BioLegato: A Programmable, Object-Oriented Graphic User Interface

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GenomeCanada

MGCB2 Microbial Genomics for Biofuels and Co-Products from Biorefining Processes

GenomePrairie

Bioinformatics Team

Intellectual critical mass

Continuity of expertise

Faculty
Brian Fristensky

Bioinformaticists
Graham Alvare
Justin Zhang

Synergies

PhD Student
Abiel Roche

Research Associate
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Biostatistician TBA

Undergraduate Students
Dale Hamel

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BioLegato

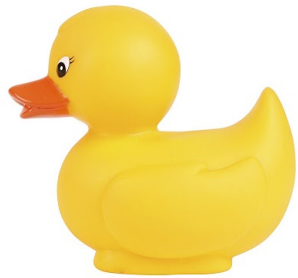**Why a Duck?**

The Object-Oriented World View

Common wisdom: "If it looks like a duck, and waddles like a duck, and quacks like a duck, then it's probably a duck."

OO: If you want a duck, then design it to look like a duck, and waddle like a duck, and quack like a duck.

BioLegato - The OO World View

1. A class is a formula for creating an object
2. Everything is an Object
3. Objects have Data and Methods
4. You can make new classes by reusing and extending an existing class

Class: BIRD
Data: Wing, Feathers
Methods: Waddle

Reuse and extend BIRD to to create new BIRD classes

Class: DUCK
Data: Wing, Feathers, Bill
Methods: Waddle, Quack, Fly, Swim

Class: PENGUIN
Data: Wing, Feathers, Bill
Methods: Waddle, Honk, Swim

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The BioLegato Concept

➢ **Unique concept in software design.***
➢ **Almost no functionality is written into the program itself.**
➢ **Menus, and a choice of canvas to display data, are read when the program launches.**
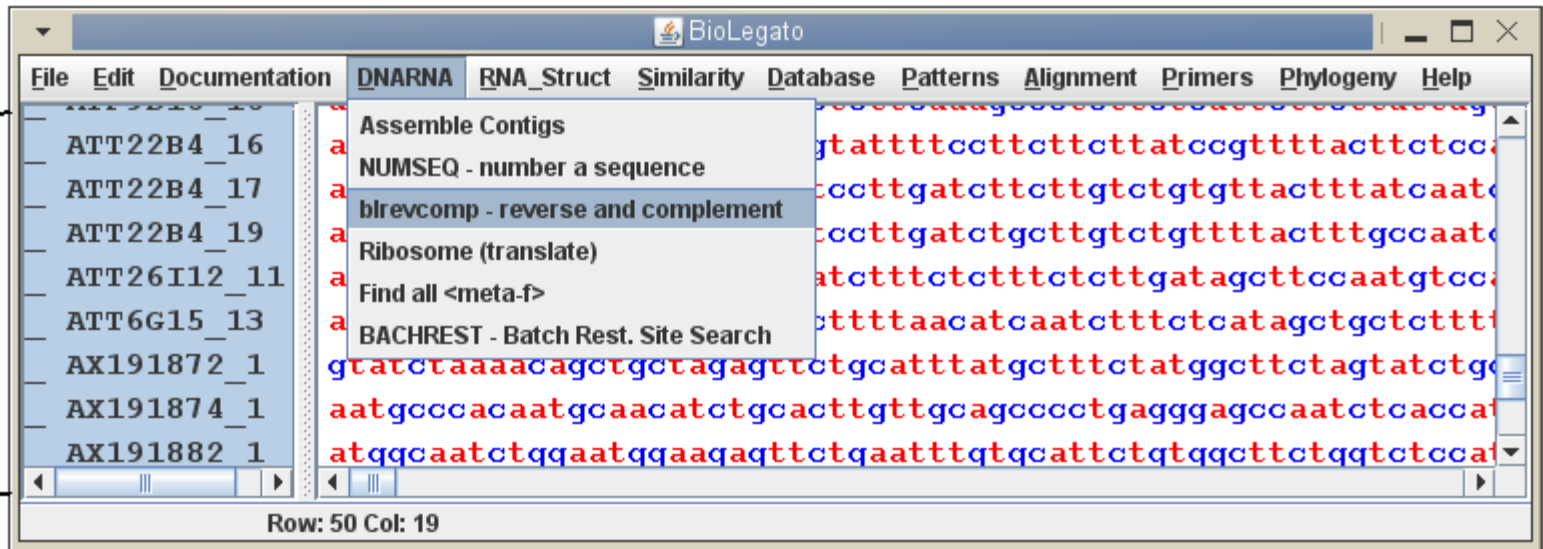
Empty BioLegato interface: null menus, empty canvas
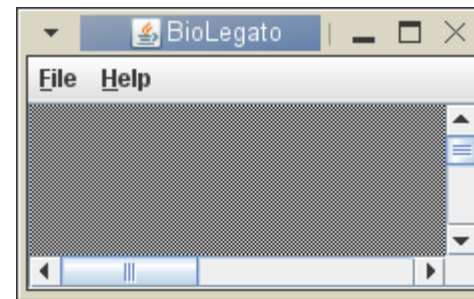
* Inspired by GDE/SeqLab of Steven Smith

