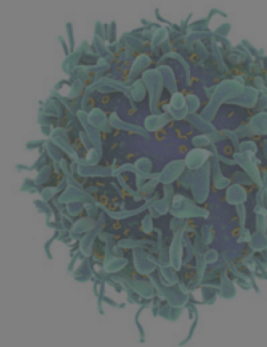
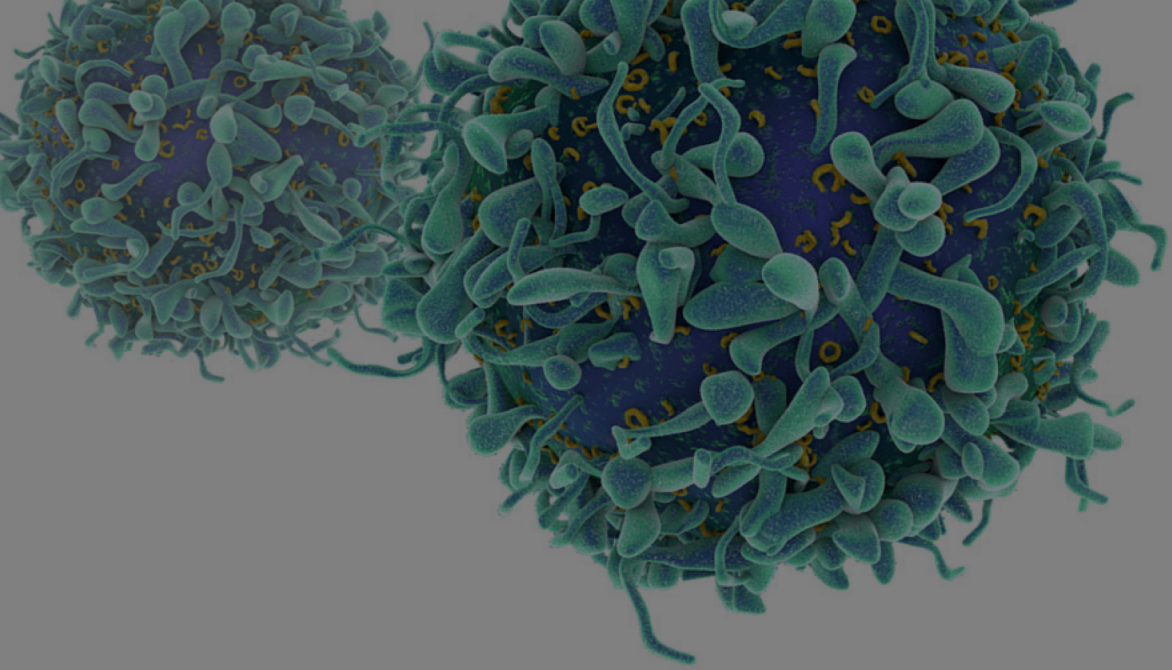


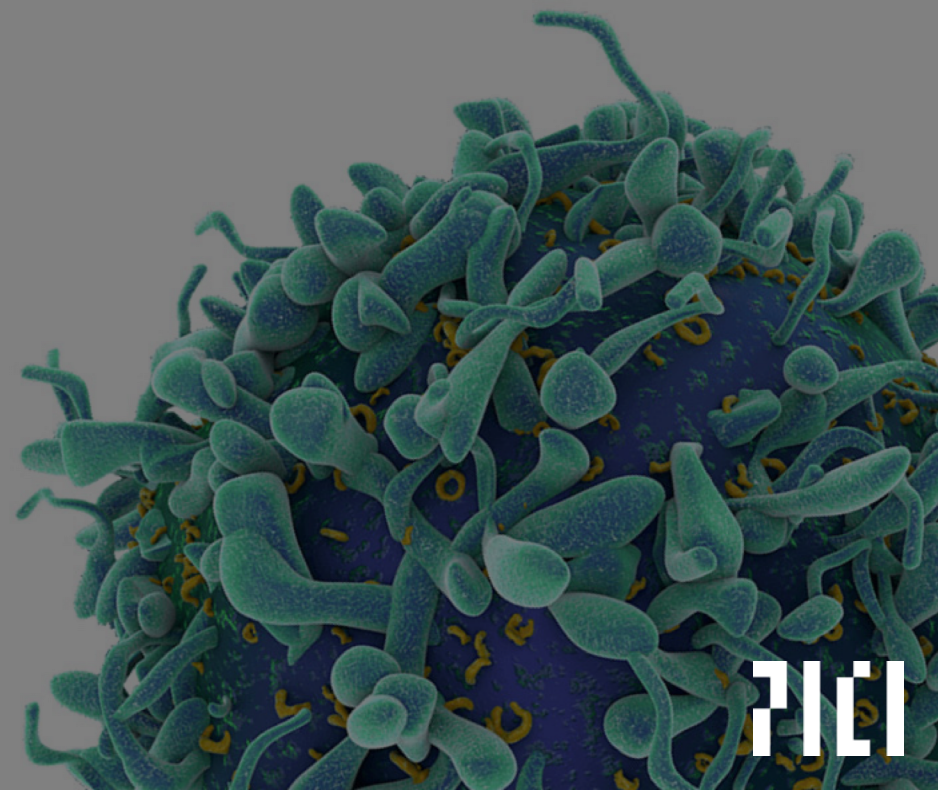
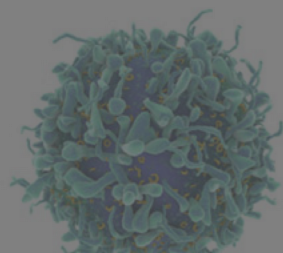
# A visual query builder for knowledge graphs

Mike Travers  
mtravers@parkerici.org

**ICI** PARKER  
INSTITUTE  
FOR CANCER  
IMMUNOTHERAPY



Background



211

# Parker Institute for Cancer Immunotherapy

The background of the slide features a grayscale scanning electron micrograph (SEM) of several cancer cells. These cells are spherical and covered in numerous small, protruding, finger-like projections, giving them a textured, bumpy appearance. The cells are scattered across the dark background, with some appearing more prominent than others.

## Mission

To accelerate the development of *breakthrough immune therapies* to turn cancer into a *curable disease*.

