May 2022 Connectathon

Timelines

Date	Event	Notes
3/1/22	Track Proposals Due	
3/1/22 4:00 PM ET	Connectathon Track Lead Information Session Join Zoom Meeting	Slides Recording
3/10/22	Track Schedules Due	
3/15/22 4:00 PM ET 3/29/22 4:00 PM ET 4/12/22 4:00 PM ET 4/26/22 4:00 PM ET	Track Lead Check In Calls 4:00 PM ET Join Zoom Meeting	email me if you have questions! Sandy@counterpointsol.com
4/18-29/22	Host your Track Kick Off Call	Please schedule your call and post the time and link on Confluence. After the call, post your recording to Confluence.

SURVEY QUESTIONS?

Name

Clinical Genomics Operations for Genomic Applications

Short

Operations expand the capabilities of a FHIR server to deliver genomics functionality to answer key clinical queries in a streamlined fashion, that is agnostic to the format used to report genetic data (i.e. the input parameters use a single format modality rather than an application needing to know a priori how the data is stored in the server). New operations are proposed that return associated Diagnostic or Therapeutic implications – answering such a request as ‘return the diagnostic implications associated with my patient’s genetic variation’ without needing to know the variant formatting on the server.

Long

Operations expand the capabilities of a FHIR server to deliver genomics functionality. Key clinical queries such as ‘find all patients with genetic variants like my patient,’ ‘does my patient have a specific variant?’, ‘does my patient have a variation in a specific gene of interest?’, and ‘does the patient’s tumor qualify for a specific trial’ are all examples of queries that are simplified using operations. Now, there are operations proposed that can answer the question ‘do any of my patient’s genetic variations have diagnostic or therapeutic implications?’ We invite you to try these operations out using a reference implementation of the operations with data from oncology, pharmacogenomic and general genomic knowledge resources. Use cases such as pharmacogenomics reanalysis, therapeutic treatment recommendations, ACMG screening for common conditions and population – cohort – based retrieval are now supported.

Our goal is to try out as many of the proposed operations as possible. We are seeking feedback, including utility of responses, additional parameters, speed of development (with/out operations), coverage of use cases and gaps.

We invite application developers, EHR vendors, Business and Data analysts/scientists, especially, to make use of the reference server. See the scenario section for example scenarios, additional scenarios are welcome during the connectathon. If one would like to develop their own server that is in-scope and we will be happy to try out your server. Additionally, if a knowledge-base, e.g. PharmGKB, would like to test out delivering their content using the Implication operations that would be encouraged.

Type

Submitting WG

Clinical Genomics

Track leads

Bob Dolin
Bret Heale

FHIR VERSION

R4

SPECIFICATIONS

https://build.fhir.org/ig/HL7/genomics-reporting//operations.html

ZULIP STREAM

TRACK DETAILS

Reference implementation server for FHIR Genomics Operations found at:

https://fhir-genomics-apis.herokuapp.com/

CLIENTS

Available operations:
https://build.fhir.org/ig/HL7/genomics-reporting/operations.html#summary-of-operations

	Subject Operations	**Population Operations**
Genotype Operations		
simple variants	find-subject-variants; find-subject-specific-variants	find-population-specific-variants
structural variants	find-subject-structural-intersecting-variants; find-subject-structural-subsuming-variants	find-population-structural-intersecting-variants; find-population-structural-subsuming-variants
haplotype/genotypes	find-subject-haplotypes; find-subject-specific-haplotypes	find-population-specific-haplotypes
Phenotype Operations		

therapeutic implications	find-subject-tx-implications	find-population-tx-implications
diagnostic implications	find-subject-dx-implications	find-population-dx-implications
Metadata Operations		
study metadata	find-study-metadata	

