

# BIO390: Introduction to Bioinformatics

## Lecture I: What is Bioinformatics?

Michael Baudis - 2019-09-17



University of  
Zurich<sup>UZH</sup>

# BIO390: Course Schedule

- 2019-09-17: Michael Baudis - What is Bioinformatics? Introduction and Resources
- 2019-09-24: Christian von Mering - Sequence Bioinformatics
- 2019-10-01: Shinichi Sunagawa (ETHZ) - Metagenomics
- 2019-10-08: Mark Robinson - Statistical Bioinformatics
- 2019-10-15: Izaskun Mallona - Regulatory Genomics and Epigenomics
- 2019-10-22: Abdullah Kahraman (USZ) - Molecular Interaction Networks
- 2019-10-29: Katja Baerenfaller (SIAF) - Proteomics
- 2019-11-05: Amedeo Caflisch - Molecular Dynamics
- 2019-11-12: Elif Ozkirimli - Protein Structure and Interactions
- 2019-11-19: Christophe Dessimoz (UniL) - Sequence evolution and phylogenetics
- 2019-11-26: Valérie Barbie (SIB) - Clinical Bioinformatics
- 2019-12-03: Andreas Wagner - Biological Networks
- 2019-12-10: Alex Handler Wagner (WUSTL) & Michael Baudis - Human Genome Variation Resources
- 2019-12-17: Exam (Multiple Choice)

# Course Information BIO390

- Tuesdays at 08:00; 2x45min
- 13 presentations by different lecturers
- course language is English
- course slides may/should be made available through the website
- written exam at end of course (== 14th course - December 17th)
- Organizer:

Prof. Dr. Michael Baudis

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<https://compbiozurich.org/UZH-BIO390/>



## UZH BIO390

Introduction to Bioinformatics

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## UZH BIO390 - Introduction to Bioinformatics Lecture Series

This is a repository for materials related to the BIO390 *Introduction to Bioinformatics* lecture series at the University of Zürich.

### [Final Program](#) and day-by-day [Schedule](#)

### Summary

The handling and analysis of biological data using computational methods has become an essential part in most areas of biology. In this lecture, students will be introduced to the use of bioinformatics tools and methods in different topics, such as molecular resources and databases, standards and ontologies, sequence and high performance genome analysis, biological networks, molecular dynamics, proteomics, evolutionary biology and gene regulation. Additionally, the use of low level tools (e.g. Programming and scripting languages) and specialized applications will be demonstrated. Another topic will be the visualization of quantitative and qualitative biological data and analysis results.

### Learning Goals

The overall learning goals - especially the (limited) set necessary for passing the test - will be updated throughout the semester.

- Core [Learning Goals](#)

This list is not exhaustive; additional information about "need to know" topics will be provided during the individual lectures.

### Literature and Resources

- [Literature links](#) and recommendations
- [Resource links](#) (browsers and online repositories)

### Links

- BIO390 HS 2019 in the [UZH OLAT](#) system
- BIO390 HS 2019 in the [UZH directory](#)



# Some Recommended Books

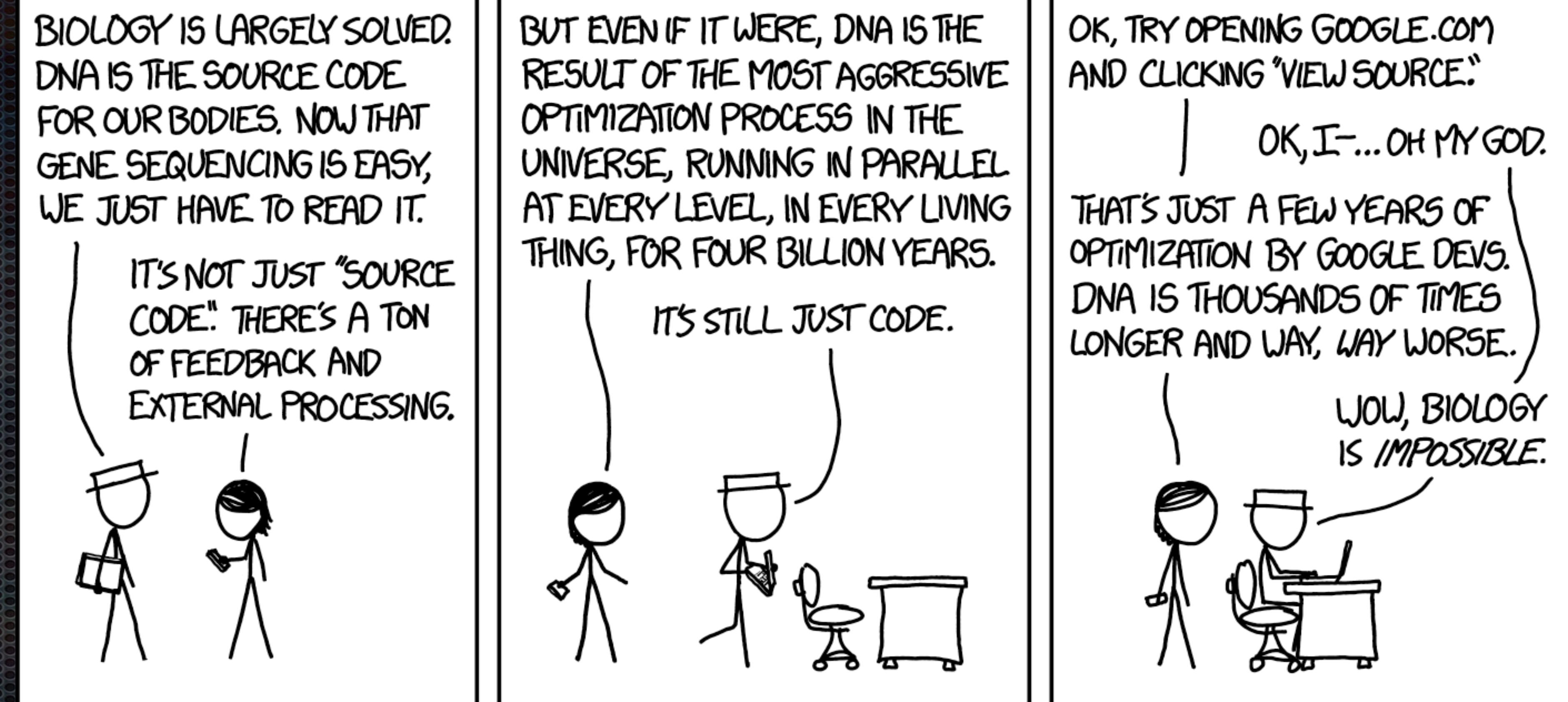
- Anna Tramontano: Introduction to Bioinformatics
- Susan Holmes and Wolfgang Huber: Statistics for Biology
- Robert Gentleman: R Programming for Bioinformatics
- John Maindonald & W. John Braun: Data Analysis and Graphics Using R
- Andy Hector: The New Statistics with R
- Neil C. Jones & Pavel A. Pevzner: Bioinformatics Algorithms
- Edward Tufte: The Visual Display of Quantitative Information (& other works by Tufte)



# Why Bioinformatics?

- **hypotheses** are the basis of biological experiments
- biological experiments produce **data**, the quantitative and/or qualitative read-outs of experiments
- both quantitative as well as qualitative data need to be **processed** for
  - statistical significance
  - categorisation
  - communication
- many datatypes are beyond the proverbial "intuitive understanding"
- analysis of data confirms or refutes initial hypotheses - or requires new hypotheses and new data

# Biology is *impossibly* complex - But bioinformatics might help



# So, What is Bioinformatics?

- Bioinformatics is "the science that uses the instruments of informatics to analyze biological data in order to formulate hypotheses about life." (Anna Tramontano)

# What is Bioinformatics?



- Bioinformatics is "the **science** that uses the instruments of informatics to analyze biological data in order to formulate hypotheses about life." (Anna Tramontano)

a : knowledge or a system of knowledge covering general truths or the operation of general laws especially as obtained and tested through **scientific method**

b : such knowledge or such a system of knowledge concerned with the physical world and its **phenomena** : NATURAL SCIENCE



# What is Bioinformatics?

Bioinformatics **uses** informatics tools for analyses

- Bioinformatics is "the science that **uses** the instruments of informatics to analyze biological data in order to formulate hypotheses about life." (Anna Tramontano)
- **software** (programming languages, statistics & visualisation, program and web APIs, databases, hardware drivers)
- **hardware** (HPC, data storage, signal measurement & processing)
- **algorithms** (modeling, encryption...)

# What is Bioinformatics?

Bioinformatics **develops** informatics tools for analyses

- Bioinformatics is "the science that uses the **instruments of informatics** to analyze biological data in order to formulate hypotheses about life." (Anna Tramontano)
- **software** (statistics & visualisation packages, program and web APIs, file formats)
- **hardware** (drivers and procedures...)
- **algorithms** (modeling, encryption...)

# What is Bioinformatics?

**biological data**

- Bioinformatics is "the science that uses the instruments of informatics to analyze **biological data** in order to formulate hypotheses about life." (Anna Tramontano)

sequences, graphs, high-dimensional data, spatial/geometric information, scalar and vector fields, patterns, constraints, images, models, prose, declarative knowledge ... \*

# What is Bioinformatics?



Bioinformatics **analyzes**

- Bioinformatics is "the science that uses the instruments of informatics to **analyze** biological data in order to formulate hypotheses about life."  
(Anna Tramontano)

1 : to study or determine the nature and relationship of the parts of (something) by **analysis**

# What is Bioinformatics?



- Bioinformatics is "the science that uses the instruments of informatics to analyze biological data in order to **formulate hypotheses** about life." (Anna Tramontano)

