



CDA Implementation Guide for Genetic Testing Report (GTR): Towards a Clinical Genomic Statement

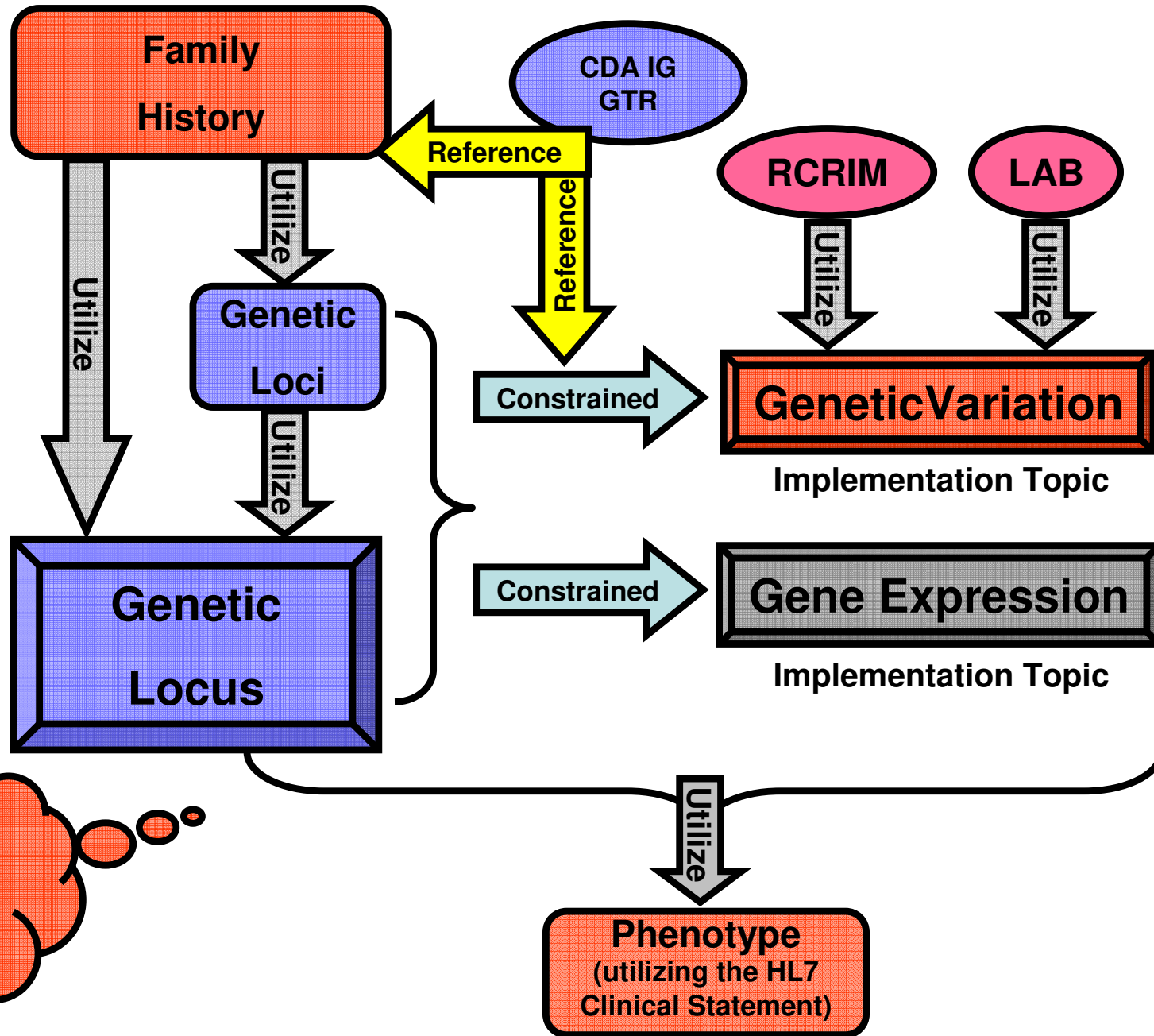
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CDA R2 Co-editor
CCD Implementation Guide Co-editor

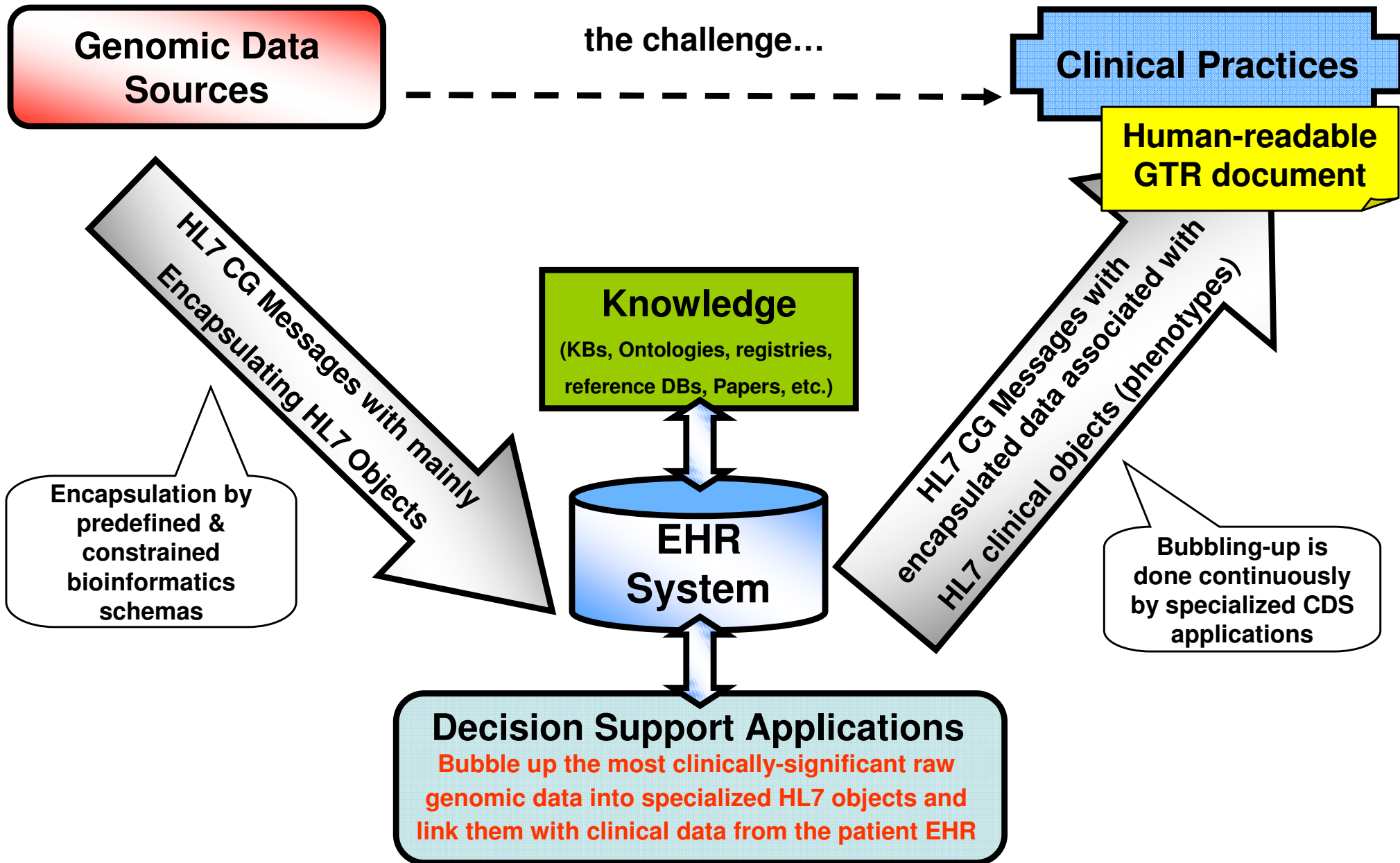
GTR & HL7 Clinical Genomics v3 Static Models



