TOC for all levels

BioPerl-1.6.1::Bio::SeqFeature::Tools
BioPerl-1.6.1::Bio::Annotation
BioPerl-1.6.1::Bio::Tree
BioPerl-1.6.1::Bio::Tree::Draw
BioPerl-1.6.1::Bio::Ontology
BioPerl-1.6.1::Bio::Ontology::SimpleGOEngine
BioPerl-1.6.1::Bio::FeatureIO
BioPerl-1.6.1::Bio::PhyloNetwork
BioPerl-1.6.1::Bio::Cluster
BioPerl-1.6.1::Bio::Matrix
BioPerl-1.6.1::Bio::Matrix::IO
BioPerl-1.6.1::Bio::Matrix::PSM
BioPerl-1.6.1::Bio::Matrix::PSM::IO
BioPerl-1.6.1::Bio::Event
BioPerl-1.6.1::Bio::TreeIO
BioPerl-1.6.1::Bio::Map
BioPerl-1.6.1::Bio::Phenotype
BioPerl-1.6.1::Bio::Phenotype::OMIM
BioPerl-1.6.1::Bio::Phenotype::MeSH
BioPerl-1.6.1::Bio::Root
BioPerl-1.6.1::Bio::Root::Test
BioPerl-1.6.1::Bio::Biblio
BioPerl-1.6.1::Bio::Biblio::IO
BioPerl-1.6.1::Bio::Structure
BioPerl-1.6.1::Bio::Structure::SecStr
BioPerl-1.6.1::Bio::Structure::SecStr::DSSP
BioPerl-1.6.1::Bio::Structure::SecStr::STRIDE
BioPerl-1.6.1::Bio::Structure::IO
BioPerl-1.6.1::Bio::DB
BioPerl-1.6.1::Bio::DB::HIV
BioPerl-1.6.1::Bio::DB::Taxonomy
BioPerl-1.6.1::Bio::DB::Expression
BioPerl-1.6.1::Bio::DB::SeqFeature
BioPerl-1.6.1::Bio::DB::SeqFeature::Store
BioPerl-1.6.1::Bio::DB::SeqFeature::Store::DBI
BioPerl-1.6.1::Bio::DB::TFBS
BioPerl-1.6.1::Bio::DB::GFF
BioPerl-1.6.1::Bio::DB::GFF::Util
BioPerl-1.6.1::Bio::DB::GFF::Aggregator
BioPerl-1.6.1::Bio::DB::GFF::Adaptor
BioPerl-1.6.1::Bio::DB::GFF::Adaptor::dbi
BioPerl-1.6.1::Bio::DB::GFF::Adaptor::berkeleydb

BioPerl-1.6.1::Bio::DB::GFF::Adaptor::memory
BioPerl-1.6.1::Bio::DB::Flat
BioPerl-1.6.1::Bio::DB::Flat::BDB
BioPerl-1.6.1::Bio::DB::Biblio
BioPerl-1.6.1::Bio::DB::SeqVersion
BioPerl-1.6.1::Bio::DB::Query
BioPerl-1.6.1::Bio::Search
BioPerl-1.6.1::Bio::Search::Tiling
BioPerl-1.6.1::Bio::Search::Result
BioPerl-1.6.1::Bio::Search::Hit
BioPerl-1.6.1::Bio::Search::Iteration
BioPerl-1.6.1::Bio::Search::HSP
BioPerl-1.6.1::Bio::LiveSeq
BioPerl-1.6.1::Bio::LiveSeq::IO
BioPerl-1.6.1::Bio::CodonUsage
BioPerl-1.6.1::Bio::MolEvol
BioPerl-1.6.1::Bio::Factory
BioPerl-1.6.1::Bio::Assembly
BioPerl-1.6.1::Bio::Assembly::IO
BioPerl-1.6.1::Bio::Assembly::Tools
BioPerl-1.6.1::Bio::Variation
BioPerl-1.6.1::Bio::Variation::IO
BioPerl-1.6.1::Bio::Das
BioPerl-1.6.1::Bio::Tools
BioPerl-1.6.1::Bio::Tools::Run
BioPerl-1.6.1::Bio::Tools::Signalp
BioPerl-1.6.1::Bio::Tools::SeqPattern
BioPerl-1.6.1::Bio::Tools::EMBOSS
BioPerl-1.6.1::Bio::Tools::SiRNA
BioPerl-1.6.1::Bio::Tools::SiRNA::Ruleset
BioPerl-1.6.1::Bio::Tools::Phylo
BioPerl-1.6.1::Bio::Tools::Phylo::Molphy
BioPerl-1.6.1::Bio::Tools::Phylo::Phylip
BioPerl-1.6.1::Bio::Tools::Phylo::PAML
BioPerl-1.6.1::Bio::Tools::Primer
BioPerl-1.6.1::Bio::Tools::Primer::Assessor
BioPerl-1.6.1::Bio::Tools::Prediction
BioPerl-1.6.1::Bio::Tools::Sim4
BioPerl-1.6.1::Bio::Tools::Spidey
BioPerl-1.6.1::Bio::Tools::EUtilities
BioPerl-1.6.1::Bio::Tools::EUtilities::Link
BioPerl-1.6.1::Bio::Tools::EUtilities::Summary

BioPerl-1.6.1::Bio::Tools::EUtilities::Info
BioPerl-1.6.1::Bio::Tools::EUtilities::Query
BioPerl-1.6.1::Bio::Tools::Analysis
BioPerl-1.6.1::Bio::Tools::Analysis::Protein
BioPerl-1.6.1::Bio::Tools::Analysis::DNA
BioPerl-1.6.1::Bio::Tools::HMMER
BioPerl-1.6.1::Bio::Tools::Alignment
BioPerl-1.6.1::Bio::Restriction
BioPerl-1.6.1::Bio::Restriction::Enzyme
BioPerl-1.6.1::Bio::Restriction::IO
BioPerl-1.6.1::Bio::Symbol

BioPerl-1.6.1 **Top**

BioPerl(1)	Perl Modules for Biology

BioPerl-1.6.1::ide **Top**

Nothing here

BioPerl-1.6.1::ide::bioperl-mode **Top**

Nothing here

BioPerl-1.6.1::ide::bioperl-mode::site-lisp **Top**

Nothing here

BioPerl-1.6.1::ide::bioperl-mode::dist **Top**

Nothing here

BioPerl-1.6.1::ide::bioperl-mode::etc **Top**

Nothing here

BioPerl-1.6.1::ide::bioperl-mode::etc::images **Top**

Nothing here

BioPerl-1.6.1::maintenance **Top**

Nothing here

BioPerl-1.6.1::Bio **Top**

AlignIO	Handler for AlignIO Formats
AnalysisI(1)	An interface to any (local or remote) analysis tool
AnalysisParserI	Generic analysis output parser interface
AnalysisResultI	Interface for analysis result objects
AnnotatableI	the base interface an annotatable object must implement
AnnotationCollectionI(1)	Interface for annotation collections
AnnotationI	Annotation interface
Biblio	A Bibliographic Query Service module

ClusterI	Cluster Interface
ClusterIO	Handler for Cluster Formats
DBLinkContainerI	Abstract interface for any object wanting to use database cross references
DasI	DAS-style access to a feature database
DescribableI	interface for objects with human readable names and descriptions
FeatureHolderI	the base interface an object with features must implement
FeatureIO	Handler for FeatureIO
HandlerBaseI	Interface class for handler methods which interact with any event-driven parsers (drivers).
IdCollectionI	interface for objects with multiple identifiers
IdentifiableI	interface for objects with identifiers
JobI	
LocatableSeq	A Bio::PrimarySeq object with start/end points on it that can be projected into a MSA or have coordinates relative to another seq.
LocationI(1)	Abstract interface of a Location on a Sequence
MapIO	A Map Factory object
OntologyIO	Parser factory for Ontology formats
ParameterBaseI	Simple interface class for any parameter-related data such as IDs, database name, program arguments, and other odds and ends.
Perl	Functional access to BioPerl for people who don't know objects
PhyloNetwork	Module to compute with Phylogenetic Networks
PrimarySeq	Bioperl lightweight Sequence Object
PrimarySeqI	Interface definition for a Bio::PrimarySeq
PullParserI	A base module for fast 'pull' parsing
Range(1)	Pure perl RangeI implementation
RangeI	Range interface
SearchDist	A perl wrapper around Sean Eddy's histogram object
SearchIO	Driver for parsing Sequence Database Searches (BLAST, FASTA, ...)
Seq	Sequence object, with features
SeqAnalysisParserI	Sequence analysis output parser interface
SeqFeatureI	Abstract interface of a Sequence Feature
SeqI(1)	[Developers] Abstract Interface of Sequence (with features)
SeqIO	Handler for SeqIO Formats
SeqUtils	Additional methods for PrimarySeq objects
SimpleAlign	Multiple alignments held as a set of sequences
SimpleAnalysisI	A simple interface to any (local or remote) analysis tool
Species	Generic species object
Taxon(1)	A node in a represented taxonomy
Taxonomy(1)	representing Taxonomy.
TreeIO	Parser for Tree files
UpdateableSeqI(1)	Descendant of Bio::SeqI that allows updates
WebAgent	A base class for Web (any protocol) access