**b** : an interpretation of a practical situation or condition taken as the ground for action

# What is Bioinformatics?

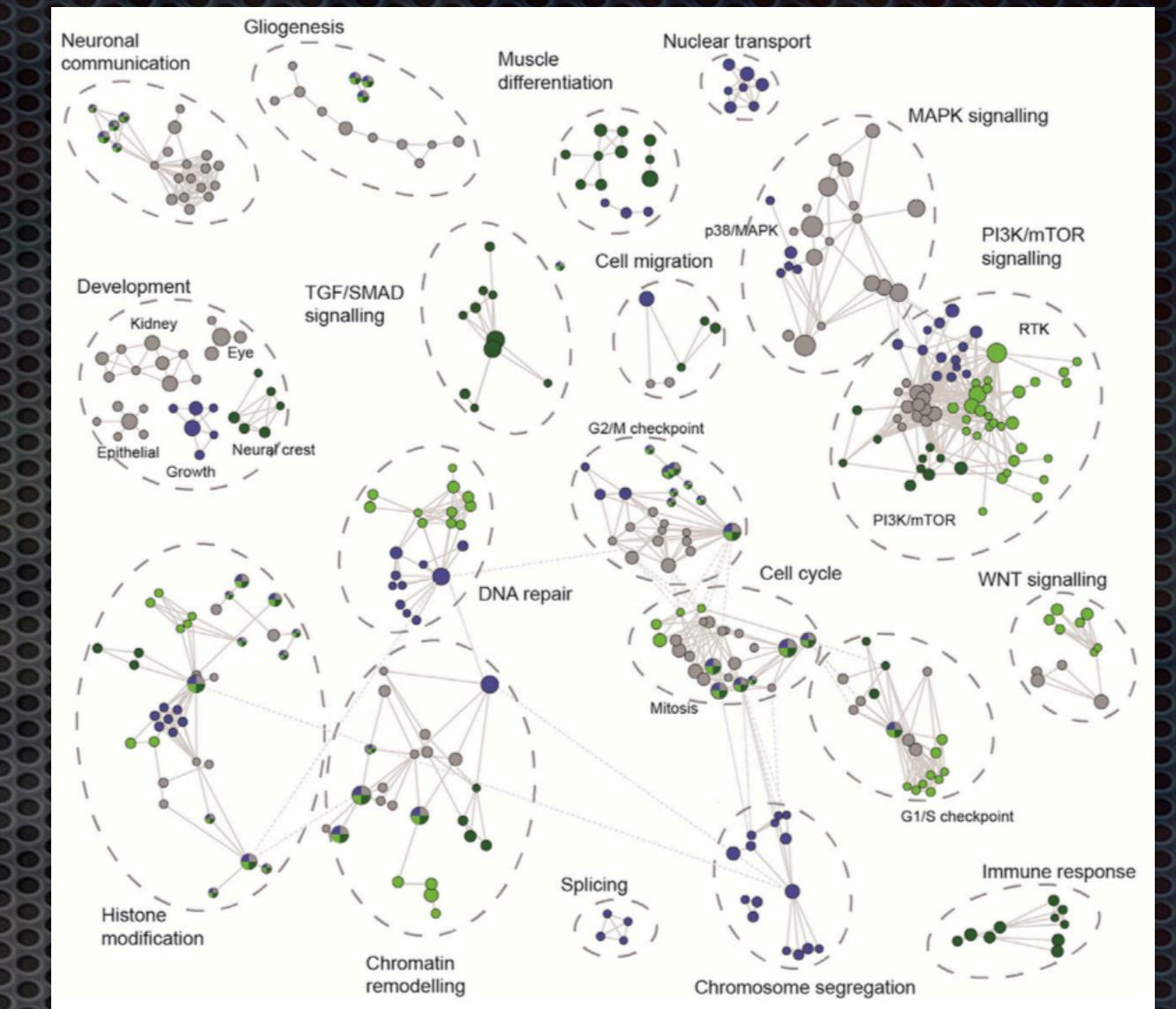
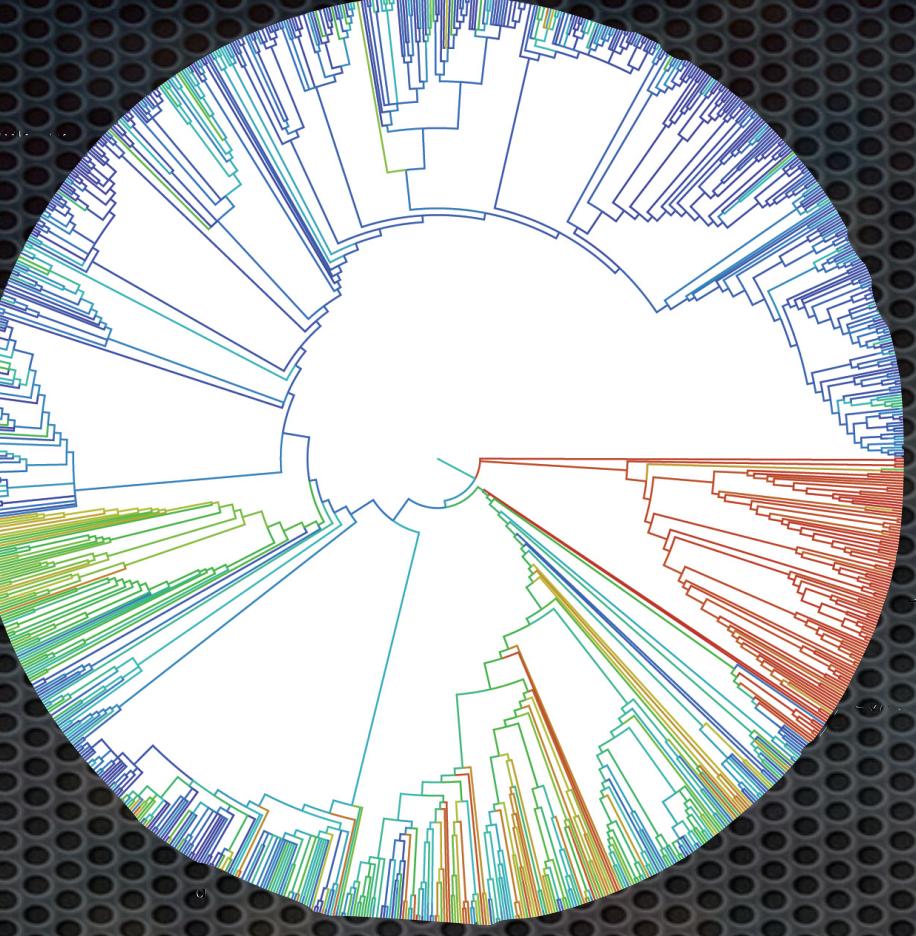


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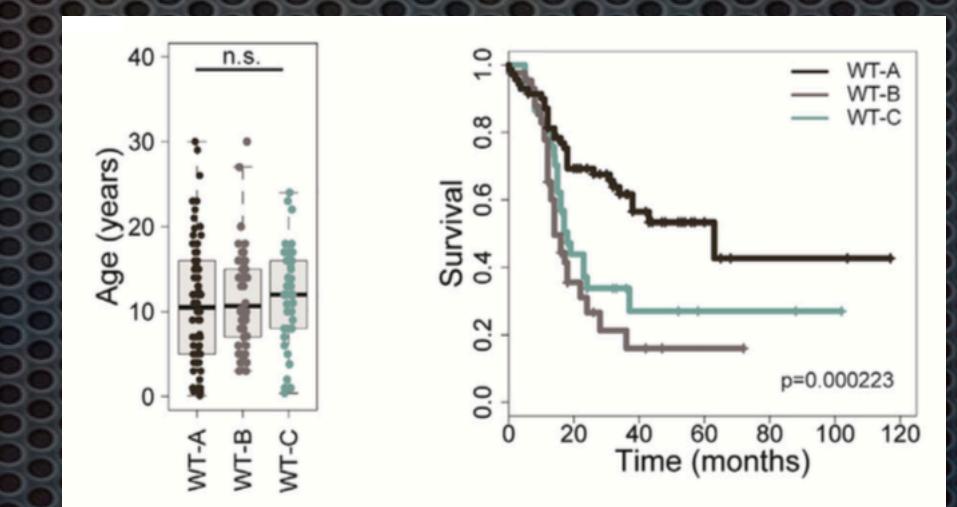
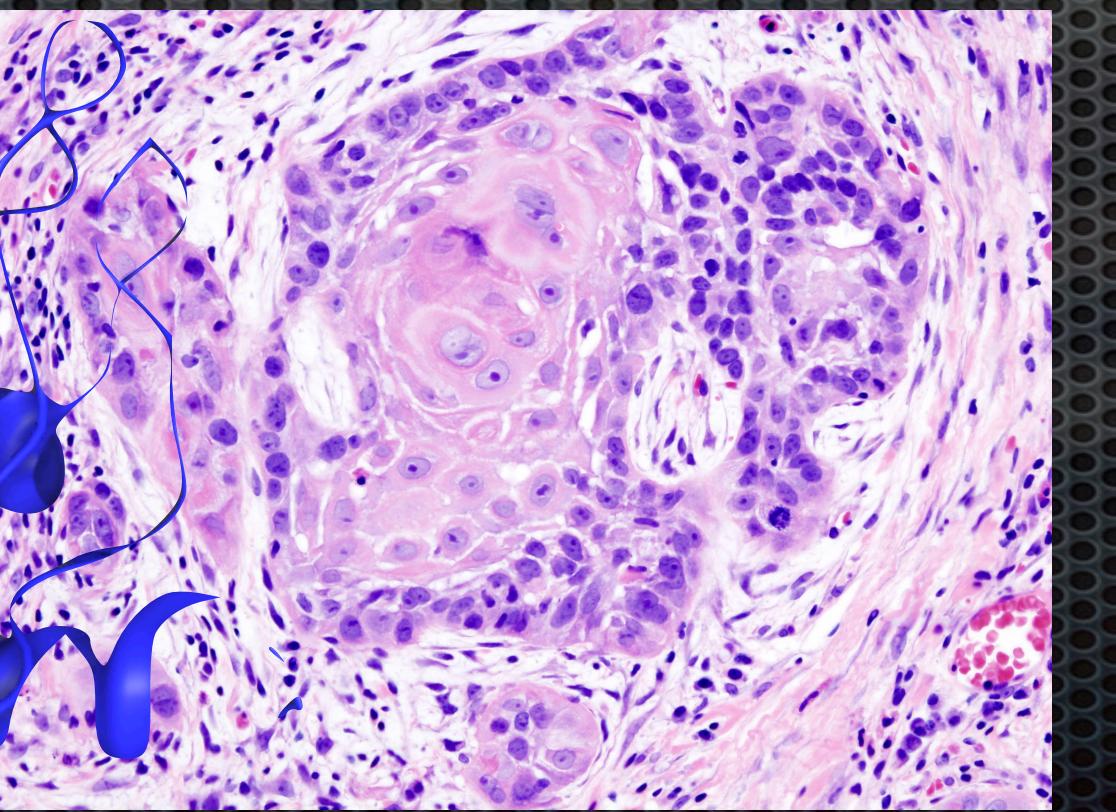
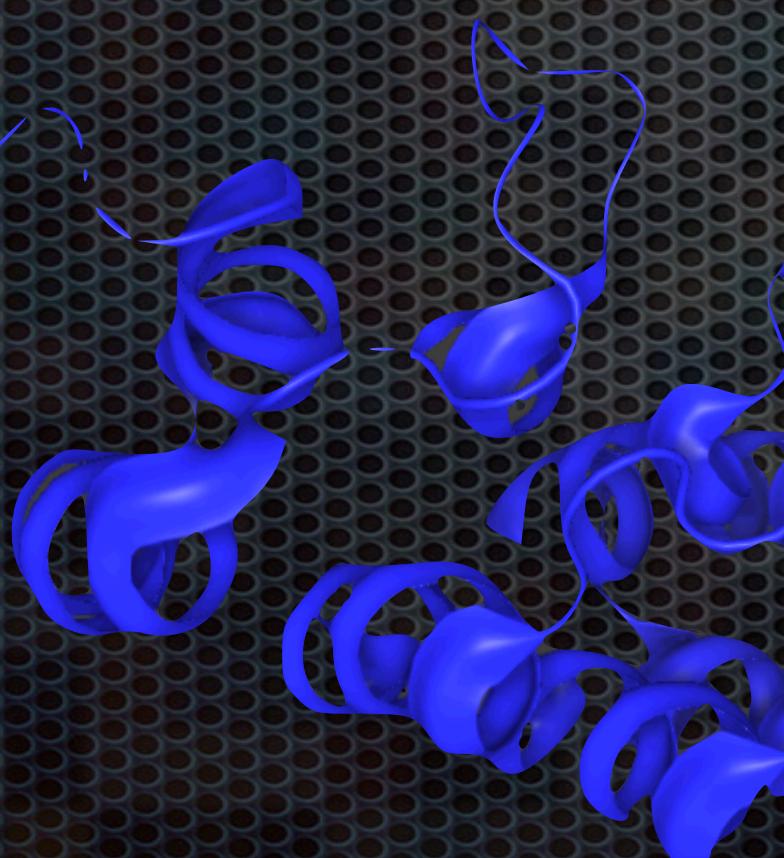
**b** : an interpretation of a practical situation or condition taken as the ground for action



# 42



- Bioinformatics is "the science that uses the instruments of informatics to analyze biological data in order to formulate hypotheses about **life.**" (Anna Tramontano)



Sources: nextprot | opentreeoflife | wikipedia | MacKay et al., Cancer Cell (2017) | original photos



# Who is a Bioinformatician?

## Bioinformatician

- strong biological knowledge
- provides hypothesis and/or dataset
- sufficient statistical and computational expertise to correctly use bioinformatics tools & develop workflows (scripting ...)
- expert user of informatics tools
- may get a Nobel

## Bioinformatician

- sufficient biological background
- provides statistical, analysis methods
- sufficient biologic or medical background to understand problems presented and identify pitfalls and hidden biases arising from data generation methods
- developer of informatics tools
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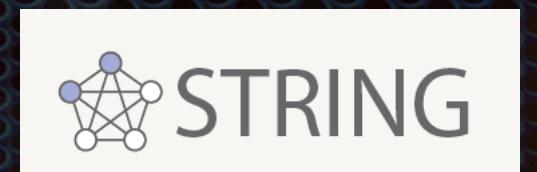
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# What do Bioinformaticians work on?

- protein **structure** definition
- DNA/RNA/protein **sequence** analysis
- **quantitative** analysis of "-omics" and cytometry data
- **functional** enrichment of target data (e.g. genes, sequence elements)
- **evolutionary** reconstruction and "tree of life" questions
- **image processing** for feature identification and spatial mapping
- **statistical** analysis of measurements and observations
- **protocols** for efficient storage, annotation and retrieval of biomedical data
- **information extraction** from prose & declarative knowledge resources (think publications & data tables)
- **clinical** bioinformatics - risk assessment and therapeutic target identification
- ...