- Normative
- DSTU
- Comments
- Other domains

Domain Information Model: "Genome"

CG and EHR: Encapsulate & Bubble-up!



CDA IG: Genetic Testing Report (GTR)

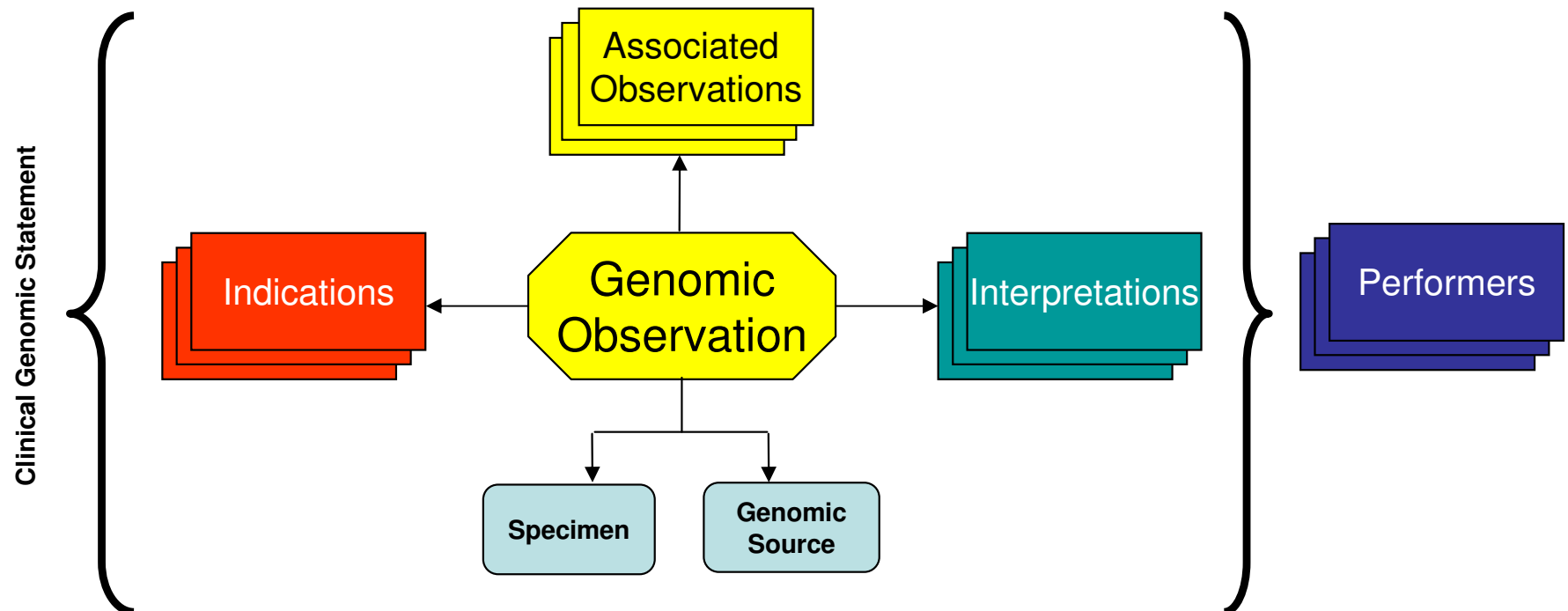
- **Define an implementation guide for genetic testing reports that is both human readable and machine-processable**
 - Target at all types of GTR producers, e.g., genetic labs, clin. geneticists
 - Readable content is larger in scope
 - E.g., detailed description of the tests performed along with references
 - Machine-processable should be limited, e.g., exclude raw data
- **Ballot a Universal IG; derive it to specific types of GTR:**
 - Healthcare & Research
 - Realm-specific guides
 - Omic-specific guides
- **Developed using the MDHT open source tool (OHT)**

GTR - Design Principles

- **Follow existing report formats commonly used in healthcare & research**
- **Emphasize interpretations & recommendations**
- **Provide general background information on tests performed**
- **Reference HL7 Clinical Genomics instances (e.g., GeneticVariation and Pedigree) as the place holders of full-blown raw genomic data and fully-structured family history data**
- **Utilize patterns of ‘genotype-phenotype’ associations in the HL7 v3 Clinical Genomics Domain**
 - **Implement them as ‘clinical genomic statement’ entry-level templates (see next slide)**

The Clinical Genomic Statement

- An abstract Clinical Genomic Statement (CGS) template that
 - Has at its core a genomic observation (e.g., a DNA sequence variation)
 - If it's a reportable finding, then it should be associated with indications and interpretations, specimen and genomic source class
 - The major finding can be associated with associated observation (e.g., amino acid change)
 - Optionally, performers may be specified (overriding header performers)
- The CGS abstract template is instantiated by specialized CGS's, e.g., for genetic variations or cytogenetics, as well as for their associated observation



Narrative and Structured Data

- **All CGS structured data items shall be part of clinical genomic statement (CGS) instances so that parsing applications can find the full semantics explicitly represented in one coherent structure**
- **Sub-sections such as Indications, Interpretations and Specimen are mainly for presenting narrative, but they may also contain structured data**
 - **In this way, it is possible to have less redundant documents, e.g., in the case where all tests reported in a GTR document have the same indication, an Indications section in the Summary section consists of a full-blown indication observation which all CGS indication observations reference**
- **CGS structured data may point to the respective narrative in sub-sections (by means of XML ID)**

GTR Rendered – The Header

Hearing Loss: Connexin 26 and 30 Full Gene Sequencing Panel Test Report - Windows Internet Explorer

D:\Amnon-eHealth\CDA\CDA Implementation Guides\GTR - Genetic Testing Report\CDA-GeneticTestingReport-Sample-v7.xml

File Edit View Favorites Tools Help

★ Favorites TeamForge : Project Home Hearing Loss: Connexin 2... X

Hearing Loss: Connexin 26 and 30 Full Gene Sequencing Panel Test Report

Patient	John Doe		
Date of birth	May 5, 1947	Sex	Male
Contact info	address not available Telecom information not available	Patient IDs	123456789 2.16.840.1.113883.18.12.7.30.9.2
Document Id	c266 2.16.840.1.113883.18.12.7.30.9.1		
Document Created:	August 9, 2010		
Author	Jean Genome,		
Legal authenticator	Jean Genome of The New Genetic Testing Laboratory signed at February 12, 2006		
Document maintained by	2.16.840.1.113883.19.3.2409		

Table of Contents

- [Summary Section](#)
- [Genetic Variations Section](#)
- [Genetic Variations Section](#)
- [Genetic Variations Section](#)

Draft that has not been clinically validated

GTR Rendered – Summary Section

Summary Section

Indications

- Indication: Profound sensorineural hearing loss

Specimen and Genomic Source

- Peripheral Blood
- Genomic source class: Germline

Tests Performed

- Connexin 26 Full Gene Test
- Mitochondrial Hearing Loss Genes Test
- Connexin 30 Deletion Test

Overall Interpretation

- **Inconclusive.** DNA sequencing detected two mutations in the connexin 26 gene, 79G>A (V27I) and 109G>A (V37I). GJB6-D13S1830 Deletion: A PCR-based analysis of the GJB6-D13S1830 region of chromosome 13 was performed and did not detect the deletion. This test does not assess the DNA sequence of the GJB6 gene or detect other mutations that could affect the expression of the gene. Mitochondrial Hearing Loss Genes: DNA sequencing did not detect the presence of any mutations in the MTTTS1 and MTRNR1 genes. Although this test examines all regions known to contain pathogenic mutations in these genes, it does not include sequencing of the 5' end of the MTRNR1 gene. The V27I mutation has been reported as a benign variant (references) and is not believed to cause hearing loss. The V37I mutation has been previously reported in patients with hearing loss. This mutation, in homozygosity or combined with another GJB2 disease causing mutation, typically results in a mild to moderate hearing loss (Cryns et al. 2005). Mutations in both copies of the GJB2 gene are necessary to assume that GJB2 is responsible for the hearing loss. Although two mutations were identified in this patient, we would assume that the combination of a benign variant and a mild pathogenic mutation would result in a mild to moderate hearing loss rather than a moderately-severe one, as in this patient. It is most likely that the hearing loss in this patient is the result of the V37I mutation and an unknown second pathogenic mutation. It should be noted that a second mutation is not identified in a large percentage (10-50%) of patients with nonsyndromic hearing loss and GJB2 mutations (del Castillo et al. 2003).

Recommendations

- Although some cases may represent a coincidental carrier state, all of the studies have concluded that there are likely to be other genetic mutations that have not yet been identified. Unfortunately, this precludes further testing. Genetic counseling is recommended for this patient and his/her family members.

Draft that has not been clinically validated

GTR Rendered – Summary Section (cont.)

Test Information

Background

- Mutations in the GJB2 (connexin 26) gene are the most common cause of hearing loss and are most often seen in a person with hearing loss that was found at birth or in early childhood without any other medical problems. The severity of the hearing loss can range from mild to profound. The inheritance pattern is usually autosomal recessive, requiring two mutations, one in each copy of the gene, to cause hearing loss. The GJB6-D13S1830 deletion removes most of the GJB6 gene, which encodes the connexin 30 protein (Cx30). This deletion, when present in two copies or when combined with a single connexin 26 mutation, causes hearing loss.

Methodology

- Exon 1 and the coding region of exon 2 of the connexin 26 (GJB2) gene are amplified using flanking primer sets. PCR products are sequenced using an ABI fluorescence automatic DNA sequencer. This test does not detect large deletions or mutations in non-coding regions that could affect gene expression. This assay is greater than 99.9% accurate in detecting mutations in the sequences analyzed. Polymerase chain reaction (PCR) analysis is performed to detect the presence or absence of a deletion spanning the GJB6-D13S1830 region of chromosome 13.

References

- Azaiez H, Chamberlin GP, Fischer SM, Welp CL, Prasad SD, Taggart RT, del Castillo, I, Van Camp G and Smith RJ. GJB2: the spectrum of deafness-causing allele variants and their phenotype. *Hum Mutat.* 2004;24(4): 305-11.
- Calvo J, Rabionet R, Gasparini P, Estivill X. Connexins and Deafness Homepage. <http://www.crg.es/deafness>.
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- Kelley PM, Harris DJ, Comer BC, Askew JW, Fowler T, Smith SD, Kimberling WJ. Novel mutations in the connexin 26 gene (GJB2) that cause autosomal recessive (DFNB1) hearing loss. *Am J Hum Genet.* 1998 Apr;62(4):792-9.
- Kenna MA, Wu BL, Cotanche DA, Korf BR, Rehm HL. Connexin 26 studies in patients with sensorineural hearing loss. *Arch Otolaryngol Head Neck Surg.* 2001 Sep;127(9):1037-42.
- Kenneson A, Van Naarden Braun K and Boyle C. GJB2 (connexin 26) variants and nonsyndromic sensorineural hearing loss: a HuGE review. *Genet Med.* 2002;4(4): 258-74.
- Park HJ, Hahn SH, Chun YM, Park K, Kim HN. Connexin26 mutations associated with nonsyndromic hearing loss. *Laryngoscope.* 2000 Sep;110(9):1535-8.
- Rickard S, Kelsell DP, Sirimana T, Rajput K, MacArdle B, Bitner-Glindzicz M. Recurrent mutations in the deafness gene GJB2 (connexin 26) in British Asian families. *J Med Genet.* 2001 Aug;38(8):530-3.
- Smith RJH, Van Camp G. Nonsyndromic hearing loss and deafness, DFNB1 (Updated March 14, 2005) In: GeneReviews at GeneTests: Medical Genetics Information Resource (database online). <http://www.genetests.org>.
- Snoeckx RL, Huygen PLM, Feldmann D, Marlin S, Denoyelle F, Waligora J, Mueller-Malesinska M, Pollak A, Ploski R, Murgia A, Orzan E, Castorina P, Ambrosetti U, Nowakowska-Szyrwinska E, Bal J, Wiszniewski W, Janecke AR, Nekahm-Heis D, Seeman P, Bendova O, Kenna MA, Frangulov A, Rehm HL, Tekin M, Incesulu A, Dahl H-HM, du Sart D, Jenkins L, Lucas D, Bitner-Glindzicz M, Avraham KB, Brownstein Z, del Castillo I, Moreno F, Blin N, Pfister M, Sziklai I, Toth T, Kelley PM, Cohn ES, Maldergem LV, Hilbert P, Roux A-F, Mondain M, Hoefsloot, LH Cremers CWRJ, Löppönen T, Löppönen H, Parving A, Gronskov K, Schrijver I, Roberson J, Gualandi F, Martini A, Lina-Granade G, Pallares-Ruiz N, Correia C, Fialho G, Cryns K, Hilgert N, Van de Heyning P, Nishimura CJ, Smith RJH, and Van Camp G. A genotype-phenotype correlation for GJB2 (connexin 26) deafness. *Am J Med Genet* 2005 Dec;77(6):945-57.

GTR Rendered – Genetic Variation Sections

Genetic Variations Section

Test Performed

- Connexin 26 Full Gene Test

Findings

- DNA VARIANTS: Homozygous 109G>A (V37I), Exon 2, GJB2, Pathogenic
- INCIDENTAL VARIANTS: Heterozygous 79G>A (V27I), Exon 2, GJB2, Benign

Interpretation

- DNA sequencing detected two mutations in the connexin 26 gene, 79G>A (V27I) and 109G>A (V37I). The V27I mutation has been reported as a benign variant (references) and is not believed to cause hearing loss. The V37I mutation has been previously reported in patients with hearing loss. This mutation, in homozygosity or combined with another GJB2 disease causing mutation, typically results in a mild to moderate hearing loss (Cryns et al. 2005). Mutations in both copies of the GJB2 gene are necessary to assume that GJB2 is responsible for the hearing loss. Although two mutations were identified in this patient, we would assume that the combination of a benign variant and a mild pathogenic mutation would result in a mild to moderate hearing loss rather than a moderately-severe one, as in this patient. It is most likely that the hearing loss in this patient is the result of the V37I mutation and an unknown second pathogenic mutation. It should be noted that a second mutation is not identified in a large percentage (10-50%) of patients with nonsyndromic hearing loss and GJB2 mutations (del Castillo et al. 2003).

Genetic Variations Section

Test Performed

- Mitochondrial Hearing Loss Genes Test

Findings

- Negative.

Interpretation

- DNA sequencing did not detect the presence of any mutations in the MTT51 and MTRNR1 genes. Although this test examines all regions known to contain pathogenic mutations in these genes, it does not include sequencing of the 5' end of the MTRNR1 gene.

Genetic Variations Section

Test Performed

- Connexin 30 Deletion Test

Findings

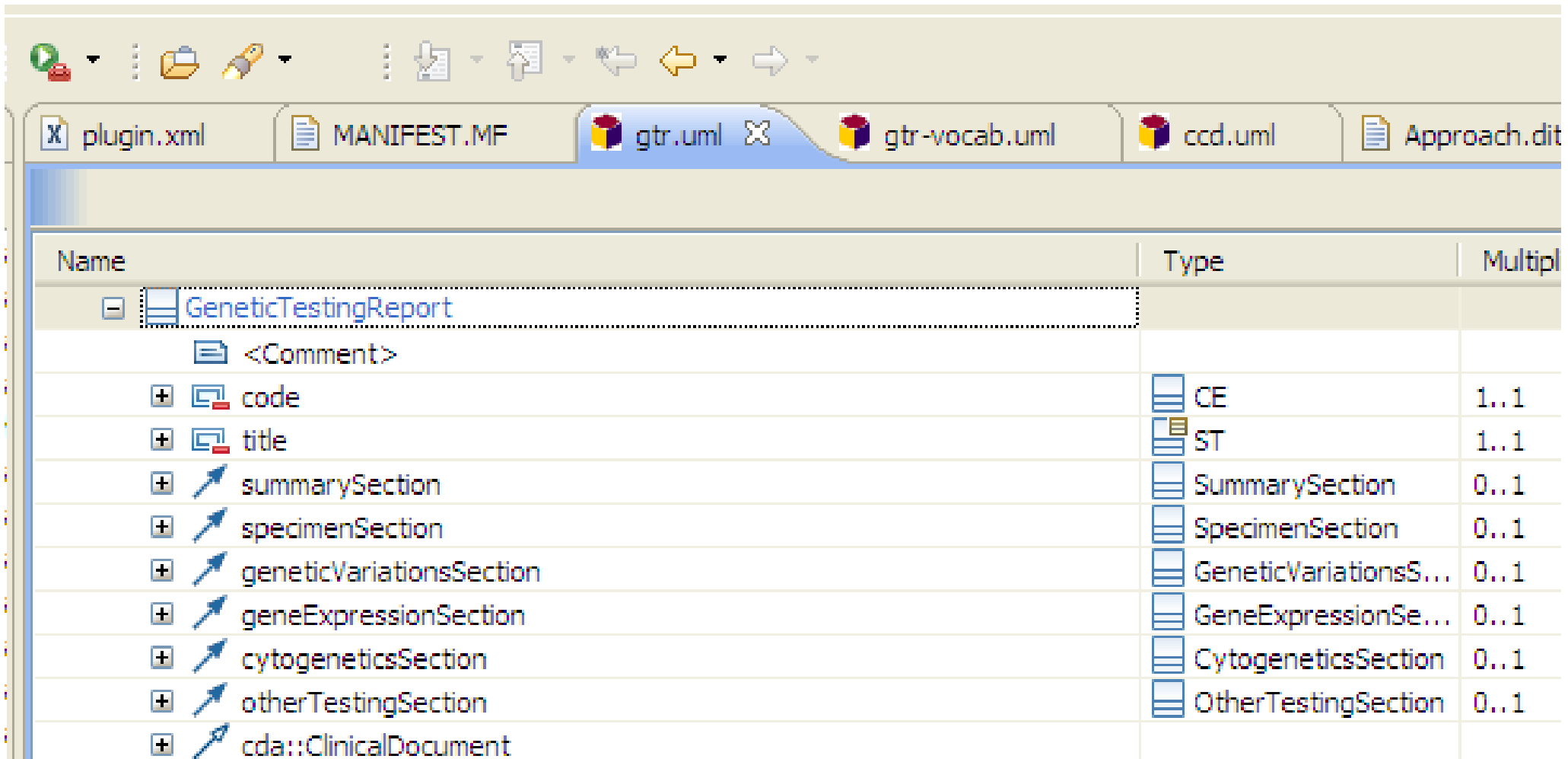
- Negative.

Interpretation

- GJB6-D13S1830 Deletion: A PCR-based analysis of the GJB6-D13S1830 region of chromosome 13 was performed and did not detect the deletion. This test does not assess the DNA sequence of the GJB6 gene or detect other mutations that could affect the expression of the gene.

Draft that has not been clinically validated

GTR UML Model - Section Outline



The screenshot shows a UML modeling tool interface with a toolbar at the top and a tabbed workspace. The active tab is 'gtr.uml'. Below the tabs, a table displays the class hierarchy for 'GeneticTestingReport'.

Name	Type	Multiple
GeneticTestingReport		
<Comment>		
code	CE	1..1
title	ST	1..1
summarySection	SummarySection	0..1
specimenSection	SpecimenSection	0..1
geneticVariationsSection	GeneticVariationsS...	0..1
geneExpressionSection	GeneExpressionSe...	0..1
cytogeneticsSection	CytogeneticsSection	0..1
otherTestingSection	OtherTestingSection	0..1
cda::ClinicalDocument		

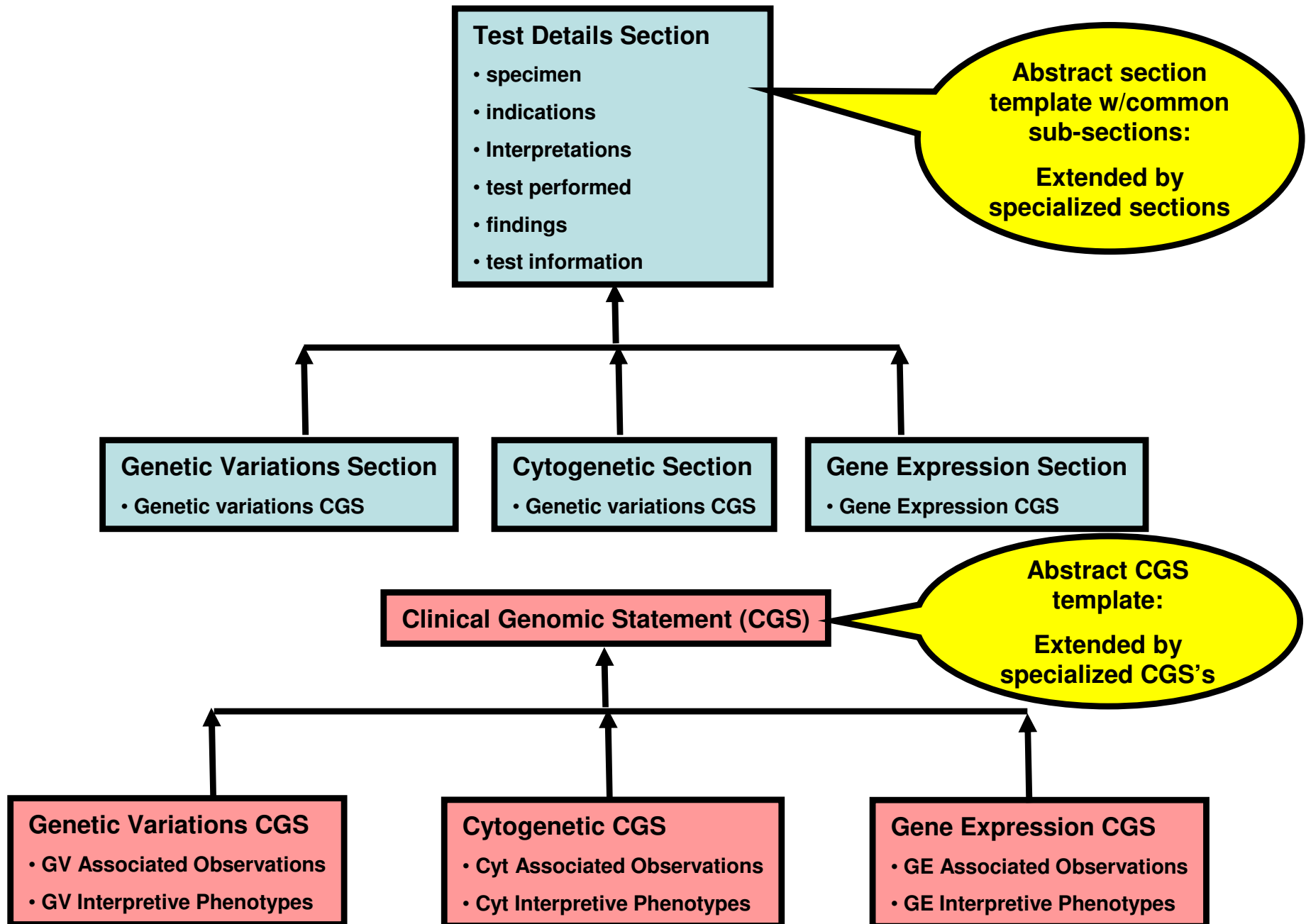
GTR UML Model - Summary Section

SummarySection		
<Comment>		
code	CE	1..1
title	ST	1..1
+ overallInterpretationSection	OverallInterpretat...	0..*
+ testsPerformedSection	TestsPerformedSe...	0..1
+ testInformationSection	TestInformationSe...	0..1
+ recommendationsSection	Recommendations...	0..1
+ cda::Section		



