

BIPMed: Bioinformatics challenges and solutions

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Genomic Databases

- LOVD interface offers a lot of extra annotation;
- Loading data to this system requires a lot of computational resources;
- DB performance may be sub-optimum on the client-side;
- Testing transition to column-based DBMS;



Brazilian Initiative on Precision Medicine



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Showing entries 1 - 100.

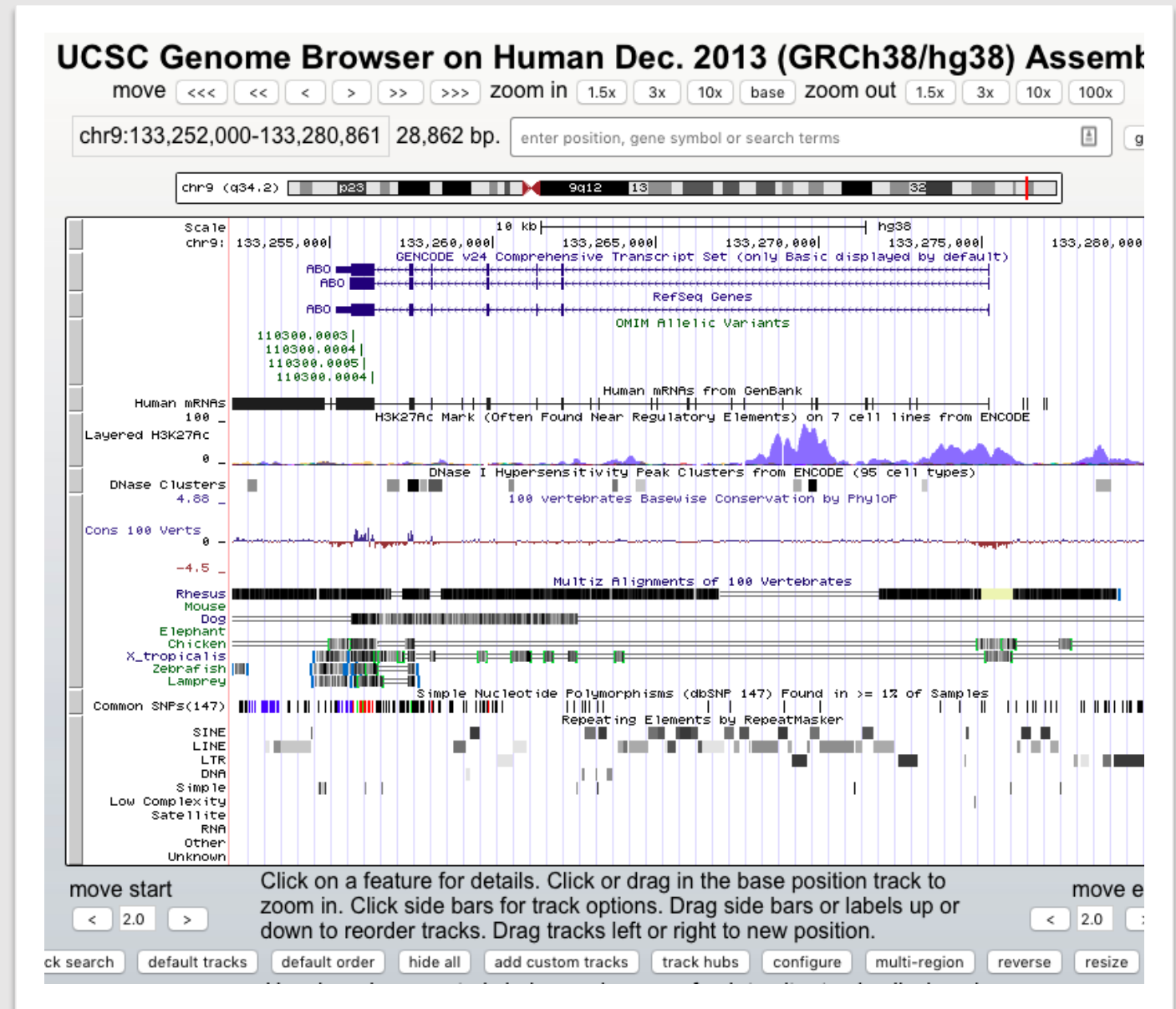
« First < Prev **1** 2 3 4 5 6 7 8 9 10 11 ... Next > Last »