# Bioinformatics: Data Categories & Databases

- biological data comes in **3 main categories**:
  - **sequence** data (nucleic acids, aminoacids)
  - **structural** data (DNA, RNA, proteins; intracellular organisation, tissues ...)
  - **functional** data (interactions in time and space)
- data storage & retrieval: importance of local and connected **databases**
  - **primary databases** - for deposition of original, raw data (e.g. SRA - sequence read archive; ENA - European Nucleotide Archive; GEO - NCBI Gene Expression Omnibus; EBI arrayExpress...)
  - **derived databases** - information resources providing agglomerated & **curated** data derived from primary sources (e.g. UniprotKB, nextProt, String, KEGG, arrayMap...)



SRA



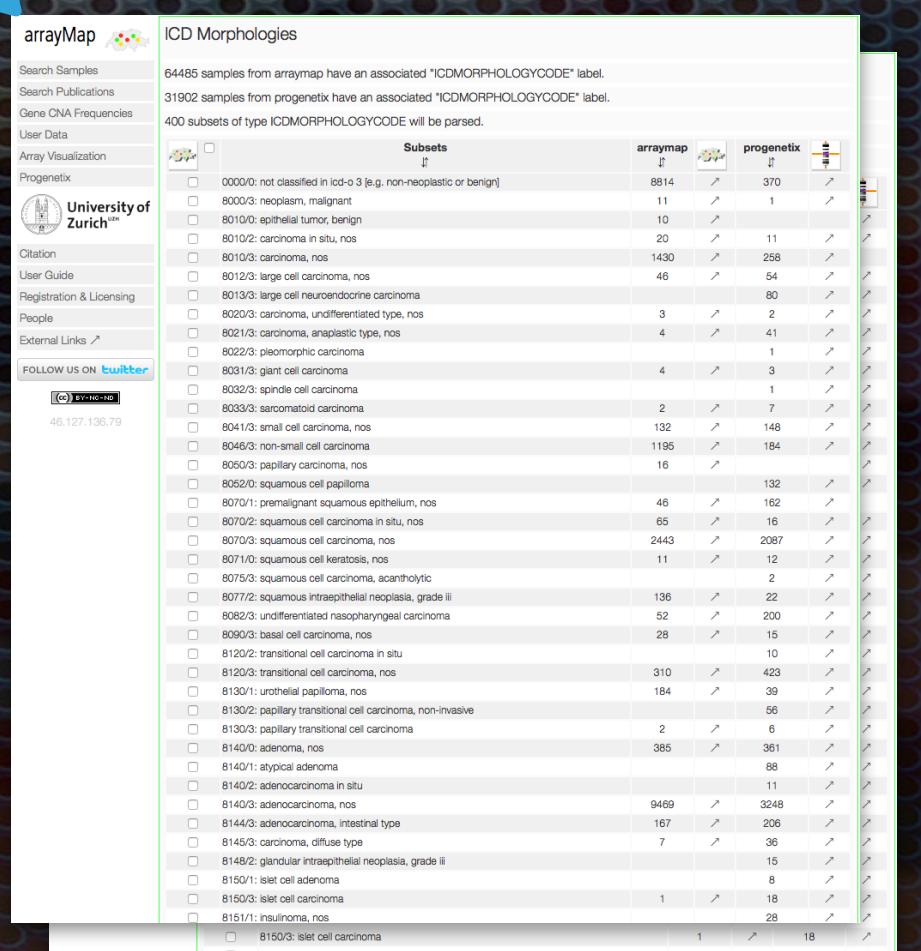
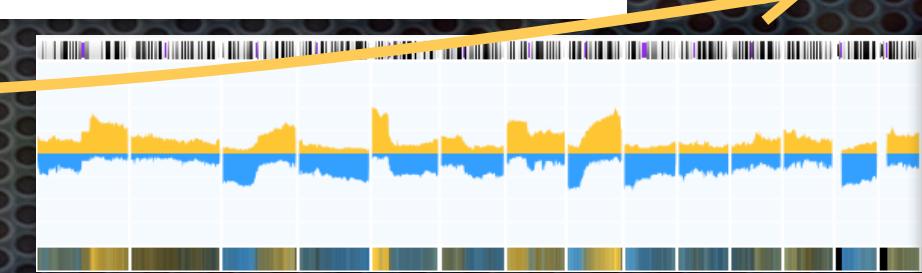
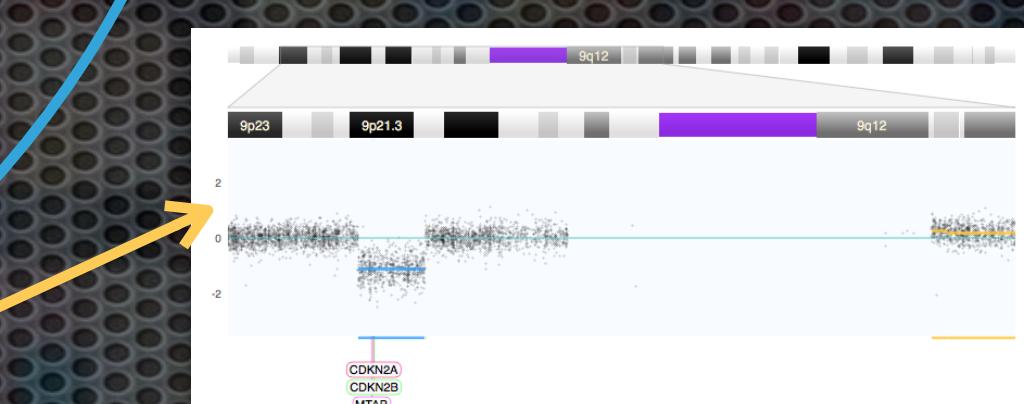
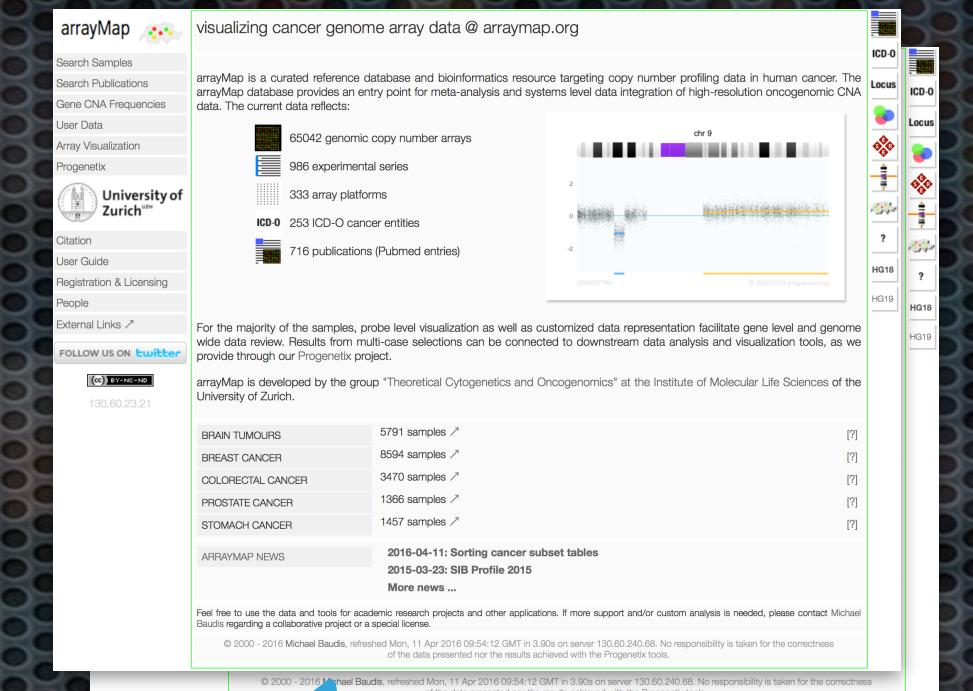
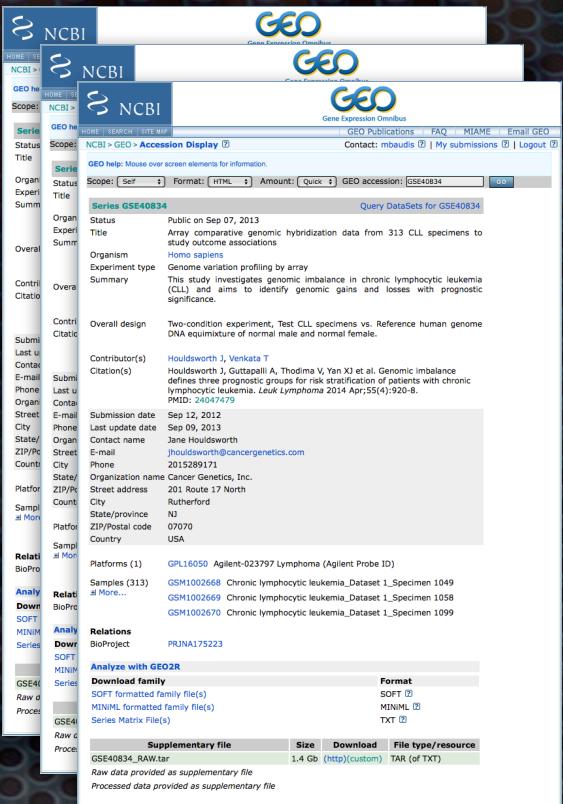
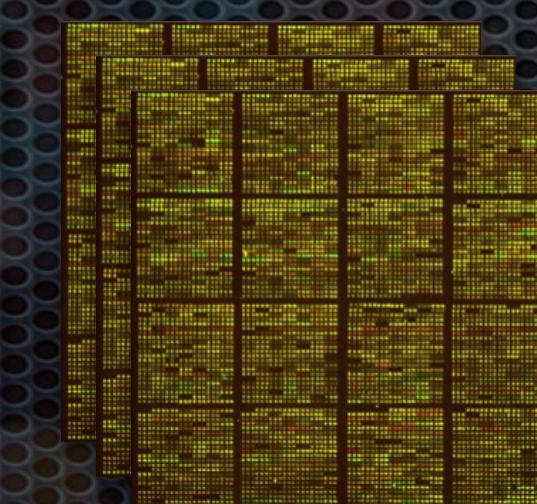
# ARRAYMAP DATA PIPELINE

