MuGeN

Multi-Genome Navigator

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

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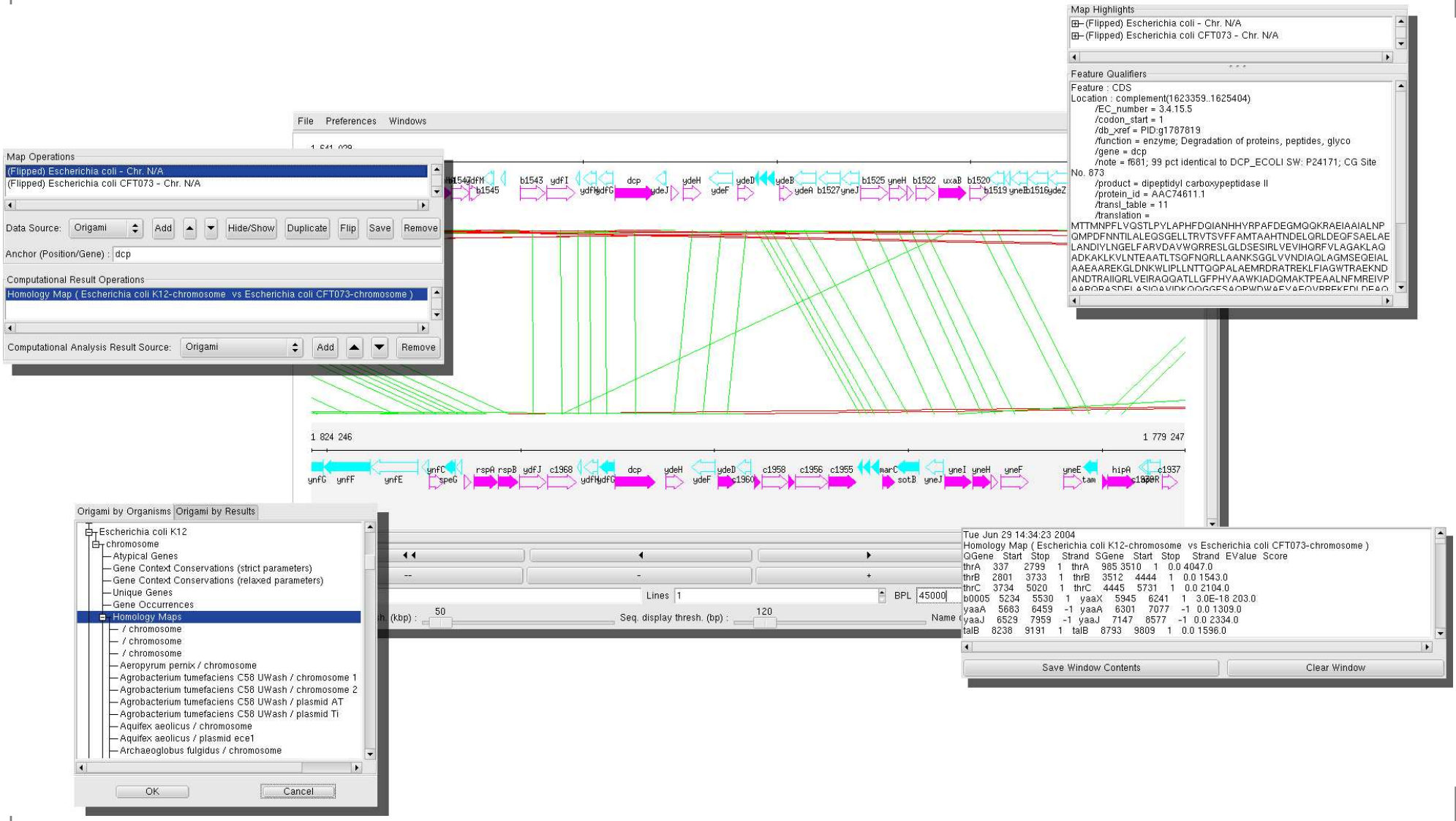
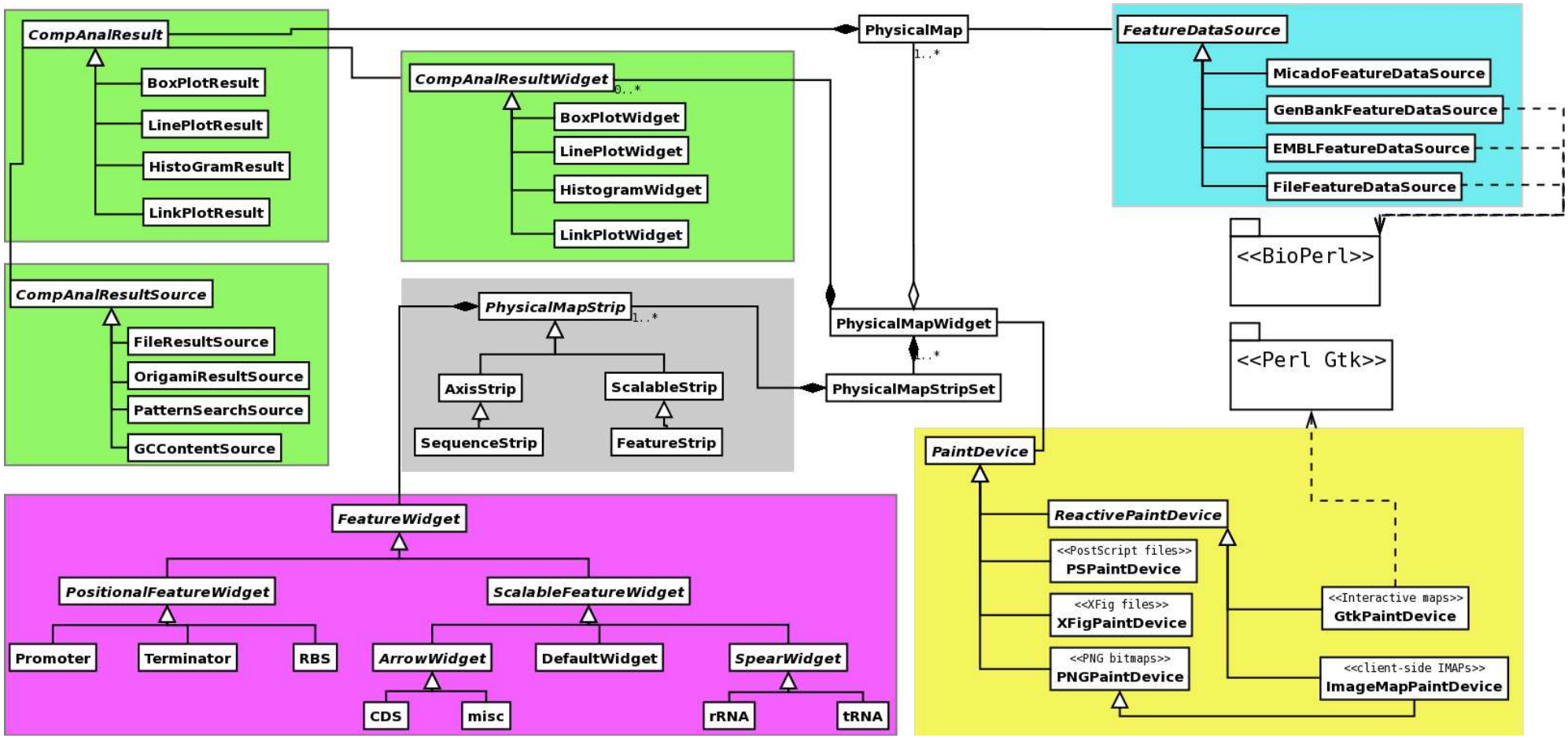
OBJECTIVES