BioPerl-1.6.1::Bio::SearchIO

Top

EventHandlerI(1)	An abstract Event Handler for Search Result parsing
FastHitEventBuilder	Event Handler for SearchIO events.
IteratedSearchResultEventBuilder	Event Handler for SearchIO events.
SearchResultEventBuilder	Event Handler for SearchIO events.
SearchWriterI	Interface for outputting parsed Search results
axt	a parser for axt format reports
blast	Event generator for event based parsing of blast reports
blast_pull	A parser for BLAST output
blasttable	Driver module for SearchIO for parsing NCBI -m 8/9 format
blastxml	A SearchIO implementation of NCBI Blast XML parsing.
cross_match	CrossMatch-specific subclass of Bio::SearchIO
erpin	SearchIO-based ERPIN parser
exonerate	parser for Exonerate
fasta(1)	A SearchIO parser for FASTA results
gmap_f9	Event generator for parsing gmap reports (Z format)
hmmer	A parser for HMMER output (hmmpfam, hmmsearch)
hmmer_pull	A parser for HMMER output
infernal	SearchIO-based Infernal parser
megablast	a driver module for Bio::SearchIO to parse megablast reports (format 0)
psl	A parser for PSL output (UCSC)
rnamotif	SearchIO-based RNAMotif parser
sim4	parser for Sim4 alignments
waba	SearchIO parser for Jim Kent WABA program alignment output
wise	Parsing of wise output as alignments

BioPerl-1.6.1::Bio::SearchIO::Writer Top

BSMLResultWriter	BSML output writer
GbrowseGFF	Interface for outputting parsed search results in Gbrowse GFF format
HSPTableWriter	Tab-delimited data for Bio::Search::HSP::HSPI objects
HTMLResultWriter	write a Bio::Search::ResultI in HTML
HitTableWriter	Tab-delimited data for Bio::Search::Hit::HitI objects
ResultTableWriter	Outputs tab-delimited data for each Bio::Search::Result::ResultI object.
TextResultWriter	Object to implement writing a Bio::Search::ResultI in Text.

BioPerl-1.6.1::Bio::SearchIO::XML Top

BlastHandler	XML Handler for NCBI Blast XML parsing.
PsiBlastHandler	XML Handler for NCBI Blast PSIBLAST XML parsing.

BioPerl-1.6.1::Bio::AlignIO Top

arp	ARP MSA Sequence input/output stream
bl2seq	bl2seq sequence input/output stream
clustalw	clustalw sequence input/output stream
emboss	Parse EMBOSS alignment output (from applications water and needle)
fasta(2)	fasta MSA Sequence input/output stream

largemultifasta	Largemultifasta MSA Sequence input/output stream
maf	Multiple Alignment Format sequence input stream
mase	mase sequence input/output stream
mega	Parse and Create MEGA format data files
meme(1)	meme sequence input/output stream
metafasta(1)	Metafasta MSA Sequence input/output stream
msf	msf sequence input/output stream
nexus(1)	NEXUS format sequence input/output stream
pfam	pfam sequence input/output stream
phylip(1)	PHYLIP format sequence input/output stream
po	po MSA Sequence input/output stream
proda	proda sequence input/output stream This provides the basic capabilities to parse the output alignments from the ProDA multiple sequence alignment program (http://proda.stanford.edu)
prodom	prodom sequence input/output stream
psi	Read/Write PSI-BLAST profile alignment files
selex	selex sequence input/output stream
stockholm	stockholm sequence input/output stream
xmfa	XMFA MSA Sequence input/output stream

BioPerl-1.6.1::Bio::AlignIO::Handler Top

GenericAlignHandler	Bio::HandlerI-based generic data handler class for alignment-based data

BioPerl-1.6.1::Bio::Location Top

Atomic	Implementation of a Atomic Location on a Sequence
AvWithinCoordPolicy	class implementing Bio::Location::CoordinatePolicy as the average for WITHIN and the widest possible and reasonable range otherwise
CoordinatePolicyI	Abstract interface for objects implementing a certain policy of computing integer-valued coordinates of a Location
Fuzzy	Implementation of a Location on a Sequence which has unclear start and/or end locations
FuzzyLocationI	Abstract interface of a Location on a Sequence which has unclear start/end location
NarrowestCoordPolicy	class implementing Bio::Location::CoordinatePolicy as the narrowest possible and reasonable range
Simple	Implementation of a Simple Location on a Sequence
Split	Implementation of a Location on a Sequence which has multiple locations (start/end points)
SplitLocationI	Abstract interface of a Location on a Sequence which has multiple locations (start/end points)
WidestCoordPolicy	class implementing Bio::Location::CoordinatePolicy as the widest possible and reasonable range

BioPerl-1.6.1::Bio::Coordinate Top

Chain(1)	Mapping locations through a chain of coordinate mappers
Collection(1)	Noncontinuous match between two coordinate sets

ExtrapolatingPair	Continuous match between two coordinate sets
GeneMapper	transformations between gene related coordinate systems
Graph	Finds shortest path between nodes in a graph
MapperI	Interface describing coordinate mappers
Pair(1)	Continuous match between two coordinate sets
Result(1)	Results from coordinate transformation
ResultI(1)	Interface to identify coordinate mapper results
Utils	Additional methods to create Bio::Coordinate objects

BioPerl-1.6.1::Bio::Coordinate::Result

Top

Gap	Another name for Bio::Location::Simple
Match(1)	Another name for Bio::Location::Simple

BioPerl-1.6.1::Bio::MapIO

Top

fpc	A FPC Map reader
mapmaker	A Mapmaker Map reader

BioPerl-1.6.1::Bio::Index

Top

Abstract	Abstract interface for indexing a flat file
AbstractSeq	base class for AbstractSeq
Blast	Indexes Blast reports and supports retrieval based on query accession(s)
BlastTable	Indexes tabular Blast reports (-m 9 format) and supports retrieval based on query accession(s)
EMBL(1)	Interface for indexing (multiple) EMBL/Swissprot .dat files (i.e. flat file EMBL/Swissprot format).
Fasta(1)	Interface for indexing (multiple) fasta files
Fastq	Interface for indexing (multiple) fastq files
GenBank(1)	Interface for indexing one or more GenBank files (i.e. flat file GenBank format).
Hmmer	indexes HMMER reports and supports retreival based on query
Qual	Interface for indexing (multiple) fasta qual files
Stockholm	Indexes Stockholm format alignments (such as those from Pfam and Rfam. Retrieves raw stream data using the ID or a Bio::SimpleAlign (via Bio::AlignIO)
SwissPfam	Interface for indexing swisspfam files
Swissprot	Interface for indexing one or more Swissprot files.