# BioLegato - Objects have data and methods

PCD - GUI scripting language

```
name            "blrevcomp - reverse and complement"
var "in1"
    type        tempfile
    direction   in
    format      flat
var "strand"
    type        chooser
    label       "Strand"
    default     0
    choices
        "reverse complement" "-r"
        "complement only" "-c"
        "flip (reverse only)" "-f"
var "out1"
    type        tempfile
    direction   out
    format      flat
var "gdeoutput"
    type        chooser
    label       "Output to new bldna window?"
    default     1
    choices
        "Yes"       "(echo '' > %out1%; bldna %in1%.blrevcomp; $RM_CMD -f %in1%.blrevcomp)&"
        "No"        "mv %in1%.blrevcomp %out1%"
panel
    var "Run"
        type        button
        label       "Run"
        shell       "blrevcomp %STRAND% %in1% %in1%.blrevcomp; $RM_CMD %in1%; %GDEOUTPUT%"
        close       true
    var "Help"
        type        button
        label       "Help"
        shell       "$BIRCH/script/gde_help_viewer.csh null/$BIRCH/doc/BioLegato/blrevcomp.html"
        close       false
```


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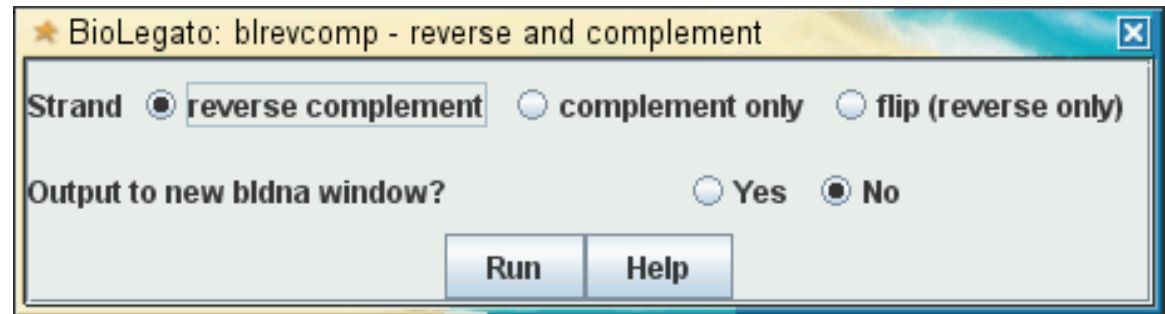
BioLegato - menus + canvas = new GUI

A GUI that will run just about any program for any kind of data can easily be made by writing new menus and choosing a canvas.

