



OECD Workshop on Pharmacogenetics

Development of international data standards to support the acquisition, exchange, submission and archiving of clinical-genomic data



Rome, Italy October 17, 2005

Amnon Shabo (Shvo), PhD IBM Research Lab in Haifa







IBM Research Worldwide



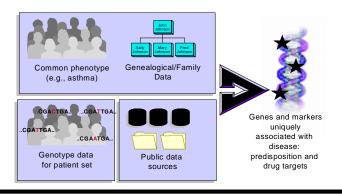




Haifa Research Lab HCLS Focal Areas

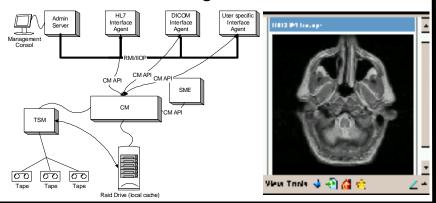
CGv2

Clinical Genomics Solutions



MCM

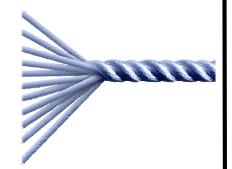
Medical Content Manager



IHII

Interoperable Health Information Infrastructure

- Targeted at regional and national EHR initiatives
- In collaboration with Almaden Research Center and HCLS



Health Standards Practice

HL7 / IHE / CEN / DICOM / HIPAA

Offering Education & Services

My HL7 roles:

- •Co-chair and facilitator of Clinical Genomics SIG
- •Co-editor of CDA Release Two (Clinical document)



Agenda / Key Points

Health Information Standards

- should be based on a central Health Reference Information Model (RIM)

Clinical Genomics & Clinical Trials Standards

- should implement the 'encapsulate & bubble-up' paradigm

The Final Frontier: EHR – Electronic Health Record

- personalized longitudinal and cross-institutional EHR
- personal genetic data should be part of the EHR
- inter/national Health Information Infrastructure is focused on EHR
- the inevitable sustainability model:
 - 'Independent Health Records Banks'

Types of Health Informatics Standard Artifacts

- Codes & Identifiers (SNOMED, ICD, LOINC, CPT, GenBank, etc.)
- Messages (HL7, DICOM, X12)
- Clinical Documents (HL7-CDA)
- Records (CEN, ISO, OpenEHR, HL7-Functional Model)
- Integration profiles (IHE: implement best-practice workflows)
- Claims (HIPAA / X12, HL7-Attachements)
- Others: Knowledge Representation (e.g., Clinical Guidelines GLIF); Context Synchronization (CCOW)



HL7 – The Dominant SDO



Focus on the 7th layer in ISO OSI (Open Systems Interconnection)

V2→V3: Quantum Leap
like the shift from 'structured' to OO
programming

ies; 25 ii
specs

V2 saging specifications – ANSI standa
DT, Billing, Observations, Medications,

V2.XML is under ballot (XML Encoding F



♦ Dedicated Data Types (e.g., CD – Conce

♦ Mandatory & Central RIM – Reference Ir

New specs: CDA, Public Health Reporting, Clinical Trials, Clin. Genom.



HL7's **mission** is clinical interoperability

"To provide standards for the exchange, management and integration of data that supports clinical patient care and the management, delivery and evaluation of healthcare services."

Source: HL7 Mission statement (1997)

interoperability

: ability of two or more systems or components to exchange information and to use the information that has been exchanged.

Functional interoperability

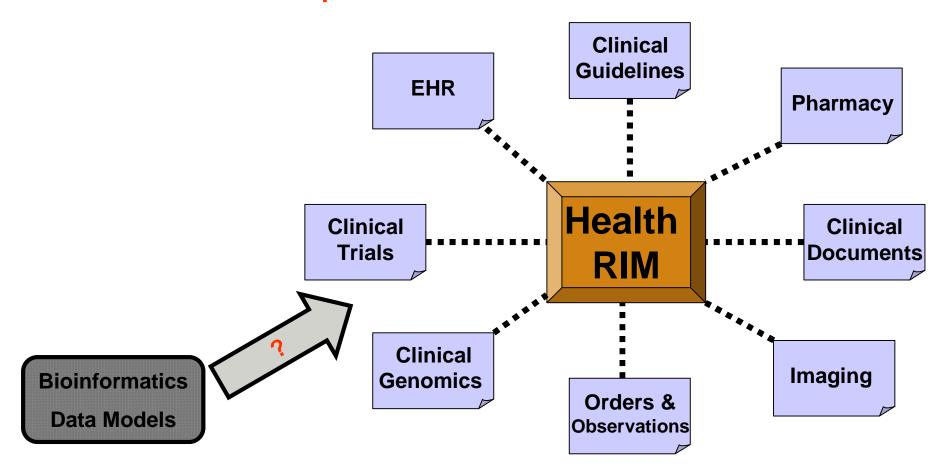
Source: IEEE Standard Computer Dictionary: A Compilation of IEEE Standard Computer Glossaries, IEEE, 1990]

Semantic interoperability



To achieve semantic interoperability...

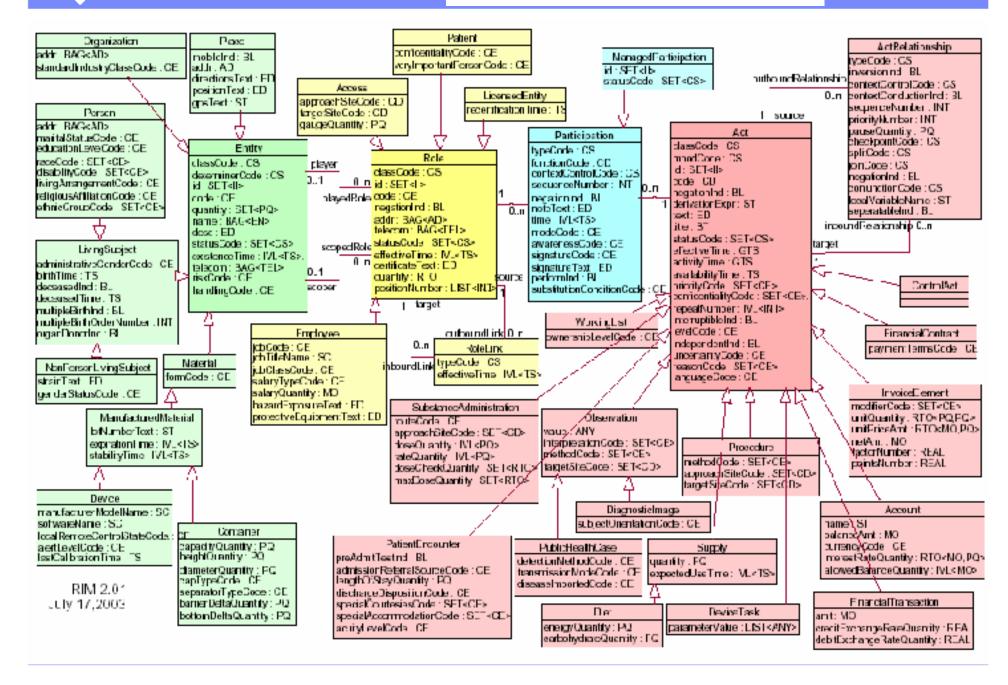
...we need standard specs derived from a Central Health RIM:



