ALGAEFUN with MARACAS

microALGAE FUNctional enrichment tool for MicroAlgae RnA-seq and Chip-seq AnalysiS

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(1)

AlgaeFUN allows researchers to perform **functional annotation** over gene sets. **Gene Ontology (GO) enrichment** analysis as well as **KEGG (Kyoto Encyclopedia of Genes and Genomes) pathway enrichment** analysis are supported. The gene set of interest can be obtained, for example, as the result of a differential expression analysis carried out using **MARACAS**. See our **video tutorial** for details or follow the next steps to perform your analysis:

1. In the left panel choose your **microalgae** of interest, the type of enrichment analysis to perform and the **p-value threshold**.
2. Insert your **gene set** in the text box or load it from a file using the **Browse ...** button. An example can be loaded by clicking on the **Example** button. Click on **Clear** button to remove the loaded gene set.
3. Users can choose between the default **background** gene provided by AlgaeFUN of a custom one that can be specified.
4. Click on the **Have Fun** button to perform the specified functional enrichment analysis. The results will be shown in the different tabs below.

Choose your favourite microalgae

Ostreococcus tauri ▼

(2)

Choose your desirable analysis
● GO terms enrichment
○ KEGG pathways enrichment analysis
○ Both

(3)

Choose gene ontology:
● Biological process
○ Cellular Component
○ Mollecular Function

Which will be your chosen p-value?

0,05 ⬍

Insert a set of genes

Insert set of genes

(4)

| Example | Clear |

Choose File with Gene Set to Upload

| Browse... | No file selected |

Would you rather use your own background set?
○ Yes
● No

⏍ Have fun!

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AlgaeFUN allows researchers to perform **annotation analysis of genomic loci or regions.** These are typically generated from **ChIP-seq** studies of the genome-wide distribution of **epigenetic marks or transcription factor binding sites.** Our tool **MARACAS** can be used to perform this type of analysis. The set of marked genes can be obtained as well as the distribution of the genomic loci overlapping specific genes parts. Also, individual marked genes and the average signal level around the TSS (Transcription Start Site) and TES (Transcription End Site) over the complete set of marked genes can be visualized. See our **video tutorial** for details or follow the next steps to perform your analysis:

1. In the left panel choose your **microalgae** of interest, the gene **promoter length** and the **gene parts** that will be considered when determining the marked genes.
2. Insert in the text box your **set of genomic regions** as a table consisting of three tab-separated columns representing the chromosome, the start and end position of the regions. An example can be loaded by clicking on the **Example** button. Click on **Clear** button to remove the loaded gene set. Alternatively, using the **Browse...** button, the genomic regions can be uploaded from a file in BED format as described previously containing as least three columns. This file can be obained using our tool **MARACAS.**
3. Optionally, users can upload the genome wide signal level of a epigenetic mark or transcription factor binding in a BigWig file. This file can be obained using our tool **MARACAS.**
4. Click on the **Have Fun** button to perform the specified analysis. The results will be shown in the different tabs below.

Choose your favourite microalgae

Ostreococcus tauri ▾

Choose the distance in base pairs around the Transcriptional Start Site defining gene promoters

| 100 | 1,000 | 2,000 |

100 300 500 700 900 1,100 1,300 1,500 1,700 1,900 2000
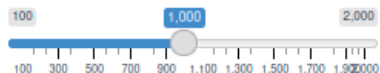
A gene will be associated to an input genomic locus when it overlaps one of the following gene features:

☑ Promoter
☑ 5' UTR
☑ Exon
☑ Intron
☑ 3' UTR

Insert a set of genomic regions

Insert set of genomic regions

Example   Clear

Choose File with the Genomic Regions to Upload

Browse...   No file selected

Choose BigWig File to Upload for Profile Representations: (Optional)

Browse...   No file selected

⏀ Have fun!

(1)

(2)

(3)

(4)

CHYB - HaLaN_13011

PSY - HaLaN_19207

PDHE2 - HaLaN_06535

(5)