BioPerl

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PDF

BioPerl

Principe

- Collection de module Perl
- Objectif: Faciliter le developpement de scripts Perl pour des applications bioinformatiques
- Open-source via une organisation GitHub
- Soutenu par Open Bioinformatics Foundation

Histoire

- 1996 : Début
- 2002
  - Premier Open Bio Hackathon
  - BioPerl 1.0
  - Article

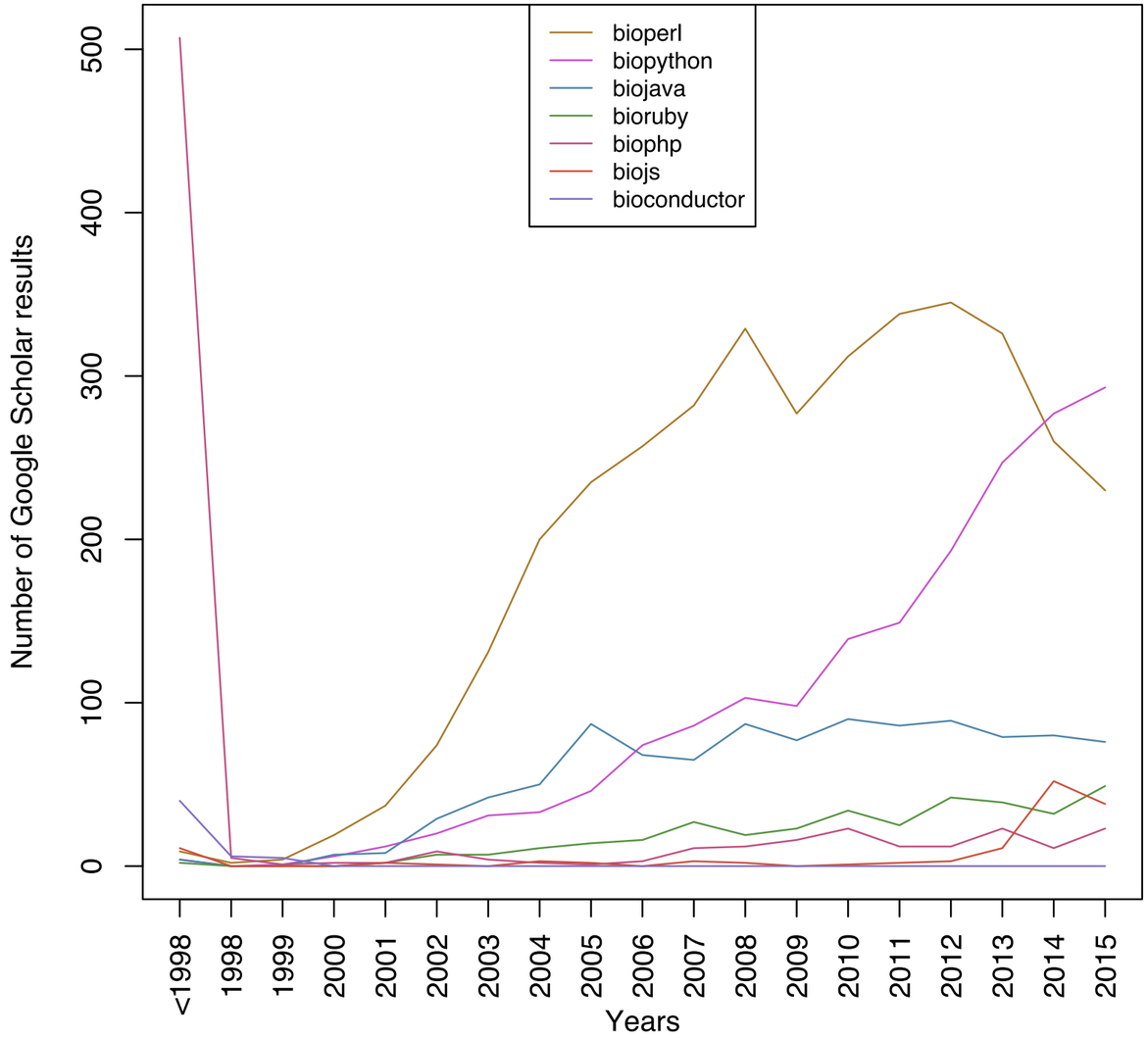
Actuellement

- GitHub
  - 31 contributeurs
- Dernière release : 1.6.924 en Juillet 2014
- Orienté-objet
- > 40 Modules Perl

Comparaison avec les autres Bio Toolkits

Bio Toolkits

	Release 1.0	Dernière release	Article majeur	Citations
BioPerl	2002	07/2014	2002	1 306
BioPython	2000	10/2015	2009	608
BioJava	2008	07/2015	2008	201
BioRuby	2006	07/2015	-	-
BioPHP	2003	?	-	-
BioJS	2013	09/2014	2013	44
Bioconductor	2001	10/2015		


bioperl
biopython
biojava
bioruby
biophp
biojs
bioconductor
Number of Google Scholar results
0
100
200
300
400
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<1998
1998
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2015
Years

Installation

Installation sous Linux/Mac OS

```
$ (sudo) cpan -i CPAN
$ cpan
cpan[1]> d /BioPerl/
Reading '/Users/cidam/.cpan/Metadata'
  Database was generated on Thu, 14 Jan 2016 13:53:43 GMT
Distribution    BOZO/Fry-Lib-BioPerl-0.15.tar.gz
Distribution    CDRAUG/Dist-Zilla-PluginBundle-BioPerl-0.20.tar.gz
Distribution    CJFIELDS/BioPerl-1.6.901.tar.gz
Distribution    CJFIELDS/BioPerl-1.6.923.tar.gz
Distribution    CJFIELDS/BioPerl-1.6.924.tar.gz
...
11 items found

cpan[2]> install CJFIELDS/BioPerl-1.6.924.tar.gz
```

Installation sous Windows

DSSL

Manipulation de séquences