- 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



ARCHITECTURE



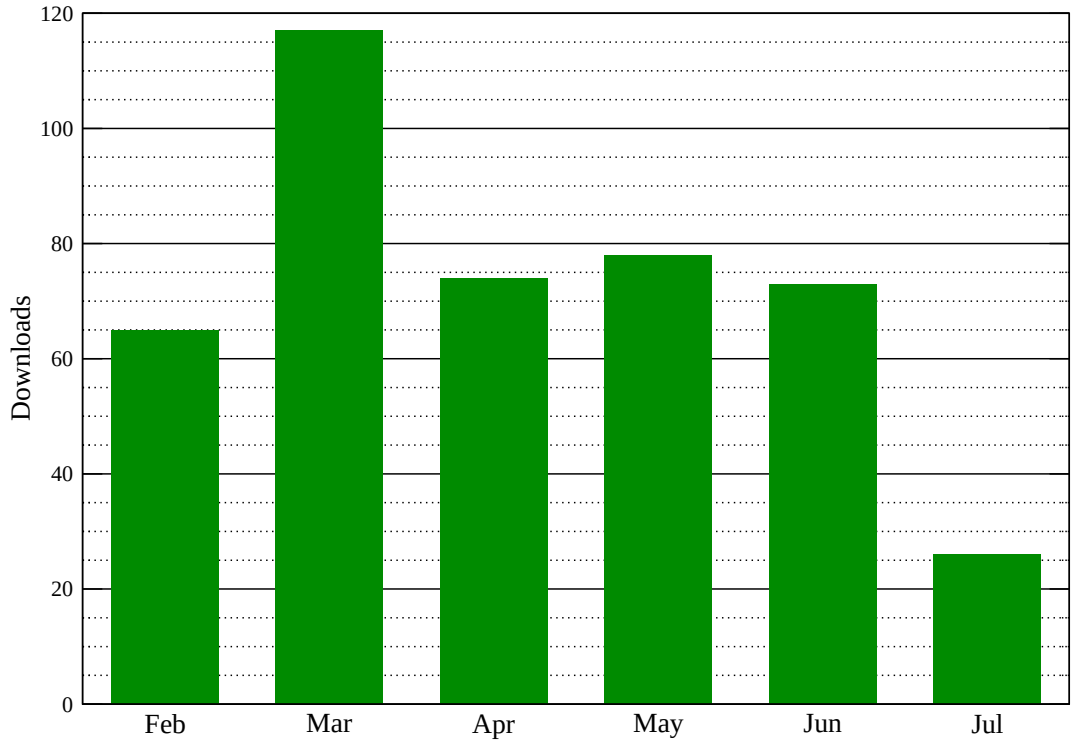
Analysis Results

- 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.