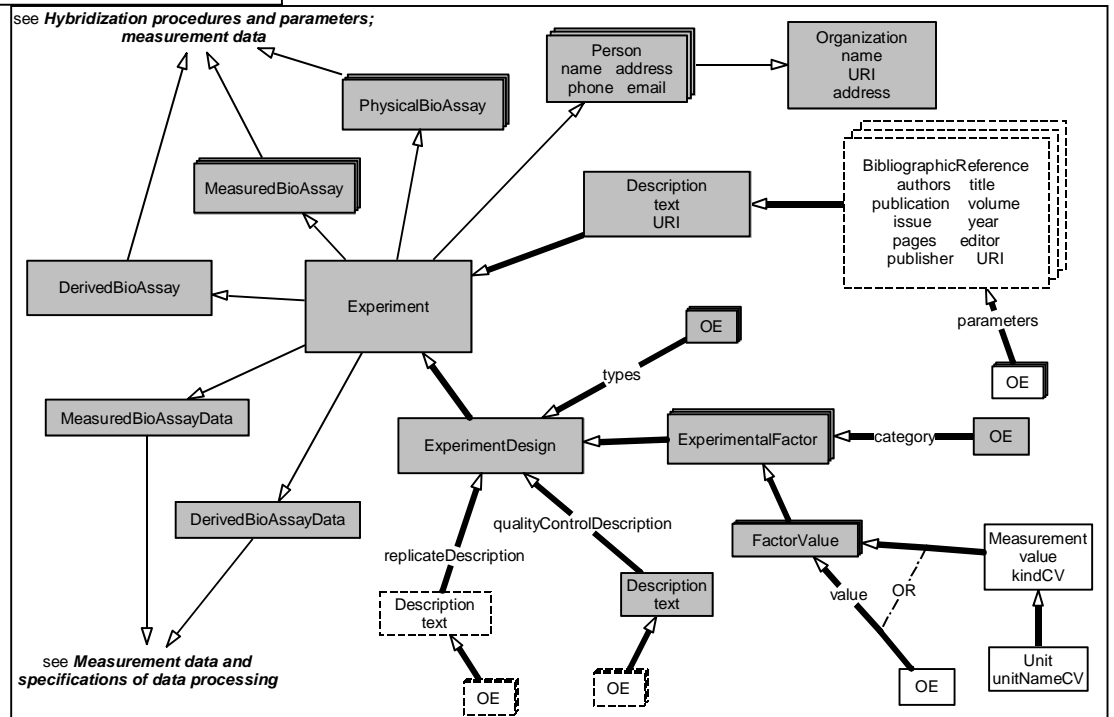
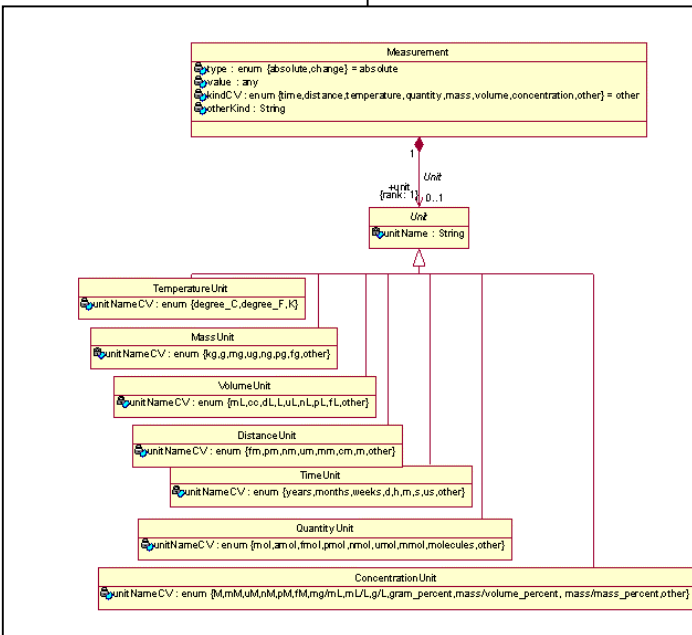
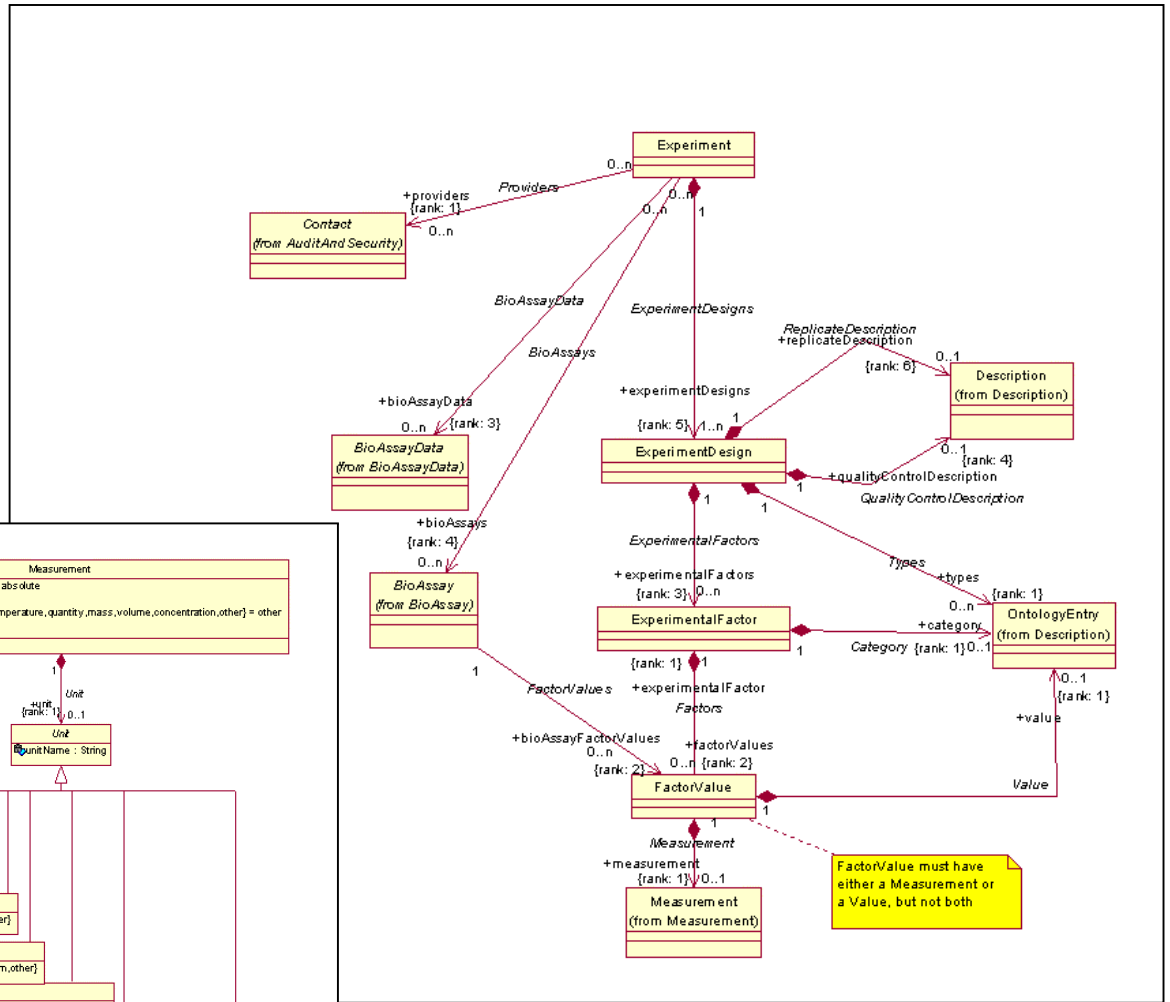


Experimental design - diagrams



Experimental design - DTD

```
<!ELEMENT Experiment_package (Experiment_assnlist?) >
<!ELEMENT Experiment_assnlist (Experiment+) >
<!ELEMENT Experiment (...Descriptions_assnlist?,...Providers_assnreflist?,...BioAssayData_assnreflist?,
    BioAssays_assnreflist?,ExperimentDesigns_assnlist) >
<!ATTLIST Experiment
    identifier CDATA #REQUIRED
    name CDATA #IMPLIED >
<!ELEMENT Providers_assnreflist (Person_ref+) >
<!ELEMENT BioAssayData_assnreflist ((DerivedBioAssayData_ref |
    MeasuredBioAssayData_ref)+) >
<!ELEMENT ExperimentDesigns_assnlist (ExperimentDesign+) >

<!ELEMENT ExperimentDesign (...Types_assnlist?,...ExperimentalFactors_assnlist?,
    QualityControlDescription_assn?,...ReplicateDescription_assn?) >
<!ELEMENT ExperimentalFactors_assnlist (ExperimentalFactor+) >
<!ELEMENT QualityControlDescription_assn (Description) >
<!ELEMENT ReplicateDescription_assn (Description) >

<!ELEMENT ExperimentalFactor (...Category_assn?,FactorValues_assnlist?,...) >
<!ATTLIST ExperimentalFactor
    identifier CDATA #REQUIRED
    .. >

<!ELEMENT Category_assn (OntologyEntry) >
<!ELEMENT FactorValues_assnlist (FactorValue+) >

<!ELEMENT FactorValue_ref EMPTY >
<!ATTLIST FactorValue_ref identifier CDATA #REQUIRED >
<!ELEMENT FactorValue (...,(Measurement_assn? | Value_assn?)) >
<!ATTLIST FactorValue
    identifier CDATA #REQUIRED
    .. >
<!ELEMENT Measurement_assn (Measurement) >
<!ELEMENT Value_assn (OntologyEntry) >

<!ELEMENT Measurement (Unit_assn?) >
<!ATTLIST Measurement
    type (absolute | change) "absolute"
    value CDATA #IMPLIED
    kindCV (time|distance|temperature|quantity|mass|volume|concentration|other) "other"
    otherKind CDATA #IMPLIED >
<!ELEMENT Unit_assn (TimeUnit|DistanceUnit|TemperatureUnit|QuantityUnit|MassUnit|VolumeUnit|ConcentrationUnit) >

<!ELEMENT TimeUnit (...) >
<!ATTLIST TimeUnit
    unitName CDATA #IMPLIED
    unitNameCV (years|months|weeks|d|h|m|s|us|other) #REQUIRED >

<!ELEMENT DistanceUnit_assn (DistanceUnit) >
<!ELEMENT DistanceUnit (...) >
<!ATTLIST DistanceUnit
    unitName CDATA #IMPLIED
    unitNameCV (fm|pm|nm|um|mm|cm|m|other) #REQUIRED >

<!ELEMENT TemperatureUnit (...) >
<!ATTLIST TemperatureUnit
    unitName CDATA #IMPLIED
    unitNameCV (degree_C|degree_F|K) #REQUIRED >

<!ELEMENT QuantityUnit (...) >
<!ATTLIST QuantityUnit
    unitName CDATA #IMPLIED
    unitNameCV (mol|amol|fmol|pmol|nmol|umol|mmol|molecules|other) #REQUIRED >

<!ELEMENT MassUnit (...) >
<!ATTLIST MassUnit
    unitName CDATA #IMPLIED
    unitNameCV (kg|g|mg|ug|ng|pg|fg|other) #REQUIRED >

<!ELEMENT VolumeUnit (...) >
<!ATTLIST VolumeUnit
    unitName CDATA #IMPLIED
    unitNameCV (mL|cc|dL|L|uL|nL|pL|fL|other) #REQUIRED >

<!ELEMENT ConcentrationUnit (...) >
<!ATTLIST ConcentrationUnit
    unitName CDATA #IMPLIED
    unitNameCV (M|mM|uM|nM|pM|fM|mg_per_mL|mL_per_L|g_per_L|
        gram_percent|mass_per_volume_percent|mass_per_mass_percent|other) #REQUIRED >
```

Experimental design - example

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE Experiment_package PUBLIC "-//OMG//DTD MAGE-ML 1.1//EN"
"http://schema.omg.org/lsr/gene_expression/1.1/MAGE-ML.dtd" >

<!--MAGE-ML Good Practice Guidelines-->
<!--MAGE-ML Good Practice tag: to highlight recommended encoding-->
<!--MIAME requirement tag: to indicate content requirement-->
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->

<Experiment identifier="ebi.ac.uk:MIAMExpress/Experiment:E-MEXP-#">
  <Descriptions_assnlist>
    <Description URI="" text="description">

    <BibliographicReferences_assnlist>
      <!--MIAME requirement (if Publication exists-Provide Bibliographic Reference)-->
      <BibliographicReference URI="my uri"
        authors="my name"
        editor="my editor"
        issue="my issue"
        pages="my pages"
        publication="my publication"
        publisher="my publisher"
        title="my title"
        volume="my volume"
        year="my year">

      <!--MO Rules: requires MO rules for appropriate coding-->
      <!--MO TERMS: use of MGED Ontology instances required -->
      <Parameters_assnlist>
        <OntologyEntry category="PublicationType" value="journal_article"/>
      </Parameters_assnlist>
    </BibliographicReference>
  </BibliographicReferences_assnlist>

</Description>
</Descriptions_assnlist>

<Providers_assnreflist>
  <!--MIAME requirement- Mandatory>
  <!--MAGE-ML Good Practice:-- Mandatory >
  <Person_ref identifier="ebi.ac.uk:MIAMExpress/Person:<object>"/>
  <Organization_ref identifier=" ebi.ac.uk:MIAMExpress/Organization:<object>"/>
</Providers_assnreflist>

<BioAssayData_assnreflist>
  <!--MAGE-ML Good Practice:--Strongly Recommended-->
  <!--Provide references to ALL BioAssayData objects (MeasuredBioAssayData and
DerivedBioAssayData in Experiment Package even if not required by DTD-->
  <!--enhances data retrieval options-->
  <MeasuredBioAssayData_ref
identifier="ebi.ac.uk:MIAMExpress/MeasuredBioAssayData:<object>"/>
  <DerivedBioAssayData_ref
identifier="ebi.ac.uk:MIAMExpress/MeasuredBioAssayData:<object>"/>
</BioAssayData_assnreflist>

<BioAssays_assnreflist>
  <!--MAGE-ML Good Practice:-- :--Strongly Recommended-->
  <!--Provide all references to BioAssays objects in Experiment Package even if not
required by DTD-->
  <!--enhances data retrieval options-->
  <PhysicalBioAssay_ref identifier="ebi.ac.uk:MIAMExpress/PhysicalBioAssay:<object>"/>
```

```

    <MeasuredBioAssay_ref identifier="ebi.ac.uk:MIAMExpress/MeasuredBioAssay:<object>" />
    <DerivedBioAssay_ref identifier="ebi.ac.uk:MIAMExpress/DerivedBioAssay:<object>" />
</BioAssays_assnreflist>

<ExperimentDesigns_assn>
  <ExperimentDesign>
    <!--MGED TERMS: -->
    <Types_assnlist>
    <OntologyEntry category="EpidemiologicalDesign" value="family_history_design"/>
    </Types_assnlist>

    <ExperimentalFactors_assnlist>
    <!--MIAME requirement-->
    <!--MAGE-ML Good Practice:-->
    <!--Declare here all variables (factor and values) related to the experiment-->
    <!--MAGE-ML Good Practice: all Factor Values should be recalled at the Level of
BioAssays-->
    <!--MAGE-ML Good Practice: see also BioAssays Package for more information-->
    <ExperimentalFactor identifier="ebi.ac.uk:MIAMExpress/ExperimentalFactor:<object>">

<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
    <Category_assn>
    <OntologyEntry category="BiologicalFactorCategory" value="Compound"/>
    </Category_assn>

    <FactorValues_assnlist>

    <!--For Qualitative Values, use OntologyEntry association-->

        <FactorValue identifier="ebi.ac.uk:MIAMExpress/FactorValue:$compound"
name="$compound">
<!--MO Rules: requires MO rules for appropriate coding-->
        <Value_assn>
        <OntologyEntry category="Compound" value="$compound">
        </OntologyEntry>
        </Value_assn>
        </FactorValue>
    </FactorValues_assnlist>

        <ExperimentalFactor identifier="ebi.ac.uk:MIAMExpress/ExperimentalFactor:Duration"
name="Duration of Exposure">
        <Category_assn>
        <OntologyEntry category="BiologicalFactorCategory" value="Time"/>
        </Category_assn>
        <FactorValues_assnlist>

