Archaea EvoMining Results

Archaea kingdom was discovered by Woese in 1977 [@woese_phylogenetic_1977]
Actinobacteria has proved that natural products can be found on expansions from central metabolic pathways
Archaea is interesting because as we will see has a phylum that contains expansions (Central and pangenomic) on Actinobacteria previously known natural products can be detected by software like antiSMASH and clusterfinder, nevertheless on Archaea a whole kingdom, this products are not found. Does Archaea not produce NP's or traditionally known method are nos switable for finding them? Archea has operons?? Archaea has introns?

Tables

Table 1: Families on Archaeabacteria

Factors	Correlation between Parents & Child
GenomeDB	876
Phylum	12
Order	23

Expansions BoxPlot by metabolic family

```
label(path = "chapter3/expansion_plotArchaeas.pdf", caption = "Expansions Boxplot",label = "Archaea_exp
```
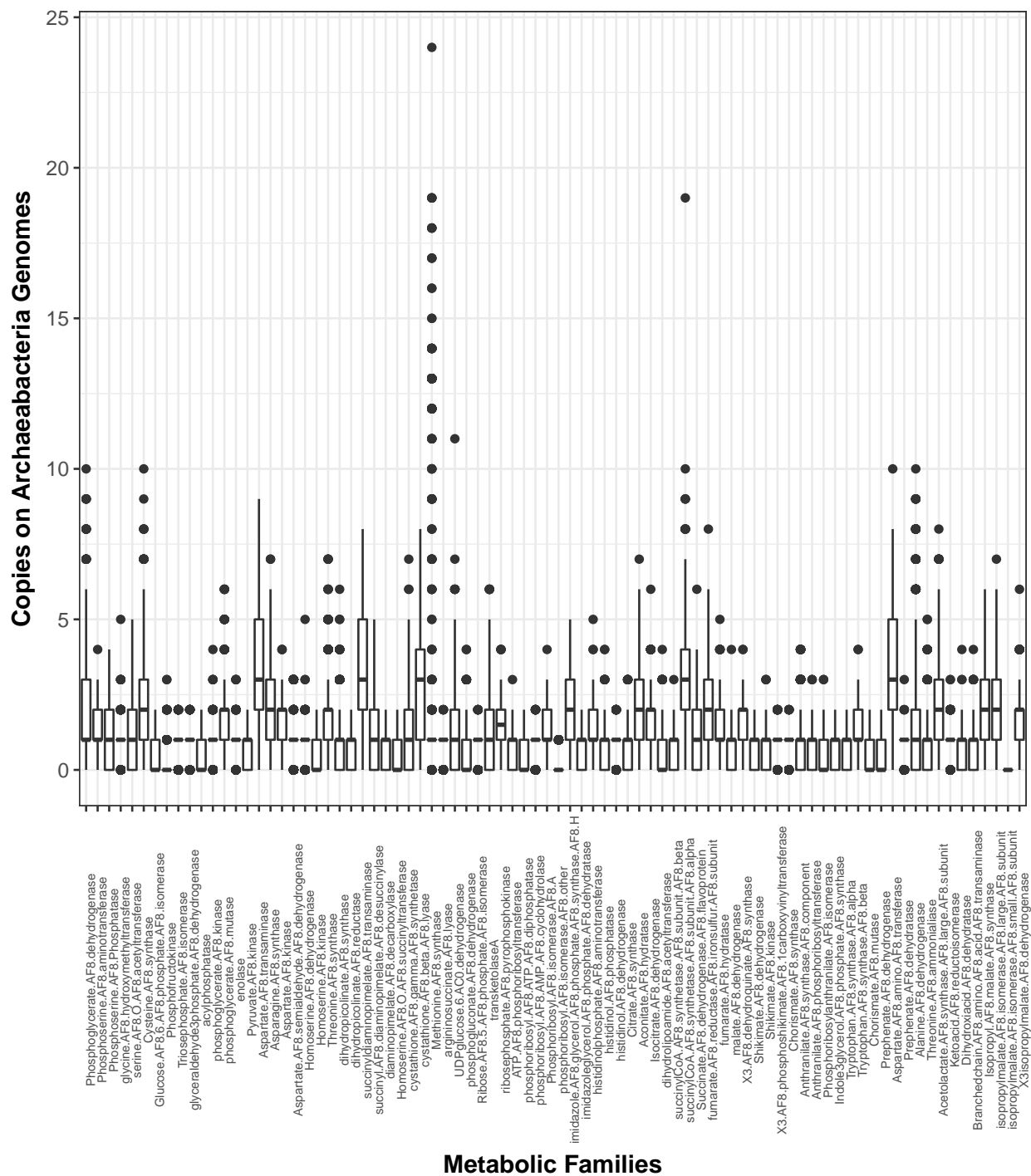