bldna -
- **menus for DNA programs**
- **multiple alignment canvas**
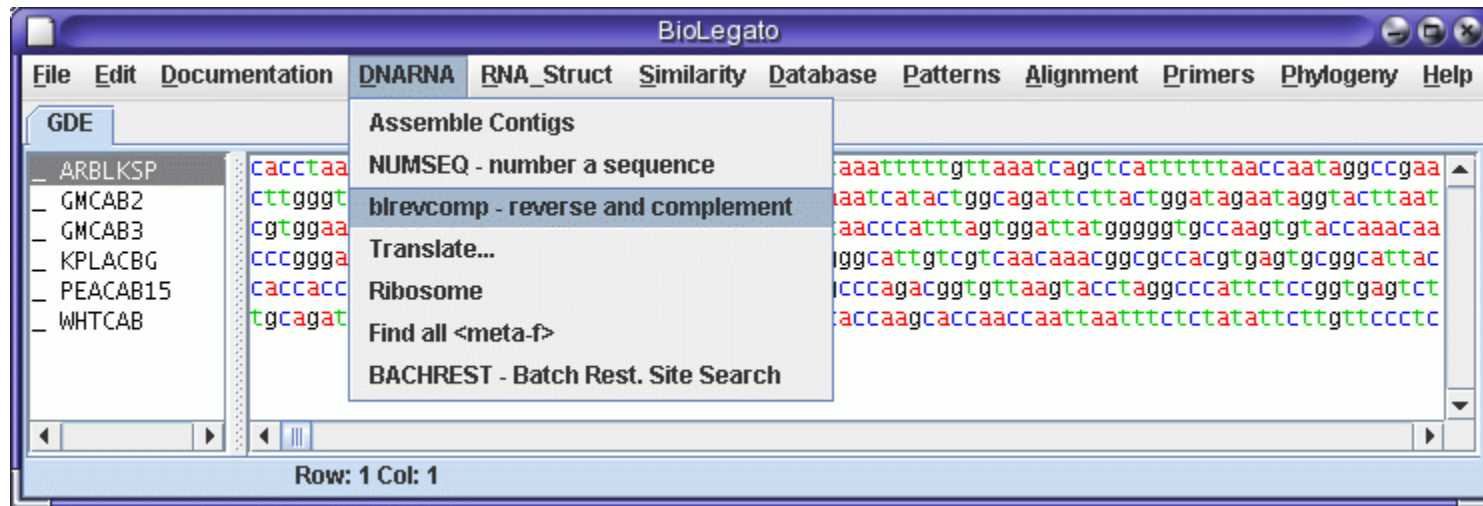
blprotein -
- **menus for protein programs**
- **multiple alignment canvas**