BioPerl-1.6.1::Bio::Seq

Top

BaseSeqProcessor	Base implementation for a SequenceProcessor
EncodedSeq	subtype of L to store DNA that encodes a protein
LargeLocatableSeq	LocatableSeq object that stores sequence as files in the tempdir
LargePrimarySeq	PrimarySeq object that stores sequence as files in the tempdir (as found by File::Temp) or the default method in Bio::Root::Root
LargeSeq	SeqI compliant object that stores sequence as files in /tmp
LargeSeqI	Interface class for sequences that cache their residues in a temporary file
Meta	Generic superclass for sequence objects with residue-based meta information
MetaI	Interface for sequence objects with residue-based meta information

PrimaryQual	Bioperl lightweight Quality Object
PrimedSeq	A representation of a sequence and two primers flanking a target region
QualI	Interface definition for a Bio::Seq::Qual
Quality	Implementation of sequence with residue quality and trace values
RichSeq	Module implementing a sequence created from a rich sequence database entry
RichSeqI	interface for sequences from rich data sources, mostly databases
SeqBuilder	Configurable object builder for sequence stream parsers
SeqFactory	Instantiates a new Bio::PrimarySeqI (or derived class) through a factory
SeqFastaSpeedFactory	Instantiates a new Bio::PrimarySeqI (or derived class) through a factory
SeqWithQuality	Bioperl object packaging a sequence with its quality. Deprecated class, use Bio::Seq::Quality instead!
SequenceTrace	Bioperl object packaging a sequence with its trace
TraceI	Interface definition for a Bio::Seq::Trace

BioPerl-1.6.1::Bio::Seq::Meta

Top

Array	array-based generic implementation of a sequence class with residue-based meta information

BioPerl-1.6.1::Bio::SeqIO

Top

FTHelper	Helper class for Embl/Genbank feature tables
MultiFile	Treating a set of files as a single input stream
abi	abi trace sequence input/output stream
ace(1)	ace sequence input/output stream
agave	AGAVE sequence output stream.
alf	alf trace sequence input/output stream
asciitree	asciitree sequence input/output stream
bsml	BSML sequence input/output stream
bsml_sax	BSML sequence input/output stream using SAX
chadoxml	chadoxml sequence output stream
chaos	chaos sequence input/output stream
chaosxml	chaosxml sequence input/output stream
ctf	ctf trace sequence input/output stream
embl(1)	EMBL sequence input/output stream
embldriver	EMBL sequence input/output stream
entrezgene	Entrez Gene ASN1 parser
excel	sequence input/output stream from a MSExcel-formatted table
exp	exp trace sequence input/output stream
fasta(3)	fasta sequence input/output stream
fastq	fastq sequence input/output stream
flybase_chadoxml	FlyBase variant of chadoxml with sequence output stream
game	- a class for parsing and writing game-XML
gbdriver	GenBank handler-based push parser
gcg	GCG sequence input/output stream
genbank(1)	GenBank sequence input/output stream

interpro(1)	InterProScan XML input/output stream
kegg	KEGG sequence input/output stream
largefasta	method i/o on very large fasta sequence files
lasergene	Lasergene sequence file input/output stream
locuslink	LocusLink input/output stream
metafasta(2)	metafasta sequence input/output stream
phd	.phd file input/output stream
pir	PIR sequence input/output stream
pln	pln trace sequence input/output stream
qual	.qual file input/output stream
raw	raw sequence file input/output stream
scf	.scf file input/output stream
strider	DNA strider sequence input/output stream
swiss(1)	Swissprot sequence input/output stream
swissdriver	SwissProt/UniProt handler-based push parser
tab	nearly raw sequence file input/output stream. Reads/writes id"\t"sequence"\n"
table	sequence input/output stream from a delimited table
tigr(1)	TIGR XML sequence input/output stream
tigrxml	Parse TIGR (new) XML
tinyseq	reading/writing sequences in NCBI TinySeq format
ztr	ztr trace sequence input/output stream

BioPerl-1.6.1::Bio::SeqIO::tinyseq

Top

tinyseqHandler	XML event handlers to support NCBI TinySeq XML parsing

BioPerl-1.6.1::Bio::SeqIO::game

Top

featHandler	- a class for handling feature elements
gameHandler	- PerlSAX handler for game-XML
gameSubs	- a base class for game-XML parsing
gameWriter	- a class for writing game-XML
seqHandler	- a class for handling game-XML sequences

BioPerl-1.6.1::Bio::SeqIO::Handler

Top

GenericRichSeqHandler	Bio::HandlerI-based data handler for GenBank/EMBL/UniProt (and other) sequence data

BioPerl-1.6.1::Bio::ClusterIO

Top

dbsnp	dbSNP input stream
unigene	UniGene input stream

BioPerl-1.6.1::Bio::Taxonomy

Top

FactoryI	interface to define how to access NCBI Taxonoy
Node(1)	A node in a represented taxonomy
Taxon(2)	Generic Taxonomic Entity object

Tree(1)	An Organism Level Implementation of TreeI interface.

BioPerl-1.6.1::Bio::OntologyIO

Top

InterProParser	Parser for InterPro xml files.
dagflat	a base class parser for GO flat-file type formats
goflat	a parser for the Gene Ontology flat-file format
obo	a parser for OBO flat-file format from Gene Ontology Consortium
simplehierarchy	a base class parser for simple hierarchy-by-indentation type formats
soflat	a parser for the Sequence Ontology flat-file format

BioPerl-1.6.1::Bio::OntologyIO::Handlers

Top

BaseSAXHandler	base class for SAX Handlers
InterProHandler	XML handler class for InterProParser
InterPro_BioSQL_Handler	parse an InterPro XML file and persist the resulting terms to a Biosql database

BioPerl-1.6.1::Bio::PopGen

Top

Genotype	An implementation of GenotypeI which is just an allele container
GenotypeI	A marker and alleles for a specific individual
HtSNP	Select htSNP from a haplotype set
IO(1)	Input individual,marker,allele information
Individual	An implementation of an Individual who has Genotype or Sequence Results
IndividualI	An individual who has Genotype or Sequence Results
Marker(1)	A genetic marker which one uses to generate genotypes
MarkerI(1)	A Population Genetic conceptual marker
PopStats	A collection of methods for calculating statistics about a population or sets of populations
Population	A population of individuals
PopulationI	Interface for Populations
Statistics(1)	Population Genetics statistical tests
TagHaplotype	Haplotype tag object.
Utilities(1)	Utilities for working with PopGen data and objects

BioPerl-1.6.1::Bio::PopGen::IO

Top

csv	Extract individual allele data from a CSV parser
hapmap	A parser for HapMap output data
phase	A parser for Phase format data
prettybase	Extract individual allele data from PrettyBase format

BioPerl-1.6.1::Bio::PopGen::Simulation

Top

Coalescent	A Coalescent simulation factory
GeneticDrift	A simple genetic drift simulation

BioPerl-1.6.1::Bio::Align

Top

AlignI	An interface for describing sequence alignments.

DNAStatistics	Calculate some statistics for a DNA alignment
PairwiseStatistics	Base statistic object for Pairwise Alignments
ProteinStatistics	Calculate Protein Alignment statistics (mostly distances)
StatisticsI(1)	Calculate some statistics for an alignment
Utilities(2)	A collection of utilities regarding converting and manipulating alignment objects

BioPerl-1.6.1::Bio::SeqEvolution Top

DNAPoint	evolve a sequence by point mutations
EvolutionI	the interface for evolving sequences
Factory(1)	Factory object to instantiate sequence evolving classes

BioPerl-1.6.1::Bio::Expression Top

Contact	DESCRIPTION of Object
DataSet	DESCRIPTION of Object
FeatureGroup	a set of DNA/RNA features. ISA Bio::Expression::FeatureI
FeatureI	an interface class for DNA/RNA features
Platform	DESCRIPTION of Object
ProbeI	an interface class for DNA/RNA probes
Sample	DESCRIPTION of Object

BioPerl-1.6.1::Bio::Expression::FeatureSet Top

FeatureSetMas50	utility class for Mas50 FeatureSet

BioPerl-1.6.1::Bio::Expression::FeatureGroup Top

FeatureGroupMas50	utility class for Mas50 FeatureGroup

BioPerl-1.6.1::Bio::SeqFeature Top

Annotated	PLEASE PUT SOMETHING HERE
AnnotationAdaptor	integrates SeqFeatureIs annotation
Collection(2)	A container class for SeqFeatures suitable for performing operations such as finding features within a range, that match a certain feature type, etc.
CollectionI	An interface for a collection of SeqFeatureI objects.
Computation	Computation SeqFeature
FeaturePair	hold pair feature information e.g. blast hits
Generic(1)	Generic SeqFeature
Lite	Lightweight Bio::SeqFeatureI class
PositionProxy	handle features when truncation/revcom sequences span a feature
Primer	Primer Generic SeqFeature
Similarity	A sequence feature based on similarity
SimilarityPair	Sequence feature based on the similarity of two sequences.
TypedSeqFeatureI	a strongly typed SeqFeature

BioPerl-1.6.1::Bio::SeqFeature::SiRNA Top

Oligo	Perl object for small inhibitory RNAs.