Figure 1: Expansions Boxplot

Here is a reference to the expansion boxplot: Figure 1.

Central pathway expansions

Heat plot of central pathways expansions, Needs to be phylogenetically sorted.

```
## Warning: Ignoring unknown aesthetics: width
```
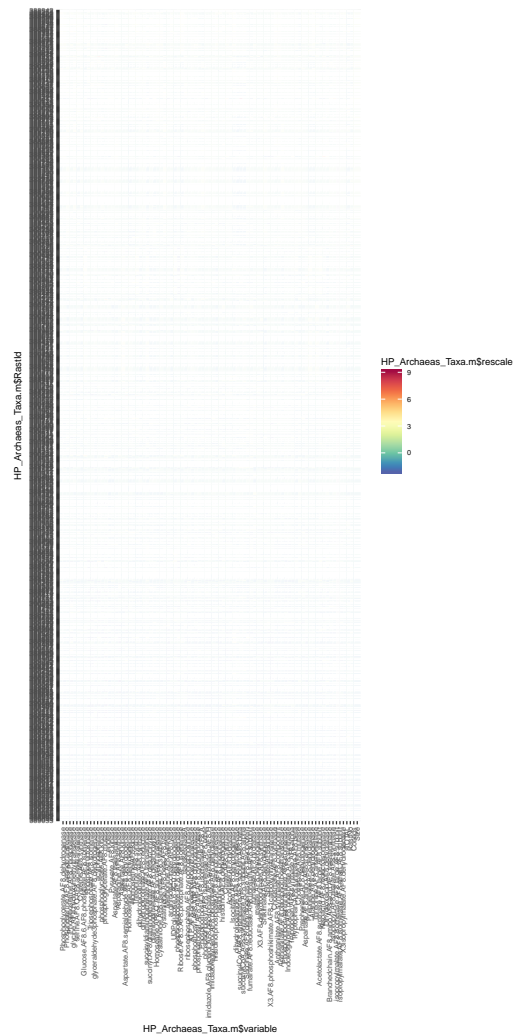
Figure 2: Archaeas Heatplot

Here is a reference to the HeatPlot: Figure 2.

