Anatomic Pathology Structured Report (APSR)
From Release 1 to Release 2

An evolution, proposed by Gunter Haroske, Thomas Schrader, Rajesh Dash, Christel Daniel, François Macary, Frank Oemig

IHE AP in cooperation with HL7 AP and CAP

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Anatomic Pathology Structured Report (APSR)
Release 1

• APSR profile R1 published in 2011 for Trial Implementation on www.ihe.net/technical_framework#pathology

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• A set of 21 CDA document templates:
  • A generic template usable for any anatomic location and any pathology
  • 20 specialized templates for 20 anatomic locations/specimen collection procedures
A common structure for the 5 first sections

- **AP <section>**
  - 1.1
    - <code>
    - <title>
    - <text> human-readable content of a section

- **AP <entry>**
  - 1.1 specimen information <organizer> machine-readable content: a specimen or group of specimens
  - 1.1 specimen collection <procedure> properties of a specimen

- **AP <observation>**
  - 0..* problem <organizer> a problem investigated
  - 0..* image(s), comment(s) related to the observation
  - 0..* clinical laboratory <observation>
  - 0..* image(s), comment(s) related to the problem
  - 0..* image(s), comment(s) related to the specimen or group

Only for the Clinical Information section

**Sub-section**
The Procedure Steps section is only human readable

The issues pointed out by Germany

- All observations are currently sorted by problem. However observations on the specimen itself (e.g.; specimen size) should be distinguished from the other AP observations. They are not related to a particular problem.

- The various steps performed on the specimen should be traceable as structured data (machine-readable):
  Part → Block → Slide

- There is potentially a high number of templates. Can we obtain the same precision with less templates?
Add zero to n <entry> to the Procedure Steps Section

- Each entry carries as machine-readable content, the hierarchy of steps that were applied to a primary specimen, or group of primary specimens (e.g.; prostate biopsies)

- Each step carries:
  - The type of step that was performed
  - The anatomic site the specimen comes from (only for the primary specimen)
  - Who performed the step
  - When
  - What material it produced:
    - the resulting specimen (part, block, slide, ...),
    - with its unique identifier
  - The list of further steps that were applied to this material
Application on Raj's example "Case 1"

CASE #1
A. "RIGHT BREAST FIVE CORES 8-9:00" (ULTRASOUND GUIDED NEEDLE CORE BIOPSY):

INVASIVE ADENOCARCINOMA OF THE BREAST.
HISTOLOGIC TYPE: DUCTAL.
NOTTINGHAM COMBINED HISTOLOGIC GRADE: 1 OF 3.
NODULE FORMATION SCORE: 2.
NUCLEAR PLEOMORPHISM SCORE: 2.
MITOTIC RATE SCORE: 1.

IN-SITU CARCINOMA: EQUIVOCAL.

BREAST CANCER BIOMARKER STUDIES:

ER INTERPRETATION: POSITIVE ESTROGEN RECEPTOR ACTIVITY (ALLRED SCORE = 8).
PR INTERPRETATION: POSITIVE PROGESTERONE RECEPTOR ACTIVITY (ALLRED SCORE = 8).
HER2/NEU IMMUNOHISTOCHEMISTRY: NEGATIVE (0) FOR EXPRESSION OF 

HER2/NEU IMMUNOHISTOCHEMISTRY: EQUIVOCAL (2+) FOR OVEREXPRESS OF HER2/NEU 

HER2/NEU FISH RESULTS WILL BE ISSUED IN AN ADDENDUM TO THIS REPORT.

Hierarchy of specimens proposed by Gunter/Raj

- Part - RIGHT BREAST FIVE CORES 8-9:00 — ID = "A7102400008"
  - PARAFFIN BLOCK NUMBER: A1 — ID = "block_A_1"
    - slide from A1
      - targetSite = "Level 1"
      - Resulting material = "H&E"
      - id = "slide_A_1_HE"
    - slide from A1
      - targetSite = "Level 2"
      - Resulting material = "ER Immunohistochemistry"
      - id = "slide_A_1_ER"
    - slide from A1
      - targetSite = "Level 3"
      - Resulting material = "PR Immunohistochemistry"
      - id = "slide_A_1_PR"
    - slide from A1
      - targetSite = "Level 4"
      - Resulting material = "HER2 Immunohistochemistry"
      - id = "slide_A_1_HER2"
The CDA case #1 report (Raj, Christel, Gunter, François)

APS_Raj_breastCancer_Case1gen_20140925.xml