# BIOCURATION

# BIOINFORMATICS

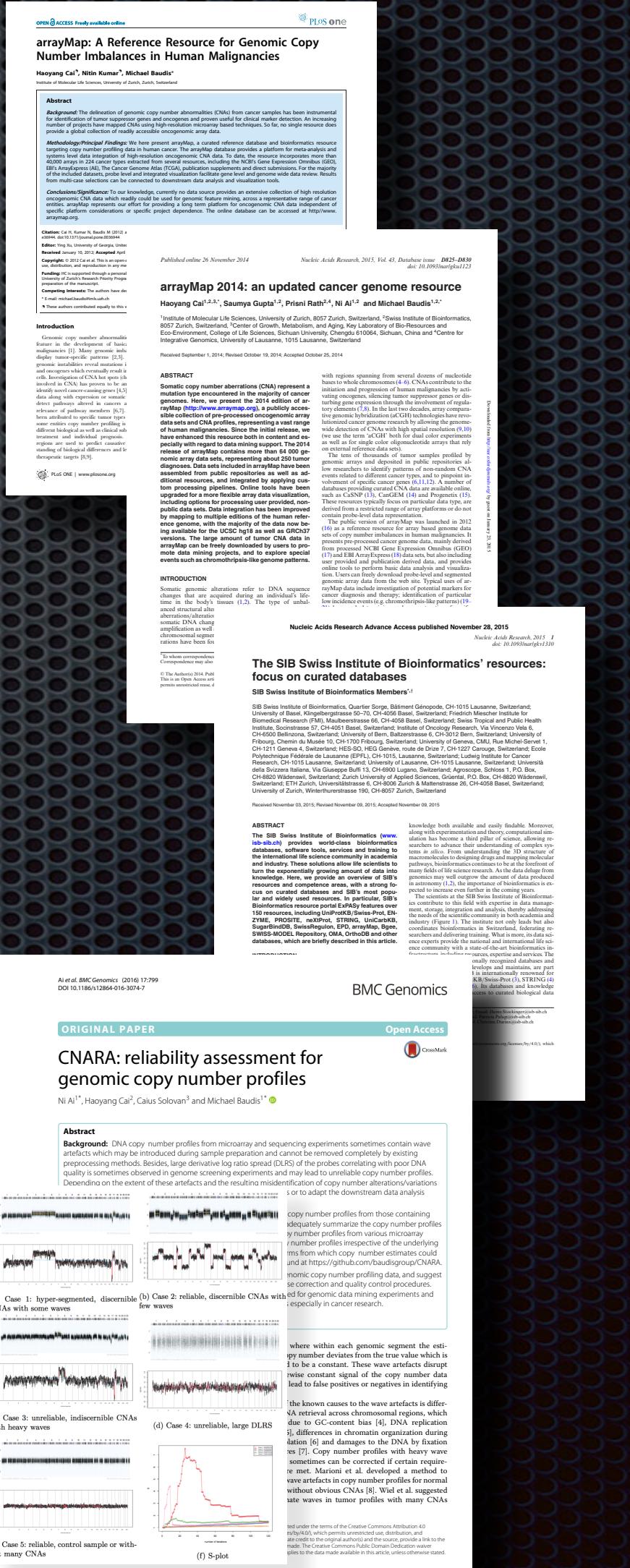
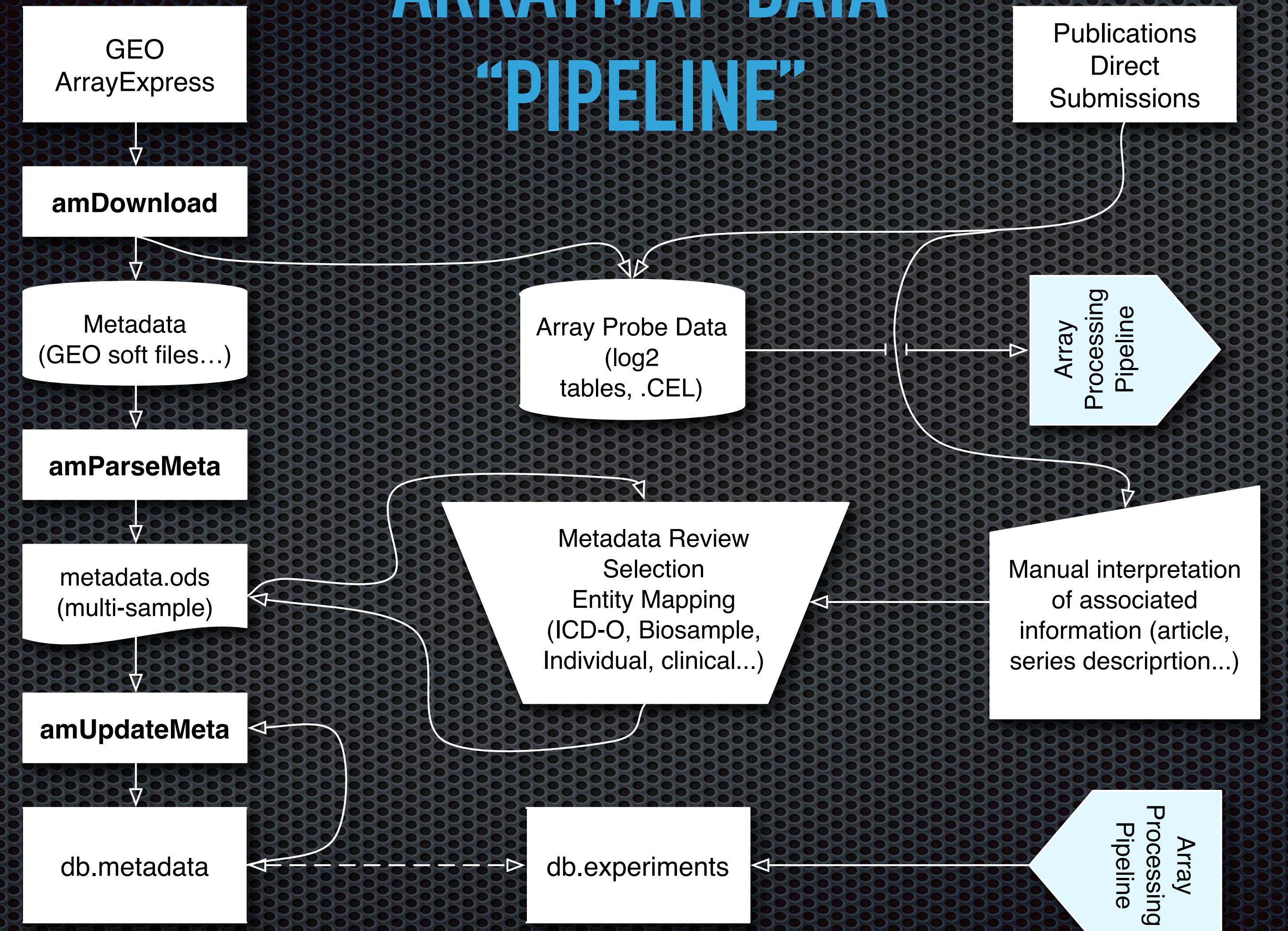


# arrayMap



# BIOINFORMATICS & CURATION

## ARRAYMAP DATA “PIPELINE”



# Bioinformatics: **File Formats**, Ontologies & APIs

- **text** or **binary** file formats, optimised for specific types of biological data
- examples from genomics:
  - **BAM** - compressed binary version of Sequence Alignment/ Map (SAM)
  - **BED** (Browser Extensible Data) -flexible way to define the data lines in an genome browser annotation tracks
  - **VCF** (Variant Call Format)

GSM1904006.CEL 69.1 MB  
Modified: 3 February 2016 at 17:46  
Add Tags...

General:

Kind: FLC animation  
Size: 69'078'052 bytes (69.1 MB on disk)  
Where: arrayRAID • arraymapln • affyRaw  
→ GSE73822 • GPL6801  
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chr7 127472363 127473530 Pos2 0 + 127472363 127473530 255,0,0  
chr7 127473530 127474697 Pos3 0 + 127473530 127474697 255,0,0  
chr7 127474697 127475864 Pos4 0 + 127474697 127475864 255,0,0  
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chr7 127480532 127481699 Neg4 0 - 127480532 127481699 0,0,255

BED file example

# Bioinformatics: File Formats, Ontologies & **APIs**

- databases can be accessed through **Application Programming Interfaces**
- *API : set of routines, protocols, and tools that specifies how software components interact, to exchange data and processing capabilities*
- web API example: implementing geographic maps, with parameters provided by the client (e.g. location coordinates, quantitative payload)
- web APIs provide a *machine readable* response to queries over HTTP
- bioinformatic applications frequently make use of web APIs for **data retrieval** or genome browser APIs for **data display**
- bioinformatics software libraries for API functionality are usually implemented in **Perl**, **Python** and/or **R**

# Bioinformatics: File Formats, Ontologies & **APIs**

[http://progenetix.org/api/?db=progenetix&api\\_out=samples&api\\_doctype=json&icdm\\_m=817&randno=20](http://progenetix.org/api/?db=progenetix&api_out=samples&api_doctype=json&icdm_m=817&randno=20)

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```

# Bioinformatics: File Formats, **Ontologies** & APIs

- ontologies in information sciences describe concrete and abstract **objects**, there precisely defined **hierarchies** and **relationships**
- ontologies in bioinformatics support the move from a descriptive towards an **analytical science** in describing biological data and relations among it

"The widest use of ontologies within biology is for conceptual annotation – a representation of stored knowledge more computationally amenable than natural language."\*

- Gene ontology (GO)
- NCI Neoplasm Core
- Uberon anatomical structures
- Experimental Factor Ontology (EFO)
- Disease Ontology (DO)



```
id: GO:0000118
name: histone deacetylase complex
namespace: cellular_component
def: "A protein complex that possesses histone deacetylase activity." [GOC:mah]
comment: Note that this term represents a location, not a function; the activity possessed by this complex is mentioned in the definition for the purpose of describing and distinguishing the complex. The function of this complex is represented by the molecular function term 'histone deacetylase activity'.
synonym: "HDAC complex" EXACT []
is_a: GO:0044451 ! nucleoplasm ;
is_a: GO:1902494 ! catalytic complex ;
```

- □ Neoplasm by Morphology
  - Epithelial Neoplasm [C3709](#)
  - Germ Cell Tumor [C3708](#)
  - Giant Cell Neoplasm [C7069](#)
  - Hematopoietic and Lymphoid Cell Neoplasm [C27134](#)
  - Melanocytic Neoplasm [C7058](#)
    - Benign Melanocytic Skin Nevus [C7571](#)
    - Dysplastic Nevus [C3694](#)
    - Melanoma [C3224](#)
      - Amelanotic Melanoma [C3802](#)
      - Cutaneous Melanoma [C3510](#)
      - Epithelioid Cell Melanoma [C4236](#)
      - Mixed Epithelioid and Spindle Cell Melanoma [C66756](#)
      - Non-Cutaneous Melanoma [C8711](#)
      - Spindle Cell Melanoma [C4237](#)
    - Meningothelial Cell Neoplasm [C6971](#)

But: What is **not bioinformatics**, though being "bio" and using computers?

- "I do not think all biological computing is bioinformatics, e.g. **mathematical modelling** is not bioinformatics, even when connected with biology-related problems. In my opinion, bioinformatics has to do with management and the subsequent use of biological information, particular genetic information." (Richard Durbin)
- **biologically-inspired computation** (neural networks etc.) - though their application may be part of bioinformatics
- **computational & systems biology**, where the emphasis is on **modelling** rather than on **data interpretation**

# Bioinformatics OR Computational / Systems Biology?

- Bioinformatics

Research, development, or application of computational tools and approaches to make the vast, diverse and complex life sciences data more understandable and useful

- Computational biology

The development and application of mathematical and computational approaches to address theoretical and experimental questions in biology