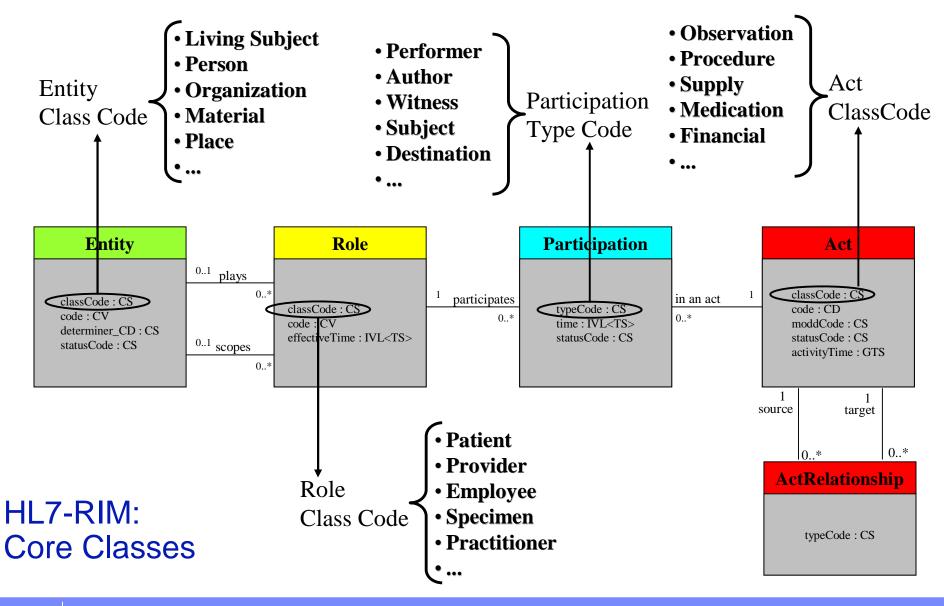
Central Health RIM (e.g., an extended HL7 V3 Reference Information Model): Bio- & medical-informatics standard specs are derived from the same RIM

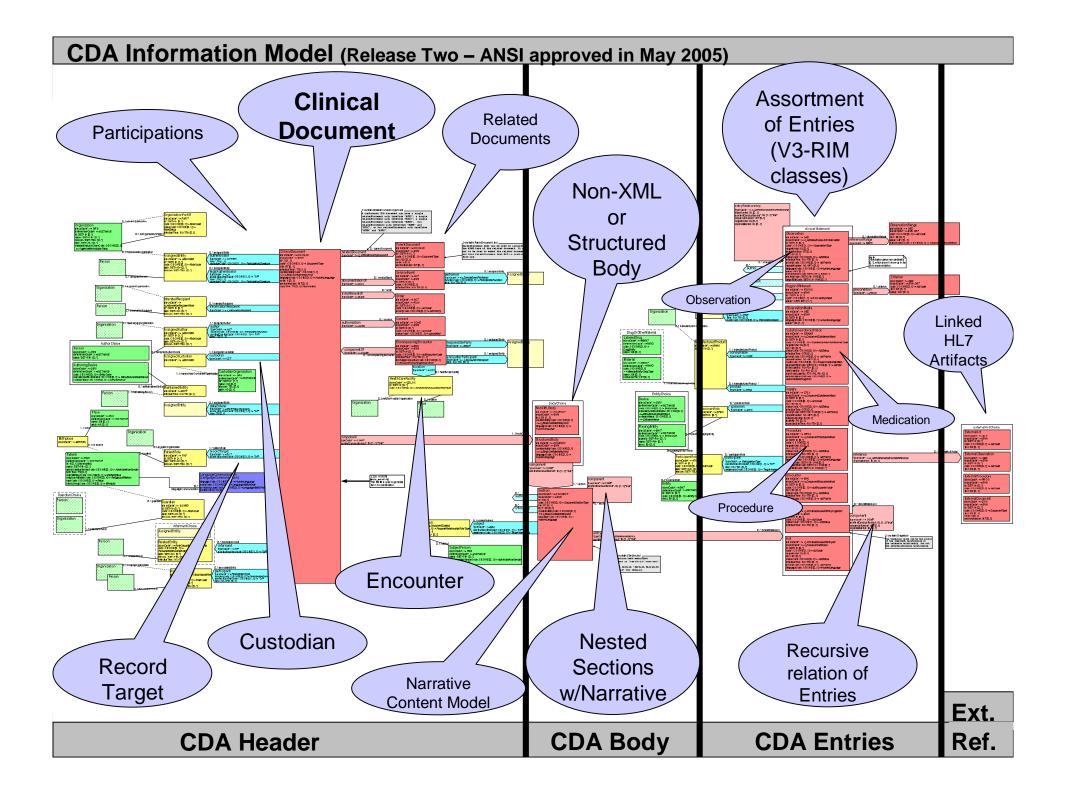
HL7 RIM – The USAM Model











Clinical Document – Structured to Narrative Links

```
<text>
                                                                                                                                                                                            Anchors
                       <caption>Complications
 Human readable
                       <content>
                                                                                                                                                                              To be pointed by the clones
                                              <content ID="a1">
                                              Thrombocytes were taken on the second day after transplantation and the count of Thrombocytes was not less than 25k during the transplantation
                                              </content>
                                                                                              Optional nesting content tags to nail down
                       </content>
                                                                                              specific narrative pieces:
         </text>
oches

oc
                                                                                               <content ID="a2">not less than 25k during</content>
                       <moodCode V="EVN"/>
                       <originalText><reference url="#a1"/></originalText>
                       <code displayName="Thrombocytes" System="SNOMED"/>
                       <value low="25" lowClosed ="true" unit="k">
                                              <originalText>not less than 25k</originalText</pre>
                                                                                                                                                                                                                                                                                      Direct Excerpts
                       <effectiveTime value="second day post-bmt" />
                                                                                                                                                                                                                                                                                                       From the narrative
         </Observation>
```

