

DIAGRAMA 2:

public class Project {

| members

public void name;

public void description;

Source [] source;

Reference Sequence [] reference_sequence;

Feature [] feature;

Alignment [] alignment;

}

public class Source {

public String name;

Sequence [] sequence;

}

public class Sequence {

public String sequence_id;

public String format;

}

public class Alignment {

public String name;

public String display_name;

public String description;

AlignmentMember [] alignment_member;

}

public class AlignmentMember {

public String reference;

AlignmentSegment [] alignment_segment;

}

```
public class AlignedSegment {  
    public String) refStart;  
    public String) refEnd;  
    public String) memberStart;  
    public String) memberEnd;  
}
```

```
public class ReferenceSequence {
```

```
    public String) name;  
    public String) displayName;
```

```
featureLocation [ ] featureLocation;
```

```
}
```

E amazgut

```
public class FeatureLocation {
```

```
    FeatureSegment [ ] featureSegments;
```

```
    Variation [ ] variations;
```

```
}
```

```
public class Variation {
```

```
    public String) name;
```

```
    public String) displayName;
```

```
    public String) description;
```

```
    public String) commonModuleName;
```

```
    public String) translationType;
```

```
    PatternLocation [ ] patternLocations;
```

```
}
```

```
public class PatternLocation {
```

```
    public String) refStart;
```

```
    public String) end;
```

```
    public String) pattern;
```

```
}
```

public class FeatureSegments {

 public String) refStart;

 public String refEnd;

}

public class Feature {

 public String) name;

 public String display-name;

 public String) description;

}

Diagrama 3

import java.util.ArrayList;

public class Population {

 public String) race;

 public String etnia;

 public String linguagem_primitiva;

 public String linguagem_familiar;

 ArrayList <taxon> taxon;

}

public class Individual extends Population {

 public String id_pai;

 public String id_mae;

 public String user;

 public String) data_comiversario;

 public String) data_falecimento;

}

```
public class Painel extends Population {
```

```
    public long tamanho;
```

```
    public String unidade_contagem;
```

```
    public Boolean organizacao;
```

```
    public String tipo;
```

```
    ArrayList<Painel> painel,
```

```
}
```

```
import java.util.ArrayList
```

```
public class Molecular_Sample {
```

```
    public String molecule;
```

```
    Population population;
```

```
    ArrayList<Molecular_Sample> molecular_sample;
```

```
    ArrayList<Anatomic_Location> anatomic_location;
```

```
}
```

```
import java.util.ArrayList;
```

```
public class Anatomic_Location {
```

```
    ArrayList<Molecular_Sample> molecular_sample;
```

```
}
```

```
import java.util.ArrayList;
```

```
public class Token {
```

```
    public String rank;
```

```
    public String nome_certificado;
```

```
    ArrayList<Population> Population,
```

```
}
```

```
import java.util.ArrayList
```

```
public class Geographic_Location {
```

```
    public double max_longitude;
```

```
    public double max_latitude;
```

```
    public double min_longitude;
```

```
    public double min_latitude;
```

```
    ArrayList<Population> population; }
```