

PHENOTATOR – a tool for annotation cellular phenotypes using ontologies

This short document shows you how to use Phenotator to annotate cellular phenotypes using existing ontologies.

To test Phenotator go to <http://wwwdev.ebi.ac.uk/fgpt/phenotator/> (Figure 1)

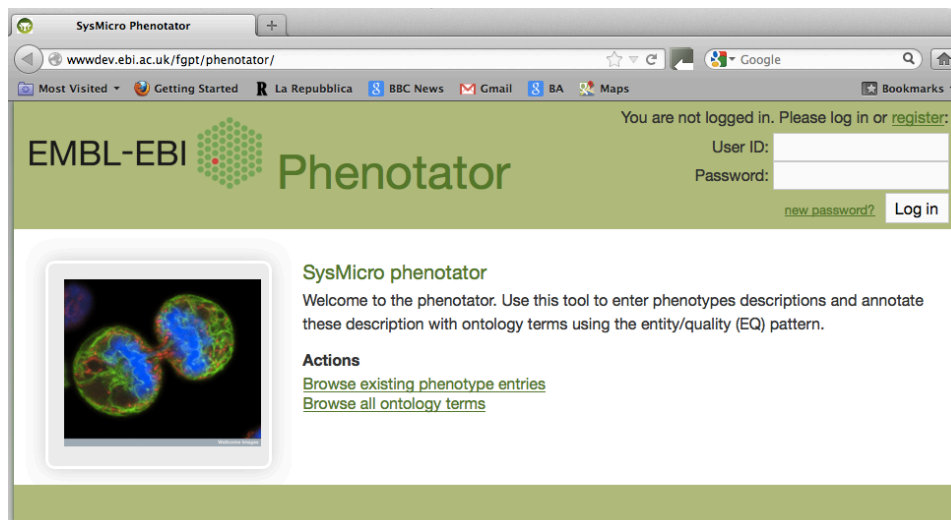


Figure 1

You will first need to register and get your log in details. The system has been configured so that users can't see each others annotations. In this way we can see how much inter annotator agreement we get.

Once you register, you should log in using your user name and password. Once you log in, you will have four options available to you (Figure 2):

- Browse existing phenotype entries
- Create new phenotype entry
- Browse all ontology terms
- Submit new ontology term request



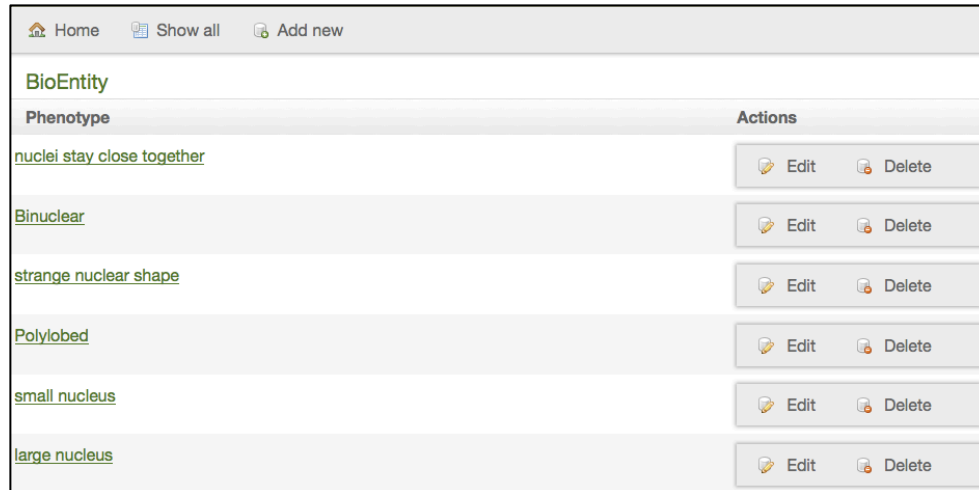
Figure 2

Let's take a look at each one of them.

Browse existing phenotype entries

This option allows browsing the phenotypes that we have already entered. The terms already available are all from the Mitochek study.

When clicking on the 'Browse existing phenotype entries' link you will get a list of such terms (Figure 3).