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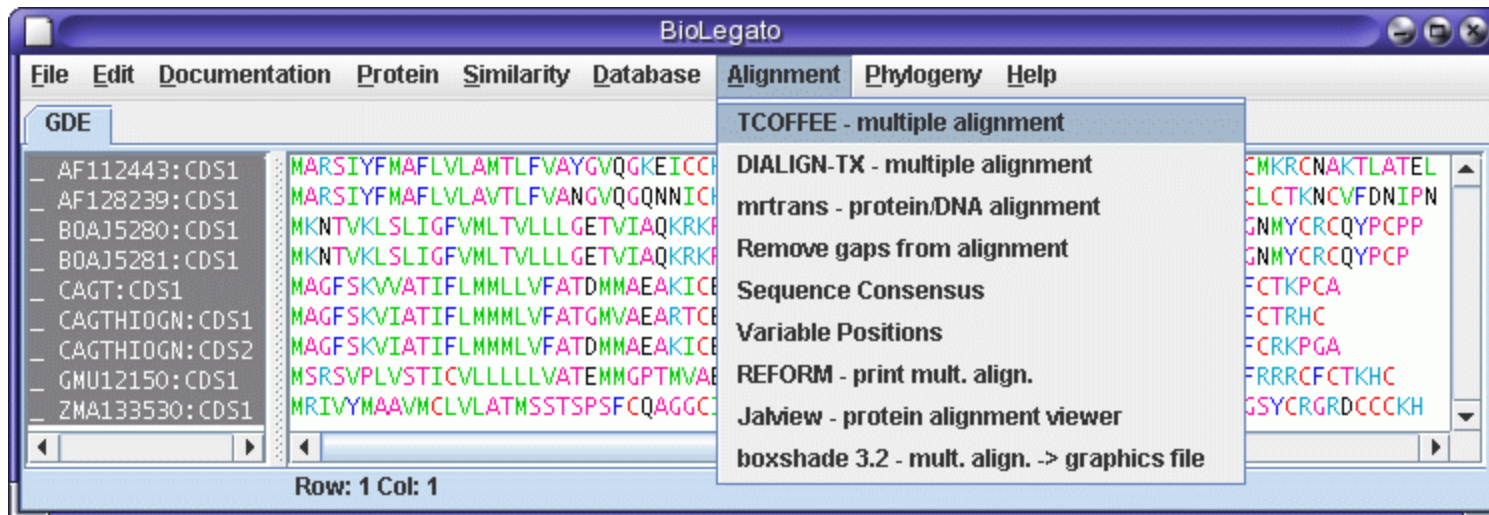
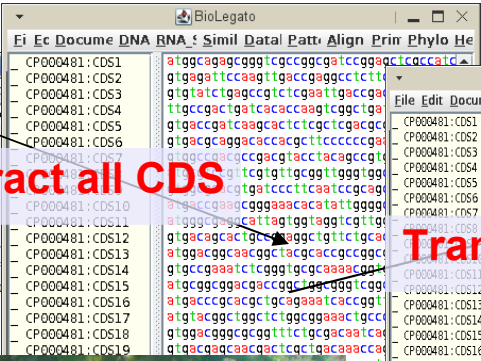# BioLegato - rapid deployment of new GUIs
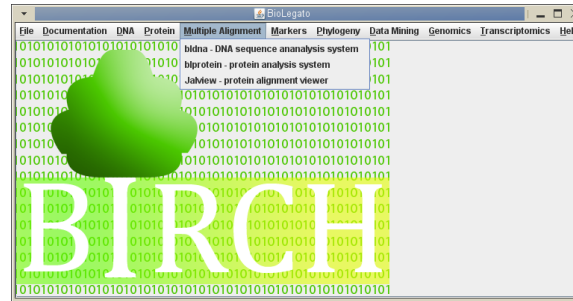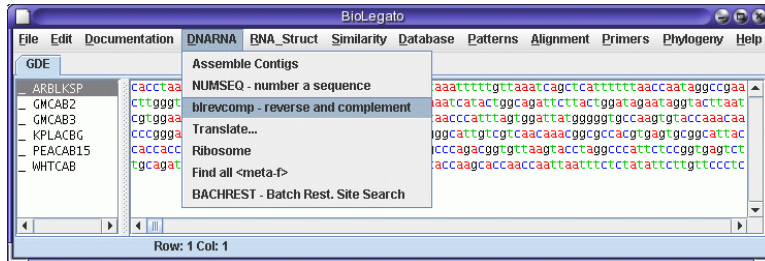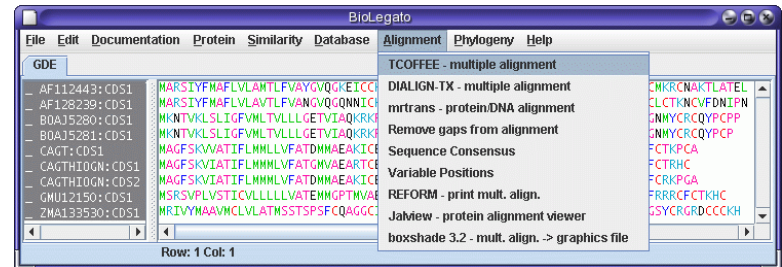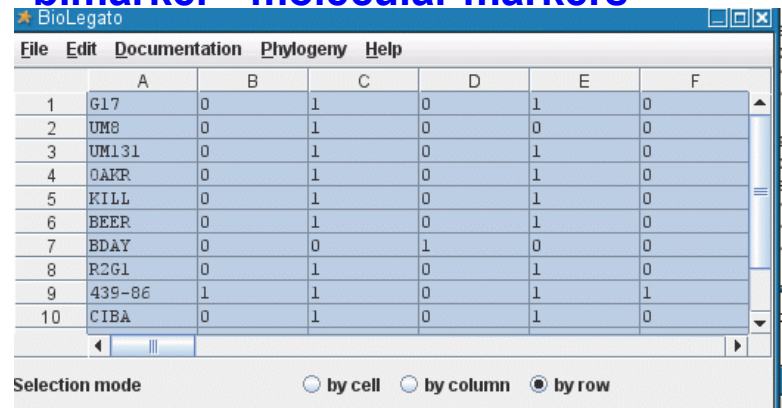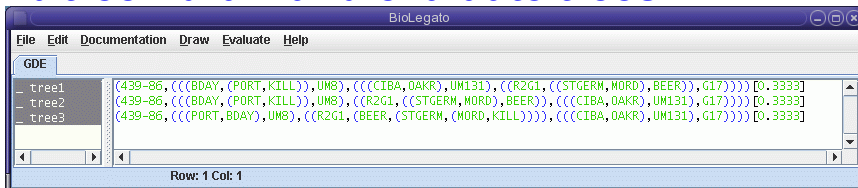
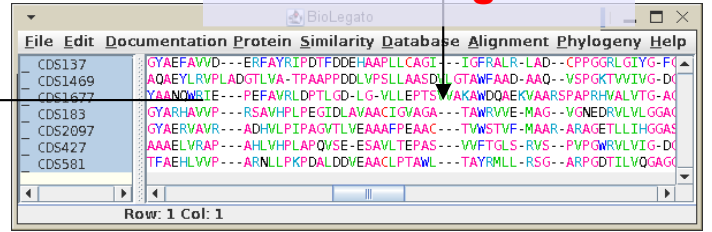# BioLegato - Point and click data pipelining

