# Beacon 2.0 Draft Première

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## Have you seen a...

## Mutation

...like that?



Have you seen...

Calls, Variants,

Samples, Patients...

...like that?

But I'm only interested in the ones related to a... still YES! Disease, Gene, Tissue...

## What can you tell me about it?

Well...

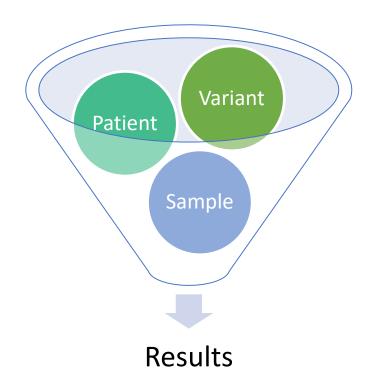
- This is the effect of the mutation
- These are the phenotypes I've seen
- This is how to get to the source data
- ...

... but I can only provide some details about patients if you are granted

#### To consider...



 If we are having data on Variants, Patients, Samples, etc. we are not restricted to a single entry point for the query





### Have you seen a...?



- Allow for entity queries
  - Lists
    - .../variants
    - .../samples
    - .../patients
  - Individual entities
    - .../variants/{id}
    - .../samples/{id}
    - .../patients/{id}
  - Filtering
    - .../variants?chr=1&pos=1001&alt=T
    - .../patients?filter=... (see later)



#### Get linked entities ...



- Just one entity. REST approach
  - E.g. Variants of a Sample
    - .../samples/{sampleid}/Variants
- More complex: Variants & Patients of several samples
  - Parameter includeDetails
    - .../samples?includeDetails:variants,patients
    - .../samples/{sampleid}?includeDetails:variants,patie nts



#### Returned structure



- Sample1,
  - PatientA
  - Variant1, Variant2,...
- Sample2
  - PatientE
  - Variant2, Variant3,...
- (...)

 To consider: This distribution allows for independent schemas for each object (see later)



#### Returned structure



- Patient1,
  - Sample1, Sample2,...
  - Variant1, Variant2,...
- Patient2
  - Sample3, Sample4,...
  - Variant2, Variant3,...
- (...)

- Variant1,
  - Sample1, Sample2,...
  - Patient1
- Variant2
  - Sample3, Sample4,...
  - Patient1, Patient2,...
- (...)



### Dealing with unstable schemas



Declare requested schema at query time

```
"request": {
    "Patient": "beacon-patient-v1.0",
    "Variant": "beacon-variant-representation-v0.1",
    "VariantAnnotation": "beacon-variant-annotation-v1.0"
}
```

State returned schema in the response

- Beacon to declare supported schemas
- Beacon to support a default schema for each entity



#### Variant schema

```
"variantsFound": [
 "variant": {
   "version": "beacon-variant-v1.0",
   "value": [
     "variantDetails": {
       "chromosome": "",
       "referenceBases": "",
       "alternateBases": "",
       "variantType": "",
       "start": 0,
       "end": 0
       },
     "info": { }
 "variantAnnotations": {
```

```
variantAnnotations": {
"version": "beacon-variant-annotation-v1.0",
 "value": {
  "variantMetadata": {
    "version": "beacon-variant-metadata-v1.0",
     "value": [
       "geneId": "",
       "HGVSId": "",
       "transcriptId": "",
       "alleleId": "",
       "variantClassification": "",
       "variantType": "",
       "disease": "",
       "proteinChange": "",
       "clinVarId": "",
       "pubmedId": "",
       "timestamp": "",
       "info": { }
   "info": {
    "cellBase": { },
    "dbSNP": { },
     "clinVar": { }
```

#### Initial schemas to consider



- Patient
  - \*Beacon default
  - Phenopackets: Individual
  - SchemaBlocks: Individual
- Sample
  - \*Beacon default
  - PhPck: Biosample
  - SB: Biosample

- Variant Representation
  - \*Beacon default
  - Beacon "legacy"
  - GA4GH VR
  - SchemaBlocks
- Variant Annotation
  - Many...



### But only if...



- Extension to \*each\* Beacon Query
- Leveraging ontologies
- Backend should know the mapping between ontology term (e.g. AgeOfOnset) and the "database column" (e.g. Age)
- Allowing for custom dictionaries (customFilters section)

```
// female
Filters:
"PATO:0000383"
// neoplastic sample (not study, nor individual)
customFilters:
 "sample.provenance.id=EFO:0009656"
// female, age of onset, abnormal sample (~case)
Filters:
     "PATO:0000383"
     "HP:0011007=>49"
     "EFO:0009656"
```



#### Transversal features



- Details per dataset
- handovers
- Authentication and /access\_levels
- /filtering\_terms
- Endpoint aliases to allow simpler queries

