PhyloGeoRef Manual

Google Summer of Code 2010, 2011.

Downloading and Setting Up the Environment

Using phyloGeoRef is easy. You can obtain phyloGeoRef from
https://github.com/dapurv5/phyloGeoRef/

This can be directly opened up as a netbeans project. If you want to use the library in your own application then the best way would be to obtain the jar for the project and include it in the classpath for your project. (phyloGeoRef/dist/phyloGeoRef.jar)
If however you want to create rich kml from your phylogenetic data then you need to write a Main class.

To use the library the following jars must be placed in the classpath for the project.

1. activation.jar
2. jaxb-api.jar
3. jaxb-impl.jar
4. jsr173_1.0_api
5. JavaAPIforKml.jar
6. Junit-4.8.2.jar

For convenience of the users these jars are placed in phyloGeoRef/dist/lib folder. To place them in the classpath Right click the project -> Properties -> Libraries -> Add JAR/Folder. Browse to the location of these jars and add them.

If you want to obtain the latest versions of these jars download the following.

- JAXB2_200xxxxx.jar (https://jaxb.dev.java.net/)
  Unjar it using the command. java –jar JAXB2_200xxxxx.jar
  In windows if you have WinZip installed you can unzip it simply via right clicking and choosing extract here.
  The libraries that are needed in the classpath are found in jaxb-ri-200xxxxx/bin created after doing the above procedure.

- JavaAPIforKml.jar (http://code.google.com/p/javaapiforkml/downloads/list)

Now that we have resolved all reference problems we can move on to write some code.

Input File Formats Supported

There are two input files required by the program

1) Tree file
2) Geospatial/Metadata file

The tree file contains the tree structure i.e. the nodes and the parent child relationship between them. If the lengths of the edges are to be used they must also be given in the tree file itself. Tree files in the following formats are supported.
NeXML, nwk, nexus, phyloxml, tol, nhx.

The geospatial/metadata file contains the location information and other metadata that might be attached to each of the taxonomic units. If the clade information is to be used then it must also be given in the metadata file itself. Metadata files in the following formats are supported.
csv, txt.

There are a few sample files placed in the /samples folder.
See the samples/treeHypothetical/tree.xml file and samples/treeHypothetical/tree.nwk file. Both these files represent the same tree in two different formats namely NeXML format and newick file format respectively.

See the samples/treeHypothetical/test.csv file.
This is a sample metadata file in the csv format. The first line must contain the tags or the column name. It is not mandatory to have the label as the first column and latitude as the second and longitude as the third. The library allows the freedom of using any type order of tags in the input metadata file. However before using the library it must be specified to the library which columns correspond to what values in the metadata file.

Writing a Main class

If you want to create kml files using the library you need to create a Main class named Phylogeoref.

```
public class Phylogeoref{
    public static void main(String...args) throws Throwable{
    //Place the code here.
    }
}
```

Before writing the main code, we need to setup the logger. To setup the logger copy paste the following code in your class. Now the overall class looks like.

```
/**
 * Main class
 * @author apurv
 */
public class Phylogeoref {

    private final static Logger LOGGER = Logger.getLogger("nescent");

    static{
        setupLogger(); //Setup the logger at class load
    }

    /**
   * Sets up the logger.
   */
    private static void setupLogger(){
        LOGGER.setLevel(Level.ALL);
        try {
                FileHandler fhandler = new FileHandler("Logfile.txt");
                SimpleFormatter sformatter = new SimpleFormatter();
                fhandler.setFormatter(sformatter);
                LOGGER.addHandler(fhandler);

        } catch (IOException ex) {
            LOGGER.log(Level.SEVERE, ex.getMessage(), ex);
        } catch (SecurityException ex) {
            LOGGER.log(Level.SEVERE, ex.getMessage(), ex);
        }
    }

    /**
   * Utility main method, used for testing this file during development.
   * @param args
   * @throws Throwable
   */
    public static void main(String...args) throws Throwable{
    //Place the code here.
    }
}
```

The setupLogger() function sets up the logger. Setting up a logger is a good practice as all the logs get recorded in a log file. In our case a Logfile.txt gets created which contains all the logs.

Now we need to put the code in the main() function.

The phyloGeoRef pipeline consists of four essential steps.

i. read (nescent.phylogeoref.reader)
ii. validate (nescent.phylogeoref.validator)
iii. process (nescent.phylogeoref.processor)
iv. write (nescent.phylogeoref.writer)

The source code has been organized in a way to modularize each of the steps in the pipeline.

Reading

Create the files which are to be read as.

```
File treeFile = new File("samples\\treeHypothetical\\tree.nwk");
File metaFile=new File("samples\\treeHypothetical\\test.csv");
```

It is to be noted that the path has been specified for a windows machine. On a Linux machine you need to do something slightly different.

```
File treeFile = new File("samples/treeHypothetical/tree.nwk");
File metaFile=new File("samples/treeHypothetical/test.csv");
```

Linux used forward slashes in path.

