Modware: An Object-Oriented Perl Inteface to Chado

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Outline

- Chado Features and Modware
- Architectural Overview
- Sample Problem
  - Insert Chromosome
  - Insert and Update Gene/mRNAs
  - Display Gene Reports
- Other Modware Highlights
- Coming soon
- Limitations

What is in the Feature Table? (the core of Chado)

- Chromosome
- Contig
- Gene
- mRNA
- Exon
- Lots of other things - See Sequence Ontology!

Modware Features

- Multiple Feature classes

  CHROMOSOME, GENE, MRNA, CONTIG
- Each class provides type specific methods
- Logic such as building exon structure of mRNA features is encapsulated
- Parent class Modware::Feature
  - Provides common methods
  - Abstract factory for various feature types

Architectural Overview

- Object-oriented Perl interface to Chado
- Built on top of Chado::AutoDBI
- Connection handled by GMOD
- Database transactions supported
- BioPerl used to represent and manipulate sequence and feature structure
- ‘Lazy’ evaluation

Create and Insert Chromosome

```
my $seq_io = new Bio::SeqIO(
   -file   => "../data/fake_chromosome.txt",
   -format => 'fasta'
);

# Bio::SeqIO will return a Bio::Seq object which
# Modware uses as its representation
my $seq = $seq_io->next_seq();

my $reference_feature = new Modware::Feature(
   -type          => 'chromosome',
   -bioperl       => $seq,
   -description   => "This is a test",
   -name          => 'Fake',
   -source        => 'GMOD 2007 Demo'
);

# Inserts chromosome into database
$reference_feature->insert();
```

Create and Insert a Gene

1) Enter the information about the following three novel genes, including the associated mRNA structures, into your database. Print the assigned feature_id for each inserted gene.

```
Gene Feature
    symbol: x-ray
    synonyms: none
    mRNA Feature
        exon:
            start: 1703
            end: 1900
            strand: 1
            srcFeature_id:
              Id of genomic sample
```

Create and Insert a Gene

1) Enter the information about the following three novel genes, including the associated mRNA structures, into your database. Print the assigned feature_id for each inserted gene.

```
Gene Feature
  symbol: x-men
  synonyms: wolverine
  mRNA Feature
     exon_1:
        start: 12648
        end: 13136
        strand: 1
        srcFeature_id:
           Id of genomic sample
```

Create and Insert a Gene

1) Enter the information about the following three novel genes, including the associated mRNA structures, into your database. Print the assigned feature_id for each inserted gene.

```
Gene Feature
    symbol: xfile
    synonyms: mulder, scully
    description: A test gene for
                 GMOD meeting
    mRNA Feature
        exon_1:
            start: 13691
            end: 13767
            strand: 1
            srcFeature_id:
               Id of genomic sample
        exon_2:
            start: 14687
            end: 14720
             strand: 1
             srcFeature_id:
                 Id of genomic sample
```

Create and Insert a Gene

symbol: xfile
    synonyms: mulder, scully
    description: A test gene for GMOD meeting
...

```
my $gene_feature = new Modware::Feature(
   -type          => 'gene',
   -name          => 'xfile',
   -description   => 'A test gene for GMOD meeting',
   -source        => 'GMOD 2007 Demo‘
);

$gene_feature->add_synonym( 'mulder' );
$gene_feature->add_synonym( 'scully' );

# inserts object into database
$gene_feature->insert();
print 'Inserted gene with feature_id:'.$gene_feature->feature_id()."\n";
```