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The Final Frontier: EHR – Electronic Health Record

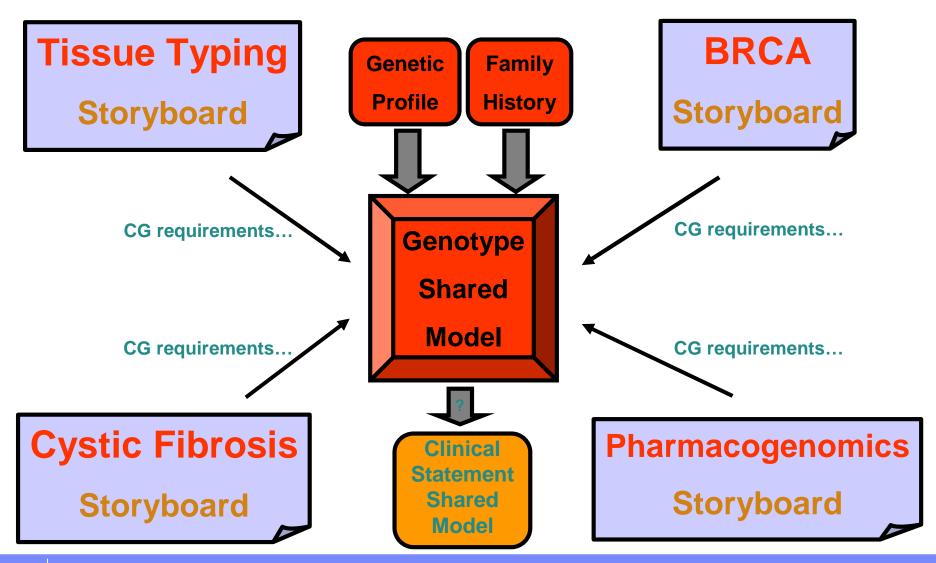
- personalized longitudinal and cross-institutional EHR
- personal genetic data should be part of the EHR
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The HL7 Clinical Genomics SIG Efforts



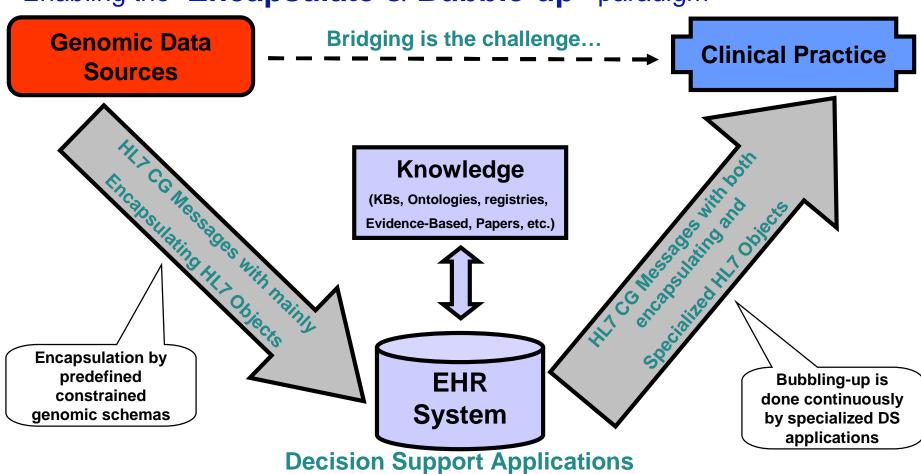
HL7 Clinical Genomics Specs (DSTU)

- DSTU = Draft Standard for Trial Use (collaborations with early adopters)
- The Genotype / Genetic Profile Modela
 - "Encapsulate & Bubble-Up" paradigm...
 - Bridging HL7 and bio-informatics markups
- Family History
 - Standardization of Patient's Pedigree for risk assessment of cancer patient

The Genotype Model - Focal Areas: Sequence **Expression** The Genotype and **Data** and its Alleles **Proteomics** Sequence **Clinical Variations Phenotypes**



Coexistence of HL7 schemas and Bioinformatics Markup: Enabling the "Encapsulate & Bubble-up" paradigm

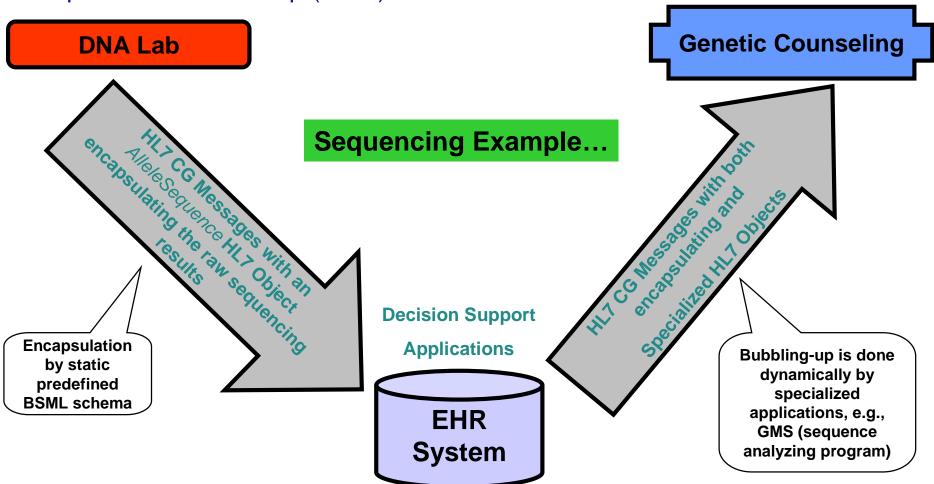


Bubbling up the clinically-significant raw genomic data into specialized HL7 objects and link them with clinical data from the patient EHR





