Extending the model

Often the schema of a clinical domain will be a superset of the VMR. For example, this tutorial considers the situation of a diabetic foot clinic where additional information along with standard observations is recorded in the EHR and presentable through an extended VMR. The VMR extension can be captured in a Package (in a similar way to the way we did a Library). Its also possible to import the new extended model as a 'hardwired' internal package. Another way to customise an extended data model is to use an archetype.

A diabetic clinic exam will look at the things like the ankle brachial index (a measure of blood flow), the pulses, and abnormalities that may be present. Compile and then save the following as *ExtendedDiabeticFoot.gello_model* :

```
Package ExtendedDiabeticFoot

imports
 iso_21090_datatypes,
 HL7_v2_VMR_V1

class DiabeticFootObservations extends Any
     diabeticFootExamDate: TS
     leftDorsalisPedisPulseFull: Boolean
     rightDorsalisPedisPulseFull: Boolean
     leftPosteriorTibialPulseFull: Boolean
     rightPosteriorTibialPulseFull: Boolean
     leftAnkleBrachialIndex: Real
     rightAnkleBrachialIndex: Real
     anyFootDeformity: Boolean
     anyNeurologicalChanges: Boolean
     anyUlcerPresent: Boolean

class ExtendedDiabeticFootExample_SinglePatient extends SinglePatient
     diabeticFootObservations: Sequence(DiabeticFootObservations)

class InfrastructureRoot extends Any
     singlePatient: ExtendedDiabeticFootExample_SinglePatient

EndPackage
```

As before with a Library, this file needs to be saved to the same folder as any GELLO files that use it.

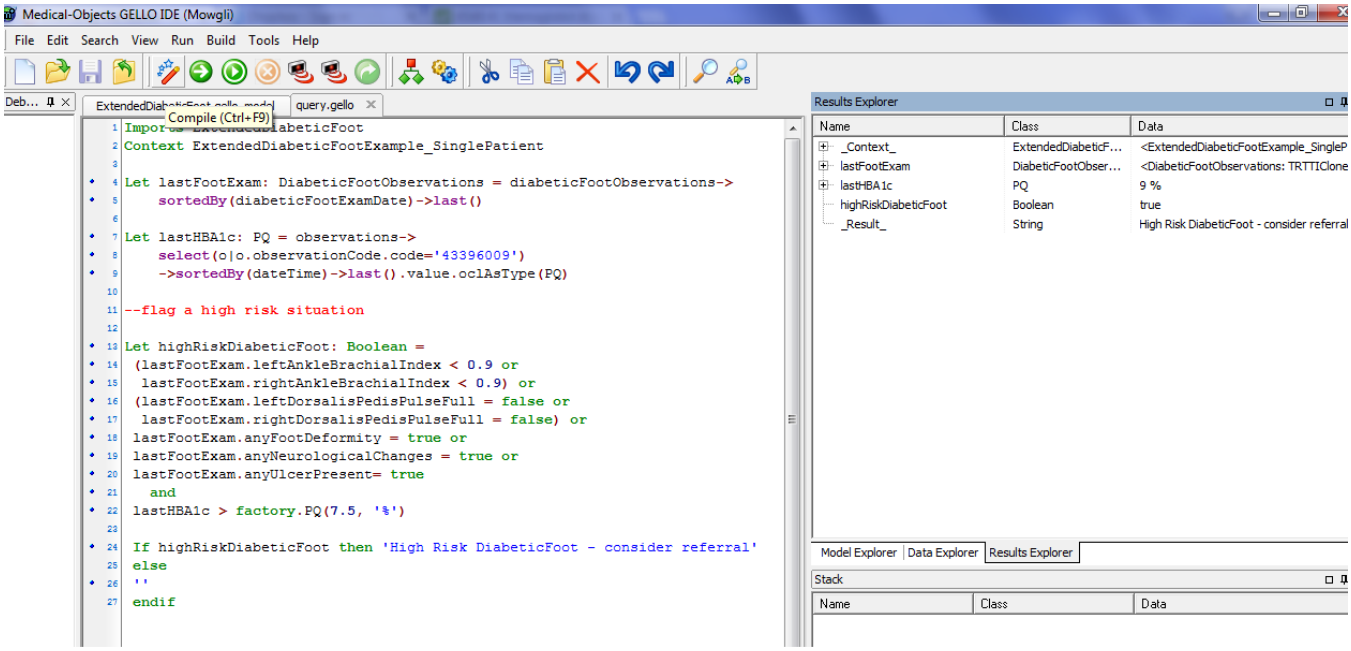
Now lets add some more clinical data to *fifthTest.xml* and save it as *SeventhTuteTest.xml.*

Add it between </vitals> and </singlePatient> at the end:

```
<observations>
    <observationCode code="43396009"
      codeSystem="2.16.840.1.113883.6.96"
      codeSystemName="SNOMED-CT">
    <displayName value = "Hemoglobin A1c measurement " />
    <translation code="4548-4"
      codeSystem="2.16.840.1.113883.6.1"
      codeSystemName="LN">
      <displayName value = "Hemoglobin A1c/Hemoglobin.Total In Blood" />
    </translation>
    </observationCode>
    <dateTime value = "20160616" />
    <value xsi:type = "PQ" value = "9.0" unit = "%"/>
 </observations>
 <diabeticFootObservations>
    <diabeticFootExamDate value = "20160616" />
    <leftDorsalisPedisPulseFull value = "false" />
    <rightDorsalisPedisPulseFull value = "true" />
    <leftPosteriorTibialPulseFull value = "true" />
    <rightPosteriorTibialPulseFull value = "true" />
    <leftAnkleBrachialIndex value = "0.7" />
    <rightAnkleBrachialIndex value = "0.9" />
    <anyFootDeformity value = "false" />
    <anyNeurologicalChanges value = "false" />
    <anyUlcerPresent value = "false" />
 </diabeticFootObservations>
```

Cut and paste the following GELLO into a new workspace:

```
Imports ExtendedDiabeticFoot
Context ExtendedDiabeticFootExample_SinglePatient

Let lastFootExam: DiabeticFootObservations = diabeticFootObservations->
 sortedBy(diabeticFootExamDate)->last()

Let lastHBA1c: PQ = observations->
 select(o|o.observationCode.code='43396009')
 ->sortedBy(dateTime)->last().value.oclAsType(PQ)
```

```
    --flag a high risk situation

    Let highRiskDiabeticFoot: Boolean =
     (lastFootExam.leftAnkleBrachialIndex < 0.9 or
      lastFootExam.rightAnkleBrachialIndex < 0.9) or
     (lastFootExam.leftDorsalisPedisPulseFull = false or
      lastFootExam.rightDorsalisPedisPulseFull = false) or
     lastFootExam.anyFootDeformity = true or
     lastFootExam.anyNeurologicalChanges = true or
     lastFootExam.anyUlcerPresent= true
      and
     lastHBA1c > factory.PQ(7.5, '%')

    If highRiskDiabeticFoot then 'High Risk DiabeticFoot - consider referral'
     else
      ''


endif
```

And after compiling and saving it say as *tuteSeven.gello* , run: