GrapeMine Documentation

GrapeMine is a data warehouse which contains grapevine data. It allows you to perform complex queries, making lists of your favorite features or search for features using a range of positions.

GrapeMine content

GrapeMine allows retrieving information/data from:

- the v1 **annotation** of the grapevine genome (mrnas, genes, exons and polypeptides)
- **ontologies** (Plant Ontology, Gene Ontology, Prosite, Pfam and so on)
- **polymorphisms data** (Snp, indels or markers)
- **phenotyping data** (Accessions, evaluation data)

Additional external links allow you to complete your searches:

- URGI GBrowse → https://urgi.versailles.inra.fr/gb2/gbrowse/vitis_12x_pub
- GnpIS → https://urgi.versailles.inra.fr/gnpis/
- BioMart → https://urgi.versailles.inra.fr/biomart/martview/
- Ontologies website → http://www.ebi.ac.uk/QuickGO/, http://www.plantontology.org/ ...

Data access

1) **Using the QuickSearch**

   You can search for features by entering a word in the search box, it will return all the features containing the word you entered. You can also search by type of features, for example "marker". You can use wild-card "*" to search for partial matches and also a specific syntax like "**or**" or "**and not**". You will see data categories appear in the left box.

   Examples:

   - marker
   - kinase or membrane
   - *Cabernet* (always use a wild card before a cultivar name to avoid empty return)
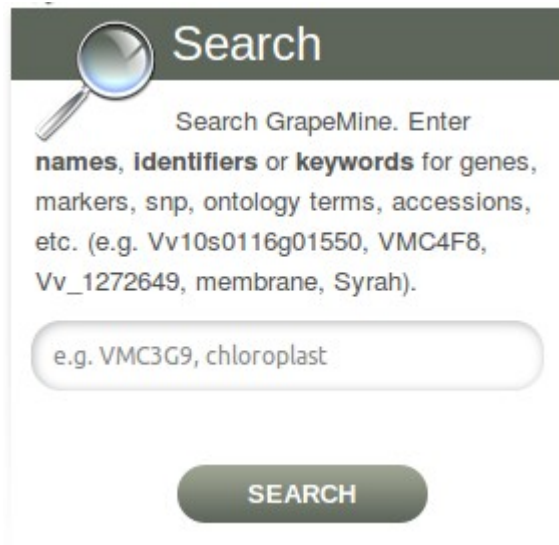   - Vv* and not *orf

Figure 1: Using the QuickSearch

2) Using "QueryBuilder"

The QueryBuilder is a flexible query interface that allows to construct data mining queries. The QueryBuilder provides you with the type of features you can query on. After clicking on a feature type, a new window appears with the direct attributes of the feature and the other linked features, togetherwith their own attributes (click on (+) to see them). To display an attribute click on "show". To filter with an attribute data click on "constrain".

First, you should select a feature on which the query will be focused. Only then you will be able to work with all the features linked to this "target" or "pivotal" feature.

Example:

We want to get the name of all the mRNAs located on the chromosome 3 and also the Plant Ontologies linked to these mRNAs.

– Select mRNA in the listbox. You will see the mRNA, its attributes and all the features linked to mRNA on the left.
– Then click on "[+] Chromosome", find DB identifier (chromosome name) and click on "show" then click on "constrain", here select "chr3" in the list box and click on "Add to query".
– Finally, click on "Plant Ontologies" and select the code and description by clicking on "show".
– Press "Show results" top right and you will get a table with all the attributes you have selected previously.

You can sort, hide or remove columns. You can also modify columns order by clicking on "Manage columns". Data are downloadable (top right). If you click on a mRNA attribute (the name for example) you will go on the mRNA card.

When you are on the mRNA card, you can see all its attributes, all the items linked to this mRNA (Gene, Exons, Ontologies...). You can get the fasta sequence by cliking on "FASTA". On the right you have an external link to URGI GBrowse.

Figure 2: Using "QueryBuilder"

3) Using "Region"

The "Region" page allows you searching for features using a range of positions. To begin, select which features you want to search for, then enter one or several positions and get the results.

Example:
Enter:
chr1:500000..700000
chr15:200..600000

To finish, click on search, results are ordered by the regions you entered. If too many results are found, you will have to create a list. As with the QueryBuilder, you can download data in many kind of formats (csv, gff3 and so on...).

Figure 3: Using "Regions"

4) Using "Templates"

The "Templates" section allows you to run pre-computed queries. There are default queries but you can create your own queries (only if you have created an account and if you are logged under this account). Queries have a title and a description. When you run a query from "Templates" you see a summary of the constraints of the query. For example in GrapeMine, there is a precomputed query : "Green accessions". Click on this query and you will see the constraint that you can edit (here the descriptor and the descriptor value). Just click on "Show results" to see the results.

If you want to make your own queries, go in the QueryBuilder, when building a query, just look down, you will see "Start building a template queries". If you have no account, click on "Log in", "Create account now".
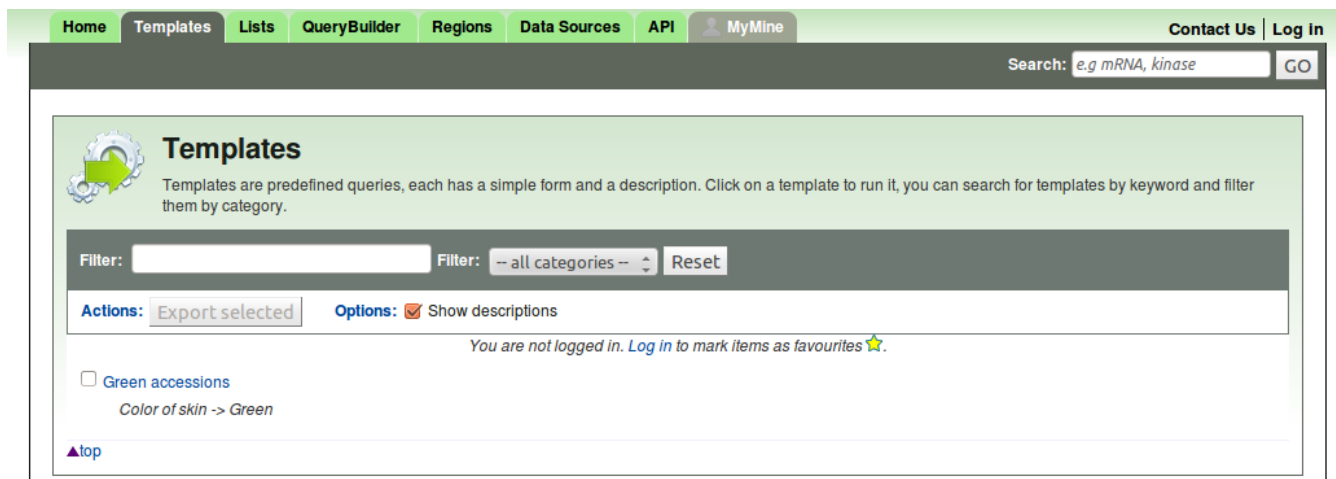

Figure 4: Using "Templates"

Using "Lists"

"Lists" allows you to create lists of your favorite features that can be further manipulated with GrapeMine functionalities. Go in "Upload" to make a new list (top left), and in "View" to see all the lists available. In the "Upload" section, click on "show examples" to display some genes identifier, then click on "create a list", give a name to this list, then you will see a table containing your genes, to the bottom a widget represents genes chromosomal distribution. When you are on a feature card, if this feature is included in a list, it will appear on the right side.

You can also create lists directly on a results page. For example, search for "mrna and kinase" in the QuickSearch, on the top of the results page you will have a button "create list".

In the "View" section, you will see all your lists, you can copy or delete them. Moreover, you can realize intersections, unions or subtractions on your lists to compare lists result.

Figure 5 : Genes list creation

Using "API"

This section is for advanced users that whish to query GrapeMine using programming language like Java or Python for example.

MyMine

MyMine is your private space on GrapeMine. It's very easy to create an account, just provide an email and a password. Thanks to your account you will be able to:

– Save lists and queries
– Modify and save templates