

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.oc1AsType(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
```

endif

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

The screenshot displays the Medical-Objects GELLO IDE (Mowgli) interface. The main editor shows a GELLO script for a diabetic foot assessment. The script includes imports, context definitions, and a logic block that evaluates various foot exam parameters to determine if a patient is at high risk for a diabetic foot. The script concludes with a referral recommendation based on the risk assessment.

The Results Explorer on the right shows the execution results of the script. It lists the variables and their values:

Name	Class	Data
Context	ExtendedDiabeticFoot	<ExtendedDiabeticFootExample_SingleP
lastFootExam	DiabeticFootObservations	<DiabeticFootObservations: TRTTIClone
lastHBA1c	PQ	9 %
highRiskDiabeticFoot	Boolean	true
Result	String	High Risk DiabeticFoot - consider referral

The bottom of the IDE shows the Stack and Model Explorer tabs, which are currently empty.