

BeaconResponse - a Perl CGI for Beacon+ queries on GA4GH compatible databases

Query parameters

- datasetId
 - the dataset to be queried
 - example: arraymap, which will expand to arraymap_ga4gh as database name
 - default: arraymap
- assemblyId
 - the genome assembly
 - example: GRCh38

Database naming

The script uses some naming conventions for databases and collections:

- MongoDB database (in our implementation)
 - datasetId_ga4gh
- collections
 - individuals
 - biosamples
 - callsets
 - variants

Example use, web call:

SNV query on dataset "dipg" with phenotype response:

- <http://progenetix.org/beacon/query/?referenceName=17&referenceBases=G&variants.alternatebases>

CNV query on dataset "dipg", with phenotype response:

- <http://progenetix.org/beacon/query/?referenceName=9&alternateBases=DEL&startMin=19000000&s>

CNV query (defaults do dataset "arraymap") with bio-metadata component and phenotype response:

- <http://progenetix.org/beacon/query/?referenceName=chr9&alternateBases=DEL&startMin=2000000>