# Cancer Immunotherapy

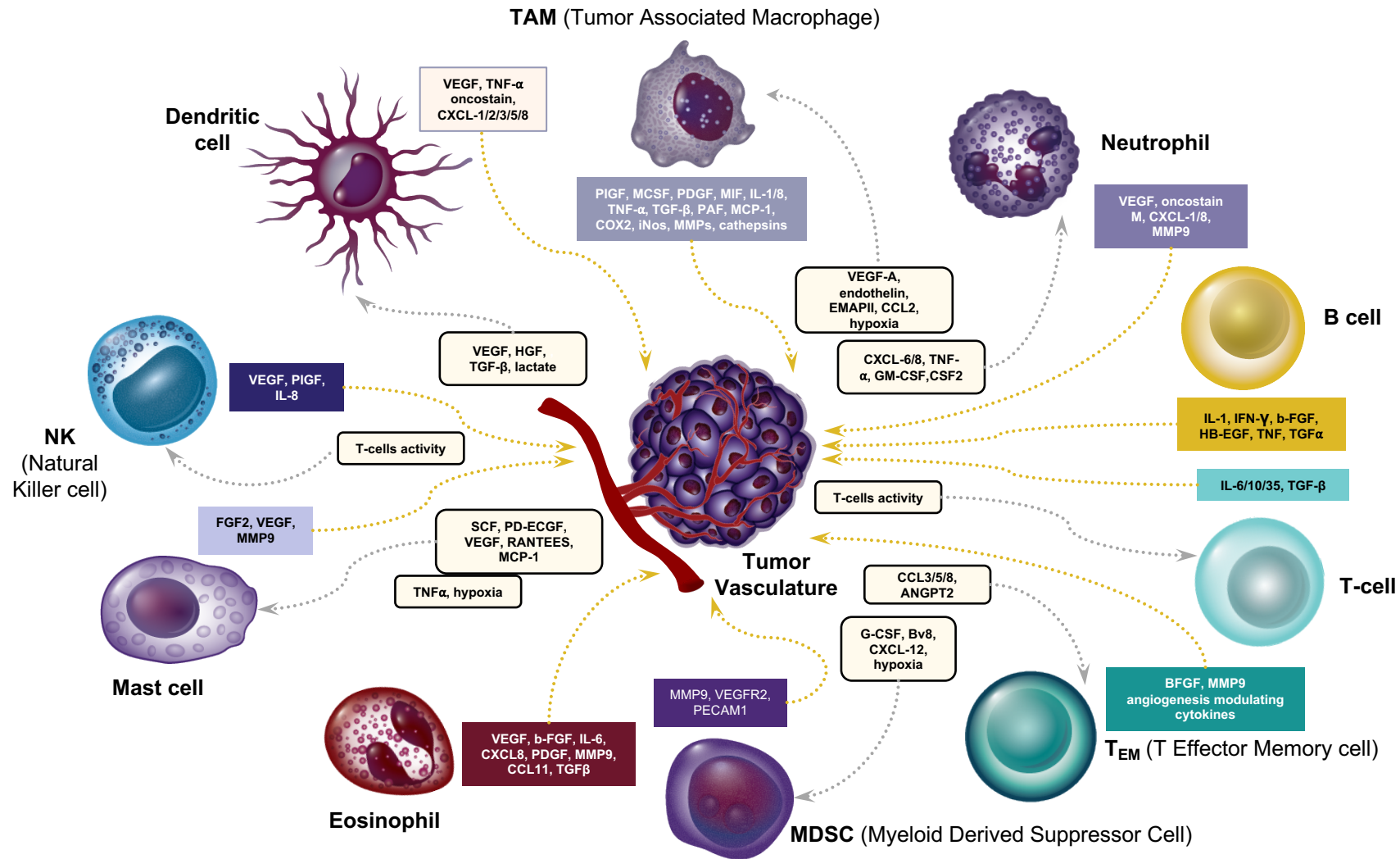
Treatments that use the body's immune system to destroy cancerous cells.

## Benefits

- Works on non-local tumors and many types of cancer
- Lower toxicity than chemo
- Works well in conjunction with other therapies
- In some patients, **long-lasting responses.**

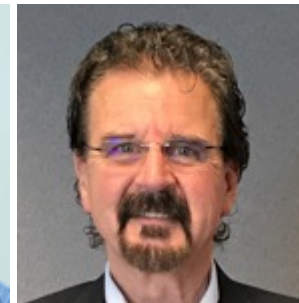
**Relatively new area, lots of unknowns, lots of research to be done**

# Tumor-Immune interactions are complex, but critical to understand



1. Stockmann C et al. *Front Oncol.* 2014;4:69.
2. Balkwill FR et al. *J Cell Sci.* 2012;125(Pt 23):5591-5596.

# PICI Informatix Team



Contact us: [data@parkerici.org](mailto:data@parkerici.org)

# CANDEL: CANcer Data & Evidence Library

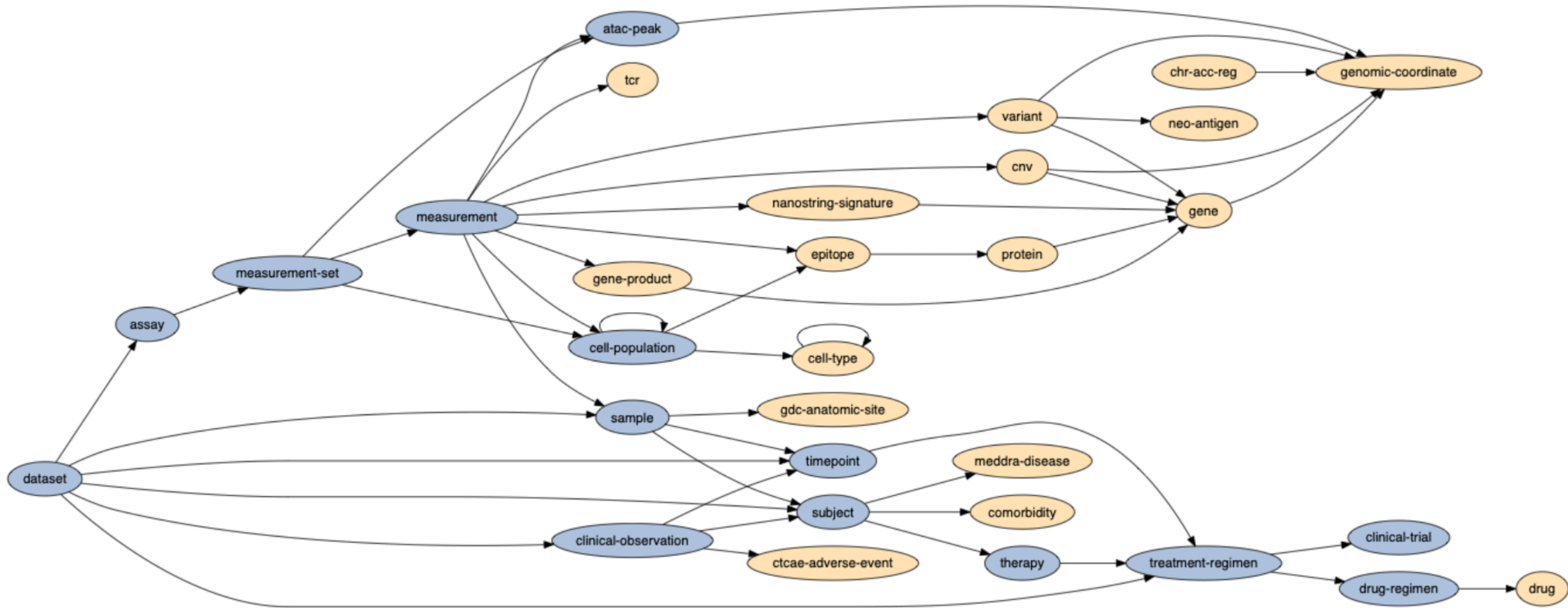
- Knowledgebase for research data
- Based on Datomic (and built in partnership with Cognitect)
- ingesting **experimental** and **reference** data from our own trials and from published research
- organizing it into a common framework
- providing it to downstream tasks (querying, analysis, visualization)
- Some objects: subjects, samples, genes, variants, clinical trials

StrangeLoop 2019: **Building a Unified Cancer Immunotherapy Data Library**

Lacey Kitsch, Ben Kamphaus

<https://youtu.be/vwZxHVcfuw>

# Medium-complex schema





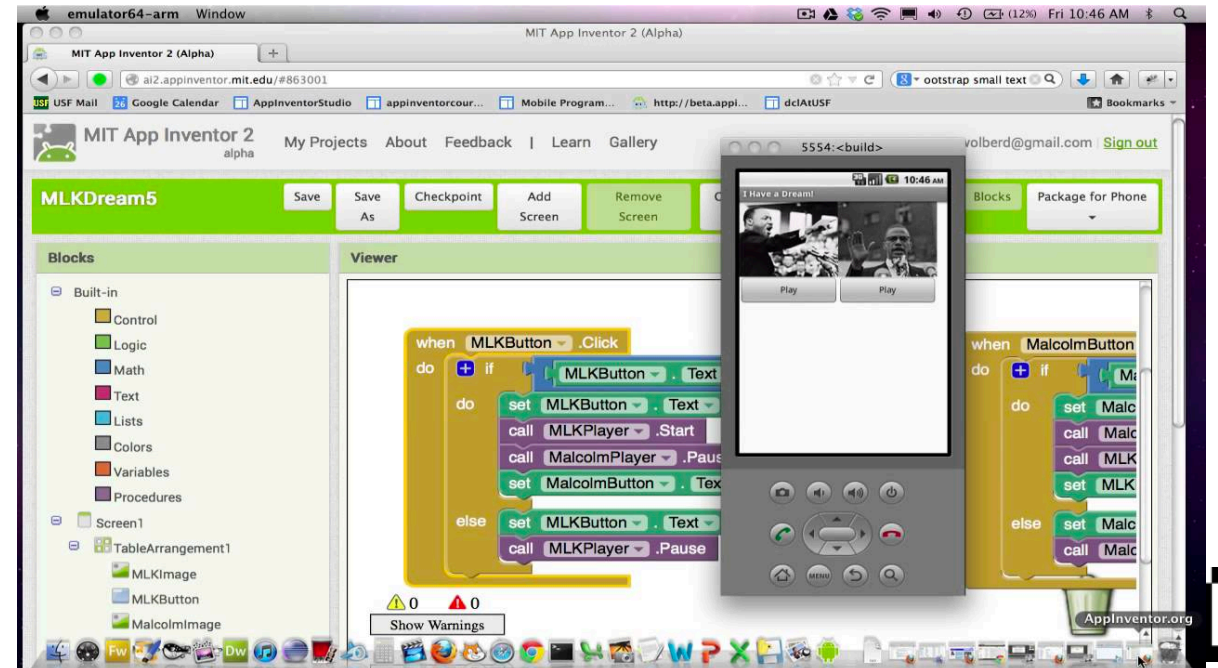
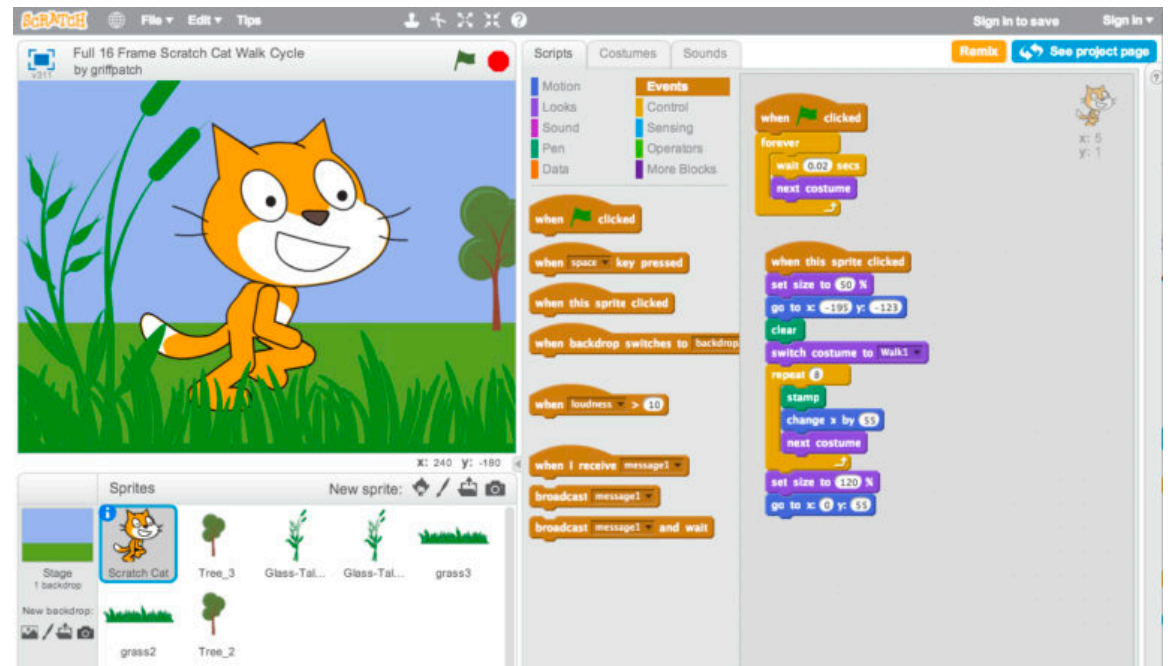
# Block languages

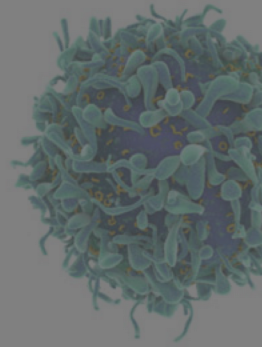
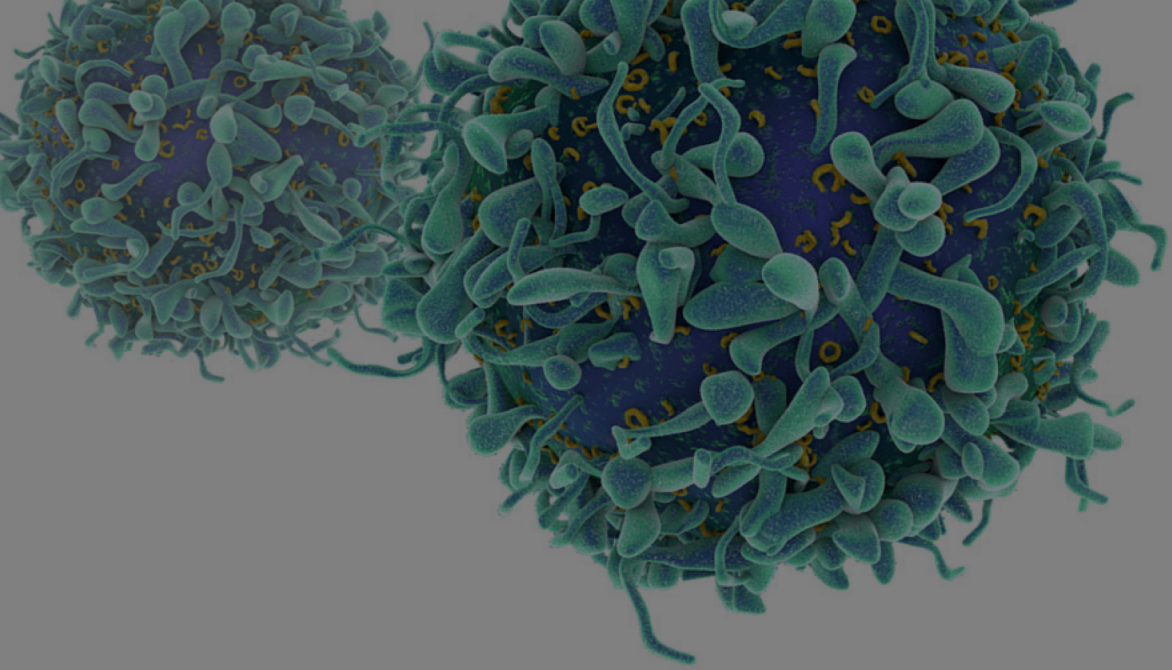
## Scratch

MIT Media Lab (2003).