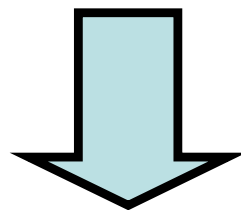
OverallInterpretationSection		
<Comment>		
code	CE	1..1
title	ST	1..1
+ overallInterpretivePhenotypeObservationPharmacogenomicDrugEfficacy	OverallInterpretiv...	0..1
+ overallInterpretivePhenotypeObservationPharmacogenomicDrugMetaboli	OverallInterpretiv...	0..1
+ overallInterpretivePhenotypeObservationGeneticDisease	OverallInterpretiv...	0..1
+ overallInterpretivePhenotypeObservationGeneticDiseaseCarrier	OverallInterpretiv...	0..1
+ cda::Section		

GTR Main Hierarchies



GTR Genetic Variation Section

GeneticVariationsSection		
<Comment>		
code	CE	1..1
title	ST	1..1
clinicalGenomicStatementGeneticVariation	ClinicalGenomicSta...	0..*
gtr::TestDetailsSection		



TestDetailsSection		
<Comment>		
code	CE	0..1
title	ST	0..1
specimenSection	SpecimenSection	0..1
indicationsSection	IndicationsSection	0..1
testsPerformedSection	TestsPerformedSe...	0..1
findingsSection	FindingsSection	0..1
interpretationSection	InterpretationSect...	0..1
testInformationSection	TestInformationSe...	0..1
cda::Section		

Clinical Genomic Statement

ClinicalGenomicStatement		
<Comment>		
code	CD	1..1
value	ANY	0..1
indicationObservation	IndicationObserva...	0..1
interpretivePhenotypeObservation	InterpretivePheno...	0..1
{?} Disallowance of interpretationCode		
cda::Observation		

Extended by specialized Clinical Genomic Statements

Name	Type	Multi
ClinicalGenomicStatementGeneticVariation		
<Comment>		
code	CD	1..1
value	ANY	0..1
interpretivePhenotypeGeneticVariation	InterpretivePhen...	0..1
interpretivePhenotypePharmacogenomicDrugEfficacy	InterpretivePhen...	0..1
interpretivePhenotypePharmacogenomicDrugMetabolism	InterpretivePhen...	0..1
geneticVariationAssociatedObservationAminoAcidChange	GeneticVariation...	0..1
geneticVariationAssociatedObservationDNACChange	GeneticVariation...	0..1
geneticVariationAssociatedObservationDNARegionName	GeneticVariation...	0..1
geneticVariationAssociatedObservationZygotity	GeneticVariation...	0..1
{?} value		
gtr::ClinicalGenomicStatement		

Interpretive Phenotype Observation

InterpretivePhenotypeObservationGeneticVariation			
<Comment>			
code	CD		1..1
value	CD		0..1
{?} value			
gtr::InterpretivePhenotypeObservation			

Name	Type	Multiplicity	Annotation
gtr-vocab			
Allelic State			53034-5
Clinical Genomic Statement Genetic Variation Amino Acid Change			48006-1
Clinical Genomic Statement Genetic Variation DNA Change			48019-4
Genetic disease analysis overall interpretation			51968-6
Genetic disease sequence variation interpretation			53037-8
Interpretive Phenotype Observation Pharmacogenomic Drug Efficacy			51961-1
Interpretive Phenotype Observation Pharmacogenomic Drug Metabolism			53040-2
Overall Interpretive Phenotype Observation Genetic Disease Carrier			53039-4
Overall Interpretive Phenotype Observation Pharmacogenomic Drug Efficacy			51964-5
Overall Interpretive Phenotype Observation Pharmacogenomic Drug Metabolism			51971-0
(CodeSystems)			

Genetic disease sequence variation interpretation			53037-8
LA6668-3			Pathogenic
LA6669-1			Presumed pathogenic
LA6682-4			Unknown significance
LA6675-8			Benign
LA6674-1			Presumed benign

GTR XML Snippets – Indications Section

```

102 .....
103 Summary Section
104 .....
105 -->
106 <component>
107   <section>
108     <code code="TBD" codeSystem="2.16.840.1.113883.6.1" codeSystemName="LOINC" displayName="Genetic Testing Sum
109     <title>Summary Section</title>
110     <!--
111 .....
112 Indications Section
113 .....
114 -->
115 <component>
116   <section>
117     <code code="TBD" codeSystem="2.16.840.1.113883.6.1" codeSystemName="LOINC" displayName="Genetic Testing Indications Section"/>
118     <title>Indications</title>
119     <text>
120       <list>
121         <item>
122           <content ID="a2">Indication: Profound sensorineural hearing loss</content>
123         </item>
124       </list>
125     </text>
126     <entry>
127       <observation classCode="COND" moodCode="EVN">
128         <id root="2.16.840.1.113883.18.12.7.30.9.2.1"/>
129         <code code="MTHU008863" codeSystemName="LOINC" displayName="Indications description"/>
130         <!-- the effective time should be the time of onset of the disease -->
131         <effectiveTime value="1950"/>
132         <value xsi:type="CD" code="C26973" codeSystemName="NCI Thesaurus" displayName="Sensory Hearing Loss">
133           <originalText>
134             <reference value="#a2"/>
135           </originalText>
136         </value>
137         <!-- the following reference could point to the full description of the disease, residing in the patient records -->
138         <reference typeCode="XCRPT">
139           <externalObservation>
140             <id root="2.16.840.1.113883.19.1.2765"/>
141           </externalObservation>
142         </reference>
143       </observation>
144     </entry>
145   </section>
146 </component>

