

# BioPython GUI

A new Graphical User Interface for BioPython

# What's a GUI?

- GUI stands for Graphical User Interface
- Allows users without in depth computer knowledge to use some code
- Makes things prettier

# What is already out there?

- Open Source:
  - GUIBlast
    - “With GUI BAST you would be able to run a graphical BLAST from your own computer, even if you run MS-Windows!”
    - Demo
    - Has not been developed since 2002/07/29 which is a while ago
  - Saturated BLAST
    - Much more mature code
    - Written in Perl using Tk libraries (very hard to install)
    - Must run on linux (or cygwin)
    - Only interfaces to BLAST

# What is already out there?

- Proprietary:
  - PatternHunter by BSI
    - Comparable to BLAST
    - “PatternHunter is a general-purpose homology search tool, based on innovative and proprietary technologies.”
    - “PatternHunter is sensitive. BLAST was invented to trade speed with sensitivity. With our proprietary multiple optimal spaced seed technology...”
- Mostly just GUI's to run BLAST
  - not really anything to help you with the DB lookups and preparing the Sequences for BLAST

# Goals in Mind

- Automated Database lookups
- Browser for all of the current sequences
- Modify the sequences (translate, transcribe)
- In the long run: Interface with BLAST

# Implementation

- Python!!!
  - All of the code for this project was written in 100% pure python
  - I was planning to use the Tk graphics library, but that was too annoying
  - So I used the GTK (GIMP tool kit) library instead
    - Mostly for linux and specifically Gnome users
    - However, can be run on Windows without too much work
  - Using GTK allowed me to easily make the UI much prettier and more user friendly

# Implementation

- You probably don't want to know this but...
- I have 4 files
  - BioPythonGui.py
    - This is where all of the GUI code is, it's nasty and organized
  - functions.py
    - This is theoretically where all of the functions the GUI code calls is, but that was a bad idea in retrospect

# Implementation

- `objects.py`
  - These are my classes that hold all the information for the 3 types of objects (Sequences, Db Items and Db queries)
- `proj.py`
  - This is where the project object is that holds all of the data

**Let's see it!**

# Further Work—Short Term

- Add ability to change the name of the items
- Make things look prettier
- Edit sequences
  - Edit the sequence
  - Able to transpose, transcribe...
- Open a new SourceForge project to let the community use it

# Further Work—Long Term

- Add BLAST Support
- Add support for other BioPython Features
  - GA (Genetic Algorithm) support
  - Read/Write FASTA and GenBank files
  - Graphics features—Draw chromosome
- Add a command line in GUI
- Allow user scripts