Représentation d'une séquence

3 types d'objets pour une séquence

- `Bio::PrimarySeq`
  - Séquence + nom
  - Fichier fasta

3 types d'objets pour une séquence

- `Bio::SeqFeatureI`
  - Caractéristique sur une séquence (séquence, localisation et annotation)
  - Entrée simple d'une table de caractéristique EMBL/GenBank/DDBJ

3 types d’objets pour une séquence

- `Bio::Seq`
  - 1 séquence et une collection de caractéristiques
  - Entrée simple d'une table EMBL/GenBank/DDBJ

Classe `Bio::Seq`

Classe `Bio::Seq`

```
$ perldoc Bio::Seq

NAME
       Bio::Seq - Sequence object, with features

...

DESCRIPTION
   A Seq object is a sequence with sequence features placed on it.
   The Seq object contains a PrimarySeq object for the actual sequence
   and also implements its interface.

   ...
```

Créer d'un objet `Bio::Seq`

```
use Bio::Seq;

my $seqobj = Bio::Seq->new(
    -seq => "ACTGTGTGTCC",
    -id => "Chlorella sorokiniana",
    -accession_number => "CAA41635"
);
```

Méthodes (1)

Méthodes renvoyant des chaines de caractères et acceptant parfois des chaine de caractères pour modifier des propriétés

```
$seqobj->seq();               # string of sequence
$seqobj->subseq(5,10);        # part of the sequence as a string
$seqobj->accession_number(); # when there, the accession number
$seqobj->alphabet();          # one of 'dna','rna',or 'protein'
$seqobj->version()            # when there, the version
$seqobj->length()             # length
$seqobj->desc();              # description
$seqobj->primary_id();        # a unique id for this sequence regardless
# of its display_id or accession number
$seqobj->display_id();        # the human readable id of the sequence
```