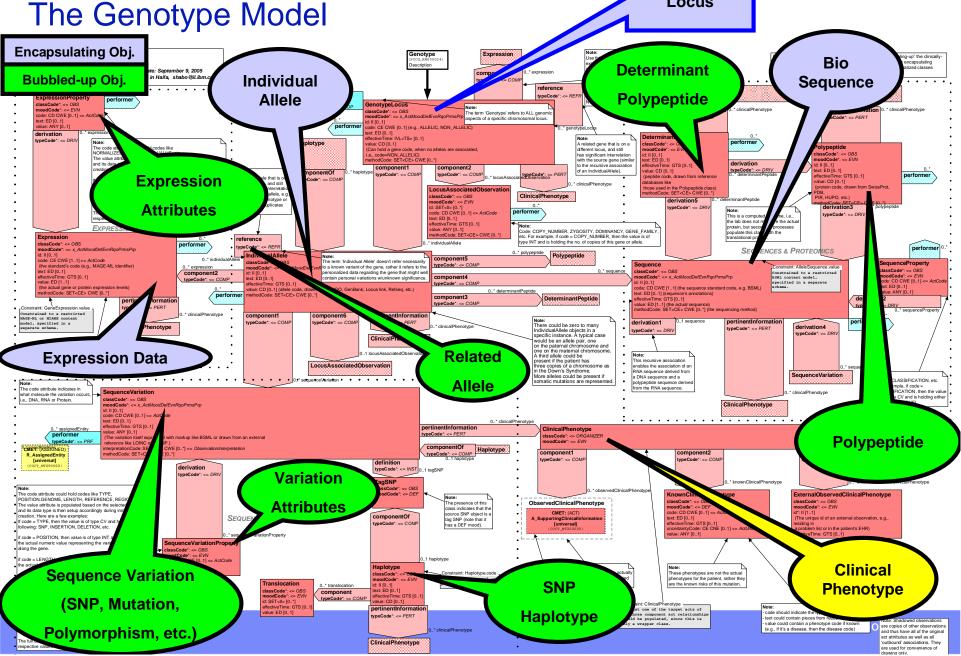
Encapsulate & bubble-up (cont.)



Bubbling up the clinically-significant SNP data into HL7 SNP and Mutation objects and link them with clinical data from the patient EHR

IBM

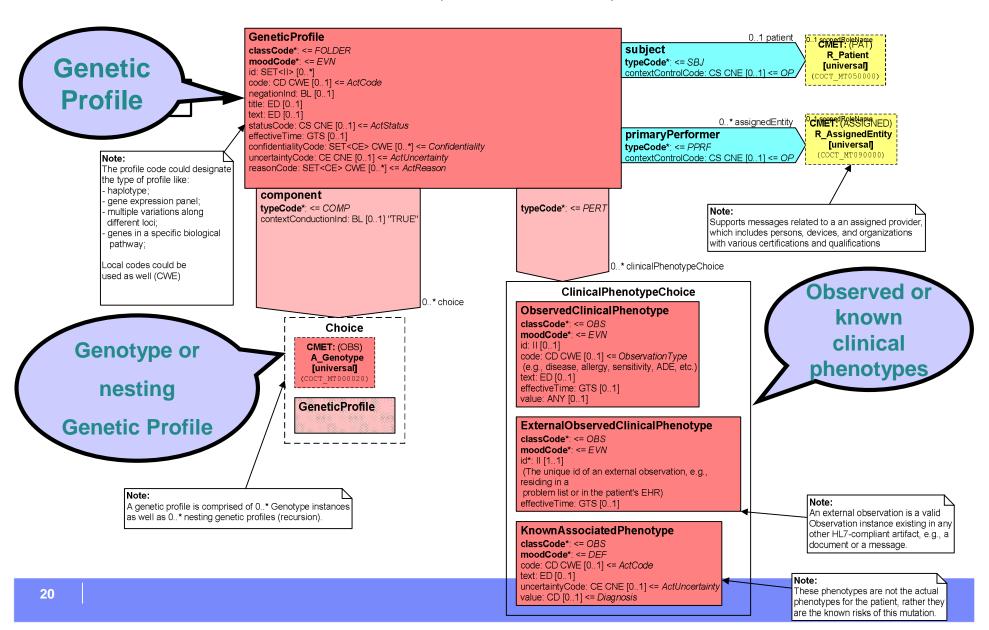
Entry Point:







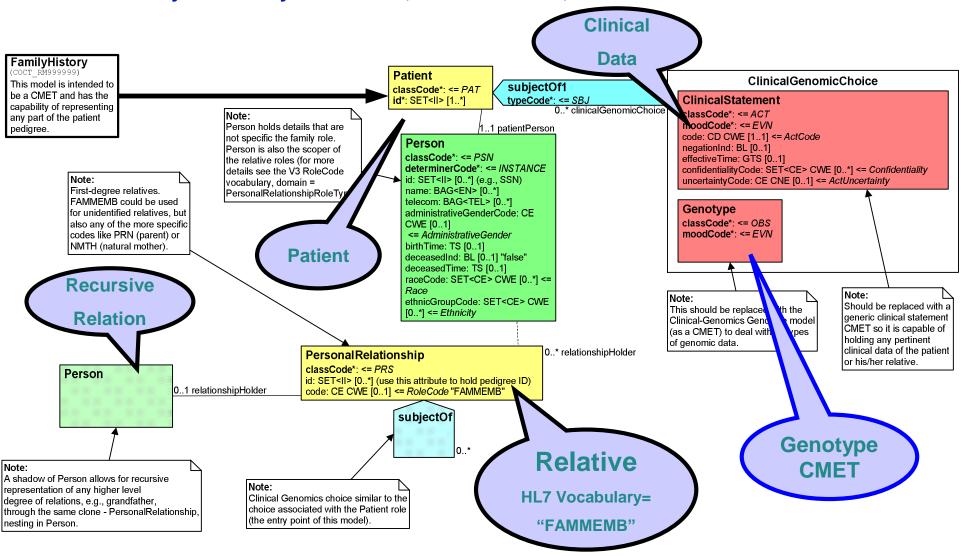
The Genetic Profile Model (since ballot #10)







The Family History Model (initial version)