Genomic sequence
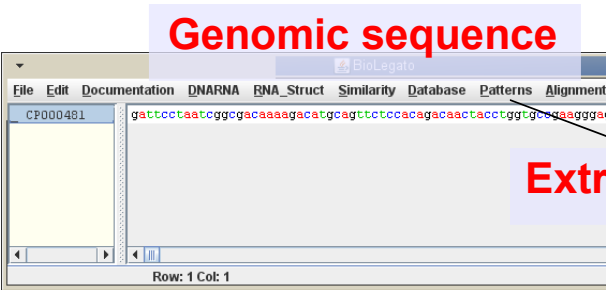
Extract all CDS

Translate to protein
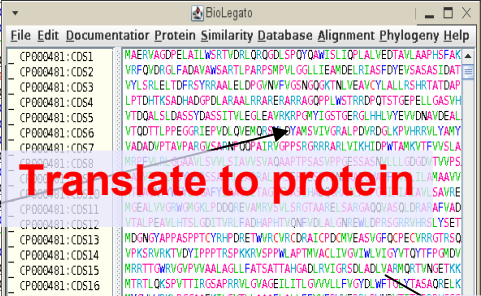
Select proteins of interest
eg. alcohol dehydrogenases
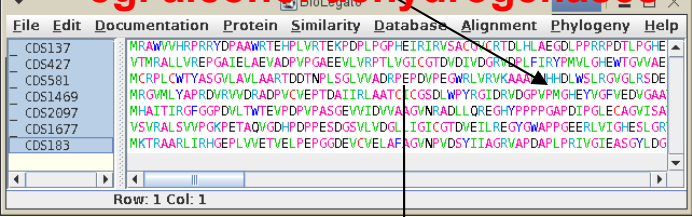
TCOFFEE alignment

PROML
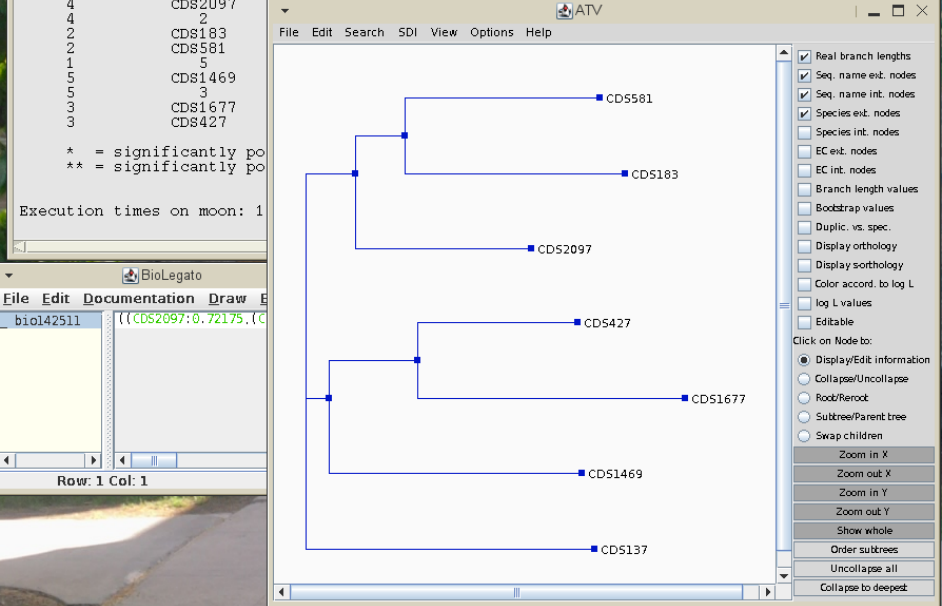maximum likelihood phylogeny

Bioinformatics - BioLegato Database Client

BioLegato lets us quickly build a database client tailored for the project.
Most databases just let you view and query the data.
BioLegato lets you select data, and run programs on it.