	Chr	Band	Transcripts	Variants	Unique variants	Last
β glycoprotein	19	q13.43	1	0	0	2015-
antisense RNA 1	19	q13.43	1	0	0	2015-
complementation factor	10	q21.1	10	0	0	2015-
nacroglobulin	12	p13.31	2	0	0	2015-
sense RNA 1 (head to head)	12	p13.31	1	0	0	2015-
nacroglobulin-like 1	12	p13	4	0	0	2015-
nacroglobulin pseudogene 1	12	p13.31	1	0	0	2015-
-galactosyltransferase 2	1	p35.1	1	9	9	2015-
-galactosyltransferase	22	q13.2	10	0	0	2015-
-N-acetylglucosaminyltransferase	3	p14.3	1	0	0	2015-
, adrenocortical insufficiency, alacrimia	12	q13	9	0	0	2015-
yl-CoA synthetase	12	q24.31	5	0	0	2015-
yl-CoA synthetase pseudogene 1	5	q35	1	0	0	2015-
mide deacetylase	3	q25.1	2	0	0	2015-
mide deacetylase-like 2	3	q25.1	2	0	0	2015-
antisense RNA 1	3	q25.1	1	0	0	2016-
mide deacetylase-like 3	1	p36.21	2	24	24	2015-
mide deacetylase-like 4	1	p36.21	5	14	14	2015-
mide deacetylase pseudogene 1	3	q25.1	1	0	0	2016-
pate aminotransferase	4	q33	6	0	0	2015-
antioxidant enzyme domain containing 1	9	q22.32	3	0	0	2015-

