An evaluation of feasibility of implementation of computable cancer phenotyping with pathology records from Cerner® EHR System

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Context: Electronic health record (EHR)-driven phenotyping has been widely used in biomedical and translational research as well as in precision medicine. Hochheiser et al. (2016) proposed the DeepPhe information model for cancer phenotyping. As many academic institutes, the Cerner EHR system in Loma Linda University Health (LLUH) is mainly used for patient care and billing purposes. Here, we evaluated the availability and structure of Cerner pathology data for implementing the DeepPhe database model.

Design: We surveyed recent neoplastic pathology reports from LLUH Cerner system (n=30), and manually mapped Cerner pathology information to data elements in the DeepPhe.

Results: The correct diagnosis codes are available in 22 reports (73%) as structured data automatically extracted by Cerner as Systematized Nomenclature of Medicine (SNOMED) Morphology (M) code. However, average 0.83 incorrect M-codes per case are also captured by Cerner (mostly "benign lymph nodes" as "tumor, benign"). Body sites are captured as SNOMED topography (T) codes in 28 reports (93%), but body sites and diagnoses are not paired in cases with multiple specimens. Synoptic summaries (whenever available) provide paired and structured tumor diagnosis, body sites, and other tumor parameters. “Observations” for immunophenotyping are reported as either templated tables or free texts. On Level 3 of DeepPhe (episodes), current pathology records are capable of representing at least three scenarios: 1) treatment and re-biopsy; 2) precancerous to cancer; 3) leukemia follow-ups.

Conclusion: For future use of DeepPhe database in research, the required information is mostly available and structured in the current Cerner EHR pathology data system.

References:
1. Hochheiser et al., An information model for computable cancer phenotypes., BMC Medical Informatics and Decision Making, 2016; 16:121. (DeepPhe model)

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