


## RvLab interface and access through the LifeWatchGreece portal

The R virtual laboratory (RvLab) is now available through the LifeWatchGreece portal with a new user friendly graphical interface for efficiency and ease in execution of RvLab functions.

RvLab is available at <https://portal.lifewatchgreece.eu/>

 Lifewatch Greece Portal

E-mail


Password

Sign In

 or 


ORCID

[Forgot your password?](#) [Register](#) [How To](#)

**RvLab**


The R vLab makes use of "R" which is a statistical processing environment widely used by scientists working in many biodiversity related disciplines. It supports an integrated and optimized (in respect to computational speed-up and data manipulation) online R environment. This vLab tackles common problems faced by R users, such as severe computational power deficit. Many of the routines operating under the R environment, such as the calculation of several biodiversity indices and the running of the multivariate analyses, are often of high computational demand and cannot deliver a result when the respective datasets are in the form of large matrices.

Available after  
Sign In

**MedOBIS vLab**


The MedOBIS [Mediterranean node of Ocean Biogeographic Information System (IOBIS: <http://www.iobis.org/>)] vLab provides reliable and quality controlled marine species datasets, meta-data and satellite data from all over the Mediterranean Sea. The concept of MedOBIS, in agreement with OBIS, is to create a comprehensive system for the retrieval of Mediterranean biological data and to deliver them to OBIS and ultimately to GBIF.

Available after  
Sign In

**Ecological Modeling**

This vLab comprises of two online coupled models, which are parameterised and initialised for the specific conditions at a few specifically identified areas for which the required datasets exist. In an attempt to make the tool user friendly a graphic user interface (GUI) developed in the course of previous projects will be used. The GUI allows the user to view model results dynamically through any internet browser. Model results will be stored at the HCMR servers and the user will be able to select the area, scenario, and parameter required, which will then be returned as results in the form of plots. All model parameters and options will be available to the user online. The ultimate operation, therefore, of this vLab will be to allow the user to submit a request for the model to run under a different scenario than those already available.

Available after  
Sign In

**Literature Mining**

Biodiversity literature and data constitute a vast public resource open to mining and knowledge extraction. Associating organisms to key features of their life e.g. the environment in which they live, the way they feed, their breeding habits, is cornerstone in explaining biodiversity patterns and informing ecological decisions. Eco-Systems Biology, and in particular network-based analysis, can provide holistic pictures of such associations, highlight novel relations and support hypothesis formulation and knowledge discovery. Initial aim of this vLab is to augment species related information based on data available in global biodiversity knowledge and literature aggregators, such as the Encyclopedia of Life (EOL) and the Biodiversity Heritage Library (BHL). Main focus of this virtual lab is the extraction of species - traits associations starting with the environment in which occur. Species and environments associations will be extracted by mining relevant text field clauses of: a) in-house LifewatchGreece data, b) the EOL and the BHL text collection. Also, interactive web-based visualizations will be developed to summarise the extracted species - environments association and support data exploration and landscape ecology studies.

Available without  
Sign In

Figure 1: The main page of the LifeWatchGreece portal.

If you are using RvLab for the first time, you should first register, by clicking the relevant link at the top of the portal's main page.



The screenshot shows the registration page of the Lifewatch Greece Portal. At the top, there is a header with the portal's logo and name on the left, and login fields for E-mail and Password on the right, with a 'Sign In' button. Below the login fields are links for 'Forgot your password?' and 'Register'. The main registration form contains several input fields: 'First name \*', 'Last name \*', 'E-mail \*', 'Password: \*', 'Repeat password: \*', 'Affiliation', and 'Position'. To the right of these fields is a large icon depicting two people sitting at a table. Below the registration fields is a CAPTCHA section with the text 'Fill in the image text:' and a box containing the letters 'Ampf q' with a refresh button. A 'Sign Up' button is located at the bottom of the form. The footer of the page states 'Developed by HCMR and FORTH'.

*Figure 2: The registration page of the LifeWatchGreece portal.*

After registration, you can sing in the portal, using your credentials.