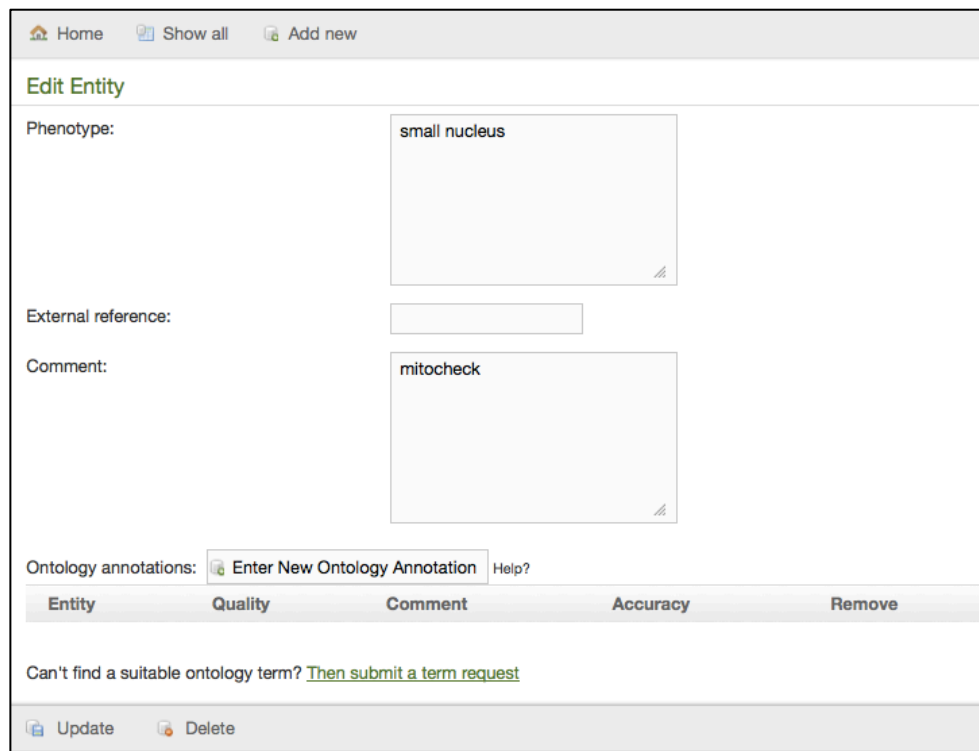
The screenshot shows a web interface for 'BioEntity'. At the top, there are navigation links: 'Home', 'Show all', and 'Add new'. Below this is a table with two columns: 'Phenotype' and 'Actions'. The table lists six phenotypes: 'nuclei stay close together', 'Binuclear', 'strange nuclear shape', 'Polylobed', 'small nucleus', and 'large nucleus'. Each phenotype has two buttons in the 'Actions' column: 'Edit' and 'Delete'.

Phenotype	Actions
nuclei stay close together	Edit Delete
Binuclear	Edit Delete
strange nuclear shape	Edit Delete
Polylobed	Edit Delete
small nucleus	Edit Delete
large nucleus	Edit Delete

Figure 3

For each term, two options are available: "Edit" and "Delete".

Click on the "Edit" button to add an ontology annotation to the selected term or edit the phenotype name or add any comment (Figure 4).



The screenshot shows the 'Edit Entity' page for the 'small nucleus' phenotype. It includes fields for 'Phenotype:' (containing 'small nucleus'), 'External reference:' (empty), and 'Comment:' (containing 'mitocheck'). Below these is a section for 'Ontology annotations:' with a button 'Enter New Ontology Annotation' and a 'Help?' link. A table with columns 'Entity', 'Quality', 'Comment', 'Accuracy', and 'Remove' is present. At the bottom, there is a link 'Can't find a suitable ontology term? Then submit a term request' and buttons for 'Update' and 'Delete'.

Entity	Quality	Comment	Accuracy	Remove
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Figure 4

To add an ontology annotation for the selected term "small nucleus", click on the "Enter New Ontology Annotation" button. When doing this, additional boxes will

appear under “Entity”, “Quality” and “Comment”, towards the bottom of the page (Figure 5).

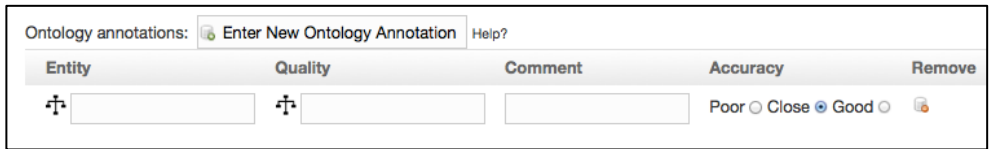


Figure 5

Let’s add an annotation for the phenotype “small nucleus”. Based on the terminology that we are using in Phenotator, an “entity” is the cellular structure or the biological process for which you have observed a phenotype and the “quality” is the phenotypic alteration that you have observed for the selected entity.

We first start typing “nucleus” in the text box under “Entity” (Figure 6).

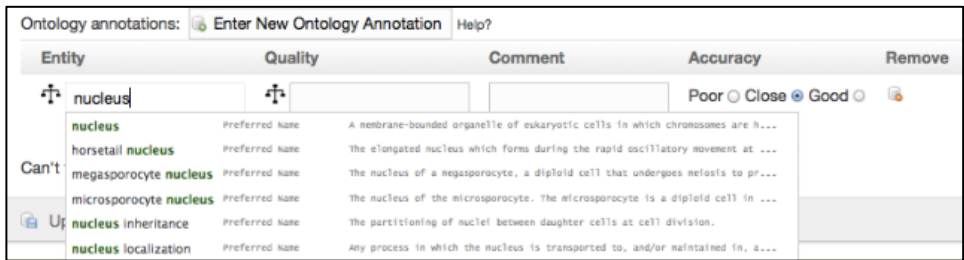


Figure 6

A list of terms from existing ontologies containing the word “nucleus” is made available to you. Please select the appropriate term from the list.

