



BioLegato: A Programmable, Object-Oriented Graphic User Interface

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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.



ABSTRACT

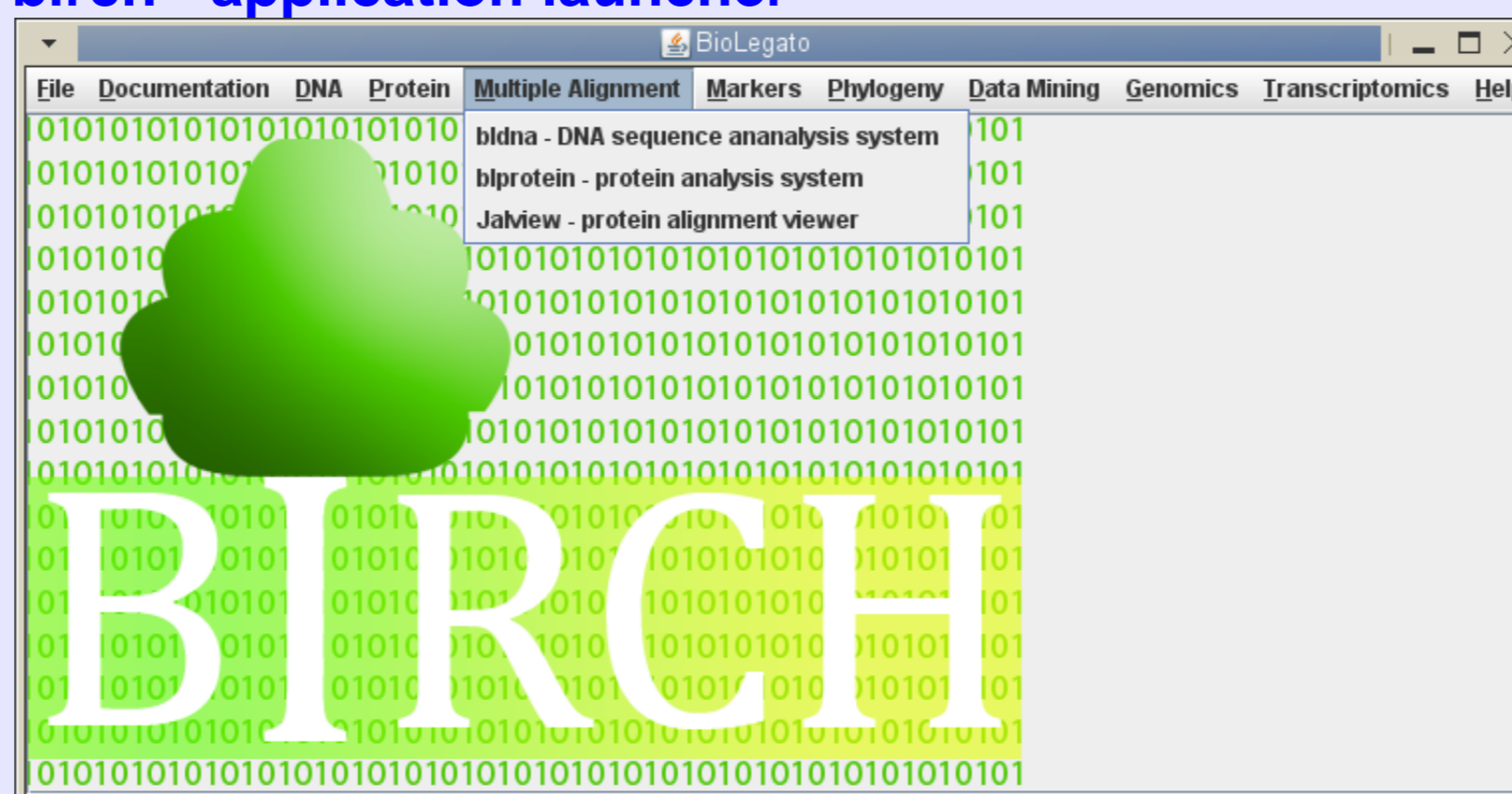
Object-oriented (OO) concepts are built into most modern programming languages and databases. BioLegato brings OO concepts to the laboratory biologist. BioLegato is best thought of as a GUI that launches other programs. As in most GUIs, each bioLegato window consists of a canvas for displaying and manipulating data, and a set of pull-down menus. In the OO paradigm, the canvas corresponds to the data, and the menus correspond to the methods associated with that data. Rather than being hard-coded, menus and canvases are read at runtime. To specify the contents of menus, we have created a small language, PCD. Canvases are implemented as Java plugins. Thus, a new GUI can be created by choosing a canvas appropriate to the data and writing menus in PCD. By analogy, bioLegato can be thought of as a generic Object class, which can be reused and extended.