Alternatively, you can sign in directly using your ORCID account. You can click the relevant button at the top of the portal's main page and you will be redirected to ORCID (figure 3).



### LifewatchGreece Portal ?

has asked for the following access to your ORCID Record



Get your ORCID iD



Allow this permission until I revoke it.

*You may revoke permissions on your account settings page. Unchecking this box will grant permission this time only.*

This application will not be able to see your ORCID password, or other private info in your ORCID Record. [Privacy Policy](#).

Sign into ORCID or [Register now](#)



Personal Account



Institutional Account

Sign in with your ORCID account

Email or iD \*

ORCID Password

[Forgotten password?](#)

Deny

Authorize

Sign in with a social media account ?



Figure 3: The sign in page in ORCID.

After signing in, you will be re-directed to the portal's home page, where you can select the RvLab (figure 4).

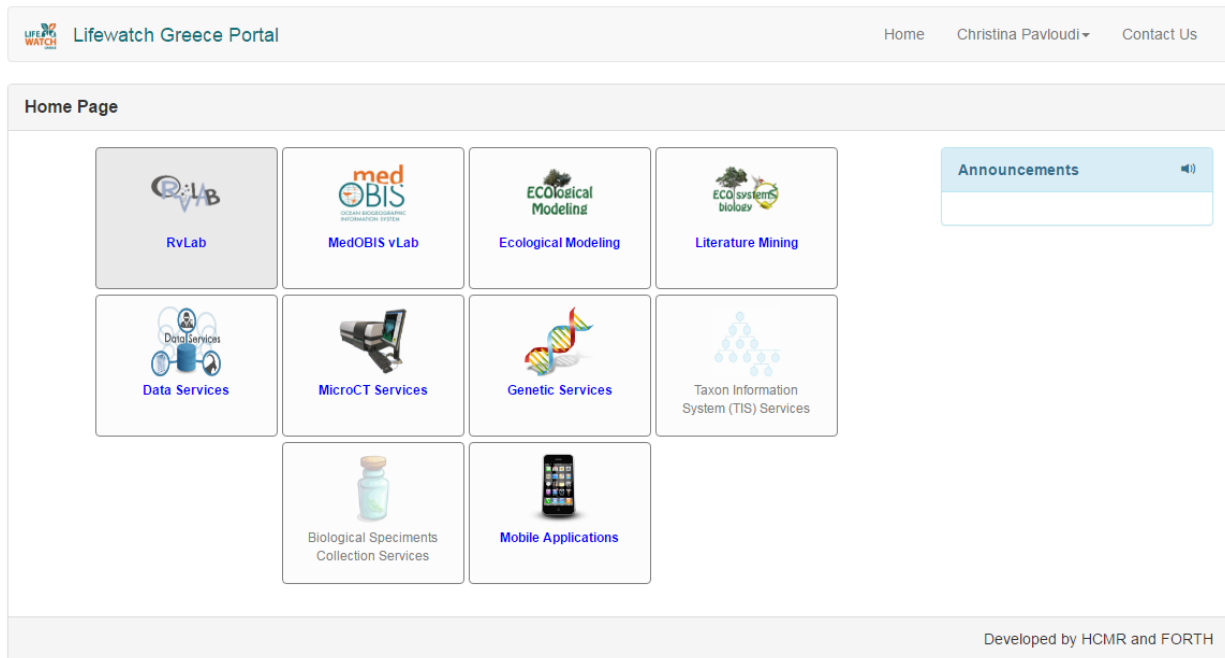


Figure 4: The home page of the LifeWatchGreece portal (available after signing in).

The main interface of the RvLab is comprised of four main tabs, as shown in figure 5.

