Cheatsheet of metaprotr
by: Aaron Millan Oropeza

From X!Tandempipeline

INPUTS

- **peptide_counts.txt**
- **protein_list.txt**
- **metadata.csv**
- **metaHIT99_db.tsv**

1) load_protspeps Loads peptides counts, proteins list and metadata. Creates: **metaproteome_object**

2) add_taxonomy Integrates the taxonomic DB into a **metaproteome_object**. Creates: **metaproteome_object**

FORMAT

5) remove_element Removes elements from a spectral_count object. Creates: **spectral_count_object**

6) select_element Selects elements from a spectral_count object. Creates: **spectral_count_object**

7) filter_unshared Keeps the non shared elements (peptides, subgroups or groups) from a spectral_count object in function of a metadata feature (sample, condition, etc.). Creates: **spectral_count_object**

8) filter_shared Keeps the common elements (peptides, subgroups or groups) from a spectral_count object in function of a metadata feature (sample, condition, etc.). Creates: **spectral_count_object**

9) filter_text Keeps or discards the elements (peptides, subgroups or groups) that matched a chunk of text in a variable of peptides_proteins dataframe from a spectral_count object. Creates: **spectral_count_object**

10) crumble_taxonomy Express the the abundance of peptides, subgroups or groups from a spectral_count object in function of a taxonomic level (specie, genus, family, order, class, phylum or superkingdom). Creates: **spectral_count_object** with taxonomy

3) getsc_specific
Obtains abundance of specific spectral counts by peptides, subgroups or groups. Creates **spectral_count object**

EXPORT

4) export_robject Exports a metaproteome or a spectral count object. Creates: **RDATA / rds file**

13) export_vennlists Exports the lists from a **venn_lists_object**. Creates: **csv files**

23) export_ipath3 Exports the **spectral_count _object** with taxonomy and annotation. Creates: **csv file**

ANALYSIS

19) inspect_sample_elements Displays the frequency of the entities (peptides, subgroups, groups) per sample. Creates: **PDF file**

20) plot_PCA Displays the PCA results from peptides, subgroups, groups or taxonomic levels. Creates: **PDF file** and **csv**

21) identify_differences Displays the most over and under represented taxonomic elements from an **spectral_count_object** with taxonomy . Creates: **PDF and csv files**

22) add_kegg Integrates the functional annotation to the taxonomic elements in **spectral_count_object** with taxonomy . Creates: **spectral_count_object** with taxonomy and annotation

VISUALIZATION

11) plot_dendocluster Plots a non-supervised clustering dendogram from a spectral_count object. Creates: **PDF file**

12) plot_venn Creates a venn diagram of 2 or 3 conditions from a spectral_count object. Creates: **PDF file** and a **venn_lists object**

14) plot_intensities_ratio Creates a scatter plot of the abundance ratio of the elements (peptides, subgroups, groups) between 2 conditions/samples from a spectral_count object. Creates: **PDF file**

15) plot_intensities Creates violin plots of the mean of abundances per sample/condition of the elements (peptides, subgroups, groups) from a spectral_count_object. Creates: **PDF file**

16) plot_fulltaxonomy Creates bar plots of the mean of abundances per sample of the elements (peptides, subgroups, groups) from a spectral_count_object. Creates: **PDF** and **csv file**

17) plot_stackedtaxo Creates stacked bar plots of samples or conditions with the spectral abundance as counts or as percentage, these values are formated based on **spectral_count_object** with taxonomy. Creates: **PDF file**

18) plot_pietaxo Creates a pie chart of one sample or condition with the spectral abundance as counts, these values are formated based on **spectral_count_object** with taxonomy. Creates: **PDF** and **csv file**

24) plot_biomarkers Creates boxplots of the spectral abundance as counts of all the taxonomic entities, these values are obtained from **spectral_count_object** with taxonomy. Creates: **PDF**
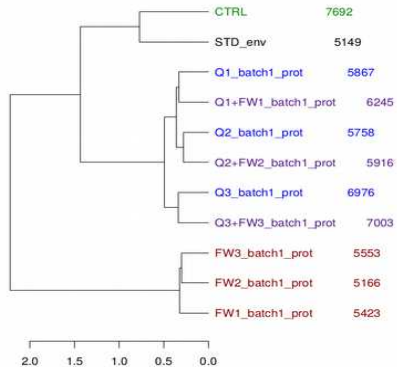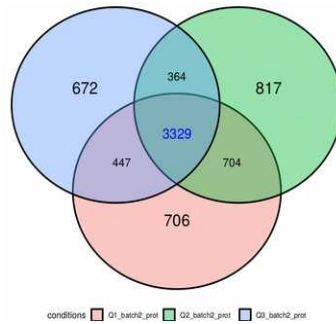
plot_dendocluster