Programs in the BIRCH bioinformatics system can be run through five bioLegato interfaces: bldna, for DNA sequences; blprotein for proteins; blmarker for molecular markers; bltree for phylogenetic trees, and birch, a launcher for programs in BIRCH. Virtually all methods in bioLegato call external programs, meaning that bioLegato can run either locally-installed programs or remote web services. Wherever possible, the output appears in a new bioLegato window, allowing *ad hoc* pipelining. For example, when bldna translates a DNA sequence, the protein output pops up in a blprotein window. The programmability of bioLegato speeds development of new GUIs for almost any sort of data, giving biologists objects that behave like the real-world entities they represent.

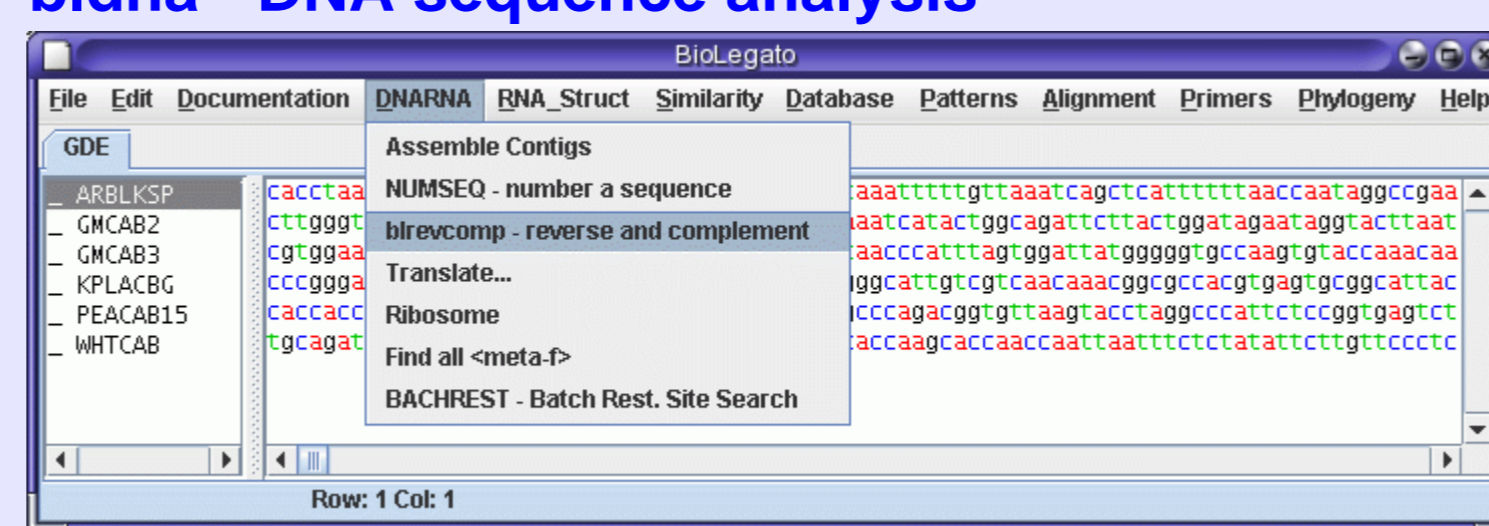
BIRCH Web site: <http://home.cc.umanitoba.ca/~psgendb>