    <!--For Quantitative Values, use the Measurement association-->

        <FactorValue identifier="ebi.ac.uk:MIAMExpress/FactorValue:$duration"
name="$duration">
        <Measurement_assn>
        <Measurement kindCV="time" type="absolute" value="$duration_value">
        <Unit_assn>
        <TimeUnit unitName="Hours" unitNameCV="h"/>
        </Unit_assn>
        </Measurement>
        </Measurement_assn>
        </FactorValue>
    </FactorValues_assnlist>
    </ExperimentalFactor>
</ExperimentalFactors_assnlist>

```

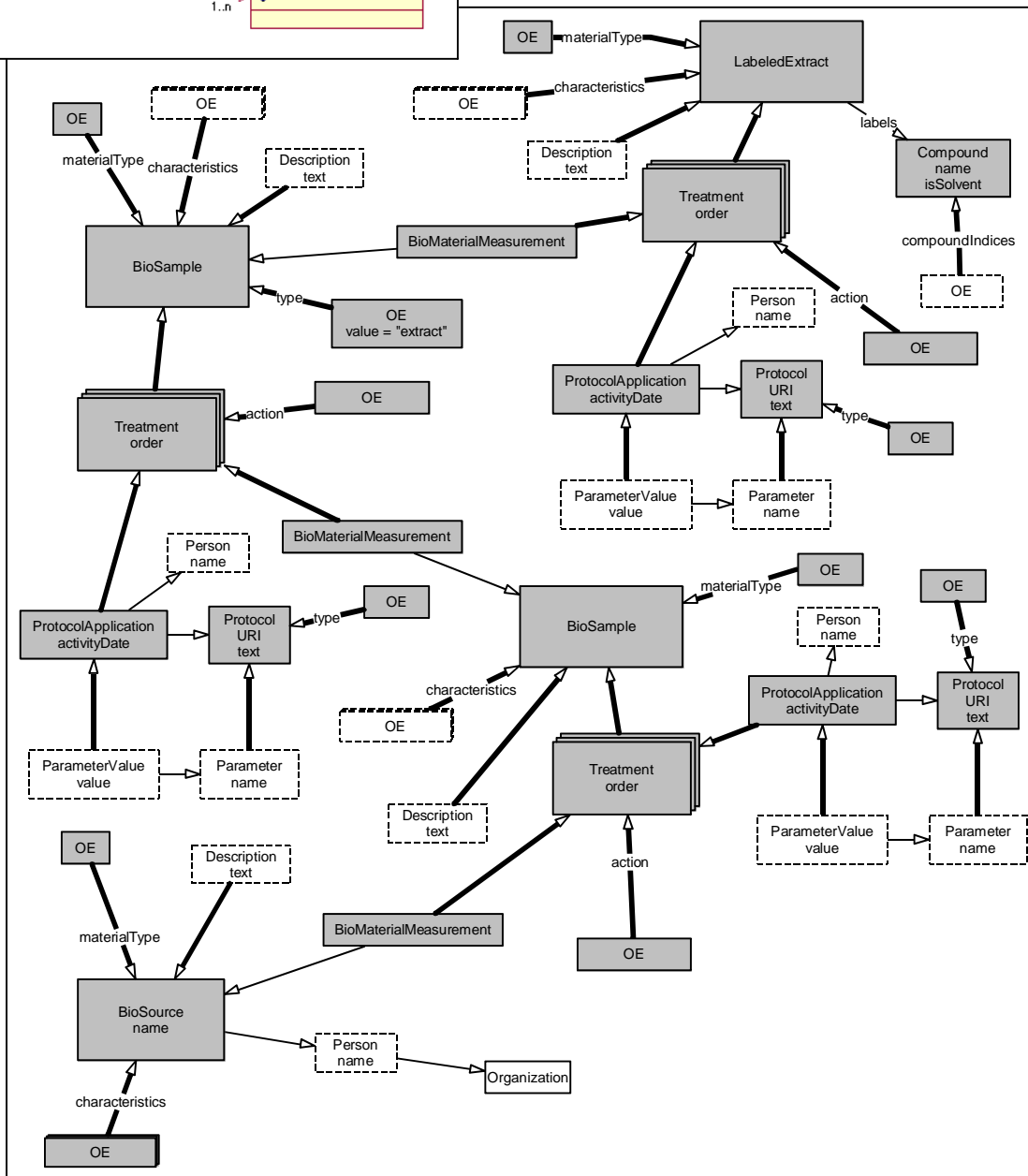
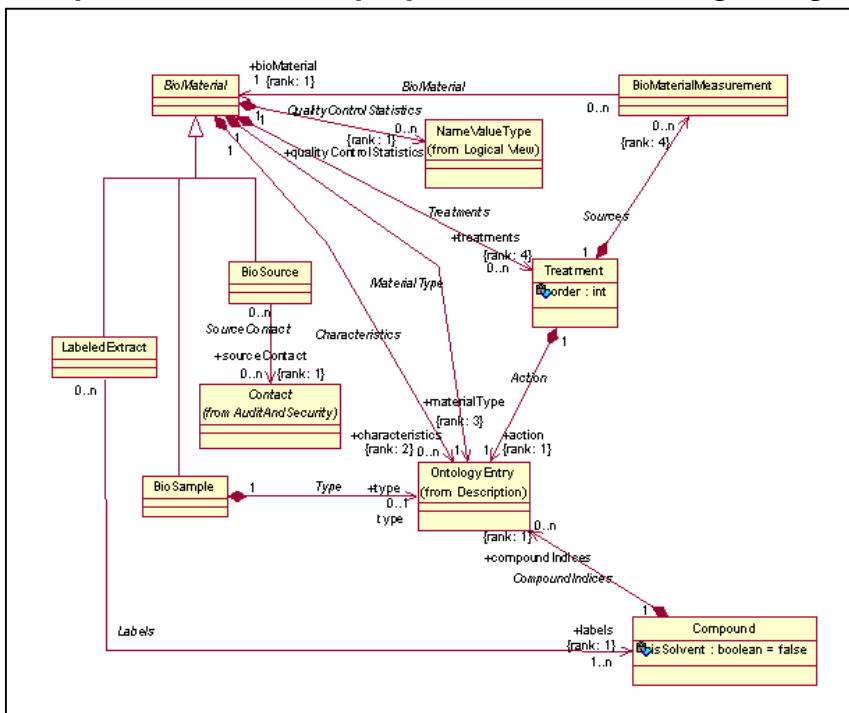
```
<!--MIAME requirement-->
  <QualityControlDescription_assn>
    <Description text="description text"/>
    <Annotations_assnlist>
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
      <OntologyEntry category="QualityControlDescription" value="dye_swap"/>
    </Annotations_assnlist>
  </QualityControlDescription_assn>

  <!-- OPTIONAL association -->
  <ReplicateDescription_assn>
    <Description text="description text"/>
    <Annotations_assnlist>
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
      <OntologyEntry category="ReplicateDescription" value="biological_duplicate"/>
    </Annotations_assnlist>
  </ReplicateDescription_assn>

</ExperimentDesign>
</ExperimentDesigns_assn>

</Experiment>
```

Samples used, extract preparation and labeling - diagrams



Samples used, extract preparation and labeling - DTD

```
<!ELEMENT BioMaterial_package (Compound_assnlist?,
    BioMaterial_assnlist?) >

<!ELEMENT Compound_assnlist (Compound+) >
<!ELEMENT BioMaterial_assnlist ((BioSource |
    LabeledExtract |
    BioSample)+) >

<!ELEMENT Labels_assnreflist (Compound_ref+) >

<!ELEMENT Compound_ref EMPTY >
<!ATTLIST Compound_ref identifier CDATA #REQUIRED >
<!ELEMENT Compound (..,CompoundIndices_assnlist?,..) >
<!ATTLIST Compound
    identifier CDATA #REQUIRED
    name CDATA #IMPLIED
    isSolvent CDATA "false" >

<!ELEMENT CompoundIndices_assnlist (OntologyEntry+) >

<!ELEMENT BioSource_ref EMPTY >
<!ATTLIST BioSource_ref identifier CDATA #REQUIRED >
<!ELEMENT BioSource (..,Descriptions_assnlist?,..,
    Characteristics_assnlist?,
    MaterialType_assn,..,
    SourceContact_assnreflist?) >
<!ATTLIST BioSource
    identifier CDATA #REQUIRED
    name CDATA #IMPLIED >

<!ELEMENT Characteristics_assnlist (OntologyEntry+) >
<!ELEMENT MaterialType_assn (OntologyEntry) >
<!ELEMENT SourceContact_assnreflist (Person_ref+) >

<!ELEMENT LabeledExtract_ref EMPTY >
<!ATTLIST LabeledExtract_ref identifier CDATA #REQUIRED >
<!ELEMENT LabeledExtract (..,Descriptions_assnlist?,..,
    Characteristics_assnlist?,
    MaterialType_assn,
    Treatments_assnlist?,
    Labels_assnreflist) >
<!ATTLIST LabeledExtract
    identifier CDATA #REQUIRED
    .. >

<!ELEMENT Treatments_assnlist (Treatment+) >

<!ELEMENT Treatment (..,ProtocolApplications_assnlist?,
    Action_assn,..,
    SourceBioMaterialMeasurements_assnlist?) >
<!ATTLIST Treatment
    identifier CDATA #REQUIRED
    ..
    order CDATA #IMPLIED >

<!ELEMENT Action_assn (OntologyEntry) >
<!ELEMENT SourceBioMaterialMeasurements_assnlist (BioMaterialMeasurement+) >

<!ELEMENT BioMaterialMeasurement (..,BioMaterial_assnref,..) >

<!ELEMENT BioMaterial_assnref (BioSource_ref |
    LabeledExtract_ref |
    BioSample_ref) >

<!ELEMENT BioSample_ref EMPTY >
<!ATTLIST BioSample_ref identifier CDATA #REQUIRED >
<!ELEMENT BioSample (..,Descriptions_assnlist?,..,
    Characteristics_assnlist?,
    MaterialType_assn,
    Treatments_assnlist?,
    Type_assn?) >
<!ATTLIST BioSample
    identifier CDATA #REQUIRED
    .. >
```

Samples used, extract preparation and labeling - example

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE Biomaterial_package PUBLIC "-//OMG//DTD MAGE-ML 1.1//EN"
"http://schema.omg.org/lsr/gene_expression/1.1/MAGE-ML.dtd" >

<BioMaterial_package>

  <Compound_assnlist>
<!--IMPORTANT: PROVIDE NAMES TO ALL COMPOUNDS-->
    <Compound identifier=" ebi.ac.uk:MIAMExpress/Compound:<object> " isSolvent="false"
name="cy3 dye">
      </Compound>

<!--OPTIONAL association: only if MIAME information can not be provided otherwise-->
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
      <CompoundIndices_assn>
        <OntologyEntry category="LabelCompound" value="Cy3"/>
      </CompoundIndices_assn>

    </Compound_assnlist>

  <BioMaterial_assnlist>
<!--IMPORTANT: PROVIDE NAMES TO ALL BIOMATERIALS-->

<BioSource identifier=" ebi.ac.uk:MIAMExpress/BioSource:<object> " name="BioSource">

<!--IMPORTANT: BioSource should have NO association to Treatment-->

<!--OPTIONAL association: only if MIAME information can not be provided otherwise-->
    <Descriptions_assnlist>
      <Description text="Description of my bioSource:this is free text"/>
    </Descriptions_assnlist>

    <Characteristics_assnlist>
<!--MIAME-REQUIREMENT: Provide Species using MGED ontology class ORGANISM-->
<!--MO TERMS: use of MGED Ontology instances required-->
<!--MO RULES: use of MGED Ontology Rules for representing complex biomaterial
characteristics instances requires-->
      <OntologyEntry category="Organism" value="Mus musculus"/>
    </Characteristics_assnlist>

<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
    <MaterialType_assn>
      <OntologyEntry category="MaterialType" value="whole_organism"/>
    </MaterialType_assn>

<!--MIAME-REQUIREMENT: to Track BioSource Provider-->
    <SourceContact_assnreflist>
      <Person_ref identifier=" ebi.ac.uk:MIAMExpress/Person:<object> " name="Person"/>
    </SourceContact_assnreflist>
  </BioSource>

  <BioSample identifier=" ebi.ac.uk:MIAMExpress/BioSample:<object> ">
<!--OPTIONAL association: only if MIAME information can not be provided otherwise-->
    <Descriptions_assnlist>
      <Description/>
    </Descriptions_assnlist>
<!-- OPTIONAL association -->
    <Characteristics_assnlist>
<!--MAGE-ML BEST PRACTICE: -->
```

```

<!--MO RULES: use of MGED Ontology Rules for representing complex biomaterial
characteristics -->
<!--IMPORTANT: BioSamples can have new characteristics compared to BioSources they are
derived from-->
<!--USE CASE: mutagenesis which causes change in genotype-->
  <OntologyEntry category="Genotype" value="p53-/-" />
</Characteristics_assnlist>

<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
  <MaterialType_assn>
    <OntologyEntry category="MaterialType" value="cell" />
  </MaterialType_assn>

  <Treatments_assnlist>
<!--MAGE-ML BEST PRACTICE: provide association to protocol when applying a treatment-->
<!--MAGE-ML BEST PRACTICE: provide an order to Treatment-->
<!--MAGE-ML BEST PRACTICE: provide association to protocol & to performer for QC checks-->

<Treatment identifier="ebi.ac.uk:MIAMExpress/Treatment:<object>" order="1">
  <ProtocolApplications_assnlist>
    <!--MAGE-ML BEST PRACTICE: DATE FORMATTING ISSUE-->
    <ProtocolApplication activityDate="YYYY-MM-DD">
<!-- OPTIONAL association -->
    <ParameterValues_assnlist>
      <ParameterValue value="1">
        <ParameterType_assnref>
          <Parameter_ref identifier="ebi.ac.uk:MIAMExpress/Parameter:<object>" />
        </ParameterType_assnref>
      </ParameterValue>
    </ParameterValues_assnlist>
<!-- OPTIONAL association -->
    <Performers_assnreflist>
      <Person_ref identifier=" ebi.ac.uk:MIAMExpress/Person:<object>" />
    </Performers_assnreflist>
    <Protocol_assnref>
      <Protocol_ref identifier=" ebi.ac.uk:MIAMExpress/Protocol:P-MEXP-XX" />
    </Protocol_assnref>
  </ProtocolApplication>
</ProtocolApplications_assnlist>
  <Action_assn>
<!--MO TERMS: use of MGED Ontology instances required-->
<!--MO RULES: use of MGED Ontology Rules for representing ComplexAction class-->
    <OntologyEntry category="Action" value="grow" />
  </Action_assn>
</Treatment>
</Treatments_assnlist>
</BioSample>

```

```

  <BioSample identifier="ebi.ac.uk:MIAMExpress/BioSample:<object>">
<!-- OPTIONAL association -->
  <Descriptions_assnlist>
    <Description/>
  </Descriptions_assnlist>
<!-- OPTIONAL association -->
  <Characteristics_assnlist>
<!--MO RULES: use of MGED Ontology Rules for representing complex biomaterial characteristics -->
<!--MO TERMS: use of MGED Ontology instances required-->
    <OntologyEntry category="Genotype" value="pten -/-" />
  </Characteristics_assnlist>
  <MaterialType_assn>
<!--MO TERMS: use of MGED Ontology instances required-->
    <OntologyEntry category="MaterialType" value="cell_lystate" />
  </MaterialType_assn>
  <Treatments_assnlist>
<!--MAGE-ML BEST PRACTICE: provide association to protocol when applying a treatment-->
<!--MAGE-ML BEST PRACTICE: provide an order to Treatment-->
<!--MAGE-ML BEST PRACTICE: provide association to performer for QC checks-->
<Treatment identifier="ebi.ac.uk:MIAMExpress/Treatment:<object>" order="1">

```

```

    <ProtocolApplications_assnlist>
<!--MAGE-ML BEST PRACTICE: DATE FORMATTING ISSUE-->
    <ProtocolApplication activityDate="YYYY-MM-DD">
<!-- OPTIONAL association -->
    <ParameterValues_assnlist>
        <ParameterValue value="1">
            <ParameterType_assnref>
                <Parameter_ref identifier="ebi.ac.uk:MIAMExpress/Parameter:<object>" />
            </ParameterType_assnref>
        </ParameterValue>
    </ParameterValues_assnlist>
<!-- OPTIONAL association -->
    <Performers_assnreflist>
        <Person_ref identifier=" ebi.ac.uk:MIAMExpress/Person:<object> " />
    </Performers_assnreflist>
    <Protocol_assnref>
        <Protocol_ref identifier=" ebi.ac.uk:MIAMExpress/Protocol:P-MEXP-XX" />
    </Protocol_assnref>
    </ProtocolApplication>
</ProtocolApplications_assnlist>
<Action_assn>
<!--MO TERMS: use of MGED Ontology instances requires-->
    <OntologyEntry category="Action" value="purify" />
</Action_assn>

<!--MAGE-ML BEST PRACTICE: provide association to SourceBiomaterial -->
    <SourceBioMaterialMeasurements_assnlist>
    <BioMaterialMeasurement>
        <BioMaterial_assnref>
            <BioSource_ref identifier=" ebi.ac.uk:MIAMExpress/BioSource:<object>" />
        </BioMaterial_assnref>
    </BioMaterialMeasurement>
    </SourceBioMaterialMeasurements_assnlist>
</Treatment>
</Treatments_assnlist>
</BioSample>

    <BioSample identifier=" ebi.ac.uk:MIAMExpress/BioSample:<object>">
<!-- OPTIONAL association -->
    <Descriptions_assnlist>
        <Description />
    </Descriptions_assnlist>
<!-- OPTIONAL association -->
    <Characteristics_assnlist>
<!--MO RULES: use of MGED Ontology Rules for representing complex biomaterial characteristics instances required-->
    <OntologyEntry category="Genotype" value="pten -/-" />
</Characteristics_assnlist>
    <MaterialType_assn>
        <OntologyEntry category="MaterialType" value="total_RNA" />
    </MaterialType_assn>
    <Treatments_assnlist>
<!--MAGE-ML BEST PRACTICE: provide an order to Treatment-->
<!--MAGE-ML BEST PRACTICE: provide association to protocol when applying a treatment-->
<!--MAGE-ML BEST PRACTICE: provide association to performer for QC checks-->
    <Treatment identifier=" ebi.ac.uk:MIAMExpress/Treatment:<object>" order="1">
        <ProtocolApplications_assnlist>
<!--MAGE-ML BEST PRACTICE: DATE FORMATTING ISSUE-->
            <ProtocolApplication activityDate=" YYYY-MM-DD ">
<!-- OPTIONAL association -->
                <ParameterValues_assnlist>
                    <ParameterValue value="1">
                        <ParameterType_assnref>
                            <Parameter_ref identifier=" ebi.ac.uk:MIAMExpress/Parameter:<object>" />
                        </ParameterType_assnref>
                    </ParameterValue>
                </ParameterValues_assnlist>
<!-- OPTIONAL association -->
                <Performers_assnreflist>
                    <Person_ref identifier=" ebi.ac.uk:MIAMExpress/Person:<object> " />
                </Performers_assnreflist>
                <Protocol_assnref>
                    <Protocol_ref identifier=" ebi.ac.uk:MIAMExpress/Protocol:P-MEXP-XX" />
                </Protocol_assnref>
            </ProtocolApplication>
        </ProtocolApplications_assnlist>
    </Treatment>
</Action_assn>