The treeFile may contain multiple trees in it. But the metaFile is required to contain the metadata for a single tree therefore an array of metafiles needs to be prepared.

```
File[] metaFiles = new File[]{metaFile};
```

Now we can use the GrandUnifiedReader class which wraps all the reading capabilities provided by the other classes in the package.

```
GrandUnifiedReader gur = new GrandUnifiedReader();
```

Create an instance of the GrandUnifiedReader class.

```
gur.setTreeFile(treeFile).setMetaFile(metaFiles).setDelim(',').setCladeDiv(4)
```

Set the various parameters for it.

setDelim() sets the delimeter for the metadata file. A csv file normally uses a comma as the delimiter. If the metadata file is a text file and the delimiter character is a tab then you can specify it as `setDelim('\t')`

setCladeDiv(4) is used to specify that the 4th column in the input metadata file will be used as the clade of the specie. You can also choose not to specify this in which case all the nodes will be colored in the same color.

The next thing to do is to tell the program which columns mean what in the input metadata file.

```
gur.setArgs(1,2,3);
```

args[0] = 1 , the 1st column contains the labels for the species. These uniquely define each of the species and should be the same as those used as in the input tree file.

args[1] = 2, the 2nd column contains the latitude values.
args[2] = 3, the 3rd column contains the longitude values.

Having configured the GrandUnifiedReader now invoke the following function to build the phylogenies.

```
gur.buildUnifiedPhylogeny();
```

This command does all the internal construction work done. A phylogeny and a mould map gets built which can be extracted as

```
Phylogeny phyArray[] =  gur.getPhylogenyArray();
Map mouldMapArray[] = gur.getMouldMaps();
```

If you are sure that the tree file contains only a single phylogeny then you can use.

```
Phylogeny phy = gur.getPhylogeny();
Map mouldMap = gur.getMouldMap();
```

The mouldMap is map from the name of the taxonomic unit to the mould associated with that taxonomic unit. Each named taxonomic unit has an external mould attached with it. This mould contains additional information for the taxonomic unit, like clade and the number of observations, etc. Having obtained the phylogeny and the mould map the reading part is over.

Validating and Processing

The validation and processing steps are combined into a single class. Obtain an instance of the PhylogenyProcessor through its factory in the following manner.

```
PhylogenyProcessor processor = ProcessorFactory.getInstance(false);
```

A false value indicates that weights are not associated with the edges. That is edge lengths are not given for the edges, or if given they are not to be used in any processing.

Now you need to phylogenify the phylogeny.

```
processor.phylogenify(phy);
```

Phylogenify means to assign location and color values to the internal nodes in the phylogeny. A false value specified before means that the midpoints will be non weighted. A true value indicates that a weighted mean algorithm is to be used.

Writing

The last step requires writing the phylogeny into a kml. This is done via the AdvancedKmlWriter.

```
AdvancedKmlWriter kmlw = new AdvancedKmlWriter(PaintStyle.HIERARCHICAL);
```

Here we also need to specify a PaintStyle. Two kinds of PaintStyles are supported at present. HIERARCHICAL and LEVELWISE. LEVELWISE divides the kml drawn into folders for each level, whereas HIERARCHICAL draws it hierarchically.

You can create the kml or you can also prepare a compressed kmz file.

```
kmlw.createKMZ(phy, mouldMap, "mojo");
```

Here mojo is the name of the kmz file that is to be created. To create an uncompressed KML invoke the createKML() method as.

```
kmlw.createKML(phy, mouldMap, "mojo");
```