Genome Size correlations

Correlation between genome size and AntiSMASH products

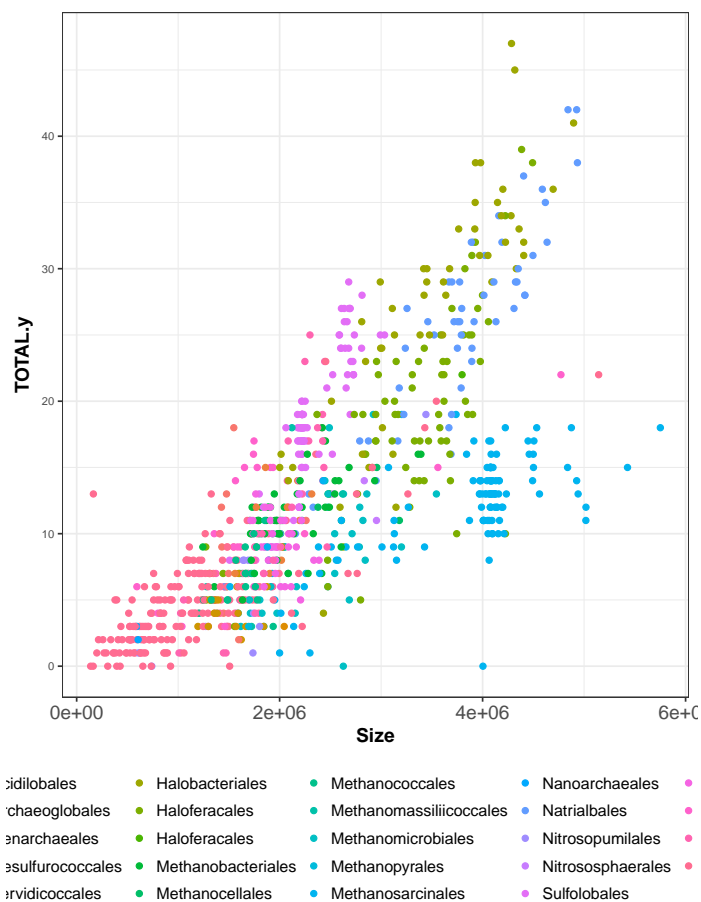Genome size vs Total antismash cluster coloured by order

Figure 3: Correlation between Archaeas genome size and antismash Natural products detection colored by Order

Here is a reference to Genome size vs Total antismash cluster: Figure 3.

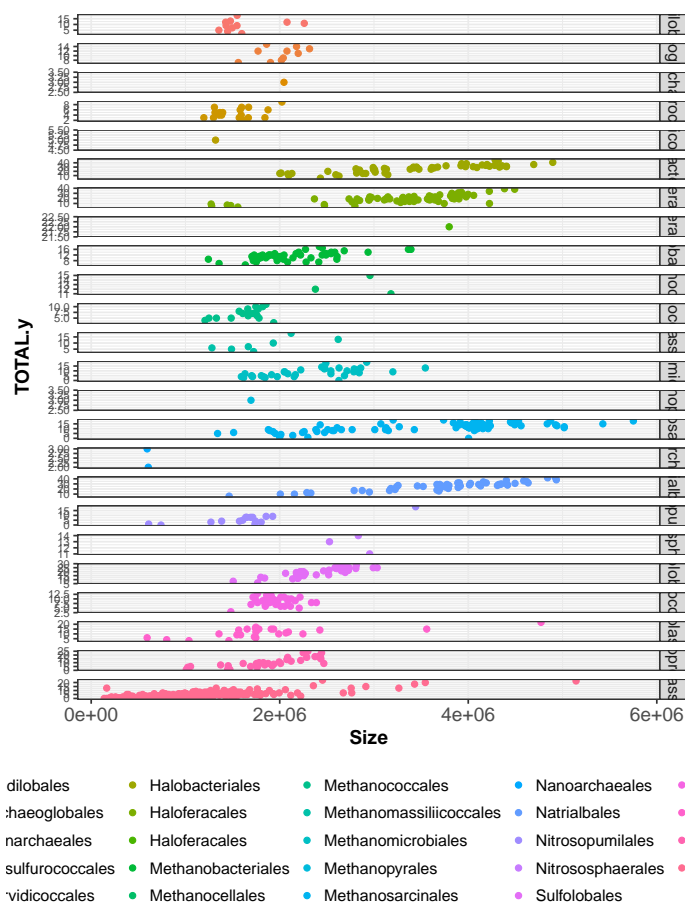Genome size vs Total antismash cluster detected splitted by order

Figure 4: Correlation between Archaeas genome size and antismash Natural products detection grided by Order

Here is a reference to Correlation between genome size and antismash Natural products detection grided by Order plot: Figure 4.

