LOINC Clinical Committee Meeting
Date: 2026-05-26
Time: 2:00 p.m. - 3:00 p.m. EDT / 6:00 p.m. - 7:00 p.m. UTC
Chair: Stan Huff & Ted Klein

ATTENDEES

Committee Members:

1. **Stan Huff (Chair)**
2. Ted Klein (Chair)
3. Anil Patel / **Linda Monico**
4. Dan Vreeman
5. Greg Melitski
6. **June Bronnert**
7. **Susan Matney**
8. **Jessie Wright**
9. **Rob McClure**
10. **Lisa Wolf**
11. **John Snyder /** Liz Amos
12. Rachael Seeley

Regenstrief Staff:

Eza Hafeza, April Lackey, Elizabeth Lumakovska, Marjorie Rallins, Geoffrey Ratemo

Guests:

None

Committee Members = 13 | # Attending = 8 | Quorum = Yes

Meeting Summary

Review Open Items

1. Connect with SHIELD and LIDR for input on making Method a post-coordinated attribute. // Marjorie Rallins, Eza Hafeza // Next available opportunity
2. Research existing groupings for potential duplication of new laborders groupers. // Stan Huff // 2025-09-23

Updates:

- Radiology as a priority domain in the LOINC Ontology

  - The LOINC Radiology Committee has indicated that radiology is central to the EHDS work, which must be operational by 2031.
  - Supporting examples raised included that imaging and testing often occur before a patient is fully examined by a treating clinician and how deeply engaged radiology experts were during the recent IHE meetings and discussions.
  - Regenstrief noted this consideration as related to the LOINC Ontology roadmap.
- Reminder to complete the open polls to reschedule the September and November 2026 meetings.
  - LOINC Clinical CMTE - September 2026 reschedule Poll
  - LOINC Clinical CMTE - November 2026 reschedule Poll
- Registration is open for the LOINC Conference, taking place October 6-9 in Cologne, Germany.
  - 2026 LOINC Conference in Cologne and Online

Decisions: none
Next steps: none

Representing human genetic information
Discussion:

- There is much current activity in this space to be aware of including:
  - Ongoing meetings with the HL7 Clinical Genomics Workgroup, attended by Stan Huff and Eza Hafeza
  - SNOMED CT establishing a formal relationship with HGNC (HUGO) to add approximately 18,000 gene concepts, with code names and identifiers exactly matching HGNC. This work is hierarchical, covering both gene structure and chromosomal location.
- Preferred modeling approach is to avoid combinatorial explosion
  - The suggested method is to use message structure and external gene-variant codes rather than creating every gene-variant combination possible in LOINC:
    - Identify the study or test in LOINC
    - Reference the gene or variant using an external code set such as HGNC or SNOMED
    - Use result values like detected/not detected where appropriate.
  - There is a distinction between
    - Pre-coordinating observation codes for a specific gene-variant result, and

        - Using a post coordination approach where the variant or gene concept is the value of the result
- The genomic concepts in discussion are mostly used in HL7 implementation guides and knowledge-sharing contexts, not necessarily in lab-EHR exchange.
- There are existing codes that relate to genomic testing attributes that are used in transmitting genomic results
    - There are about 39 codes used for transmitting genetic information in lab results.
    - These support attributes like allele name, allelic state, amino acid change, and DNA change.
- Regenstrief is investigating whether new codes are needed for sharing genetics knowledge.
    - Molecular genetics knowledge definition resources are not currently used in transmission of laboratory results. They are used to share new knowledge among researchers. The knowledge resource is used to represent foundational genetic knowledge like where the gene is located, what disease or conditions are associated with gene variants and mutations, etc.
    - No new LOINC concepts for the genetic knowledge base will be added yet, we are still learning what is needed. The HL7 Genomics Workgroup is actively working on this topic and discussion regarding whether LOINC concepts are needed.

Decisions: none
Next steps: none

Approach to "risk of" calculations
Discussion:

- LOINC has 277 "risk-of" concepts encompassing ordinal, quantitative, narrative, and nominal risks. 82 of these are risk-of genetic condition concepts.
- The primary concern is combinatorial explosion if a new code is created for every disease, condition, or genetic variant,
- In rethinking the model, representation should consider:
    - A quantitative risk mode
    - The condition or situation being assessed
    - The formula or authoritative source used
    - Potentially the class of risk model used by specific organization
- SNOMED CT has done significant work revising its risk models. Their "increased risk/decreased risk" approach is more precise than "at risk" because it preserves the direction of the risk assignment. This model is worth considering in LOINC to avoid creating separate concepts for every condition-specific risk statement.

Decisions: None
Next steps: None

Representing outputs from AI or other CDS logic
Not discussed

Follow-up Tasks

1. None

Reference Materials

- LOINC Clinical Committee meeting summary_final_2026-04-28.docx
- Clinical Committee_Meeting Slides_2026-0-26_final.pptx

Next Meeting

- 2026-07-28, 2:00 p.m. - 3:00 p.m. EDT / 6:00 p.m. - 7:00 p.m. UTC
- Anticipated Topics: continue risk-of discussions

Parked Topics

1. Property definition discrepancies // John Snyder
2. Synoptic reporting concepts // Eza Hafeza, Rob McClure
    a. Synoptic reports by SCT and History in LOINC .zip
    b. Cancer Reporting Update_2018-12-06.pptx
3. Calibration and normalization of raw measurements, e.g. continuous glucose monitors
4. Consider the binding strength between value sets and LOINC codes for better clarity // John Snyder // TBD
5. European group microbiology results representation (deferred from OCT 2025 meeting)
6. Nursing head to toe assessment // Susan Matney