particular holds great potential that could be used in the oil and gas industry. The MetaHCR project aims to be a platform for the cataloguing, storage and analysis of microorganisms that have been identified in hydrocarbon-rich environments, and are related to hydrocarbon degradation, oil souring, metal corrosion and methane emissions.

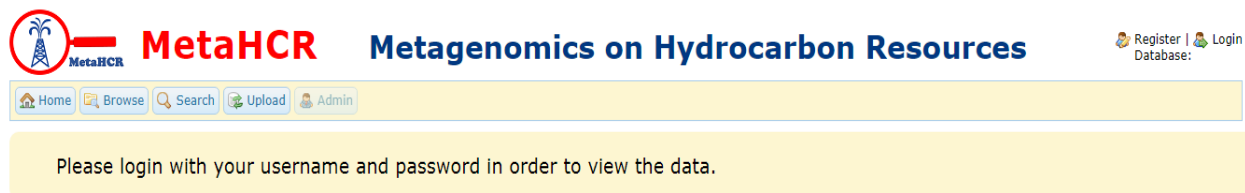
MetaHCR Milestones

- Development of a database containing microbial species, taxonomic and functional marker genes identified in the literature or the analyzed samples
- Implementation of a cyber-infrastructure to be used for data storage, analysis and sharing
- Creation of a user-friendly front-end allowing easy access to the data by the non-expert

» Read more about this project on the [about MetaHCR page](#).

Pumpjack during sunset. Monahans, Texas USA, 2013
(Photo: Laura Upshaw)

You must login to access MetaHCR's facilities. Click on the Login icon in the upper right-hand corner of the web page. You will be presented with the following dialog:



The image shows the MetaHCR web interface. At the top, there is a navigation bar with the MetaHCR logo, the text "MetaHCR Metagenomics on Hydrocarbon Resources", and links for "Register" and "Login Database:". Below the navigation bar is a yellow banner with the text "Please login with your username and password in order to view the data." In the center, there is a "Login to MetaHCR" dialog box with fields for "Email Address:" and "Password:", and "Login" and "Cancel" buttons.

Note if you are using a freshly-installed version of the public database, you should log in with user name of admin and the password of admin.

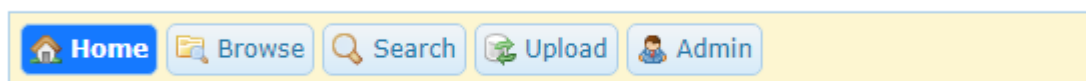
Enter your email address and password and click on the Login button. If the login is successful the Home page will be re-displayed:



The image shows the MetaHCR web interface after a successful login. The navigation bar now includes a "Logout (admin)" link. The yellow banner below the navigation bar contains the text "Home Browse Search Upload Admin".

In the upper right hand corner, your user name, organization and the name of the database that you are currently accessing is displayed. In addition, there is an icon for logging out.

After logging in, the administrative functions are reached by clicking on the *Admin* button at the top of a MetaHCR web page. This button is disabled if you do not have the correct privileges.



The image shows the MetaHCR navigation bar with buttons for "Home", "Browse", "Search", "Upload", and "Admin".

Clicking on the *Admin* button will take you to the administrators web page. It has a different look and organization than the MetaHCR application pages:

MetaHCR administration
[Back to MetaHCR Home](#)
Welcome, **An Admin**. [Change password](#) / [Log out](#)

Site administration

Authentication and Authorization	
Groups	+ Add Change
Users	+ Add Change

Sites	
Sites	+ Add Change

Webapp	
Attributes	+ Add Change
Curator details	+ Add Change
Environments	+ Add Change
Hydrocarbon chemistries	+ Add Change
Hydrocarbon resources	+ Add Change
Investigations	+ Add Change
MetaHCR databases	+ Add Change
Metabolism types	+ Add Change
Metagenome analyses	+ Add Change
Mineralogies	+ Add Change
Organisms	+ Add Change
Organizations	+ Add Change
Samples	+ Add Change
Single gene analyses	+ Add Change
User profiles	+ Add Change
Water chemistries	+ Add Change

Recent Actions

My Actions

- + User profile
- + guest User
- ✎ An Admin Administrator User profile
- ✎ admin User
- ✎ admin User
- ✎ An Admin Administrator User profile
- ✎ admin User
- ✗ pcmarks User

On the left-hand side, under the Authentication and Authorization, are the Groups and Users currently available in MetaHCR. *Note that the Django Groups facilities are not utilized in the MetaHCR application. Similarly, for Sites.*

Under Webapp are all the data items (tables) whose entries can be created, deleted and modified via general data maintenance.

General Data Maintenance

Any of the data items (tables) listed under Webapp can be clicked on resulting in a page showing a list of the entries (rows) in that table. There is a button on the upper right that allows you to add a new entity to this table. Clicking on one of these entries will show all the data fields in that entry and allow you to also modify the data and save the changes. There is also a Delete button that will delete this entry from its table. A typical maintenance web page – in this case Sample – looks like the following:

[Home](#) > [Webapp](#) > [Samples](#) > Id: 2 Name: MHC.PW.SRR088837

Change sample

History

Source mat id:

Samp well name:

Win:

Samp type:

sample.samp_type => produced water

+

Samp subtype:

.....