```

```
        <OntologyEntry category="Action" value="purify"/>
    </Action_assn>
    <SourceBioMaterialMeasurements_assnlist>
<!--MAGE-ML BEST PRACTICE: provide association to SourceBiomaterial & Measurement-->
    <BioMaterialMeasurement>
        <BioMaterial_assnref>
            <BioSource_ref identifier="ebi.ac.uk:MIAMExpress/BioSource:<object>" />
        </BioMaterial_assnref>
    </BioMaterialMeasurement>
    </SourceBioMaterialMeasurements_assnlist>
</Treatment>
</Treatments_assnlist>
</BioSample>
```

```
<LabeledExtract identifier="ebi.ac.uk:MIAMExpress/LabeledExtract:<object>">
<!--NOTE: LabeledExtracts can be created from other LabeledExtracts-->
<!--USE CASE: Example, make labeled mRNA, separate by size, run on arrays-->
<!-- OPTIONAL association -->
    <Descriptions_assnlist>
        <Description/>
    </Descriptions_assnlist>
```

```
<!--MO TERMS: use of MGED Ontology instances required-->
    <MaterialType_assn>
        <OntologyEntry category="MaterialType" value="synthetic_DNA"/>
    </MaterialType_assn>

    <Treatments_assnlist>
<!--IMPORTANT: LabeledExtracts can be created from other LabeledExtracts-->
<!--USE CASE: Example, prepare labeled mRNA, separate by size, run on arrays-->
<!--USE CASE: specify how using 'Treatment' object-->
```

```
        <Treatment identifier="ebi.ac.uk:MIAMExpress/Treatment:<object>" order="1">
            <ProtocolApplications_assnlist>
<!--MAGE-ML BEST PRACTICE: DATE FORMATTING ISSUE-->
                <ProtocolApplication activityDate="YYYY-MM-DD">
<!-- OPTIONAL association -->
                    <ParameterValues_assnlist>
                        <ParameterValue value="1">
                            <ParameterType_assnref>
                                <Parameter_ref identifier="ebi.ac.uk:MIAMExpress/Parameter:<object>" />
                            </ParameterType_assnref>
                        </ParameterValue>
                    </ParameterValues_assnlist>
<!-- OPTIONAL association -->
                    <Performers_assnreflist>
                        <Person_ref identifier=" ebi.ac.uk:MIAMExpress/Person:<object> " />
                    </Performers_assnreflist>
                    <Protocol_assnref>
                        <Protocol_ref identifier="ebi.ac.uk:MIAMExpress/Protocol:P-MEXP-XX" />
                    </Protocol_assnref>
                </ProtocolApplication>
            </ProtocolApplications_assnlist>
```

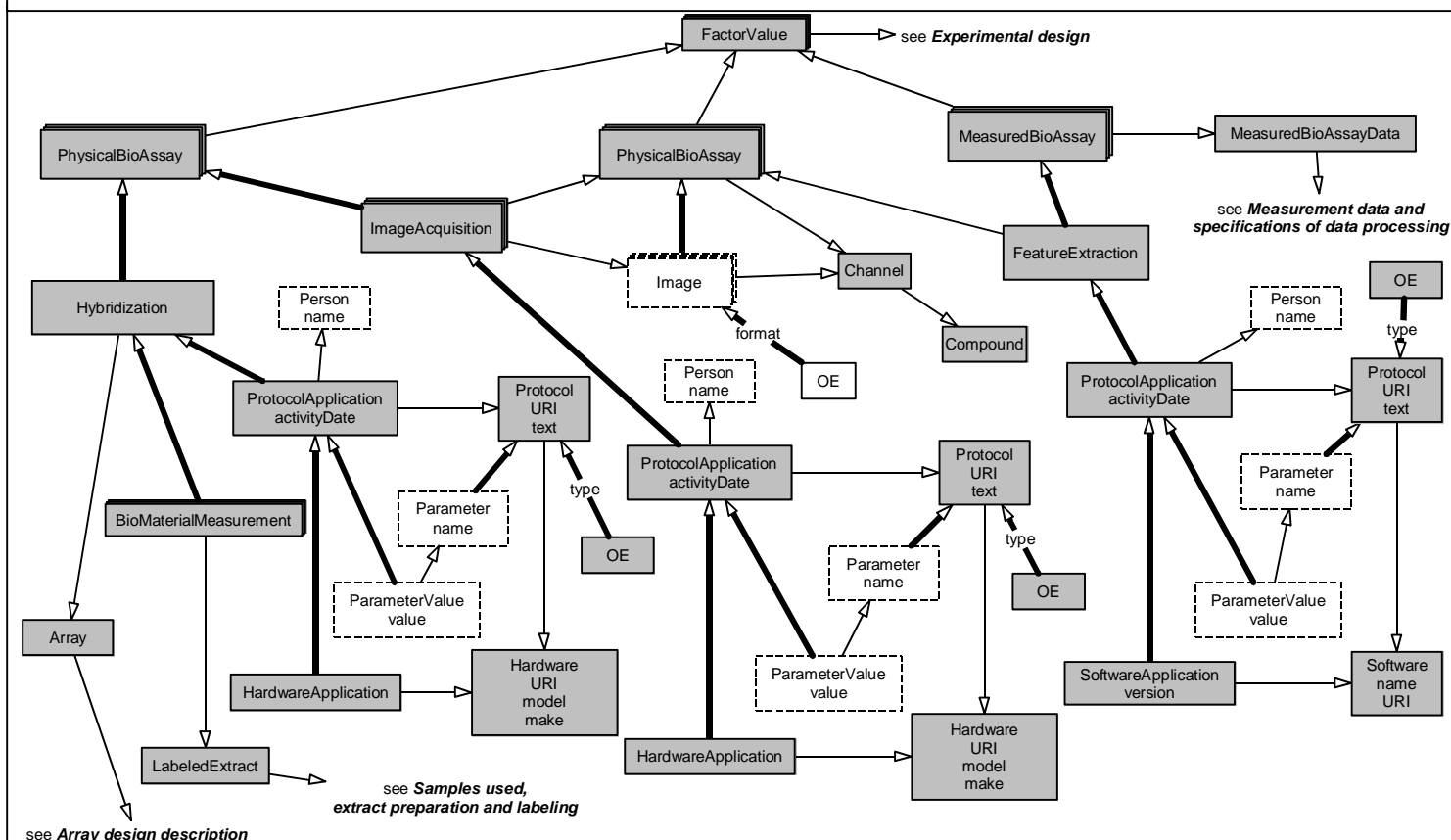
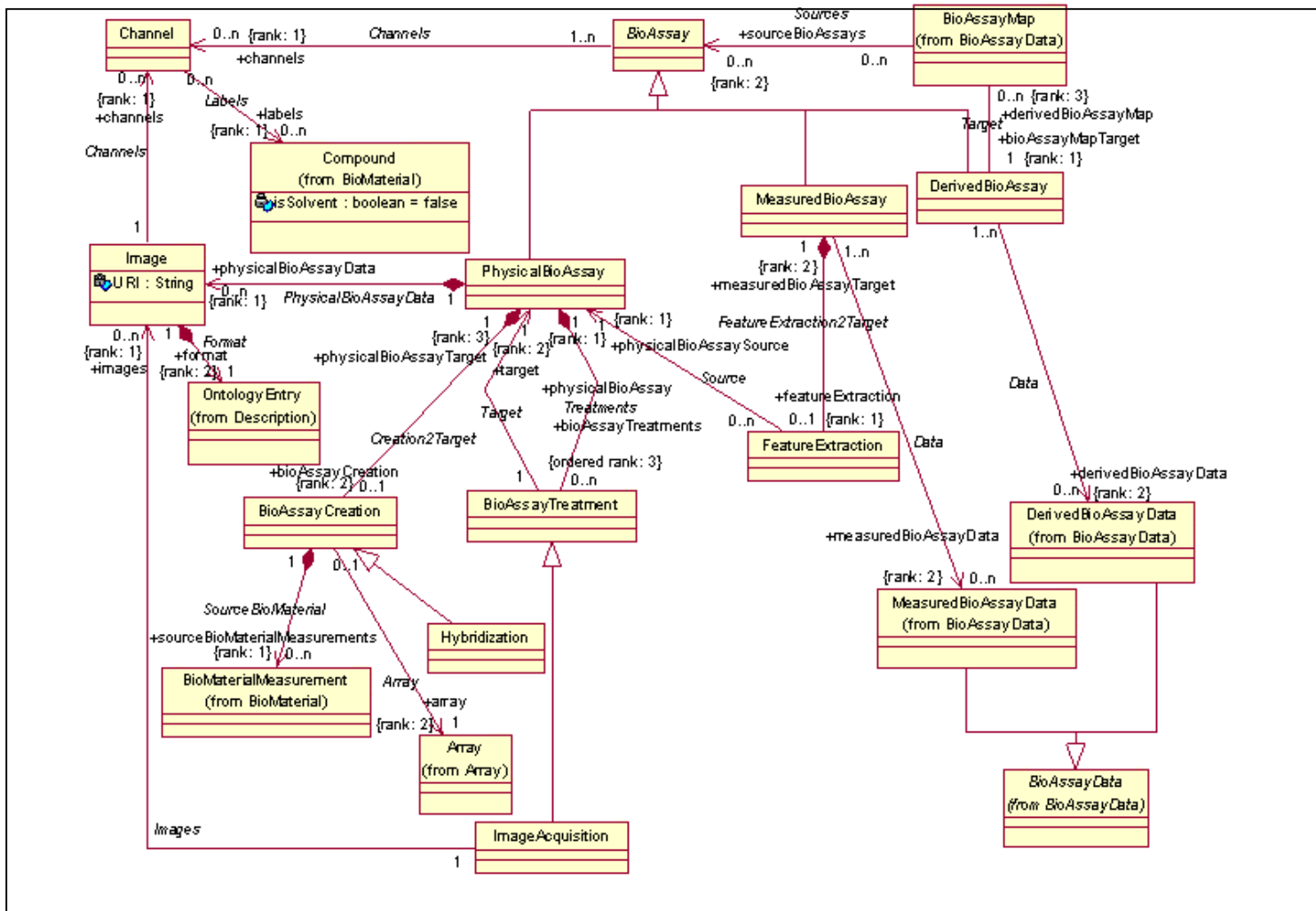
```
<!--MO TERMS: use of MGED Ontology instances required-->
    <Action_assn>
        <OntologyEntry category="Action" value="labeling"/>
    </Action_assn>

<!--MAGE-ML BEST PRACTICE: provide association to SourceBiomaterial & Measurement-->
    <SourceBioMaterialMeasurements_assnlist>
        <BioMaterialMeasurement>
            <BioMaterial_assnref>
                <BioSample_ref identifier="ebi.ac.uk:MIAMExpress/BioSample:<object>" />
            </BioMaterial_assnref>
        </SourceBioMaterialMeasurements_assnlist>
    </Treatment>
```

```
</Treatments_assnlist>
<Labels_assnreflist>
  <Compound_ref identifier="ebi.ac.uk:MIAMExpress/Compound:<object>" />
</Labels_assnreflist>
</LabeledExtract>
</BioMaterial_assnlist>

</BioMaterial_package>
```

Hybridization procedures and parameters, measurement data - diagrams



Hybridization procedures and parameters, measurement data - DTD

```
<!ELEMENT BioAssay_package (Channel_assnlist?, BioAssay_assnlist?) >
<!ELEMENT Channel_assnlist (Channel+) >
<!ELEMENT BioAssay_assnlist ((PhysicalBioAssay | DerivedBioAssay | MeasuredBioAssay)+) >

<!ELEMENT Channel_ref EMPTY >
<!ATTLIST Channel_ref identifier CDATA #REQUIRED >
<!ELEMENT Channel (..,Labels_assnreflist?) >
<!ATTLIST Channel
    identifier CDATA #REQUIRED
    name CDATA #IMPLIED >

<!ELEMENT BioAssays_assnreflist ((PhysicalBioAssay_ref | DerivedBioAssay_ref | MeasuredBioAssay_ref)+) >

<!ELEMENT PhysicalBioAssay_ref EMPTY >
<!ATTLIST PhysicalBioAssay_ref identifier CDATA #REQUIRED >
<!ELEMENT PhysicalBioAssay (..,Channels_assnreflist?,BioAssayFactorValues_assnreflist?,
    PhysicalBioAssayData_assnlist?, BioAssayCreation_assn?, BioAssayTreatments_assnlist?) >
<!ATTLIST PhysicalBioAssay
    identifier CDATA #REQUIRED
    .. >

<!ELEMENT Channels_assnreflist (Channel_ref+) >
<!ELEMENT BioAssayFactorValues_assnreflist (FactorValue_ref+) >
<!ELEMENT PhysicalBioAssayData_assnlist (Image+) >
<!ELEMENT BioAssayCreation_assn (Hybridization) >
<!ELEMENT BioAssayTreatments_assnlist (( .. | ImageAcquisition )+) >

<!ELEMENT Image_ref EMPTY >
<!ATTLIST Image_ref identifier CDATA #REQUIRED >
<!ELEMENT Image (..,Channels_assnreflist?,Format_assn) >
<!ATTLIST Image
    identifier CDATA #REQUIRED
    ..
    URI CDATA #IMPLIED >
<!ELEMENT Format_assn (OntologyEntry) >

<!ELEMENT Hybridization (..,ProtocolApplications_assnlist?,SourceBioMaterialMeasurements_assnlist?,Array_assnref) >
<!ATTLIST Hybridization
    identifier CDATA #REQUIRED
    .. >

<!ELEMENT Array_assnref (Array_ref) >

<!ELEMENT ImageAcquisition (..,ProtocolApplications_assnlist?,Target_assnref,Images_assnreflist?) >
<!ATTLIST ImageAcquisition
    identifier CDATA #REQUIRED
    .. >

<!ELEMENT Target_assnref (PhysicalBioAssay_ref) >
<!ELEMENT Images_assnreflist (Image_ref+) >

<!ELEMENT DerivedBioAssay_ref EMPTY >
<!ATTLIST DerivedBioAssay_ref identifier CDATA #REQUIRED >
<!ELEMENT DerivedBioAssay (..,BioAssayFactorValues_assnreflist?,..,DerivedBioAssayData_assnreflist?,
    DerivedBioAssayMap_assnreflist?) >
<!ATTLIST DerivedBioAssay
    identifier CDATA #REQUIRED
    .. >

<!ELEMENT DerivedBioAssayData_assnreflist (DerivedBioAssayData_ref+) >
<!ELEMENT DerivedBioAssayMap_assnreflist (BioAssayMap_ref+) >

<!ELEMENT MeasuredBioAssay_ref EMPTY >
<!ATTLIST MeasuredBioAssay_ref identifier CDATA #REQUIRED >
<!ELEMENT MeasuredBioAssay (..,BioAssayFactorValues_assnreflist?,FeatureExtraction_assn?,
    MeasuredBioAssayData_assnreflist?) >
<!ATTLIST MeasuredBioAssay
    identifier CDATA #REQUIRED
    .. >

<!ELEMENT FeatureExtraction_assn (FeatureExtraction) >
<!ELEMENT MeasuredBioAssayData_assnreflist (MeasuredBioAssayData_ref+) >

<!ELEMENT FeatureExtraction (..,ProtocolApplications_assnlist?,PhysicalBioAssaySource_assnref) >
<!ATTLIST FeatureExtraction
    identifier CDATA #REQUIRED
    .. >

<!ELEMENT PhysicalBioAssaySource_assnref (PhysicalBioAssay_ref) >
```

Hybridization procedures and parameters, measurement data - example

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE BioAssay_package PUBLIC "-//OMG//DTD MAGE-ML 1.1//EN"
"http://schema.omg.org/lsr/gene_expression/1.1/MAGE-ML.dtd" >

<!--Example coded after graphical description produced by Angel Pizarro-->
<!--According to this example, one PhysicalBioAssay is Created as an "Hybridization"-->
<!--Then, 2 other Physical BioAssays are created corresponding to the Image Acquisition Event
that occurs for each channel-->
<!--Then, 2 MeasuredBioAssays are created to represent the "FeatureExtraction" event, leading
to creation of Raw Data in each of the 2 channels-->
<!--Both MeasuredBioAssays are referencing the same MeasuredBioAssayData object (see
BioAssayData_package for additional information)-->

<BioAssay_package>
  <BioAssay_assnlist>

    <PhysicalBioAssay identifier="ebi.ac.uk:MIAMExpress/PhysicalBioAssay:<object>">

<!--IMPORTANT--: Association to Channel should be present only the Level of
PhysicalBioAssays !>
<!--IMPORTANT--: Association to Channel is discouraged at the Level of
Measured/DerivedBioAssays !>
<!--IMPORTANT--: Use the Dye name to specify Channel, so it can be related to Compound !>
    <Channels_assnreflist>
      <Channel_ref identifier="ebi.ac.uk:MIAMExpress/Channel:<object>" />
      <Channel_ref identifier="ebi.ac.uk:MIAMExpress/Channel:<object>" />
    </Channels_assnreflist>

    <!--MAGE-ML Good Practice: Recall "Factor Values" (declared in Experiment Package) at the
level of ALL BioAssays-->
      <BioAssayFactorValues_assnreflist>
        <FactorValue_ref identifier="ebi.ac.uk:MIAMExpress/FactorValue:<object>" />
        <FactorValue_ref identifier="ebi.ac.uk:MIAMExpress/ FactorValue:<object>" />
      </BioAssayFactorValues_assnreflist>

      <BioAssayCreation_assn>
<!--IMPORTANT: -->
<!--MAGE-ML Good Practice: If BioEvent is an actual "hybridization" then use "Hybridization"
object as shown-->
        <Hybridization identifier="ebi.ac.uk:MIAMExpress/Hybridization:<object>">
          <ProtocolApplications_assnlist>
<!--MAGE-ML BEST PRACTICE: DATE FORMATTING ISSUE-->
            <ProtocolApplication activityDate="YYYY-MM-DD">

<!-- OPTIONAL association -->
              <HardwareApplications_assnlist>
                <HardwareApplication>
                  <ParameterValues_assnlist>
                    <ParameterValue value="1">
                      <ParameterType_assnref>
<!--MAGE-ML good practice: if information recorded, always provided association to
Performer-->
                        <Parameter_ref identifier="ebi.ac.uk:MIAMExpress/Parameter:<object>" />
                      </ParameterType_assnref>
                    </ParameterValue>
                  </ParameterValues_assnlist>
                </Hardware_application>
              </HardwareApplications_assnlist>
            </ProtocolApplication>
          </ProtocolApplications_assnlist>
        </Hybridization>
      </BioAssayCreation_assn>
    </PhysicalBioAssay>
  </BioAssay_assnlist>
</BioAssay_package>
```

```

<!--MAGE-ML good practice: if information recorded, always provided association to
Performer-->
<!--Enhances QC possibilities-->
  <Person_ref identifier="ebi.ac.uk:MIAMExpress/Person:<object>" />
  </Performers_assnreflist>

  <Protocol_assnref>
    <Protocol_ref identifier="ebi.ac.uk:MIAMExpress/Protocol:<object>" />
  </Protocol_assnref>
</ProtocolApplication>
</ProtocolApplications_assnlist>

