<!-- Add name attribute for each FeatureExtraction element in a MeasuredBioAssay. -->
<!-- Compute the name by concatenating: -->
<!-- 1) The name of the Hybridization for the PhysicalBioAssay to which the MeasuredBioAssay refers with a PhysicalBioAssay_ref -->
<!-- 2) The string " feature extraction ". -->
<!-- 3) The name of the Compound for a LabeledExtract to which the above Hybridization refers with a LabeledExtract_ref -->

<TranslationStep>
  <changeLocationQuery><![CDATA[doc("-target")//MeasuredBioAssay//FeatureExtraction]]></changeLocationQuery>
  <locationValueQuery>
    <![CDATA[
      for $pba in doc("-value")/ancestor::BioAssay_assnlist/PhysicalBioAssay,
      $le in doc("-value")/ancestor::MAGE-ML//LabeledExtract,
      $c   in doc("-value")/ancestor::MAGE-ML//Compound_assnlist/Compound
        where
          $pba/@identifier = doc("-value")/ancestor::MeasuredBioAssay//PhysicalBioAssay_ref/string(@identifier) and
          $le/string(@identifier) = $pba//Hybridization//LabeledExtract_ref/string(@identifier) and
          $c/string(@identifier)  = $le//Labels_assnreflist/Compound_ref/string(@identifier)
        return concat($pba//Hybridization/string(@name), " feature extraction ", $c/string(@name))
    ]]>"
  </locationValueQuery>
  <XmlModify>
    <op>addAttribute</op>
    <newNodeName>name</newNodeName>
  </XmlModify>
</TranslationStep>