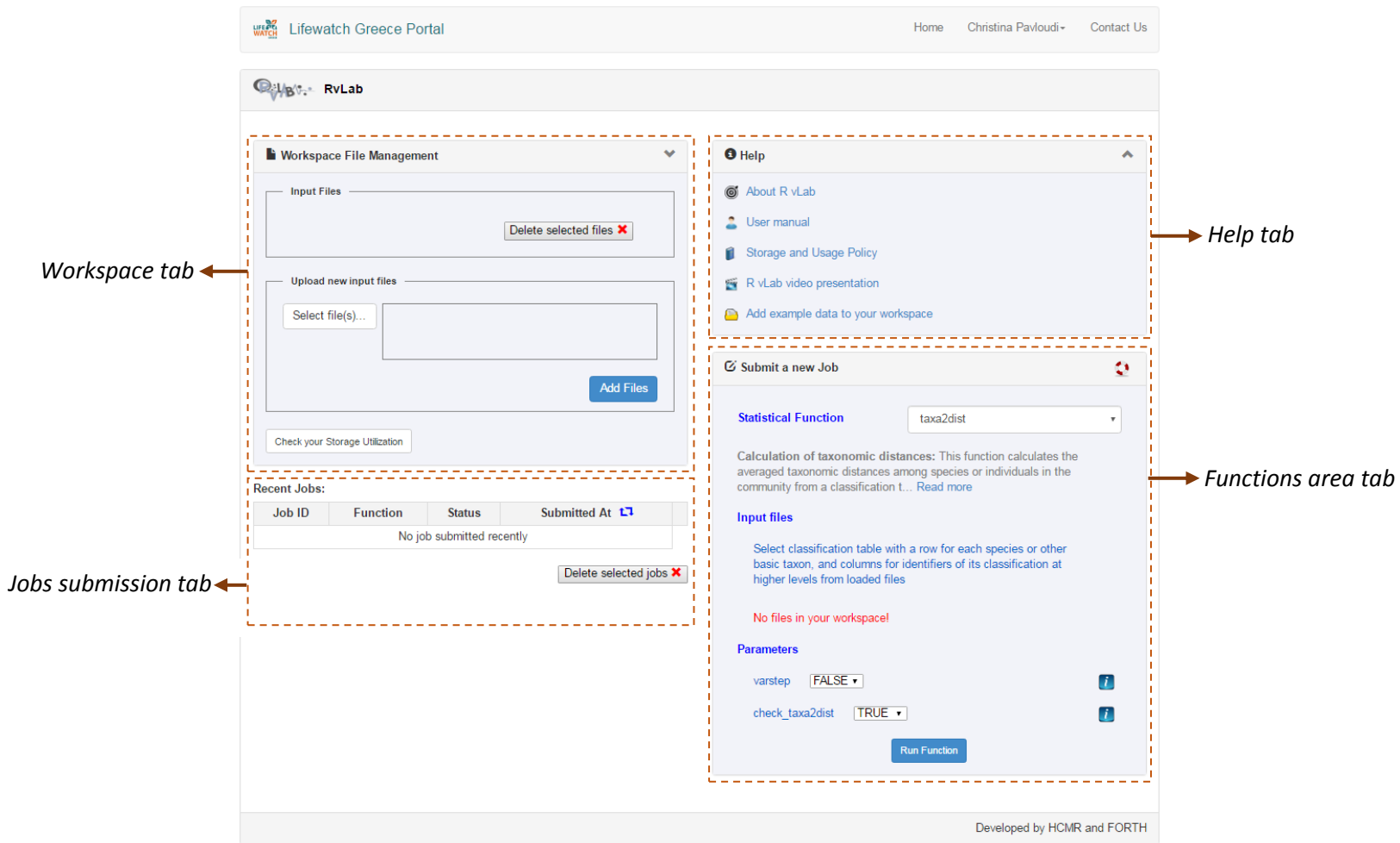


Figure 5: The main interface of the RvLab.


On the top left, you can see the *Workspace* tab, where you can upload specific files in predefined formats, such as text document (.txt) or comma separated values (.csv) file format.


On the top right, you can see the *Help* tab, where you can see some general information on the RvLab. Also, you can add some example datasets to your workspace to run certain analyses.

On the bottom right, you can see the *Functions area* tab where you can select the analysis you want to run and choose its parameters.

On the bottom left, you can see the *Jobs submission* tab, where you can see the progress of your submitted jobs and their results.

Click on the "Add example data to your workspace" and you will see datasets added to your workspace.

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 **RvLab**

Workspace File Management

Input Files

- Macrobenthos\_Classes\_Adundance.csv
- Macrobenthos\_Crustacea\_Adundance.csv
- Macrobenthos\_Families\_Adundance.csv
- softLagoonAbundance.csv
- softLagoonAggregation.csv
- softLagoonEnv.csv
- softLagoonFactors.csv

Delete selected files ✖

Upload new input files

Select file(s)...

Add Files

Check your Storage Utilization

Recent Jobs:

Job ID	Function	Status	Submitted At
No job submitted recently			

Delete selected jobs ✖

Help

Submit a new Job

Statistical Function

taxa2dist

Calculation of taxonomic distances:

This function calculates the averaged taxonomic distances among species or individuals in the community from a classification t... [Read more](#)

Input files

Select classification table with a row for each species or other basic taxon, and columns for identifiers of its classification at higher levels from loaded files

- Macrobenthos\_Classes\_Adundance.csv
- Macrobenthos\_Crustacea\_Adundance.csv
- Macrobenthos\_Families\_Adundance.csv
- softLagoonAbundance.csv
- softLagoonAggregation.csv
- softLagoonEnv.csv
- softLagoonFactors.csv

Parameters

varstep

FALSE

check\_taxa2dist

TRUE

Run Function

Developed by HCMR and FORTH

Figure 6: The interface of the RvLab, showing the example data loaded on your workspace.

Now you can proceed with the analyses by choosing the relevant one for your needs from the drop-down menu. You can see some of the currently available analyses in figure 7.

**Help**

**Submit a new Job**

**Statistical Function**

**Input files**

Select classification table with basic taxon, and columns for higher levels from loaded files

No files in your workspace!

**Parameters**

varstep **FALSE**

check\_taxa2dist **TRUE**

**Statistical Function List:**

- taxa2dist
- pca
- cca
- anosim
- anova
- permanova
- mantel
- metams
- 2nd stage MDS
- metams\_visual
- radfit
- bioenv
- simper
- regression
- Parallel taxa2dist
- Parallel taxa2dist postgres
- Parallel anosim
- Parallel mantel
- Parallel taxa2dist to taxondive
- Parallel permanova

**Run**

Developed by HCMR

Figure 7: Some of the currently available RvLab analyses.

Let's choose for example the analysis "metams\_visual" (figure 8). For further documentation on the chosen function, you can click on the icon of the life jacket and a new webpage will open with all the relevant information.

Also, a small text explaining the analysis is available right below.

After choosing the analysis, you can select the parameters you want and click on "Run function". Next to the parameters, there are information buttons which you can click in order to get more information on the different parameters and their values.

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RvLab

Workspace File Management

Input Files

- Macrobenthos\_Classes\_Adundance.csv
- Macrobenthos\_Crustacea\_Adundance.csv
- Macrobenthos\_Families\_Adundance.csv
- softLagoonAbundance.csv
- softLagoonAggregation.csv
- softLagoonEnv.csv
- softLagoonFactors.csv

Delete selected files

Upload new input files

Select file(s)...

Add Files

Check your Storage Utilization

Recent Jobs:

Job ID	Function	Status	Submitted At
No job submitted recently			

Delete selected jobs

Submit a new Job

Statistical Function
metamds\_visual

Alternative interactive visualization of the Nonmetric Multidimensional Scaling: This function (SUMMARIZEplot) performs a Nonmetric Multidimensional Scaling of the most abundant taxa at the provided abundance matrix and returns interactive bar charts, pie chart and nMDS plot.

Input files

Select community data as a symmetric square matrix from loaded files

- Macrobenthos\_Classes\_Adundance.csv
- Macrobenthos\_Crustacea\_Adundance.csv
- Macrobenthos\_Families\_Adundance.csv
- softLagoonAbundance.csv
- softLagoonAggregation.csv
- softLagoonEnv.csv
- softLagoonFactors.csv

Select Transformation Method: none

\* info about transformation methods

☒ Check to transpose matrix

Parameters

Number of top ranked species 21

Method: euclidean

K 12

trymax\_viz 20

Run Function

Documentation for the chosen function

Text explaining the function and the analysis

Information button

Developed by HCMR and FORTH

Figure 8: Choosing the "metamds\_visual" analysis.