Correlation between genome size and Central pathway expansions

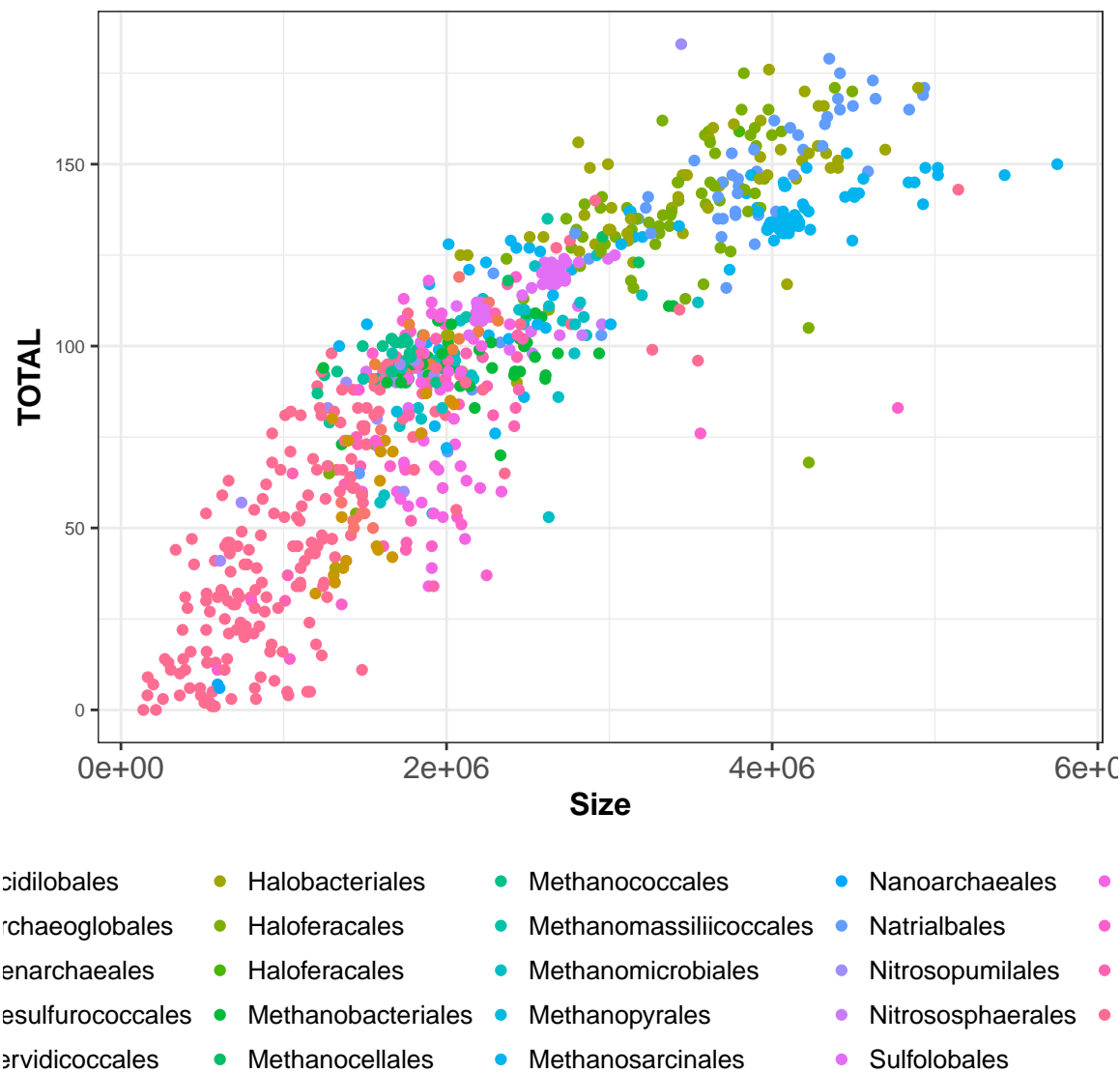Genome size vs Total central pathway expansion coloured by order

Figure 5: Correlation between Archaeas genome size and central pathway expansions

Here is a reference to the size vs Total central pathway expansion plot: Figure 5.