<SourceBioMaterialMeasurements_assnlist>
  <BioMaterialMeasurement>
    <BioMaterial_assnref>
      <LabeledExtract_ref
identifier="ebi.ac.uk:MIAMExpress/LabeledExtract:<object>" />
      </BioMaterial_assnref>
    </BioMaterialMeasurement>
    <BioMaterialMeasurement>
      <BioMaterial_assnref>
        <LabeledExtract_ref
identifier="ebi.ac.uk:MIAMExpress/LabeledExtract:<object>" />
        </BioMaterial_assnref>
      </BioMaterialMeasurement>
    </SourceBioMaterialMeasurements_assnlist>

  <Array_assnref>
    <Array_ref identifier="ebi.ac.uk:MIAMExpress/Array:<object>" />
  </Array_assnref>

</Hybridization>
</BioAssayCreation_assn>
<BioAssayTreatments_assnlist>
  <ImageAcquisition identifier="ebi.ac.uk:MIAMExpress/ImageAcquisition:<object>"
name="IA-Cy3">
  <ProtocolApplications_assnlist>
<!--MAGE-ML BEST PRACTICE: DATE FORMATTING ISSUE-->
    <ProtocolApplication activityDate="YYYY-MM-DD">
<!-- OPTIONAL association -->
      <HardwareApplications_assnlist>
        <HardwareApplication>
          <ParameterValues_assnlist>
            <ParameterValue value="1">
              <ParameterType_assnref>
                <Parameter_ref identifier="ebi.ac.uk:MIAMExpress/Parameter:<object>" />
              </ParameterType_assnref>
            </ParameterValue>
          </ParameterValues_assnlist>
          <Hardware_assnref>
            <Hardware_ref identifier="ebi.ac.uk:MIAMExpress/Hardware:<object>" />
          </Hardware_assnref>
        </HardwareApplication>
      </HardwareApplications_assnlist>
<!-- OPTIONAL association -->
      <Performers_assnreflist>
<!--MAGE-ML good practice: if information recorded, always provided association to Performer-->
<!--Enhances QC possibilities-->
        <Person_ref identifier="ebi.ac.uk:MIAMExpress/Person:<object>" />
        </Performers_assnreflist>
        <Protocol_assnref>
          <Protocol_ref identifier="ebi.ac.uk:MIAMExpress/Protocol:P-PROT-XX" />
        </Protocol_assnref>
      </ProtocolApplication>
    </ProtocolApplications_assnlist>
  <Target_assnref>
    <PhysicalBioAssay_ref identifier="ebi.ac.uk:MIAMExpress/PhysicalBioAssay:PBA-
Cy3" name="PBA-Cy3" />

```

```

    </Target_assnref>
    <Images_assnreflist>
      <Image_ref identifier="ebi.ac.uk:MIAMExpress/Image:<object>" />
    </Images_assnreflist>
  </ImageAcquisition>

  <ImageAcquisition identifier="ebi.ac.uk:MIAMExpress/ImageAcquisition:<object>"
name="IA-Cy5">
    <ProtocolApplications_assnlist>
<!--MAGE-ML BEST PRACTICE: DATE FORMATTING ISSUE-->
      <ProtocolApplication activityDate="YYYY-MM-DD">

<!-- OPTIONAL association -->
      <SoftwareApplications_assnlist>
        <SoftwareApplication version="1.0">
          <ParameterValues_assnlist>
            <ParameterValue value="1">
              <ParameterType_assnref>
                <Parameter_ref identifier="ebi.ac.uk:MIAMExpress/Parameter:<object>" />
              </ParameterType_assnref>
            </ParameterValue>
          </ParameterValues_assnlist>
        </SoftwareApplication>
      </SoftwareApplications_assnlist>
      <Software_assnref>
        <Software_ref identifier="ebi.ac.uk:MIAMExpress/Software:<object>" />
      </Software_assnref>
    </SoftwareApplication>
  </SoftwareApplications_assnlist>
<!-- OPTIONAL association -->
  <Performers_assnreflist>
<!--MAGE-ML good practice: if information recorded, always provided association to Performer-->
<!--Enhances QC possibilities-->
    <Person_ref identifier="ebi.ac.uk:MIAMExpress/Person:<object>" />
  </Performers_assnreflist>
  <Protocol_assnref>
    <Protocol_ref identifier="ebi.ac.uk:MIAMExpress/Protocol:P-MEXP-XX" />
  </Protocol_assnref>
</ProtocolApplication>
</ProtocolApplications_assnlist>
<Target_assnref>
  <PhysicalBioAssay_ref identifier="ebi.ac.uk:MIAMExpress/PhysicalBioAssay:PBA-
Cy5" name="PBA_Cy5" />
</Target_assnref>
  <Images_assnreflist>
    <Image_ref identifier="ebi.ac.uk:MIAMExpress/Image:<object>" name="IMAGE: Cy5" />
  </Images_assnreflist>
</ImageAcquisition>
</BioAssayTreatments_assnlist>
</PhysicalBioAssay>

  <PhysicalBioAssay identifier="ebi.ac.uk:MIAMExpress/PhysicalBioAssay:<object>"
name="PBA-Cy3">

<!--MAGE-ML Good Practice: Provide association to Channel-->
    <Channels_assnreflist>
      <Channel_ref identifier="ebi.ac.uk:MIAMExpress/Channel:<object>"
name="Channel: Cy3" />
    </Channels_assnreflist>

<!--MO TERMS: use of MGED Ontology instances required-->
    <BioAssayFactorValues_assnreflist>
      <FactorValue_ref identifier="ebi.ac.uk:MIAMExpress/FactorValue:<object>" />
    </BioAssayFactorValues_assnreflist>

<!-- OPTIONAL association -->
<!--IMPORTANT: How to ensure linking between Channel and Experimental Value -->
<!--Providing association to Channel becomes necessary -->
    <PhysicalBioAssayData_assnlist>
      <Image identifier="ebi.ac.uk:MIAMExpress/Image:<object>" name="IMAGE: Cy3">

```

```

    <Channels_assnreflist>
    <Channel_ref identifier=" ebi.ac.uk:MIAMExpress/Channel:<object> name="Channel:Cy3" />
  </Channels_assnreflist>
<!--MO TERMS: use of MGED Ontology instances required-->
  <Format_assn>
    <OntologyEntry category="ImageFormat" value="TIFF" />
  </Format_assn>
</Image>
</PhysicalBioAssayData_assnlist>

</PhysicalBioAssay>

<PhysicalBioAssay identifier="ebi.ac.uk:MIAMExpress/PhysicalBioAssay:PBA-Cy5" name="
PBA-Cy5">

<!--MAGE-ML Good Practice: Provide association to Channel-->
  <Channels_assnreflist>
<Channel_ref identifier="ebi.ac.uk:MIAMExpress/Channel:<object>" name="Channel:Cy5" />
  </Channels_assnreflist>

<!--MAGE-ML Good Practice: Provide association to Factor Value attached to BioAssay-->
<!--Greatly enhances data display and retrieval-->
  <BioAssayFactorValues_assnreflist>
    <FactorValue_ref identifier="ebi.ac.uk:MIAMExpress/FactorValue:<object>" />
  </BioAssayFactorValues_assnreflist>

  <PhysicalBioAssayData_assnlist>
<!-- OPTIONAL association -->
<!--IMPORTANT: How to ensure linking between Channel and Experimental Value -->
<!--Providing association to Channel becomes necessary -->
    <Image identifier="ebi.ac.uk:MIAMExpress/Image:<object>" name="IMAGE:Cy5">
      <Channels_assnreflist>
        <Channel_ref identifier ebi.ac.uk:MIAMExpress/Channel:<object>" name="Channel:Cy5" />
      </Channels_assnreflist>
<!--MO TERMS: use of MGED Ontology instances required-->
      <Format_assn>
        <OntologyEntry category="ImageFormat" value="TIFF" />
      </Format_assn>
    </Image>
  </PhysicalBioAssayData_assnlist>
</PhysicalBioAssay>

  <MeasuredBioAssay identifier=" ebi.ac.uk:MIAMExpress/MeasuredBioAssay:<object>"
name="MBA-Cy3">

<!--MAGE-ML Good Practice: Association to Channel Discouraged-->

<!--MAGE-ML GOOD PRACTICE: Recall Factor Value-->

  <BioAssayFactorValues_assnreflist>
    <FactorValue_ref identifier="ebi.ac.uk:MIAMExpress/FactorValue:<object>" />
  </BioAssayFactorValues_assnreflist>

  <FeatureExtraction_assn>
    <FeatureExtraction identifier="ebi.ac.uk:MIAMExpress/FeatureExtraction:<object>"
name="FE-Cy3">

    <ProtocolApplications_assnlist>
<!--MAGE-ML BEST PRACTICE: DATE FORMATTING ISSUE-->
      <ProtocolApplication activityDate="YYYY-MM-DD ">
<!-- OPTIONAL association -->

```

```

    <ParameterValues_assnlist>
      <ParameterValue value="1">
        <ParameterType_assnref>
          <Parameter_ref identifier="ebi.ac.uk:MIAMExpress/Parameter:<object>" />
        </ParameterType_assnref>
      </ParameterValue>
    </ParameterValues_assnlist>

<!-- OPTIONAL association -->
    <SoftwareApplications_assnlist>
      <SoftwareApplication version="1.0">
        <Software_assnref>
          <Software_ref identifier=" ebi.ac.uk:MIAMExpress/Software:<object> " />
        </Software_assnref>
      </SoftwareApplication>
    </SoftwareApplications_assnlist>

<!-- OPTIONAL association -->
    <Performers_assnreflist>
      <Person_ref identifier="ebi.ac.uk:MIAMExpress/Person:<object>" />
    </Performers_assnreflist>

    <Protocol_assnref>
      <Protocol_ref identifier="ebi.ac.uk:MIAMExpress/Protocol:P-MEXP-XX" />
    </Protocol_assnref>
  </ProtocolApplication>
</ProtocolApplications_assnlist>
<PhysicalBioAssaySource_assnref>
  <PhysicalBioAssay_ref
identifier="ebi.ac.uk:MIAMExpress/PhysicalBioAssay:<object>" name="PBA-Cy3" />
  </PhysicalBioAssaySource_assnref>
</FeatureExtraction>
</FeatureExtraction_assn>

<!--MAGE-ML Good Practice: Provide association to Data-->
  <MeasuredBioAssayData_assnreflist>
    <MeasuredBioAssayData_ref
identifier="ebi.ac.uk:MIAMExpress/MeasuredBioAssayData:<object>" name="FE-MBAD-root" />
    </MeasuredBioAssayData_assnreflist>

  </MeasuredBioAssay>

  <MeasuredBioAssay identifier="ebi.ac.uk:MIAMExpress/MeasuredBioAssayData:<object>"
name="MBA-Cy5" >
<!--MAGE-ML Good Practice: Association to Channel Discouraged-->

    <BioAssayFactorValues_assnreflist>
      <!--MAGE-ML GOOD PRACTICE: Recall Factor Value-->
      <FactorValue_ref identifier="ebi.ac.uk:MIAMExpress/FactorValue:<object>" />
    </BioAssayFactorValues_assnreflist>

    <FeatureExtraction_assn>
      <FeatureExtraction identifier="ebi.ac.uk:MIAMExpress/FeatureExtraction:<object>"
name="FE-Cy5" >
        <ProtocolApplications_assnlist>
          <!--MAGE-ML BEST PRACTICE: DATE FORMATTING ISSUE-->
          <ProtocolApplication activityDate="YYYY-MM-DD" >
            <!-- OPTIONAL association -->
            <ParameterValues_assnlist>
              <ParameterValue value="1">
                <ParameterType_assnref>
                  <Parameter_ref identifier="ebi.ac.uk:MIAMExpress/Parameter:<object>" />
                </ParameterType_assnref>
              </ParameterValue>
            </ParameterValues_assnlist>
          </ProtocolApplication>
        </ProtocolApplications_assnlist>
      </FeatureExtraction>
    </MeasuredBioAssay>
  </MeasuredBioAssay>

```

```

        </ParameterValue>
    </ParameterValues_assnlist>

<!-- OPTIONAL association -->
    <SoftwareApplications_assnlist>
        <SoftwareApplication version="1.0">
            <Software_assnref>
                <Software_ref identifier="ebi.ac.uk:MIAMExpress/Software:<object>" />
            </Software_assnref>
        </SoftwareApplication>
    </SoftwareApplications_assnlist>

<!-- OPTIONAL association -->
    <Performers_assnreflist>
        <Person_ref identifier="ebi.ac.uk:MIAMExpress/Person:<object>" />
    </Performers_assnreflist>
    <Protocol_assnref>
        <Protocol_ref identifier="ebi.ac.uk:MIAMExpress/Protocol:P-MEXP-XX" />
    </Protocol_assnref>
</ProtocolApplication>
</ProtocolApplications_assnlist>
<PhysicalBioAssaySource_assnref>
    <PhysicalBioAssay_ref
identifier="ebi.ac.uk:MIAMExpress/PhysicalBioAssay:<object>" name="PBA-Cy5" />
    </PhysicalBioAssaySource_assnref>
</FeatureExtraction>
</FeatureExtraction_assn>

<!--MAGE-ML Good Practice: Provide association to Data-->
    <MeasuredBioAssayData_assnreflist>
        <MeasuredBioAssayData_ref
identifier="ebi.ac.uk:MIAMExpress/MeasuredBioAssayData:<object>" name="MBAD-root" />
    </MeasuredBioAssayData_assnreflist>
</MeasuredBioAssay>

    <DerivedBioAssay identifier="ebi.ac.uk:MIAMExpress/DerivedBioAssay:<object>" name="">

<!--MAGE-ML Good Practice: Association to Channel Discouraged-->

<!--MO TERMS: use of MGED Ontology instances required-->
<!--MO RULES: use of MGED Ontology Rules for representing Compound-->
    <Type_assn>
        <OntologyEntry category="DerivedBioAssayType" value="ratio" />
    </Type_assn>

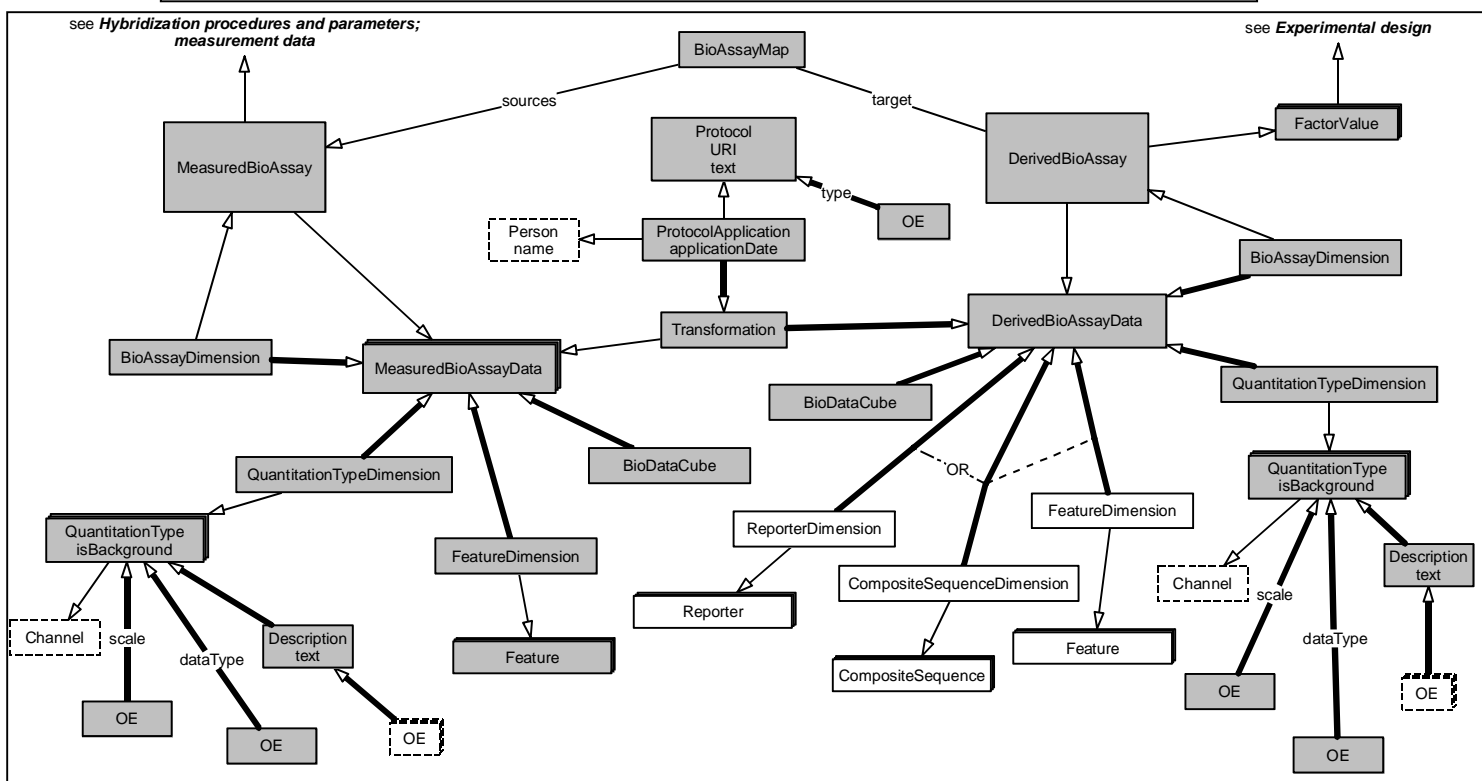
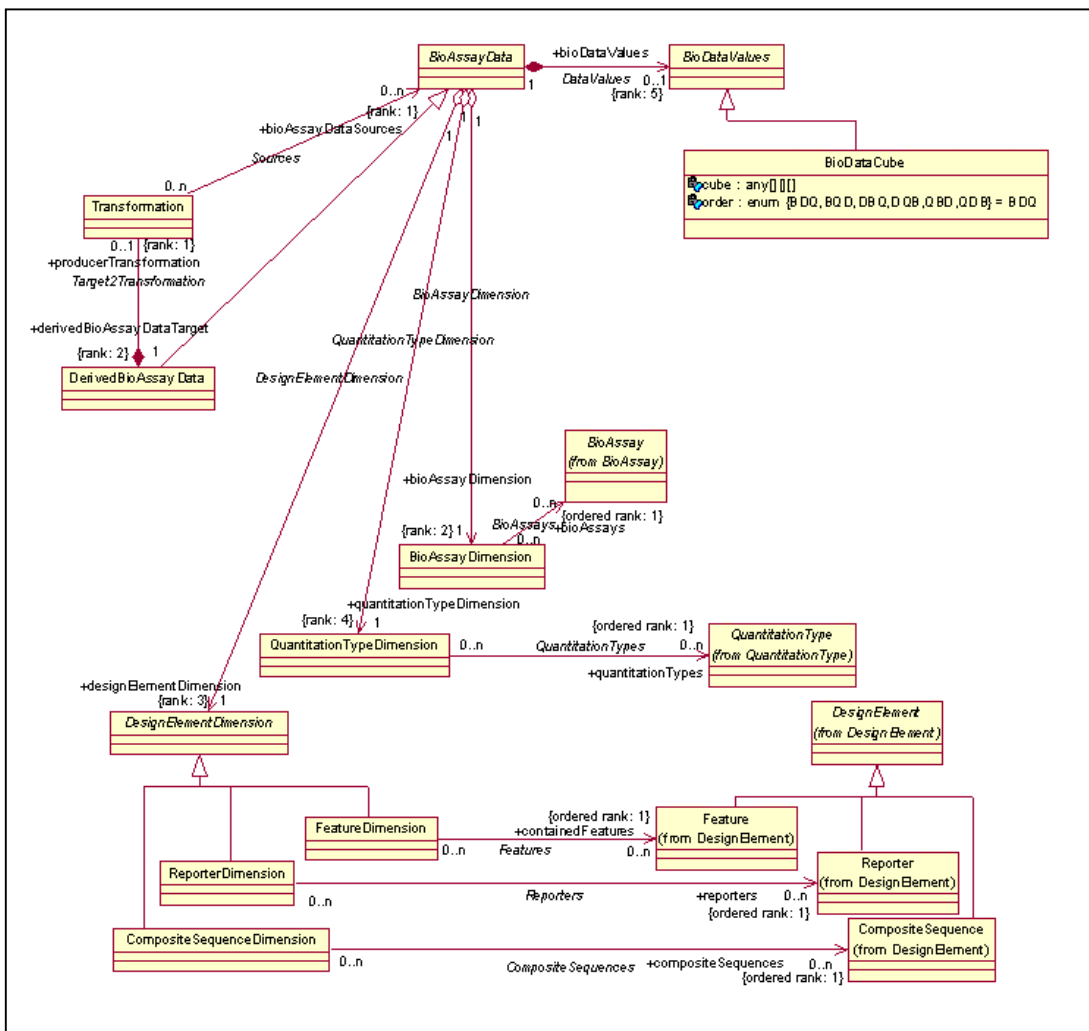
<!--MAGE-ML Good Practice: Provide association to Data-->
    <DerivedBioAssayData_assnreflist>
        <BioAssayFactorValues_assnreflist>
            <!--MAGE-ML GOOD PRACTICE: Recall Factor Value-->
            <FactorValue_ref identifier="ebi.ac.uk:MIAMExpress/FactorValue:<object>" />
        </BioAssayFactorValues_assnreflist>
        <DerivedBioAssayData_ref
identifier="ebi.ac.uk:MIAMExpress/DerivedBioAssayData:<object>" name="" />
    </DerivedBioAssayData_assnreflist>