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How the Genotype fits in a F.Hx XML?

```
<!-- DAUGHTER -->
                                                   Taken from a patient pedigree, the
       - <relationshipHolder>
                                                   portion related to patient's daughter
           <id extension="555.011" />
           <code code="DAU" />
                                                   (in collaboration with Partners HealthCare
         + <relationshipHolder>
                                                   & other HL7 CG SIG members)
           <!-- CENOMIC DATA -->
         <subjectOf>
             <cli>dinicalGenomicChoice>
               <cli>inicalGenomicChoiceGenotype>
                 <Genotype>

    <individualAllele>

                     <code code="BRCA1" codeSystem="[inscrt GcnBank OID]"
                      codeSystemName="GenBank" />
                     <text>Homo sapiens breast and ovarian cancer susceptibility (BRCA1)
                      complete cds.</text>
                                                  Point
                   + < AlleleSequence >
                                                                    Need to assure uniqueness
                    <SequenceVariation>
                                                                     across the various type
   To
                   </individualAllele>
                                                                       encapsulated data
                 </Genotype>
phenotype
               </clinicalGenomicChoiceGenotype>
and beyond.... </clinicalGenomicChoice>
           </subjectOf>
                                                   Click here to browse the entire XML...
                 CLINICAL DATA
         + <subjectOf>
                                                   Click here for the same sample with
         </relationshipHolder>
                                                   sequence data...
         <!-- end of DAUGHTER data
```





Sequence Sample XML

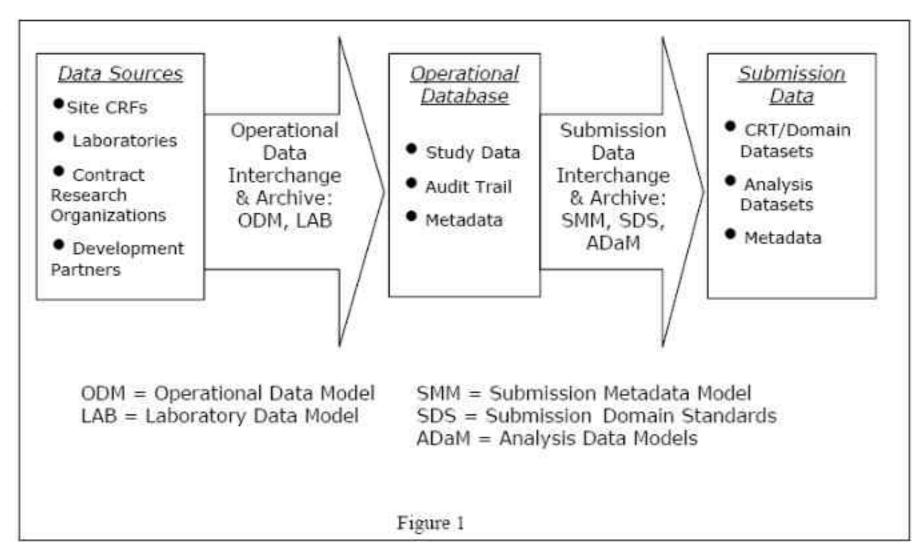
```
<sequence>
  <code code="BSMLcon3"/>
  <effectiveTime value="20050901"/>
  <value>
    <Definitions>
       <Sequences>
          <Sequence id="seq1" molecule="dna" title="EGFR - Homo sapiens epidermal growth factor</p>
           receptor" length="5616" representation="raw">
            <Seq-data>
                 1 ccccggcgca gcgcggccgc agcagcctcc gcccccgca cggtgtgagc gcccgacgcg
                 61 geogaggegg ceggagteec gagetageec eggeggeege egeegeecag aceggaegae
                  121 aggecacete geoggegee geoggagee eggetegee geoggegea caaceacege
            </Seq-data>
          </Sequence>
       </Sequences>
       <lsoforms>
          <lsoform-set>
            <lsoform id="snp1" segref="seg1" location="190" change="T"/>
            <lsoform id="snp2" segref="seg1" location="1099" change="G"/>
            <lsoform id="snp3" segref="seg1" location="2418" change="C"/>
            <lsoform id="snp4" segref="seg1" location="3721" change="T"/>
                                                                              Notes:
            <lsoform id="snp5" segref="seg1" location="4982" change="G"/>
          </lsoform-set>
       </lsoforms>
     </Definitions>
```

The use of the BSML 'segref' attribute is to point to the sequence where this SNP occurs - value is the sequence id value.

</value>

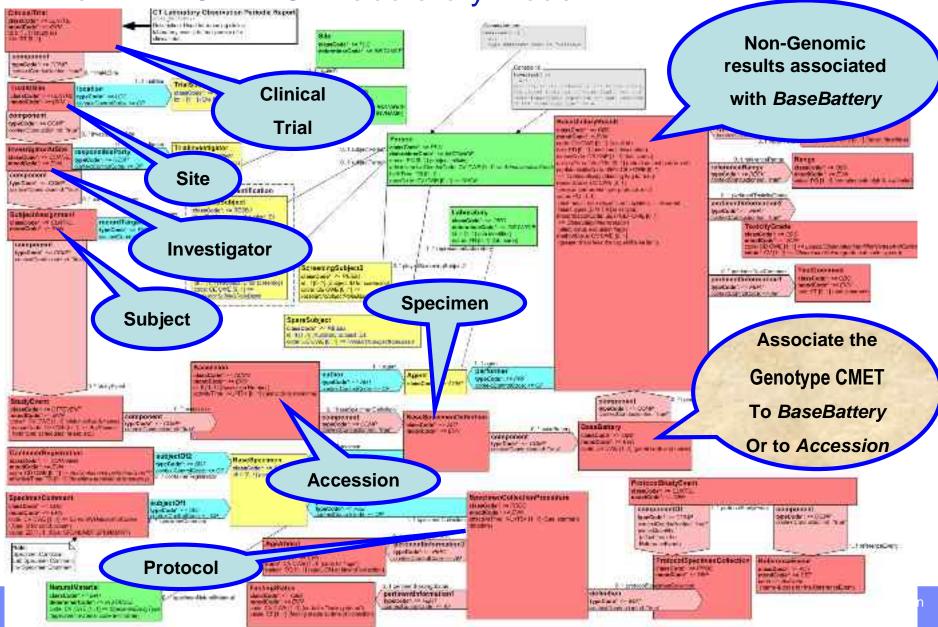
sequence>

The CDISC Standardization Activities in Clinical Trials





The HL7 RCRIM CT Laboratory Model



HL7 RCRIM-Clinical Genomics Joint Effort to address the need for information standards in FDA VGDS

- The Clinical Genomics SIG develops the Genotype Model
- The RCRIM TC develops Pharmacogenomics Message based on the CDISC Clinical Trials models
- The Pharmacogenomics Message utilizes the Genotype Model to convey genetic/genomic data
- The Pharmacogenomics Message will be proposed as the data standard in the FDA Guidance for VGDS – Voluntary Genomic Data Submission
- * "The Agency has heard that pharmaceutical sponsors have been reluctant to embark on programs of pharmacogenomic testing during FDA-regulated phases of drug development because of uncertainties in how the data will be used by FDA in the drug application review process."

