

Diagrama 1

```
public interface Collection {  
    public void equals();  
    } public void add();
```

```
public interface list extends Collection {  
    } public void get();
```

```
public class Pedido implements list {  
    } public static void Itens de linha [*]
```

```
public class Abstractlist implements list {  
    public void equal();  
    public void get();  
    } public void add();
```

```
public class Arraylist extends Abstractlist {  
    } public void get();  
    } public void add();
```

Diagrama 2

```
public class Project {  
    public void name;  
    public void description;  
    source [] sources;  
    ReferenceSequence [] referencesequences;  
    Feature [] features  
    Alignment [] alignments;  
}  
  
public class Source {  
    public String name;  
    Sequence [] sequences;  
}  
  
public class Sequence {  
    public String sequence id;  
    public String format;  
}  
  
public class Alignment {  
    public String name;  
    public String display name;  
    public String description;  
    AlignmentMember [] alignmentmembers;  
}  
  
public class AlignMember {  
    public String reference;  
    AlignedSegment [] alignedsegment;  
}
```

```
public class AlignSegment {
    public String refStart;
    public String refEnd;
    public String memberStart;
    public String memberEnd;
}

public class ReferenceSequence {
    public String name;
    public String displayName;
    } featureLocation [] featureLocation

public class featureLocation {
    FeatureSegment [] featureSegments;
    Variation [] variations;
}

public class Variation {
    public String name;
    public String displayName;
    public String description;
    public String scannerModuleName;
    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 displayName;  
    public String description;
```

Diagrama 3

Population

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

```
public class Population {  
    public String raca;  
    public String etnia;  
    public String linguagemPrimaria;  
    public String linguagemFamiliar;  
    ArrayList<Taxon> taxon;  
}
```

Individual

```
public class Individual extends Population {  
    public String idPai;  
    public String idMae;  
    public String sexo;  
    public String dataAnversario;
```

```
public int data - document;
```

Painel

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

```
public class Painel extends Population {  
    public long tamanho;  
    public String unidade - contagem;  
    public Boolean organizacao;  
    public String tipo;  
    ArrayList < Painel > painel;  
}
```

Molecular

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

```
public class Molecular - Sample {
```

```
    public String molecule;
```

```
    Population population;
```

```
    ArrayList < Molecular - Sample > molecular - sample;
```

```
    ArrayList < Anatomic - Location > anatomic - location;
```

```
}
```

Anatomic

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

```
public class Anatomic - Location {
```

```
    ArrayList < Molecular - Sample > molecular - sample }
```

Taxon

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

```
public class Taxon {  
    public String rank;  
    public String nome_cientifico;  
    ArrayList<Population> Population;  
}
```

Geographic

```
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;  
}
```