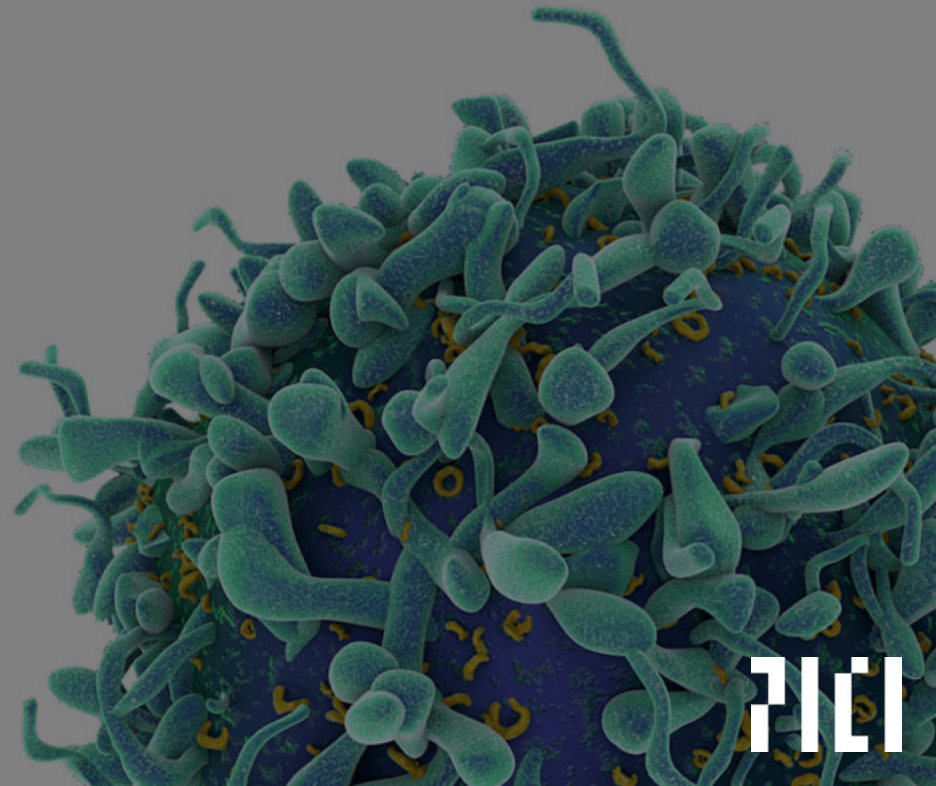
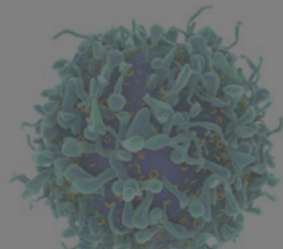
Scratch-like languages:

- **Tynker** (commercial)
- **Snap** from Berkeley (high-order procedures!)
- Android app inventor / **Blockly** (from Google)



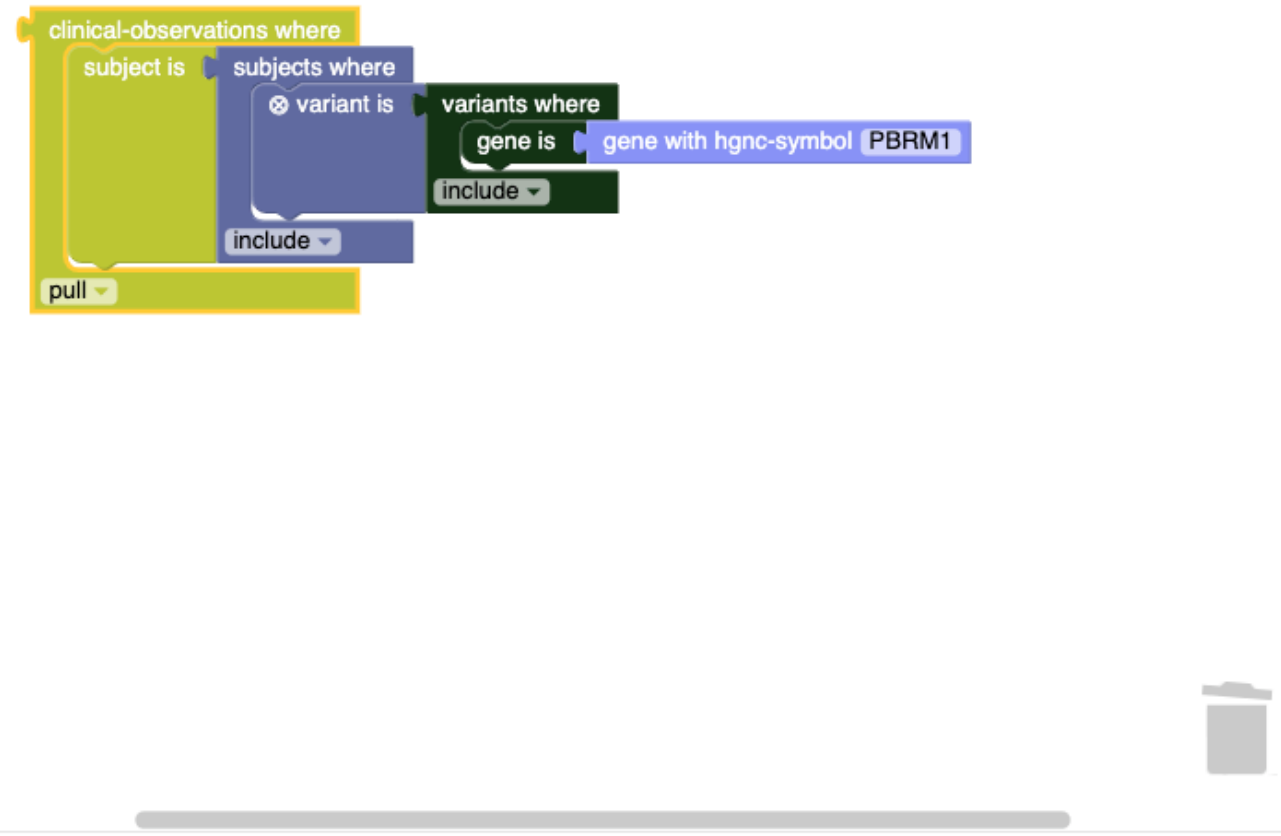


Enflame 



211

- ▼ Experimental
  - assay
  - atac-peak
  - cell-population
  - clinical-observation
  - clinical-trial
  - dataset
  - drug-regimen
  - measurement
  - measurement-set
  - sample
  - subject
  - therapy
  - timepoint
  - treatment-regimen
- ▼ Reference
  - cell-type
  - chr-acc-reg
  - cnv
  - comorbidity
  - ctcae-adverse-event
  - drug
  - epitope
  - gdc-anatomic-site
  - gene
  - gene-product