# BIO390: Introduction to Bioinformatics

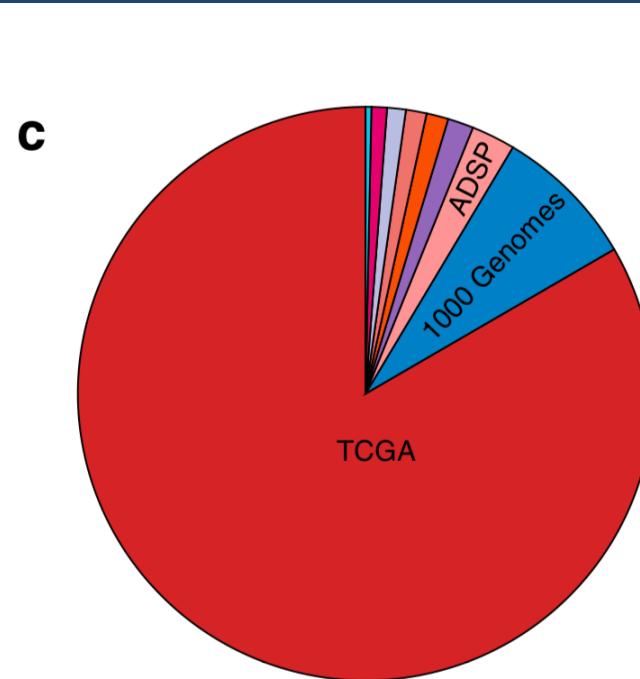
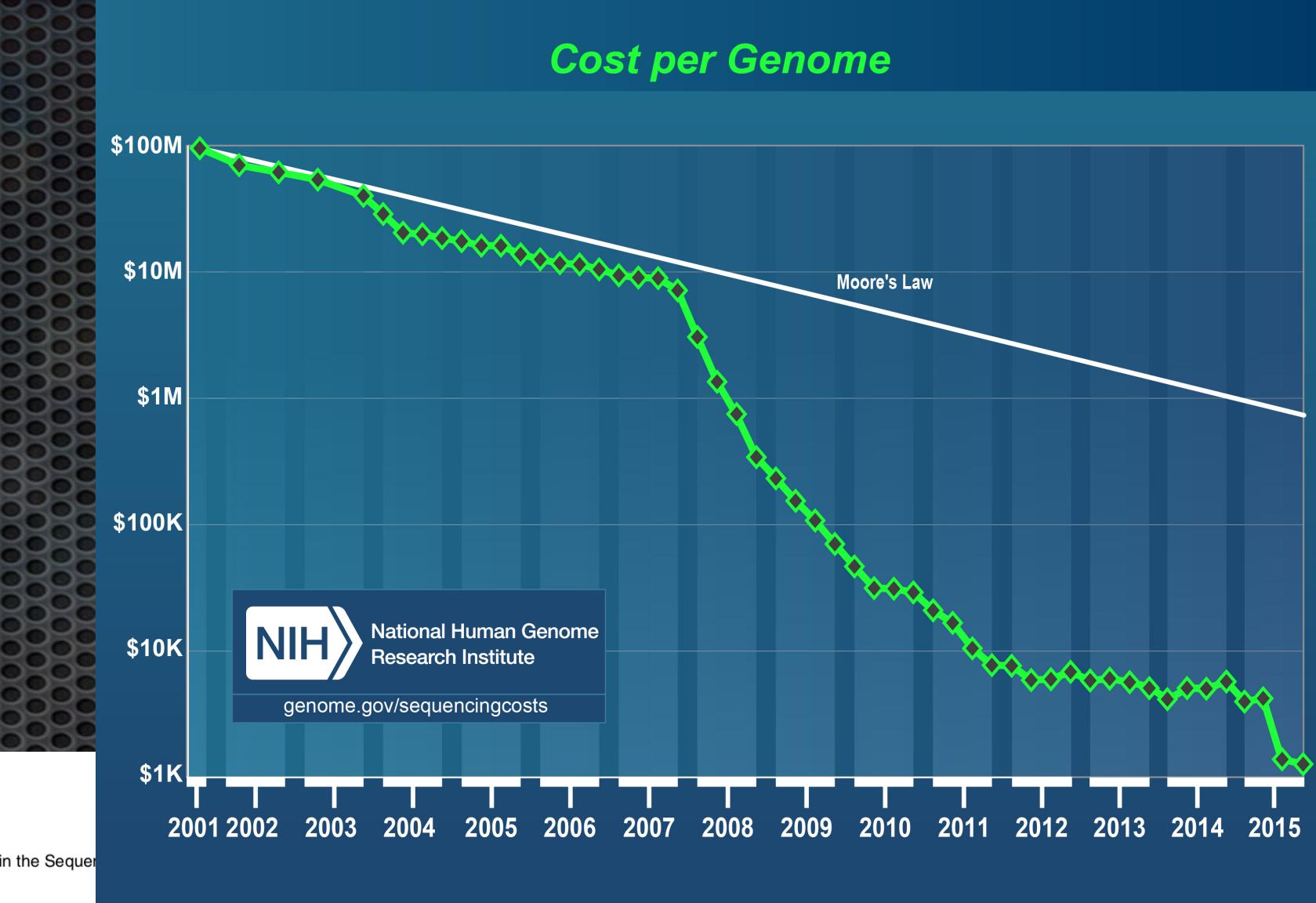
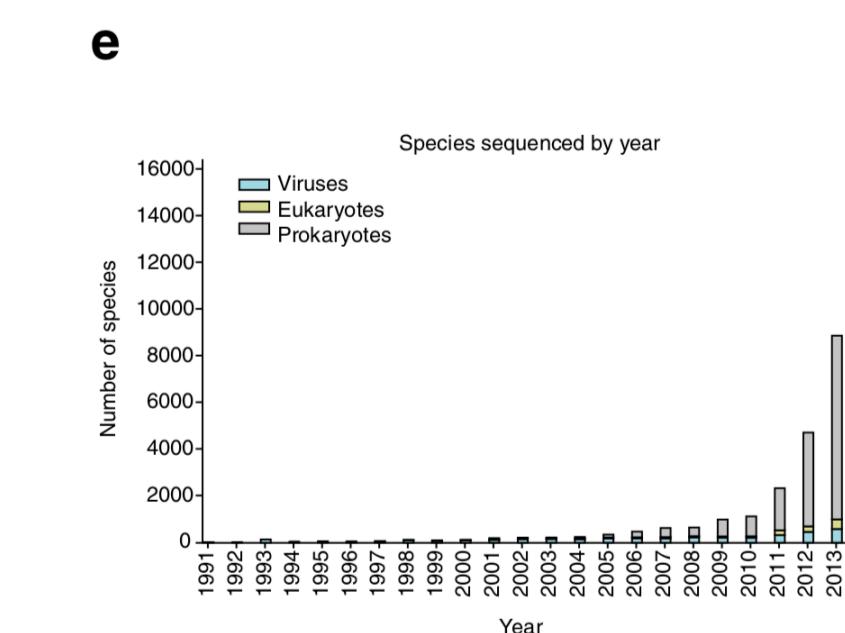
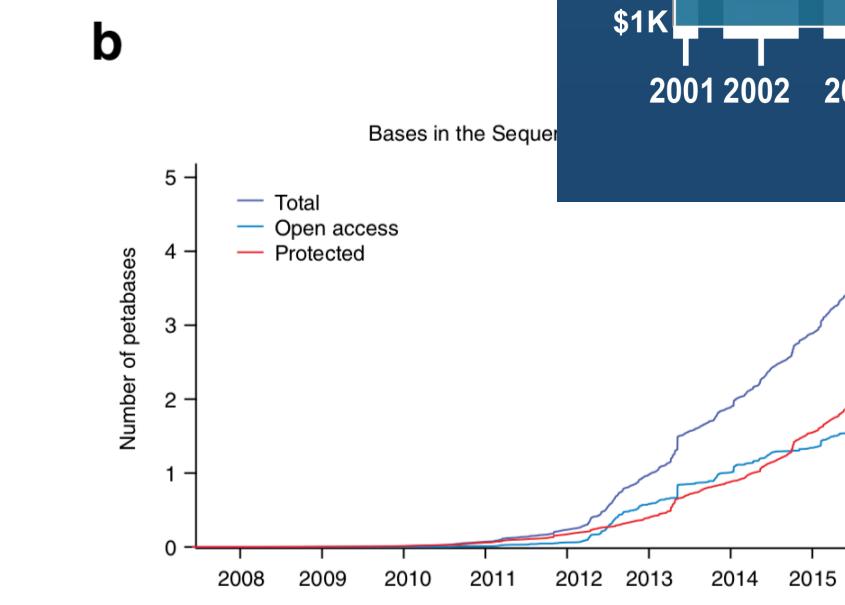
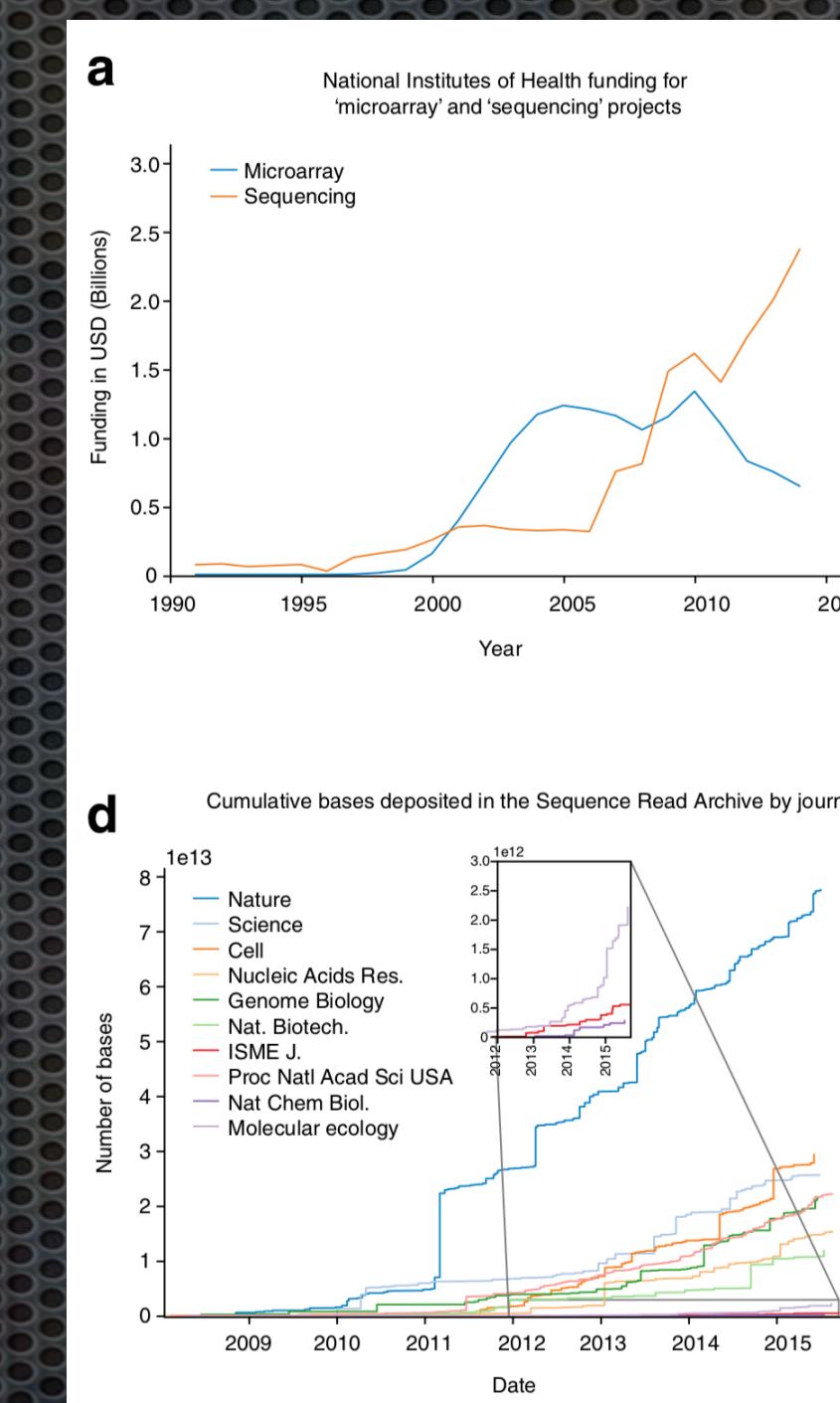
Lecture I: What is Bioinformatics? Examples from  
Sequencing & Human Genome Variation