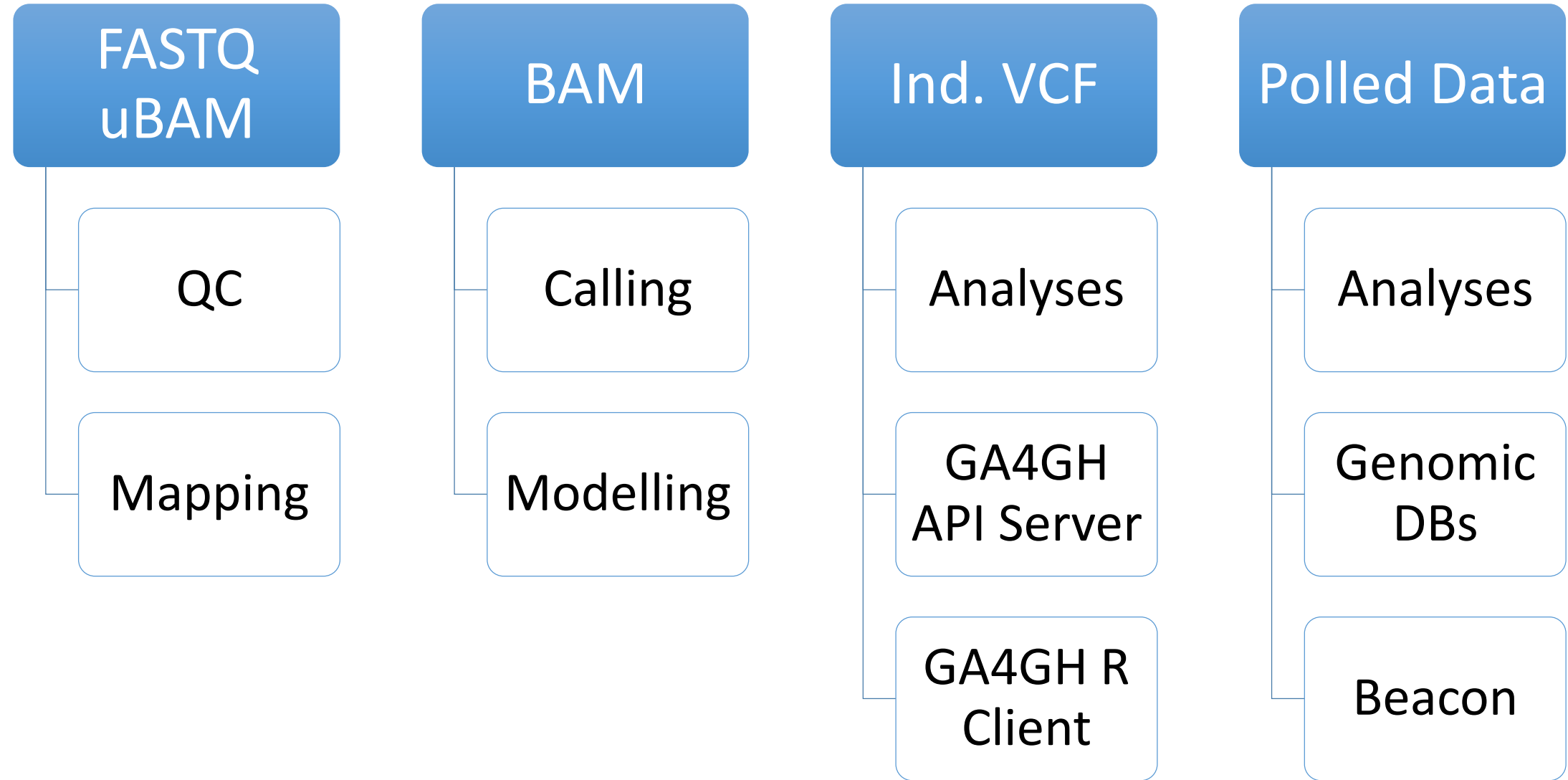


Integration with existing tools

- Creating custom-tracks for use with UCSC Genome Browser;
 - All variants;
 - All variants found in at least 1%;
 - All variants found in at least 5%;
- Setting up a local infra-structure to accommodate BIPMed data via UCSC Genome Browser;

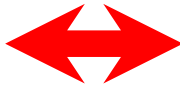
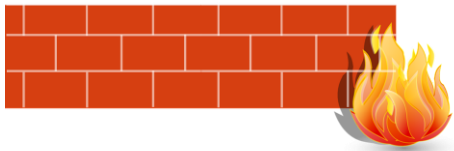


Data Management



Data Management – Security – API

```
int ilength, iN;  
double dblTemp;  
bool again = true;  
  
while (again) {  
    iN = -1;  
    again = false;  
    getline(cin, sInput);  
    system("cls");  
    stringstream(sInput) >> dblTemp;  
    ilength = sInput.length();  
    if (ilength < 4) {  
        again = true;  
        continue;  
    } else if (sInput[ilength - 3] != '.') {  
        again = true;  
        continue;  
    }  
    while (++iN < ilength) {  
        if (isdigit(sInput[iN])) {  
            continue;  
        } else if (iN == (ilength - 3)) {  
            continue;  
        }  
    }  
}
```



Ind. VCF

Analyses

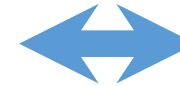
Restricted Access

Polled Data

Analyses

Genomic DBs

Beacon



```
int ilength, iN;  
double dblTemp;  
bool again = true;  
  
while (again) {  
    iN = -1;  
    again = false;  
    getline(cin, sInput);  
    system("cls");  
    stringstream(sInput) >> dblTemp;  
    ilength = sInput.length();  
    if (ilength < 4) {  
        again = true;  
        continue;  
    } else if (sInput[ilength - 3] != '.') {  
        again = true;  
        continue;  
    }  
    while (++iN < ilength) {  
        if (isdigit(sInput[iN])) {  
            continue;  
        } else if (iN == (ilength - 3)) {  
            continue;  
        }  
    }  
}
```