Méthodes (2)

Méthodes renvoyant des nouveaux objet `Bio::Seq`

```
$seqobj->trunc(5,10)  # truncation from 5 to 10 as new object
$seqobj->revcom       # reverse complements sequence
$seqobj->translate    # translation of the sequence
```

Méthodes (3)

Méthode pour déterminer si une chaine de caractère peut être accepter par la méthode `seq()`

```
$seqobj->validate_seq($string)
```

Manipulation de séquences

```
$seq = $seqobj->seq();
$length = $seqobj->length();
$subseq = $seqobj->subseq($length/2, $length);
$new_seq = $seq.$subseq;
if($seqobj->validate_seq($new_seq)){
    $seqobj->seq($new_seq);
}
print $seqobj->seq()," ",$seqobj->length()\n";
```

Que sera affiché?

Traduction

```
$translated_obj = $seqobj;
if( $seqobj->alphabet() == 'dna'){
    $translated_obj = $seqobj->translate();
}
print $translated_obj->seq(),"\n";
```

Que sera affiché?

Récupération de statistiques sur une séquence

Classe `Bio::Tools::SeqStats`

```
$ perldoc Bio::Tools::SeqStats

NAME
       Bio::Tools::SeqStats - Object holding statistics
       for one particular sequence

...

DESCRIPTION
   Bio::Tools::SeqStats is a lightweight object for the calculation of
   simple statistical and numerical properties of a sequence. By
   "lightweight" I mean that only "primary" sequences are handled by t
   object.  The calling script needs to create the appropriate primary
   sequence to be passed to SeqStats if statistics on a sequence featu
   are required.  Similarly if a codon count is desired for a frame-
   shifted sequence and/or a negative strand sequence, the calling scr
   needs to create that sequence and pass it to the SeqStats object.
```

Création

```
$seq_stats  =  Bio::Tools::SeqStats->new(-seq => $seqobj);
```

Méthodes

- `count_monomers`
  - Comptage du nombre de chaque type de monomère
- `get_mol_wt`
  - Calcul du poids moléculaire
- `count_codons`
  - Comptage du nombre de chaque type de codons
- `hydropathicity`
  - Calcul l'hydrophaticité moyenne de Kyte-Doolittle

Manipulation de fichiers de séquences

Classe `Bio::SeqIO`

```
$ perldoc Bio::SeqIO

NAME
    Bio::SeqIO - Handler for SeqIO Formats

...

DESCRIPTION
   Bio::SeqIO is a handler module for the formats in the SeqIO set (eg
   Bio::SeqIO::fasta). It is the officially sanctioned way of getting
   the format objects, which most people should use.

   The Bio::SeqIO system can be thought of like biological file handle
   They are attached to filehandles with smart formatting rules (eg,
   genbank format, or EMBL format, or binary trace file format) and ca
   either read or write sequence objects (Bio::Seq objects, or more
   correctly, Bio::SeqI implementing objects, of which Bio::Seq is one
```

Création d'un objet `Bio::SeqIO`

Ouverture d'un flux sur le fichier ou la chaine de caractères

Constructeur

Paramètres possibles

- `-file`
- `-string`
- `-format` : `fasta`, `nexus`, `fastq`, `quality`, `excel`, `raw`, `tab`, ...
- `-alphabet` : `dna`, `rna` ou `protein`

Méthodes

- `next_seq`
  - Lecture du prochain objet "séquence" dans le flux
  - Renvoi d'un objet `Bio::Seq` ou rien si aucune séquence disponible
- `write_seq`
  - Ecriture d'un object `Bio:Seq` dans le flux
- `format`, `alphabet`, ...

