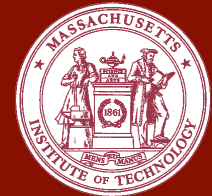


# dBabble\*: Cross-platform Language Interfacing To Facilitate Open Science Collaborations



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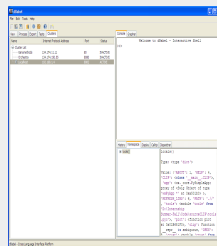
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## Abstract

- Open science promises increased productivity via communication and collaboration in what is now a global research community.
- Bioinformatics and biocomputing open science research is unique in that it joins very different disciplines such as biology, mathematics, engineering, and computer science together.
- Researchers in bioinformatics thus typically come with their own computer languages. Perhaps more importantly, each researcher knows and can access vast libraries of code within his/her specialty's community (written in his/her native language).
- Current programming models for cross-language use (e.g. swig, <http://www.swig.org/>) assume one high level language for prototyping and a low level one for optimizing code.
- dBabel is open source and available via GPL at: <http://bcl.med.harvard.edu/proj/dbabel>

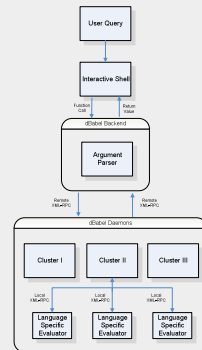
## Introduction

- dBabel provides a novel means of communication between various languages and platforms.
- dBabel automatically detects and integrate code from different languages spread over different platforms and locations- so that they can communicate easily with one another.
- dBabel offers the user an intuitive graphical interface with a powerful interactive shell to manage various clusters spread in various facilities all around the world.



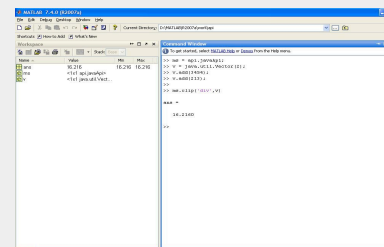
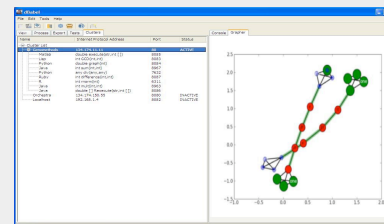
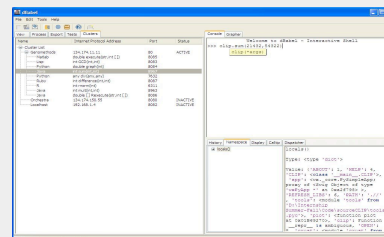
## Methods

- dBabel uses XML-RPC, a simple yet robust remote procedure calling mechanism. It uses HTTP as the transport and XML as the encoding, thus allowing complex data structures to be transmitted, processed and returned.
- The user query is parsed by the dBabel backend and a list of clusters running the dBabel daemon service are contacted to check for the existence of the function.
- On finding the required function, the language specific XML-RPC service is spawned in the cluster, the function is evaluated, and the result sent back to dBabel.



## Results

- dBabel is implemented in python and currently supports Python, Java, Lisp, Matlab, R, Perl, C, C++, and Ruby.
- dBabel interfaces with the outside world via a powerful and interactive GUI shell. Among its many features are smart syntax highlighting and auto-detection of code from different languages.
- dBabel also supports Application Programming Interfaces (API's) in Python, Java, Matlab, R, and Lisp- enabling virtually any language to communicate with one another.



## Conclusions

- dBabel's combines languages and platforms together within a single framework.
- Most of the major languages used in bioinformatics and biocomputing are currently supported allowing researchers all over the world to communicate seamlessly.
- dBabel has already been used to foster both international open science collaborations as well local initiatives.
- Current directions for dBabel include: recruiting social networks to share computational resources, integrating more languages, and creating additional APIs.
- For more information on dBabel, please see: <http://bcl.med.harvard.edu/proj/dbabel>

## References

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Biomedical Cybernetics Laboratory

\* Formerly called: dBabble