

MuGeN

Multi-Genome Navigator

<http://www-mig.jouy.inra.fr/bdsi/MuGeN>

M. Hoebeke

`Mark.Hoebeke@jouy.inra.fr`



OBJECTIVES

- Explore multiple genomes simultaneously:
 - No theoretical limit but practical limit around 5.
- Mix annotated genomes and *in silico* analysis results:
 - Easily distinguish main feature types (CDSs, different kinds of RNA)
 - Add plots generated by bioinformatics tools either directly on top of the features or in between feature “strips”.
- Provide multiple output formats for images:
 - Bitmap (PNG, IMAP), vector (PS, EPS), editable (XFig).
- Be usable as standalone application and as batch tool:
 - Provide a decent GUI and a means to embed image generation in Web pages.

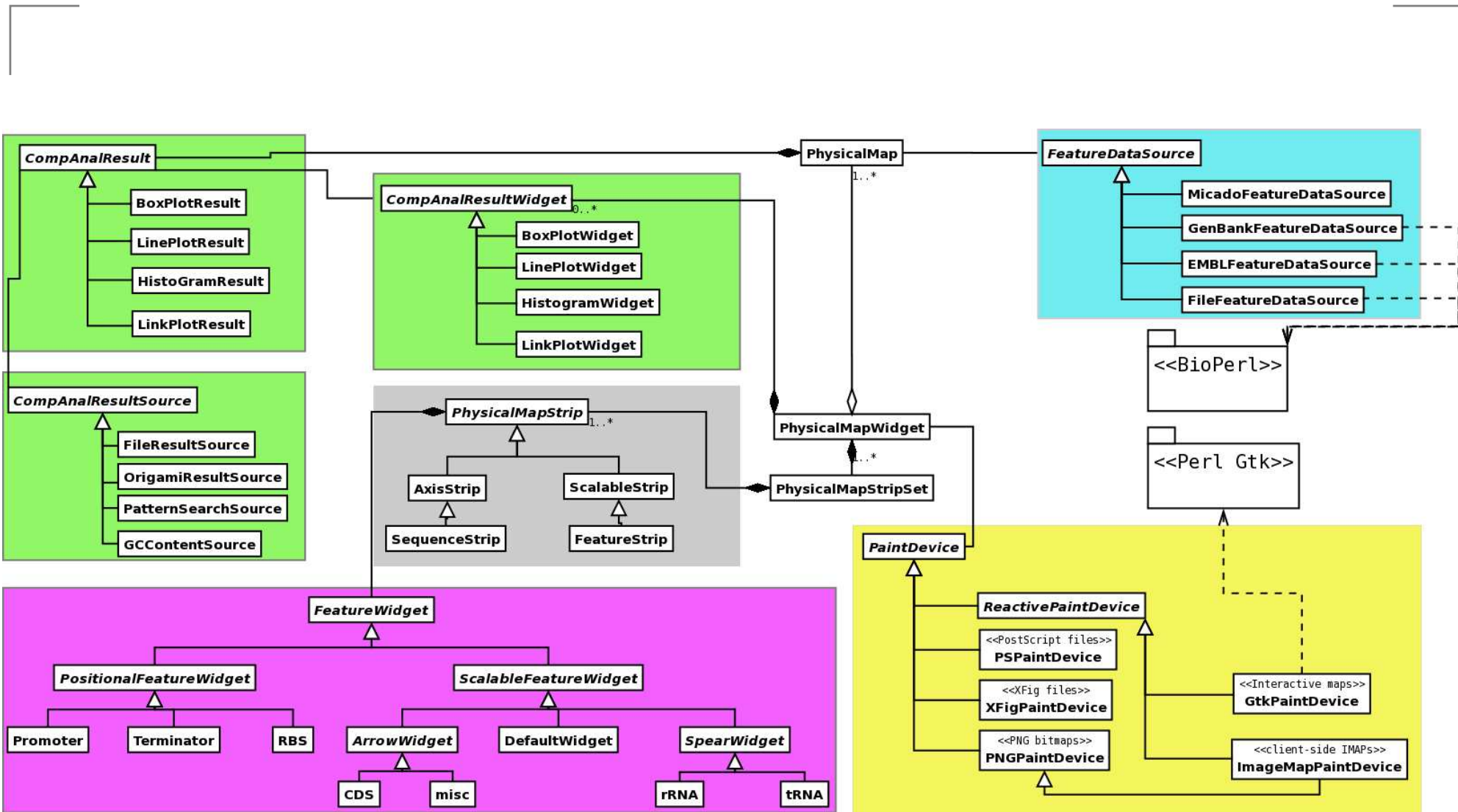
GUI OVERVIEW

The screenshot displays the MuGen software interface with several key components:

