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

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BOSC’04
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.

```xml
<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'/>
  \end{histogram>
</companalresults>
```

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**Usage**

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

- **Third-party:**

![Bar chart showing downloads from February to July](http://www-mig.jouy.inra.fr/bdsi/MuGeN)
PERSPECTIVES: WHAT’S LACKING?

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

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