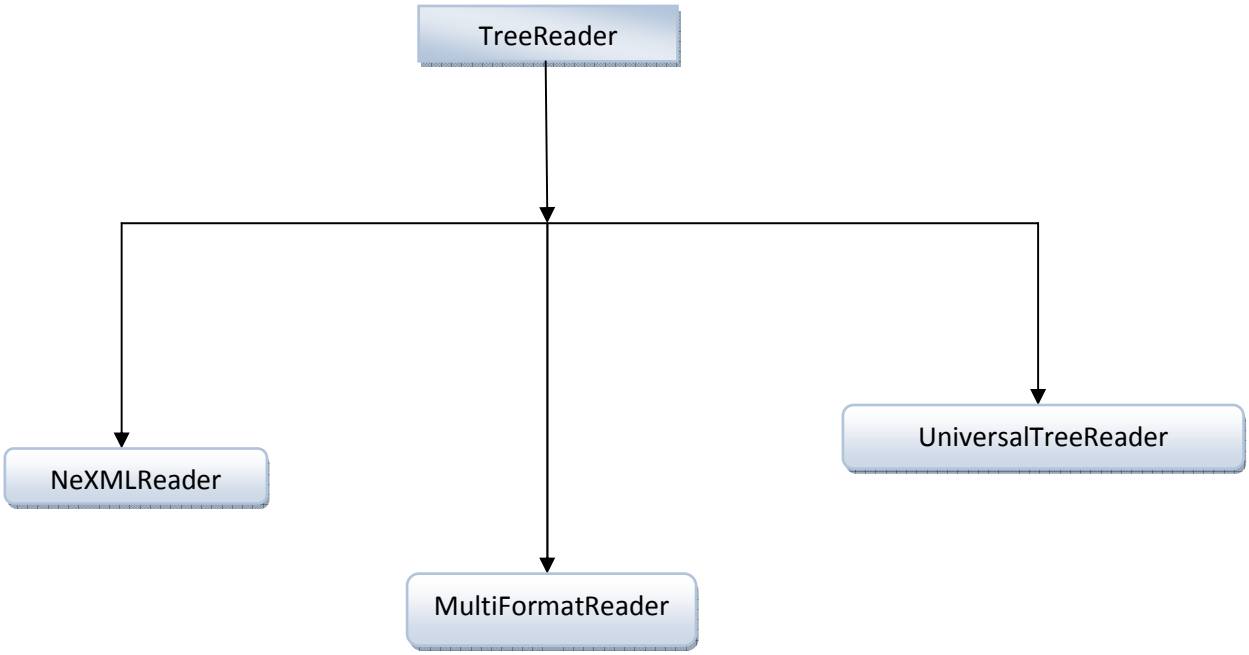
The next section deals with the internal details about the library. See src/nescent/DemoMain.java

Caveat

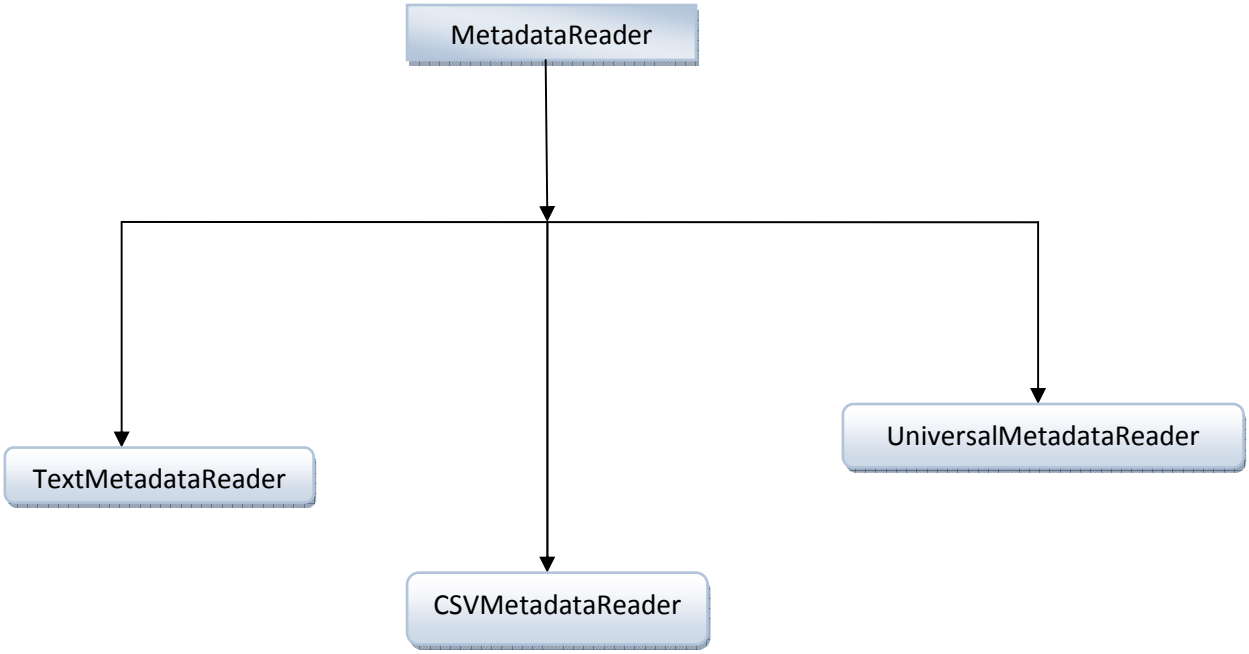
The org.forester library used with the project has some problems which have been overlooked. Though these errors do not raise any concerns because they are not used by the nescent library.
Here are the errors.
Some of the lines in the class in the file org/forester/application/nj.java have been commented. Search for “TODO” to find the exact lines that have been commented. These lines refer to components that do not exist in the org.forester library.

Understanding the Reader

This section explains how the reader component has been written and how it functions. The nescent.phylogeoref.reader package contains all the classes for reading input files. Here is the class diagram.