```

Summary
Section

Indication's
narrative

Indication's
structured data

GTR XML Snippets – Specimen Section

```
148 *****
149 Specimen Section
150 *****
151 -->
152 <component>
153   <section>
154     <code code="TBD" codeSystem="2.16.840.1.113883.6.1" codeSystemName="LOINC"
155           displayName="Genetic Testing Specimen and Genomic Source Section"/>
156     <title>Specimen and Genomic Source</title>
157     <text>
158       <list>
159         <item>Peripheral Blood</item>
160         <item>Genomic source class: Germline</item>
161       </list>
162     </text>
163     <entry>
164       <observation classCode="OBS" moodCode="EVN">
165         <code code="TBD" displayName="Specimen Type"/>
166         <value xsi:type="CD" code="TBD" displayName="Peripheral Blood"/>
167         <entryRelationship typeCode="SUBJ">
168           <observation classCode="OBS" moodCode="EVN">
169             <code code="48002-0" codeSystemName="LOINC" displayName="Genomic source class"/>
170             <value xsi:type="CD" code="LA6683-2" codeSystemName="LOINC" displayName="Germline"/>
171           </observation>
172         </entryRelationship>
173       </observation>
174     </entry>
175   </section>
176 </component>
```

Specimen's narrative

Specimen's structured data

GTR XML Snippets – Overall Interpretation Section

Interpretation's narrative

Structured Interpretation

```

207 *****
208 Overall Interpretation section
209 *****
210 -->
211 <component>
212   <section>
213     <code code="TBD" codeSystem="2.16.840.1.113883.6.1" codeSystemName="LOINC" displayName="Genetic Test
214     Section"/>
215     <title>Overall Interpretation</title>
216     <text>
217       <list>
218         <item>
219           <content>
220             <content styleCode="Bold">Inconclusive.</content> DNA sequencing detected two mutations in the connexin 26 gene,
221             79G>A (V27I) and 109G>A (V37I). GJB6-D13S1830 Deletion: A PCR-based analysis of the GJB6-D13S1830 region of
222             chromosome 13 was performed and did not detect the deletion. This test does not assess the DNA sequence of the GJB6
223             gene or detect other mutations that could affect the expression of the gene. Mitochondrial Hearing Loss Genes: DNA
224             sequencing did not detect the presence of any mutations in the MTT51 and MTRNR1 genes. Although this test examines
225             all regions known to contain pathogenic mutations in these genes, it does not include sequencing of the 5' end of
226             the MTRNR1 gene. The V27I mutation has been reported as a benign variant (references) and is not believed to cause
227             hearing loss. The V37I mutation has been previously reported in patients with hearing loss. This mutation, in
228             homozygosity or combined with another GJB2 disease causing mutation, typically results in a mild to moderate
229             hearing loss (Cryns et al. 2005). Mutations in both copies of the GJB2 gene are necessary to assume that GJB2 is
230             responsible for the hearing loss. Although two mutations were identified in this patient, we would assume that the
231             combination of a benign variant and a mild pathogenic mutation would result in a mild to moderate hearing loss
232             rather than a moderately-severe one, as in this patient. It is most likely that the hearing loss in this patient is
233             the result of the V37I mutation and an unknown second pathogenic mutation. It should be noted that a second
234             mutation is not identified in a large percentage (10-50%) of patients with nonsyndromic hearing loss and GJB2
235             mutations (del Castillo et al. 2003).
236           </content>
237         </item>
238       </list>
239     </text>
240     <entry>
241       <observation classCode="PHN" moodCode="DEF">
242         <code code="51968-6" codeSystemName="LOINC" displayName="Genetic disease analysis overall
243         <statusCode code="completed"/>
244         <effectiveTime value="200512011500"/>
245         <value xsi:type="CD" code="LA9663-1" displayName="Inconclusive"/>
246       </observation>
247     </entry>
248   </section>
249 </component>

```

GTR XML Snippets – Genetic Variation Section

```

373 *****
374 Genetic Variations Section: Connexin 26 Full Gene Test
375 *****
376 --->
377 <component>
378   <section>
379     <code code="TBD" codeSystem="2.16.840.1.113883.6.1" codeSystemName="LOINC" displayName="Genetic Variations Section" />
380     <title>Genetic Variations Section</title>
381     <!-- Structured representation of: Homozygous 109G>A (V37I), Exon 2, GJB2, Pathogenic -->
382     <entry>
383       <observation classCode="GEN" moodCode="EVN">
384         <code code="55208-3" codeSystemName="LOINC" displayName="DNA Analysis Discrete Sequence Variant Panel"/>
385         <statusCode code="completed"/>
386         <effectiveTime value="200512011500"/>
387         <entryRelationship typeCode="SUBJ">
388           <observation classCode="LOC" moodCode="EVN">
389             <code code="48018-6" codeSystemName="LOINC" displayName="Gene Identifier"/>
390             <value xsi:type="CD" code="GJB2" codeSystemName="HUGO"/>
391           </observation>
392         </entryRelationship>
393         <entryRelationship typeCode="SUBJ">
394           <observation classCode="LOC" moodCode="EVN">
395             <code code="51958-7" codeSystemName="LOINC" displayName="Transcript Reference Sequence Identifier"/>
396             <value xsi:type="CD" code="NM_004004.5" codeSystem="REFSEQ" codeSystemName="NCBI Reference Sequence"/>
397           </observation>
398         </entryRelationship>
399         <entryRelationship typeCode="SUBJ">
400           <observation classCode="LOC" moodCode="EVN">
401             <code code="48003-8" codeSystemName="LOINC" displayName="DNA Sequence Variation Identifier"/>
402             <value xsi:type="CD" code="rs72474224" codeSystemName="dbSNP"/>
403           </observation>
404         </entryRelationship>
405         <entryRelationship typeCode="SUBJ">
406           <observation classCode="LOC" moodCode="EVN">
407             <code code="48004-6" codeSystemName="LOINC" displayName="DNA Sequence Variation"/>
408             <value xsi:type="CD" code="109G>A" codeSystemName="HGVS nomenclature for the description of sequence variations"/>
409           </observation>
410         </entryRelationship>
411         <entryRelationship typeCode="SUBJ">
412           <observation classCode="LOC" moodCode="EVN">
413             <code code="48019-4" codeSystemName="LOINC" displayName="DNA Sequence Variation Type"/>
414             <value xsi:type="CD" code="LA6690-7" codeSystemName="LOINC" displayName="Substitution"/>
415           </observation>
416         </entryRelationship>
417         <entryRelationship typeCode="SUBJ">
418           <observation classCode="LOC" moodCode="EVN">
419             <code code="48005-3" codeSystemName="LOINC" displayName="Amino Acid Change"/>
420             <value xsi:type="CD" code="Val37Ile"/>