Create mRNA BioPerl Object

```
exon_1:
   start: 13691
   end: 13767
   strand: 1
   srcFeature_id: Id of genomic sample
```

```
exon_2:
   start: 14687
   end: 14720
   strand: 1
   srcFeature_id: Id of genomic sample
```

```
# First, create exon features (using Bioperl)
my $exon_1   = new Bio::SeqFeature::Gene::Exon (
   -start     => 13691,
   -end       => 13767,
   -strand    => 1,
   -is_coding => 1
);

my $exon_2   = new Bio::SeqFeature::Gene::Exon (
   -start     => 14687,
   -end       => 14720,
   -strand    => 1,
   -is_coding => 1
);

# Next, create transcript feature to 'hold' exons (using Bioperl)
my $bioperl_mrna = new Bio::SeqFeature::Gene::Transcript();

# Add exons to transcript (using Bioperl)
$bioperl_mrna->add_exon( $exon_1 );
$bioperl_mrna->add_exon( $exon_2 );
```

Create and Insert mRNA

The BioPerl object holds the location information, but now we want to create a Modware object and link it to the gene as well as locate it on the chromosome.

```
    # Now create Modware Feature to 'hold' bioperl object
    my $mrna_feature = new Modware::Feature(
       -type             => 'mRNA',
       -bioperl          => $bioperl_mrna,
       -source           => 'GMOD 2007 Demo',
       -reference_feature => $reference_feature
    );

    # Associate mRNA to gene (required for insertion)
    $mrna_feature->gene( $gene_feature );

# inserts object into database
    $mrna_feature->insert();
```

Writing the Report

2) Retrieve and print the following report for gene xfile

```
symbol: xfile
synonyms: mulder, scully
description: A test gene for GMOD meeting
type: gene
exon1 start: 13691
exon1 end: 13767
exon2 start: 14687
exon2 end: 14720
>xfile cds
ATGGCGTTAGTATTCATGGTTACTGGTTTCGCTACTGATATCACCCAGCGTGTAGGCTGT
GGAATCGAACACTGGTATTGTATAAATGTTTGTGAATACACTGAGAAATAA
```

```perl
use Modware::Gene;
use GMODWriter;

my $xfile_gene = new Modware::Gene( -name => 'xfile' );
GMODWriter->Write_gene_report( $xfile_gene );
```

Writing the Report

```
package GMODWriter;
sub Write_gene_report {
   my ($self, $gene)     = @_;

   my $symbol      = $gene->name();
   my @synonyms    = @{ $gene->synonyms() };
   my $syn_string  = join ",", @synonyms;
   my $description = $gene->description();
   my $type        = $gene->type();
   # get features associated with the gene that are of type 'mRNA'
   my ($mrna)      = grep { $_->type() eq 'mRNA' } @{ $gene->features() };
   # use bioperl method to get exons from mRNA
   my @exons       = $mrna->bioperl->exons_ordered();
   # Modware will return a nice fasta file for you.
   my $fasta       = $mrna->sequence( -type => 'cds', -format => 'fasta' );

   # Now print the actual report
   print "symbol: $symbol\n";
   print "synonyms: $syn_string\n";
   print "description: $description\n";
   print "type: $type\n";

   my $count = 0;
   foreach my $exon ( @exons ) {
      $count++;
      print "exon${count} start: ".$exon->start()."\n";
      print "exon${count} end: ".$exon->end()."\n";
   }
   print "$fasta";
}
. . .
```

Updating a Gene Name

3) Update the gene xfile: change the name symbol to x-file and retrieve the changed record. Regenerate gene report

```
use Modware::Gene;
use Modware::DBH;
use GMODWriter;

eval{

  # get xfile gene
  my $xfile_gene = new Modware::Gene( -name => 'xfile' );

  # change the name
  $xfile_gene->name( 'x-file' );
   # write changes to database
  $xfile_gene->update();

  # we can use the original object if we want, but instead
  # we refetch from the database to 'prove' the name has been changed
  my $xfile_gene2 = new Modware::Gene( -name => 'x-file' );
  # use our GMODWriter package to write report for x-file
  GMODWriter->Write_gene_report( $xfile_gene2 );

};
if ($@){
  warn $@;
  new Modware::DBH->rollback();
}
```