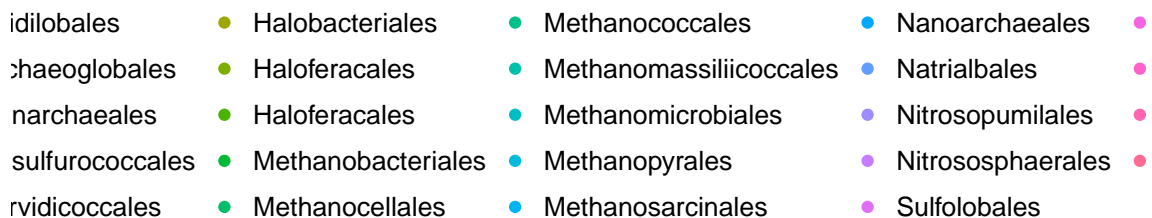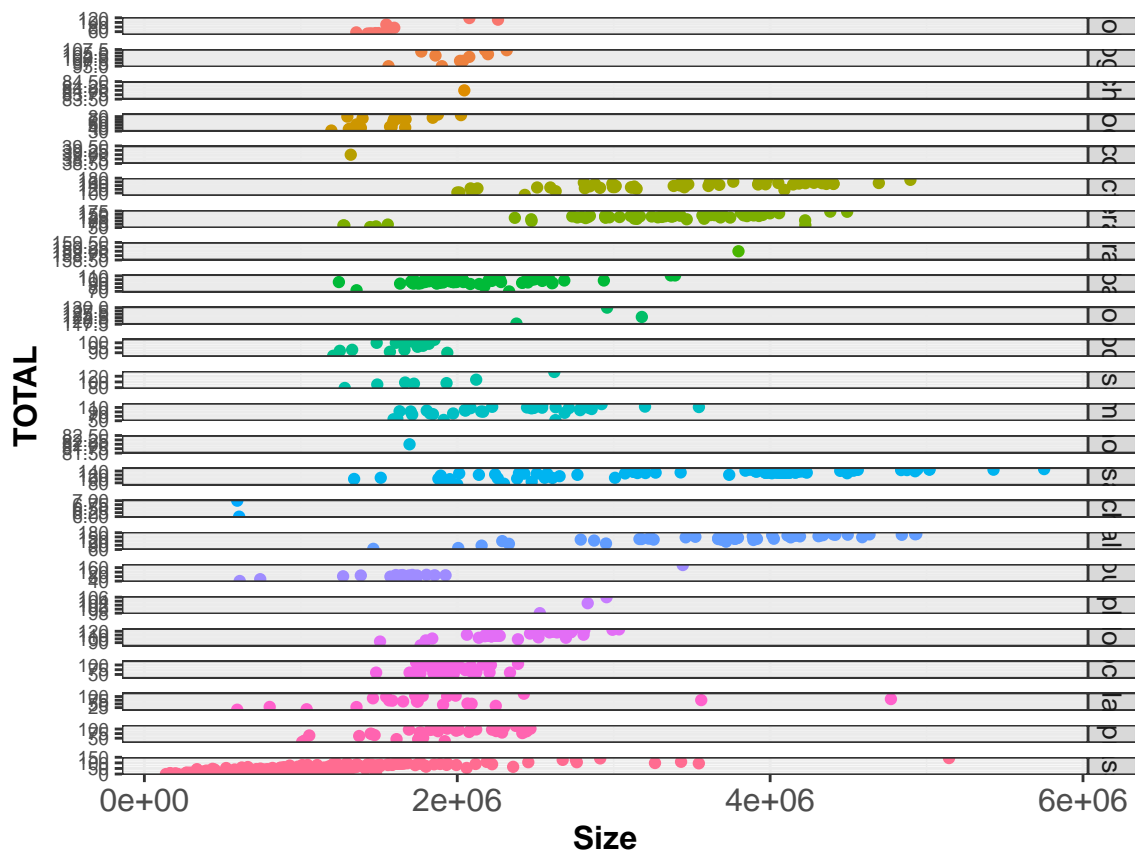Genome size vs Total central pathway expansion grided by order

Figure 6: Correlation between Archaeas genome size and central pathway expansions grided by order

Here is a reference to the Genome size vs Total central pathway expansion grided by order plot: Figure 6.

