

# 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)...