Search and Display Results

4) Search for all genes with symbols starting with "x-*". With the results produce the following simple result list (organism will vary):

```
1323    x-file  Xenopus laevis
1324    x-men   Xenopus laevis
1325    x-ray   Xenopus laevis
```

```
use Modware::Gene;
use Modware::DBH;
use GMODWriter;

# find genes starting with 'x-'
my $results = Modware::Search::Gene->Search_by_name( 'x-*' );

# write the search results
GMODWriter->Write_search_results( $results )
```

Search and Display Results

4) Search for all genes with symbols starting with "x-*". With the results produce the following simple result list (organism will vary):

```
1323    x-file  Xenopus laevis
1324    x-men   Xenopus laevis
1325    x-ray   Xenopus laevis
```

```
sub Write_search_results {
    my ($self, $itr)      = @_;

    # loop through iterator
    while ( my $gene = $itr->next() ) {
       # simply print the requested information
       print $gene->feature_id()."\t".$gene->name().
       "\t".$gene->organism_name()."\n";
    }
}
```

Delete a Gene

5) Delete the gene x-ray. Run the search and report again.

```
1323   x-file  Xenopus laevis
1324   x-men   Xenopus laevis
```

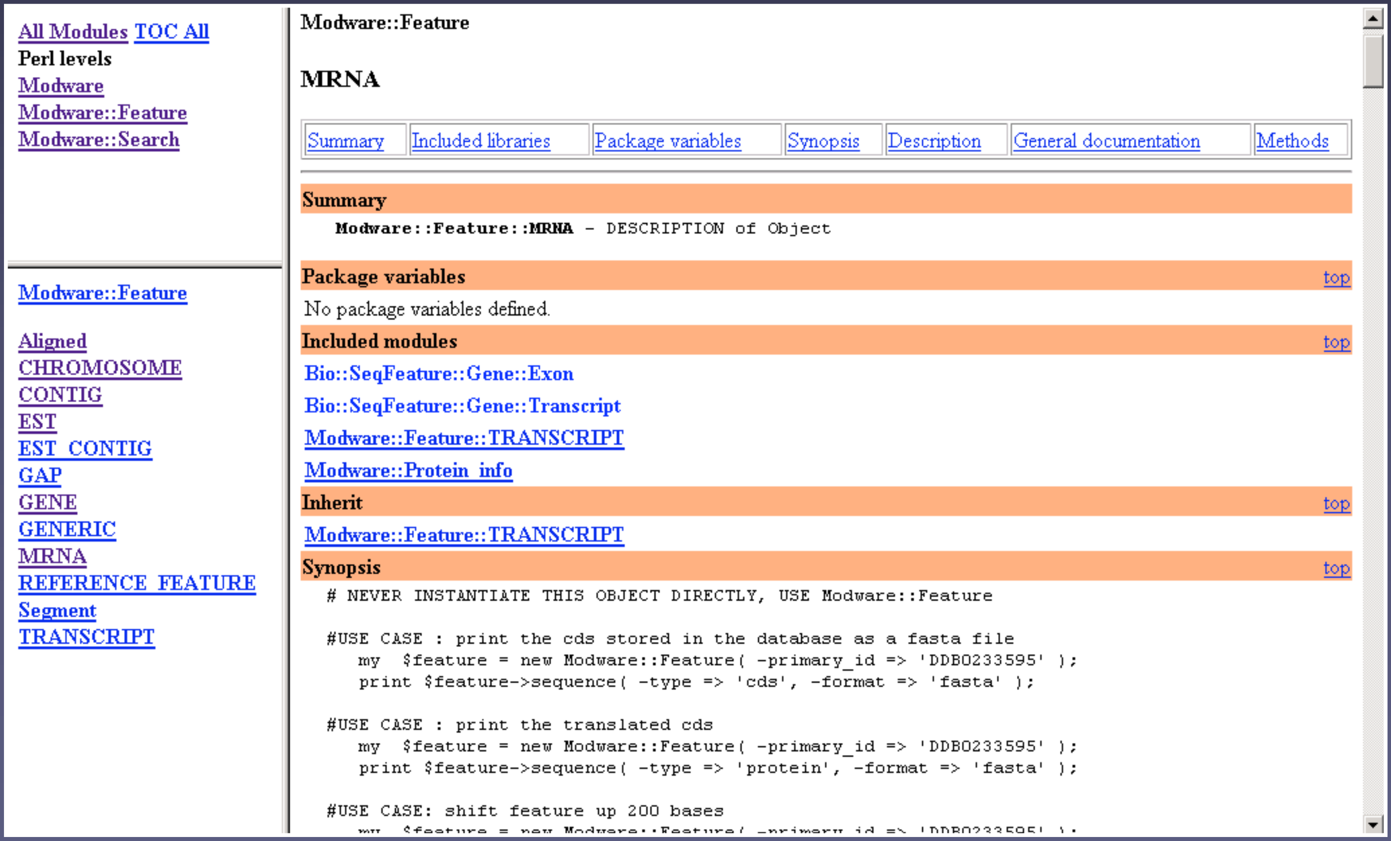
```
# get the xray gene
my $xray = new Modware::Gene( -name => 'x-ray' );

# set is_deleted = 1, this will 'hide' the gene from Searches
$xray->is_deleted(1);

# write change to database
$xray->update();

# find genes starting with 'x-'
my $results = Modware::Search::Gene->Search_by_name( 'x-*' );

# write the search results
GMODWriter->Write_search_results( $results )
```

