



Global Alliance
for Genomics & Health
Collaborate. Innovate. Accelerate.

SchemaBlocks

Michael Baudis



SchemaBlocks - Perceived Need

- “GA4GH schemas” by the DWG provided object model and documentation
- rigid, top-down managed development model was abandoned => WS + DP
- now no place - outside individual WS & DP - in GA4GH ecosystem to provide
 - Data models
 - Standard recommendations
 - Object prototypes
- lack of shared objects & documentation leads to duplicate development efforts and lack of citable references - examples:
 - Use of genome coordinates in GA4GH products?
 - Variant formats (placeholders, future ...) e.g. for Beacon, Search ...?
 - Dataset specific parameters related to consent code (DURI)?
 - Object hierarchies & relations (e.g. dataset | subject | sample | callset | variant ...)?
 - How to use external reference systems (e.g. ontologies) in queries and data delivery?



SchemaBlocks - History & Status

- Started by members of C/P & GKS, as ***continuation*** of former DWG Metadata work & other parts from GA4GH Schemas
 - core data model, objects
 - documentation
- Integration and exchange with *Phenopackets*, *Beacon* developments
- Maintained updated documentation and models in the Metadata repository
- December 2018:
 - first call with participants of different WS (GKS, C/P, Discovery)
 - launch of Github organisation “ga4gh-schemablocks”
 - New website @ schemablocks.org, with some initial documentation
- This SC meeting: Feedback & visibility will shape future directions



SchemaBlocks - Emerging Principles

- Machine readable “blocks”, with lightweight structure
 - e.g. JSON schema as YAML
 - precedence of *documentation* over implementation
- Human readable documentation
 - representing block descriptions & examples, also standards & conventions
- Competing standards and alternative objects entirely possible
 - e.g. different variant standards & coordinate systems - VCF | VMC | Beacon
 - external references to non-GA4GH standards, e.g. ISO, IEEE
- Cross-cutting initiative: Not “part of” a single WS
 - **C/P** & **GKS** (+ others, drivers...) for **standards**; requirements ... by Discovery
- Aligns with GA4GH standard setting mission

Not an attempt to build a “one size fits all”, monolithic schema



SchemaBlocks - Standards and Code



GA4GH::SchemaBlocks

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Data Formats

Identifiers and CURIEs
Genome Coordinates
Dates & Times

Data Schemas

Examples, Guides & FAQ

Meeting minutes

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Related Sites

GA4GH::Discovery
GA4GH::CLP
GA4GH::GKS
SchemaBlocks at Metadata
ELIXIR Beacon
Phenopackets
GA4GH
Beacon+

Tags



Formats

Schema elements previously developed as part of various GA4GH efforts had been assembled in the [SchemaBlocks demonstrator](#). Those schemas and documentation will be re-implemented in this space.

Additional information about data formats can be found on the [GA4GH::Metadata](#) site.

Identifiers and CURIEs

One of the GA4GH conventions is to use CURIEs as (external) identifiers.
mbaudis, 2018-12-24: more ...

Genome Coordinates

This documentation needs to be edited, to represent the GA4GH convention of using "... 0-based, inclusive coordinates".

For now please see

- the [documentation of the Variant](#) object for the original *GA4GH schema*
- a [recent discussion on Github](#), and the links from there
- a [nice explanation of coordinate systems at Biostars.org](#) by Obi Griffith

mbaudis, 2018-12-21: more ...

Dates & Times

Date and time formats are specified as ISO8601 compatible strings, both for time points as well as for intervals and durations.

mbaudis, 2018-12-21: more ...

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Ontology_term

The original schema definitions are provided in the [YAML file](#).

Properties of the *Ontology_term* class

Property	Type	Format	Description
id	string		properly prefixed CURIE of the ontology term
label	string		the text label associated with the term

Ontology_term represents the core object used to reference domain-specific entities, as well as to identify their domains through the appropriate prefix. CURIEs are case sensitive, although for prefixes this practice is inconsistently followed.

Examples

```
{
  "id": "DUO:000004",
  "label": "no restriction"
}
```

```
{
  "label": "Juvenile onset",
  "id": "HP:0003621"
}
```

```
{
  "id": "ncit:C3058",
  "label": "Glioblastoma"
}
```

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Tags

Beacon CP Discovery
GA4GH GKS MME admins
code contacts contributors
coordinates dates
developers identifiers
leads press times

GA4GH Intervals

Status: **draft**

Contributors

- Andy Yates

Definition

Two integers that define the start and end positions of a range of residues, possibly with length zero, and specified using interbase coordinates. Coordinates are assumed to be positioned on a non-circular sequence.

Model

- start (uint64) start position >= 0 (required)
- end (uint64) end position >= start (required)

Background

When humans refer to a range of residues within a sequence, the most common convention is to use an interval of ordinal residue positions in the sequence i.e. start counting residues from 1. This system is also referred to as "1-start, fully-closed", biological coordinates and "Ensembl style". While natural for humans, this convention has several shortcomings for data modelling and programming. GA4GH prefers the use of interbase or "0-based, half-open" coordinates (also known as Chado or "UCSC style") and strongly advises that all future products prefer their use for future products unless the product visually displays data to a human. Interbase coordinates refer to the zero-width points before and after residues. An interval of interbase coordinates permits referring to any span, including an empty span, before, within, or after a sequence.

The Interbase Coordinate System

While interbase is numerically equivalent to "0-start, fully-closed" they are semantically different. Interbase does not refer to residues and therefore can model events occurring between residues, the start and end of a sequence. For non-circular sequences the following holds true.

- Interbase coordinates start at 0
- Start must be >= 0
- End must be >= start
- The length of an interval is (end - start)
- The reverse start is (sequence length - end)
- The reverse end is (sequence length - (start-1))
- A zero-length interval (start == end) is a point between two residues
- An interval of length 1 is a residue position
- Two intervals are equal if their start and end are equal
- Two intervals intersect if start or end occurs between the start and end of the other
- Two intervals coincide if they intersect or they are equal

GA4GH Products and Their Supported Interval Systems

Product	Interbase	0-start, half-open	1-start, fully-closed
BAM/CRAM		X	
----			..

*** DRAFT ***

GA4GH::SchemaBlocks

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Michael Baudis
Melanie Courtot
all ...

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People

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Senior Web Developer, Wellcome Sanger
Institute, Hinxton
Primary work: DECIPHER
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SchemaBlocks - Future Directions

- Receive continuous contributions from WS in form of “blocks” and documentation through interaction w/ different development teams
 - Variant annotation types and models from **GKS**
 - Ontology, phenotype format & recommendations from **C/P** (*phenopackets...*)
 - Search components from **Discovery** & Beacon, use conditions (**DURI**)...
- Formalise approval levels & governance model
- Become part of GA4GH product approval process
 - products document awareness of SchemaBlocks through
 - Contribution of code or documentation
 - Use of existing code or formats
 - (Or Statement about lack of applicability...)



SchemaBlocks - Feedback?

- How do we formalise this in the GA4GH structure?
 - Currently “An initiative by members of the GA4GH”, linked from Discovery...
 - GA4GH staff support (since need for regular calls, minutes)
- Depending on that - Structure, leadership?
 - “Self-assembly” (w/ direction from WS leads) or formal set-up with dedicated WS interaction?
- Future place in product development & approval processes?
 - Early for decision - but suggestions about direction?