Correlation between genome size and each of the central pathway families. Data are coloured by metabolic family instead of coloured by taxonomical order. This treatment allows to answer how differente metabolic families grows when genome size grow.

Also I want to add form given by taxonomical order.

```
## Warning: The shape palette can deal with a maximum of 6 discrete values
## because more than 6 becomes difficult to discriminate; you have
## 24. Consider specifying shapes manually if you must have them.
```

```
## Warning: Removed 64823 rows containing missing values (geom_point).
```

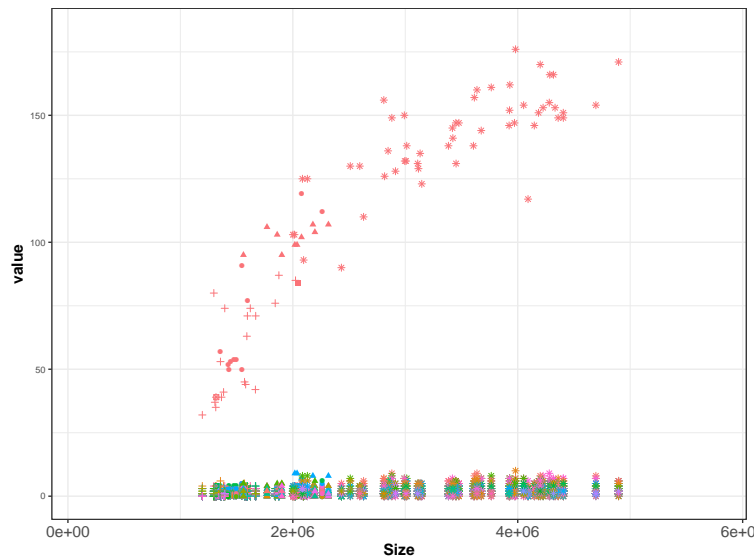Genome size vs Total central pathway expansion coloured by metabolic Family

Figure 7: Correlation between Archaeas Genome size vs Total central pathway expansion coloured by metabolic Family

Here is a reference to the Genome size vs Total central pathway expansion coloured by metabolic Family plot: Figure 7.

Future Work: Genome size vs Total central pathway expansion grided by metabolic Family For clarity I need to also grid and group by Metabolic Pathway

Here is a reference to Genome size vs Total central pathway expansion grided by metabolic Family plot: **??**.

Natural products

Natural products recruitments from EvoMining heatplot

We can see natural products recruitment after central pathways expansions colored by their kingdom. Natural products recruited by metabolic family, colored by phylogenetic origin.

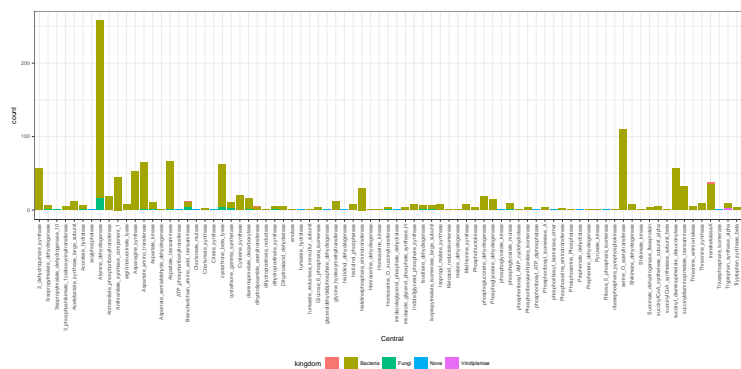Recruitments after central pathways expansions coloured by Kingdom

Figure 8: Archaeas Recruitmens on central families coloured by kingdom

Here is a reference to Recruitments after central pathways expansions colourd by Kingdom plot: Figure 8.