Operation	Description
find-subject-variants	Determine if simple variants are present that overlap range(s).
find-subject-specific-variants	Determine if specified simple variants are present.
find-subject-structural-intersecting-variants	Determine if structural variants are present that overlap range(s).
find-subject-structural-subsuming-variants	Determine if structural variants are present that fully subsume a range.
find-subject-haplotypes	Retrieve haplotypes/genotypes for specified genes.
find-subject-specific-haplotypes	See if specified haplotypes/genotypes are present.
find-subject-tx-implications	Retrieves genetic therapeutic implications for variants/haplotypes/genotypes.
find-subject-dx-implications	Retrieves genetic diagnostic implications for variants.
find-population-specific-variants	Retrieve count or list of patients having specified variants.
find-population-structural-intersecting-variants	Retrieve count or list of patients having structural intersecting variants in specified regions.
find-population-structural-subsuming-variants	Retrieve count or list of patients having structural subsuming variants in specified regions.

find-population-specific-haplotypes	Retrieve count or list of patients having specified genotypes/haplotypes.
find-population-tx-implications	Retrieve count or list of patients having therapeutic implications.
find-population-dx-implications	Retrieve count or list of patients having diagnostic implications.
find-study-metadata	Retrieve metadata about sequencing studies performed on a subject.

Security and Privacy Considerations

No security or privacy considerations for use of the reference server. The data is synthetic. If implementing a server for Genomics Operations be sure to use test patient data and not expose real patient information.

Scenarios

- Do operations speed application development
- Cancer tx implications scenario
- HLA scenario
- Bret: I'm looking at this scenario. 1st find-population-specific-variants and then using that list of patients to limit the output of find-population-tx-implications. there's a couple of ways to mix and match these operations to get to the question of 'what do patients with my patient's variants have in common with regards to reported diagnostic implications'...I think you've been pretty thorough. A calling application might need to perform more than one, or perform then sequentially but by giving the operations at a more granular level it provides the opportunity for creativity and expanding the use cases met.
- Over the course of the past two years, many patients have been tested for variants pathogenic for hereditary breast and ovarian cancer syndrome (HBOC), Lynch syndrome (LS), and familial hypercholesterolemia (FH). Recent knowledge base updates have added to the list of known pathogenic variants, and have reclassified the pathogenicity of many variants. We now want to find patients that have pathogenic variants for HBOC, LS, or FH, based on the new knowledge base.
- A researcher has developed a new drug, designed for cancer patients with large deletions involving all or part of BRCA1 (NC_000017.11:43044294-43125364) or BRCA2 (NC_000013.11:32315507-32400268), and wants a list of potential clinical trial participants.

Useful links

- May 2022 confluence page

Agenda

4/28	10 am - 12 pm Eastern time	Track Kick-off and Orientation - brief overview on operations and orientation to Track, scenarios and CG IG Discuss resources available Solicit additional scenarios - 'this is your connectathon, what would you like to test out that's not covered?' Follow-up discussions on Zulip thread or confluence.
2-May	4 pm Eastern TIme	LIVE Connectathon kick-off

We will be hosting one zoom call it will be on all day (encouraging use of chat and zoom hand-raise to ask questions, and Zulip chat!)

3-May	9:00 am - 10:00 am Eastern Time	Track Orientation - brief review of operations, scenarios and CG IG Zulip channel is a must! Please use it

10:00 am - 10:15 am EST	(educational breakout) Focus on scenario 0 - why operations
10:15 am - 10:45 am EST	(educational breakout) Focus on implication operations - why operations
11:00 am - 1:00 pm EST	Testing scenarios open office hours/work-session/troubleshooting - issue handling
1:00 pm - 2:00 pm EST	Bring your own topic
2:00 pm - 3:00 pm EST	Testing scenarios open office hours/work-session/troubleshooting - issue handling
3:00 pm - 4:30 pm EST	Demo or descriptions of days efforts - regroup of participants
5:30 pm - 8:00 pm EST	late zoom session
	When zoom closes, the zulip channel will still be live - please use it.

4-May	9:00 am - 9:30 am EST	Check-in
		Check-in for anyone with questions, comments, or feedback.
	9:30 am - 11 am EST	Recap day 1. Challenges/what-learned
	11:00 am - 12:30 pm EST	Continue scenario testing/Open office hours/work session
	12:30 pm - 2 pm EST	Special topics as decided by group
	1:30 pm - 3:30 pm EST	Track Final Demos/Discussion
		Future Connectathons
		Track report-out
After connectathon		Zulip channel will still be available (as are all the Clinical Genomics zulip channels and CG calls). Join the accelerator!