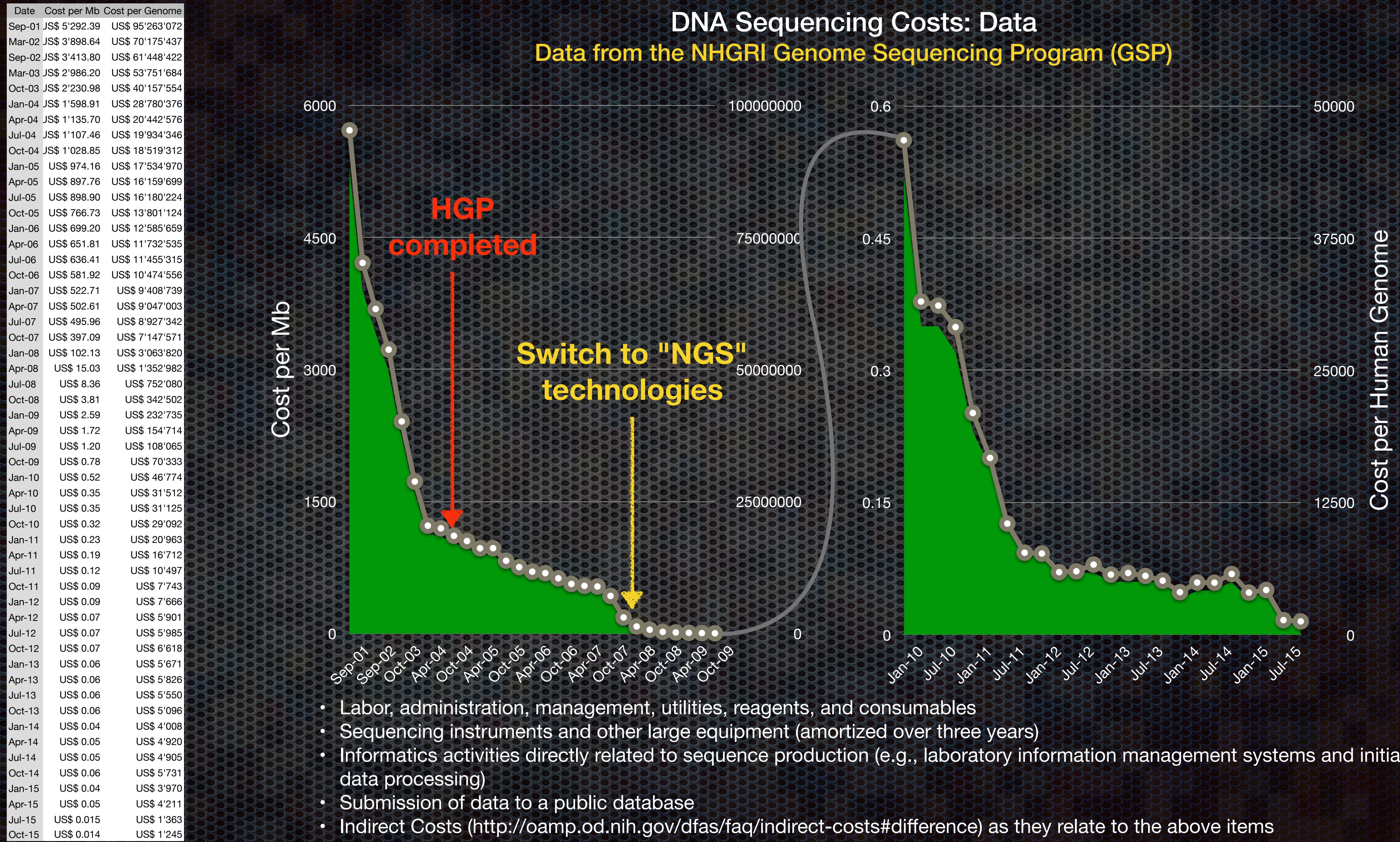


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# Sequencing everywhere, and everything

- dramatic increase in genome sequencing, both for human / disease related projects as well as basic biology (species identification, metagenome analyses, evolutionary modeling ...)

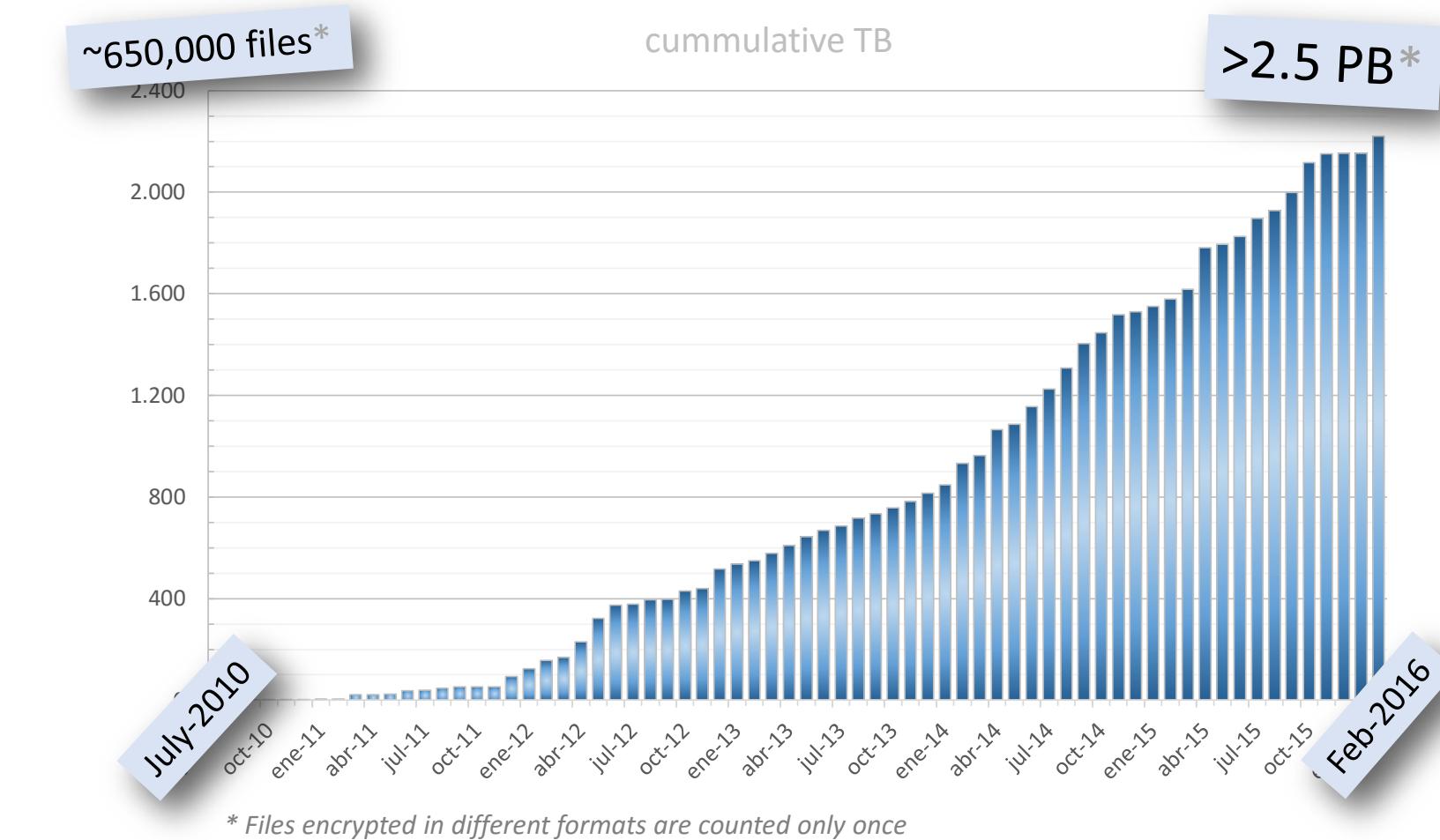




# Bioinformatics - Databases & Data Driven Science

- "post-genomic era": shift in biology from being descriptive/qualitative to being analytical/quantitative ("data driven science")
- typical examples here are genomic screening assays to map genome variants, and statistically associate them with phenotypes/traits (e.g. Genome Wide Association Studies - GWAS)

The EGA contains a growing amount of data



6

population based and cancer research studies produce a rapidly increasing amount of genome sequence data - growth of the European Genome - Phenome Archive (EGA)

The trouble with human genome variation



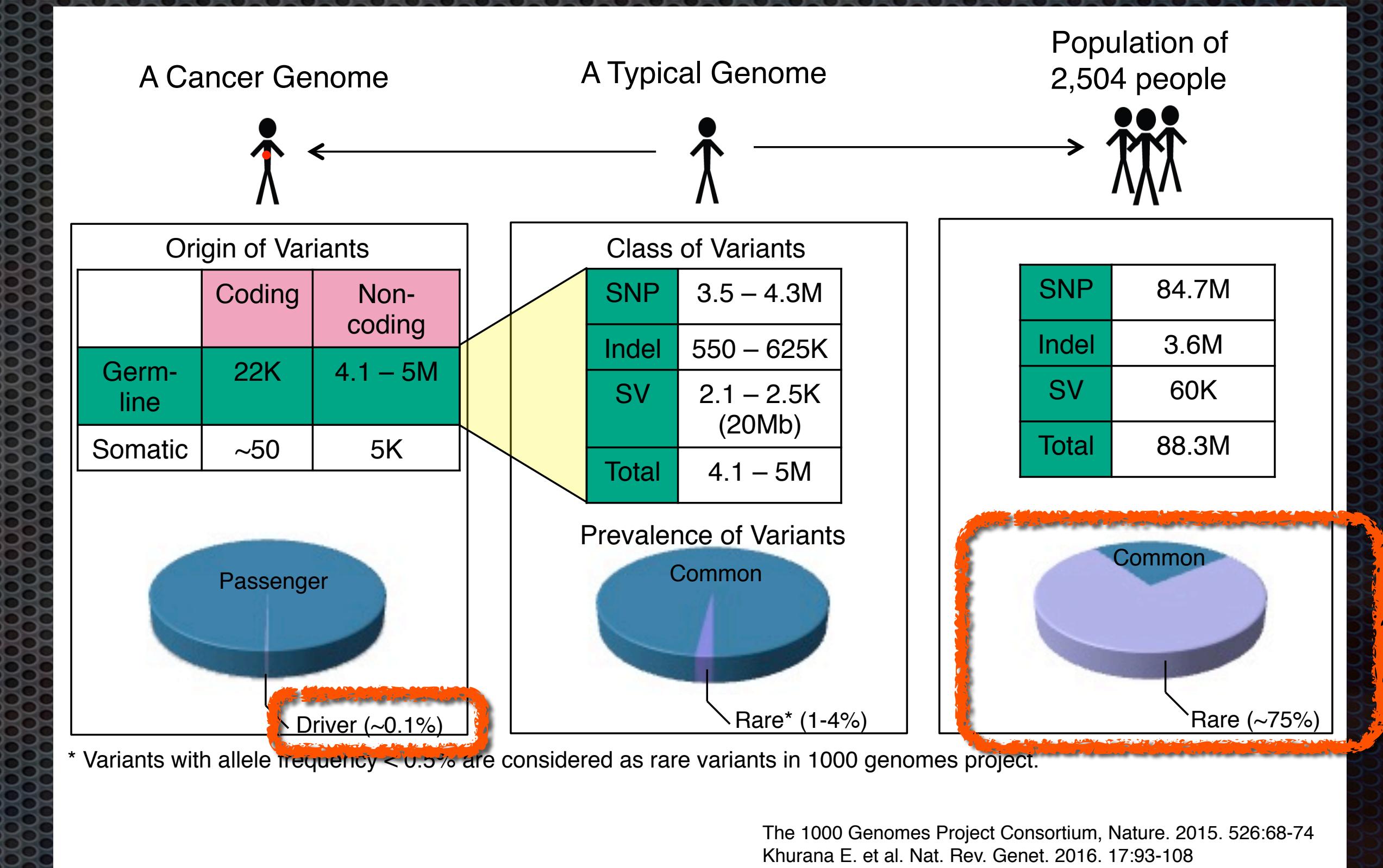
# Conclusions from the analysis of variation in the human genome

---

- 1. Humans are all very similar to each other
  - Two humans will show about 99.9% sequence identity with each other. In other words, only about 1 in 1'000 bp is different between two individuals.
  - Humans show about 98% sequence identity to chimps. So two humans are still much more similar to each other than either is to the monkey.
- 2. Humans are very different from each other
  - Two typical humans will likely have over 1'000'000 independent sequence differences in their genomes.

# Finding Somatic Mutations In Cancer: Many Needles in a Large Haystack

- a typical human genome (~3 billion base pairs) has ~5 million variants
- most of them are "**rare**"; i.e. can only be identified as recurring when sequencing thousands of people
- cancer cells accumulate additional variants, only **few** of which ("**drivers**") are relevant for the disease



The 1000 Genomes Project Consortium, Nature. 2015. 526:68-74  
Khurana E. et al. Nat. Rev. Genet. 2016. 17:93-108

Graphic adapted from Mark Gerstein ([GersteinLab.org](http://GersteinLab.org); @markgerstein)

# What is a PB, for human genomes? It depends.

- 2 bits per base are sufficient to encode TCGA
  - using 00, 01, 10, 11
  - [TCGA]{3'000'000'000}
  - $2 * 3 * 10^9 b = 6,000,000,000 b$
  - perfect genome (no overhead): ~715 MB
  - 1PB => ~1'400'000 genomes
- according to Swiss online store (Sep 2019) ~35'000CHF (65x16TB disks)
- this is less than a PhD position per year in Switzerland ...
- (real costs are 2x that, + duplication, facilities, service ... => ~500'000CHF)
- **However: A single 30x BAM file => 100GB**
- Still: 500'000CHF => 1PB => 10'000 genomes => 50CHF/genome (BAM format)



# Reference Resources for Human Genome Variants

- NCBI:dbSNP

- single nucleotide polymorphisms (SNPs) and multiple small-scale variations
  - including insertions/deletions, microsatellites, non-polymorphic variants

- NCBI:dbVAR

- genomic structural variation
  - insertions, deletions, duplications, inversions, multinucleotide substitutions, mobile element insertions, translocations, complex chromosomal rearrangements

- NCBI:ClinVar

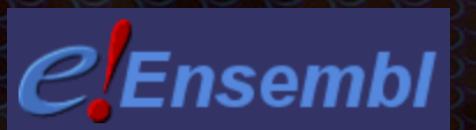
- aggregates information about genomic variation and its relationship to human health

- EMBL-EBI:EVA

- open-access database of all types of genetic variation data from all species

- Ensembl

- portal for many things genomic...