+

Samp location point:

.....

+

Temp:

Pressure:

Samp tvdss:

Depth of the sample i.e. the vertical distance between the sea level and the sampled position in the subsurface. Depth can be reported as an interval for subsurface samples e.g. 1325.75-1362.25 m

Note the Samp type field. It is example of a field that uses the controlled vocabulary values that can be found in the Attributes table. With a controlled vocabulary the user is limited to entering only valid values. More on Attributes below.

Adding Organizations, Databases, Users and User Profiles

There are relationships and dependencies amongst Organizations, Databases, Users and User Profiles. Users must belong to an Organization and Users must have a User Profile. Moreover, Organizations must specify the name of the database. Typically, the following steps are executed in this order:

1. Add an Organization unless the proper one exists.
2. Add a MetaHCR database
3. Add a User.
4. Add a User Profile associating it with a User and a User Profile

Clicking on Organizations under Webapp will display a list of organizations:

Home > Webapp > Organizations

Select organization to change

[Add organization +](#)

Action: Go 0 of 1 selected

<input type="checkbox"/>	Organization
<input type="checkbox"/>	MetaHCR Public

1 organization

Clicking on an organization will display its fields:

Home > Webapp > Organizations > MetaHCR Public

Change organization

[History](#)

Name:	<input type="text" value="MetaHCR Public"/>
Address1:	<input type="text"/>
Address2:	<input type="text"/>
Postcode:	<input type="text"/>
Country:	<input type="text"/>
Contact name:	<input type="text"/>
Contact email:	<input type="text"/>

[✖ Delete](#) [Save and add another](#) [Save and continue editing](#) [Save](#)

Selecting MetaHCR databases displays the following list:

Select meta hcr database to change Add meta hcr database +

Action: Go 0 of 1 selected

<input type="checkbox"/>	Meta hcr database
<input type="checkbox"/>	default of MetaHCR Public

1 meta hcr database

The field values for a database entry are:

Name:	<input type="text" value="default"/>
Description:	<input type="text" value="MetaHCR Public Data"/>
Creation date:	Date: <input type="text"/> Today Time: <input type="text"/> Now
Last update:	Date: <input type="text"/> Today Time: <input type="text"/> Now
Version:	<input type="text" value="v34"/>
Organization:	<input type="text" value="MetaHCR Public"/> +

The Name field corresponds to the database name that is specified in the MetaHCR settings.py file (see the section on Settings).

To add a User, click on its + Add button. The following page will be displayed:

Home > Authentication and Authorization > Users > Add user

Add user



First, enter a username and password. Then, you'll be able to edit more user options.

Username:	<input type="text"/>
Required. 30 characters or fewer. Letters, digits and @/./+/-/_ only.	
Password:	<input type="password"/>
Password confirmation:	<input type="password"/>
Enter the same password as above, for verification.	

Note that passwords are never saved in plain text.

Finally, to add a User Profile, click on its + *Add button*. This page will appear:

Add user profile

User:	guest ▼	+
Organization:	MetaHCR Public ▼	+
Default database:	default of MetaHCR Public ▼	+
<input checked="" type="checkbox"/> Reset password		
Date of password:	Date:	<input type="text"/> Today 
	Time:	<input type="text"/> Now 

Controlled Vocabulary

MetaHCR employs a controlled vocabulary for many of the field values of its data resources. Each field has associated with it a set of valid values. The entries in the Attribute table can be added, deleted and changed. Similarly for the set of valid values associated with an attribute.

Select the Attributes entry from list under Webapp on the main Maintenance page. A list (partial) of the attributes is shown:

Select attribute to change

Action: 0 of 100 selected

<input type="checkbox"/>	Attribute
<input type="checkbox"/>	all.all => n/a
<input type="checkbox"/>	biological_analysis.type => Metagenome
<input type="checkbox"/>	biological_analysis.type => Single Gene

Attributes are identified by table and field names. In the above, the valid values for the type field in the biological_analysis table are Metagenome and Single Gene. You must use the database table and field names that are found in the database's schema. Note the all.all Attribute. These are attributes that can be used across all tables and their fields.

Settings

All Django applications rely on a settings file named setting.py. The file is found in the metahcr/metahcr directory under the top-level directory. It is read when the application starts. It consists of a number of parameters - variables and their values. In general, the parameters in the first part of the file are the ones whose values may need to be changed. In particular, the following are important:

- CATEGORY_CHOICES – a list of pairs of values that specify the names and corresponding attribute display values of all of the tables that contain controlled vocabulary fields.
- DATABASES – these are values specific to the database(s) that are being used. Each database entry is identified by a name – default in the public database. This name is used in the User Profile described earlier in this document. The values within this database record are specific to the type of database being used. MetaHCR is currently configured to use a PostgreSQL database.
- AWS_ACCESS_KEY, AWS_SECRET_ACCESS_KEY, AWS_STORAGE_BUCKET_NAME – these are values that must be supplied if you want upload data files stored in an AWS S3 bucket.