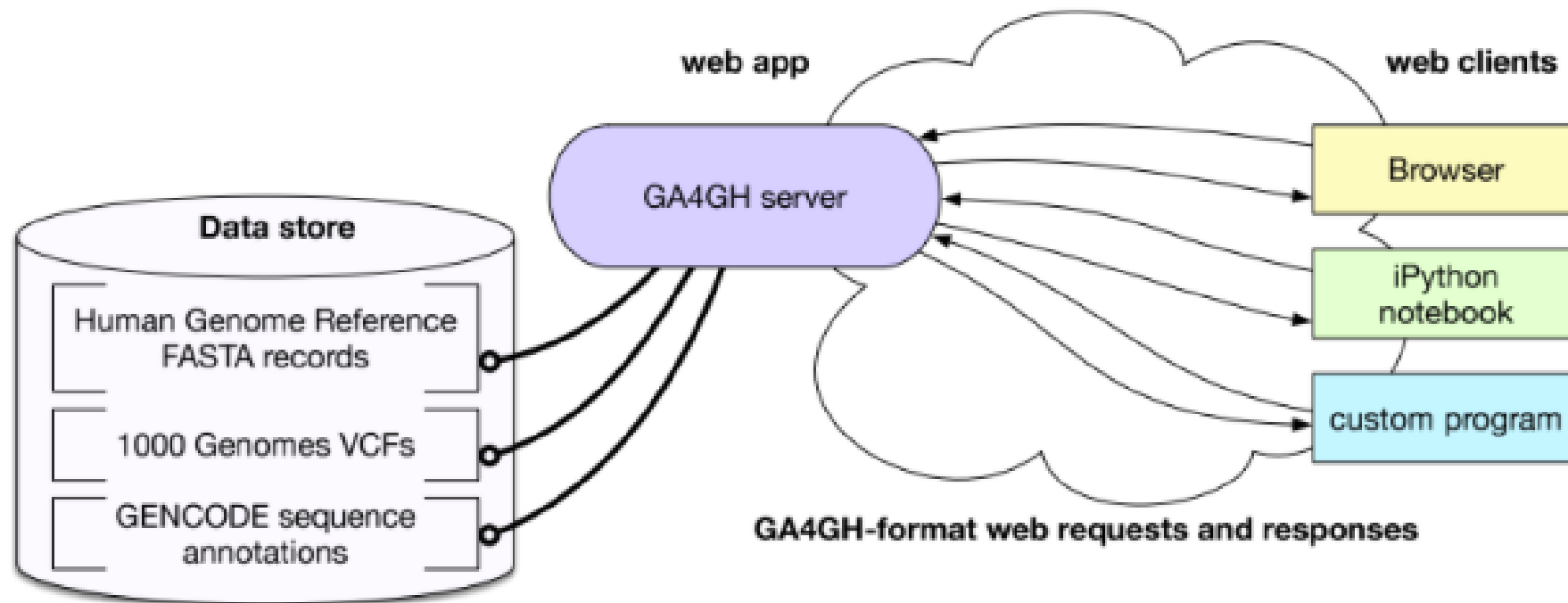
Programmatic Access – Databases

- DB infra-structure uses GA4GH Server API;
- We developed the GA4GH R Client to assist on programmatic access;
- DB access via GA4GH API is possible but not allowed as of today, as authentication is still being developed;
- Tools can be used internally;

GA4GH Server API

- The ga4gh-server software implements data schema for representing genomic variation data.
- It provides an application program interface (API) through the internet.
- Example: <http://1kgenomes.ga4gh.org/>
- Project page: <https://github.com/ga4gh/server>

GA4GH Server API



Source: GA4GH

GA4GHclient package

- GA4GHclient is a Bioconductor package for accessing GA4GH API data servers.
- Provides tools to perform programmatic access to genomic data servers that follow the GA4GH standards.
- Integrates with other Bioconductor packages allowing creation of complex genomic data analysis.
- Also provides a web application to interact with genomic data.
- Project page: <https://github.com/labbcg/GA4GHclient>