<!-- OPTIONAL association -->
    <DerivedBioAssayMap_assnreflist>
        <BioAssayMap_ref identifier="ebi.ac.uk:MIAMExpress/DerivedBioAssayMap:object" />
    </DerivedBioAssayMap_assnreflist>

    </DerivedBioAssay>
</BioAssay_assnlist>
</BioAssay_package>

```

Measurement data and specifications of data processing - diagrams



Measurement data and specifications of data processing - DTD

```
<!ELEMENT BioAssayData_package (BioAssayDimension_assnlist?,DesignElementDimension_assnlist?,
    QuantitationTypeDimension_assnlist?,BioAssayMap_assnlist?,...,BioAssayData_assnlist?) >

<!ELEMENT BioAssayDimension_assnlist (BioAssayDimension+) >
<!ELEMENT DesignElementDimension_assnlist ((CompositeSequenceDimension |
    ReporterDimension | FeatureDimension)+) >
<!ELEMENT QuantitationTypeDimension_assnlist (QuantitationTypeDimension+) >
<!ELEMENT BioAssayMap_assnlist (BioAssayMap+) >
<!ELEMENT BioAssayData_assnlist ((DerivedBioAssayData | MeasuredBioAssayData)+) >

<!ELEMENT BioAssayDimension_ref EMPTY >
<!ATTLIST BioAssayDimension_ref identifier CDATA #REQUIRED >
<!ELEMENT BioAssayDimension (... ,BioAssays_assnreflist?) >
<!ATTLIST BioAssayDimension identifier CDATA #REQUIRED .. >

<!ELEMENT CompositeSequenceDimension_ref EMPTY >
<!ATTLIST CompositeSequenceDimension_ref identifier CDATA #REQUIRED >
<!ELEMENT CompositeSequenceDimension (... ,CompositeSequences_assnreflist?) >
<!ATTLIST CompositeSequenceDimension identifier CDATA #REQUIRED .. >

<!ELEMENT ReporterDimension_ref EMPTY >
<!ATTLIST ReporterDimension_ref identifier CDATA #REQUIRED >
<!ELEMENT ReporterDimension (... ,Reporters_assnreflist?) >
<!ATTLIST ReporterDimension identifier CDATA #REQUIRED .. >

<!ELEMENT FeatureDimension_ref EMPTY >
<!ATTLIST FeatureDimension_ref identifier CDATA #REQUIRED >
<!ELEMENT FeatureDimension (... ,ContainedFeatures_assnreflist?) >
<!ATTLIST FeatureDimension identifier CDATA #REQUIRED .. >
<!ELEMENT ContainedFeatures_assnreflist (Feature_ref+) >

<!ELEMENT QuantitationTypeDimension_ref EMPTY >
<!ATTLIST QuantitationTypeDimension_ref identifier CDATA #REQUIRED >
<!ELEMENT QuantitationTypeDimension (... ,QuantitationTypes_assnreflist?) >
<!ATTLIST QuantitationTypeDimension identifier CDATA #REQUIRED .. >
<!ELEMENT QuantitationTypes_assnreflist ((SpecializedQuantitationType_ref | DerivedSignal_ref |
    MeasuredSignal_ref | Error_ref | PValue_ref |
    ExpectedValue_ref | Ratio_ref | PresentAbsent_ref | Failed_ref)+) >

<!ELEMENT BioAssayMap_ref EMPTY >
<!ATTLIST BioAssayMap_ref identifier CDATA #REQUIRED >
<!ELEMENT BioAssayMap (... ,BioAssayMapTarget_assnref,SourceBioAssays_assnreflist?) >
<!ATTLIST BioAssayMap identifier CDATA #REQUIRED .. >
<!ELEMENT BioAssayMapTarget_assnref (DerivedBioAssay_ref) >
<!ELEMENT SourceBioAssays_assnreflist (( .. | MeasuredBioAssay_ref )+) >

<!ELEMENT DerivedBioAssayData_ref EMPTY >
<!ATTLIST DerivedBioAssayData_ref identifier CDATA #REQUIRED >
<!ELEMENT DerivedBioAssayData (... ,BioAssayDimension_assnref?,DesignElementDimension_assnref?,
    QuantitationTypeDimension_assnref?,BioDataValues_assn?,ProducerTransformation_assn?) >
<!ATTLIST DerivedBioAssayData identifier CDATA #REQUIRED .. >
<!ELEMENT BioAssayDimension_assnref (BioAssayDimension_ref) >
<!ELEMENT DesignElementDimension_assnref (CompositeSequenceDimension_ref | ReporterDimension_ref |
    FeatureDimension_ref) >
<!ELEMENT QuantitationTypeDimension_assnref (QuantitationTypeDimension_ref) >
<!ELEMENT BioDataValues_assn (BioDataCube | ..) >
<!ELEMENT ProducerTransformation_assn (Transformation) >

<!ELEMENT BioDataCube (... ,(DataInternal_assn | DataExternal_assn)) >
<!ATTLIST BioDataCube order (BDQ|BQD|DBQ|DQB|QBD|QDB) "BDQ" >
<!ELEMENT DataInternal_assn (DataInternal) >
<!ELEMENT DataExternal_assn (DataExternal) >

<!ELEMENT DataInternal (#PCDATA) >
<!ELEMENT DataExternal EMPTY >
<!ATTLIST DataExternal dataFormat CDATA "whitespace"
    ..
    filenameURI CDATA #REQUIRED >

<!ELEMENT Transformation (... ,ProtocolApplications_assnlist?,BioAssayDataSources_assnreflist?,..) >
<!ATTLIST Transformation identifier CDATA #REQUIRED .. >

<!ELEMENT BioAssayDataSources_assnreflist (( .. | MeasuredBioAssayData_ref )+) >

<!ELEMENT MeasuredBioAssayData_ref EMPTY >
<!ATTLIST MeasuredBioAssayData_ref identifier CDATA #REQUIRED >
<!ELEMENT MeasuredBioAssayData (... ,BioAssayDimension_assnref?,DesignElementDimension_assnref?,
    QuantitationTypeDimension_assnref?,BioDataValues_assn?) >
<!ATTLIST MeasuredBioAssayData identifier CDATA #REQUIRED .. >
```

Measurement data and specifications of data processing - example

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE BioAssayData_package PUBLIC "-//OMG//DTD MAGE-ML 1.1//EN"
"http://schema.omg.org/lsr/gene_expression/1.1/MAGE-ML.dtd" >

<BioAssayData_package>

  <BioAssayDimension_assnlist>
    <BioAssayDimension identifier="ebi.ac.uk:MIAMExpress/BioAssayDimension:<object>">
      <BioAssays_assnreflist>
        <PhysicalBioAssay_ref identifier="ebi.ac.uk:MIAMExpress/PhysicalBioAssay:<object>" />
      </BioAssays_assnreflist>
    </BioAssayDimension>
  </BioAssayDimension_assnlist>

  <DesignElementDimension_assnlist>

    <FeatureDimension identifier="ebi.ac.uk:MIAMExpress/FeatureDimension:<object>">
      <Features_assnreflist>
        <Feature_ref identifier="ebi.ac.uk:MIAMExpress/Feature:<object>" />
      </Features_assnreflist>
    </FeatureDimension>

    <ReporterDimension identifier="ebi.ac.uk:MIAMExpress/ReporterDimension:<object>">
      <Reporters_assnreflist>
        <Reporter_ref identifier="ebi.ac.uk:MIAMExpress/Reporter:<object>" />
      </Reporters_assnreflist>
    </ReporterDimension>

    <CompositeSequenceDimension
identifier="ebi.ac.uk:MIAMExpress/CompositeSequenceDimension:<object>">
      <CompositeSequences_assnreflist>
        <CompositeSequence_ref
identifier="ebi.ac.uk:MIAMExpress/CompositeSequence:<object>" />
      </CompositeSequences_assnreflist>
    </CompositeSequenceDimension>

  </DesignElementDimension_assnlist>

  <QuantitationTypeDimension_assnlist>
    <QuantitationTypeDimension
identifier="ebi.ac.uk:MIAMExpress/QuantitationTypeDimension:<object>">
      <QuantitationTypes_assnreflist>
        <DerivedSignal_ref identifier="ebi.ac.uk:MIAMExpress/DerivedSignal:<object>" />
      </QuantitationTypes_assnreflist>
    </QuantitationTypeDimension>
  </QuantitationTypeDimension_assnlist>

  <!-- OPTIONAL association -->
  <!--MIAME REQUIREMENT:-->

  <BioAssayMap_assnlist>
    <BioAssayMap identifier="ebi.ac.uk:MIAMExpress/BioAssayMap:<object>">
      <BioAssayMapTarget_assnref>
        <DerivedBioAssay_ref identifier="ebi.ac.uk:MIAMExpress/DerivedBioAssay:<object>" />
      </BioAssayMapTarget_assnref>
      <SourceBioAssays_assnreflist>
        <MeasuredBioAssay_ref identifier="ebi.ac.uk:MIAMExpress/MeasuredBioAssay:<object>" />
      </SourceBioAssays_assnreflist>
    </BioAssayMap>
  </BioAssayMap_assnlist>
```

```

<BioAssayData_assnlist>
  <DerivedBioAssayData identifier="ebi.ac.uk:MIAMExpress/DerivedBioAssayData:<object>">
    <BioAssayDimension_assnref>
      <BioAssayDimension_ref
identifier="ebi.ac.uk:MIAMExpress/BioAssayDimension:<object>" />
    </BioAssayDimension_assnref>
    <DesignElementDimension_assnref>
      <ReporterDimension_ref
identifier="ebi.ac.uk:MIAMExpress/ReporterDimension:<object>" />
    </DesignElementDimension_assnref>
    <QuantitationTypeDimension_assnref>
      <QuantitationTypeDimension_ref
identifier="ebi.ac.uk:MIAMExpress/QuantitationTypeDimension:<object>" />
    </QuantitationTypeDimension_assnref>

<!--IMPORTANT: BioData Values should not be coded using Tuples -->
<!--ARRAYExpress favours BioDataCube coded as External-->
  <BioDataValues_assn>
    <BioDataCube order="DBQ">
      <DataExternal_assn>
        <DataExternal filenameURI="www.ebi.ac.uk/datafile.txt" />
      </DataExternal_assn>
    </BioDataCube>
  </BioDataValues_assn>
  <ProducerTransformation_assn>

    <Transformation identifier=" ebi.ac.uk:MIAMExpress/Transformation:<object>">
      <ProtocolApplications_assnlist>

<!--MAGE-ML BEST PRACTICE: DATE FORMATTING ISSUE-->
      <ProtocolApplication activityDate="YYYY-MM-DD">
<!-- OPTIONAL association -->
        <Performers_assnreflist>
          <Person_ref identifier="ebi.ac.uk:MIAMExpress/Person:<object>" />
        </Performers_assnreflist>
        <Protocol_assnref>
          <Protocol_ref identifier="ebi.ac.uk:MIAMExpress/Protocol:P-MEXP-XX" />
        </Protocol_assnref>
      </ProtocolApplication>
    </ProtocolApplications_assnlist>
    <BioAssayDataSources_assnreflist>
      <MeasuredBioAssayData_ref
identifier="ebi.ac.uk:MIAMExpress/MeasuredBioAssayData:<object>" />
    </BioAssayDataSources_assnreflist>
  </Transformation>

  </ProducerTransformation_assn>
</DerivedBioAssayData>

  <MeasuredBioAssayData identifier="ebi.ac.uk:MIAMExpress/MeasuredBioAssayData:<object>">
    <BioAssayDimension_assnref>
      <BioAssayDimension_ref
identifier="ebi.ac.uk:MIAMExpress/BioAssayDimension:<object>" />
    </BioAssayDimension_assnref>
    <DesignElementDimension_assnref>
      <FeatureDimension_ref identifier="ebi.ac.uk:MIAMExpress/FeatureDimension:<object>" />
    </DesignElementDimension_assnref>
    <QuantitationTypeDimension_assnref>
      <QuantitationTypeDimension_ref
identifier="ebi.ac.uk:MIAMExpress/QuantitationTypeDimension:<object>" />
    </QuantitationTypeDimension_assnref>
  </MeasuredBioAssayData>
  <BioDataValues_assn>

```

```
<BioDataCube>
  <DataExternal_assn>
    <DataExternal filenameURI="www.ebi.ac.uk/datafile.txt"/>
  </DataExternal_assn>
</BioDataCube>
</BioDataValues_assn>
</MeasuredBioAssayData>
</BioAssayData_assnlist>
</BioAssayData_package>
```