# Beacon Project

An open web service that tests the willingness of international sites to share genetic data.



Beacon Network

Search Beacons

Search all beacons for allele

GRCh37 ▾ 10:118969015 C / CT Search

Response All None  
 Found 16  
 Not Found 27  
 Not Applicable 22

Organization All None  
 AMPLab, UC Berkeley  
 BGI  
 BioReference Laborato...  
 Brazilian Initiative on ...  
 BRCA Exchange  
 Broad Institute  
 Centre for Genomic R...  
 Centro Nacional de A...  
 Curoverse  
 EMBL European Bio...  
 Global Alliance for G...  
 Google  
 Institute for Systems ...  
 Instituto Nacional de ...

Response	All	None
<input checked="" type="checkbox"/> Found	16	
<input type="checkbox"/> Not Found	27	
<input type="checkbox"/> Not Applicable	22	

BioReference BioReference Hosted by BioReference Laboratories Found

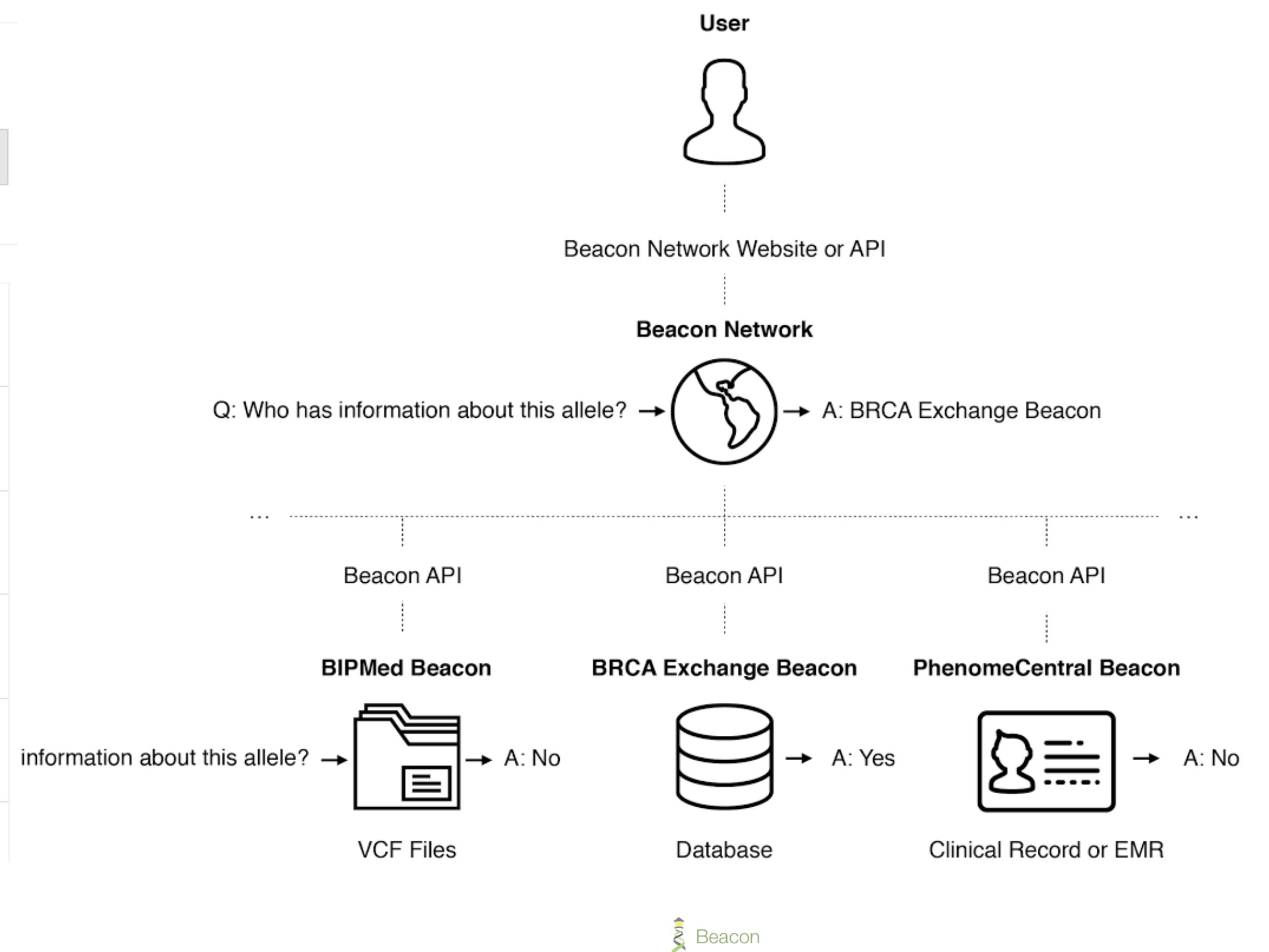
Catalogue of Somatic Mutations in Cancer Catalogue of Somatic Mutations in Cancer Hosted by Wellcome Trust Sanger Institute Found

Cell Lines Cell Lines Hosted by Wellcome Trust Sanger Institute Found

Conglomerate Conglomerate Hosted by Global Alliance for Genomics and Health Found

COSMIC COSMIC Hosted by Wellcome Trust Sanger Institute Found

dbGaP: Combined GRU Catalog and NHLBI Exome Seq... dbGaP: Combined GRU Catalog and NHLBI Exome Seq... Found



Date	Tag	Title
2018-01-24	v0.4.0	Beacon
2016-05-31	v0.3.0	Beacon

# Beacon+ Concept

- Implementation of cancer beacon prototype, backed by arrayMap and DIPG data set  
(MacKay *et al.*, Cancer Cell 2017, in print)
- structural variations (DUP, DEL) in addition to SNV
- diagnosis queries using ontology codes (NCIT, ICD-O)
- quantitative responses
- current version uses **GA4GH schema compatible** database

Beacon+

This forward looking Beacon interface implements additional, planned features beyond the current GA4GH specifications. [Info](#)

Query

Dataset: DIPG (CNV + selected SNV)

Reference name\*: 17

Genome Assembly\*: GRCh36 / hg18

Variant type\*: SNV / indel

Position\*: 7577121

Ref. Base(s)\*: G

Alt. Base(s)\*: A

Bio-ontology: pgx:icdom:9380\_3

[Beacon Query](#)

Response

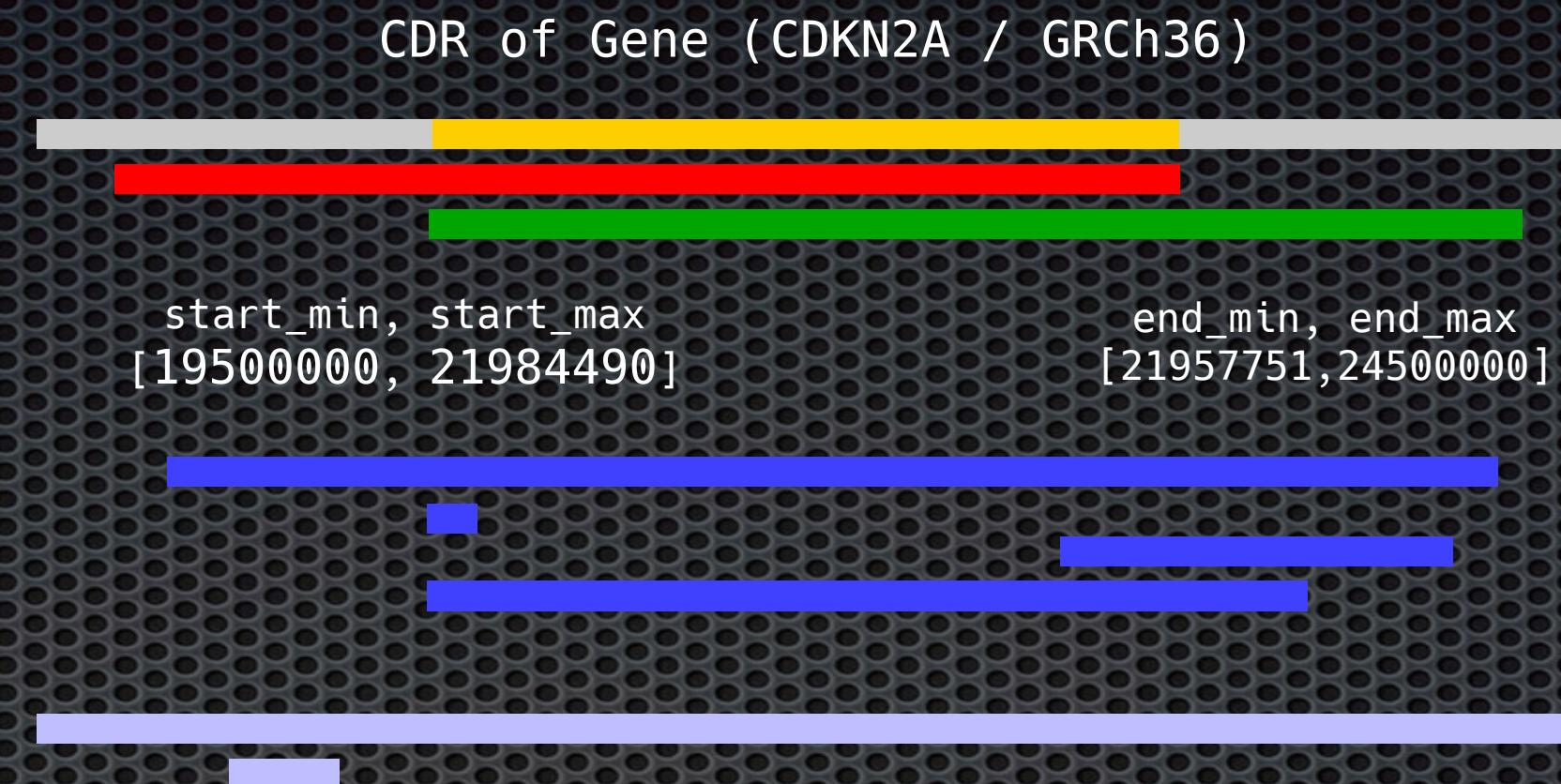
Dataset	Chro.	Assembly	Var. Type	Start Min	Start Max	End Min	End Max	Pos.	Ref.	Alt.	Bio Query	Call Count	Samples	f	Query
arraymap	9	GRCh36	DEL	19000000	21984490	21900000	25000000				pgx:icdom:8140_3	3781	403	0.0065	<a href="#">show JSON</a>
dipg	17	GRCh36	SNV			7577121		G	A	pgx:icdom:9380_3	21	20	0.0187	<a href="#">show JSON</a>	

arrayMap  University of Zurich UZH  This Beacon implementation is developed by the Computational Oncogenomics Group at the [University of Zurich](#), with support from the [SIB Technology group](#) and [ELIXIR](#).   

```

"allele_request" : {
  "$and" : [
    { "reference_name" : "9" },
    { "variant_type" : "DEL" },
    { "start" : { "$gte" : 19500000 } },
    { "start" : { "$lte" : 21984490 } },
    { "end" : { "$gte" : 21957751 } },
    { "end" : { "$lte" : 24500000 } }
  ]
},
"api_version" : "0.4",
"beacon_id" : "org.progenetix:progenetix-beacon",
"exists" : true,
"info" : {
  "query_string" :
"dataset_id=arraymap&variants.reference_name=chr9&assembly_id=GRCh36&variants.variant_type=DEL&variants.start_max=19000000&variants.start_min=21984490&variants.end_min=21900000&variants.end_max=25000000&biosamples.bio_characteristics.ontology_terms.term_id=pgx:icdom:9440_3",
  "version" : "Beacon+ implementation based on a development branch of the beacon-team project: https://github.com/ga4gh/beacon-team/pull/94",
  "url" : "http://progenetix.org/beacon/info/",
  "dataset_allele_responses" : [
    {
      "dataset_id" : "arraymap",
      "error" : null,
      "exists" : true,
      "external_url" : "http://arraymap.org",
      "sample_count" : 584,
      "call_count" : 3781,
      "variant_count" : 3244,
      "frequency" : 0.0094,
      "info" : {
        "description" : "The query was against database \\"arraymap_ga4gh\\", variant collection \\"variants_cnv_grch36\\". 3781 / 59428 matched callsets for 3602919 variants. Out of 62105 biosamples in the database, 2047 matched the biosample query; of those, 584 had the variant."
      },
      "ontology_ids" : [
        "ncit:C3058",
        "pgx:icdom:9440_3",
        "pgx:icdot:C71.9",
        "pgx:icdot:C71.0"
      ]
    }
  ]
}