After clicking on "Run function", you will see the submitted analysis in the *Jobs submission* tab. While the analysis is being executed, the status of the job will be yellow (figure 9). All jobs are submitted to a queuing system on the HCMR PC cluster. You can submit multiple jobs, one after the other, without having to wait for each one to finish first.



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RvLab

Workspace File Management

Input Files

Macrobenthos\_Classes\_Adundance.csv

Macrobenthos\_Crustacea\_Adundance.csv

Macrobenthos\_Families\_Adundance.csv

softLagoonAbundance.csv

softLagoonAggregation.csv

softLagoonEnv.csv

softLagoonFactors.csv

Delete selected files

Upload new input files

Select file(s)...

Add Files

Check your Storage Utilization

Recent Jobs:

Job ID	Function	Status	Submitted At
Job2297	metamds_visual	Submitted	31 May 2016 12:03:58

Delete selected jobs

Help

Submit a new Job

Statistical Function

metamds\_visual

Alternative interactive visualization of the Nonmetric Multidimensional Scaling: This function (SUMMARIZEplot) performs a Nonmetric Multidimensional Scaling of the... [Read more](#)

Input files

Select community data as a symmetric square matrix from loaded files

Macrobenthos\_Classes\_Adundance.csv

Macrobenthos\_Crustacea\_Adundance.csv

Macrobenthos\_Families\_Adundance.csv

softLagoonAbundance.csv

softLagoonAggregation.csv

softLagoonEnv.csv

softLagoonFactors.csv

Select Transformation Method:

none

\* info about transformation methods

Check to transpose matrix

☒

Parameters

Number of top ranked species

21

Method:

euclidean

K

12

trymax\_viz

20

Run Function

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Figure 9: The chosen analysis is being executed.

Once the analysis is completed, the status will change its colour to green. If there was some problem with your analysis and it had failed, the status would have changed to red.

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Workspace File Management

Input Files

Macrobenthos\_Classes\_Adundance.csv

Macrobenthos\_Crustacea\_Adundance.csv

Macrobenthos\_Families\_Adundance.csv

softLagoonAbundance.csv

softLagoonAggregation.csv

softLagoonEnv.csv

softLagoonFactors.csv

Delete selected files

Upload new input files

Select file(s)...

Add Files

Check your Storage Utilization

Recent Jobs:

Job ID	Function	Status	Submitted At
Job2297	metamds_visual	Completed	31 May 2016 12:03:58

Delete selected jobs

Help

Submit a new Job

Statistical Function

metamds\_visual

Alternative interactive visualization of the Nonmetric Multidimensional Scaling: This function (SUMMARIZEplot) performs a Nonmetric Multidimensional Scaling of the...

Read more

Input files

Select community data as a symmetric square matrix from loaded files

Macrobenthos\_Classes\_Adundance.csv

Macrobenthos\_Crustacea\_Adundance.csv

Macrobenthos\_Families\_Adundance.csv

softLagoonAbundance.csv

softLagoonAggregation.csv

softLagoonEnv.csv

softLagoonFactors.csv

Select Transformation Method:

none

info

\* info about transformation methods

Check to transpose matrix

Parameters

Number of top ranked species

21

info

Method:

euclidean

info

K

12

info

trymax\_viz

20

info

Run Function

Developed by HCMR and FORTH

Figure 10: The analysis is completed.

Once your analysis is completed, you can click on its Job ID (in this example on *Job2297*) and you will be redirected to the results page (figure 11). If your analysis had failed, clicking on the Job ID would show you the generated error message.