Non-supervised clustering dendogram of the experimental samples. Display the number of entities.
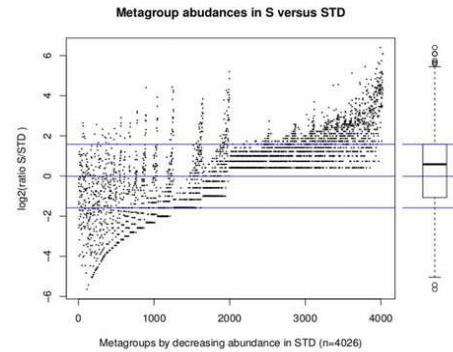

plot_venn

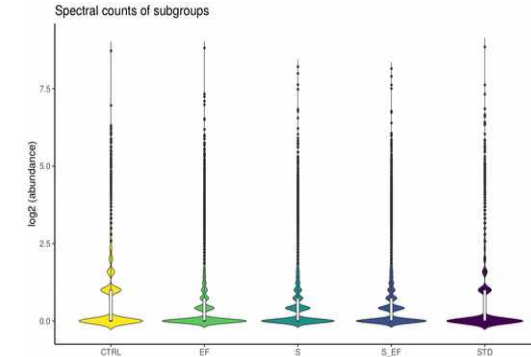Venn diagram of the entities of 2 or 3 conditions.

plot_intensities_ratio

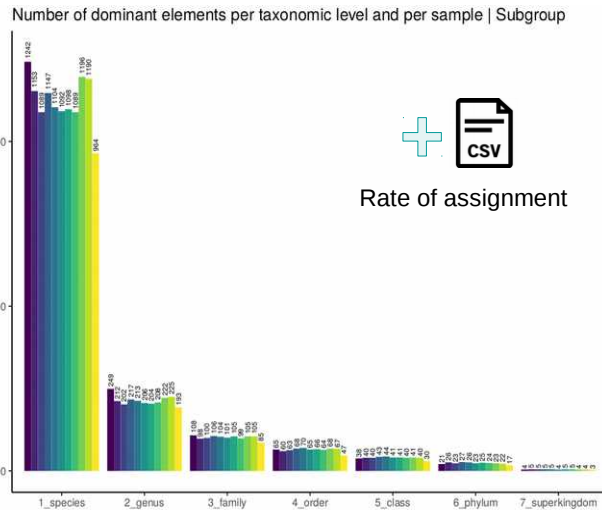Scatter plot of the abundance ratio of the entities between 2 conditions.

plot_intensities

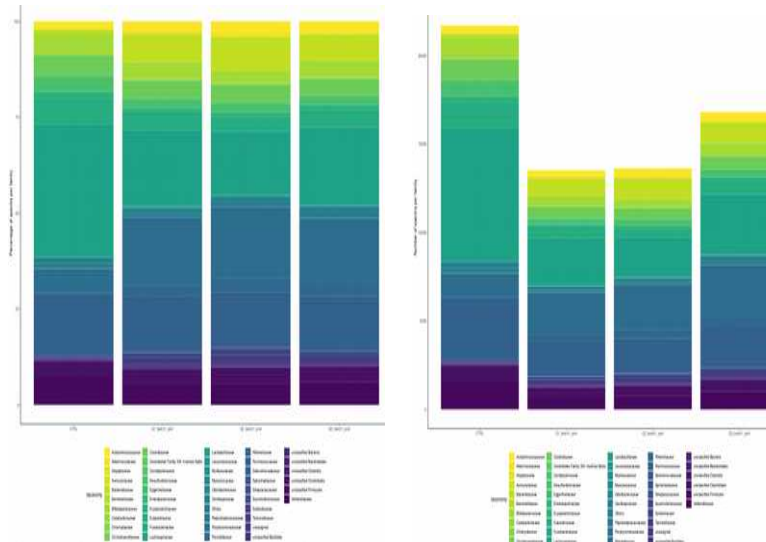Violin plots of the mean of abundances of the entities per condition .

plot_full_taxonomy

Bar plots of the mean of abundances of the entities per sample. Seven taxonomic levels are displayed.

