**Course: Advanced Bioinformatics**

**Module title: Features and Annotations**

**Module no. : 196**

Features & Annotations

* Sequence data often comes with added information about the various properties of the sequence (Genbank, SwissProt etc).
* BioJava divides this information into global properties (Annotations) and Localized properties (Features).

Annotatable

* Annotatable is an “mix-in” interface that indicates the implementing object contains a Annotation object.
* It defines one method.
  + Annotation getAnnotation();

Annotations

* org.biojava.bio.Annotation
* Annotations are used for Global properties.
* Species, Accession Number, xrefs, date, publication.
* Key – value maps.
* Key and Value are objects but almost always are Strings.
* Annotation.EMPTY\_ANNOTATION
  + static convenience class
  + good place holder, avoids null pointer exceptions
  + immutable

Annotation API

Map [**asMap**](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\Annotation.html)()   
Return a map that contains the same key/values as this Annotation.

boolean [**containsProperty**](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\Annotation.html)(java.lang.Object key)   
Returns whether there the property is defined.

Object [**getProperty**](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\Annotation.html)(java.lang.Object key)   
Retrieve the value of a property by key.

Set [**keys**](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\Annotation.html)()   
Get a set of key objects.

void [**removeProperty**](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\Annotation.html)(java.lang.Object key)   
Delete a property

void [**setProperty**](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\Annotation.html)(java.lang.Object key, java.lang.Object value)   
Set the value of a property.

FeatureHolder

* FeatureHolder is another “mix-in” interface which allows the implementing object to hold Features.
* Sequence implements FeatureHolder.
* Features are created by FeatureHolders.
* FeatureHolders can be filtered

FeatureHolder Methods

boolean [**containsFeature**](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\FeatureHolder.html)([Feature](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\Feature.html) f)   
Check if the feature is present in this holder.

int [**countFeatures**](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\FeatureHolder.html)()   
Count how many features are contained.

[Feature](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\Feature.html) [**createFeature**](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\FeatureHolder.html)([Feature.Template](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\Feature.Template.html) ft)   
 Create a new Feature, and add it to this FeatureHolder.

Iterator [**features**](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\FeatureHolder.html)()   
 Iterate over the features in no well defined order.

[FeatureHolder](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\FeatureHolder.html) [**filter**](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\FeatureHolder.html)([FeatureFilter](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\FeatureFilter.html) filter)   
 Query this set of features using a supplied FeatureFilter.

[FeatureHolder](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\FeatureHolder.html) [**filter**](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\FeatureHolder.html)([FeatureFilter](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\FeatureFilter.html) fc, boolean recurse)   
 Return a new FeatureHolder that contains all of the children of this one that passed the filter fc.

[FeatureFilter](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\FeatureFilter.html) [**getSchema**](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\FeatureHolder.html)()   
Return a schema-filter for this FeatureHolder.

void [**removeFeature**](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\FeatureHolder.html)([Feature](file:///\\PHSGRI-S3002\schrema6$\src\cvs\biojava-live\doc\org\biojava\bio\seq\Feature.html) f)   
 Remove a feature from this FeatureHolder.

Features may be nested

* Features implement FeatureHolder!
  + Therefore Features may hold nested Features
  + c.f. The AWT Menu is a MenuItem
  + e.g. A gene has exons and introns
  + Filtering can be recursive
  + A Feature *cannot* hold itself (directly or indirectly)