```



Match using query ranges “at least one base in interval affected”

Example “focal” matches

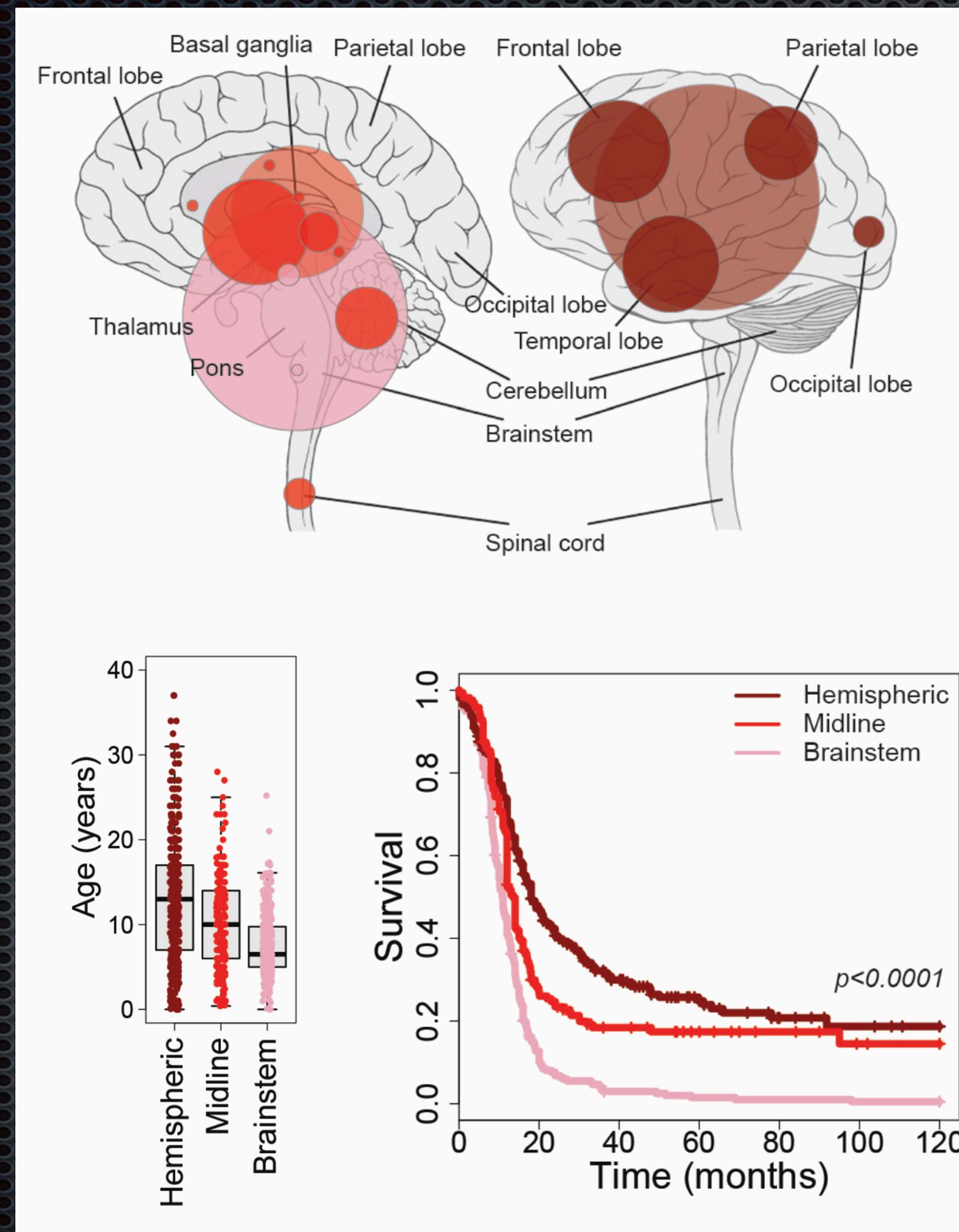
Mismatches

- Beacon+ **range queries** allow the definition of a genome region of interest, containing a specified variant or potentially other position related feature
- “fuzzy” matching of region ends essential for inexact features
- quantitative reporting



Mackay A, Jones C, Baudis M and many, many others:  
Integrated molecular meta-analysis of 1000 paediatric  
high grade and diffuse intrinsic pontine glioma (2017,  
Cancer Cell, in press)

## Implementing real-world datasets for federated access using GA4GH schema specifications: pHGG



```
{  
  "_id" : ObjectId("591eb73709d374442fcc6b2a"),  
  "individual_id" : "DIPG_IND_0809",  
  "id" : "DIPG_BS_0809",  
  "name" : "pHGG_META_0809",  
  "description" : "glioma, paediatric, high grade",  
  "individual_age_at_collection" : {  
    "age_class" : {  
      "term" : "Adult onset",  
      "term_id" : "HP:0003581"  
    },  
    "age" : "P17Y0M"  
  },  
  "bio_characteristics" : [  
    {  
      "ontology_terms" : [  
        {  
          "term_label" : "Glioma",  
          "term_id" : "ncit:C3059"  
        },  
        {  
          "term_label" : "Brain NOS",  
          "term_id" : "pgx:icdot:C71.9"  
        }  
      ],  
      "description" : "Juvenile high grade glioma",  
    },  
    "external_identifiers" : [  
      {  
        "database" : "Pubmed",  
        "identifier" : "25752754",  
        "relation" : "reported_in"  
      }  
    ],  
    "attributes" : {  
      "grade" : { "values" : [ { "string_value" : "4" } ] },  
      "histone" : { "values" : [ { "string_value" : "wt" } ] },  
    }  
  }
```

# GA4GH API promotes sharing

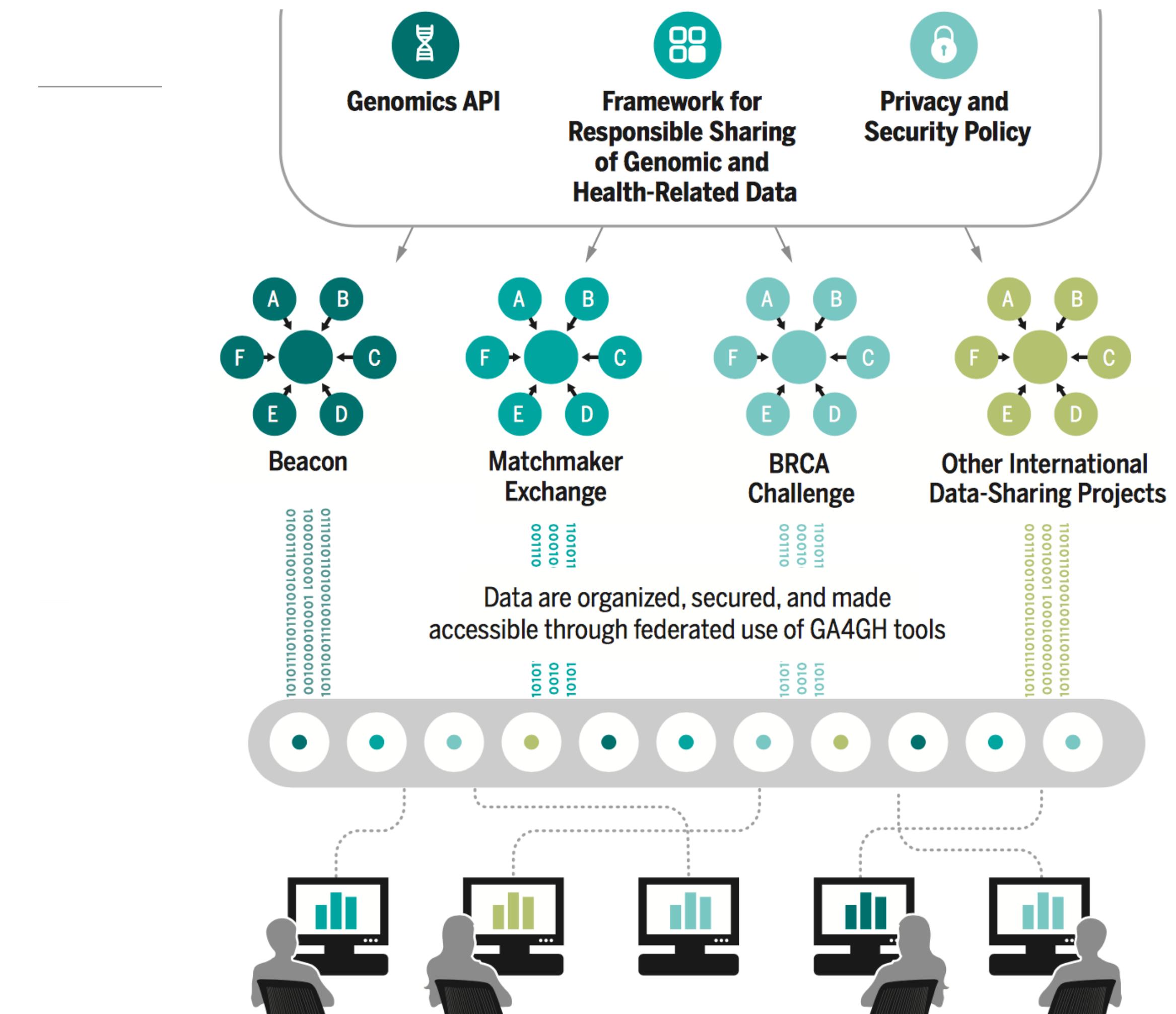
**A federated data ecosystem.** To share genomic data globally, this approach furthers medical research without requiring compatible data sets or compromising patient identity.



GENOMICS

# *A federated ecosystem for sharing genomic, clinical data*

Silos of genome data collection are being transformed into seamlessly connected, independent systems



# BIO390: Course Schedule

- 2019-09-17: Michael Baudis - What is Bioinformatics? Introduction and Resources
- **2019-09-24: Christian von Mering - Sequence Bioinformatics**
- 2019-10-01: Shinichi Sunagawa (ETHZ) - Metagenomics
- 2019-10-08: Mark Robinson - Statistical Bioinformatics
- 2019-10-15: Izaskun Mallona - Regulatory Genomics and Epigenomics
- 2019-10-22: Abdullah Kahraman (USZ) - Molecular Interaction Networks
- 2019-10-29: Katja Baerenfaller (SIAF) - Proteomics
- 2019-11-05: Amedeo Caflisch - Molecular Dynamics
- 2019-11-12: Elif Ozkirimli - Protein Structure and Interactions
- 2019-11-19: Christophe Dessimoz (UniL) - Sequence evolution and phylogenetics
- 2019-11-26: Valérie Barbie (SIB) - Clinical Bioinformatics
- 2019-12-03: Andreas Wagner - Biological Networks
- 2019-12-10: Alex Handler Wagner (WUSTL) & Michael Baudis - Human Genome Variation Resources
- 2019-12-17: Exam (Multiple Choice)



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Switzerland



Global Alliance  
for Genomics & Health



[arraymap.org](http://arraymap.org)

[progenetix.org](http://progenetix.org)

[info.baudisgroup.org](mailto:info.baudisgroup.org)

[sib.swiss/baudis-michael](http://sib.swiss/baudis-michael)

[imls.uzh.ch/en/research/baudis](http://imls.uzh.ch/en/research/baudis)