Other Modware Highlights

- Easy to write applications with Modware
- Extensible
- Available through Sourceforge
  - http://gmod-ware.sourceforge.net
- Easy to install
- Large unit test coverage
- Current release 0.2-RC1
  - Works with GMOD's latest release
  - Sample script demoed here are available
    - sample_scripts directory

Other Nice Things About Modware

http://gmod-ware.sourceforge.net/doc/



All Modules TOC All
Perl levels
Modware
Modware::Feature
Modware::Search

Modware::Feature

Aligned
CHROMOSOME
CONTIG
EST
EST_CONTIG
GAP
GENE
GENERIC
MRNA
REFERENCE_FEATURE
Segment
TRANSCRIPT

Modware::Feature

MRNA

Summary	Included libraries	Package variables	Synopsis	Description	General documentation	Methods

Summary

```
Modware::Feature::MRNA - DESCRIPTION of Object
```

Package variables top

No package variables defined.

Included modules top

Bio::SeqFeature::Gene::Exon
Bio::SeqFeature::Gene::Transcript
Modware::Feature::TRANSCRIPT
Modware::Protein_info

Inherit top

Modware::Feature::TRANSCRIPT

Synopsis top

```
  # NEVER INSTANTIATE THIS OBJECT DIRECTLY, USE Modware::Feature

  #USE CASE : print the cds stored in the database as a fasta file
     my  $feature = new Modware::Feature( -primary_id => 'DDB0233595' );
     print $feature->sequence( -type => 'cds', -format => 'fasta' );

  #USE CASE : print the translated cds
     my  $feature = new Modware::Feature( -primary_id => 'DDB0233595' );
     print $feature->sequence( -type => 'protein', -format => 'fasta' );

  #USE CASE: shift feature up 200 bases
     my  $feature = new Modware::Feature( -primary_id => 'DDB0233595' );
```

Coming Attractions

- Support for changing genomic sequence
- ncRNAs
- UTRs
- Onotology modules
- Phenotype Annotations
- Send us your ideas!

Limitations

- Does not have full flexibility of Chado
- Not enough users to get quality feedback
- Performance (?)
- Language dependent

Acknowlegments

dictyBase

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- GMOD
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  - Brian O'connor
  - Everyone else
- BioPerl
- SGD

Why Modware Was Developed

- Each feature type requires different behavior
- Want to leave schema semantics out of application
- Want to leverage work done in BioPerl
- Re-use code developed for common use cases