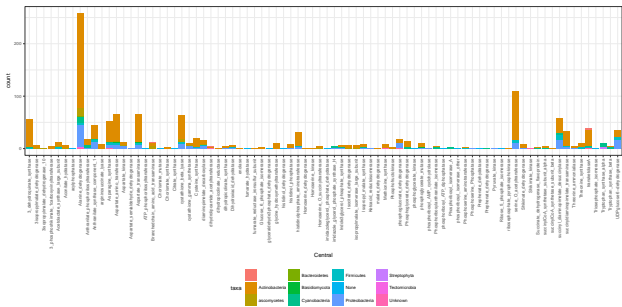Recruitments after central pathways expansions colourd by taxonomy

Figure 9: Archaeas Recruitmens on central families coloured by taxonomy

Here is a reference to Recruitments after central pathways expansions colourd by taxa plot: Figure 9.

Archaeas AntiSMASH

Taxonomical diversity on Archaeasbacteria Data

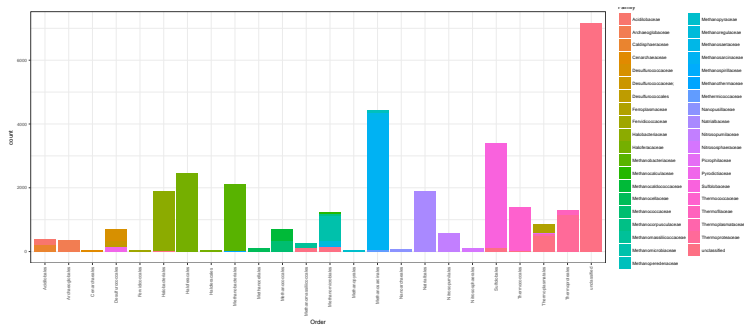

Figure 10: Archaeas Diversity

Here is a reference to Recruitments after central pathways expansions colourd by taxa plot: Figure 10.
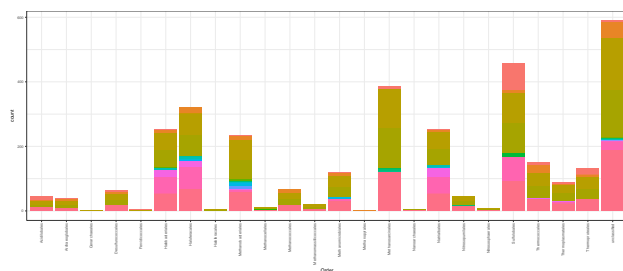
Smash diversity

Figure 11: Archaeas Smash Taxonomical Diversity

Here is a reference to Recruitments after central pathways expansions colourd by taxa plot: Figure 11.

AntisSMASH vs Central Expansions

Is it a correlation between pangenome grow and central pathways expansions?

Total central pathway expansions by genome vs Total antismash cluster detected coloured by order

Figure 12: Correlation between Archaeas central pathway expansions and antismash Natural products detection

Here is a reference to the expansions vs antismash NP's clusters plot: Figure 12.

Total central pathway expansions by genome vs Total antismash cluster detected splitted by order
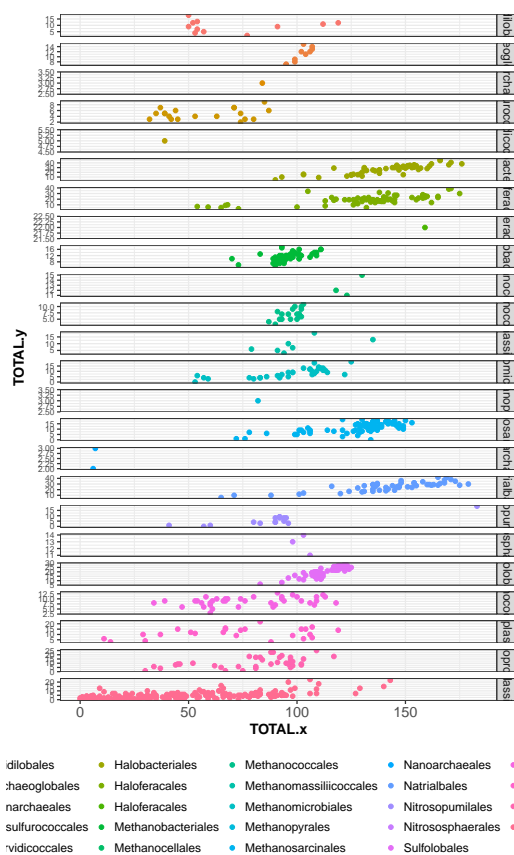

Figure 13: Correlation between Archaeas central pathway expnasions and antismash Natural products detection

Here is a reference to the expansions vs antismash NP's clusters splitted by order plot Figure 13.