Array design description (1) - DTD

```
<!ELEMENT ArrayDesign_package (ReporterGroup_assnlist?, CompositeGroup_assnlist?, ArrayDesign_assnlist?) >

<!ELEMENT ReporterGroup_assnlist (ReporterGroup+) >
<!ELEMENT ReporterGroup_ref EMPTY >
<!ATTLIST ReporterGroup_ref identifier CDATA #REQUIRED >
<!ELEMENT ReporterGroup (...Types_assnlist?,Species_assn?,Reporters_assnreflist) >
<!ATTLIST ReporterGroup identifier CDATA #REQUIRED .. >
<!ELEMENT Species_assn (OntologyEntry) >

<!ELEMENT CompositeGroup_assnlist (CompositeGroup+) >
<!ELEMENT CompositeGroup_ref EMPTY >
<!ATTLIST CompositeGroup_ref identifier CDATA #REQUIRED >
<!ELEMENT CompositeGroup (...Types_assnlist?,Species_assn?,CompositeSequences_assnreflist) >
<!ATTLIST CompositeGroup identifier CDATA #REQUIRED .. >

<!ELEMENT ArrayDesign_assnlist (... | PhysicalArrayDesign)+) >
<!ELEMENT PhysicalArrayDesign_ref EMPTY >
<!ATTLIST PhysicalArrayDesign_ref identifier CDATA #REQUIRED >
<!ELEMENT PhysicalArrayDesign (...FeatureGroups_assnlist?,ReporterGroups_assnreflist?,
    CompositeGroups_assnreflist?,DesignProviders_assnreflist?,SurfaceType_assn?,ZoneGroups_assnlist?) >
<!ATTLIST PhysicalArrayDesign identifier CDATA #REQUIRED
    name CDATA #IMPLIED
    ..
    numberOfFeatures CDATA #IMPLIED >

<!ELEMENT FeatureGroups_assnlist (FeatureGroup+) >
<!ELEMENT ReporterGroups_assnreflist (ReporterGroup_ref+) >
<!ELEMENT CompositeGroups_assnreflist (CompositeGroup_ref+) >
<!ELEMENT DesignProviders_assnreflist ((Person_ref | Organization_ref)+) >
<!ELEMENT SurfaceType_assn (OntologyEntry) >
<!ELEMENT ZoneGroups_assnlist (ZoneGroup+) >

<!ELEMENT FeatureGroup (...Types_assnlist?,...TechnologyType_assn?,...DistanceUnit_assn?,Features_assnlist) >
<!ATTLIST FeatureGroup identifier CDATA #REQUIRED ..
    featureWidth CDATA #IMPLIED
    featureLength CDATA #IMPLIED
    featureHeight CDATA #IMPLIED >
<!ELEMENT TechnologyType_assn (OntologyEntry) >
<!ELEMENT Features_assnlist (Feature+) >

<!ELEMENT Feature_ref EMPTY >
<!ATTLIST Feature_ref identifier CDATA #REQUIRED >
<!ELEMENT Feature (...Zone_assnref?,FeatureLocation_assn?) >
<!ATTLIST Feature identifier CDATA #REQUIRED .. >

<!ELEMENT Zone_assnref (Zone_ref) >
<!ELEMENT FeatureLocation_assn (FeatureLocation) >
<!ELEMENT FeatureLocation (...) >
<!ATTLIST FeatureLocation row CDATA #REQUIRED
    column CDATA #REQUIRED >

<!ELEMENT ZoneGroup (...ZoneLocations_assnlist?) >
<!ELEMENT ZoneLocations_assnlist (Zone+) >
<!ELEMENT Zone_ref EMPTY >
<!ATTLIST Zone_ref identifier CDATA #REQUIRED >
<!ELEMENT Zone (...) >
<!ATTLIST Zone identifier CDATA #REQUIRED ..
    row CDATA #IMPLIED
    column CDATA #IMPLIED .. >

<!ELEMENT Array_package (ArrayGroup_assnlist?, Array_assnlist?, ArrayManufacture_assnlist?) >
<!ELEMENT ArrayGroup_assnlist (ArrayGroup+) >
<!ELEMENT Array_assnlist (Array+) >
<!ELEMENT ArrayManufacture_assnlist (ArrayManufacture+) >

<!ELEMENT ArrayGroup_ref EMPTY >
<!ATTLIST ArrayGroup_ref identifier CDATA #REQUIRED >
<!ELEMENT ArrayGroup (...Arrays_assnreflist,SubstrateType_assn?,DistanceUnit_assn?) >
<!ATTLIST ArrayGroup identifier CDATA #REQUIRED ..
    numArrays CDATA #IMPLIED ..
    width CDATA #IMPLIED
    length CDATA #IMPLIED >
<!ELEMENT Arrays_assnreflist (Array_ref+) >
<!ELEMENT SubstrateType_assn (OntologyEntry) >

<!ELEMENT Array_ref EMPTY >
<!ATTLIST Array_ref identifier CDATA #REQUIRED >
<!ELEMENT Array (...ArrayDesign_assnref,Information_assnref,ArrayGroup_assnref?,...) >
<!ATTLIST Array identifier CDATA #REQUIRED .. >

<!ELEMENT ArrayDesign_assnref (... | PhysicalArrayDesign_ref) >
<!ELEMENT Information_assnref (ArrayManufacture_ref) >
<!ELEMENT ArrayGroup_assnref (ArrayGroup_ref) >

<!ELEMENT ArrayManufacture_ref EMPTY >
<!ATTLIST ArrayManufacture_ref identifier CDATA #REQUIRED >
<!ELEMENT ArrayManufacture (...Arrays_assnreflist,...ProtocolApplications_assnlist?) >
<!ATTLIST ArrayManufacture
    identifier CDATA #REQUIRED
    name CDATA #IMPLIED .. >
```

Array design description (1) - examples

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE ArrayDesign_package PUBLIC "-//OMG//DTD MAGE-ML 1.1//EN"
"http://schema.omg.org/lsr/gene_expression/1.1/MAGE-ML.dtd" >

<!--MAGE-ML Good Practice Guidelines-->
<!--MIAME requirement: to indicate content requirement-->
<!--MO TERMS: MGED Controlled vocabulary must be provided-->
<!--ADF CREATION / ADF PARSING: Points to object that should used when creating an ADF-->
<!--MO Rules: requires MO rules for appropriate coding-->

<ArrayDesign_package>
<!--IMPORTANT: One of FeatureGroups, ReporterGroups and CompositeGroups should have
association to
species -->

  <ReporterGroup_assnlist>
    <ReporterGroup identifier="ebi.ac.uk:MIAMExpress/ReporterGroup:<object>">
<!--MIAME-REQUIREMENT: Provide Type 'Role' to specify if reporter is Control or
Experimental-->
<!--ADF-CREATION / ADF PARSING: Create Field 'Reporter Group [role] to specify if reporter
is 'Control' or
'Experimental'-->

<!--OPTIONAL: If Type Association not specified at the Level of CompositeGroup, Specify it
here-->
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
<Types_assnlist>
  <OntologyEntry category="DesignElementGroupType" value="
experimental_design_element_group_type "/>
</Types_assnlist>

<!--OPTIONAL: If Species Association not specified at the Level of Composite Group, Specify
it here-->
<Species_assn>
<!--MIAME-REQUIREMENT: Provide Species using MGED ontology class ORGANISM-->
<!--MO Rules: Mandatory use of MGED Ontology class 'Organism'-->
  <OntologyEntry category="Organism" value="Homo sapiens"/>
</Species_assn>

  <Reporters_assnreflist>
    <Reporter_ref identifier="ebi.ac.uk:MIAMExpress/Reporter:<object>"/>
    <!--See DesignElement package for more information about Reporter and Composite -->
  </Reporters_assnreflist>
</ReporterGroup>
</ReporterGroup_assnlist>

  <CompositeGroup_assnlist>
    <CompositeGroup identifier="ebi.ac.uk:MIAMExpress/CompositeGroup:<object>">

<!--OPTIONAL: If Type Association not specified at the Level of Reporter Group, Specify it
here-->
  <Types_assnlist>
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
    <OntologyEntry category="DesignElementGroupType" value="
experimental_design_element_group_type "/>
  </Types_assnlist>
<!--OPTIONAL: If Species Association not specified at the Level of Reporter Group, Specify
it here-->
  <Species_assn>
```

```

<!--MIAME-REQUIREMENT: Provide Species using MGED ontology class ORGANISM--><!--MO Rule:
Mandatory use of MGED Ontology class 'Organism'-->
  <OntologyEntry category="Organism" value="Homo sapiens"/>
</Species_assn>

  <CompositeSequences_assnreflist>
    <CompositeSequence_ref
identifier="ebi.ac.uk:MIAMExpress/CompositeSequence:<object>" />
    </CompositeSequences_assnreflist>
  </CompositeGroup>
</CompositeGroup_assnlist>

<ArrayDesign_assnlist>

<!--MAGE-ML BEST PRACTICE: use PhysicalArrayDesign instead of ArrayDesign-->
<!--MIAME-REQUIREMENT:Attribute [number of feature] MUST BE PROVIDED -->
<!--ADF-CREATION/ ADF PARSING:Attribute [Name] should be formatted following
rule:[institute][species][number of feature][version]-->

  <PhysicalArrayDesign identifier="ebi.ac.uk:MIAMExpress/PhysicalArrayDesign:<object>"
name="convention for naming" numberOfFeatures="6500">

    <Descriptions_assnlist>
      <Description text=""/>
    </Descriptions_assnlist>

    <FeatureGroups_assnlist>
<!--MAGE-ML BEST PRACTICE: Do NOT provide Species association despite the model allows it as
well as the DTD Species should be specified only at the level of Reporter Group and
Composite Group-->

<FeatureGroup featureHeight="0" featureLength="10 um"
  featureWidth="10 um" identifier="ebi.ac.uk:MIAMExpress/FeatureGroup:<object>">

<!-- OPTIONAL association -->
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
  <Types_assnlist>
    <OntologyEntry category=" DesignElementGroupType " value="
control_design_element_group_type "/>
  </Types_assnlist>

<!--MIAME-REQUIREMENT: TechnologyType required-->
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
  <TechnologyType_assn>
    <OntologyEntry category="TechnologyType" value="spotted_ss_oligo_features" />
  </TechnologyType_assn>

<!-- OPTIONAL association -->
  <DistanceUnit_assn>
    <DistanceUnit unitNameCV="um" />
  </DistanceUnit_assn>

  <Features_assnlist>
<!--Identify all Features present in that group-->
  <Feature identifier="ebi.ac.uk:MIAMExpress/Feature:<object>">

<!--MIAME-REQUIREMENT:if feature of Control_type-->
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
<!-- OPTIONAL association -->
  <ControlType_assn>
    <OntologyEntry category="ControlType" value="control_empty" />

```

```

</ControlType_assn>
<Zone_assnref>
  <Zone_ref identifier="ebi.ac.uk:MIAMExpress/Zone:object"/>
</Zone_assnref>

  <FeatureLocation_assn>
<!--MIAME-REQUIREMENT: FeatureLocation-->
  <FeatureLocation column="y" row="x">
<!--MIAME REQUIREMENT: must be supplied-->
<!--ADF-Creation/ADF Parsing:Create Fields [Column] and [Raw] in ADF for specifying feature
location within Zone (aka Grid)-->
<!--PROVIDE x and y coordinate for feature within a Zone -->
  </FeatureLocation>
</FeatureLocation_assn>
</Feature>
</Features_assnlist>
</FeatureGroup>
</FeatureGroups_assnlist>

<!--MIAME REQUIREMENT: either 'Person' or 'Organization' must be supplied-->
<DesignProviders_assnreflist>
  <Person_ref identifier="ebi.ac.uk:MIAMExpress/Person:<object>"/>
  <Organization_ref identifier="ebi.ac.uk:MIAMExpress/Organization:<object>"/>
</DesignProviders_assnreflist>

<!--MIAME REQUIREMENT: Surface Type required-->
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
<SurfaceType_assn>
  <OntologyEntry category="Surfacetyp" value="aminosilane "/>
</SurfaceType_assn>

  <ZoneGroups_assnlist>
    <ZoneGroup>
      <ZoneLocations_assnlist>
<!--MIAME REQUIREMENT: must be supplied-->
<!--ADF-CREATION/ ADF PARSING:Create Fields [MetaColumn] and [MetaRaw] in ADF for specifying
Zone location within Array-->
<!--PROVIDE X and Y coordinates for Zone-->
  <Zone column="Y" identifier="ebi.ac.uk:MIAMExpress/Zone:<object>" row="X">
    </Zone>

      </ZoneLocations_assnlist>
    </ZoneGroup>
  </ZoneGroups_assnlist>
</PhysicalArrayDesign>
</ArrayDesign_assnlist>
</ArrayDesign_package>

<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE Array_package PUBLIC "-//OMG//DTD MAGE-ML 1.1//EN"
"http://schema.omg.org/lsr/gene_expression/1.1/MAGE-ML.dtd" >
<!--MAGE-ML Good Practice Guidelines-->
<!--MIAME requirement: to indicate content requirement-->
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->

<Array_package>
  <ArrayGroup_assnlist>
    <ArrayGroup identifier="ebi.ac.uk:MIAMExpress/ArrayGroup:<object>">
      <Arrays_assnreflist>
        <Array_ref identifier="ebi.ac.uk:MIAMExpress/Array:<object>"/>
      </Arrays_assnreflist>
    </ArrayGroup>
  </ArrayGroup_assnlist>
</Array_package>

```

```

<!--MIAME REQUIREMENT: Substrate Type required-->
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
  <SubstrateType_assn>
    <OntologyEntry category="SubstrateType" value="glass"/>
  </SubstrateType_assn>

  <DistanceUnit_assn>
    <DistanceUnit unitName="micrometer" unitNameCV="um"/>
  </DistanceUnit_assn>
</ArrayGroup>
</ArrayGroup_assnlist>
<Array_assnlist>
  <Array identifier="ebi.ac.uk:MIAMExpress/Array:<object>">
    <ArrayDesign_assnref>
      <PhysicalArrayDesign_ref
identifier="ebi.ac.uk:MIAMExpress/PhysicalArrayDesign:<object>" />
    </ArrayDesign_assnref>
    <Information_assnref>
      <ArrayManufacture_ref identifier="ebi.ac.uk:MIAMExpress/ArrayManufacture:<object>" />
    </Information_assnref>
  </Array>
</Array_assnlist>
<ArrayManufacture_assnlist>
  <ArrayManufacture identifier="ebi.ac.uk:MIAMExpress/ArrayManufacture:<object>">
    <Arrays_assnreflist>
      <Array_ref identifier="ebi.ac.uk:MIAMExpress/Array:<object>" />
    </Arrays_assnreflist>
    <ProtocolApplications_assnlist>
<!--MAGE-ML BEST PRACTICE: DATE FORMATTING ISSUE-->
      <ProtocolApplication activityDate="YYYY-MM-DD">
<!--OPTIONAL association-->
        <Performers_assnreflist>
          <Person_ref identifier="ebi.ac.uk:MIAMExpress/Person:<object>" />
        </Performers_assnreflist>
        <Protocol_assnref>
          <Protocol_ref identifier="ebi.ac.uk:MIAMExpress/Protocol:<object>" />
        </Protocol_assnref>
      </ProtocolApplication>
    </ProtocolApplications_assnlist>
  </ArrayManufacture>
</ArrayManufacture_assnlist>
</Array_package>

```


Array design description (2) - DTD

```
<!ELEMENT DesignElement_package (CompositeSequence_assnlist?,Reporter_assnlist?,..
    ReporterCompositeMap_assnlist?,FeatureReporterMap_assnlist?) >

<!ELEMENT CompositeSequence_assnlist (CompositeSequence+) >
<!ELEMENT Reporter_assnlist (Reporter+) >
<!ELEMENT ReporterCompositeMap_assnlist (ReporterCompositeMap+) >
<!ELEMENT FeatureReporterMap_assnlist (FeatureReporterMap+) >

<!ELEMENT CompositeSequences_assnreflist (CompositeSequence_ref+) >
<!ELEMENT CompositeSequence_ref EMPTY >
<!ATTLIST CompositeSequence_ref identifier CDATA #REQUIRED >
<!ELEMENT CompositeSequence (..,Descriptions_assnlist?,..
    ControlType_assn?,
    BiologicalCharacteristics_assnreflist?,
    (ReporterCompositeMaps_assnreflist? | ..)) >
<!ATTLIST CompositeSequence
    identifier CDATA #REQUIRED
    name CDATA #IMPLIED >

<!ELEMENT ControlType_assn (OntologyEntry) >
<!ELEMENT BiologicalCharacteristics_assnreflist (BioSequence_ref+) >
<!ELEMENT ReporterCompositeMaps_assnreflist (ReporterCompositeMap_ref+) >

<!ELEMENT Reporters_assnreflist (Reporter_ref+) >
<!ELEMENT Reporter_ref EMPTY >
<!ATTLIST Reporter_ref identifier CDATA #REQUIRED >
<!ELEMENT Reporter (..,Descriptions_assnlist?,..,ControlType_assn?,ImmobilizedCharacteristics_assnreflist?,..,
    FailTypes_assnlist?, FeatureReporterMaps_assnreflist?) >
<!ATTLIST Reporter
    identifier CDATA #REQUIRED
    name CDATA #IMPLIED >

<!ELEMENT ImmobilizedCharacteristics_assnreflist (BioSequence_ref+) >
<!ELEMENT FailTypes_assnlist (OntologyEntry+) >
<!ELEMENT FeatureReporterMaps_assnreflist (FeatureReporterMap_ref+) >

<!ELEMENT ReporterCompositeMap_ref EMPTY >
<!ATTLIST ReporterCompositeMap_ref identifier CDATA #REQUIRED >
<!ELEMENT ReporterCompositeMap (..,CompositeSequence_assnref,ReporterPositionSources_assnlist) >
<!ATTLIST ReporterCompositeMap
    identifier CDATA #REQUIRED .. >

<!ELEMENT CompositeSequence_assnref (CompositeSequence_ref) >
<!ELEMENT ReporterPositionSources_assnlist (ReporterPosition+) >
<!ELEMENT ReporterPosition (..,Reporter_assnref,..) >
<!ELEMENT Reporter_assnref (Reporter_ref) >

<!ELEMENT FeatureReporterMap_ref EMPTY >
<!ATTLIST FeatureReporterMap_ref identifier CDATA #REQUIRED >
<!ELEMENT FeatureReporterMap (..,Reporter_assnref,FeatureInformationSources_assnlist) >
<!ATTLIST FeatureReporterMap
    identifier CDATA #REQUIRED .. >

<!ELEMENT FeatureInformationSources_assnlist (FeatureInformation+) >
<!ELEMENT FeatureInformation (..,Feature_assnref,..) >
<!ELEMENT Feature_assnref (Feature_ref) >

<!ELEMENT BioSequence_package (BioSequence_assnlist?) >
<!ELEMENT BioSequence_assnlist (BioSequence+) >

<!ELEMENT BioSequence_ref EMPTY >
<!ATTLIST BioSequence_ref identifier CDATA #REQUIRED >
<!ELEMENT BioSequence (..,SequenceDatabases_assnlist?,..,PolymerType_assn,Type_assn,..) >
<!ATTLIST BioSequence
    identifier CDATA #REQUIRED ..
    length CDATA #IMPLIED
    isApproximateLength CDATA #IMPLIED ..
    sequence CDATA #IMPLIED >

<!ELEMENT SequenceDatabases_assnlist (DatabaseEntry+) >
<!ELEMENT PolymerType_assn (OntologyEntry) >

<!ELEMENT DatabaseEntry (..,Database_assnref) >
<!ATTLIST DatabaseEntry
    accession CDATA #REQUIRED
    accessionVersion CDATA #IMPLIED
    URI CDATA #IMPLIED >