Enflame Help Schema Library

DB dannys-database-1.2

Query Go

```

{:find
 ((pull
  ?clinical-observation1
  [*
   {:clinical-observation/ctcae-adve
    [:db/id :ctcae-adverse-event/nam
     {:clinical-observation/timepoint
      {:clinical-observation/subject [:
       (pull ?subject1 [:db/id :subject/id
        (pull ?variant1 [:db/id :variant/id
         :where
          ([?measurement1 :measurement/variant
           [?measurement1 :measurement/sample
            [?sample1 :sample/subject ?subject1
             [?gene1 :gene/hgnc-symbol "PBRM1"]
              [?variant1 :variant/gene ?gene1]
               [?clinical-observation1 :clinical-o
  
```

Wick

Share Library

Browser

Showing 6 of 6 [Download](#)

clinical-observation	age	recist	responder	subject	timepoint	subject	variant
17592186367292		PR		M4945	Pembrolizumab-2wk/eos	M4945	GRCh38:chr3+:52696148:52696148/C/A
17592186367289	66			M4945	Pembrolizumab-2wk/baseline	M4945	GRCh38:chr3+:52696148:52696148/C/A
17592186367298		PD		MA7027	Pembrolizumab-2wk/eos	MA7027	GRCh38:chr3+:52598231:52598231/G/A
17592186367296	56			MA7027	Pembrolizumab-2wk/baseline	MA7027	GRCh38:chr3+:52598231:52598231/G/A

▼ Experimental

- assay
- atac-peak
- cell-population
- clinical-observation
- clinical-trial
- dataset
- drug-regimen
- measurement
- measurement-set
- sample
- subject**
- therapy
- timepoint
- treatment-regimen

▼ Reference

- cell-type
- chr-acc-reg
- cnv
- comorbidity
- ctcae-adverse-event
- drug
- epitope
- gdc-anatomic-site
- gene
- gene-product

any subject  
include ▼

subjects where  
include ▼

subject with HLAI-type

subject with HLAII-type

subject with id

subject with uid

or

HLAI-type is

HLAII-type is

⊗ age <

clinical-observation is

subjects where  
race is asian ▼  
include ▼

```
{:find ((pull ?subject1 [:db/id :subject/id]))
:where ([?subject1 :subject/race :race/asian])}
```

# Side panes

DB selection; query in various formats, other controls

[Share](#) **Library**

**Text**

```
[clinical-observations where [subject is [subjects where [⊗ variant is [variants where [gene is [gene with hgnc-symbol PBRM1]]]]]]]]
```

**Description**

clear Save

**URL**

```
http://localhost:1991/index.html?server=park
```

Copy

**Browser**

<b>subject</b>	M4945
<b>HLAI-type</b>	A0201,A3001,B1302,B4403,C0601
<b>id</b>	M4945
<b>meddra-disease</b>	Lung adenocarcinoma
<b>sex</b>	male
<b>smoker</b>	former
<b>therapies</b>	17592186422301
<b>uid</b>	Rizvi2015/M4945

Blockify

subject with id M4945

# Design philosophy

A slightly higher-level language than Datalog

Training wheels:

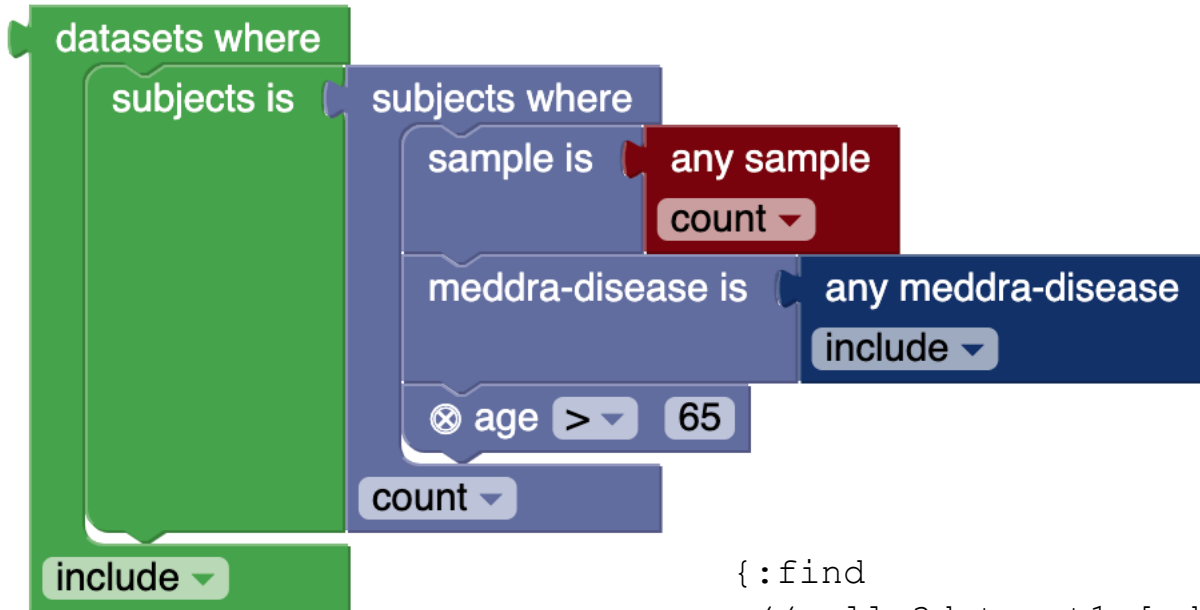
- shows how to do it the adult way

- doesn't need to provide full power of underlying system

```
{:find ((pull ?gene1 [:db/id :gene/hgnc-symbol]) ?hgnc-symbol1),  
:where  
  [(re-find ?regex ?hgnc-symbol1)]  
  [(re-pattern ".*XX.*") ?regex]  
  [?gene1 :gene/hgnc-symbol ?hgnc-symbol1]] }
```