Custom Database Client for the MGCB2 project

bldb -
- **menus for project-related programs**
- **table canvas**

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Example: Compare pathways between two species

In the database client, select two species to compare

Choose pathway and click RUN

BioLegato calls the KEGG [3] API to create a custom KEGG map, highlighting enzymes present only in either species, or both
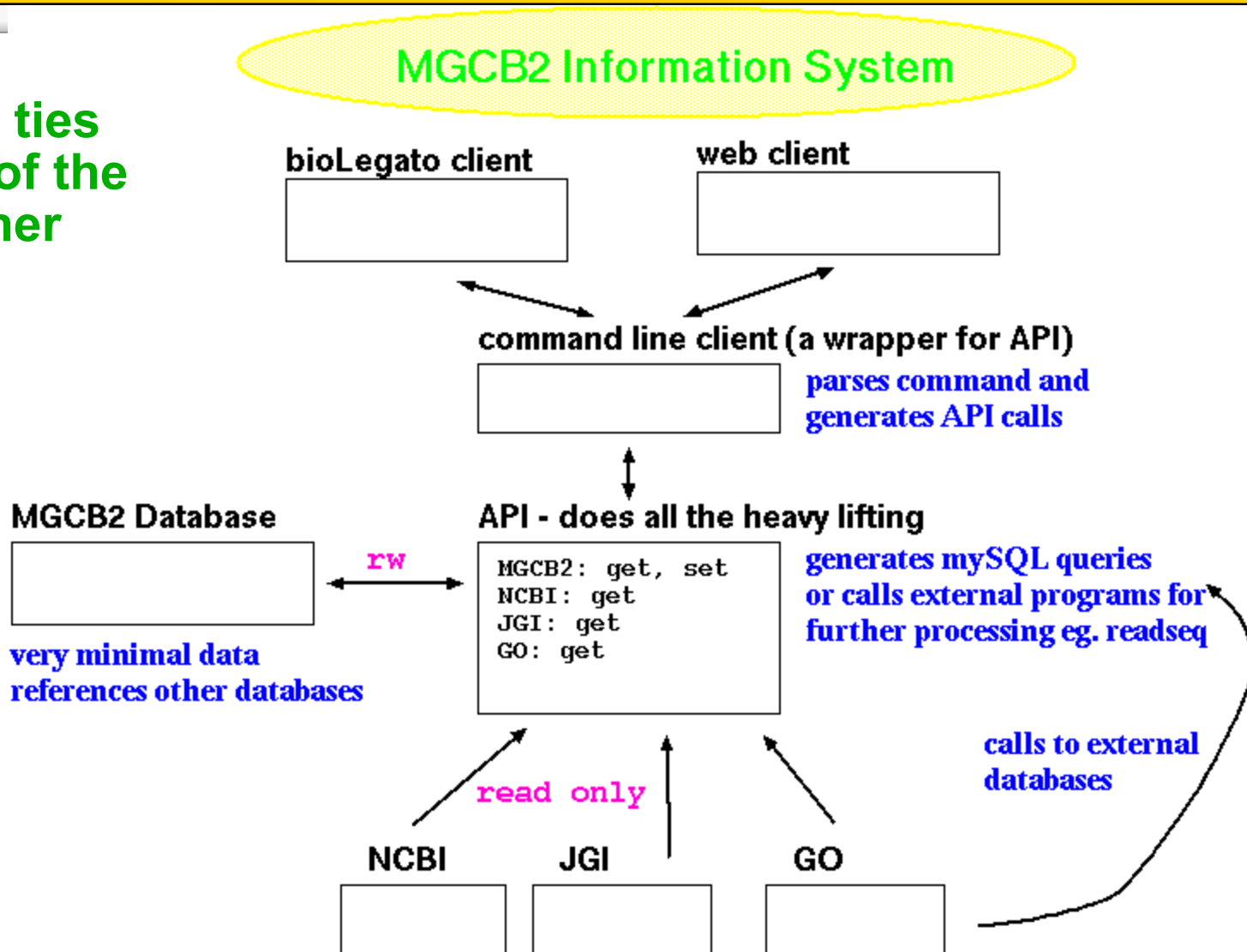
Click on an enzyme to display KEGG info

Bioinformatics - Database

The database ties components of the project together

BioLegato - To Do List

➢ **Inheritance**
➢ **Relations between classes**
➢ **More canvases**
➢ **More widgets eg. menu bars, buttons, side-panels**

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BioLegato/BIRCH

BioLegato is distributed with the BIRCH bioinformatics system

http:/home.cc.umanitoba.ca/~frist

- ➤ **Solaris**
- ➤ **Linux**
- ➤ **Mac OSX**
- ➤ **Windows (2nd Quarter 2012)**