BioRuby: Object Oriented Open Source Library for Bioinformatics

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\section{Introduction}

BioRuby \cite{6} is the project to build a useful library for bioinformatics tasks with the object oriented scripting language Ruby, started in late 2000. Ruby is made in Japan and is getting popularity by its simple and powerful syntax in recent years.

For Perl, Java and Python programmers, there are already existing BioPerl \cite{4}, BioJava \cite{3} and BioPython \cite{5} projects as precedent efforts, and organized by the open bio foundation \cite{7, 2, 1}. However, they tend to be complicated unnecessarily because of the limitation of each language characteristics and historical reasons that they have gradually developed. Taking these state into consideration, we find the ruby language is suitable for constructing simple and easy to use open bio library.

In 2002, the first invited-only Open Bio\textsuperscript{*} developers meeting called BioHackathon was held in Arizona and Cape Town, and we have agreed on five new ways to retrieve a record given an identifier from the biological sequence databases. These methods are named OBDA (open bio sequence database access) and include file indexing (simple, Berkeley DB), BioFetch (CGI/HTTP), BioSQL (MySQL, PostgreSQL, Oracle), XEMBL and Corba described below.

\section{Project Status}

Currently, we have classes for biological sequences and annotations (Bio::Sequence, Bio::Location, Bio::Feature), literature management classes for retrieving and storing reference information (Bio::Reference, Bio::PubMed), parsers for over 20 major biological databases (Bio::DB, Bio::GenBank, Bio::KEGG, etc.), wrappers for sequence analysis softwares such as BLAST, FASTA and EMBOSS (Bio::Blast, Bio::Fasta etc.) and classes for pathway computation (Bio::Pathway, Bio::Relation). Additionally, we have already implemented accessing methods for OBDA via Bio::Registry, Bio::FlatFile, Bio::Fetch and Bio::SQL classes (XEMBL and Corba interfaces are planned).

As for OBDA, Bio::Registry is a mechanism to select accessing methods by using initialization files (\texttt{~/.bioinformatics/seqdatabase.ini}). Since, OBDA has five different ways to retrieve the same entry from several databases, users can determine which method to use for obtaining an entry. File indexing is a simplest method to build against file databases. BioFetch is a method to retrieve an