Pair(2)	Perl object for small inhibitory RNA (SiRNA) oligo pairs

BioPerl-1.6.1::Bio::SeqFeature::Gene	**Top**
Exon(1)	a feature representing an exon
ExonI	Interface for a feature representing an exon
GeneStructure	A feature representing an arbitrarily complex structure of a gene
GeneStructureI	A feature representing an arbitrarily complex structure of a gene
Intron(1)	An intron feature
NC_Feature	superclass for non-coding features
Poly_A_site	poly A feature
Promoter	Describes a promoter
Transcript(1)	A feature representing a transcript
TranscriptI	Interface for a feature representing a transcript of exons, promoter(s), UTR, and a poly-adenylation site.
UTR	A feature representing an untranslated region that is part of a transcriptional unit

BioPerl-1.6.1::Bio::SeqFeature::Tools	**Top**
FeatureNamer	generates unique persistent names for features
IDHandler	maps $seq_feature-Eprimary_tag
TypeMapper	maps $seq_feature-Eprimary_tag
Unflattener	turns flat list of genbank-sourced features into a nested SeqFeatureI hierarchy

BioPerl-1.6.1::Bio::Annotation	**Top**
AnnotationFactory	Instantiates a new Bio::AnnotationI (or derived class) through a factory
Collection(3)	Default Perl implementation of AnnotationCollectionI
Comment	A comment object, holding text
DBLink	untyped links between databases
OntologyTerm	An ontology term adapted to AnnotationI
Reference	Specialised DBLink object for Literature References
Relation	Relationship (pairwise) with other objects SeqI and NodeI;
SimpleValue	A simple scalar
StructuredValue	A scalar with embedded structured information
TagTree	AnnotationI with tree-like hierarchal key-value relationships ('structured tags') that can be represented as simple text.
Target	Provides an object which represents a target (ie, a similarity hit) from one object to something in another database
Tree(2)	Provide a tree as an annotation to a Bio::AnnotatableI object
TypeManager	Manages types for annotation collections

BioPerl-1.6.1::Bio::Tree	**Top**
AlleleNode	A Node with Alleles attached
AnnotatableNode	A Tree Node with support for annotation
Compatible	Testing compatibility of phylogenetic trees with nested taxa.
DistanceFactory	Construct a tree using distance based methods

Node(2)	A Simple Tree Node
NodeI	Interface describing a Tree Node
NodeNHX	A Simple Tree Node with support for NHX tags
RandomFactory(1)	TreeFactory for generating Random Trees
Statistics(2)	Calculate certain statistics for a Tree
Tree(3)	An Implementation of TreeI interface.
TreeFunctionsI	Decorated Interface implementing basic Tree exploration methods
TreeI	A Tree object suitable for lots of things, designed originally for Phylogenetic Trees.

BioPerl-1.6.1::Bio::Tree::Draw

Top

Cladogram	Drawing phylogenetic trees in Encapsulated PostScript (EPS) format.

BioPerl-1.6.1::Bio::Ontology

Top

DocumentRegistry	Keep track of where to find ontologies. Allows lookups by name.
GOterm	representation of GO terms
InterProTerm	Implementation of InterProI term interface
OBOEngine	An Ontology Engine for OBO style flat file format from the Gene Ontology Consortium
OBOterm	representation of OBO terms
Ontology	standard implementation of an Ontology
OntologyEngineI	Interface a minimal Ontology implementation should satisfy
OntologyI	Interface for an ontology implementation
OntologyStore	A repository of ontologies
Path	a path for an ontology term graph
PathI	Interface for a path between ontology terms
Relationship	a relationship for an ontology
RelationshipFactory	Instantiates a new Bio::Ontology::RelationshipI (or derived class) through a factory
RelationshipI	Interface for a relationship between ontology terms
RelationshipType	a relationship type for an ontology
SimpleOntologyEngine	Implementation of OntologyEngineI interface
Term(1)	implementation of the interface for ontology terms
TermFactory	Instantiates a new Bio::Ontology::TermI (or derived class) through a factory
TermI	interface for ontology terms

BioPerl-1.6.1::Bio::Ontology::SimpleGOEngine

Top

GraphAdaptor	Graph adaptor for Bio::Ontology::SimpleGOEngine
GraphAdaptor02	Graph adaptor (v02.x) for Bio::Ontology::SimpleGOEngine

BioPerl-1.6.1::Bio::FeatureIO

Top

bed	read/write features from UCSC BED format
gff	read/write GFF feature files
gtf	read write features in GTF format
interpro(2)	read features from InterPro XML
ptt	read/write features in PTT format

vecscreen_simple	read/write features from NCBI vecscreen -f 3 output

BioPerl-1.6.1::Bio::PhyloNetwork	Top
Factory(2)	Module to sequentially generate Phylogenetic Networks
FactoryX	Module to sequentially generate Phylogenetic Networks
GraphViz	Interface between PhyloNetwork and GraphViz
RandomFactory(2)	Module to generate random Phylogenetic Networks
TreeFactory	Module to sequentially generate Phylogenetic Trees
TreeFactoryMulti	Module to sequentially generate Phylogenetic Trees
TreeFactoryX	Module to sequentially generate Phylogenetic Trees
muVector	Module to compute with vectors of arbitrary dimension

BioPerl-1.6.1::Bio::Cluster	Top
ClusterFactory	Instantiates a new Bio::ClusterI (or derived class) through a factory
FamilyI	Family Interface
SequenceFamily	Sequence Family object
UniGene	UniGene object
UniGeneI	abstract interface of UniGene object

BioPerl-1.6.1::Bio::Matrix	Top
Generic(2)	A generic matrix implementation
IO(2)	A factory for Matrix parsing
MatrixI	An interface for describing a Matrix
Mlagan	A generic matrix with mlagan fields
PhylipDist	A Phylip Distance Matrix object
Scoring	Object which can hold scoring matrix information

BioPerl-1.6.1::Bio::Matrix::IO	Top
mlagan	A parser for the mlagan substitution matrix
phylip(2)	A parser for PHYLIP distance matricies
scoring	A parser for PAM/BLOSUM matricies

BioPerl-1.6.1::Bio::Matrix::PSM	Top
IO(3)	PSM parser
InstanceSite	A PSM site occurance
InstanceSiteI	InstanceSite interface, holds an instance of a PSM
ProtMatrix	SiteMatrixI implementation, holds a position scoring matrix (or position weight matrix) with log-odds scoring information.
ProtPsm	handle combination of site matricies
Psm	handle combination of site matricies
PsmHeader	PSM mast parser implementation
PsmHeaderI	handles the header data from a PSM file
PsmI	abstract interface to handler of site matricies

SiteMatrix	SiteMatrixI implementation, holds a position scoring matrix (or position weight matrix) and log-odds
SiteMatrixI	SiteMatrixI implementation, holds a position scoring matrix (or position weight matrix) and log-odds

BioPerl-1.6.1::Bio::Matrix::PSM::IO

Top

mast	PSM mast parser implementation
masta	motif fasta format parser
meme(2)	PSM meme parser implementation
psiblast	PSM psiblast parser
transfac	PSM transfac parser

BioPerl-1.6.1::Bio::Event

Top

EventGeneratorI	This interface describes the basic event generator class.
EventHandlerI(2)	An Event Handler Interface

BioPerl-1.6.1::Bio::TreeIO

Top

TreeEventBuilder	Build Bio::Tree::Tree's and Bio::Tree::Node's from Events
cluster	A TreeIO driver module for parsing Algorithm::Cluster::treecluster() output
lintree	Parser for lintree output trees
newick	TreeIO implementation for parsing Newick/New Hampshire/PHYLIP format.
nexus(2)	A TreeIO driver module for parsing Nexus tree output from PAUP
nhx	TreeIO implementation for parsing Newick/New Hampshire eXtendend (NHX) format.
pag	Bio::TreeIO driver for Pagel format
phyloxml	TreeIO implementation for parsing PhyloXML format.
svggraph	A simple output format that converts a Tree object to an SVG output
tabtree	A simple output format which displays a tree as an ASCII drawing

