Connectathon 27 -
FHIR Genomics Operations

Resources

- Clinical Genomics Connectathon 27 Confluence page
- FHIR Genomics Operations undergoing ballot
- GACS Postman collection. Examples are included for
    - LiftOver
    - UncallableRegions
    - Targeted NGS, with regions not studied
- Patients stored in the GACS server
    - All data is from 1000 Genomes Project, publicly available
    - Most patient data is derived from WGS Build 37 VCFs
    - Patient NB6TK328 has data derived from WGS Build 38 VCF
    - Patient HG00403A has data derived from a targeted gene panel (list of studied regions is here)
- Possible scenarios
    - Query for variants in a region, using the find-subject-variants operation.
    - Include a parameter to also get back information on uncallable regions.
    - For various SNPs of interest, where no variants are identified, determine if the region was studied and not deemed uncallable.
    - Explore liftOver capabilities (e.g. query a patient that has build37 data using a query using build38 parameters).
    - Compare Bundle vs. DiagnosticReport as operation response
- (DRAFT) Potential new FHIR Genomics operations
    - Example of revised $find-subject-variants that supports multiple regions ($find-subject-variants/?patientId=HG00404&region=NC_000005.9:112043201-112181936,NC_000017.10:41196311-41277500,NC_000019.9:38924339-39078204)

Issues / proposals

- [Jira 31565] Add 'uncallableRegions' parameter to find-subject-variants operation
    - CHANGE: OUT:regionStudied cardinality from [0..*] to [0..1].
    - Where a server has information about the studied region, a regionStudied observation should be returned. If uncallableRegions parameter is set, but server doesn't have information on uncallable regions, the server shall return a single component:uncallable-regions with dataAbsentReason='unknown'
    - Long answer:
        - change OUT:regionStudied cardinality from [0..*] to [0..1].

        - without the uncallableRegions flag
            - if studied region is unknown, do not include a regionStudied observation
            - if studied region is known, include a single regionStudied observation with
                - [1..1] component:genomic-ref-seq indicates the chromosome studied
                - [1..*] component:ranges-examined indicate the studied ranges that overlap with the queried region.
                - [1..1] component:coordinate-system, valued with '0-based interval counting'
                - [0..0] component:uncallable-regions is not included
        - with the uncallableRegions flag
            - if studied region is unknown, do not include a regionStudied observation
            - if studied region is known, include a single regionStudied observation with
                - [1..1] component:genomic-ref-seq indicates the chromosome studied
                - [1..*] component:ranges-examined indicate the studied ranges that overlap with queried region.
                - [1..1] component:coordinate-system, valued with '0-based interval counting'
                - uncallable regions
                    - if uncallable regions are not known
                        - [1..1] component:uncallable-regions with dataAbsentRegion='unknown'
                    - if uncallable regions are known
                        - [1..*] component:uncallable-regions each indicating a contiguous sub-region within a reported ranges-examined that was deemed uncallable.
- allelic-state - should only be required if genomic-source-class = 'germline'
- Error codes:
    - Background: to move from single-region to multi-region queries, we need to reexamine the use of ERROR code 404 where the region hasn't been studied. With multi-region queries, some regions will and others may not have been studied. Also, we don't have a specific way to indicate a failed liftOver.
        - 200: Successfully executed request
            - if query range not studied, include regionStudied observation with a single component:ranges-examined with dataAbsentReason='not-performed'
        - 400 ERROR: Invalid query parameters
        - 404 ERROR: Patient not found

        - 422 ERROR: Failed LiftOver
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- [] DiagnosticReport vs. Bundle for returning operation results
    - Options
        - Option 1: Bundle with full observations
        - Option 2: DiagnosticReport with referenced observations
        - Option 3: DiagnosticReport with contained observations
    - Considerations
        - Ability to query individual observations
        - Ability to retain bundle or report (to have a retained timestamp for when report was assembled)
        - Dynamic generation of FHIR instances and ability of server to keep track of assigned observation identifiers.
        - CDS pipeline vs. Lab-to-EHR pipeline, and the need for persistent identifiers in these scenarios. (Is the intent of the communication to have the contained observations stored discreetly in the EHR?)
- … (any ballot comments)...