Biolegato reuses and extends canvases and menus to create new biological objects

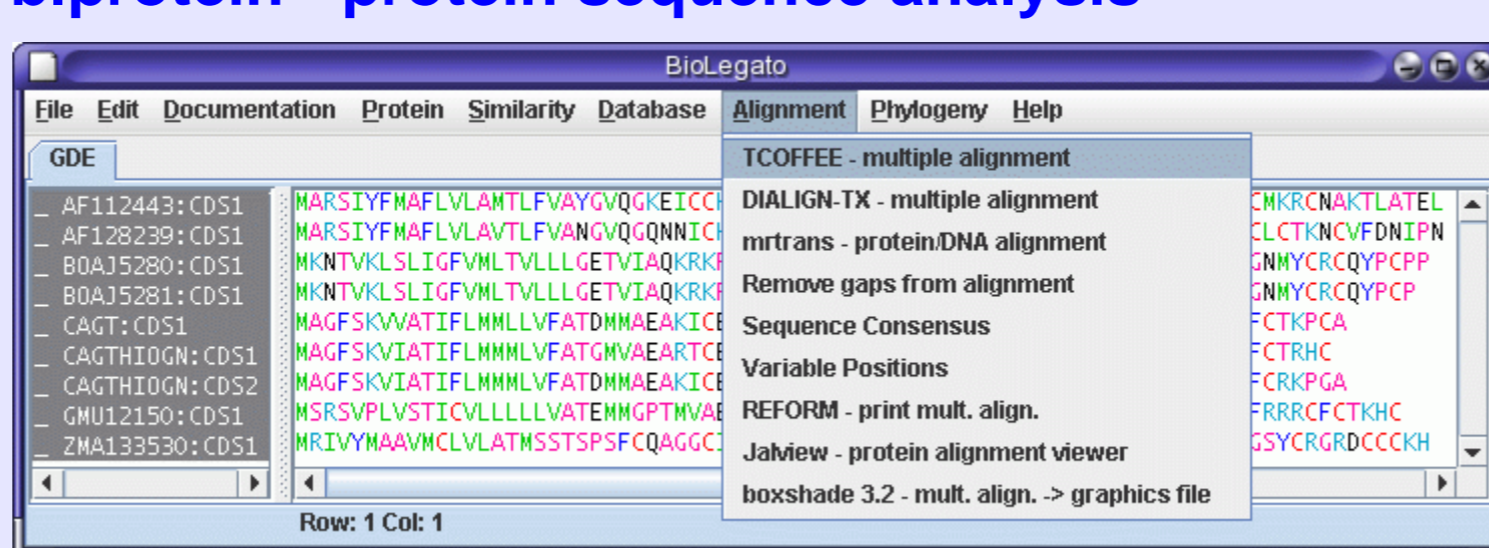
birch - application launcher



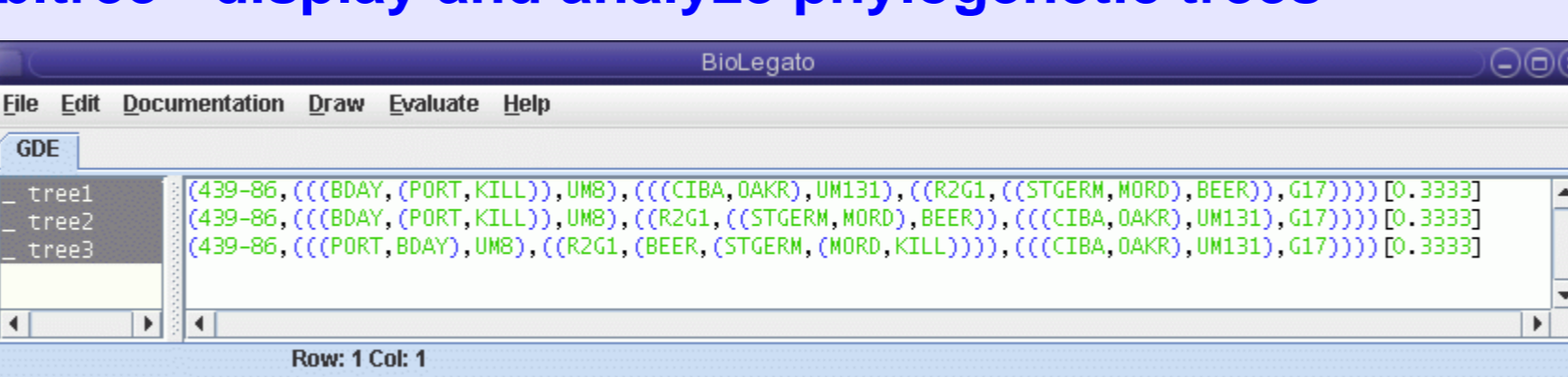
bldna - DNA sequence analysis