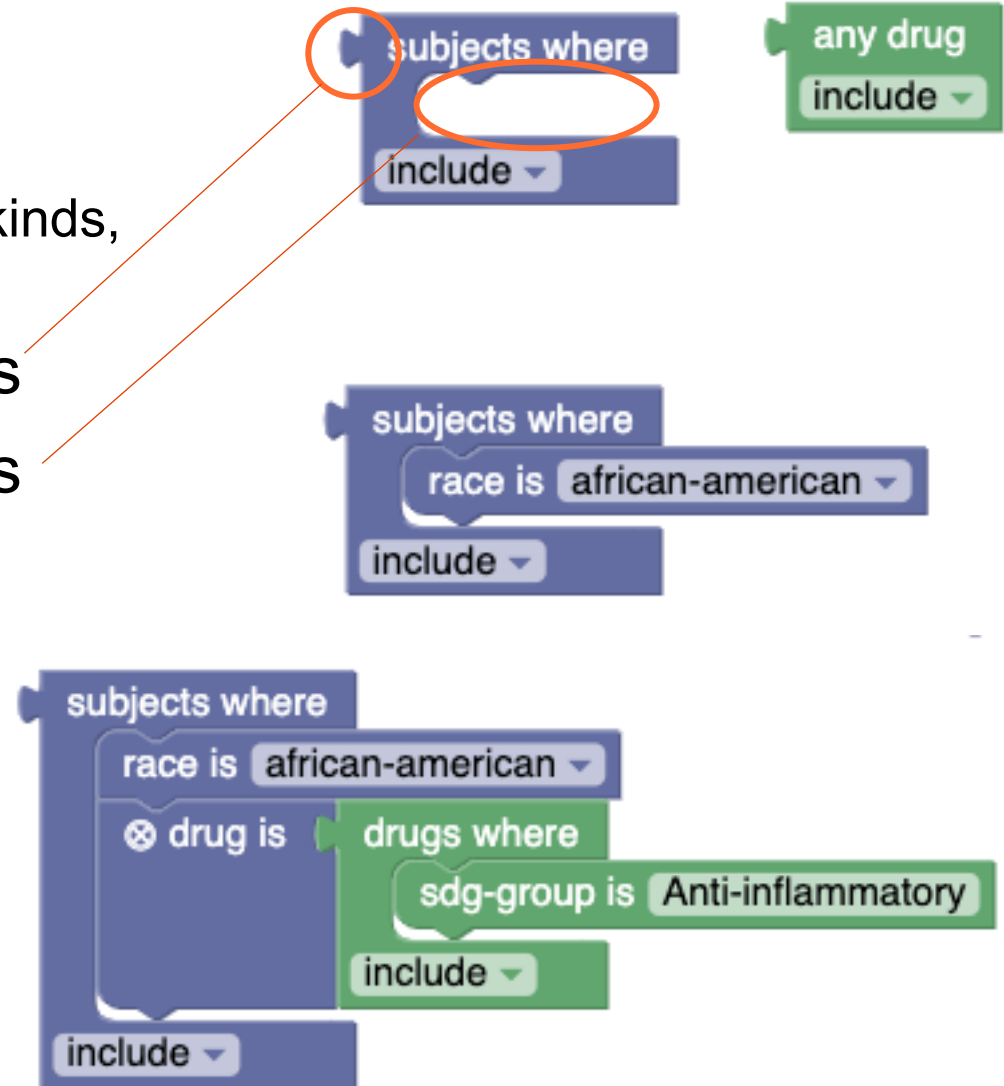
# A more complex example



```
{:find
  ((pull ?dataset1 [:db/id :dataset/name])
   (count-distinct ?subject1)
   (count-distinct ?sample1)
   (pull ?meddra-disease1 [:db/id :meddra-disease/preferred-name]) ?age1),
 :where
 ([?clinical-observation1 :clinical-observation/subject ?subject1]
  [(> ?age1 65)]
  [?clinical-observation1 :clinical-observation/age ?age1]
  [?subject1 :subject/meddra-disease ?meddra-disease1]
  [?sample1 :sample/subject ?subject1]
  [?sample1 :sample/id ?id1]
  [?dataset1 :dataset/subjects ?subject1]))}
```

# Design details

- Class (kind) mapped to color
- works OK because there are only ~30 kinds, won't scale
- Output nub produces sets of objects
- Statement input used for constraints (where clauses) because it's n-ary
- Constraint blocks primitives
- Constraint block subqueries





# Implementation





# Components

## Underlying technologies

- **Blockly**  
open source Google library for block UI
- **Clojure[script]**
- **Re-frame**
- **Alzabo**  
schema representation

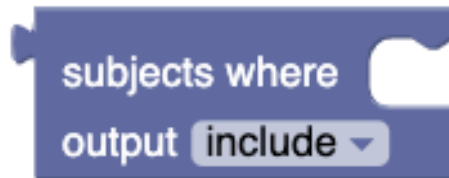
## Interacts with

- **CANDEL**  
Datomic database
- **Gaslight**  
query server
- **Wick**  
R Datalog package



# Output specifier

A **query entity block** produces a set of entities of a given type. For instance, this produces the set of all subjects:



Query entity blocks have an additional selector that lets you specify the output type. The options are:

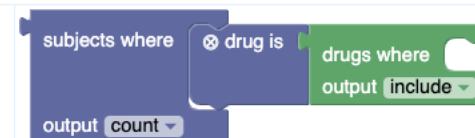
- **include**: (default) include the entity itself and its label (unique-id) if available
- **pull**: include the entity and all of its attributes
- **count**: don't return the entity itself, but instead the count of its unique values based on the rest of the query
- **omit**: don't return anything for this entity

# Sharing Features: Library

## Enflame: Library

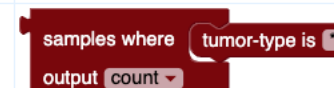
[subjects where [⊗ drug is [drugs]]]

Drugs with subject count



[samples where [tumor-type is \*]]

Sample count by tumor type

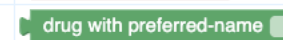


[samples where [gdc-anatomic-site is [gdc-anatomic-sites]]]

Sample counts by anatomical region

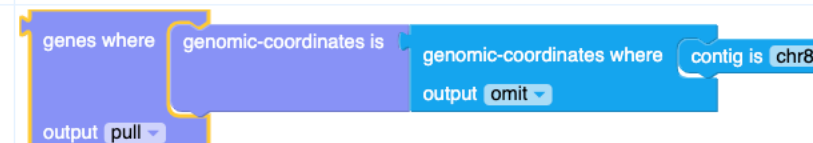


[drug with preferred-name ]



[genes where [genomic-coordinates is [genomic-coordinates where [contig is chr8]]]]

Genes on a given chromosome



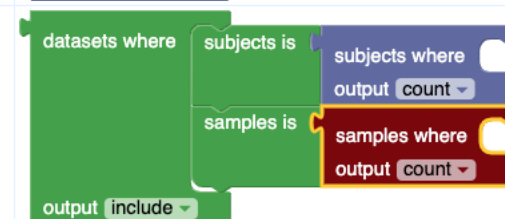
[subjects where [⊗ treatment-regimen is [treatment-regimen with name aPD1]]]

Subjects with a particular treatment regimen



[datasets where [subjects is [subjects]] and [samples is [samples]]]

Dataset census



Schema transformation

(into something basically equivalent to RDFS)

classes

attributes

entity values (eg race, cancer stage)