(http://www.fda.gov/cder/guidance/6400fnl.htm#_Toc97697894)

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EHR Standards

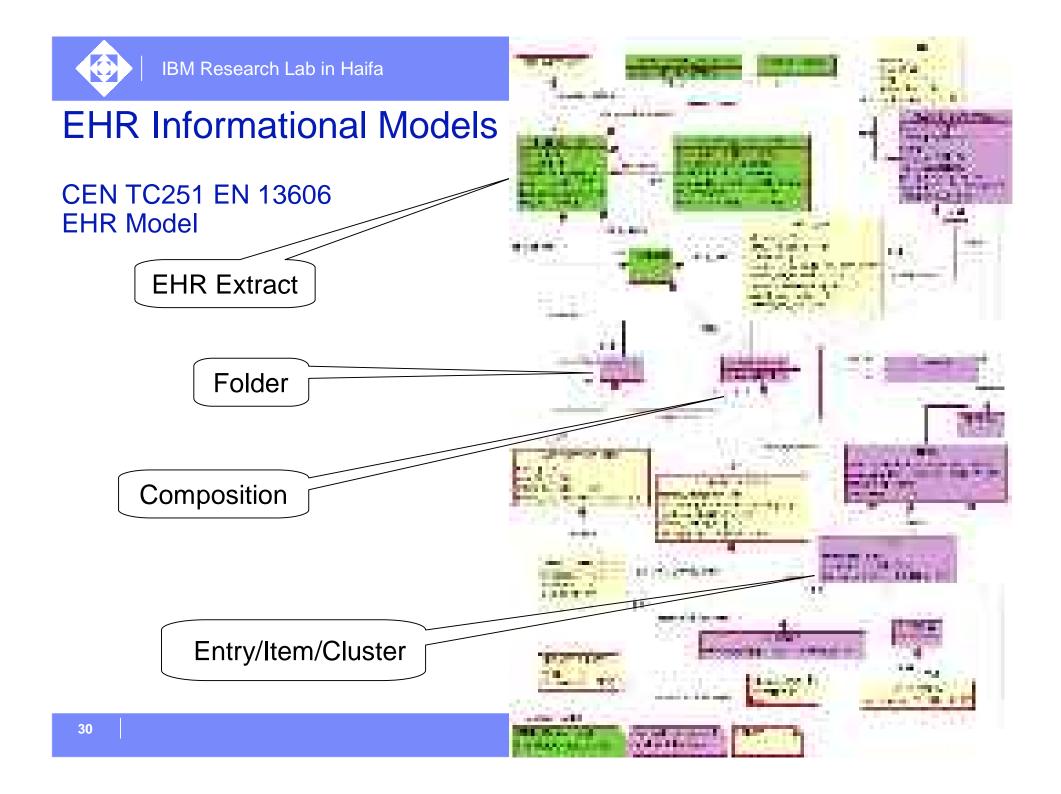
ISO assessment...

"Previous attempts to develop a definition for the Electronic Health Record have foundered due to the difficulty of encompassing all of the many and varied facets of the EHR in a single comprehensive definition."



The HL7 EHR Functional Model DSTU







IHE (Integrating the Healthcare Enterprise) XDS New Profile

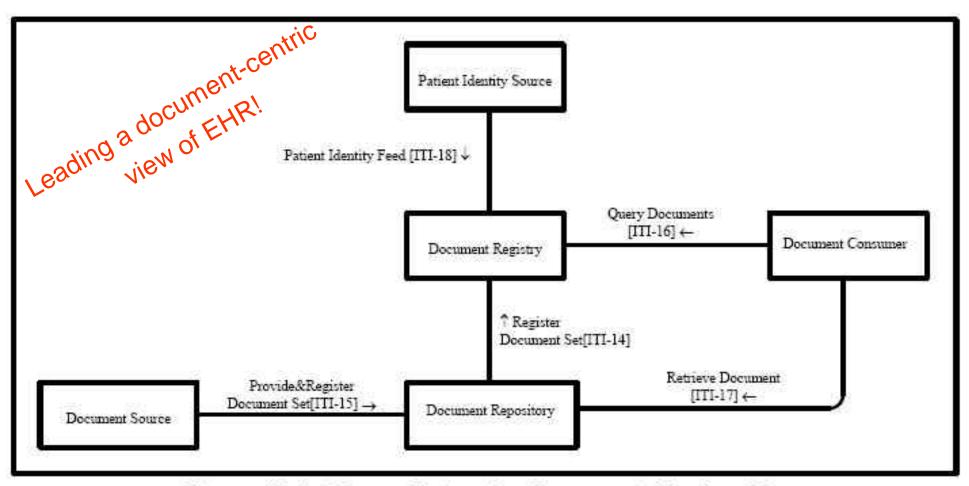


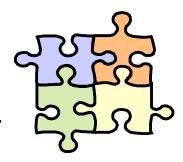
Figure 10.1-1 Cross-Enterprise Document Sharing Diagram





What's the Problem? (1)

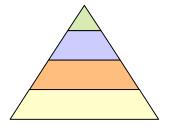
So, we integrated all medical records... ...we even standardized & indexed them (!)...



...and the patient is now requesting care:

How does the current healthcare provider make sense out of the pile of medical records and have better medical reasoning?

- Those medical records could be numerous, using different standards, different codes, different units, could contain contradictory info., etc.
- Possible solution: A lifetime electronic health record