- Main Map:** A genomic map showing genes as arrows. The top track shows genes like *dcp*, *ydeH*, *ydeI*, *ydeB*, *ydeA*, *b1527yneJ*, *b1525yneH*, *b1522*, *uxaB*, *b1520*, *b1519yneI*, and *b1516ydeZ*. The bottom track shows genes like *ynfC*, *ynfF*, *ynfE*, *ynfC*, *spe6*, *rspA*, *rspB*, *ydfJ*, *c1968*, *ydfH/ydfC*, *dcp*, *ydeH*, *ydeI*, *c1960*, *c1958*, *c1956*, *c1955*, *marC*, *sotB*, *yneJ*, *yneI*, *yneH*, *yneF*, *yneE*, *tan*, *hipA*, and *c1937*.
- Map Operations Panel (Top Left):** Contains options for data source (Origami), anchor (Position/Gene), and computational result operations (Homology Map).
- Map Highlights Panel (Top Right):** Shows details for a selected feature (CDS), including location, EC number, function (degradation of proteins), and a partial translation sequence.
- Origami by Organisms Panel (Bottom Left):** A tree view showing the current map's position within a database of various bacterial genomes.
- Homology Map Panel (Bottom Right):** Displays a table of homology results between the two Escherichia coli strains.

QGene	Start	Stop	Strand	SGene	Start	Stop	Strand	EValue	Score
thrA	337	2799	1	thrA	985	3510	1	0.0	4047.0
thrB	2801	3733	1	thrB	3512	4444	1	0.0	1543.0
thrC	3734	5020	1	thrC	4445	5731	1	0.0	2104.0
b0005	5234	5530	1	yaaX	5345	6241	1	3.0E-18	203.0
yaaA	5663	6459	-1	yaaA	6301	7077	-1	0.0	1309.0
yaaJ	6529	7359	-1	yaaJ	7147	8577	-1	0.0	2334.0
talB	8238	9191	1	talB	8793	9809	1	0.0	1596.0

ARCHITECTURE



ANALYSIS RESULTS

- Types:

- Line plots, box plots, histograms, link plots.

- Taken from:

- Local files, built-in modules or external programs, remote repositories.

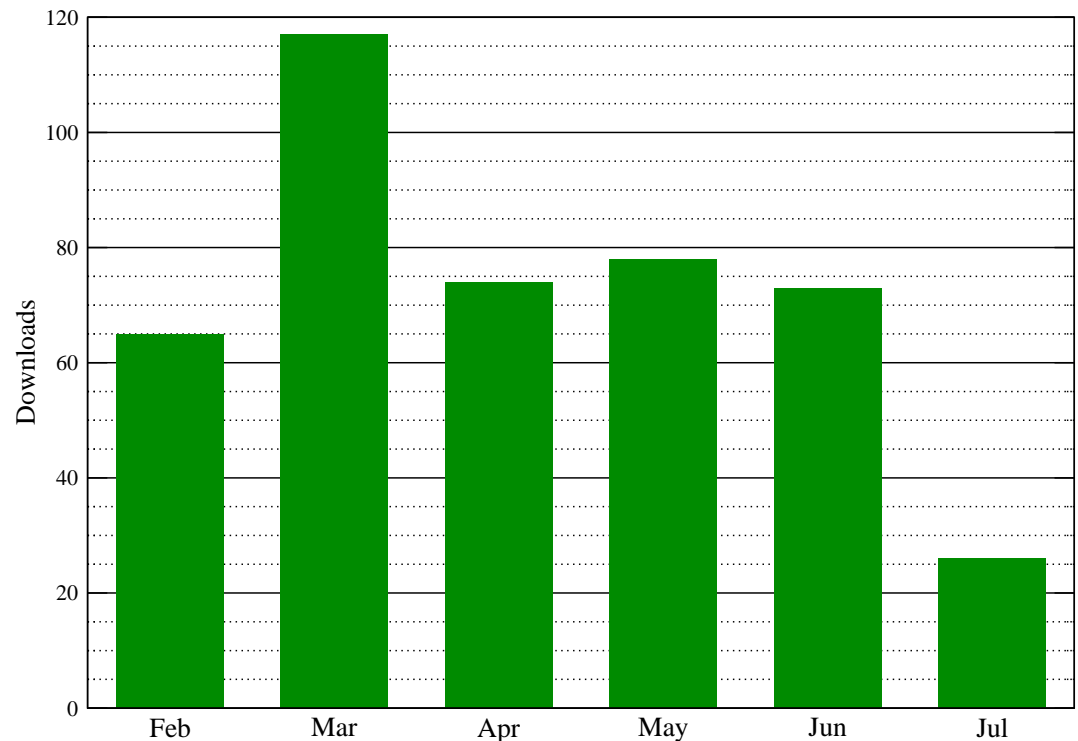
- Defined by:

- A Simple XML DTD.

```
<companalresults>
<colors>
  <color name='darkred' red='1' green='0.75' blue='0.75' />
</colors>
<histogram comment='Sample Histogram'>
  <bar height='20' start='1000' width='1000' filled='yes'
    color='darkred' info='Sample Bar' />
(...)
```

USAGE

- In-house:
 - Access to local databases (Micado, MOSAIC, Small Genes).
 - Front-end for genome annotation pipeline (work in progress).
 - Teaching.
- Third-party:



PERSPECTIVES: WHAT'S LACKING ?

- **REALLY** easy installation procedure.
- Circular views of (microbial) chromosomes.
- Annotation capabilities.
- More widespread output formats: SVG.