BioPerl-1.6.1::Bio::Map

Top

Clone	An central map object representing a clone
Contig(1)	A MapI implementation handling the contigs of a Physical Map (such as FPC)
CytoMap	A Bio::MapI compliant map implementation handling cytogenic bands
CytoMarker	An object representing a marker.
CytoPosition	Marker class with cytogenetic band storing attributes
EntityI	An Entity Interface
FPCMarker	An central map object representing a marker
Gene(1)	An gene modelled as a mappable element.
GeneMap	A MapI implementation to represent the area around a gene
GenePosition	A typed position, suitable for modelling the various regions of a gene.
GeneRelative	Represents being relative to named sub-regions of a gene.
LinkageMap	A representation of a genetic linkage map.
LinkagePosition	Create a Position for a Marker that will be placed on a Bio::Map::LinkageMap
MapI	Interface for describing Map objects in bioperl

Mappable	An object representing a generic map element that can have multiple locations in several maps.
MappableI	An object that can be placed in a map
Marker(2)	An central map object representing a generic marker that can have multiple location in several maps.
MarkerI(2)	Interface for basic marker functionality
Microsatellite	An object representing a Microsatellite marker.
OrderedPosition	Abstracts the notion of a member of an ordered list of markers. Each marker is a certain distance from the one in the ordered list before it.
OrderedPositionWithDistance	Abstracts the notion of a member of an ordered list of markers. Each marker is a certain distance from the one in the ordered list before it.
Physical	A class for handling a Physical Map (such as FPC)
Position	A single position of a Marker, or the range over which that marker lies, in a Map
PositionHandler	A Position Handler Implementation
PositionHandlerI	A Position Handler Interface
PositionI	Abstracts the notion of a position having a value in the context of a marker and a Map
PositionWithSequence	A position with a sequence.
Prediction	An object representing the predictions of something that can have multiple locations in several maps.
Relative	Represents what a Position's coordiantes are relative to.
RelativeI	Interface for describing what a Position's coordiantes are relative to.
SimpleMap	A MapI implementation handling the basics of a Map
TranscriptionFactor	A transcription factor modelled as a mappable element

BioPerl-1.6.1::Bio::Phenotype **Top**

Correlate	Representation of a correlating phenotype in a given species
Measure	Representation of context/value(-range)/unit triplets
Phenotype	A class for modeling phenotypes
PhenotypeI	An interface for classes modeling phenotypes

BioPerl-1.6.1::Bio::Phenotype::OMIM **Top**

MiniMIMentry	Representation of a Mini MIM entry
OMIMentry	represents OMIM (Online Mendelian Inheritance in Man) database entries
OMIMentryAllelicVariant	Representation of a allelic variant of the OMIM database
OMIMparser	parser for the OMIM database

BioPerl-1.6.1::Bio::Phenotype::MeSH **Top**

Term(2)	A MeSH term
Twig	Context for a MeSH term

BioPerl-1.6.1::Bio::Root **Top**

Build	A common Module::Build subclass base for BioPerl distributions
Exception	Generic exception objects for Bioperl
HTTPget	module for fallback HTTP get operations when LWP:: is unavailable

IO(4)	module providing several methods often needed when dealing with file IO
Root	Hash-based implementation of Bio::Root::RootI
RootI	Abstract interface to root object code
Storable	object serialisation methods
Test	A common base for all Bioperl test scripts.
Utilities(3)	General-purpose utility module
Version	provide global, distribution-level versioning

BioPerl-1.6.1::Bio::Root::Test

Top

Warn	Perl extension to test Bioperl methods for warnings

BioPerl-1.6.1::Bio::Biblio

Top

Article	Representation of a general article
BiblioBase	An abstract base for other biblio classes
Book	Representation of a book
BookArticle	Representation of a book article
IO(5)	Handling the bibliographic references
Journal	Representation of a journal
JournalArticle	Representation of a journal article
MedlineArticle	Representation of a MEDLINE article
MedlineBook	Representation of a MEDLINE book
MedlineBookArticle	Representation of a MEDLINE book article
MedlineJournal	Representation of a MEDLINE journal
MedlineJournalArticle	Representation of a MEDLINE journal article
Organisation	Representation of an organisation
Patent	Representation of a patent
Person	Representation of a person
Proceeding	Representation of a conference proceeding
Provider	Representation of a general provider
PubmedArticle	Representation of a PUBMED article
PubmedBookArticle	Representation of a PUBMED book article
PubmedJournalArticle	Representation of a PUBMED journal article
Ref	Representation of a bibliographic reference
Service	Representation of a provider of type service
TechReport	Representation of a technical report
Thesis	Representation of thesis
WebResource	Representation of a web resource

BioPerl-1.6.1::Bio::Biblio::IO

Top

medline2ref	A converter of a raw hash to MEDLINE citations
medlinexml	A converter of XML files with MEDLINE citations
pubmed2ref	A converter of a raw hash to PUBMED citations
pubmedxml	A converter of XML files with PUBMED citations

BioPerl-1.6.1::Bio::Structure	Top
Atom	Bioperl structure Object, describes an Atom
Chain(2)	Bioperl structure Object, describes a chain
Entry	Bioperl structure Object, describes the whole entry
IO(6)	Handler for Structure Formats
Model	Bioperl structure Object, describes a Model
Residue	Bioperl structure Object, describes a Residue
StructureI	Abstract Interface for a Structure objects

BioPerl-1.6.1::Bio::Structure::SecStr	Top
Nothing here	

BioPerl-1.6.1::Bio::Structure::SecStr::DSSP	Top
Res(1)	Module for parsing/accessing dssp output

BioPerl-1.6.1::Bio::Structure::SecStr::STRIDE	Top
Res(2)	Module for parsing/accessing stride output

BioPerl-1.6.1::Bio::Structure::IO	Top
pdb	PDB input/output stream

BioPerl-1.6.1::Bio::DB	Top
Ace	Database object interface to ACeDB servers
BiblioI	An interface to a Bibliographic Query Service
BioFetch	Database object interface to BioFetch retrieval
CUTG	for access to the Codon usage Database at http://www.kazusa.or.jp/codon.
DBFetch	Database object for retrieving using the dbfetch script
EMBL(2)	Database object interface for EMBL entry retrieval
EUtilities(1)	webagent which interacts with and retrieves data from NCBI's eUtils
EntrezGene	Database object interface to Entrez Gene
Expression	DESCRIPTION of Object
Failover	A Bio::DB::RandomAccessI compliant class which wraps a prioritized list of DBs
Fasta(1)	- Fast indexed access to a directory of fasta files
Fasta(2)	
FileCache	In file cache for BioSeq objects
Flat	Interface for indexed flat files
GFF(1)	- Storage and retrieval of sequence annotation data
GenBank(2)	Database object interface to GenBank
GenPept	Database object interface to GenPept
GenericWebAgent	helper base class for parameter-based remote server access and response retrieval.
HIV	Database object interface to the Los Alamos HIV Sequence Database
ID_Iterator	
InMemoryCache	Abstract interface for a sequence database

LocationI(2)	A RandomAccessI-like abstract interface for retrieving location data from a sequence database and returning Bio::LocationI objects
MeSH	Term retrieval from a Web MeSH database
NCBIHelper	A collection of routines useful for queries to NCBI databases.
Qual(1)	- Fast indexed access to a directory of quality files
Qual(2)	
QueryI	Object Interface to queryable sequence databases
RandomAccessI	Abstract interface for a sequence database
RefSeq	Database object interface for RefSeq retrieval
ReferenceI	A RandomAccessI-like abstract interface for retrieving Reference data from a sequence database and returning Bio::Annotation::Reference objects
Registry	Access to the Open Bio Database Access registry scheme
SeqFeature	- Normalized feature for use with Bio::DB::SeqFeature::Store
SeqHound	Database object interface to SeqHound
SeqI(2)	Abstract Interface for Sequence databases
SeqVersion	front end to querying databases for identifier versions
Stream(1)	
Stream(2)	
SwissProt	Database object interface to SwissProt retrieval
TFBS	Access to a Transcription Factor Binding Site database
Taxonomy(2)	Access to a taxonomy database
Universal	Artificial database that delegates to specific databases
UpdateableSeqI(2)	An interface for writing to a database of sequences.
WebDBSeqI	Object Interface to generalize Web Databases for retrieving sequences