Rate of assignment

plot_stackedtaxo

Stacked bar plots of conditions with the spectral abundance of the taxonomic elements as counts or as percentage.
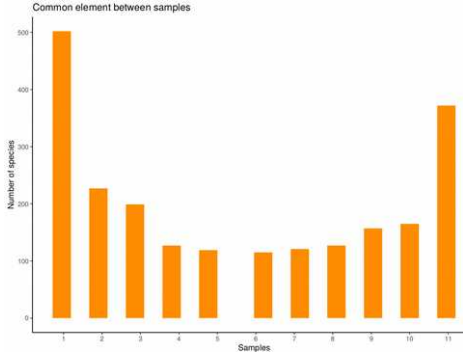

plot_pietaxo

Pie chart of one condition with the spectral abundance as counts or as percentage.
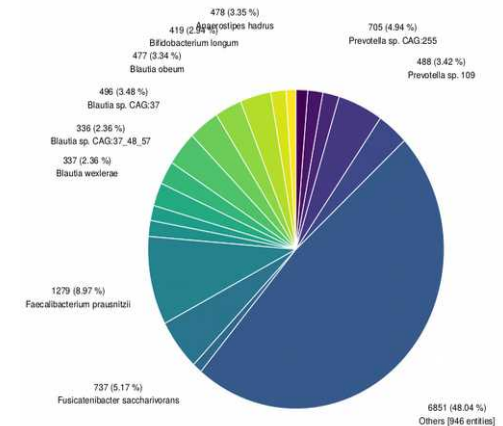
Values of abundance for each taxonomic entity
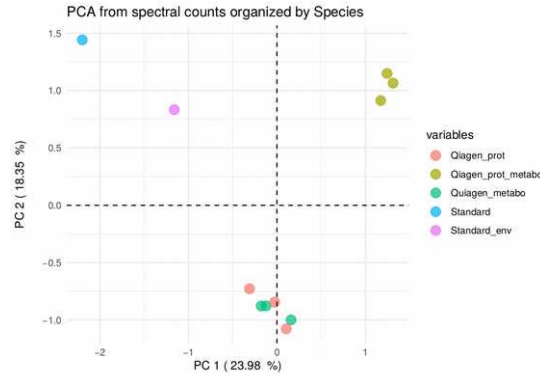
inspect_sample_elements

Barplots indicating the presence of entities per sample. Useful to observe the heterogeneity in the samples.
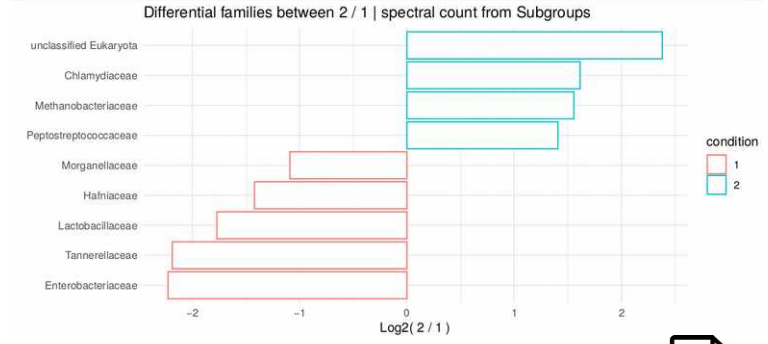

plot_PCA

Plot of two selectet axis after performing a Principal Component Analysis of the entities of a 'spectral_count_object'

identify_differences

Barplots of the most differential taxonomic entities between two conditions or samples.

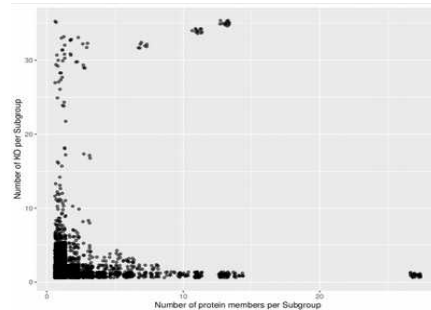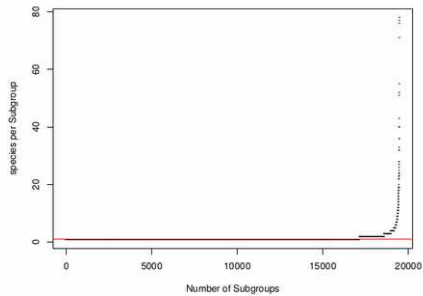List of the taxonomic entities with their ratios between conditions

add_kegg

Adds the functional annotation from KEGG DB to the taxonomic entities.

KEGG DB

spectral_count_object with taxonomy and **functional annotation**

Quality Control plots

export_ipath3

Creates a CSV file with the suitable format to display metabolic pathways using the tool iPATH3

spectral_count_object with **taxonomy** and **functional annotation**

Paste in iPATH3