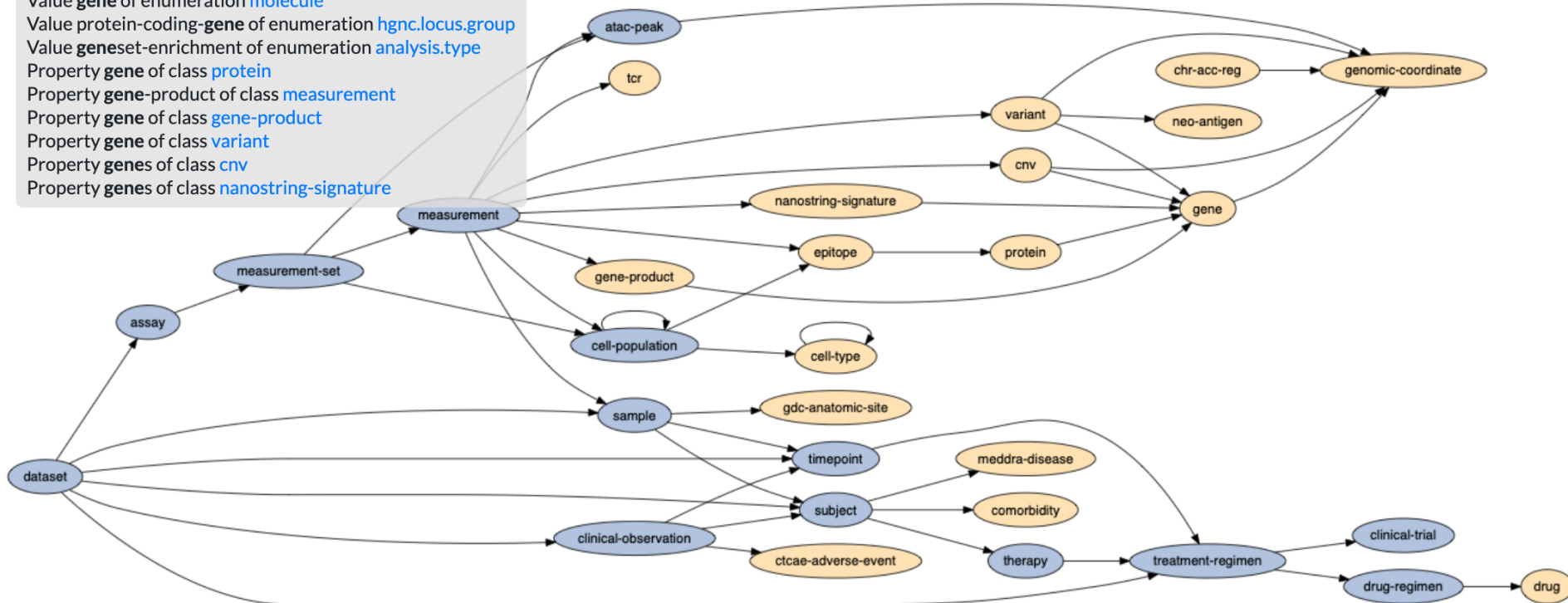
Similar to Hodur <https://github.com/hodur-org>

Generates documentation (graphviz, html, search widget)

# CANDEL Schema

search:

Class [gene](#)  
 Class [gene-product](#)  
 Value [gene](#) of enumeration [molecule](#)  
 Value protein-coding-[gene](#) of enumeration [hgnc.locus.group](#)  
 Value [geneset-enrichment](#) of enumeration [analysis.type](#)  
 Property [gene](#) of class [protein](#)  
 Property [gene-product](#) of class [measurement](#)  
 Property [gene](#) of class [variant](#)  
 Property [genes](#) of class [cnv](#)  
 Property [genes](#) of class [nanosttring-signature](#)



## Kinds

### reference

- [cell-type](#)
- [chr-acc-reg](#)
- [cnv](#)
- [comorbidity](#)
- [ctcae-adverse-event](#)

## Enums

- [ae.grade](#)
- [analysis.type](#)
- [assembly](#)
- [candel](#)
- [ethnicity](#)
- [hgnc.locus.group](#)
- [molecule](#)



Future (and past)



## **Usability**

- Hide some of schema complexity

- More control over results

- Tighter integration with Alzabo graph

- User testing

## **Support more complex queries**

“How many patients who experienced toxicity on any given therapy had a microbiome sample profiled within 10 days of the toxicity event?”

## **Adapt to other databases**

- Including SPARQL/Linked Data

# Open source (someday)

Possible components to open source:

**Alzabo**

**Blockoid** (thin CLJS wrapper for Blockly)

**Querulous** (general graph query generator)

Ultimately would like to make this useful for other datatypes, eg SPARQL endpoints like Wikidata.

# Related work

SPARQL Playground: a Block Programming Tool to Experiment with SPARQL

Paolo Bottoni and Miguel Ceriani, 2015

<http://sparqlblocks.org/demo/>

Has a lower-level approach that exposes SPARQL elements directly.

Avoids the semantic type/color problem.

The screenshot displays a block programming interface for SPARQL. The query is constructed as follows:

- select all the variables and the first 3 rows**
- where**
  - film** is a **dbo : Film**
  - & has**
    - dbo : director** → **dbpedia : Francis\_Ford\_Coppola**
    - rdfs : label** → **label**
- ordered by** **label** ↓, **by** ↓, **and by** ↓

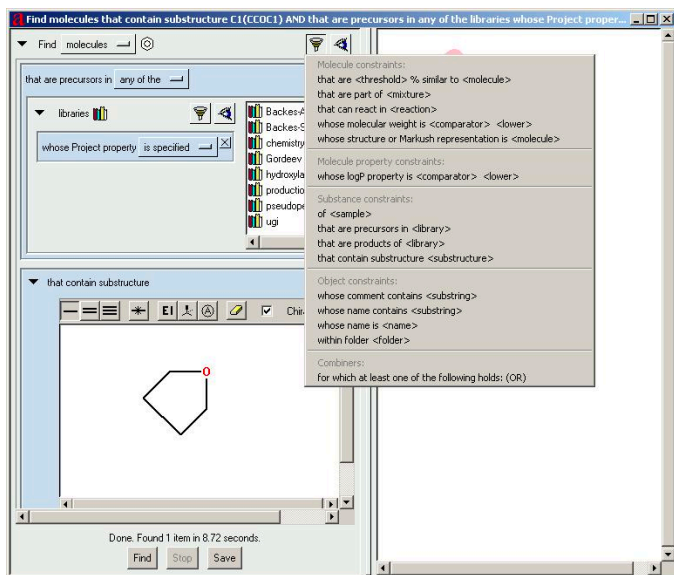
The results are displayed in two columns:

film	label
dbpedia : Apocalypse_Now	“ Apocalypse Now ”
dbpedia : Apocalypse_Now_Redux	“ Apocalypse Now Redux ”
dbpedia : Battle_Beyond_the_Sun	“ Battle Beyond the Sun ”