<!ELEMENT Database_assnref (Database_ref) >
```

Array design description (2) - example

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE DesignElement_package PUBLIC "-//OMG//DTD MAGE-ML 1.1//EN"
"http://schema.omg.org/lsrc/gene_expression/1.1/MAGE-ML.dtd" >
<!--MAGE-ML Good Practice Guidelines-->
<!--MIAME requirement: to indicate content requirement-->
<!--ADF CREATION / ADF PARSING: Points to object that should used when creating an ADF-->
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->

<DesignElement_package>
  <CompositeSequence_assnlist>
    <CompositeSequence identifier="ebi.ac.uk:MIAMEExpress/CompositeSequence:<object>">
<!--ADF CREATION / ADF PARSING: Create field 'CompositeSequence Identifier'-->
<!--ADF CREATION / ADF PARSING: Create field 'CompositeSequence Name' and provide Sensible
CompositeSequence Name as displaid in interface-->
      <Descriptions_assnlist>
<!-- ADF CREATION / ADF PARSING: Create a 'CompositeSequence Comment' to provide free text
description-->
        <Description/>
      </Descriptions_assnlist>

      <ControlType_assn>
<!--MIAME-REQUIREMENT: to be specified if reporter is a control element-->
<!--ADF CREATION / ADF PARSING: Create field 'CompositeSequence ControlType' in ADF to
specify type of control using MO term-->
<!--MO-terms: select term from controlled vocabulary-->
        <OntologyEntry category="ControlType" value="control_spike_calibration"/>
      </ControlType_assn>

      <BiologicalCharacteristics_assnreflist>
        <BioSequence_ref identifier="ebi.ac.uk:MIAMEExpress/BioSequence:<object>" />
<!--ADF CREATION / ADF PARSING: Create 'CompositeSequence BioSequence [Actual Sequence]'
field in ADF-->
      </BiologicalCharacteristics_assnreflist>

      <ReporterCompositeMaps_assnreflist>
        <ReporterCompositeMap_ref
identifier="ebi.ac.uk:MIAMEExpress/ReporterCompositeMap:<object>" />
      </ReporterCompositeMaps_assnreflist>
    </CompositeSequence>
  </CompositeSequence_assnlist>

  <Reporter_assnlist>

    <Reporter identifier="ebi.ac.uk:MIAMEExpress/Reporter:<object>" name="Reporter">
      <!--ADF CREATION / ADF PARSING: Create field 'Reporter Identifier'-->
      <!--ADF CREATION / ADF PARSING: Create field 'Reporter Name' and provide Sensible
Reporter Name as displaid in interface-->
      <Descriptions_assnlist>
        <Description text="reporter"/>
<!--ADF-CREATION / ADF PARSING:Create a 'Reporter Comment' to provide free text description-
->
      </Descriptions_assnlist>

      <ControlType_assn>
<!--MIAME-REQUIREMENT: to be specified if reporter is a control element-->
<!--ADF CREATION / ADF PARSING: Create field 'Reporter ControlType' in ADF to specify type of
control using MO term-->
<!--MO Rules: requires MO rules for appropriate coding-->
```

```

    <!--MO TERMS: use of MGED Ontology instances required -->
    <OntologyEntry category="ControlType" value="control_label"/>
</ControlType_assn>

    <ImmobilizedCharacteristics_assnreflist>
<!--Several BioSequence can be referenced hereas in case of Sequence and PCR primers.-->
    <BioSequence_ref identifier="ebi.ac.uk:MIAMExpress/BioSequence:<object>"/>
<!-- ADF CREATION / ADF PARSING: Create Field 'Reporter BioSequence [Forward Primer]' to
provide information-->
    <BioSequence_ref identifier="ebi.ac.uk:MIAMExpress/BioSequence:<object>"/>
<!-- ADF CREATION / ADF PARSING: Create Field 'Reporter BioSequence [Reverse Primer]' to
provide information-->
    <BioSequence_ref identifier="ebi.ac.uk:MIAMExpress/BioSequence:<object>"/>
<!--ADF CREATION / ADF PARSING: Create 'Reporter BioSequence [Actual Sequence]' field in
ADF-->
</ImmobilizedCharacteristics_assnreflist>

<!--OPTIONAL association-->
<!--MIAME-REQUIREMENT: provide QC checks e.g. in the case of PCR based arrays -->
<!--ADF CREATION / ADF PARSING: Create 'Reporter Failed Type' field in ADF-->

<FailTypes_assnlist>
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
    <OntologyEntry category="FailType" value="PCR_fail"/>
</FailTypes_assnlist>

    <FeatureReporterMaps_assnreflist>
    <FeatureReporterMap_ref
identifier="ebi.ac.uk:MIAMExpress/FeatureReporterMap:<object>"/>
    </FeatureReporterMaps_assnreflist>
    </Reporter>
</Reporter_assnlist>

    <ReporterCompositeMap_assnlist>
    <ReporterCompositeMap identifier="ebi.ac.uk:MIAMExpress/ReporterCompositeMap:<object>">
    <CompositeSequence_assnref>
    <CompositeSequence_ref
identifier="ebi.ac.uk:MIAMExpress/CompositeSequence:<object>"/>
    </CompositeSequence_assnref>
    <ReporterPositionSources_assnlist>
    <ReporterPosition end="35" start="10">
    <!--Provide location of reporter within CompositeSequence object -->
    <Reporter_assnref>
    <Reporter_ref identifier="ebi.ac.uk:MIAMExpress/Reporter:<object>"/>
    </Reporter_assnref>
    </ReporterPosition>
    </ReporterPositionSources_assnlist>
    </ReporterCompositeMap>
</ReporterCompositeMap_assnlist>

    <FeatureReporterMap_assnlist>
    <FeatureReporterMap identifier="ebi.ac.uk:MIAMExpress/FeatureReporterMap:<object>">
    <Reporter_assnref>
    <Reporter_ref identifier="ebi.ac.uk:MIAMExpress/Reporter:<object>"/>
    </Reporter_assnref>
    <FeatureInformationSources_assnlist>
    <FeatureInformation>
    <Feature_assnref>
    <Feature_ref identifier="ebi.ac.uk:MIAMExpress/Feature:<object>"/>
    </Feature_assnref>
    </FeatureInformation>
    </FeatureInformationSources_assnlist>
    </FeatureReporterMap>

```

```
</FeatureReporterMap_assnlist>
</DesignElement_package>
```

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE BioSequence_package PUBLIC "-//OMG//DTD MAGE-ML 1.1//EN"
"http://schema.omg.org/lsr/gene_expression/1.1/MAGE-ML.dtd" >
<!--MAGE-ML Good Practice Guidelines-->
<!--MIAME requirement: to indicate content requirement-->
<!--MO TERMS: MGED Controlled vocabulary must be provided-->
<!--ADF creation / ADF parsing: Points to object that should used when creating an ADF-->
```

```
<BioSequence_package>
```

```
<BioSequence_assnlist>
```

```
<BioSequence identifier="ebi.ac.uk:MIAMEexpress/BioSequence:<object>"
isApproximateLength="n/a" sequence="ACTCTGGGCCTGGCT" length="15">
```

```
<!--MIAME-REQUIREMENT:Attribute [sequence] required if Oligo-array -->
<!--ADF creation / ADF parsing: Create field with 'Reporter/CompositeSequence BioSequence
[Actual Sequence] '-->
```

```
<SequenceDatabases_assnlist>
```

```
<DatabaseEntry accession="NM_13243">
```

```
<!--ADF creation / ADF parsing: several accession numbers can be supplied in ADF
using semi-colon (;) as separator-->
```

```
<Database_assnref>
```

```
<!--ADF creation / ADF parsing: Database Entry Field in ADF-->
```

```
<!--ADF creation / ADF parsing: database tag should be supplied between square
brackets [] in field header-->
```

```
<Database_ref identifier="ebi.ac.uk:MIAMEexpress/Database:refseq"/>
```

```
</Database_assnref>
```

```
</DatabaseEntry>
```

```
</SequenceDatabases_assnlist>
```

```
<!--ADF creation / ADF parsing: MANDATORY Field in ADF-->
```

```
<!--ADF creation / ADF parsing: Create Field with 'BioSequence PolymerType' Header-->
```

```
<!--MO Rules: requires MO rules for appropriate coding-->
```

```
<!--MO TERMS: use of MGED Ontology instances required -->
```

```
<PolymerType_assn>
```

```
<OntologyEntry category="PolymerType" value="DNA"/>
```

```
</PolymerType_assn>
```

```
<!--ADF creation / ADF parsing: MANDATORY Field in ADF-->
```

```
<!--ADF creation / ADF parsing: Create Field with 'BioSequence PolymerType' Header-->
```

```
<!--MO Rules: requires MO rules for appropriate coding-->
```

```
<!--MO TERMS: use of MGED Ontology instances required -->
```

```
<Type_assn>
```

```
<OntologyEntry category="BioSequenceType" value="ORF"/>
```

```
</Type_assn>
```

```
</BioSequence>
```

```
</BioSequence_assnlist>
```

```
</BioSequence_package>
```

Miscellaneous: quantitation types - class diagram and DTD

```

<!ELEMENT QuantitationType_package (QuantitationType_assnlist?) >
<!ELEMENT QuantitationType_assnlist ((SpecializedQuantitationType | DerivedSignal | MeasuredSignal | Error |
    PValue | ExpectedValue | Ratio | PresentAbsent | Failed)+) >

<!ELEMENT SpecializedQuantitationType_ref EMPTY >
<!ATTLIST SpecializedQuantitationType_ref identifier CDATA #REQUIRED >
<!ELEMENT SpecializedQuantitationType (...Descriptions_assnlist?,...,Channel_assnref?,Scale_assn,DataType_assn,...) >
<!ATTLIST SpecializedQuantitationType identifier CDATA #REQUIRED
    name CDATA #IMPLIED
    isBackground CDATA #REQUIRED >

<!ELEMENT Channel_assnref (Channel_ref) >
<!ELEMENT Scale_assn (OntologyEntry) >
<!ELEMENT DataType_assn (OntologyEntry) >

<!ELEMENT DerivedSignal_ref EMPTY >
<!ATTLIST DerivedSignal_ref identifier CDATA #REQUIRED >
<!ELEMENT DerivedSignal (...Descriptions_assnlist?,Channel_assnref?,Scale_assn,DataType_assn,...) >
<!ATTLIST DerivedSignal identifier CDATA #REQUIRED
    name CDATA #IMPLIED
    isBackground CDATA #REQUIRED >

<!ELEMENT Error_ref EMPTY >
<!ATTLIST Error_ref identifier CDATA #REQUIRED >
<!ELEMENT Error (...Descriptions_assnlist?,...,Channel_assnref?,Scale_assn,DataType_assn,...,
    TargetQuantitationType_assnref) >
<!ATTLIST Error identifier CDATA #REQUIRED
    name CDATA #IMPLIED
    isBackground CDATA #REQUIRED >

<!ELEMENT TargetQuantitationType_assnref (SpecializedQuantitationType_ref | DerivedSignal_ref | MeasuredSignal_ref
    | Error_ref | PValue_ref | ExpectedValue_ref | Ratio_ref | PresentAbsent_ref | Failed_ref) >

<!ELEMENT ExpectedValue_ref EMPTY >
<!ATTLIST ExpectedValue_ref identifier CDATA #REQUIRED >
<!ELEMENT ExpectedValue (...Descriptions_assnlist?,...,Channel_assnref?,Scale_assn,DataType_assn,...,
    TargetQuantitationType_assnref) >
<!ATTLIST ExpectedValue identifier CDATA #REQUIRED
    name CDATA #IMPLIED
    isBackground CDATA #REQUIRED >

<!ELEMENT Failed_ref EMPTY >
<!ATTLIST Failed_ref identifier CDATA #REQUIRED >
<!ELEMENT Failed (...Descriptions_assnlist?,...,Channel_assnref?,Scale_assn,DataType_assn,...) >
<!ATTLIST Failed identifier CDATA #REQUIRED
    name CDATA #IMPLIED
    isBackground CDATA #REQUIRED >

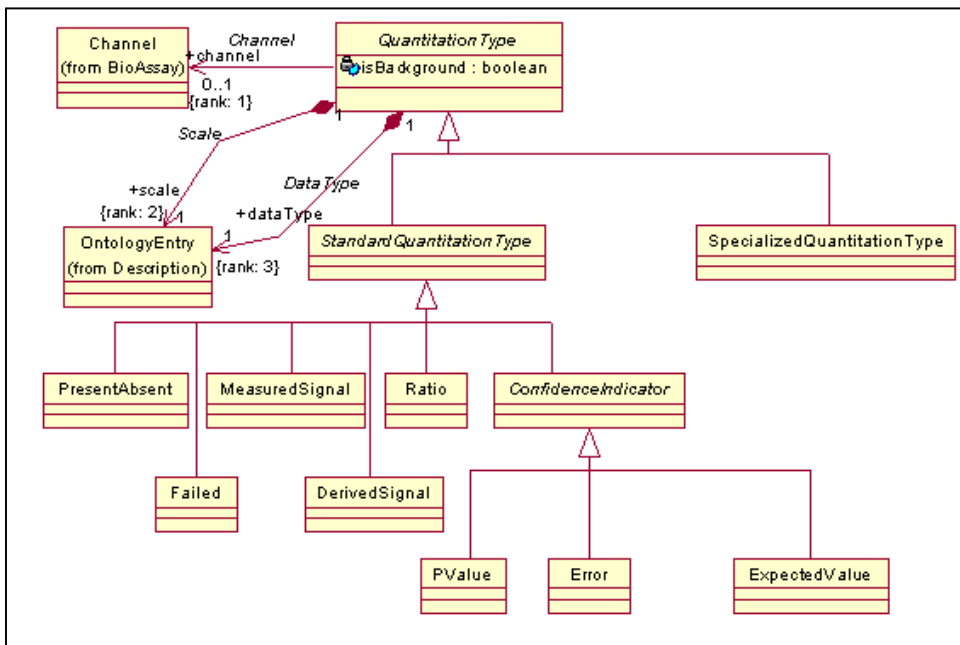
<!ELEMENT MeasuredSignal_ref EMPTY >
<!ATTLIST MeasuredSignal_ref identifier CDATA #REQUIRED >
<!ELEMENT MeasuredSignal (...Descriptions_assnlist?,...,
    Channel_assnref?,Scale_assn,DataType_assn,...) >
<!ATTLIST MeasuredSignal identifier CDATA #REQUIRED
    name CDATA #IMPLIED
    isBackground CDATA #REQUIRED >

<!ELEMENT PValue_ref EMPTY >
<!ATTLIST PValue_ref identifier CDATA #REQUIRED >
<!ELEMENT PValue (...Descriptions_assnlist?,...,
    Channel_assnref?, Scale_assn,
    DataType_assn,...,
    TargetQuantitationType_assnref) >
<!ATTLIST PValue identifier CDATA #REQUIRED
    name CDATA #IMPLIED
    isBackground CDATA #REQUIRED >

<!ELEMENT PresentAbsent_ref EMPTY >
<!ATTLIST PresentAbsent_ref identifier CDATA #REQUIRED >
<!ELEMENT PresentAbsent (...
    Descriptions_assnlist?,
    ...,Channel_assnref?, Scale_assn,
    DataType_assn,...) >
<!ATTLIST PresentAbsent
    identifier CDATA #REQUIRED
    name CDATA #IMPLIED
    isBackground CDATA #REQUIRED >

<!ELEMENT Ratio_ref EMPTY >
<!ATTLIST Ratio_ref identifier CDATA #REQUIRED >
<!ELEMENT Ratio (...Descriptions_assnlist?,...,
    Channel_assnref?,
    Scale_assn,
    DataType_assn,...) >
<!ATTLIST Ratio
    identifier CDATA #REQUIRED
    name CDATA #IMPLIED
    isBackground CDATA #REQUIRED >

```



Miscellaneous: quantitation types - example

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE QuantitationType_package PUBLIC "-//OMG//DTD MAGE-ML 1.1//EN"
"http://schema.omg.org/lsr/gene_expression/1.1/MAGE-ML.dtd" >

  <QuantitationType_package>
    <QuantitationType_assnlist>

<!--MIAME REQUIREMENT: A full description of the Quantitation Type should be provided by
Manufacturer-->
<!--MIAME REQUIREMENT: Description should include method of calculation-->
<!--MAGE-ML good practice-->

      <MeasuredSignal identifier="ebi.ac.uk:MIAMEExpress/MeasuredSignal:<object>"
isBackground="false" name=" Number of pixels in Green Channel ">

        <Descriptions_assnlist>
          <Description>
            text="Number of pixels in Green Channel: Total number of pixels used to
compute feature statistics; ie. total number of inlier pixels/per spot">

<!--MAGE-ML good practice-->
<!--MIAME REQUIREMENT: provide mapping when available to MGED approved Quantitation Type
Definitions (to be released)-->
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
          <Annotations_assnlist>
            <OntologyEntry category="QuantitationType"
description="the raw signal column gives the [raw] signal output from
the image analysis algorithm."
value="SIGNAL_RAW"/>
          </Annotations_assnlist>
        </Description>
      </Descriptions_assnlist>
<!--OPTIONAL association if QT is related to one Channel-->
      <Channel_assnref>
        <Channel_ref identifier="ebi.ac.uk:MIAMEExpress/Channel:<object>"/>
      </Channel_assnref >
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
      <Scale_assn>
        <OntologyEntry category="Scale" value="unscaled"/>
      </Scale_assn>
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
      <DataType_assn>
        <OntologyEntry category="DataType" value="string_datatype"/>
      </DataType_assn>
<!--OPTIONAL association-->
      <QuantitationTypeMaps_assnreflist>
        <QuantitationTypeMap_ref
identifier="ebi.ac.uk:MIAMEExpress/QuantitationTypeMap:<object>"/>
      </QuantitationTypeMaps_assnreflist>

    </MeasuredSignal>
  </QuantitationType_assnlist>
</QuantitationType_package>
```