BioPerl-1.6.1::Bio::DB::HIV

Top

AnnotationCollectionI(2)	
HIVAnnotProcessor	Adds HIV-specific annotations to Bio::SeqIO streams
HIVQueryHelper	Routines and packages used by Bio::DB::HIV and Bio::DB::Query::HIVQuery
HIVSchema	
Q	
QRY	
R	

BioPerl-1.6.1::Bio::DB::Taxonomy

Top

entrez	Taxonomy Entrez driver
flatfile	An implementation of Bio::DB::Taxonomy which uses local flat files
list	An implementation of Bio::DB::Taxonomy that accepts lists of words to build a database

BioPerl-1.6.1::Bio::DB::Expression

Top

geo	*** DESCRIPTION of Class

BioPerl-1.6.1::Bio::DB::SeqFeature

Top

NormalizedFeature	- Normalized feature for use with Bio::DB::SeqFeature::Store

NormalizedFeatureI	- Interface for normalized features
NormalizedTableFeatureI	- Interface for normalized features whose hierarchy is stored in a table
Segment(1)	- Location-based access to genome annotation data
Store	- Storage and retrieval of sequence annotation data

BioPerl-1.6.1::Bio::DB::SeqFeature::Store Top

FeatureFileLoader	- feature file loader for Bio::DB::SeqFeature::Store
GFF2Loader	- GFF2 file loader for Bio::DB::SeqFeature::Store
GFF3Loader	- GFF3 file loader for Bio::DB::SeqFeature::Store
Iterator(1)	
Iterator(2)	
LoadHelper	- Internal utility for Bio::DB::SeqFeature::Store
Loader(1)	- Loader
Subdir	
bdb	fetch and store objects from a BerkeleyDB
berkeleydb(1)	- Storage and retrieval of sequence annotation data in Berkeleydb files
berkeleydb3	- Storage and retrieval of sequence annotation data in Berkeleydb files
memory(1)	- In-memory implementation of Bio::DB::SeqFeature::Store

BioPerl-1.6.1::Bio::DB::SeqFeature::Store::DBI Top

Iterator	utility methods for creating and iterating over SeqFeature records
Pg	- Mysql implementation of Bio::DB::SeqFeature::Store
SQLite	- SQLite implementation of Bio::DB::SeqFeature::Store
mysql(1)	- Mysql implementation of Bio::DB::SeqFeature::Store

BioPerl-1.6.1::Bio::DB::TFBS Top

transfac_pro	An implementation of Bio::DB::TFBS which uses local flat files for transfac pro

BioPerl-1.6.1::Bio::DB::GFF Top

Aggregator	- Aggregate GFF groups into composite features
Featname	- The name of a feature
Feature(1)	- A relative segment identified by a feature type
Homol	- A segment of DNA that is homologous to another
RelSegment	- Sequence segment with relative coordinate support
Segment(2)	- Simple DNA segment object
Typename	- The name of a feature type

BioPerl-1.6.1::Bio::DB::GFF::Util Top

Binning	binning utility for Bio::DB::GFF index
Rearrange	rearrange utility

BioPerl-1.6.1::Bio::DB::GFF::Aggregator Top

alignment	- Alignment aggregator
clone	- Clone aggregator

coding	- The Coding Region Aggregator
gene	- Sequence Ontology Geene
match	- Match aggregator
none	- No aggregation
orf	- An aggregator for orf regions
processed_transcript	- Sequence Ontology Transcript
so_transcript	- Sequence Ontology Transcript
transcript	- Transcript aggregator
ucsc_acembly	- UCSC acembly aggregator
ucsc_ensgene	- UCSC ensGene aggregator
ucsc_genscan	- UCSC genscan aggregator
ucsc_refgene	- UCSC refGene aggregator
ucsc_sanger22	- UCSC sanger22 aggregator
ucsc_sanger22pseudo	- UCSC sanger22pseudo aggregator
ucsc_softberry	- UCSC softberry aggregator
ucsc_twinscan	- UCSC twinscan aggregator
ucsc_unigene	- UCSC UniGene aggregator

BioPerl-1.6.1::Bio::DB::GFF::Adaptor **Top**

FeatureStore	
ace(2)	- ace interface (for multiple inheritance)
berkeleydb(2)	- Bio::DB::GFF database adaptor for in-memory databases
biofetch(1)	- Cache BioFetch objects in a Bio::DB::GFF database
biofetch_oracle	- Cache BioFetch objects in a Bio::DB::GFF database
dbi	- Database adaptor for DBI (SQL) databases
memory(2)	- Bio::DB::GFF database adaptor for in-memory databases

BioPerl-1.6.1::Bio::DB::GFF::Adaptor::dbi **Top**

caching_handle	- Cache for database handles
faux_dbh	
iterator(1)	iterator for Bio::DB::GFF::Adaptor::dbi
mysql(2)	- Database adaptor for a specific mysql schema
mysqlace	- Unholy union between mysql GFF database and acedb database
mysqlcmap	- Database adaptor for an integraded CMap/GBrowse mysql schema
mysqlopt	- Deprecated database adaptor
oracle	- Database adaptor for a specific oracle schema
oracleace	- Unholy union between oracle GFF database and acedb database
pg	- Database adaptor for a specific postgres schema
pg_fts	- Database adaptor for a specific postgres schema with a TSearch2 implementation

BioPerl-1.6.1::Bio::DB::GFF::Adaptor::berkeleydb **Top**

iterator(2)	iterator for Bio::DB::GFF::Adaptor::berkeleydb

BioPerl-1.6.1::Bio::DB::GFF::Adaptor::memory **Top**

feature_serializer	utility methods for serializing and deserializing GFF features
iterator(3)	iterator for Bio::DB::GFF::Adaptor::memory

BioPerl-1.6.1::Bio::DB::Flat

Top

BDB	Interface for BioHackathon standard BDB-indexed flat file
BinarySearch	BinarySearch search indexing system for sequence files

BioPerl-1.6.1::Bio::DB::Flat::BDB

Top

embl(2)	embl adaptor for Open-bio standard BDB-indexed flat file
fasta(4)	fasta adaptor for Open-bio standard BDB-indexed flat file
genbank(2)	genbank adaptor for Open-bio standard BDB-indexed flat file
swiss(2)	swissprot adaptor for Open-bio standard BDB-indexed flat file

BioPerl-1.6.1::Bio::DB::Biblio

Top

biofetch(2)	A BioFetch-based access to a bibliographic citation retrieval
eutils	Access to PubMed's bibliographic query service
soap	A SOAP-based access to a bibliographic query service

BioPerl-1.6.1::Bio::DB::SeqVersion

Top

gi	interface to NCBI Sequence Revision History page

BioPerl-1.6.1::Bio::DB::Query

Top

GenBank(3)	Build a GenBank Entrez Query
HIVQuery	Query interface to the Los Alamos HIV Sequence Database
WebQuery	Helper class for web-based sequence queryies

BioPerl-1.6.1::Bio::Search

Top

BlastStatistics	An object for Blast statistics
BlastUtils	Utility functions for Bio::Search:: BLAST objects
DatabaseI	Interface for a database used in a sequence search
GenericDatabase	Generic implementation of Bio::Search::DatabaseI
GenericStatistics	An object for statistics
Processor	DESCRIPTION of Object
SearchUtils	Utility functions for Bio::Search:: objects
StatisticsI(2)	A Base object for statistics

BioPerl-1.6.1::Bio::Search::Tiling

Top

HSPI(1)	
MapTileUtils(1)	utilities for manipulating closed intervals for an HSP tiling algorithm
MapTileUtils(2)	
MapTiling	An implementation of an HSP tiling algorithm, with methods to obtain frequently-requested statistics
TilingI	Abstract interface for an HSP tiling module