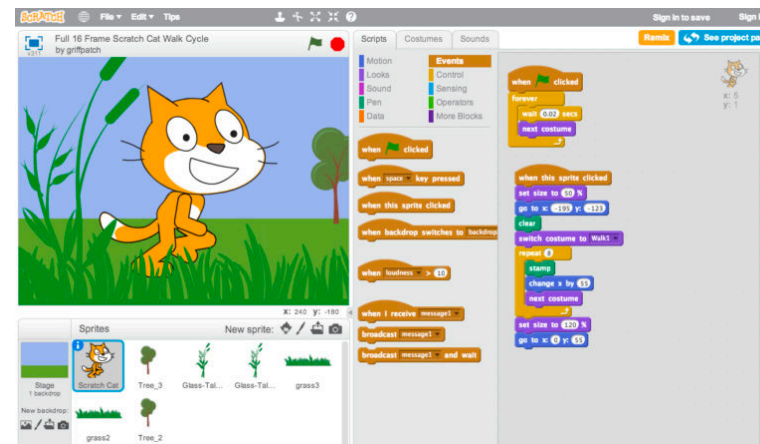
# Some history



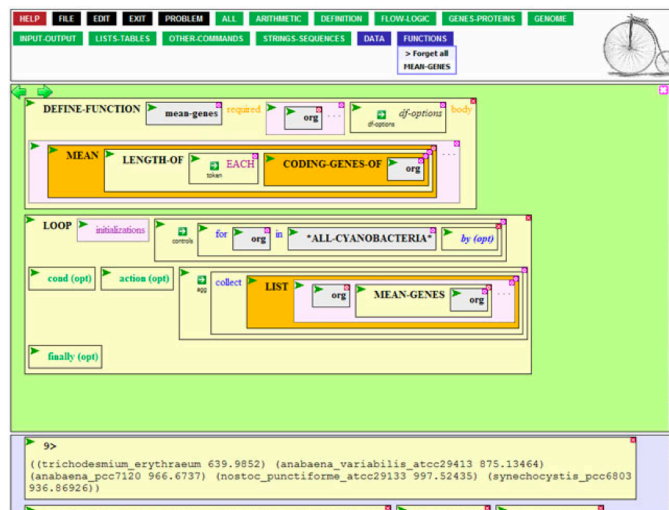
Behave, 1996



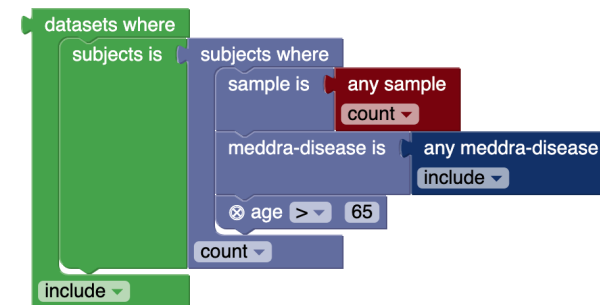
Afferent, 1999



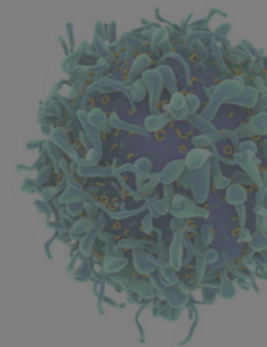
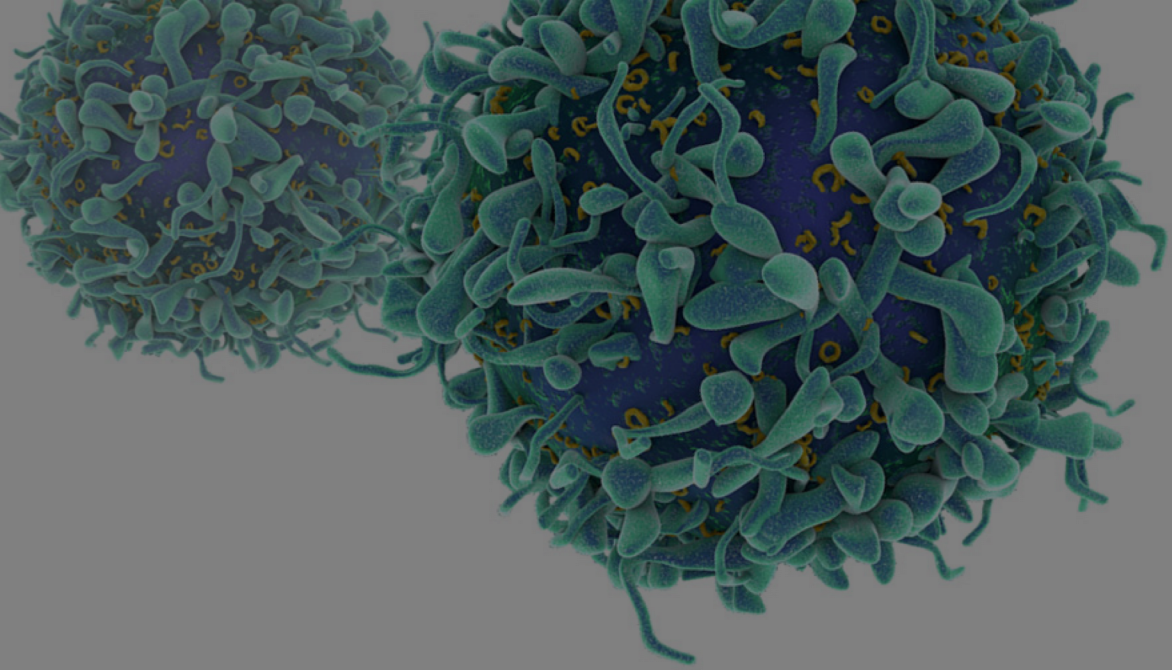
Scratch, 2003



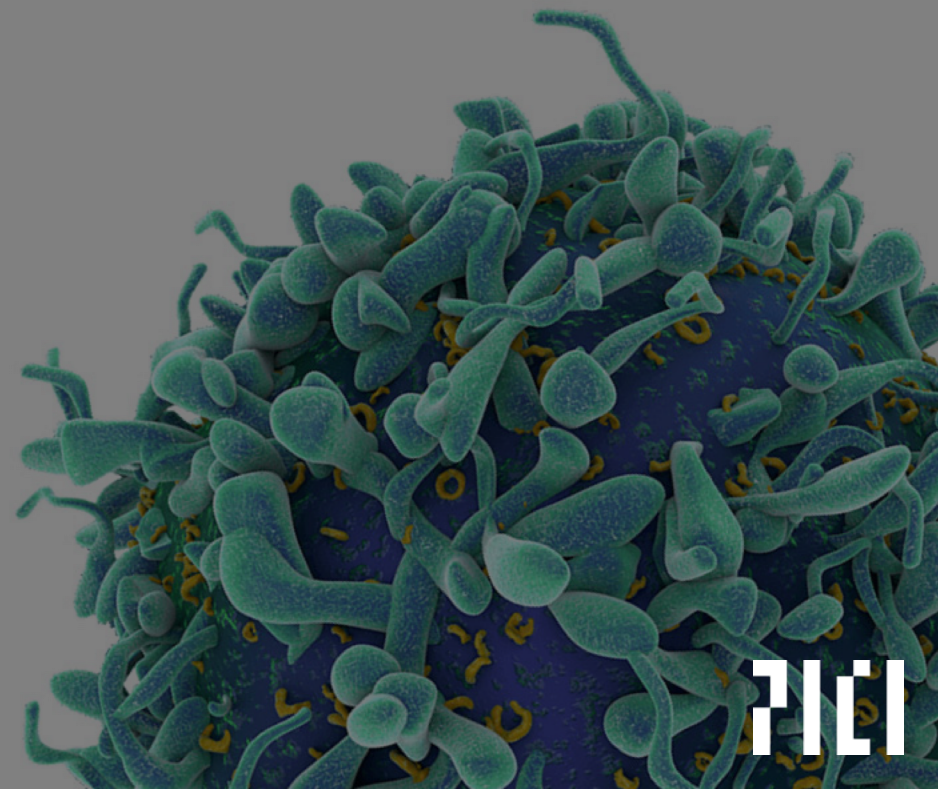
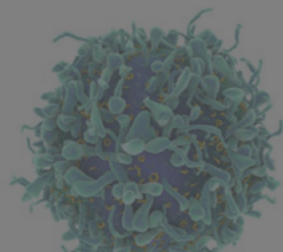
BioBike, 2006



Enflame, 2019



The End



211