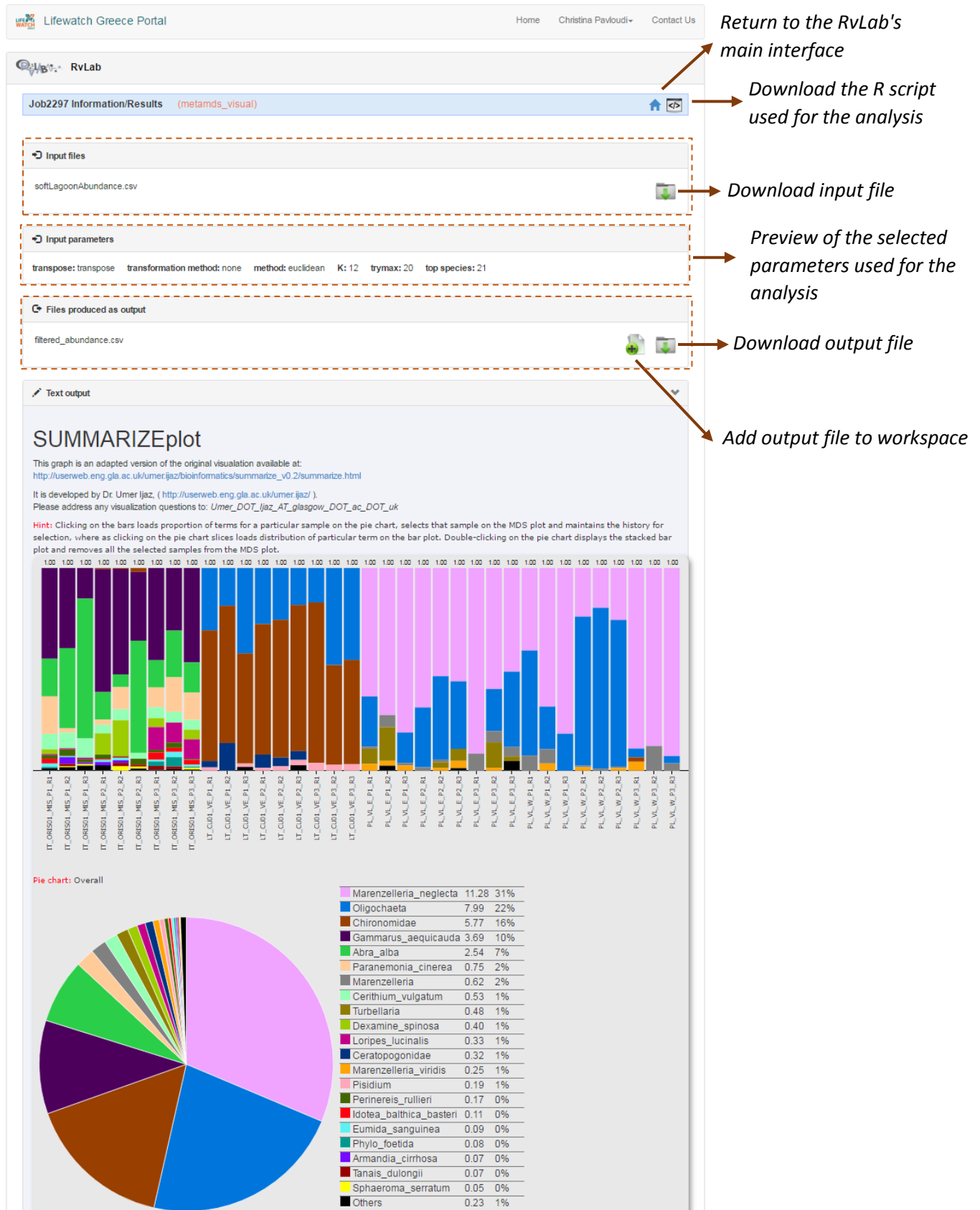



Figure 11: A preview of the results of the analysis.

If you have any suggestions about new functions to be implemented or if you are experiencing difficulties with the analyses and the interface, you can contact us by clicking the relevant link on the top of the RvLab's page. Just select from the drop-down menu that your inquiry is related to RvLab, so that it will be delivered to the relevant people.

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## Contact Form

For feedback, problem, proposals and any other issue generally related to the portal or regarding a certain vLab or web service provided by the portal, use the form of this page.

Subject \*


Related To \*

RvLab

▼

Message \*

Fill in the image text \*



C

Send Message

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Figure 12: The contact form of the RvLab.

Enjoy!!