BioPerl-1.6.1::Bio::Search::Result

Top

BlastPullResult	A parser and result object for BLASTN results
BlastResult	Blast-specific subclass of Bio::Search::Result::GenericResult
CrossMatchResult(1)	CrossMatch-specific subclass of Bio::Search::Result::GenericResult
CrossMatchResult(2)	
GenericResult	Generic Implementation of Bio::Search::Result::ResultI interface applicable to most search results.
HMMERResult	A Result object for HMMER results
HmmpfamResult	A parser and result object for hmmpfam results
PullResultI	Bio::Search::Result::ResultI interface for 'pull' parsers
ResultFactory	A factory to create Bio::Search::Result::ResultI objects
ResultI(2)	Abstract interface to Search Result objects
WABAResult	Result object for WABA alignment output

BioPerl-1.6.1::Bio::Search::Hit

Top

BlastHit	Blast-specific subclass of Bio::Search::Hit::GenericHit
BlastPullHit	A parser and hit object for BLASTN hits
Fasta(2)	Hit object specific for Fasta-generated hits
GenericHit	A generic implementation of the Bio::Search::Hit::HitI interface
HMMERHit	A Hit module for HMMER hits
HitFactory	A factory to create Bio::Search::Hit::HitI objects
HitI	Interface for a hit in a similarity search result
HmmpfamHit	A parser and hit object for hmmpfam hits
ModelHit	A model-based implementation of the Bio::Search::Hit::HitI interface
PsiBlastHit	Bioperl BLAST Hit object
PullHitI	Bio::Search::Hit::HitI interface for pull parsers.

BioPerl-1.6.1::Bio::Search::Iteration

Top

GenericIteration	A generic implementation of the Bio::Search::Iteration::IterationI interface.
IterationI	Abstract interface to an iteration from an iterated search result, such as PSI-BLAST.

BioPerl-1.6.1::Bio::Search::HSP

Top

BlastHSP	Bioperl BLAST High-Scoring Pair object
BlastPullHSP	A parser and HSP object for BlastN hsps
FastaHSP	HSP object for FASTA specific data
GenericHSP	A "Generic" implementation of a High Scoring Pair
HMMERHSP	A HSP object for HMMER results
HSPFactory	A factory to create Bio::Search::HSP::HSPI objects
HSPI(2)	Interface for a High Scoring Pair in a similarity search result
HmmpfamHSP	A parser and HSP object for hmmpfam hsps
ModelHSP	A HSP object for model-based searches
PSLHSP	A HSP for PSL output
PsiBlastHSP	Bioperl BLAST High-Scoring Pair object
PullHSPI	Bio::Search::HSP::HSPI interface for pull parsers.
WABAHSP	HSP object suitable for describing WABA alignments

BioPerl-1.6.1::Bio::LiveSeq

Top

AARange	AARange abstract class for LiveSeq
Chain(3)	DoubleChain DataStructure for Perl
ChainI	Double linked chain data structure
DNA	DNA object for LiveSeq
Exon(2)	Range abstract class for LiveSeq
Gene(2)	Range abstract class for LiveSeq
Intron(2)	Range abstract class for LiveSeq
Mutation	Mutation event descriptor class
Mutator	Package mutating LiveSequences
Prim_Transcript	Prim_Transcript class for LiveSeq
Range(2)	Range abstract class for LiveSeq
Repeat_Region	Repeat_Region class for LiveSeq
Repeat_Unit	Repeat_Unit class for LiveSeq
SeqI(3)	Abstract sequence interface class for LiveSeq
Transcript(2)	Transcript class for LiveSeq
Translation	Translation class for LiveSeq

BioPerl-1.6.1::Bio::LiveSeq::IO

Top

BioPerl(2)	Loader for LiveSeq from EMBL entries with BioPerl
Loader(2)	Parent Loader for LiveSeq

BioPerl-1.6.1::Bio::CodonUsage

Top

IO(7)	for reading and writing codon usage tables to file
Table	for access to the Codon usage Database at http://www.kazusa.or.jp/codon.

BioPerl-1.6.1::Bio::MolEvol

Top

CodonModel	Codon Evolution Models

BioPerl-1.6.1::Bio::Factory

Top

AnalysisI(2)	An interface to analysis tool factory
ApplicationFactoryI	Interface class for Application Factories
DriverFactory	Base class for factory classes loading drivers
FTLocationFactory	A FeatureTable Location Parser
LocationFactoryI	A factory interface for generating locations from a string
MapFactoryI	A Factory for getting markers
ObjectBuilderI	Interface for an object builder
ObjectFactory	Instantiates a new Bio::Root::RootI (or derived class) through a factory
ObjectFactoryI	A General object creator factory
SeqAnalysisParserFactory	class capable of creating SeqAnalysisParserI compliant parsers
SeqAnalysisParserFactoryI	interface describing objects capable of creating SeqAnalysisParserI compliant parsers
SequenceFactoryI	This interface allows for generic building of sequences in factories which create sequences (like SeqIO)

SequenceProcessorI	Interface for chained sequence processing algorithms
SequenceStreamI	Interface describing the basics of a Sequence Stream.
TreeFactoryI	Factory Interface for getting and writing trees from/to a data stream

BioPerl-1.6.1::Bio::Assembly

Top

Contig(2)	Perl module to hold and manipulate sequence assembly contigs.
ContigAnalysis	Perform analysis on sequence assembly contigs.
IO(8)	Handler for Assembly::IO Formats
Scaffold	Perl module to hold and manipulate sequence assembly data.
ScaffoldI	Abstract Inteface of Sequence Assemblies
Singlet	Perl module to hold and manipulate singlets from sequence assembly contigs.

BioPerl-1.6.1::Bio::Assembly::IO

Top

ace(3)	module to load ACE files from various assembly programs
phrap	driver to load phrap.out files.
tigr(2)	Driver to read and write assembly files in the TIGR Assembler v2 default format.

BioPerl-1.6.1::Bio::Assembly::Tools

Top

ContigSpectrum	create and manipulate contig spectra

BioPerl-1.6.1::Bio::Variation

Top

AAChange	Sequence change class for polypeptides
AAReverseMutate	point mutation and codon information from single amino acid changes
Allele	Sequence object with allele-specific attributes
DNAMutation	DNA level mutation class
IO(9)	Handler for sequence variation IO Formats
RNAChange	Sequence change class for RNA level
SNP	submitted SNP
SeqDiff	Container class for mutation/variant descriptions
VariantI	Sequence Change SeqFeature abstract class

BioPerl-1.6.1::Bio::Variation::IO

Top

flat	flat file sequence variation input/output stream
xml	XML sequence variation input/output stream

BioPerl-1.6.1::Bio::Das

Top

FeatureTypeI	Simple interface to Sequence Ontology feature types
SegmentI	DAS-style access to a feature database

BioPerl-1.6.1::Bio::Tools

Top

AlignFactory	Base object for alignment factories
AnalysisResult	Base class for analysis result objects and parsers
Blat	parser for Blat program
CodonTable	Codon table object
Coil	parser for Coil output

ECnumber	representation of EC numbers (Enzyme Classification)
EPCR	Parse ePCR output and make features
ERPIN	a parser for ERPIN output
ESTScan	Results of one ESTScan run
EUtilities(2)	NCBI eutil XML parsers
Eponine	Results of one Eponine run
Est2Genome	Parse est2genome output, makes simple Bio::SeqFeature::Generic objects
Fgenesh	parse results of one Fgenesh run
FootPrinter	write sequence features in FootPrinter format
GFF(2)	A Bio::SeqAnalysisParserI compliant GFF format parser
Gel	Calculates relative electrophoretic migration distances
Geneid	Results of one geneid run
Genemark	Results of one Genemark run
Genewise	Results of one Genewise run
Genomewise	Results of one Genomewise run
Genscan	Results of one Genscan run
Glimmer	parser for Glimmer 2.X/3.X prokaryotic and GlimmerM/GlimmerHMM eukaryotic gene predictions
Grail	Results of one Grail run
GuessSeqFormat	Module for determining the sequence format of the contents of a file, a string, or through a filehandle.
Hmmpfam	Parser for Hmmpfam program
IUPAC	Generates unique Seq objects from an ambiguous Seq object
Infernal	A parser for Infernal output
Lucy	Object for analyzing the output from Lucy, a vector and quality trimming program from TIGR
MZEF	Results of one MZEF run
Match(2)	Parses output from Transfac's match(TM)
OddCodes	Object holding alternative alphabet coding for one protein sequence
Primer3	Create input for and work with the output from the program primer3
Prints	Parser for FingerPRINTScanII program
Profile	parse Profile output
Promoterwise	parser for Promoterwise tab format output
PrositeScan	Parser for ps_scan result
Protparam	submit to and parse output from protparam ;
Pseudowise	Results of one Pseudowise run
QRNA	A Parser for qrna output
RNAMotif	A parser for RNAMotif output
RandomDistFunctions	A set of routines useful for generating random data in different distributions
RepeatMasker	a parser for RepeatMasker output
Seg	parse C output
SeqPattern	represent a sequence pattern or motif
SeqStats	Object holding statistics for one particular sequence