The NeXMLReader uses a NeXMLEngine behind it to construct a phylogeny from a NeXML file. Any kind of new TreeReader should inherit from TreeReader interface and the UniversalTreeReader must also be modified slightly to accommodate the new type.



Any kind of new MetadataReader should inherit from this interface and suitable changes must be made to the UniversalMetadataReader to accommodate the new MetadataReader type.

The GrandUnifiedReader class combines the power of UniversalTreeReader and UniversalMetadataReader into a single class. First the UniversalTreeReader prepares a raw phylogeny from the tree file specified. In the second step the GrandUnifiedReader uses the PhylogenyKitchen to cook the raw phylogeny.

Adding Custom Properties

The PhylogenyKitchen has the following predefined properties.

```
private final static String[] PROPERTIES = {"label",
                                            "latitude",
                                            "longitude",
                                            "id",
                                            "sname",     //Scientific Name
                                           };
```

Do not change the order of these properties. This is the order that is followed when you specify the column meanings in setArgs(). This is the reason why args[0] is to be given the column number for the label. args[1] the column label for latitude and so on.
You can also add custom properties to it. Suppose you wish to add a custom property common name in it. Then add a variable for common name in this array.

```
private final static String[] PROPERTIES = {"label",
                                            "latitude",
                                            "longitude",
                                            "id",
                                            "sname",     //Scientific Name
                                            "cname",     //Common Name
                                           };
```

Now while specifying the setArgs() you need to specify the column number for cname also. To use this property go to the method

```
setNodeData(NodeData nodeData, PhylogenyMould mould)
```

Here you can simply obtain the value of that property as `get("cname")`

```
taxo.setCommonName(get("cname"));
```

P.S. Append the custom properties only at the end of the array and not in between. Also see https://github.com/dapurv5/phyloGeoRef/wiki/Tutorial:-Using-the-GrandUnifiedReader,-adding-new-properties.

Understanding the Validator

The validator checks for the following errors.

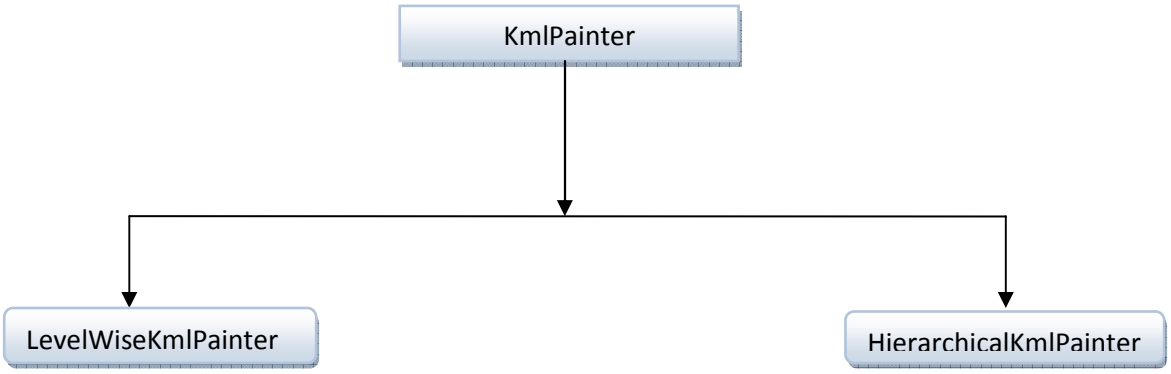
1. Tree Structure i.e. the number of children for each internal node should be at least 2
2. Latitude/Longitude values within proper bounds
3. If weighted mean algorithm is to be used then each edge should have a positive edge length associated with it.
4. Each of the external nodes must have their location information.

Understanding the Processor

The processor assigns location and color information to the internal nodes. Two kinds of processors exist. Weighted and Unweighted. The current algorithm used for finding the location of HTUs (Hypothetical Taxonomic Units) is average of latitude and longitude information. The ComputeUtility class provides the method for finding the mean longitude position. The mean is calculated in a manner so as to contain the longitude of the parent node within the bounds of the longitudes of the child nodes.

See http://www.geomidpoint.com/calculation.html

Understanding the Writer



LevelWiseKmlPainter draws the kml levelwise. Each level of the phylogenetic tree is drawn in a separate folder whereas a **HierarchicalKmlPainter** draws the tree hierarchically.
The various constants used in the drawing of kml are placed in nescent.phylogeoref.utility.**KmlConstants**
The **HTMLParlour** class prepares the HTML content that is placed in the balloons with each placemark.

Future Improvements

1. Using web services to get images for the species.
2. Adding Animations
3. Changing the centroid algorithm
4. Validating the complete NeXML file via HTTP.
5. Using confidence values in the kml