```

Genetic
Variation

Genetic
Variation
associated
observations

GTR XML Snippets – Genetic Variation Section (cont.)

```

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```

```

</observation>
</entryRelationship>
<entryRelationship typeCode="SUBJ">
  <observation classCode="GEN" moodCode="EVN">
    <code code="48006-1" codeSystemName="LOINC" displayName="Amino acid change type"/>
    <value xsi:type="CD" code="LA6698-0" displayName="Missense"/>
  </observation>
</entryRelationship>
<entryRelationship typeCode="SUBJ">
  <observation classCode="LOC" moodCode="EVN">
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    <value xsi:type="ST">Exon 2</value>
  </observation>
</entryRelationship>
<entryRelationship typeCode="SUBJ">
  <observation classCode="GEN" moodCode="EVN">
    <code code="53034-5" codeSystemName="LOINC" displayName=" Allelic State"/>
    <value xsi:type="CD" code="LA6705-3" codeSystemName="LOINC" displayName="Homozygous"/>
  </observation>
</entryRelationship>
<!-- pointing to the indication of performing this variation testing-->
<entryRelationship typeCode="RSON">
  <observation classCode="OBS" moodCode="EVN">
    <id root="2.16.840.1.113883.18.12.7.30.9.2.1"/>
    <code/>
  </observation>
</entryRelationship>
<!-- interpretation of the variation observation (should consider if MFST=manifistation as the code here) -->
<entryRelationship typeCode="SPRT">
  <observation classCode="PHN" moodCode="DEF">
    <code code="53037-8" codeSystemName="LOINC" displayName="Genetic disease sequence variation interpretation"/>
    <value xsi:type="CD" code="LA6668-3" codeSystemName="LOINC" displayName="Pathogenic"/>
  </observation>
</entryRelationship>
</observation>
</entry>

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Genetic
Variation
indication

Genetic
Variation
interpretation

uHealth: Patient Empowerment System

- **Joint project between IBM and Gil Hospital (Korea)**
- **5 years project, currently in 2nd year**
- **3 IBM centers are involved:**
 - IBM Korea
 - IBM Research in China
 - IBM Research in Haifa
- **Building an open platform and services**
- **Web-based rich portal**
- **Testing the system with patients and physicians from the hospital**
- **Support integration with external PHR (e.g. Google Health)**

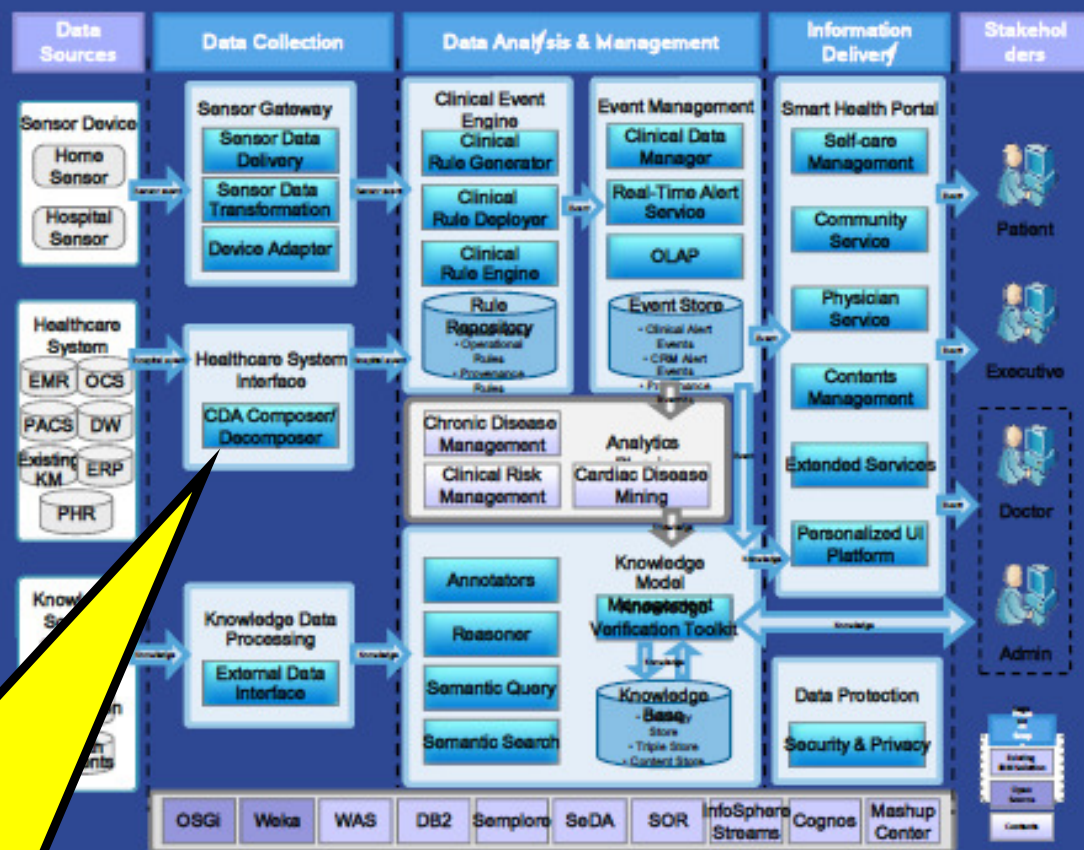
uHealth: PHR / EHR Hybrid System

uHealth – Empowering the Patient, Korea



Improve patient safety with IT

- Patients in the center; control, mgmt. and access
- Empower patients to be a data source, hub for external data, knowledge consumers and nodes in social-medical network
- Smart health Portal
 - Clinical and genomics information analysis
 - Dynamic content
 - Fully standard compliant
 - Rich data set integration
 - A platform for service provisioning
 - Easy of interaction between all users inc. physicians
- Focus
 - Social medical discovery
 - Patients like me
 - Medical recommendations
 - Personalised genomics ADE



Using CCD + GTR

The End

- Thank you for your attention... 😊
- Questions?