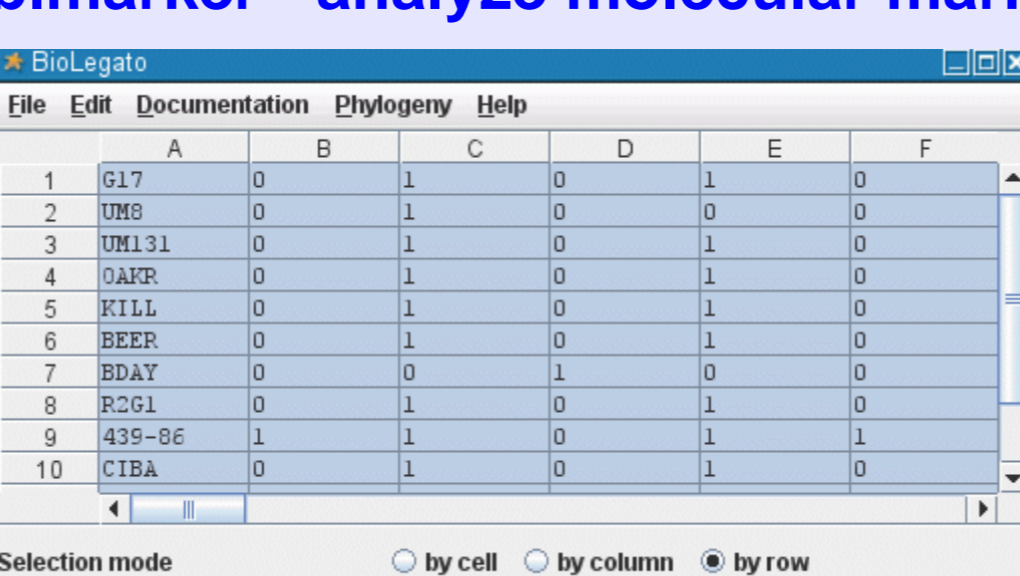
blprotein - protein sequence analysis



bltree - display and analyze phylogenetic trees

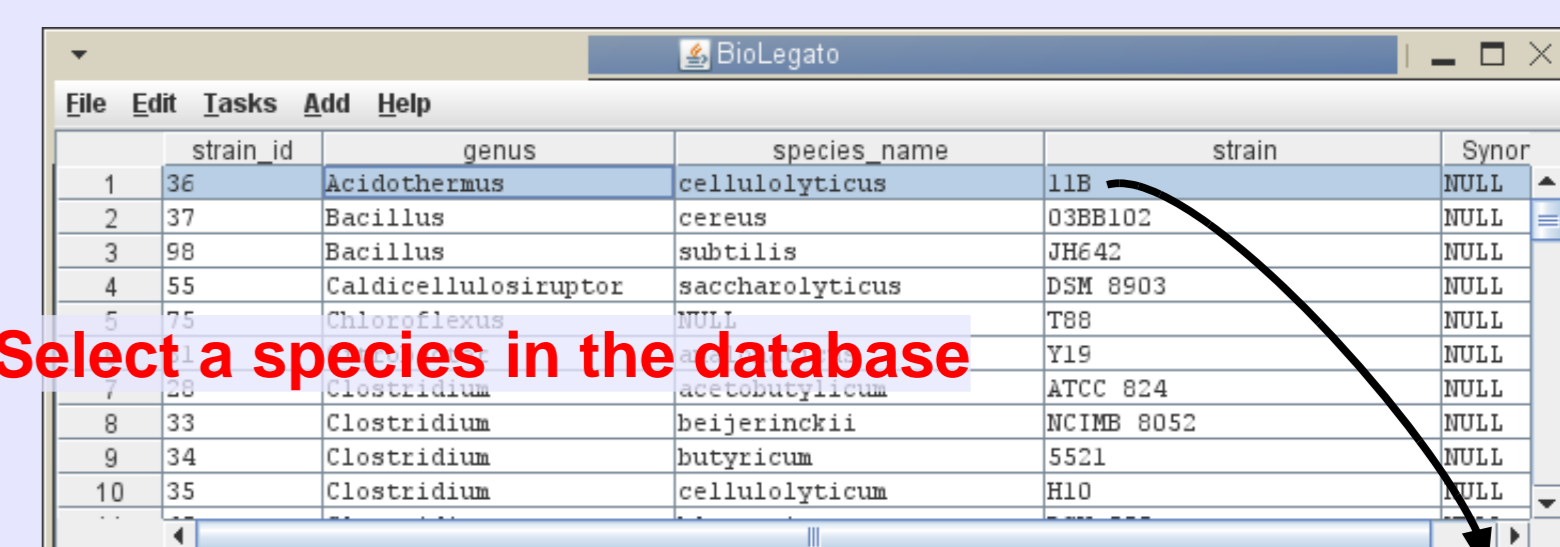


blmarker - analyze molecular marker data



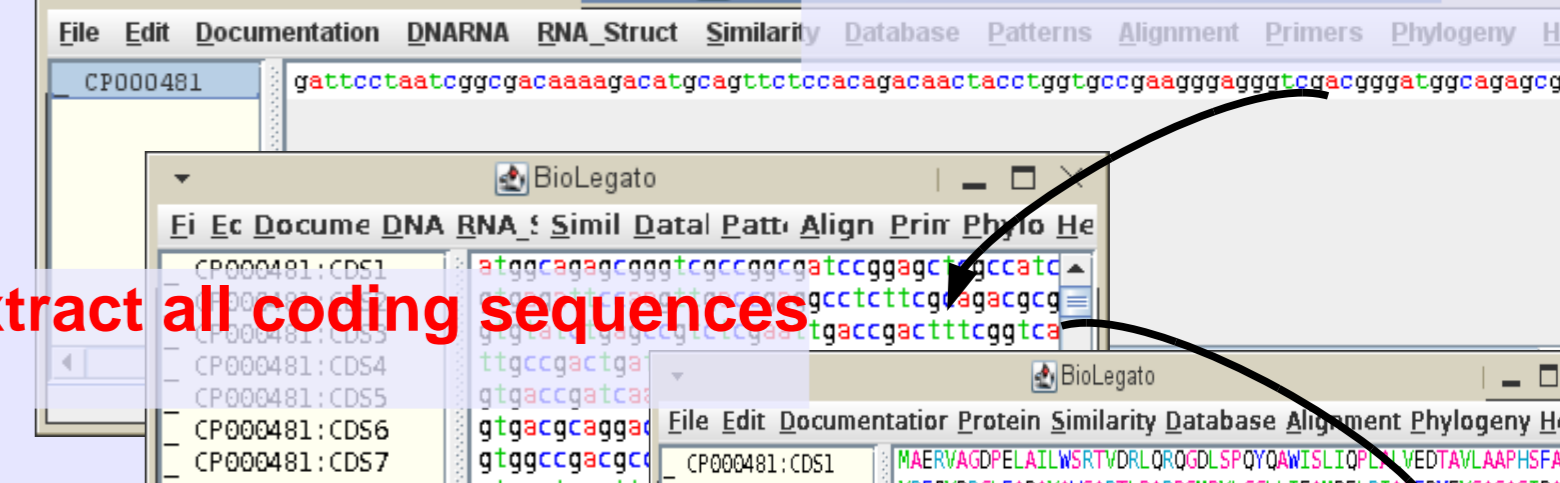
Point and click data pipelining: Run programs directly from the database

Most database clients only search and display data. The bioLegato database client lets you select data, and launch external programs, including other bioLegato programs.