Ecrire de séquences dans un fichier

```
use Bio::SeqIO;
use Bio::Seq;
my $seqio_obj = Bio::SeqIO->new(-file => '>sequence.fasta',
    -format => 'fasta' );
my $seqobj = Bio::Seq->new(
    -seq => "ACTGTGTGTCC",
    -id => "Chlorella sorokiniana"
);
$seqio_obj->write_seq($seqobj);
my $seqobj = Bio::Seq->new(
    -seq => "ACTGTGTGTCCTGTGTCC",
    -id => "Modified Chlorella sorokiniana"
);
$seqio_obj->write_seq($seqobj);
```

Que fait ce code?

Lecture des séquences d'un fichier

```
use Bio::SeqIO;

$seqio_obj = Bio::SeqIO->new(-file => "sequence.fasta",
    -format => "fasta" );

while ($seq_obj = $seqio_obj->next_seq){
    print $seq_obj->seq,"\n";
}
```

Que fait ce code?

Accès aux bases de données

Récupération d'une séquence dans une base de données

Bases de données accessibles

Base de données	Module
GenBank	`Bio::DB::GenBank`
SwissProt	`Bio::DB::SwissProt`
GenPept	`Bio::DB::GenPept`
EMBL	`Bio::DB::EMBL`
SeqHound	`Bio::DB::SeqHound`
Entrez Gene	`Bio::DB::EntrezGene`
RefSeq	`Bio::DB::RefSeq`

Classe `Bio::DB::GenBank`

```
$ perldoc Bio::DB::GenBank

NAME
    Bio::DB::GenBank - Database object interface to GenBank

...

DESCRIPTION

    Allows the dynamic retrieval of Bio::Seq sequence objects from the
    GenBank database at NCBI, via an Entrez query

    ...
```

Constructeur

```
use Bio::DB::GenBank;

$db_obj = Bio::DB::GenBank->new;
```

Méthodes

- `get_Seq_by_id($unique_id)`
- `get_Seq_by_acc($accession_number)`
- `get_Seq_by_version($versioned_accession_number)`
- `get_Seq_by_gi($genbank_gi_number)`

⚠Utiliser le bon identifiant pour la bonne méthode

Récupération d'une séquence dans une base de données

```
use Bio::DB::GenBank;
use Bio::Seq;

$db_obj = Bio::DB::GenBank->new;

$seq_obj = $db_obj->get_Seq_by_id(2);

print $seq_obj->display_id(),"\n";
```

Récupération de plusieurs séquences avec des requêtes plus complexes

Bases de données et modules pour les requêtes

Base de données	Module
GenBank	`Bio::DB::Query::GenBank`
SwissProt	`Bio::DB::Query::SwissProt`
GenPept	`Bio::DB::Query::GenPept`
EMBL	`Bio::DB::Query::EMBL`
SeqHound	`Bio::DB::Query::SeqHound`
Entrez Gene	`Bio::DB::Query::EntrezGene`
RefSeq	`Bio::DB::Query::RefSeq`

Classe `Bio::DB::Query::GenBank`

```
$ perldoc Bio::DB::Query::GenBank

NAME
    Bio::DB::Query::GenBank - Build a GenBank Entrez Query

...

DESCRIPTION

    This class encapsulates NCBI Entrez queries.  It can be used to
    store a list of GI numbers, to translate an Entrez query expressio
    into a list of GI numbers, or to count the number of terms that
    would be returned by a query.  Once created, the query object can
    be passed to a Bio::DB::GenBank object in order to retrieve the
    entries corresponding to the query.

    ...
```

Création d'un objet

`Bio::DB::Query::GenBank`

Ouverture d'un flux sur des objets `Bio::Seq`

Constructeur

Paramètres possibles

- `-db : protein, nucleotide, ...`
- `-query`
- `-mindate`
- `-maxdate`
- `-reldate`
- `-datetype`
- `-ids`
- `-maxids`

Méthodes

- `count`
  - Renvoi du nombre de résultats de la requête
- `ids`
  - Renvoi/Modifie la liste des identifiants des résultats