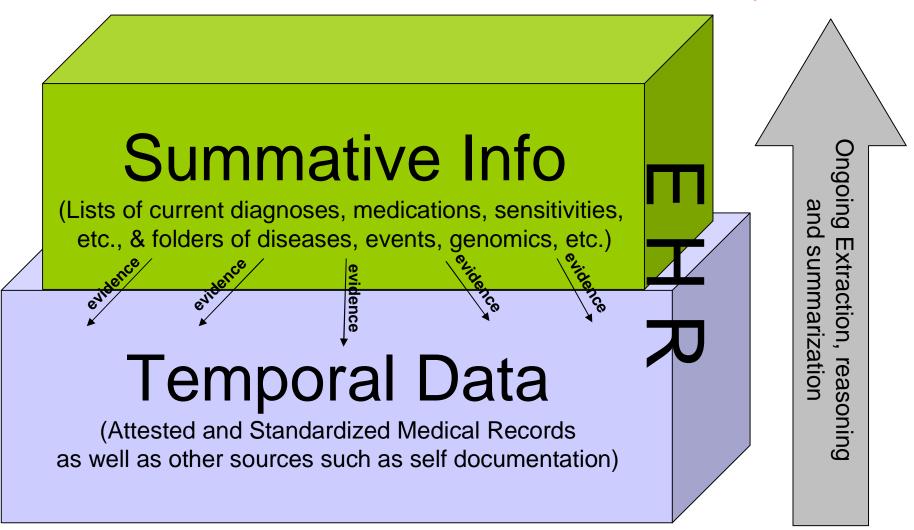
Main Features of a Lifetime EHR

- A persistent entity (not a query result!)
- Always available to authorized parties
- Continuously being updated
- Embeds the standardized medical records (preferably by value)
- Includes folders of topical & non-redundant information built on data from the standardized medical records & health records
- Folders are based on data from standardized medical records, captured as transactions into the EHR and extracted as EHR Extracts

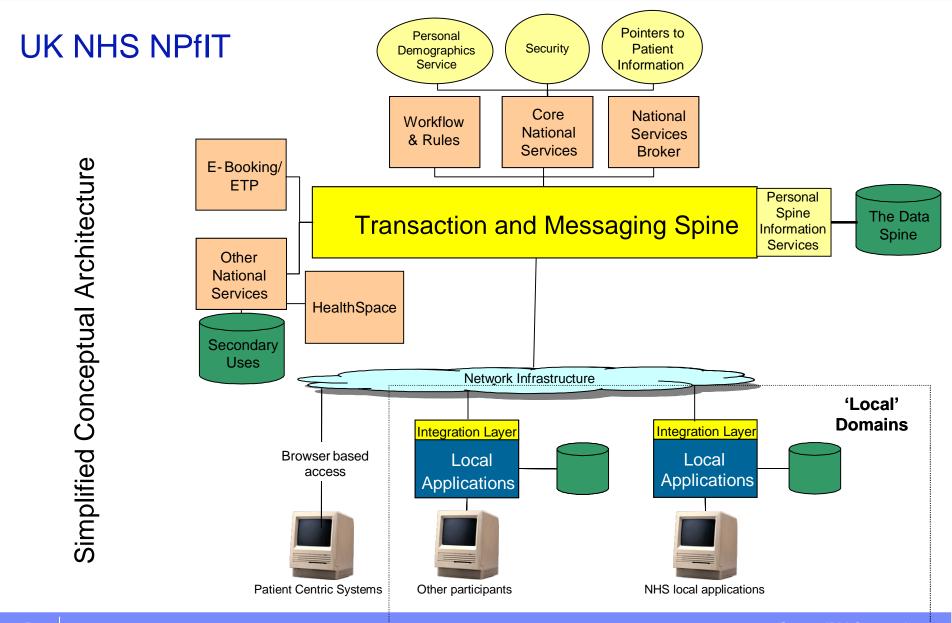


The EHR Conceptual Structure

IBM Research is creating infrastructure for these processes.





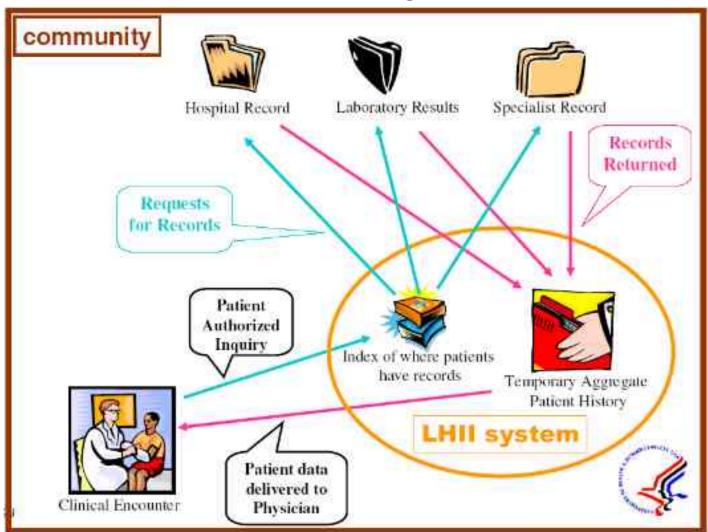


Taken from Dr. Yasnoff Presentation, NHII-2004

The USA NHII – The NHII 2004 Meeting

NOTE:

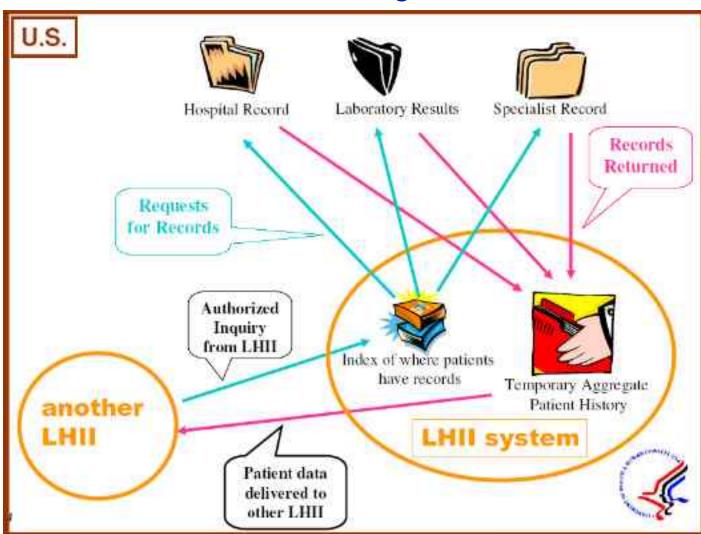
It's based on an index without meta-data, as opposed to the registry model!



Taken from Dr. Yasnoff Presentation, NHII-2004

The USA NHII – The NHII 2004 Meeting

Key point: Network of networks... not clear how it works and how do we uniquely identify a patient!



What's the Problem? (2)

Problem:

Who could possibly sustain longitudinal EHRs throughout the lifetime of its subjects?!