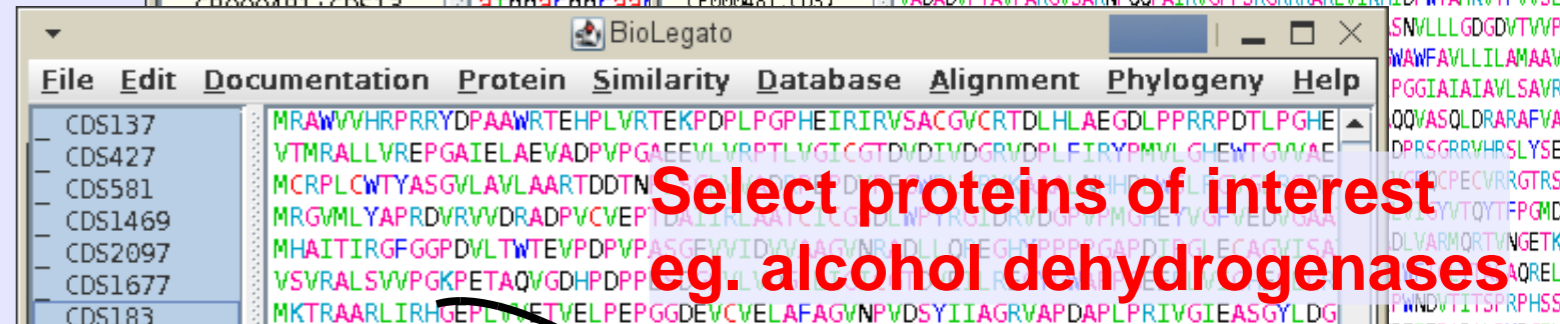
Select a species in the database

Genome is retrieved to bioLegato

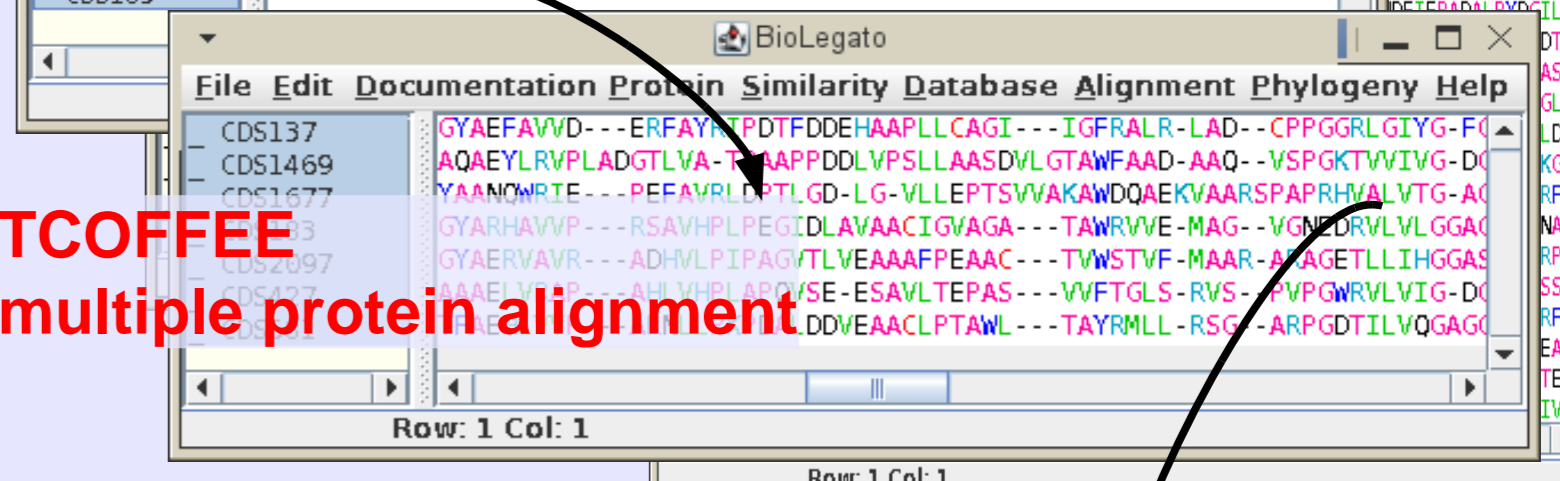


Extract all coding sequences

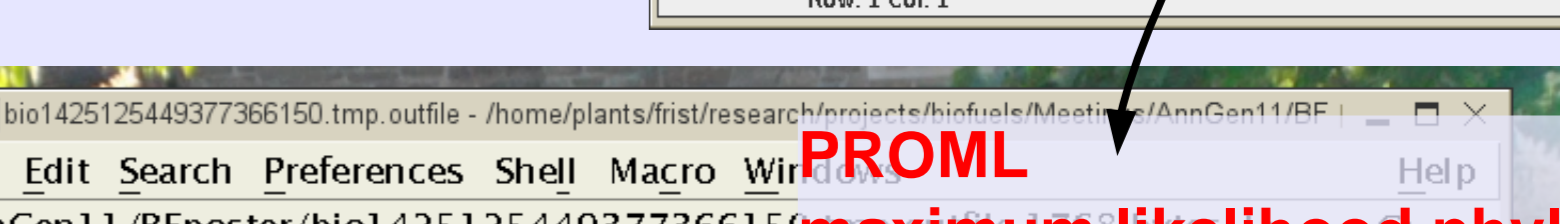
Translate all CDS to protein