Dataset
bipmed-exome

Variant Set
bipmed-exome

Gene Symbol
SCN1A

Genomic Feature

- Genes
- Transcripts
- Exons
- CDS
- Promoters

Reference Name
chr2

Start
165989160

End
166128047

Search Variants

Variants

Show 10 entries

Search:

	DNA change	dbSNP ID	Reference Name	Start	End	Reference Bases	Alternate Bases	ExcessHet	AC	BaseQRankSum	MI
1	g.165991411A>G	-	chr2	165991411	165991411	A	G	3.03090000153	2	2.78999996185	0.00
2	g.165991493G>C	-	chr2	165991493	165991493	G	C	3.01029992104	1	1.48000001907	0.00
3	g.165991857C>T	-	chr2	165991857	165991857	C	T	3.03090000153	2	-0.29699999094	0.00
4	g.165992330G>A	-	chr2	165992330	165992330	G	A	3.01029992104	1	-1.49800002575	0.00
5	g.165992388G>A	-	chr2	165992388	165992388	G	A	3.03090000153	2	0.165999993682	0.00
6	g.165992564T>A	-	chr2	165992564	165992564	T	A	0.105499997735	4	1.64999997616	0.02
7	g.165995836_165995840delinsT	-	chr2	165995836	165995840	TTTAA	T	3.03150010109	2	0.921000003815	0.00
8	g.165995889G>C	-	chr2	165995889	165995889	G	C	3.07249999046	3	-2.90499997139	0.01
9	g.165998005C>T	-	chr2	165998005	165998005	C	T	3.07369995117	3	-1.14999997616	0.01
10	g.165999649G>A	-	chr2	165999649	165999649	G	A	3.21959996223	5	2.25999999046	0.02

Showing 1 to 10 of 66 entries

Previous **1** 2 3 4 5 6 7 Next

BIPMed Beacon and Beacon Network



BIPMed Beacon

This beacon provides data on individuals from the reference population.

Chromosome:

19

Position:

58353112

Allele:

C

Submit



[Search Beacons](#)

Search [all beacons](#) for allele

GRCh38 ▾

19 : 58353113 T > C

Search

Response All None

- Found 4
- Not Found 13
- Not Applicable 54

Organization

- AMPLab, UC Be...
- Australian Geno...
- BGI
- BioReference La...
- Brazilian Initiativ...

Show All



Altruist

Hosted by Sequencing.com

Found



AMPLab - 1000 Genomes Project

Hosted by AMPLab, UC Berkeley

Found



BIPMed

Hosted by Brazilian Initiative on Precision Medicine

Found



OpenSNP - Personal Genomics in the Public Do...

Hosted by OpenSNP

Found

Programmatic Access – Beacon

- BIPMed Beacon connected to Beacon Network;
- Beacon Network can be accessed via Beacon API;
- Beacon API can access BIPMed Beacon directly;
- Tools are under development and designed to allow for queries through computer programs, assisting on variant filtering;