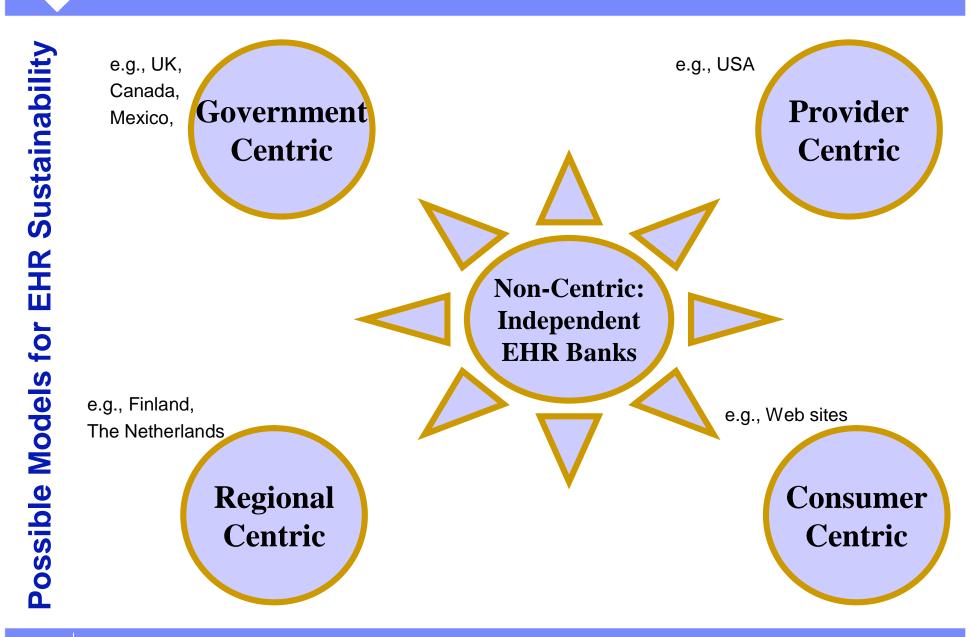
Argument:

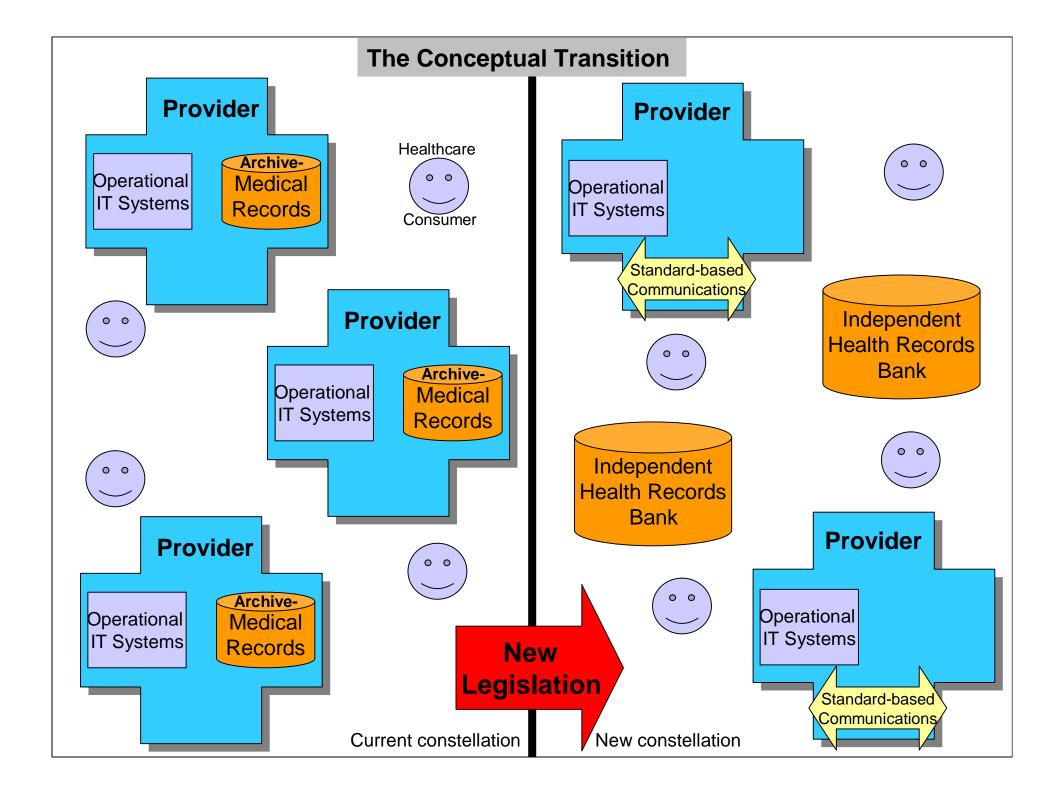
No single healthcare provider can or should sustain lifetime EHRs":

- Involves specialization in archiving IT, not in health
- Current situation occasionally leads to ethical conflicts

Possible solution:

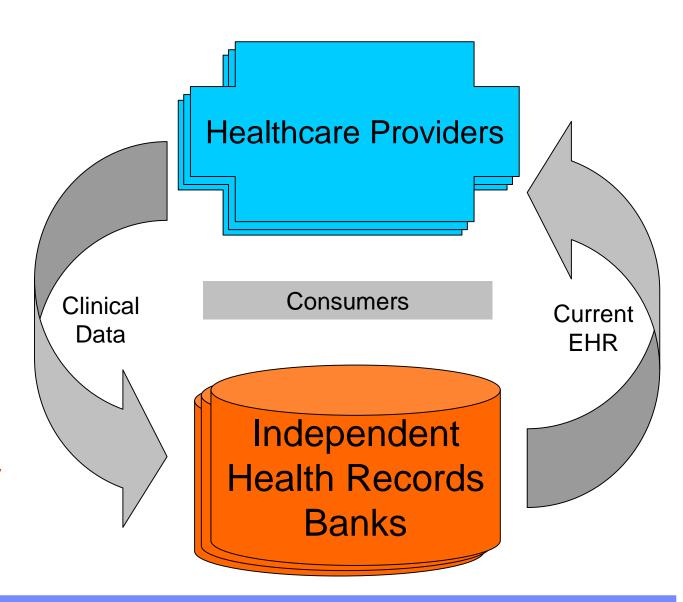
Multiple competing "Independent Health Records Banks", regulated by new legislation





The IHRB Vision

- The medico-legal copy of a medical record solely resides in an IHRB
- IHRBs are Independent of healthcare providers, insurers and gov. agencies
- Multiple competing IHRBs, regulated by international law





The End

- Thanks for your attention!
- Questions?
- Comments: shabo@il.ibm.com

