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Leading health innovation through data

201904 Analytics using SNOMED CT: results from a genomics pilot

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Summary

In this presentation we report on the results of a SNOMED CT genomics pilot that was established with the Renal Genetics Flagship in Australian Genomics. The pilot explores how SNOMED CT can be used to capture high-quality data and how these codes can be used along with FHIR to do analytics.

Audience

Clinical, Research/academic, Technical Clinical,

Learning Objectives

1. Understand the importance of capturing high quality, coded data.
2. Become familiar with the way SNOMED CT and FHIR terminology can be used together to improve data capture.
3. Learn how SNOMED CT and FHIR can be used to do analytics and provide valuable insights to clinicians

Abstract

Australian Genomics is a national initiative building evidence and developing the framework to support the implementation of genomics medicine in the Australian healthcare system. The initiative encompasses four programs of work: 1) establishing the national diagnostic and research network in genomics; 2) developing a national approach to data federation and analysis; 3) informing health policy, conducting health economic analyses, applying implementation science methods and addressing ethical implications; and 4) evaluating the needs of the genomic workforce.

The Australian eHealth Research Centre is part of Program 2 and leads the Phenotype Capture subgroup, which is standardising the phenotype data currently captured by the clinical projects. The team interacts with several flagships (the entities doing clinical research) and is currently developing information models and value sets for the flagships' clinical areas.

A pilot was established with the Renal Genetics Flagship in order to explore how SNOMED CT could be used to capture high-quality data and how this data could be used to do analytics. The project was divided in two phases. The first phase involves improving the clinical data that has already been collected, using mostly free text, for the initial cohort. Three free text fields, diagnosis at referral, diagnosis at the clinic and final diagnosis, will be coded by clinical terminologists using our open source REDCap FHIR terminology plugin, configured to use SNOMED CT codes. This data will also be used to define value sets for this clinical area and to identify gaps in SNOMED CT. Finally, a subset of the REDCap forms, including the new coded diagnosis data, will be transformed to FHIR using the open source FHIRCap transformation engine.

The second phase will use our CSIRO FHIR analytics platform to explore the behaviour of these diagnoses throughout the patients' journey. This data can help the clinicians determine if the current workflow is effective or if some steps can be optimised, for example, if some diagnosis are already accurate since referral.

This presentation will report on the results of the pilot, which is now underway, with the initial phase being close to completion and the second phase scheduled to be finalised by the end of June 2019.