Family History – Gello - vMR
What is GELLO?

- Clinical Decision Support Language
- HL7/ANSI standard
- Revised April 2010
- Based on OCL 2.0
  - Optimised for Clinical Queries
  - Unneeded features removed
  - Features added eg. Factory, list operations
- Operates on a “Virtual Medical Record” (vMR)
  - vMR standard under development currently
  - ISO 21090 data types likely to be used
GELLO Concepts

GELLO expression:

Context Patient
ProblemList -> exists(Code.equals(Factory.CodedValue("Asthma")))

Same GELLO expression in different settings
Let BreastCancer: CD = Factory.codedvalue('123456', 'SNOMED-CT', 'Breast Cancer')

Let EarlyBreastCancerCount: Integer =
    FamilyHistory.relatives -> iterate(x; i:Integer = 0 |
        if (x.clinicalGenomicObservations ->
            select(code.implies(BreastCancer) and (dateEstimatedAge() < 30)).isEmpty()) then i + 1 else i endif)

EarlyBreastCancerCount > 0

Context SinglePatient
---We use this as the test for a laparoscopic procedure
let Laparoscopic: CD = Factory.SNOMEDCD("51316009|Laparoscopic Procedure|")
---This is used to determine abdominal surgery
let AbdoSurgery: CD = Factory.SNOMEDCD("386671008|Abdominal Cavity Surgery|")
---Iterate over past history, seeing if any laparoscopic surgery
let OpenSurgeryCount: Integer =
    Procedure -> iterate(SX; i:Integer = 0 | 
        if (SX.code.implies(AbdoSurgery).value and 
            (not SX.code.implies(Laparoscopic).value)) then 
            i+1 
        else 
            i 
        endif)

--see if there has been any open abdo surgery
OpenSurgeryCount > 0
“Detailed Clinical Models”
ISO Project
Aims to be platform agnostic
Activity in HL7 Patient care working group
- UML models
- Spread sheets
- Word Documents
Currently no formal model has been done
- Interoperability unlikely without this
vMR Transform Principles

- The vMR model uses the RMIM to make the relationships explicit and easier to query without losing any data. The relationships in the RMIM are fixed and represented using the RIM whereas the VMR Model uses an explicit object model. The object model allows direct access to a collection of relatives as well as the collection of conditions that the relative suffers from.
Example Family History GELLO

Context SinglePatient

Let IBD: CD = Factory.CodedValue('24526004', 'SNOMED-CT') -- IBD
Let Colitis: CD = Factory.CodedValue('64226004', 'SNOMED-CT') -- Colitis

FamilyHistory.ClinicalGenomicChoice -> select(
    ClinicalObservation -> select(
        (code.implies(IBD).value or code.implies(Colitis).value) and (not negationInd.value)
        ).notEmpty()
    ).notEmpty()

Context SinglePatient

Let ColonCancer: CD = Factory.CodedValue('C2955', 'NCI') -- Colon Cancer NCI Code

FamilyHistory.ClinicalGenomicChoice -> select(
    (Relative.Relationship.code = 'NMTH' or Relative.Relationship.code = 'NFTH') and
    ClinicalObservation -> select(
        code.implies(ColonCancer).value and (not negationInd.value) and (DataEstimatedAge.low.value <= 50.0)
        ).notEmpty()
    ).notEmpty()
class FamilyHistory extends Observation
    ClinicalGenomicChoice: Sequence(ClinicalGenomicChoice)
    Informant: Entity
    PatientID: ST
    PedigreeAnalysisResults: Sequence(Observation)
    Relatives: Sequence(Relative)

class ClinicalGenomicChoice extends Any
    ClinicalObservation: Sequence(ClinicalObservation)
    GeneticLoci: Sequence(Observation)
    Relative: Relative

class ClinicalObservation extends Any
    causeOfDeath: BL
    code: CD
    DataEstimatedAge: IVL_REAL
    negationInd: BL

class Relative extends Any
    ClinicalGenomicChoice: Sequence(ClinicalGenomicChoice)
    deceasedEstimatedAge: REAL
    livingEstimatedAge: REAL
    naturalEstimatedAge: REAL
    naturalFatherID: ST
    naturalMotherID: ST
    patientID: ST
    person: Person
    Relationship: CD
Full Family History Model

--- HL7 V3. FHIR example
--- Step 1. make sure default model is set to FHIR.model
--- Step 2. recompile this example (only if model changed)
--- Step 3. use "Tools|Read Test Data" to load emmaHL7Compliant.xml
--- Step 4. use the Execute button to run the gello
--- Step 5. examine the query results in the data explorer

context InfrastructureRoot

```
familyHistory.subject.patient.patientPerson.relative->select(code.code = 'NSIS')
```

<table>
<thead>
<tr>
<th>Name</th>
<th>Class</th>
<th>Data</th>
</tr>
</thead>
<tbody>
<tr>
<td>:Result?2[]</td>
<td>Sequence( Relative )</td>
<td>[Collection: TOCL.Collection]</td>
</tr>
<tr>
<td>1</td>
<td>code</td>
<td>String</td>
</tr>
<tr>
<td></td>
<td>nullFlavor</td>
<td>(Relative)</td>
</tr>
<tr>
<td></td>
<td>relationshipHolder</td>
<td>Person</td>
</tr>
<tr>
<td></td>
<td>subject0</td>
<td>1[]</td>
</tr>
<tr>
<td></td>
<td>subject0</td>
<td>2[]</td>
</tr>
<tr>
<td>2</td>
<td>code</td>
<td>String</td>
</tr>
<tr>
<td></td>
<td>nullFlavor</td>
<td>(Relative)</td>
</tr>
<tr>
<td></td>
<td>relationshipHolder</td>
<td>Person</td>
</tr>
<tr>
<td></td>
<td>subject0</td>
<td>1[]</td>
</tr>
</tbody>
</table>