Repeat the same for “Quality”, typing “small” in the text box under “Quality” (Figure 7) and select the appropriate term from the list of suggestions.

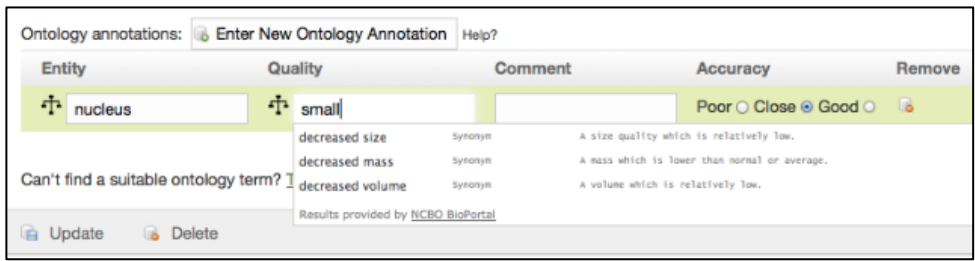



Figure 7

You can also rate the accuracy of the annotation by selecting one of the following attributes: “Poor”, “Close” or “Good”.

If you are happy with adding one annotation only, click “Update” and the newly added annotation will be stored with the phenotype.

If you wish to add more than one annotation, repeat the previous steps.

When looking for an appropriate term for either “Entity” or “Quality”, you can browse the ontologies available to you by clicking on this icon: .

This will load the ontology and you can search for a term within the ontology using the “Find” option. As result the selected branch of the ontology tree containing the term that you searched for will be loaded and you can select the term that you were looking for from the tree (Figure 8)

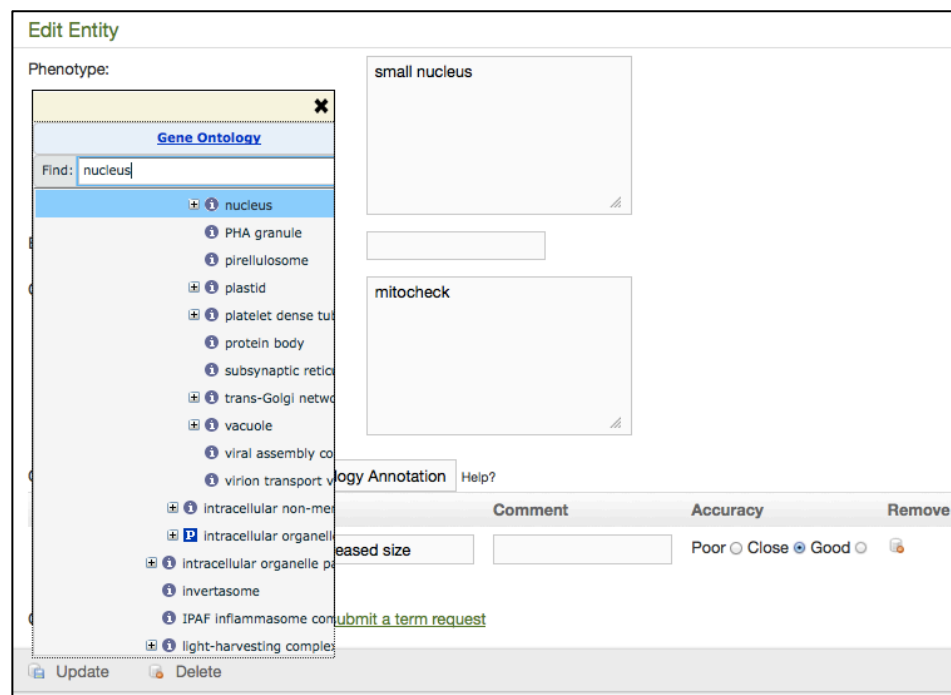


Figure 8

If you cannot find a suitable term from the ontologies available to describe the selected phenotype, click on the “[Then submit a term request](#)” link at the bottom of the page. Fill in the term request form (Figure 9) and submit the request by clicking the button “Create” at the bottom of the term request form.

The term request will be submitted to us and this will give us an idea of what terms cannot be described with the ontologies currently available.

The screenshot shows a web form titled "Create TermRequest". It contains four main input fields: "Term *" (a small text box), "Definition *" (a large text area), "Ontology *" (a dropdown menu with "Cellular component" selected), and "Comment" (a text area). At the bottom left, there is a "Create" button with a document icon.

Figure 9

Create new phenotype entry

Use this option to add a new phenotype and the corresponding annotation, following the same steps as described in the previous session.

Browse all ontology terms

This option allows you to browse the ontologies that are currently available to select terms from when creating annotations for phenotypes.

We have currently loaded the Gene Ontology for “Entity” and PATO for “Quality” but additional ontologies can be loaded. The new ontologies that we will add in future releases are based on the requests for new terms that will come from users.

Submit new ontology term request

This option allows you to submit a request for a new ontology term that you consider appropriate to describe a phenotype that you have observed in your experiment and that you could not find in the ontologies already loaded in Phenotator. This is the same functionality described in Figure 9.