SeqWords	Object holding n-mer statistics for a sequence
SiRNA	Perl object for designing small inhibitory RNAs.
Sigcleave	Bioperl object for sigcleave analysis
Signalp	parser for Signalp output
TandemRepeatsFinder	a parser for Tandem Repeats Finder output
TargetP	Results of one TargetP run
Tmhmm	parse TMHMM output (TransMembrane HMM)
dpAlign	Perl extension to do pairwise dynamic programming sequence alignment
ipcress	Parse ipcress output and make features
isPcr	Parse isPcr output and make features
pICalculator	calculate the isoelectric point of a protein
pSW	pairwise Smith Waterman object
tRNAscanSE	A parser for tRNAscan-SE output

BioPerl-1.6.1::Bio::Tools::Run

Top

GenericParameters	An object for the parameters used to run programs
ParametersI	A Base object for the parameters used to run programs
RemoteBlast	Object for remote execution of the NCBI Blast via HTTP
StandAloneBlast	Object for the local execution of the NCBI BLAST program suite (blastall, blastpgp, bl2seq). There is experimental support for WU-Blast and NCBI rpsblast.
StandAloneNCBIBlast	Object for the local execution of the NCBI BLAST program suite (blastall, blastpgp, bl2seq). With experimental support for NCBI rpsblast.
StandAloneWUBlast	Object for the local execution of WU-Blast.
WrapperBase	A Base object for wrappers around executables

BioPerl-1.6.1::Bio::Tools::Signalp

Top

ExtendedSignalp	enhanced parser for Signalp output

BioPerl-1.6.1::Bio::Tools::SeqPattern

Top

Backtranslate	Bio::Tools::SeqPattern::Backtranslate

BioPerl-1.6.1::Bio::Tools::EMBOSS

Top

Palindrome	parse EMBOSS palindrome output

BioPerl-1.6.1::Bio::Tools::SiRNA

Top

Nothing here

BioPerl-1.6.1::Bio::Tools::SiRNA::Ruleset

Top

saigo	Perl object implementing the Saigo group's rules for designing small inhibitory RNAs
tuschl	Perl object implementing the tuschl group's rules for designing small inhibitory RNAs

BioPerl-1.6.1::Bio::Tools::Phylo

Top

Gerp	Parses output from GERP
Gumby	Parses output from gumby
Molphy	parser for Molphy output

PAML	Parses output from the PAML programs codeml, baseml, basemlg, codemlsites and yn00

BioPerl-1.6.1::Bio::Tools::Phylo::Molphy

Top

Result(2)	container for data parsed from a ProtML run

BioPerl-1.6.1::Bio::Tools::Phylo::Phylip

Top

ProtDist	parser for ProtDist output

BioPerl-1.6.1::Bio::Tools::Phylo::PAML

Top

ModelResult	A container for NSSite Model Result from PAML
Result(3)	A PAML result set object

BioPerl-1.6.1::Bio::Tools::Primer

Top

AssessorI	interface for assessing primer pairs
Feature(2)	position of a single primer
Pair(3)	two primers on left and right side

BioPerl-1.6.1::Bio::Tools::Primer::Assessor

Top

Base	base class for common assessor things

BioPerl-1.6.1::Bio::Tools::Prediction

Top

Exon(3)	A predicted exon feature
Gene(3)	a predicted gene structure feature

BioPerl-1.6.1::Bio::Tools::Sim4

Top

Exon(4)	A single exon determined by an alignment
Results(1)	Results of one Sim4 run

BioPerl-1.6.1::Bio::Tools::Spidey

Top

Exon(5)	A single exon determined by an alignment
Results(2)	Results of a Spidey run

BioPerl-1.6.1::Bio::Tools::EUtilities

Top

EUtilDataI	eutil data object interface
EUtilParameters	Manipulation of NCBI eutil-based parameters for remote database requests.
History(1)	lightweight implementation of HistoryI interface (not bound to filehandles, extraneous methods, etc).
History(2)	lightweight implementation of HistoryI interface (not bound to filehandles, extraneous methods, etc).
HistoryI	simple extension of EUtilDataI interface class for classes which hold NCBI server history data
Info	interface class for storing einfo data
Link	general API for accessing data retrieved from elink queries
Query	parse and collect esearch, epost, espell, egquery information
Summary	class for handlign data output (XML) from esummary.

BioPerl-1.6.1::Bio::Tools::EUtilities::Link	**Top**
LinkSet	class for EUtils LinkSets
UrlLink	class for EUtils UrlLinks

BioPerl-1.6.1::Bio::Tools::EUtilities::Summary	**Top**
DocSum	data object for document summary data from esummary
Item	simple layered object for DocSum item data
ItemContainerI	abtract interface methods for accessing Item information from any Item-containing class. This pertains to either DocSums or to Items themselves (which can be layered)

BioPerl-1.6.1::Bio::Tools::EUtilities::Info	**Top**
FieldInfo	class for storing einfo field data
LinkInfo	class for storing einfo link data

BioPerl-1.6.1::Bio::Tools::EUtilities::Query	**Top**
GlobalQuery	container class for egquery data

BioPerl-1.6.1::Bio::Tools::Analysis	**Top**
SimpleAnalysisBase	abstract superclass for SimpleAnalysis implementations

BioPerl-1.6.1::Bio::Tools::Analysis::Protein	**Top**
Domcut	a wrapper around Domcut server
ELM	a wrapper around the ELM server which predicts short functional motifs on amino acid sequences
GOR4	a wrapper around GOR4 protein secondary structure prediction server
HNN	a wrapper around the HNN protein secondary structure prediction server
Mitoprot	a wrapper around Mitoprot server
NetPhos	a wrapper around NetPhos server
Scansite	a wrapper around the Scansite server
Sopma	a wrapper around the Sopma protein secondary structure prediction server

BioPerl-1.6.1::Bio::Tools::Analysis::DNA	**Top**
ESEfinder	a wrapper around ESEfinder server

BioPerl-1.6.1::Bio::Tools::HMMER	**Top**
Domain	One particular domain hit from HMMER
Results(3)	Object representing HMMER output results
Set	Set of identical domains from HMMER matches

BioPerl-1.6.1::Bio::Tools::Alignment	**Top**
Consed	A module to work with objects from consed .ace files
Trim	

BioPerl-1.6.1::Bio::Restriction	**Top**
Analysis	cutting sequences with restriction enzymes

Enzyme	A single restriction endonuclease (cuts DNA at specific locations)
EnzymeCollection	Set of restriction endonucleases
EnzymeI	Interface class for restriction endonuclease
IO(10)	Handler for sequence variation IO Formats

BioPerl-1.6.1::Bio::Restriction::Enzyme

Top

MultiCut	A single restriction endonuclease
MultiSite	A single restriction endonuclease

BioPerl-1.6.1::Bio::Restriction::IO

Top

bairoch	bairoch enzyme set
base	base enzyme set
itype2	itype2 enzyme set
prototype	prototype enzyme set
withrefm	withrefm enzyme set

BioPerl-1.6.1::Bio::Symbol

Top

Alphabet	BSANE/BioCORBA compliant symbol list alphabet
AlphabetI	A Symbol Alphabet
DNAAlphabet	A ready made DNA alphabet
ProteinAlphabet	A ready made Protein alphabet
Symbol	A biological symbol
SymbolI	Interface for a Symbol