GELLO is valid, no compile errors found in context of current model
HL7 V2 models

- HL7 V2
  - Has strong structural model
    - Not formally presented as such
    - No semantic attributes
    - Many class definitions eg Medication
    - Ability to create hierarchies not obvious
  - No formal Terminology binding
    - Also no conflict
  - DCM format for V2 is Word documents
  - Wide usage in many countries
    - Exclusive use of HL7V2 in Australia
Can represent Complex models in V2
  - Described by Template
  - Only data that differs needs to be in message
    - Allows default values
  - V3 Pedigree model could be duplicated
Template (EN13606) Editor
Example vMR as EN13606
Mechanism developed to persist archetyped data in HL7V2 messages

- All OBX based, medication not modelled
- Observation Sub-ID used to create hierarchy
  - Mapped to maximal Archetype data structure
- Data type Mapping
- OBR becomes COMPOSITION
- Backward compatible with existing systems
- Currently Standards Australia Technical Report
Allows Gello based CDS in V2

Let IBD: CodedValue = Factory.CodedValue('24526004', 'SNOMED-CT') -- IBD
Let Colitis: CodedValue = Factory.CodedValue('64226004', 'SNOMED-CT') -- Colitis
Let ColitisCount: Integer = FamilyHistory.Relatives -> Select(x |
  (x.ClinicalGenomicChoice.clinicalObservation -> Select(code.implies(Colitis) or code.implies(IBD)).cardinality() > 0)
  and x.LivingEstimatedAge <= 20).cardinality()
ColitisCount > 0
Mechanism is Generic

- Example of Urine Culture
  - EN13606 Archetype
    - Exports
      - GELLO Class
      - ADL file
      - Mindmap
      - UML (.xmi)
      - Spreadsheet (for V2 implementation)
GELLO Class export for CDS

```java
package PKG_CEN_UrineCulture_V1

import VH1;

class DipStick
   Blood: Observation
   Glucose: Observation
   Protein: Observation
   PH: Observation
   SpecificGravity: Observation

class Microscopy
   WhiteCells: Observation
   RedCells: Observation
   EpithelialCells: Observation
   OtherCells: Observation
   Other: Observation
```

<table>
<thead>
<tr>
<th>Name</th>
<th>Kind</th>
<th>Detail</th>
</tr>
</thead>
<tbody>
<tr>
<td>PKG_CEN_UrineCulture_V1</td>
<td>package</td>
<td>package PKG_CEN_UrineCulture_V1</td>
</tr>
<tr>
<td>CEN_UrineCulture_V1</td>
<td>class</td>
<td>CEN_UrineCulture_V1 extends Any</td>
</tr>
<tr>
<td>collection(Isolate)</td>
<td>class</td>
<td>collection(Isolate) extends collection</td>
</tr>
<tr>
<td>Culture</td>
<td>class</td>
<td>Culture extends Any</td>
</tr>
<tr>
<td>DipStick</td>
<td>class</td>
<td>DipStick extends Any</td>
</tr>
<tr>
<td>Isolate</td>
<td>class</td>
<td>Isolate extends Any</td>
</tr>
<tr>
<td>Growth</td>
<td>attribute</td>
<td>Growth: Observation</td>
</tr>
<tr>
<td>Pathogen</td>
<td>attribute</td>
<td>Pathogen: Pathogen</td>
</tr>
<tr>
<td>Microscopy</td>
<td>class</td>
<td>Microscopy extends Any</td>
</tr>
</tbody>
</table>

GELLO is valid, no compile errors found in context of current model.
ADL and Mindmap

definition
ENTRY[at0000] occurrences matches {0..1} matches
  items cardinality matches {0..*} matches
  ELEMENT[at0002] occurrences matches
    value matches {
      CODED_TEXT matches {
        code matches {
          [local: {
            at0061, -- Urine
            at0041, -- Clean
            at0057, -- Midstr
            at0042, -- Catheter
            at0043, -- Suprapubic
            at0044, -- First morning
            at0045, -- Periurethral bag
            at0056, -- Ureteric
            at0059, -- Bladder
            at0013, -- Other
            at0061] -- assumed value
          }
        }
      }
    }
  }

ENTRY[at0000] occurrences matches {0..1} matches
  -- Other specimen type:
  value matches {
    TEXT matches /\n  }
<table>
<thead>
<tr>
<th>DISPLAYNAME</th>
<th>LOCALCODE</th>
<th>OCCURRENCES</th>
<th>DATATYPE</th>
<th>V2VALUETYPE</th>
<th>SUBID</th>
<th>LOINC</th>
<th>SNOMED</th>
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<td>a0000</td>
<td>0..1</td>
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<td>-</td>
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<td>CE</td>
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<td>STRING</td>
<td>ST</td>
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</tr>
</tbody>
</table>

For V2 Implementation
Further Information

- Medical-Objects Clinical Decision Support wiki

- HL7 vMR Project

- DCM

- GELLO