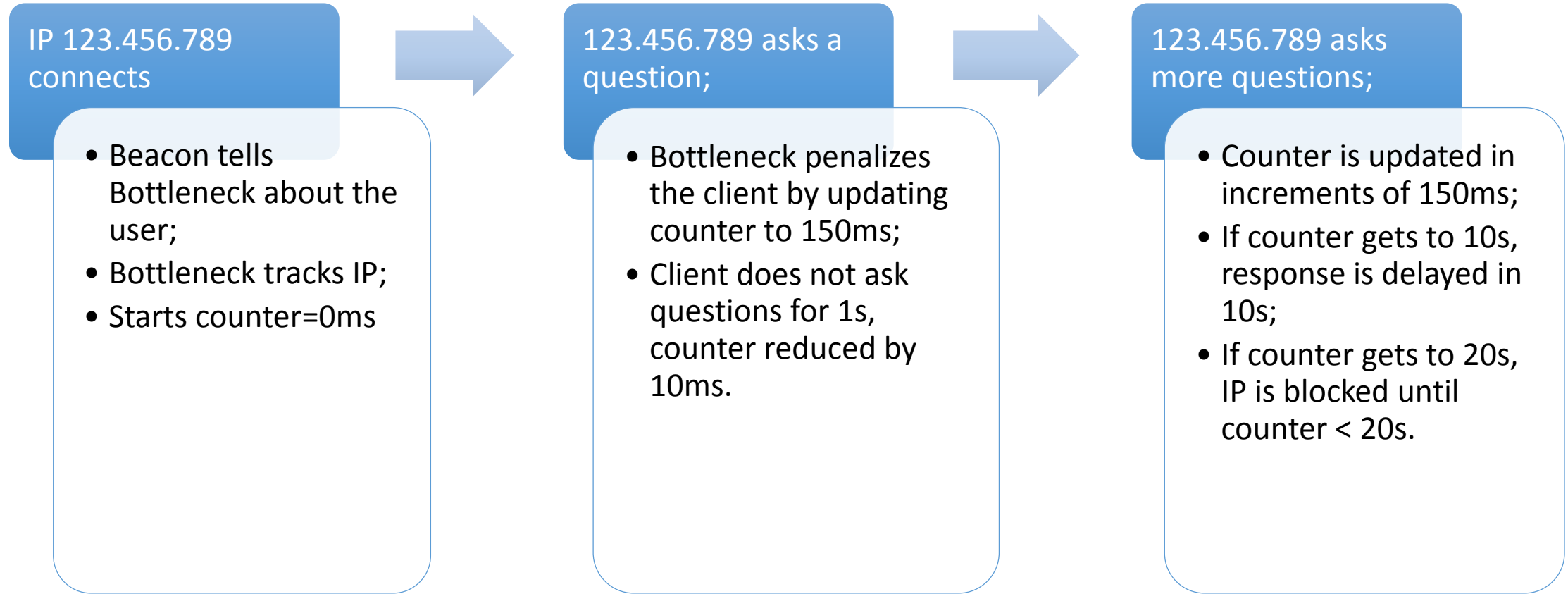
Programmatic Access – Beacon

```
> getBeaconData(1, 13272, 'C', 'GRCh38', 'bipmed')
[
  {
    "beacon": {
      "id": "bipmed",
      "name": "BIPMed",
      "organization": "Brazilian Initiative on Precision Medicine",
      "description": "Variants identified on Brazilian subjects who belong to the reference population.",
      "aggregator": false,
      "enabled": false,
      "visible": false,
      "createdDate": "2015-11-13",
      "supportedReferences": ["HG38"]
    },
    "query": {
      "chromosome": "CHR1",
      "position": 13272,
      "allele": "C",
      "reference": "HG38"
    },
    "response": true
  }
]
```