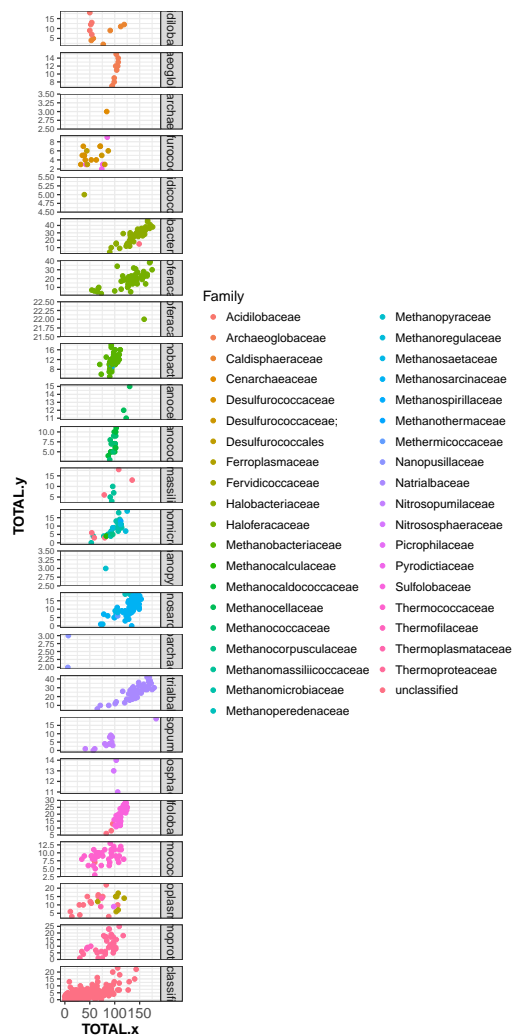AntisMAsh vs Expansions by taxonomic Family

Natural products colured by family

Figure 14: Archaeas Natural products by family

Here is a reference to the Natural products colured by family plot Figure 14.

Selected trees from EvoMining

Phosphoribosyl_isomerase_3 family
Figure from EvoMining

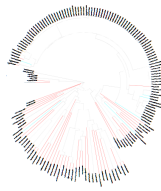Figure 15: Phosphoribosyl isomerase A EvoMiningtree

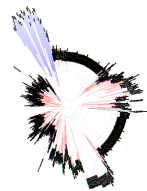Figure 16: Phosphoribosyl isomerase other EvoMiningtree

Figure 17: Phosphoribosyl anthranilate isomerase EvoMiningtree

Footnotes and Endnotes

You might want to footnote something. [1] The footnote will be in a smaller font and placed appropriately. Endnotes work in much the same way. More information can be found about both on the CUS site or feel free to reach out to data@reed.edu.

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Of course you will need to cite things, and you will probably accumulate an armful of sources. There are a variety of tools available for creating a bibliography database (stored with the .bib extension). In addition to BibTeX suggested below, you may want to consider using the free and easy-to-use tool called Zotero. The Reed librarians have created Zotero documentation at http://libguides.reed.edu/citation/zotero. In addition, a tutorial is available from Middlebury College at http://sites.middlebury.edu/zoteromiddlebury/.

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If you look at the YAML header at the top of the main .Rmd file you can see that we can specify the style of the bibliography by referencing the appropriate csl file. You can download a variety of different style files at https://www.zotero.org/styles. Make sure to download the file into the csl folder.

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- The cite key (a citation's label) needs to be unique from the other entries.
- When you have more than one author or editor, you need to separate each author's name by the word "and" e.g. `Author = {Noble, Sam and Youngberg, Jessica},`.
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[1] footnote text
[2] @reedweb2007
[3] @noble2002

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