Récupération de plusieurs séquences

```
use Bio::DB::GenBank;
use Bio::DB::Query::GenBank;

$query = "Arabidopsis[ORGN] AND topoisomerase[TITL] and 0:3000[SLEN]";
$query_obj = Bio::DB::Query::GenBank->new(-db => 'nucleotide',
    -query => $query );

$gb_obj = Bio::DB::GenBank->new;

$stream_obj = $gb_obj->get_Stream_by_query($query_obj);

while ($seq_obj = $stream_obj->next_seq) {
    print $seq_obj->display_id, "\t", $seq_obj->length, "\n";
}
```

Parser des rapports de recherche

Classe `Bio::SearchIO`

```
$ perldoc Bio::SearchIO

NAME
    Bio::SearchIO - Driver for parsing Sequence Database Searches (BLA
    FASTA, ...)

...

DESCRIPTION

     This is a driver for instantiating a parser for report files from
   sequence database searches. This object serves as a wrapper for the
   format parsers in Bio::SearchIO::* - you should not need to ever us
   those format parsers directly. (For people used to the SeqIO system
   we are deliberately using the same pattern).

     ...
```

Création d'un objet `Bio::Search`

Ouverture d'un flux sur le fichier contenant un rapport de recherche

Constructeur

Paramètres possibles

- `-file`
- `-format`
- `-output_format`
- `-inclusion_threshold`
- `-signif`
- `-check_all_hits`
- `-min_query_len`
- `-best`

Formats

Name	Format
`blast`	BLAST (WUBLAST, NCBIBLAST,bl2seq)
`fasta`	FASTA `-m9` and `-m0`
`blasttable`	BLAST `-m9` or `-m8` output (both NCBI and WUBLAST tabular)
`megablast`	MEGABLAST
`blastxml`	NCBI BLAST XML
...	...

Méthodes

- `next_result`
- `write_result`
- `write_report`
- `result_count`
- `best_hit_only`
- `check_all_hits`

Représentation des données dans `Bio::Search`

- `Bio::Search`
  - `Bio::Search::Result`
    - `Bio::Search::Hit`
      - `Bio::Search::HSP` (high-scoring segment pair)

Méthodes de `Bio::Search::Result`

- `algorithm`
- `query_name`
- `query_accession`
- `query_length`
- `query_description`
- `database_name`
- `available_statistics`
- `available_parameters`
- `num_hits`
- `hits`

Méthodes de `Bio::Search::Hit`

- `name`
- `length`
- `accession`
- `description`
- `algorithm`
- `raw_score`
- `significance`
- `hsps`
- `num_hsps`
- `locus`
- `accession_number`

Méthodes de `Bio::Search::HSP` (1)

- `algorithm`
- `evalue`
- `expect`
- `frac_identical`
- `frac_conserved`
- `gaps`
- `query_string`
- `hit_string`
- `length('total'/'hit'/'query')`
- `num_conserved`
- `num_identical`

Méthodes de `Bio::Search::HSP` (1)

- `rank`
- `seq_inds('hit'/'query', 'identical'/ 'conserved'/ 'conserved-notidentical')`
- `score`
- `range('hit'/'query')`
- `percent_identity`
- `strand('hit'/'query')`
- `start('hit'/'query')`
- `end('hit'/'query')`
- `matches('hit'/'query')`
- `get_aln`

Parcours d'un fichier issu d'une requête Blast

```
use Bio::SearchIO;

my $in = new Bio::SearchIO(
    -format => "blast",
    -file => "report.bls");
while(my $result = $in->next_result){
    while(my $hit = $result->next_hit){
        while(my $hsp = $hit->next_hsp){
            print "Query=", $result->query_name,
                " Hit=", $hit->name,
                " Length=", $hsp->length('total'),
                " Percent_id=", $hsp->percent_identity,
                "\n";
        }
    }
}
```

Références

- BioPerl GitHub Page
- Wiki BioPerl