Select proteins of interest eg alcohol dehydrogenases



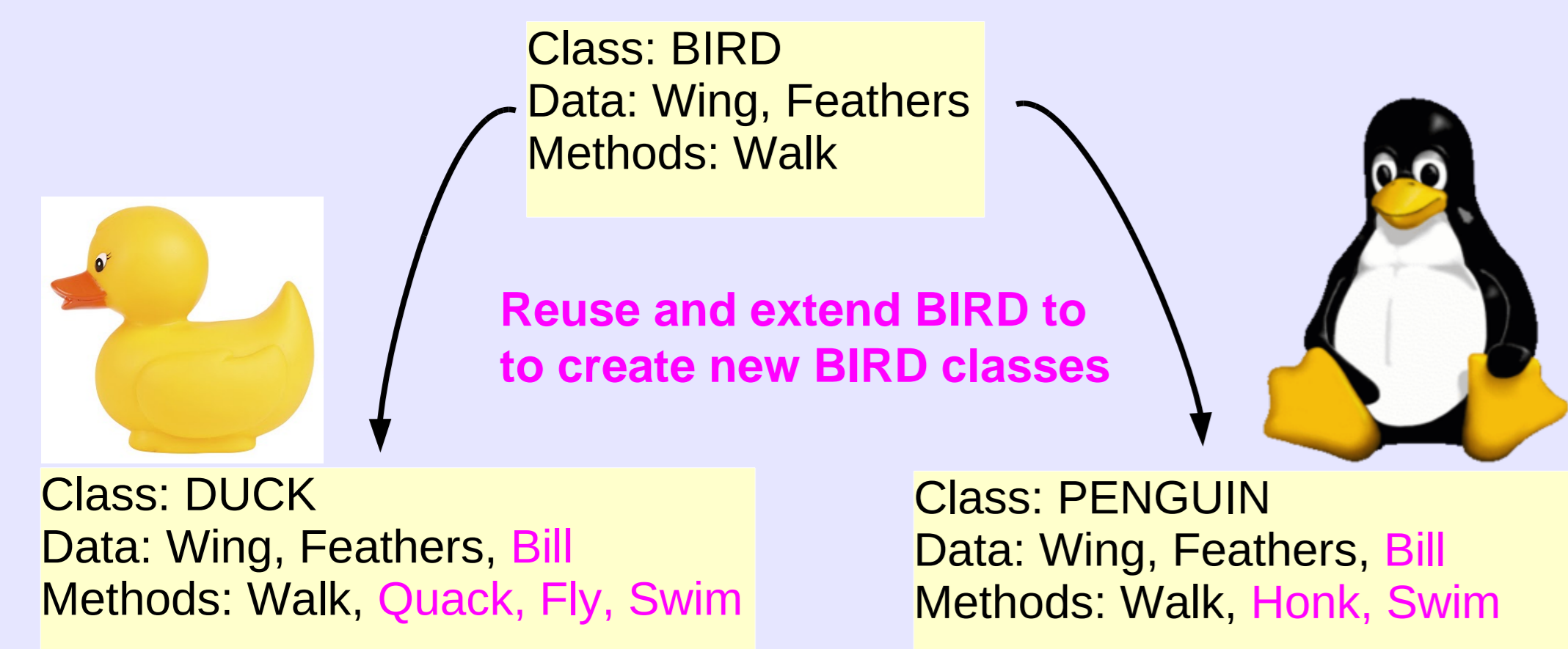
TCOFFEE multiple protein alignment



PROML maximum likelihood phylogeny

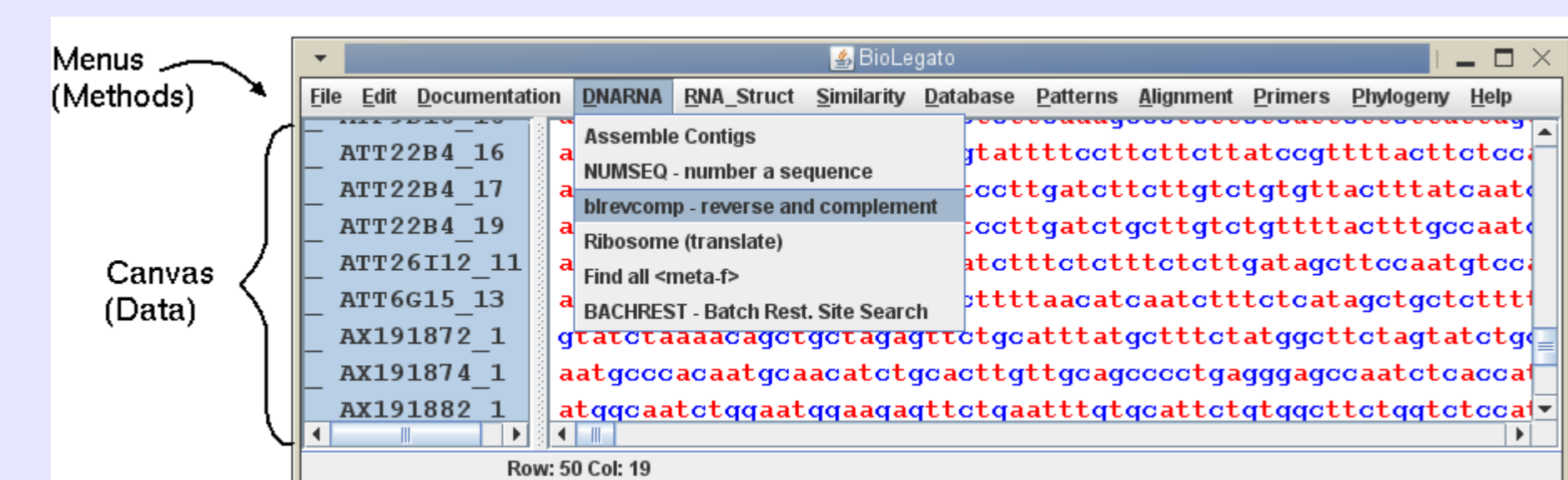
The Object-Oriented World View:

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.



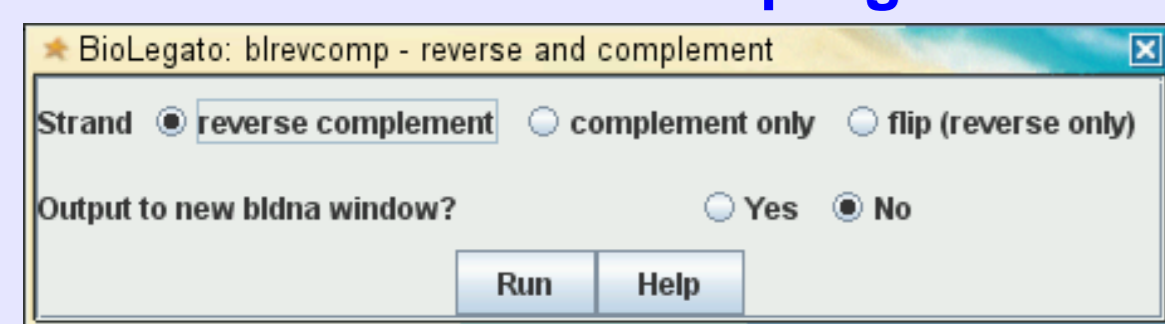
BioLegato Objects have Data and Methods

In BioLegato, the menus correspond to methods, and the canvas corresponds to the data. Both menus and canvas are read when the program is launched. Canvases are Java plugins, while menus are written in PCD, a new, compact language that describes the contents of menus, such as buttons, sliders and file choosers. Thus, new bioLegato classes can be created by reusing existing menus and canvases, or creating new menus and canvases.



PCD - A new language for creating bioLegato "methods"

All it takes to add a new program as a "method"...



... is to write a menu in PCD. Thus, any program installed on your computer, or any program on the Web, can become a bioLegato method.

```
name "brevcomp - 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
"(echo %> %out1%; bldna %in1%.brevcomp; $RM_CMD -f %in1%.brevcomp)&"
"Yes"
"No" %in1%.brevcomp %out1%"
panel
var "Run"
type button
label "Run"
shell "brevcomp %STRAND% %in1% %in1%.brevcomp; $RM_CMD %in1%; %GDEOUTPUT%"
close
var "Help"
type button
label "Help"
shell "$BIRCH/script/gde_help_viewer.csh null;$BIRCH/doc/bioLegato/brevcomp.html"
close
```

Most of the PCD code specifies "widgets", like buttons, sliders, and file choosers, that set the parameters for any program that bioLegato runs

This line tells bioLegato, which program to run, and which parameters to pass to the program, when you click on the Run button.

SUMMARY

- One GUI unifies most data and programs
- BioLegato can utilize any data, any programs, from anywhere
- OO approach models the GUI to biological concepts, which are intuitive to the scientist

REFERENCES

1. Fristensky B (2007) BIRCH: A user-oriented, locally-customizable, bioinformatics system. BMC Bioinformatics, 8:54
2. Smith, S.W., Overbeek, R., Woese, C.R., Gilbert, W., and Gillevet, P.M. (1994) The genetic data environment: an expandable GUI for multiple sequence analysis. Computer Appl. in the Biosciences 10:671-675.

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