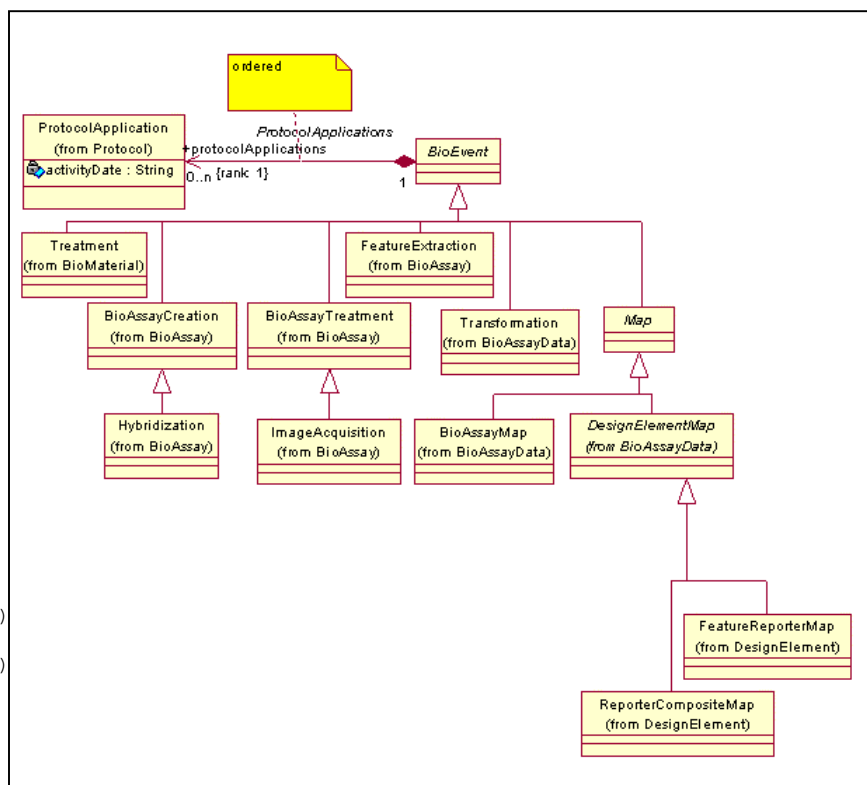
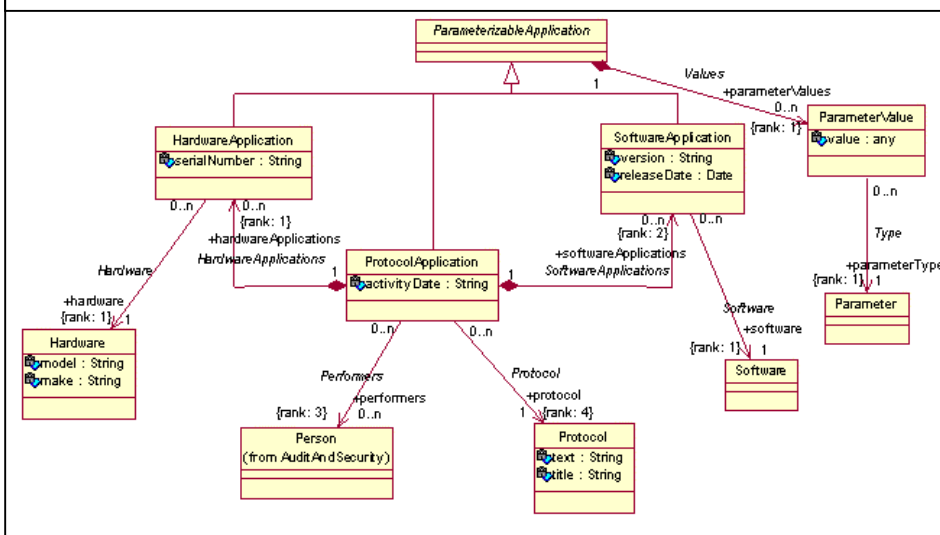
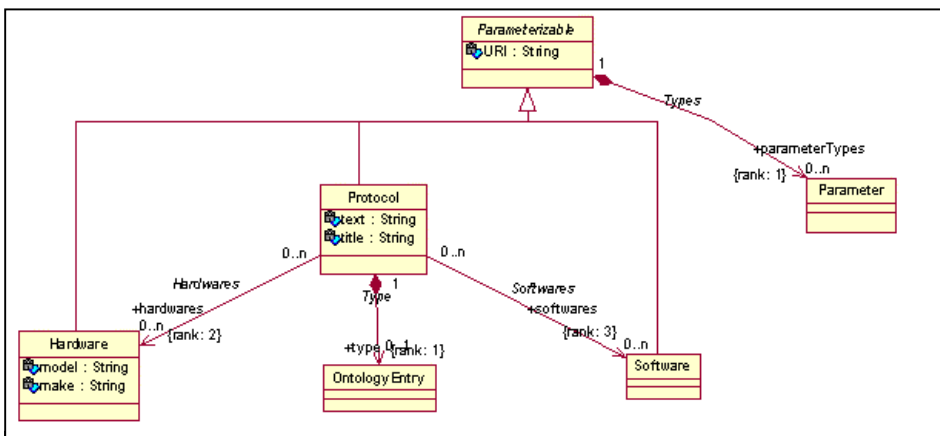
Miscellaneous: protocols - class diagrams and DTD

```
<!ELEMENT Protocol_package (Hardware_assnlist?,Software_assnlist?,Protocol_assnlist?) >
<!ELEMENT Hardware_assnlist (Hardware+) >
<!ELEMENT Software_assnlist (Software+) >
<!ELEMENT Protocol_assnlist (Protocol+) >
```

```
<!ELEMENT Hardware_ref EMPTY >
<!ATTLIST Hardware_ref
  identifier CDATA #REQUIRED >
<!ELEMENT Hardware (...) >
<!ATTLIST Hardware
  identifier CDATA #REQUIRED
  .. URI CDATA #IMPLIED
  model CDATA #IMPLIED
  make CDATA #IMPLIED >
<!ELEMENT Software_ref EMPTY >
<!ATTLIST Software_ref
  identifier CDATA #REQUIRED >
<!ELEMENT Software (...) >
<!ATTLIST Software
  identifier CDATA #REQUIRED
  name CDATA #IMPLIED
  URI CDATA #IMPLIED >
```

```
<!ELEMENT Protocol_ref EMPTY >
<!ATTLIST Protocol_ref
  identifier CDATA #REQUIRED >
<!ELEMENT Protocol (.,.,
  ParameterTypes_assnlist?,
  Type_assn,
  Hardwares_assnreflist?,
  Softwares_assnreflist?) >
<!ATTLIST Protocol
  identifier CDATA #REQUIRED
  .. URI CDATA #IMPLIED
  text CDATA #IMPLIED .. >
<!ELEMENT ParameterTypes_assnlist
  (Parameter+) >
<!ELEMENT Hardwares_assnreflist
  (Hardware_ref+) >
<!ELEMENT Softwares_assnreflist
  (Software_ref+) >
<!ELEMENT Parameter_ref EMPTY >
<!ATTLIST Parameter_ref identifier CDATA #REQUIRED >
<!ELEMENT Parameter (...) >
<!ATTLIST Parameter identifier CDATA #REQUIRED
  name CDATA #IMPLIED >
```

```
<!ELEMENT ProtocolApplications_assnlist
  (ProtocolApplication+) >
<!ELEMENT ProtocolApplication (.,.,
  ParameterValues_assnlist?,
  HardwareApplications_assnlist?,
  SoftwareApplications_assnlist?,
  Performers_assnreflist?,
  Protocol_assnref) >
<!ATTLIST ProtocolApplication
  activityDate CDATA #REQUIRED >
<!ELEMENT ParameterValues_assnlist
  (ParameterValue+) >
<!ELEMENT HardwareApplications_assnlist
  (HardwareApplication+) >
<!ELEMENT SoftwareApplications_assnlist
  (SoftwareApplication+) >
<!ELEMENT Performers_assnreflist (Person_ref+) >
<!ELEMENT Protocol_assnref (Protocol_ref) >
<!ELEMENT ParameterValue (.,.,
  ParameterType_assnref) >
<!ATTLIST ParameterValue value CDATA #IMPLIED >
<!ELEMENT ParameterType_assnref (Parameter_ref) >
<!ELEMENT HardwareApplication (.,.,Hardware_assnref) >
<!ELEMENT Hardware_assnref (Hardware_ref) >
<!ELEMENT SoftwareApplication (.,.,Software_assnref) >
<!ATTLIST SoftwareApplication
  version CDATA #IMPLIED .. >
<!ELEMENT Software_assnref (Software_ref) >
```



Miscellaneous: protocols - example

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE Protocol_package PUBLIC "-//OMG//DTD MAGE-ML 1.1//EN"
"http://schema.omg.org/lsr/gene_expression/1.1/MAGE-ML.dtd" >
<!--MIAME requirement: to indicate content requirement-->
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
<!--MAGE-ML Good Practice Guidelines-->
<!--OPTIONAL-->

<Protocol_package>
  <Hardware_assnlist>
    <Hardware identifier="ebi.ac.uk:MIAMExpress/Hardware:<object>" URI="url" make="make"
model="model">
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
    <Type_assn>
      <OntologyEntry category="HardwareType" value="array_scanner"/>
    </Type_assn>
  </Hardware>
</Hardware_assnlist>

  <Software_assnlist>
    <Software identifier="ebi.ac.uk:MIAMExpress/Hardware:<object>" URI="" model="">
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
    <Type_assn>
      <OntologyEntry category="SoftwareType" value="image_acquisition_software"/>
    </Type_assn>
  </Software>
</Software_assnlist>

  <Protocol_assnlist>
    <Protocol URI="http://www.manufacturer.com/protocoll.pdf"
identifier="ebi.ac.uk:MIAMExpress/Protocol:P-MEXP-XX" name="protocol">

<!--OPTIONAL association-->
<!--MIAME requirement: to indicate content requirement-->
<!--Provide list of parameters where necessary. Warning, values should be therefore pecified
at the level of a protocol application-->
<ParameterTypes_assnlist>
  <Parameter identifier="ebi.ac.uk:MIAMExpress/Parameter:<object>">
<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
    <DataType_assn>
      <OntologyEntry category="DataType" value="float"/>
    </DataType_assn>
  </Parameter>
</ParameterTypes_assnlist>

<!--MO Rules: requires MO rules for appropriate coding-->
<!--MO TERMS: use of MGED Ontology instances required -->
    <Type_assn>
      <OntologyEntry category="ProtocolType" value="image_acquisition"/>
    </Type_assn>

<!--OPTIONAL association-->
  <Hardwares_assnreflist>
    <Hardware_ref identifier="ebi.ac.uk:MIAMExpress/Hardware:<object>"/>
  </Hardwares_assnreflist>
<!--OPTIONAL association-->
  <Softwares_assnreflist>
    <Software_ref identifier="ebi.ac.uk:MIAMExpress/Software:<object>"/>
  </Softwares_assnreflist>
</Protocol_package>
```

```
</Softwares_assnreflist>
```

```
</Protocol>
```

```
</Protocol_assnlist>
```

```
</Protocol_package>
```

Miscellaneous: descriptions and contacts - class diagrams and DTD

```

<!ELEMENT Description_package (Database_assnlist?) >
<!ELEMENT Database_assnlist (Database+) >
<!ELEMENT Database_ref EMPTY >
<!ATTLIST Database_ref identifier CDATA #REQUIRED >
<!ELEMENT Database (...) >
<!ATTLIST Database identifier CDATA #REQUIRED
      name CDATA #IMPLIED
      version CDATA #IMPLIED
      URI CDATA #IMPLIED >

<!ELEMENT Descriptions_assnlist (Description+) >
<!ELEMENT Description (...Annotations_assnlist?,...BibliographicReferences_assnlist?) >
<!ATTLIST Description text CDATA #IMPLIED
      URI CDATA #IMPLIED >

```

```

<!ELEMENT Annotations_assnlist (OntologyEntry+) >
<!ELEMENT BibliographicReferences_assnlist (BibliographicReference+) >

```

```

<!ELEMENT BibliographicReference (...Parameters_assnlist,...) >

```

```

<!ATTLIST BibliographicReference
  title CDATA #IMPLIED
  authors CDATA #IMPLIED
  publication CDATA #IMPLIED
  publisher CDATA #IMPLIED
  editor CDATA #IMPLIED
  year CDATA #IMPLIED
  volume CDATA #IMPLIED
  issue CDATA #IMPLIED
  pages CDATA #IMPLIED
  URI CDATA #IMPLIED >

```

```

<!ELEMENT Parameters_assnlist (OntologyEntry+) >

```

```

<!ELEMENT Type_assn (OntologyEntry) >
<!ELEMENT Types_assnlist (OntologyEntry+) >

```

```

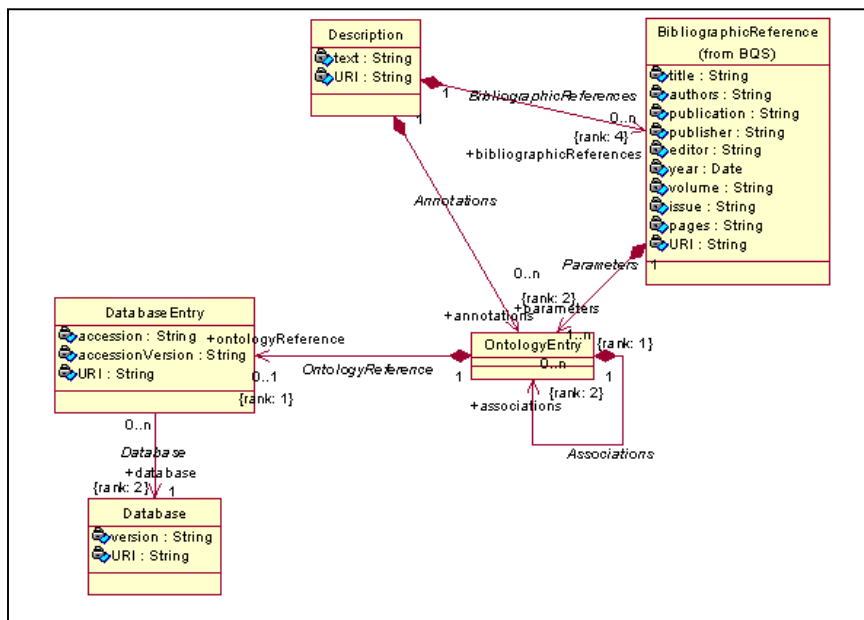
<!ELEMENT OntologyEntry (...
  OntologyReference_assn?,
  Associations_assnlist?) >
<!ATTLIST OntologyEntry category CDATA #REQUIRED
  value CDATA #REQUIRED
  description CDATA #IMPLIED >

```

```

<!ELEMENT OntologyReference_assn (DatabaseEntry) >
<!ELEMENT Associations_assnlist (OntologyEntry+) >

```



```

<!ELEMENT AuditAndSecurity_package (Contact_assnlist?,
  ..) >

```

```

<!ELEMENT Contact_assnlist ((Person | Organization)+) >

```

```

<!ELEMENT Organization_ref EMPTY >
<!ATTLIST Organization_ref identifier CDATA #REQUIRED >
<!ELEMENT Organization (...) >
<!ATTLIST Organization
  identifier CDATA #REQUIRED
  name CDATA #IMPLIED
  URI CDATA #IMPLIED
  address CDATA #IMPLIED
  .. >

```

```

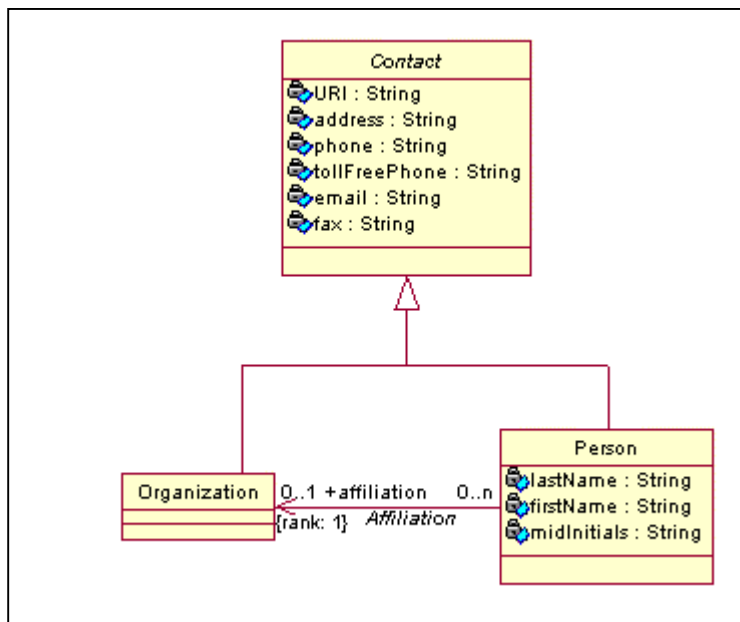
<!ELEMENT Person_ref EMPTY >
<!ATTLIST Person_ref identifier CDATA #REQUIRED >
<!ELEMENT Person (...Affiliation_assnref?) >
<!ATTLIST Person
  identifier CDATA #REQUIRED
  name CDATA #IMPLIED
  ..
  address CDATA #IMPLIED
  phone CDATA #IMPLIED
  ..
  email CDATA #IMPLIED .. >

```

```

<!ELEMENT Affiliation_assnref (Organization_ref) >

```



Miscellaneous: contacts - example

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE AuditAndSecurity_package PUBLIC "-//OMG//DTD MAGE-ML 1.1//EN"
"http://schema.omg.org/lsrc/gene_expression/1.1/MAGE-ML.dtd" >

<AuditAndSecurity_package>
  <Contact_assnlist>

<!--MIAME REQUIREMENT: Provide all necessary contact information -->

<Organization URI="http://www.ebi.ac.uk"
  address="Wellcome Trust Genome Campus"
  email="contact@ebi.ac.uk"
  fax="+44 1223 492 468"
  identifier=" ebi.ac.uk:MIAMEExpress/Organization:<object>"
  name="EMBL-EBI"
  phone="+44 1223 494 444">

<!--OPTIONAL association-->
<!--Provide information about structure in Organization-->
  <Parent_assnref>
    <Organization_ref identifier=" ebi.ac.uk:MIAMEExpress/Organization:<object>" />
  </Parent_assnref>

</Organization>

<Organization URI="http://www.embl.de"
  address="Meyerhofstrasse 1 D69117 Heidelberg"
  email="info@embl.de"
  fax="+ 49 6221 387306"
  identifier=" ebi.ac.uk:MIAMEExpress/Organization:<object>"
  name="EMBL"
  phone="+ 49 6221 3870"/>

<Person address="Wellcome Trust Genome Campus"
  email="johnsmoth@ebi.ac.uk"
  firstName="John"
  identifier=" ebi.ac.uk:MIAMEExpress/Person:<object>"
  lastName="Smith"
  midInitials="K."
  name="Smith">

<!--OPTIONAL association-->
  <Roles_assnlist>
    <OntologyEntry category="Roles" value="data_coder" />
  </Roles_assnlist>

<!--MIAME REQUIREMENT: -->
  <Affiliation_assnref>
    <Organization_ref identifier=" ebi.ac.uk:MIAMEExpress/Organization:<object>" />
  </Affiliation_assnref>
</Person>
</Contact_assnlist>

</AuditAndSecurity_package>
```

Miscellaneous: database declaration - example

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE Description_package PUBLIC "-//OMG//DTD MAGE-ML 1.1//EN"
"http://schema.omg.org/lsrc/gene_expression/1.1/MAGE-ML.dtd" >

<Description_package>
  <Database_assnlist>
    <!--MIAME REQUIREMENT:--Provide URI template when declaring a Database>
    <Database URI="http://www.ebi.ac.uk/embl/"
  identifier="ebi.ac.uk:arrayexpress/Database:embl" name="EMBL GenBank DDBJ"/>
    <!-- ... definitions of other Databases -->
  </Database_assnlist>
</Description_package>
```