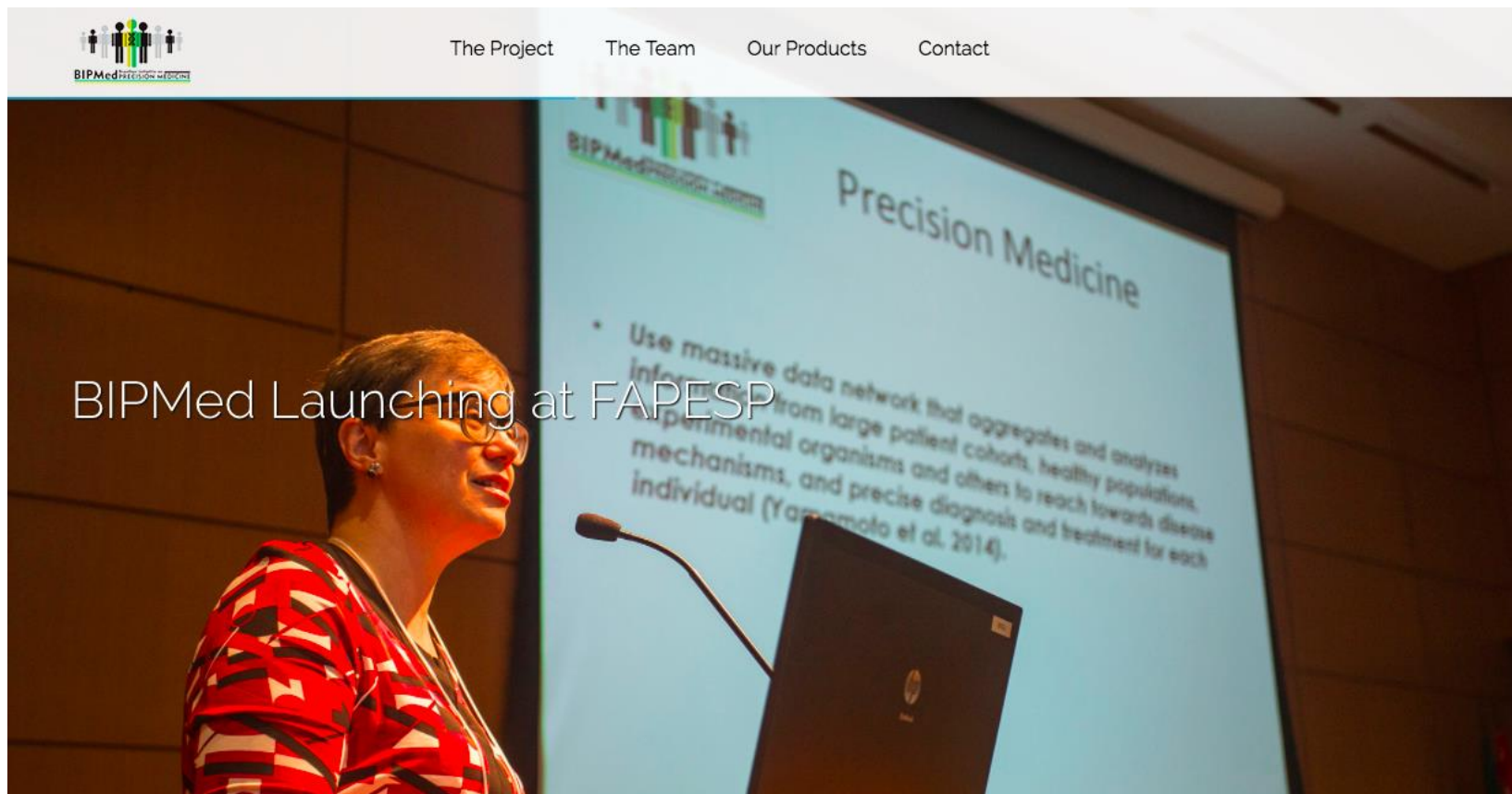
Bottleneck Server

- To avoid genome-wide queries, the BIPMed Beacon uses IP Throttling;
- IP Throttling is performed by the Bottleneck Server, as used by UCSC;
- In practice, the Beacon slows down requests when too many come from the same IP.

Bottleneck Server



BIPMed Website
<http://www.bipmed.org>



Website security

- Website is secured by Cloudflare;
- Contents are copied across many Cloudflare servers around the world;
- Every request to the website is initially sent to the Cloudflare server;
- Cloudflare analyzes requests and decides whether or not they come from a client flagged as a threat;

Website security

- If client is not a threat:
 - Cloudflare finds the server that is the closest to the client;
 - This server replies to the request by sending cached versions of the website;
 - Connection is much faster and our server does not need to handle traffic;
- If client is a threat:
 - Cloudflare will not reply to requests.
 - Our “original” server is protected from attacks.
- All services provided by us may use a similar system.

Reliability

- Genomic databases and Beacons are mirrored;
- Current mirrors:
 - USP
 - School of Medicine – UNICAMP;
 - Institute of Chemistry – UNICAMP;
- Mirrors are designed to work as backup systems in case of problems with the main server.



Thank you!

- Visit our website: <http://www.bipmed.org>
- Email us: contact@bipmed.org