Applied Comparative Genomics

Michael Schatz

August 25, 2025

Lecture 1: Course Overview

Welcome!

The primary goal of the course is for students to be grounded in theory and leave the course empowered to conduct independent genomic analyses.

- We will study the leading computational and quantitative approaches for comparing and analyzing genomes starting from raw sequencing data.
- The course will focus on human genomics and human medical applications, but the techniques will be broadly applicable across the tree of life.
- The topics will include (pan)-genome assembly & comparative genomics, variant identification & analysis, gene expression & regulation, personal genome analysis, and cancer genomics.

Course Webpage: https://github.com/schatzlab/appliedgenomics2025
Course Discussions: https://piazza.com/class/meogfdbmu7x7hf

Class Hours: Mon + Wed @ 3:00p – 4:15p, Hodson 316

Schatz Office Hours: TBD and by appointment
TA Office Hours: TBD and by appointment
Please try Piazza first!

TA: Mahler Revsine

Prerequisites and Resources

Prerequisites

- No formal course requirements
- Access to an Apple or Linux Machine, or Install VirtualBox
- Familiarity with the Unix command line for exercises
  - bash, ls, grep, sed, + install published genomics tools
- Familiarity with a major programming language for project
  - C/C++, Java, R, Perl, Python

Primary Texts

- None! We will be studying primary research papers

Other Resources:

- Google, SEQanswers, Biostars, StackOverflow
- Applied Computational Genomics Course at UU
  - https://github.com/quinlan-lab/applied-computational-genomics
- Ben Langmead's teaching materials:
  - https://www.langmead-lab.org/teaching.html
- See course webpage

Grading Policies

Assessments:

- 5 Assignments: 25% Due at 11:59pm a week later
  Practice using the tools and methods we are discussing
- 2 Exams: 40% In Class (Oct 8 & Nov 12)
  Assess your performance, focusing on the concepts
- 1 Class Project: 35% Written & Oral presentations
  Project Proposal 2% | Prelim report 3% |
  In class presentation 10 % | Written report 10 % | Oral Defense 10%
  Significant project developing a novel analysis/method
- In-class Participation: Not graded, but there to help you!

Policies:

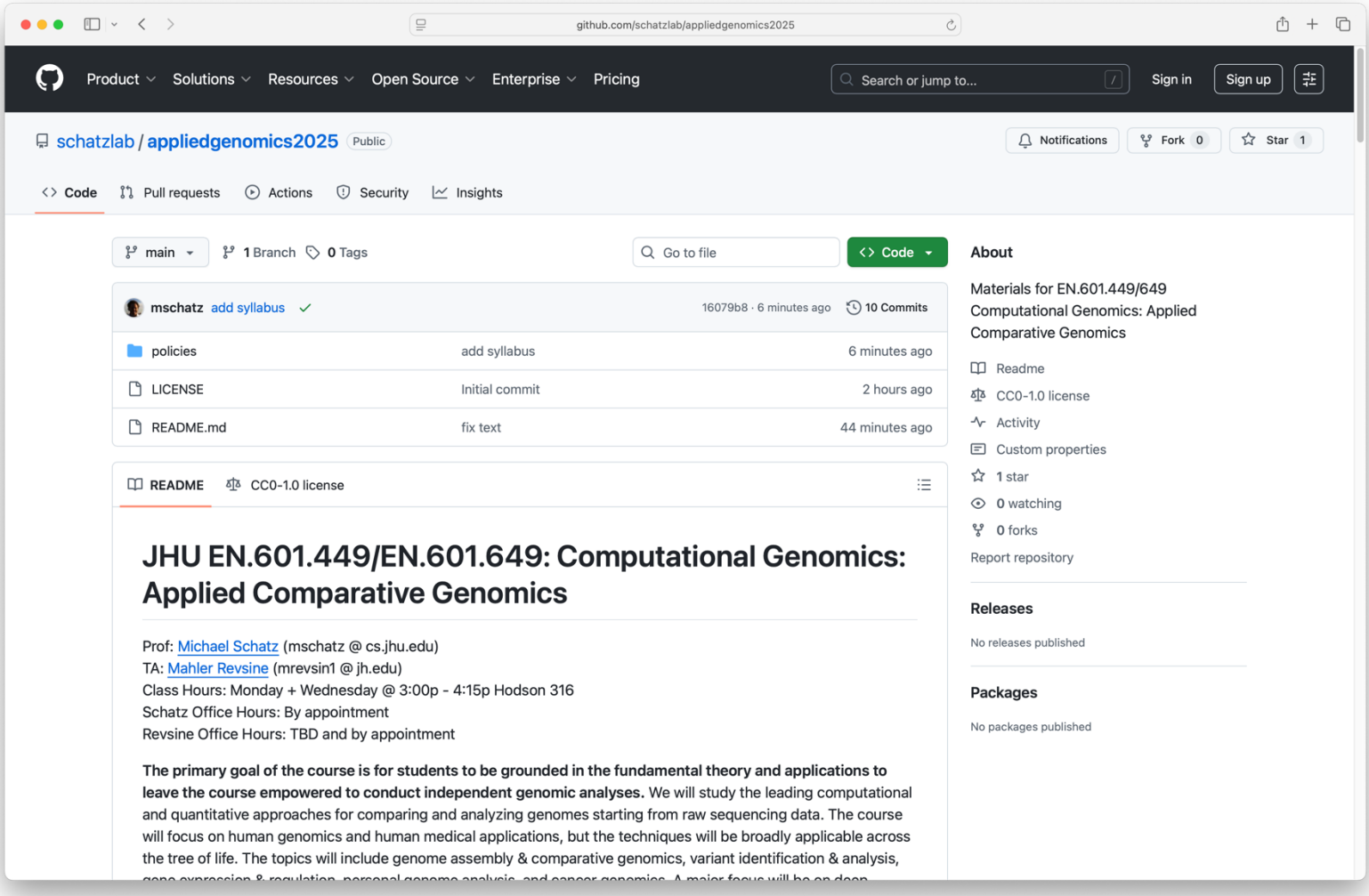
- Scores assigned relative to the highest points awarded
- Automated testing and grading of assignments
- ***Late Days:***
  - A total of 96 hours (24 x 4) can be used to extend the deadline for assignments, but not the class project, without any penalty; after that time assignments will not be accepted

On ChatGPT

whats a good policy on the use of chatgpt for a university class on genomics and data science? the instructor is generally favorable but also wants students to learn and understand the content presented in class. The instructor is also concerned that chatgpt will sometimes make up answers that are completely wrong (hallucinations)

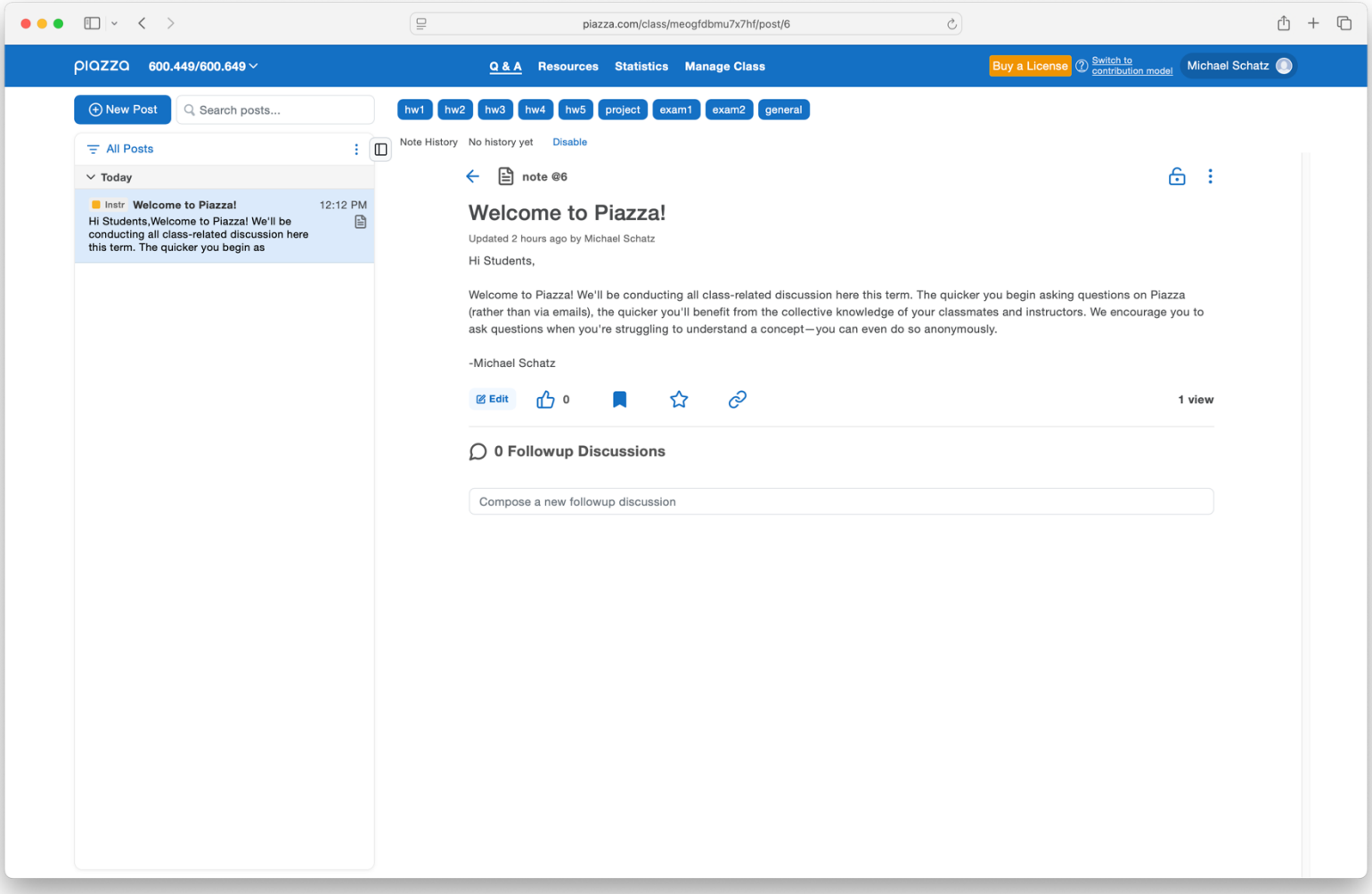
A good policy for the use of ChatGPT in a university class on genomics and data science should emphasize that the tool is a supplement to, not a replacement for, engaging with primary course materials and learning objectives. Students should be encouraged to use ChatGPT to clarify complex concepts, find additional resources, and practice coding, but not to complete assignments or exams directly from AI-generated content without proper understanding and cross-referencing with reputable scientific sources. The policy should require students to disclose when they use ChatGPT and reflect on its contributions and limitations, fostering critical thinking and awareness of potential inaccuracies or "hallucinations." Educating students on the limitations of AI, including how to fact-check responses against trusted academic sources, will enhance their ability to use the tool responsibly. Additionally, promoting ethical use and reinforcing academic integrity are crucial, with the instructor modeling appropriate use and providing clear examples of acceptable and unacceptable practices. This approach will help students develop essential skills in genomics and data science while making the most of AI tools like ChatGPT.

Course Webpage



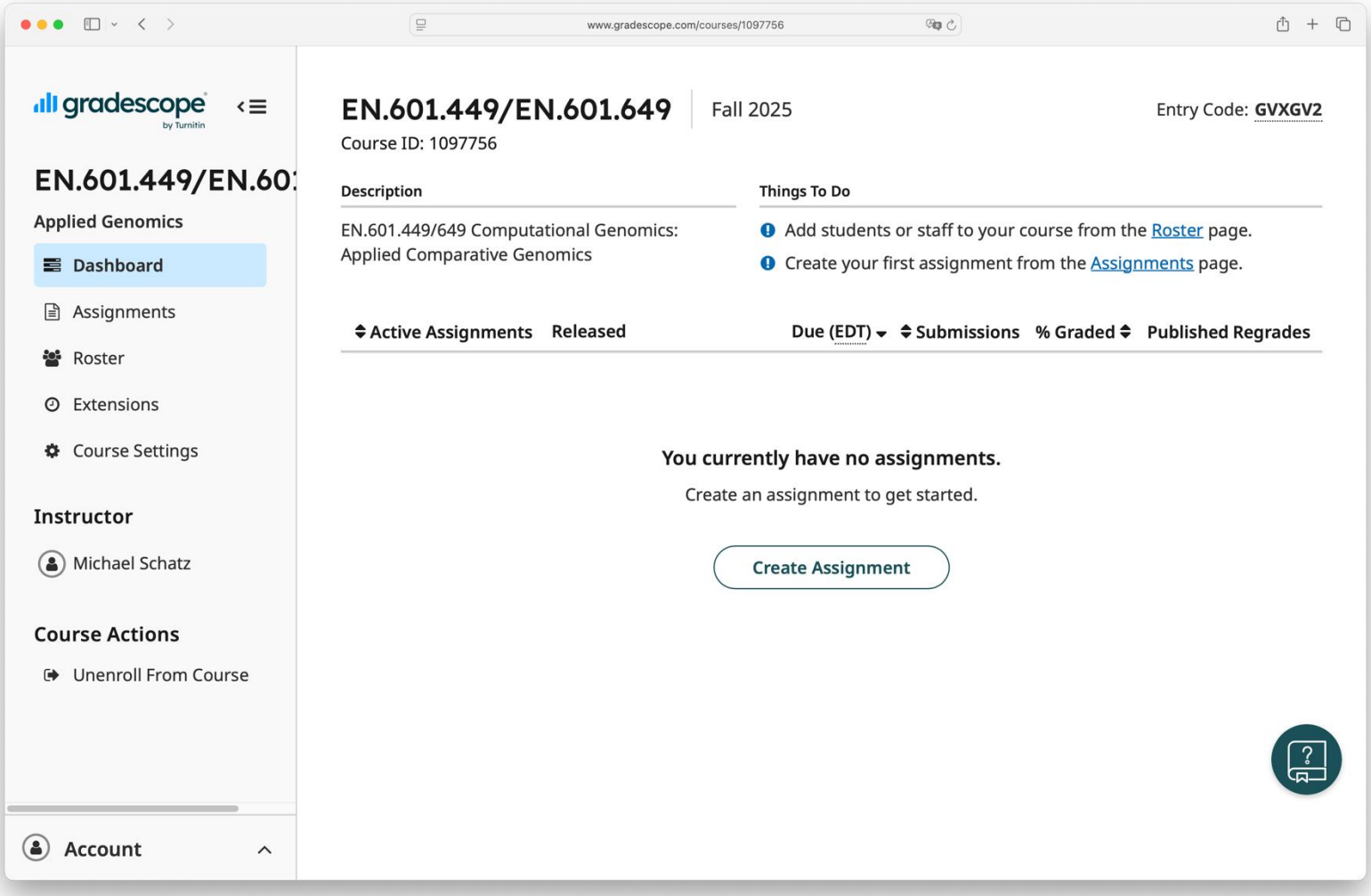
https://github.com/schatzlab/appliedgenomics2025

Piazza



https://piazza.com/jhu/fall2025/600449600649

GradeScope



https://www.gradescope.com/

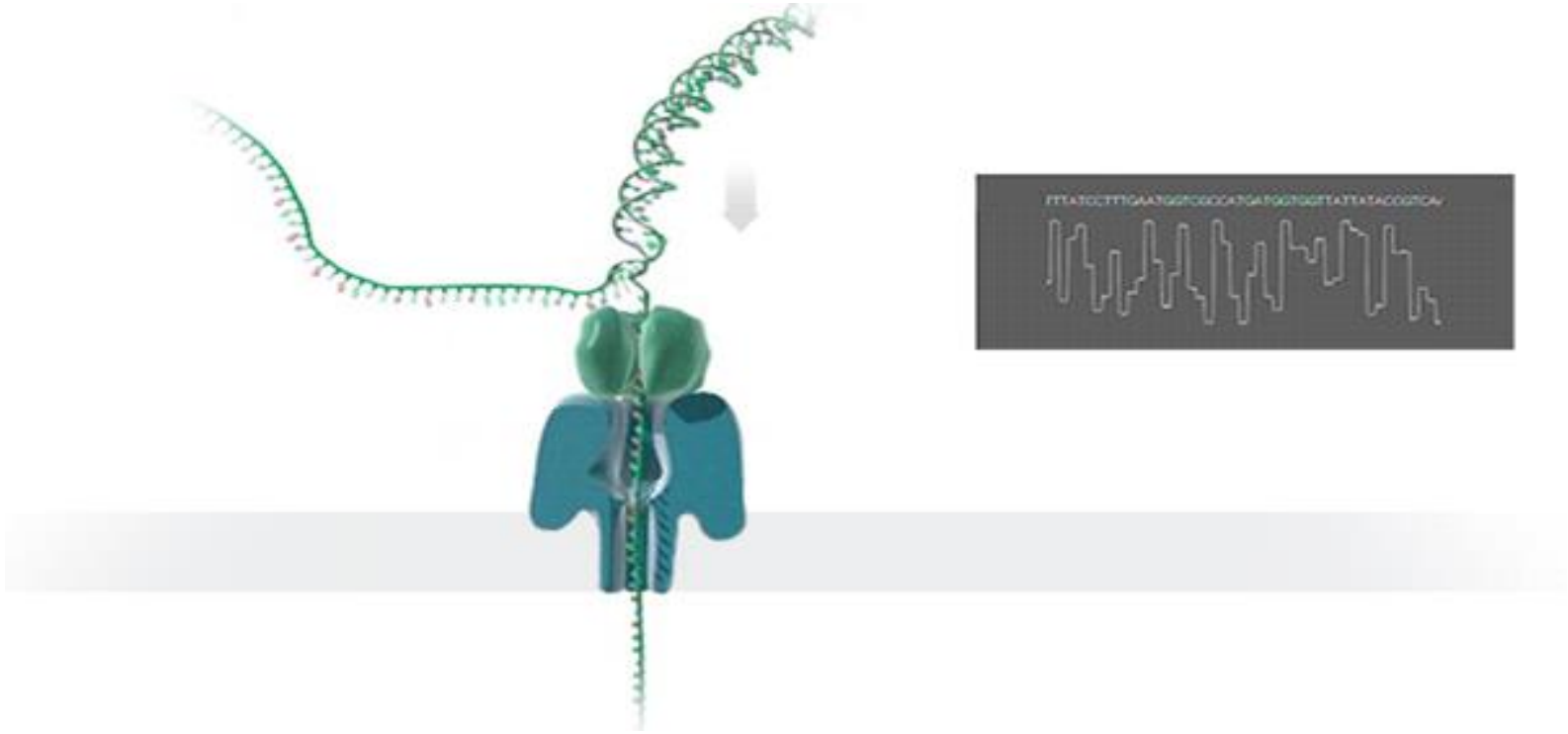
Entry Code: **GVXGV2**

25	11/19/25	W	In-class presentation		
*	11/24/25	M	Thanksgiving Break		
*	11/26/25	W	Thanksgiving Break		
26	12/1/25	M	In-class presentation		
27	12/3/25	W	In-class presentation		
*	12/10/25	W	Draft Report Due		
*	12/11/25	Th	Final project presentation		
*	12/12/25	F	Final project presentation		
*	12/15/25	M	Final project presentation		
*	12/16/25	Tu	Final Report Due		

https://github.com/schatzlab/appliedgenomics2025

Nanopore Sequencing

Sequences DNA/RNA by measuring changes in ionic current as nucleotide strand passes through a pore



https://www.youtube.com/watch?v=RcP85JHLmnI

nanoporetech.com/applications/dna-nanopore-sequencing

Bioinformatics
doi.10.1093/bioinformatics/xxxxxx
Advance Access Publication Date: TBA
Manuscript Category

Subject Section

Basecall-free alignment of Oxford Nanopore reads using the Burrow-Wheelers Transform

Yunfan Fan [1,*], Sam Kovaka [2] and Taher Mun [2,*]

[1]Department of Biomedical Engineering, Johns Hopkins University, Baltimore, 21218, USA and
[2]Department of Computer Science, Johns Hopkins University, Baltimore, USA.

* To whom correspondence should be addressed.

pre-print

Abstract

Motivation: Sequencers manufactured by Oxford Nanopore Technologies (ONT) can generate long reads while simultaneously providing the ability to sequence in the field due to the compact cell-phone-sized design of their MinION sequencer. However, the technology hinges on measuring minute changes in ionic current through a pore as DNA is simultaneously passed through. The process of basecalling, which converts these electrical signals into bases, is a time-consuming and resource intensive process, but necessary for most downstream applications such as read alignment and genome assembly. This project aims to bypass the basecalling step for alignment applications by directly aligning the signals to a reference genome that has been converted from bases into signals.
Results: results here
Availability: availability here
Contact: yfan7@jhu.edu, skovaka1@jhu.edu tmun1@jhu.edu
Supplementary information: Available upon request.

1 Introduction

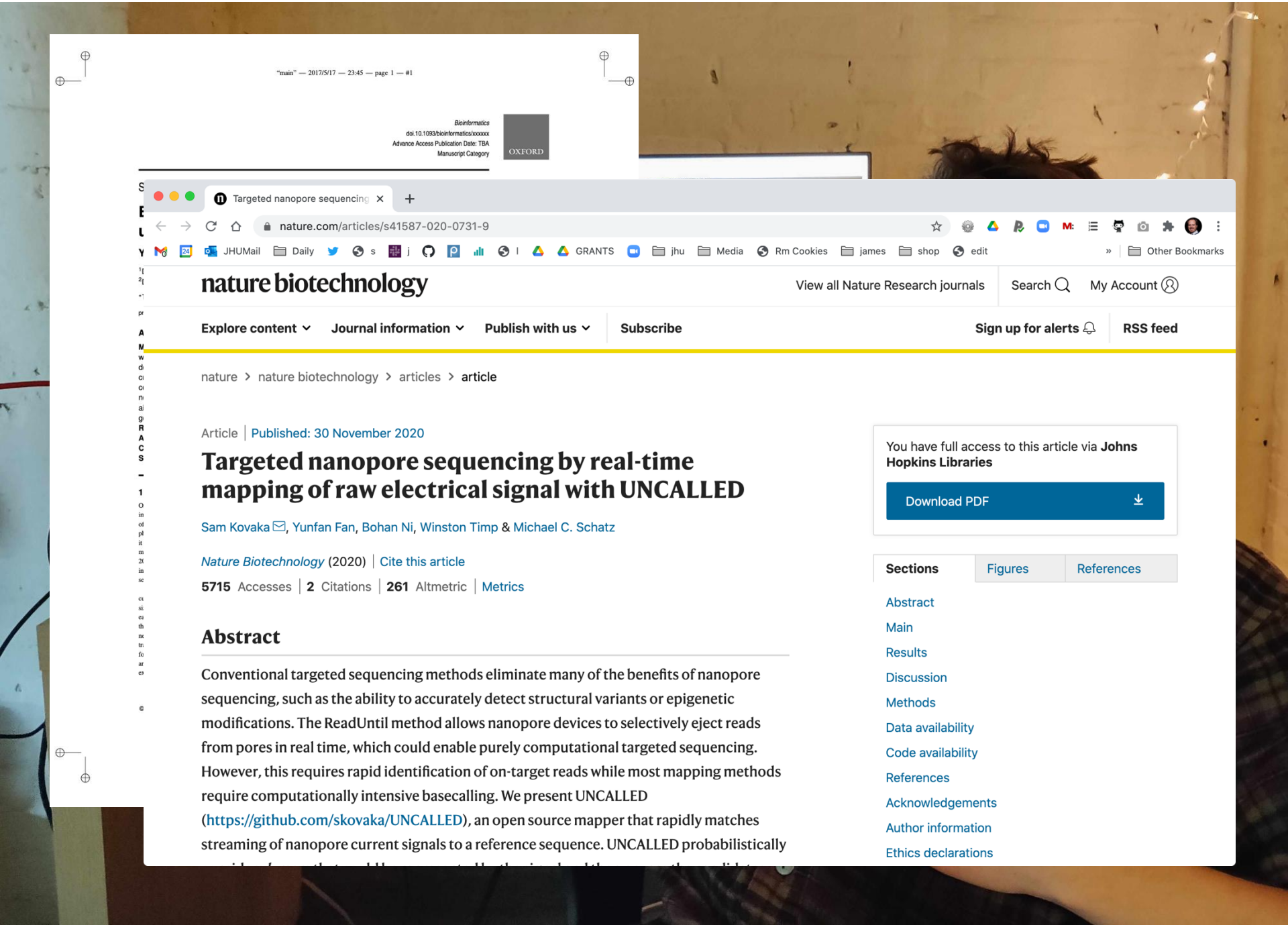
Oxford Nanopore reads provide the convenience of portability, the immediacy of real-time sequencing, as well as the novelty and usefulness of long reads. Since the ONT MinION technology is as compact as a cell-phone and connects directly to a conventional laptop via USB to operate, it has been leveraged in the field for applications including outbreak monitoring (Quick et al. 2016) and extraterrestrial sequencing (Rainey 2016). Its capability to gather and report useful data in real time has also inspired efforts to apply DNA sequencing in urgent medical diagnosis settings (Votintseva et al. 2017).

The MinION sequencer measures and records a time series of electrical current amplitudes as ions and a DNA strand pass through a nanometer sized hole. As segments of six base pairs occupy the pore sequentially, each recorded current corresponds to unique 6-mers of DNA. Due to this indirect nature of sequencing, the actual base sequence of the reads need to be eluted through a process called basecalling, where signals are translated into nucleotides. Base calling software and services are available for hire through ONT subsidiaries, but open source implementations are also available. However, the base calling process is invariably expensive computationally, and involves complicated modeling by way of Hidden Markov Models in the case of the open source software or Recurrent Neural Networks in the case of the proprietary. Previously, the proprietary basecalling software also required an internet connection, which can be prohibitive of field work applications in remote locations. As most downstream software for lynchpin genomic analysis such as read alignment and genome assembly deal only with nucleotide sequences, the basecalling step is emerging as a critical bottleneck for the efficacy of the technology.

In order to address this problem in the context of read alignment, we propose to skip the base calling step altogether and align the raw current signals directly to a reference (Laszlo et al. 2014). This can be done by converting a reference genome from base-space to signal-space using a model of expected current levels and then indexing it using the Burrows-Wheeler Transform. Then, the signals generated from the ONT reads can be directly aligned to the reference using this BWT in order to obtain an accurate mapping.

2 Methods

Resources: Development and testing was done on the MARCC langmead-bigmem server, which has 1TB RAM and 112 cores. Of this, we used up to 30GB RAM and a single core.



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Bioinformatics
doi.10.1093/bioinformatics/xxxxxx
Advance Access Publication Date: TBA
Manuscript Category

OXFORD

Targeted nanopore sequencing

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Article | Published: 30 November 2020

Targeted nanopore sequencing by real-time mapping of raw electrical signal with UNCALLED

Sam Kovaka, Yunfan Fan, Bohan Ni, Winston Timp & Michael C. Schatz

Nature Biotechnology (2020) | Cite this article

5715 Accesses | **2** Citations | **261** Altmetric | Metrics

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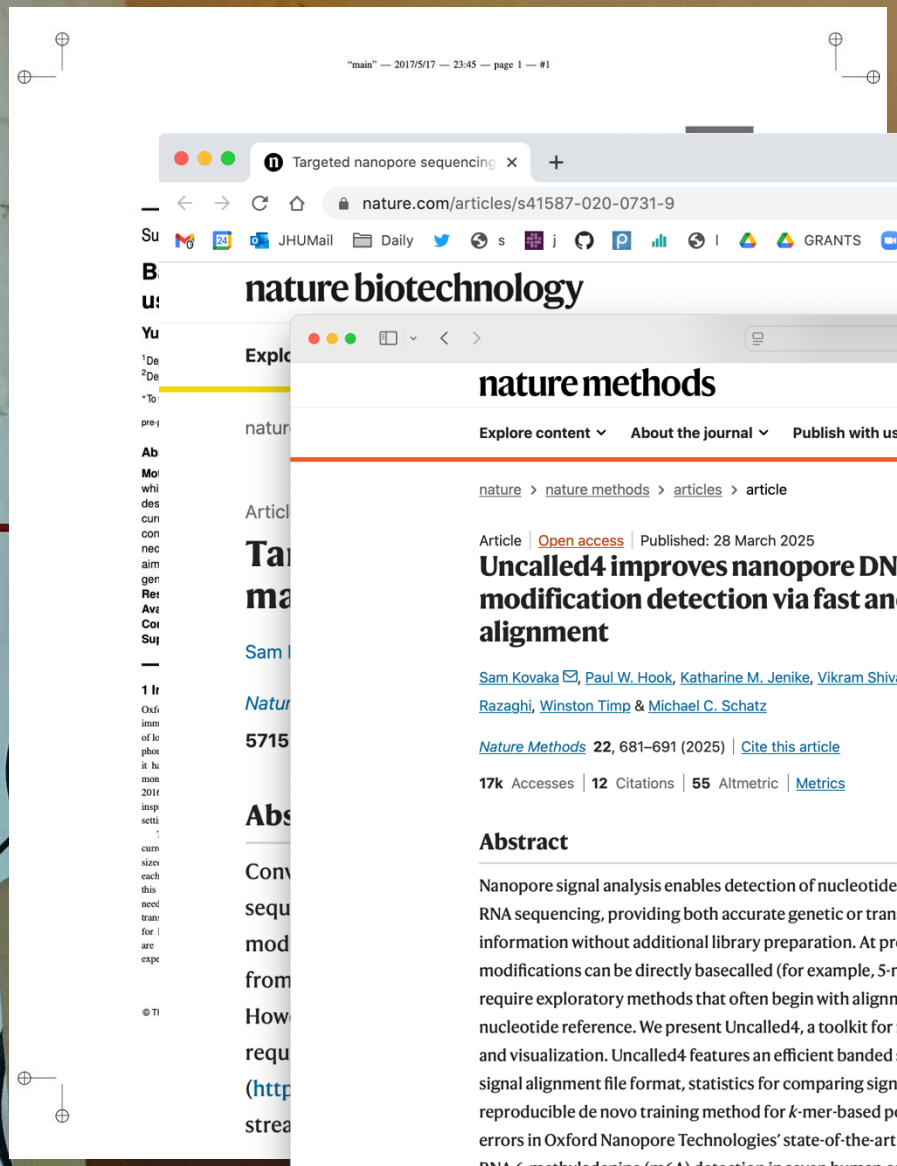
Sections Figures References

- Abstract
- Main
- Results
- Discussion
- Methods
- Data availability
- Code availability
- References
- Acknowledgements
- Author information
- Ethics declarations

Abstract

Conventional targeted sequencing methods eliminate many of the benefits of nanopore sequencing, such as the ability to accurately detect structural variants or epigenetic modifications. The ReadUntil method allows nanopore devices to selectively eject reads from pores in real time, which could enable purely computational targeted sequencing. However, this requires rapid identification of on-target reads while most mapping methods require computationally intensive basecalling. We present UNCALLED (https://github.com/skovaka/UNCALLED), an open source mapper that rapidly matches streaming of nanopore current signals to a reference sequence. UNCALLED probabilistically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Targeted nanopore sequencing
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Article | Open access | Published: 28 March 2025
Uncalled4 improves nanopore DNA and RNA modification detection via fast and accurate signal alignment
Sam Kovaka, Paul W. Hook, Katharine M. Jenike, Vikram Shivakumar, Luke B. Morina, Roham Razaghi, Winston Timp & Michael C. Schatz
Nature Methods 22, 681–691 (2025) | Cite this article
17k Accesses | 12 Citations | 55 Altmetric | Metrics
Abstract
Nanopore signal analysis enables detection of nucleotide modifications from native DNA and RNA sequencing, providing both accurate genetic or transcriptomic and epigenetic information without additional library preparation. At present, only a limited set of modifications can be directly basecalled (for example, 5-methylcytosine), while most others require exploratory methods that often begin with alignment of nanopore signal to a nucleotide reference. We present Uncalled4, a toolkit for nanopore signal alignment, analysis and visualization. Uncalled4 features an efficient banded signal alignment algorithm, BAM signal alignment file format, statistics for comparing signal alignment methods and a reproducible de novo training method for k-mer-based pore models, revealing potential errors in Oxford Nanopore Technologies' state-of-the-art DNA model. We apply Uncalled4 to RNA 6-methyladenine (m6A) detection in seven human cell lines, identifying 26% more modifications than Nanopolish using m6Anet, including in several genes where m6A has known implications in cancer. Uncalled4 is available open source at github.com/skovaka/uncalled4.
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Sections
Figures
References
Abstract
Main
Results
Discussion
Methods
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Code availability
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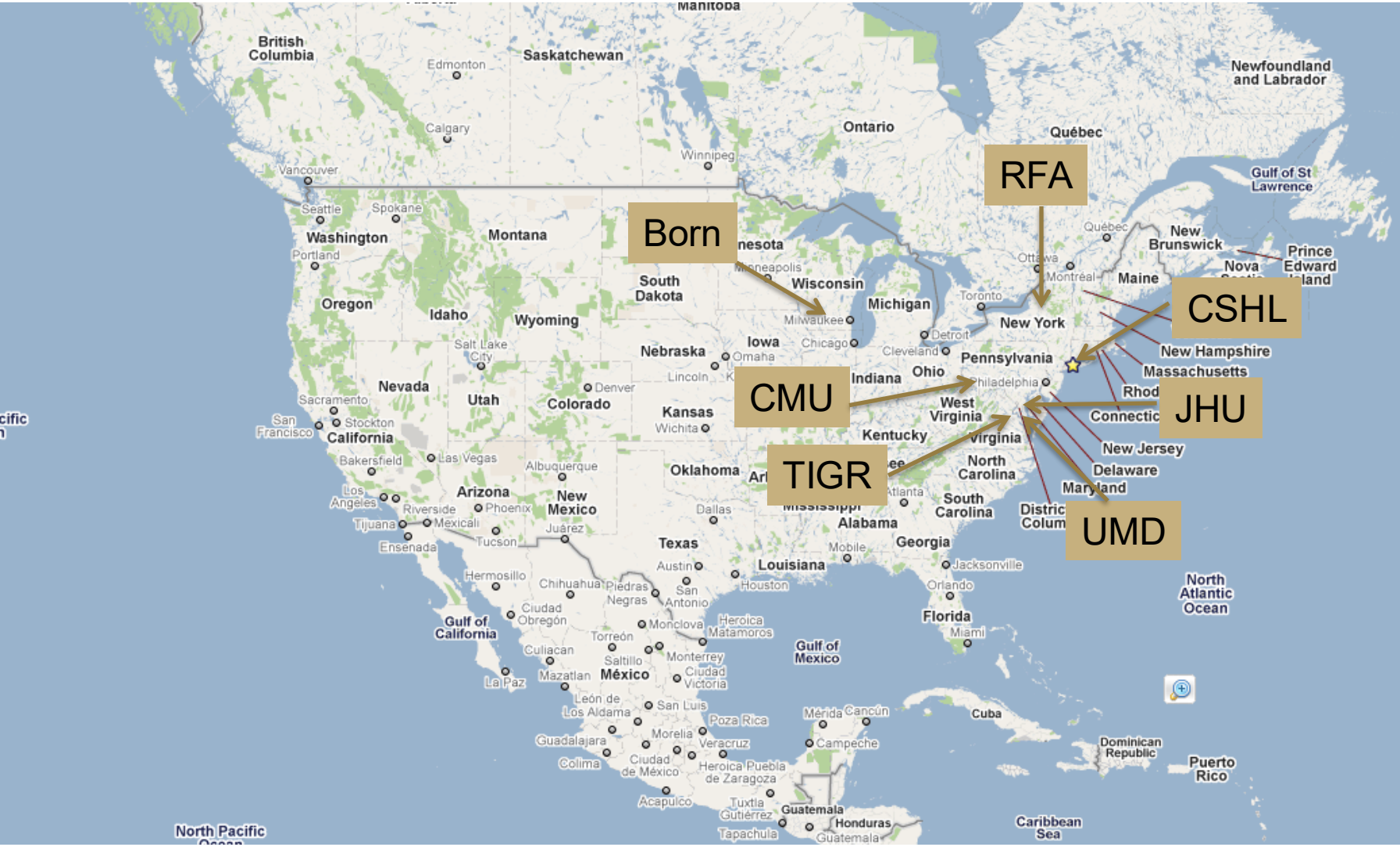
A Little About Me

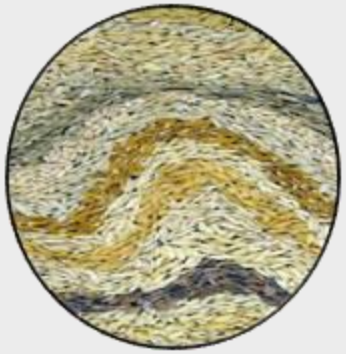


Schatzlab Overview

Human Genetics

Role of mutations in disease

Nurk *et al.* (2022)
Aganezov *et al.* (2020)



Agricultural Genomics

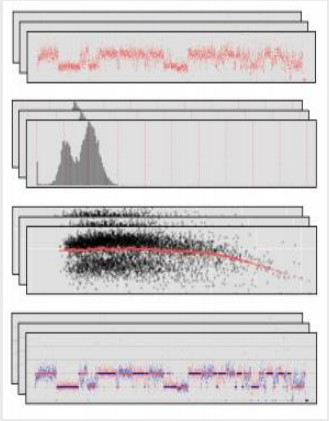
Genomes & Transcriptomes

Benoit et al. (2025)
Satterlee *et al.* (2024)

Algorithmics & Systems Research

Ultra-large scale biocomputing

Kirsche *et al.* (2023)
Schatz *et al.* (2022)



Biotechnology Development

Single Cell + Single Molecule Sequencing

Kovaka *et al.* (2024)
Rozowsky *et al.* (2023)

Why Genomics?

Discovery of the Double Helix

equipment, and to Dr. G. E. R. Deacon and the captain and officers of R.R.S. *Discovery II* for their part in making the observations.

[1] Young, F. B., Gerrard, H., and Jevons, W., *Phil. Mag.*, **40**, 149 (1920).
[2] Longuet-Higgins, M. S., *Mon. Not. Roy. Astro. Soc., Geophys. Supp.*, **5**, 285 (1949).
[3] Von Arx, W. S., Woods Hole Papers in Phys. Oceanog. Meteor., **11** (3) (1950).
[4] Ekman, V. W., *Arkiv. Mat. Astron. Fysik. (Stockholm)*, **2** (11) (1905).

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Corey[1]. They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons: (1) We believe that the material which gives the X-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.

This figure is purely diagrammatic. The two ribbons symbolize the two phosphate–sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical line marks the fibre axis

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate diester groups joining β-D-deoxyribofuranose residues with 3′,5′ linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furberg's[2] model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration', the sugar being roughly perpendicular to the attached base. There is a residue on each chain every 3·4 A. in the *z*-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 A. The distance of a phosphorus atom from the fibre axis is 10 A. As the phosphates are on the outside, cations have easy access to them.

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

The novel feature of the structure is the manner in which the two chains are held together by the purine and pyrimidine bases. The planes of the bases are perpendicular to the fibre axis. They are joined together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so that the two lie side by side with identical *z*-co-ordinates. One of the pair must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows: purine position 1 to pyrimidine position 1; purine position 6 to pyrimidine position 6.

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) it is found that only specific pairs of bases can bond together. These pairs are: adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, on either chain, then on these assumptions the other member must be thymine; similarly for guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted in any way. However, if only specific pairs of bases can be formed, it follows that if the sequence of bases on one chain is given, then the sequence on the other chain is automatically determined.

It has been found experimentally[3,4] that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribose nucleic acid.

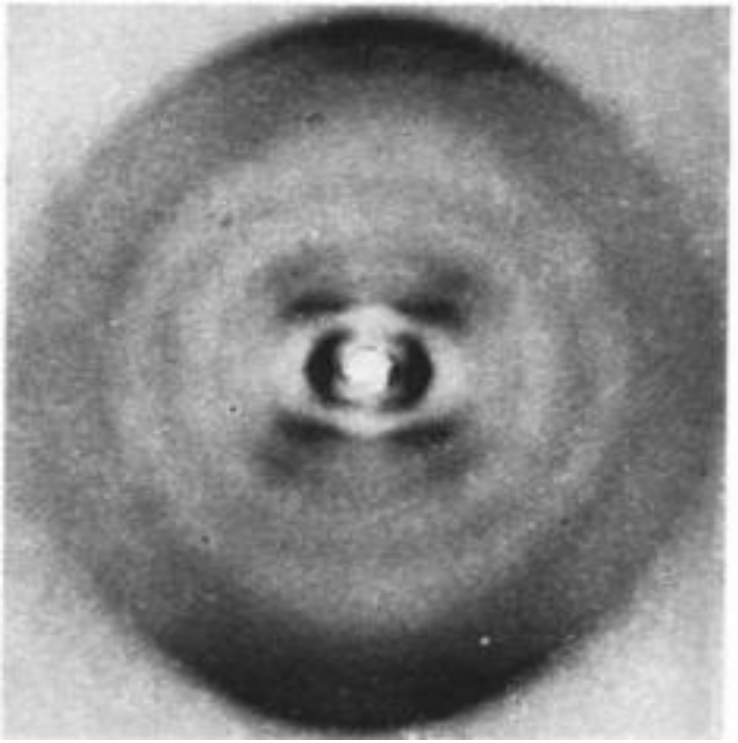
It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atom would make too close a van der Waals contact.

The previously published X-ray data[2,4] on deoxyribose nucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in the following communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on published experimental data and stereochemical arguments.

It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material.

Full details of the structure, including the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on interatomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F. Wilkins, Dr. R. E. Franklin and their co-workers at



chemical arguments.

It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material.

Full details of the structure, including the con-

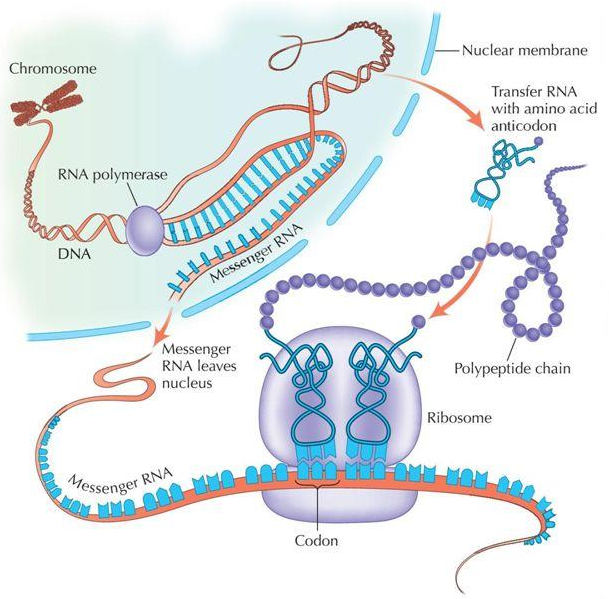
Molecular structure of nucleic acids; a structure for deoxyribose nucleic acid

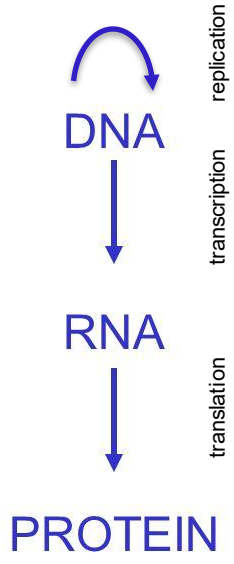
Watson JD, Crick FH (1953). *Nature* 171: 737–738.

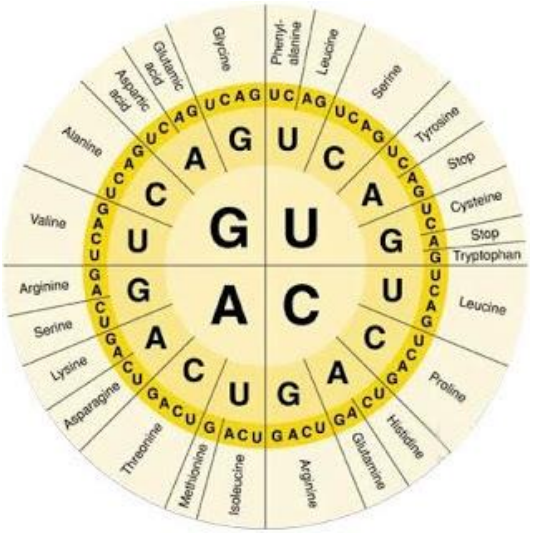
Nobel Prize in Physiology or Medicine in 1962

Central Dogma of Molecular Biology

"Once 'information' has passed into protein it cannot get out again. In more detail, the transfer of information ***from nucleic acid to nucleic acid, or from nucleic acid to protein may be possible***, but transfer from protein to protein, or from protein to nucleic acid is impossible. Information means here the precise determination of sequence, either of bases in the nucleic acid or of amino acid residues in the protein"





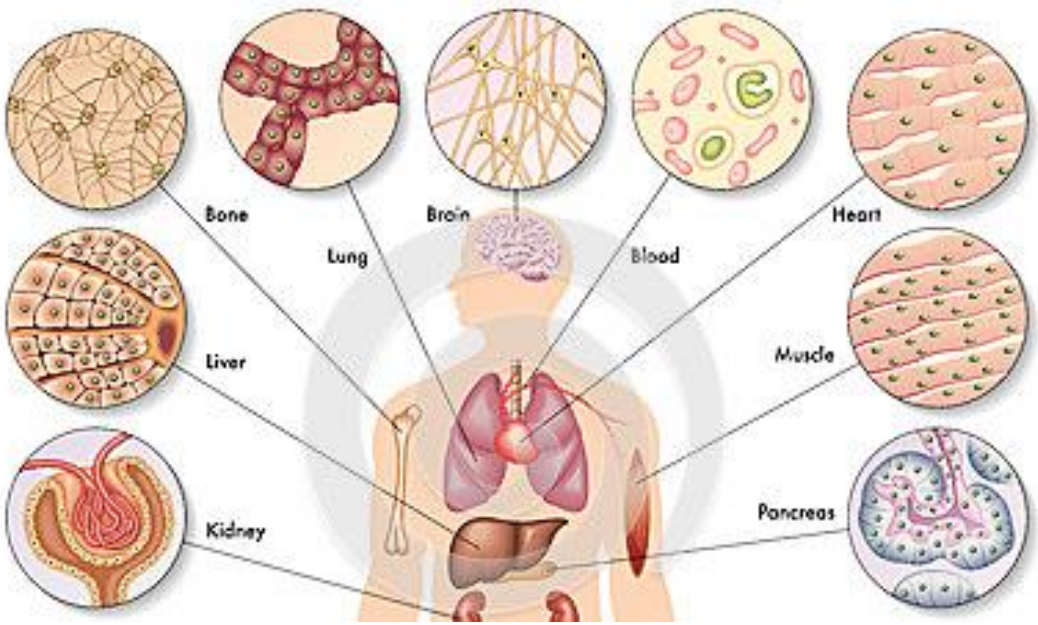


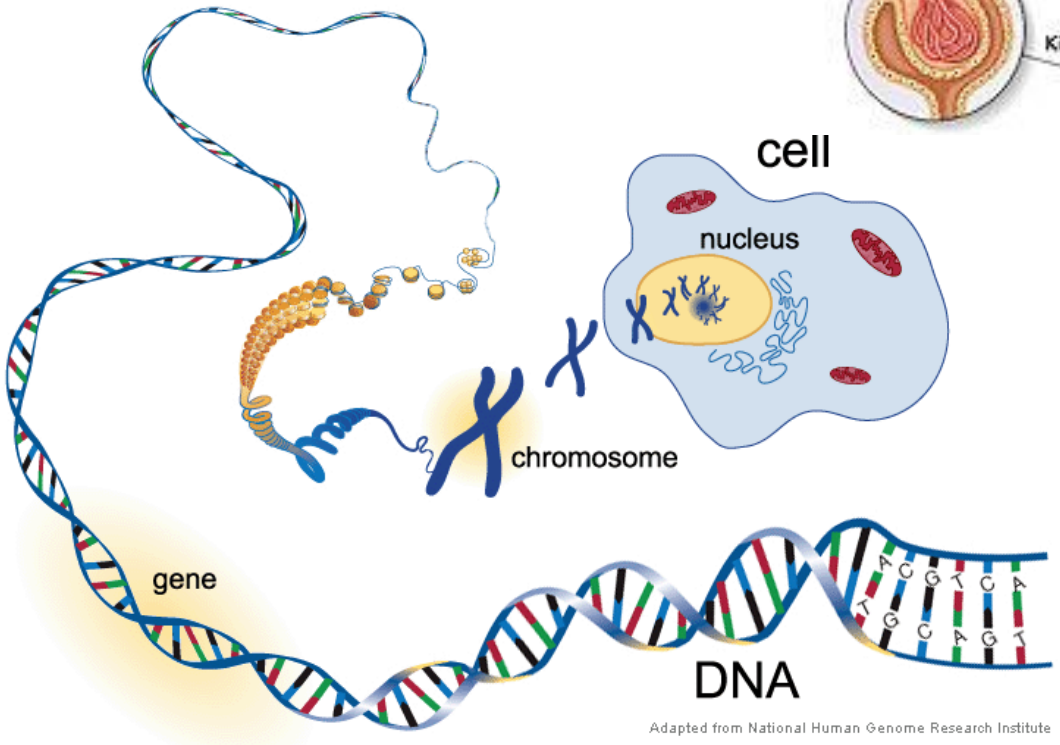
On Protein Synthesis

Crick, F.H.C. (1958). Symposia of the Society for Experimental Biology pp. 138–163.

One Genome, Many Cell Types

Each cell of your body contains an exact copy of your 3 billion base pair genome.





Your body has a few hundred (thousands?) major cell types, largely defined by the gene expression patterns

Unsolved Questions in Biology

- What is your genome sequence?
- How does your genome compare to my genome?

- Where are the genes and how active are they?
- How does gene activity change during development?
- How does splicing change during development?

- How does methylation change during development?
- How does chromatin change during development?
- How does is your genome folded in the cell?
- Where do proteins bind and regulate genes?

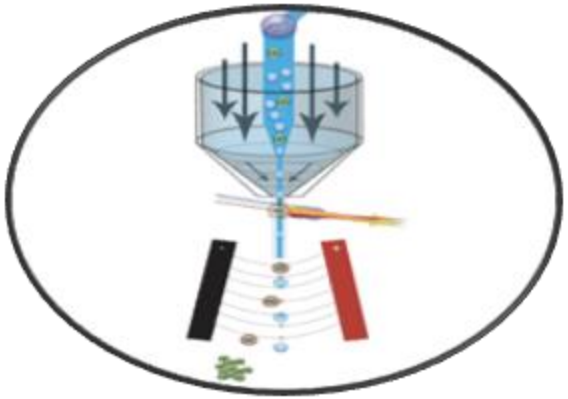
- What virus and microbes are living inside you?
- How do your mutations relate to disease?
- What drugs and treatments should we give you?

- ***Plus thousands and thousands more***

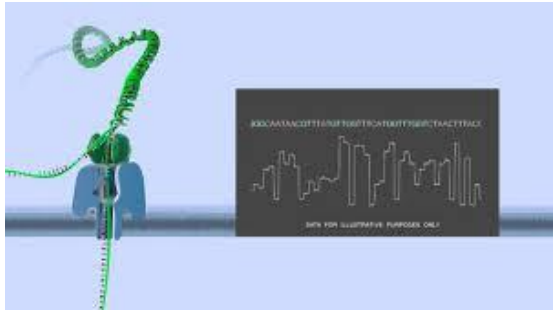
How to do Genomics?

Genomics Arsenal in the year 2025

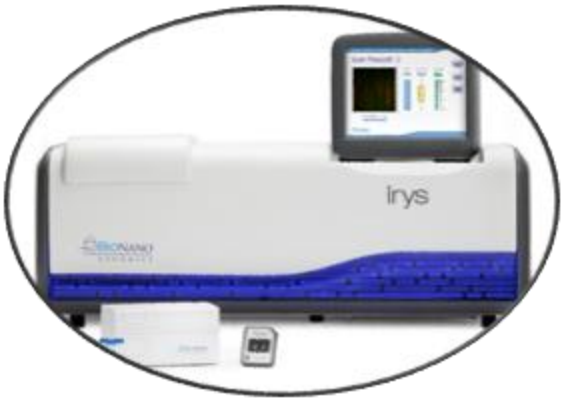
Sample Preparation

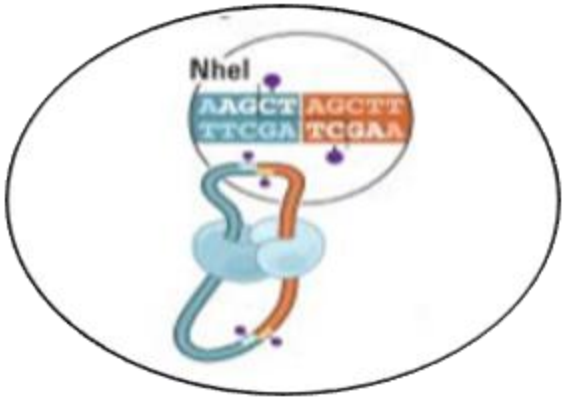


Sequencing

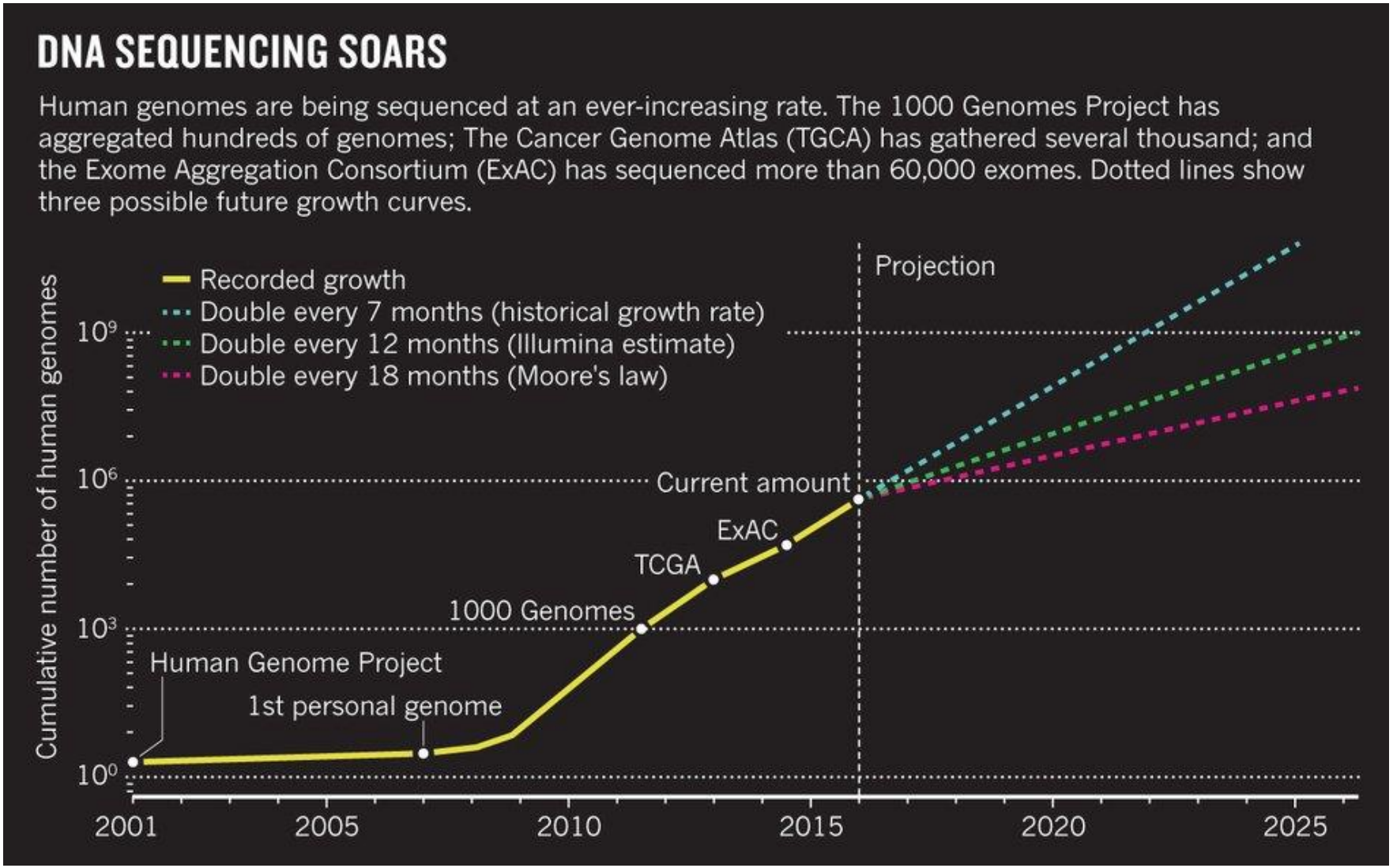


Chromosome Mapping





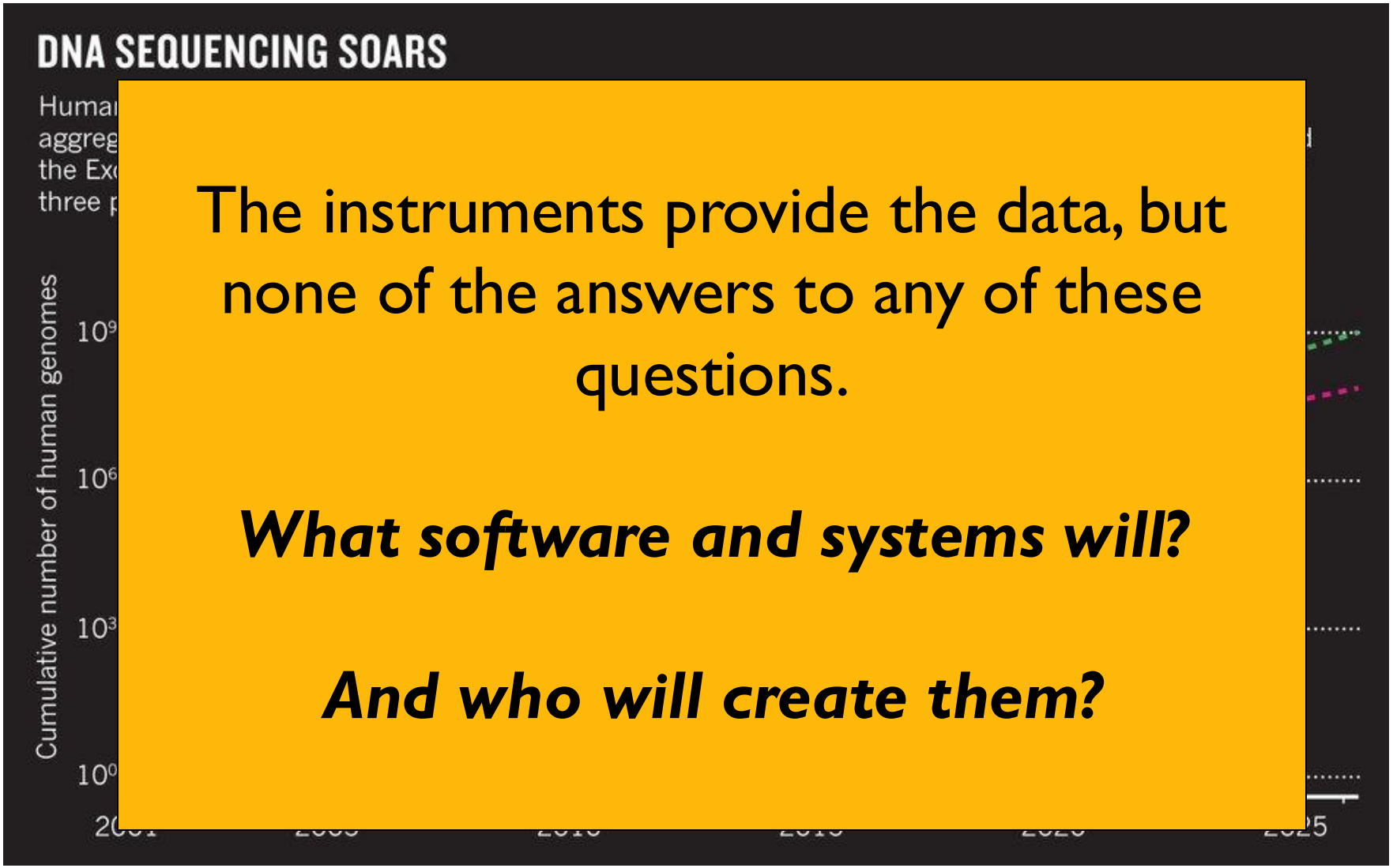
Sequencing Capacity



Big Data: Astronomical or Genomical?

Stephens, Z, et al. (2015) PLOS Biology DOI: 10.1371/journal.pbio.1002195

Sequencing Capacity



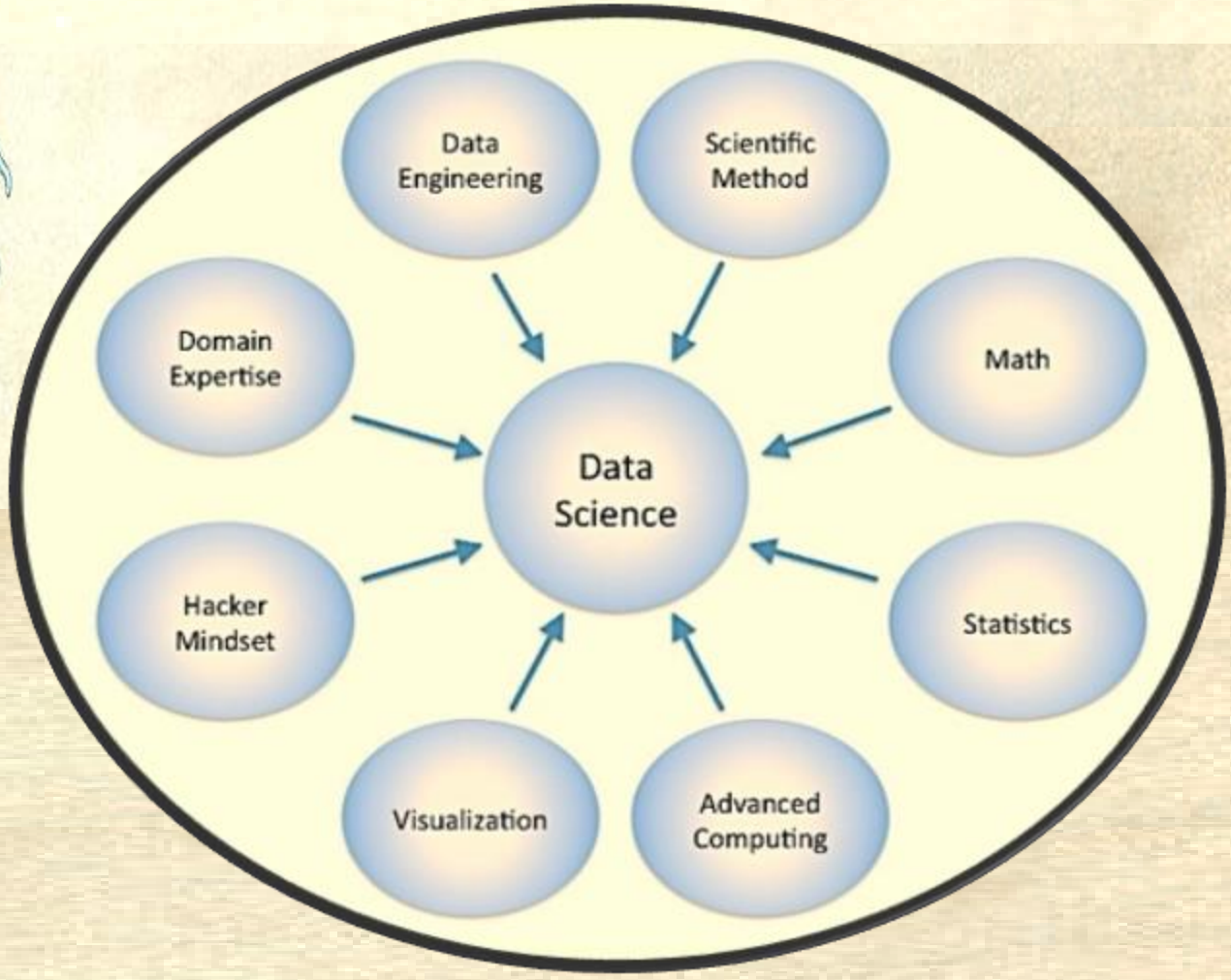
The instruments provide the data, but none of the answers to any of these questions.

What software and systems will?

And who will create them?

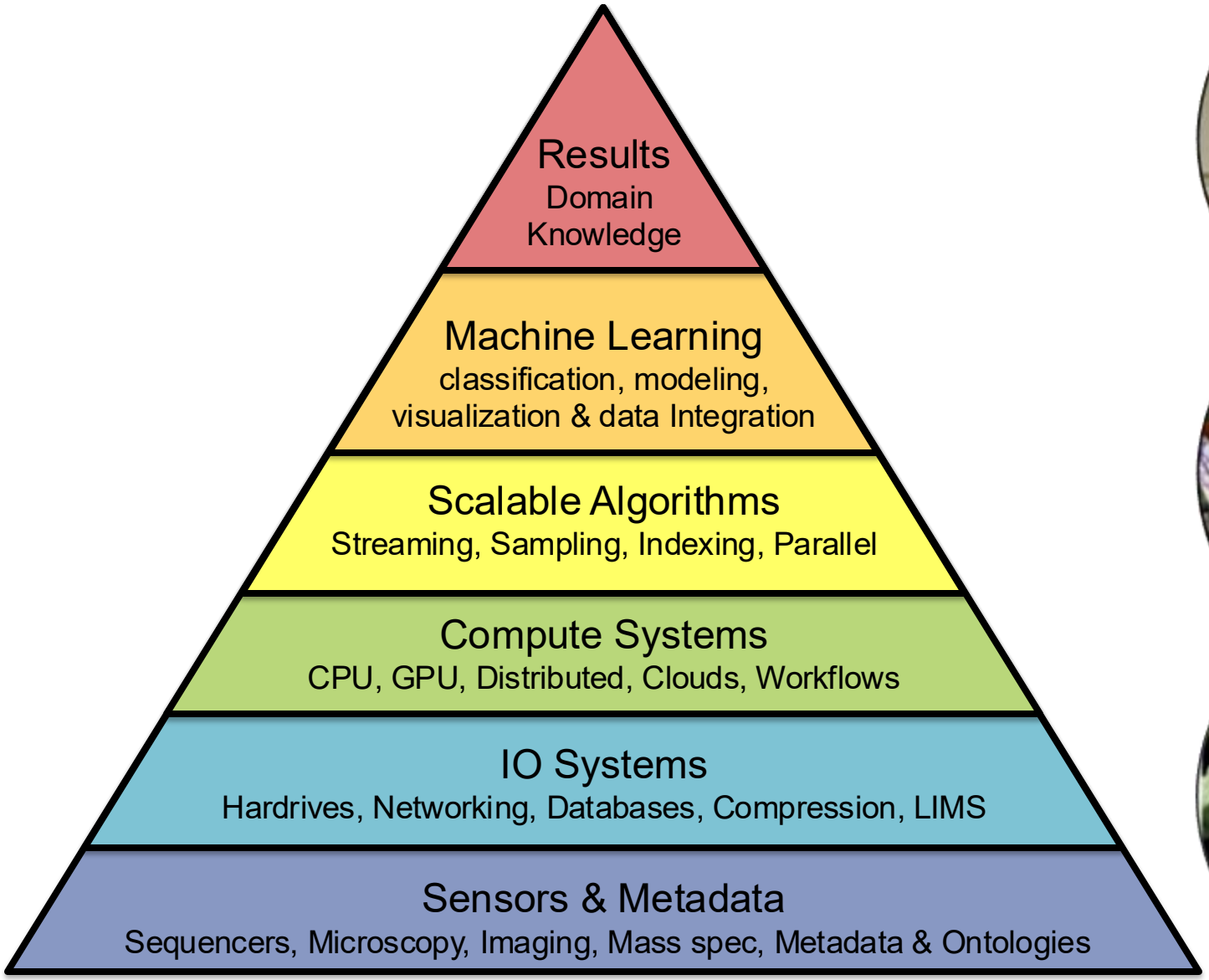
Big Data: Astronomical or Genomical?
Stephens, Z, et al. (2015) PLOS Biology DOI: 10.1371/journal.pbio.1002195

Who is a Data Scientist?

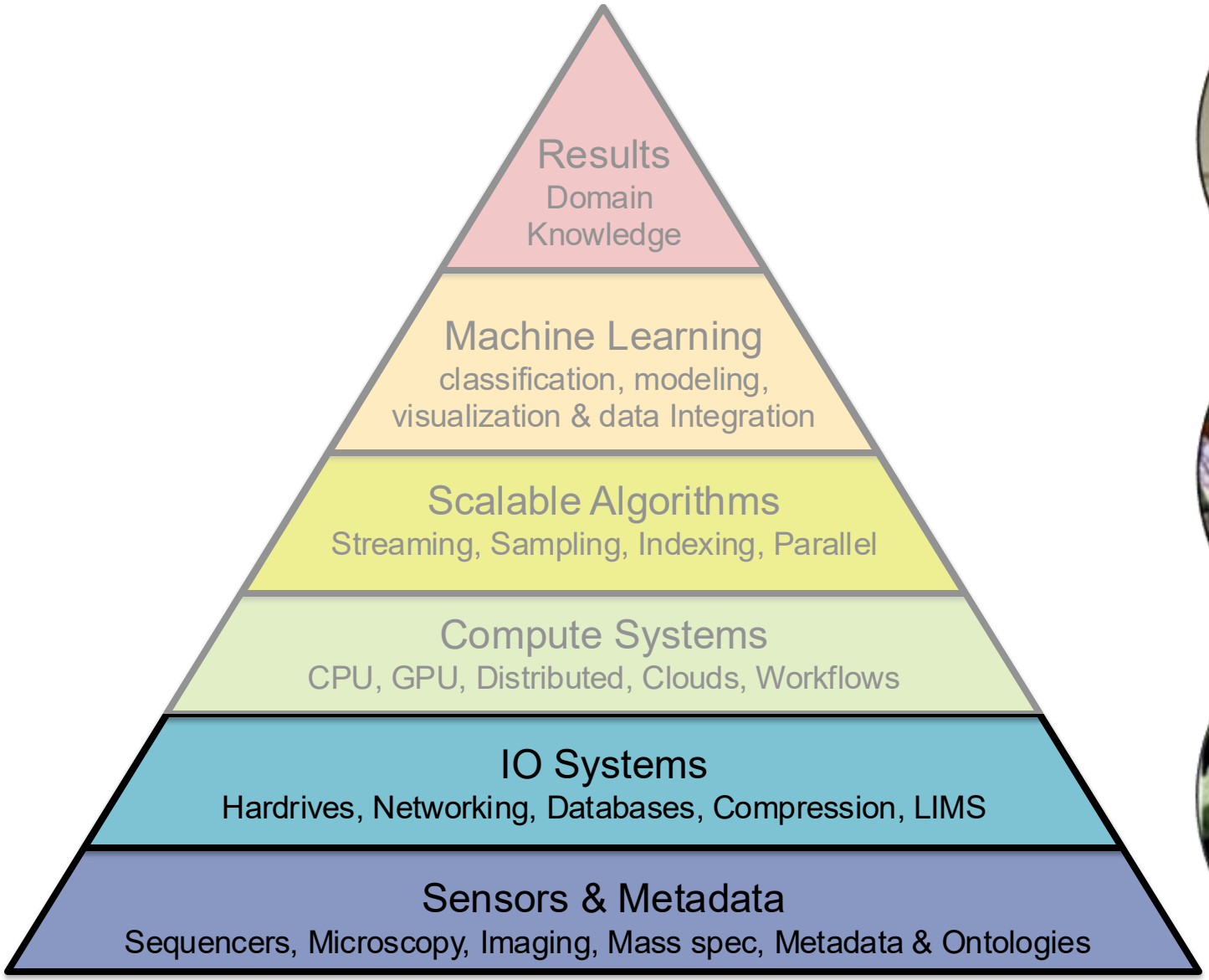


http://en.wikipedia.org/wiki/Data_science

Applied Genomics

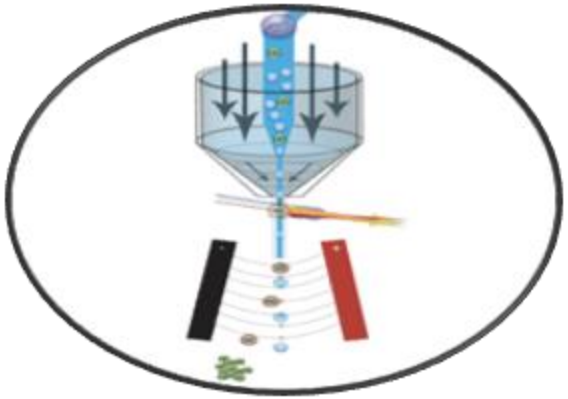


Applied Genomics

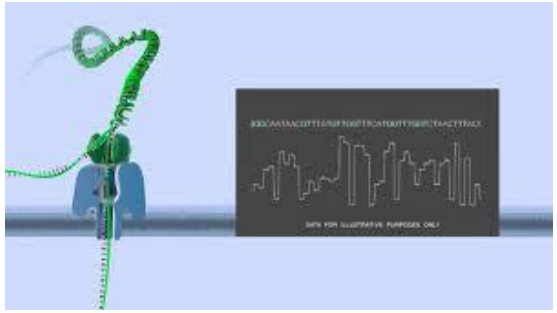


Genomics Arsenal in the year 2025

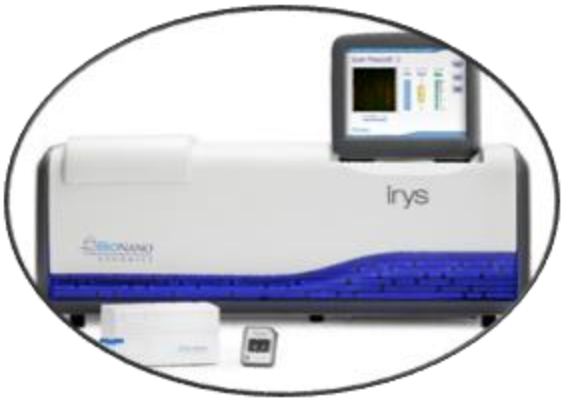
Sample Preparation

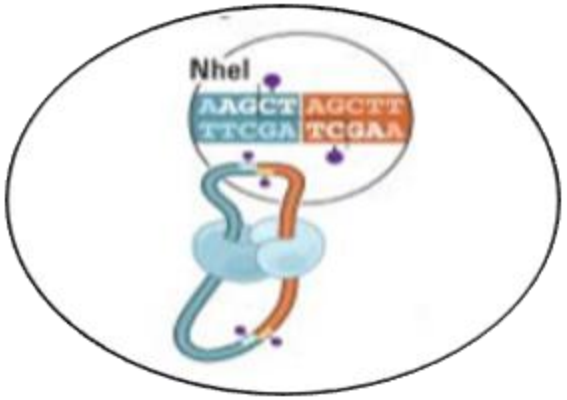


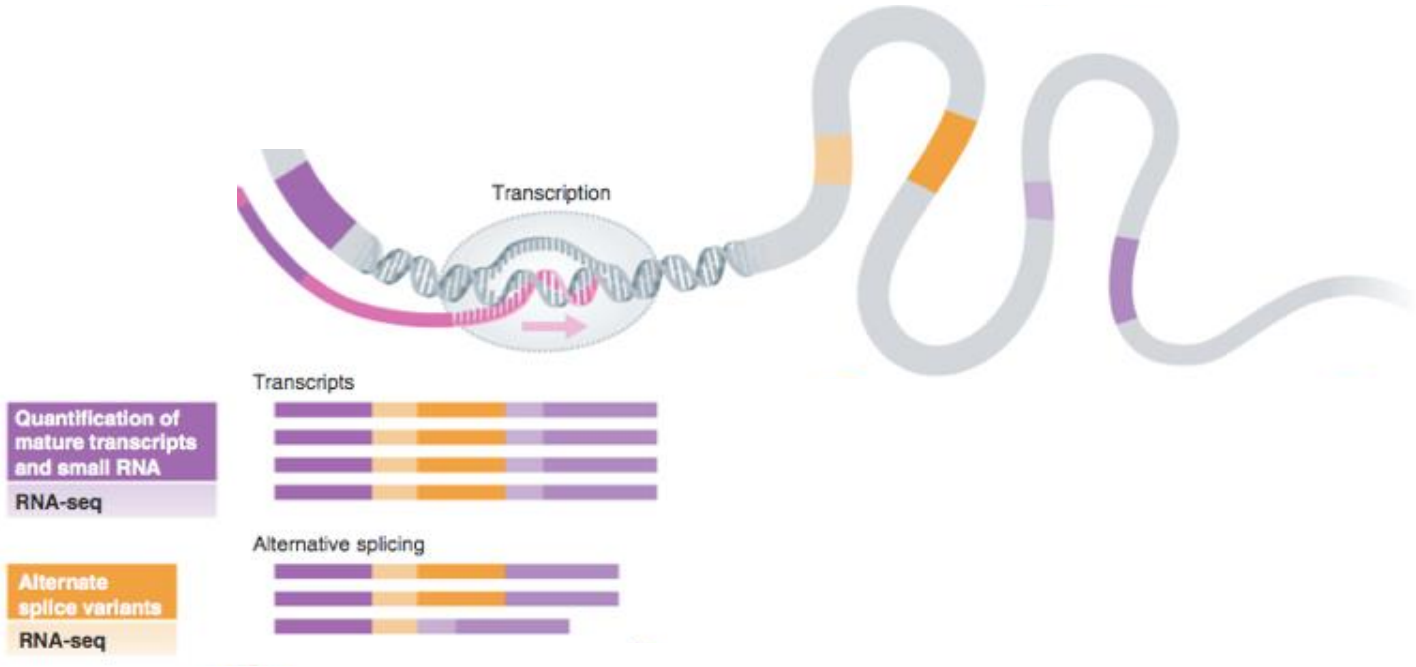
Sequencing



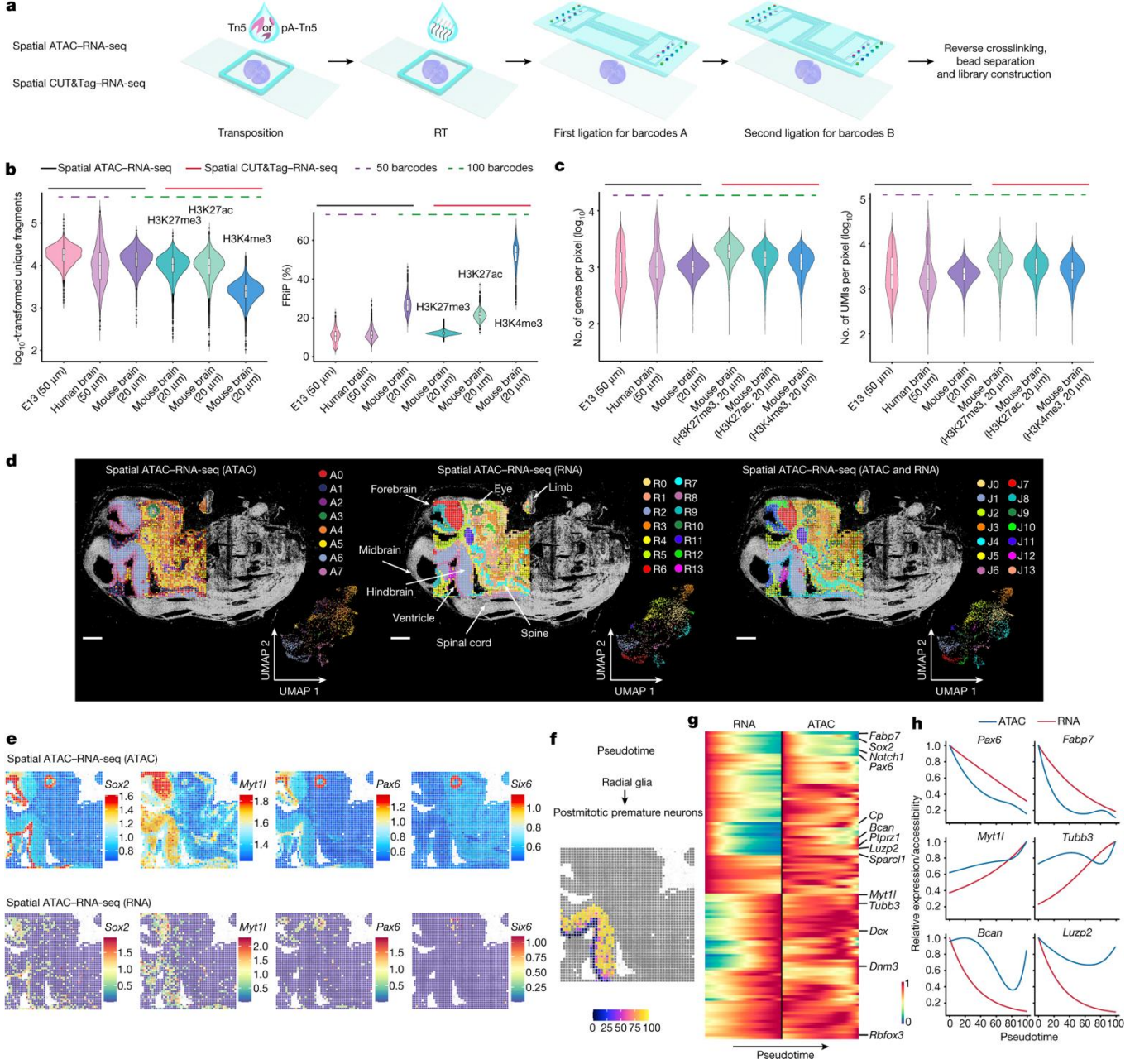
Chromosome Mapping







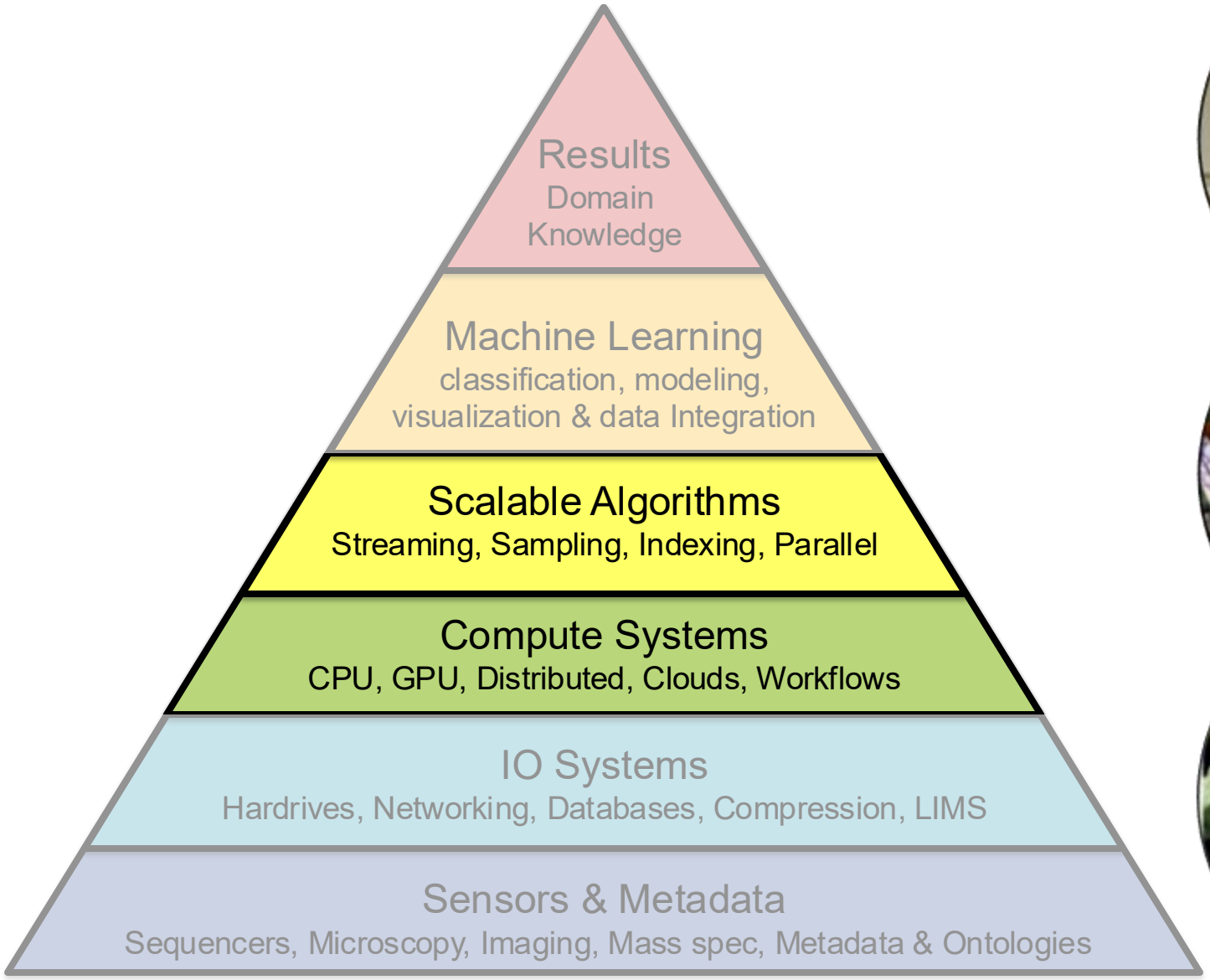
Soon et al., Molecular Systems Biology, 2013



Spatial epigenome–transcriptome co-profiling of mammalian tissues

Zhang et al. *(2023) Nature. https://doi.org/10.1038/s41586-023-05795-1*

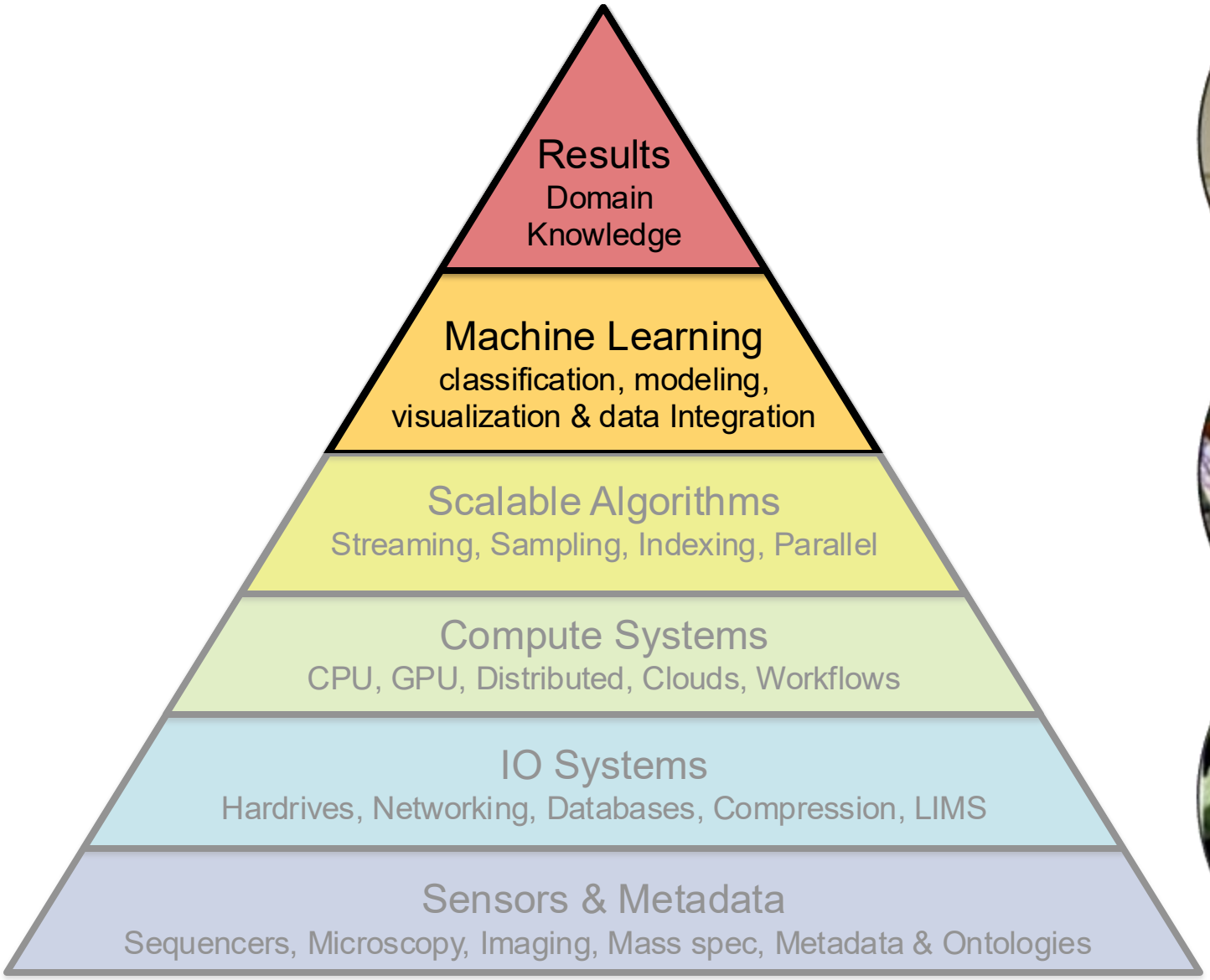
Applied Genomics



Potential Topics

- Genome assembly, whole genome alignment
- Full text indexing: Suffix Trees, Suffix Arrays, FM-index
- Dynamic Programming: Edit Distance, sequence similarity
- Read mapping & Variant identification
- Gene Finding: HMMs, Plane-sweep algorithms
- RNA-seq: mapping, assembly, quantification
- ChIP-seq: Peak finding, motif finding
- Methylation-seq: Mapping, CpG island detection
- HiC: Domain identification, scaffolding
- Chromatin state analysis: ChromHMM, Enformer
- Scalable genomics: Cloud computing, scalable data structures
- Population & single cell analysis: clustering, pseudotime
- Disease analysis, cancer genomics, Metagenomics
- Deep learning in genomics

Applied Genomics



Genetic Basis of Autism Spectrum Disorders

Complex disorders of brain development

- Characterized by difficulties in social interaction, verbal and nonverbal communication and repetitive behaviors.
- Have their roots in very early brain development, and the most obvious signs of autism and symptoms of autism tend to emerge between 2 and 3 years of age.

U.S. CDC identify around 1 in 68 American children as on the autism spectrum

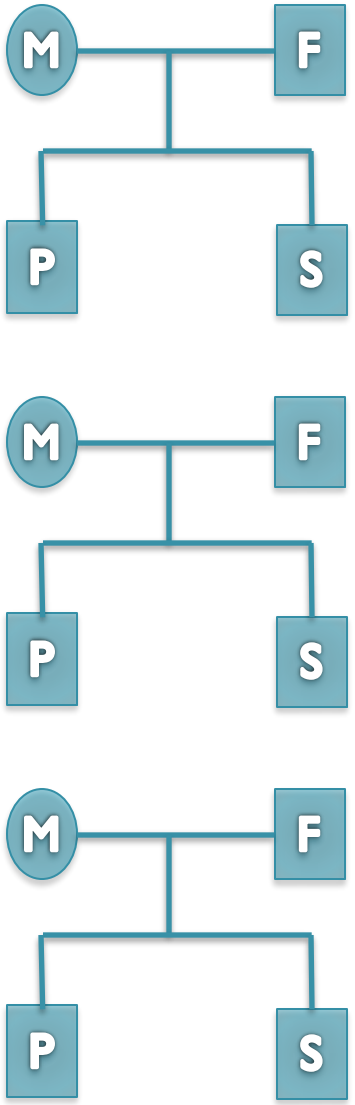
- Ten-fold increase in prevalence in 40 years, only partly explained by improved diagnosis and awareness.
- Studies also show that autism is four to five times more common among boys than girls.
- Specific causes remain elusive

Searching for the genetic risk factors

Search Strategy

- Thousands of families identified from a dozen hospitals around the United States
- Large scale genome sequencing of "simplex" families: mother, father, affected child, unaffected sibling
- Unaffected siblings provide a natural control for environmental factors

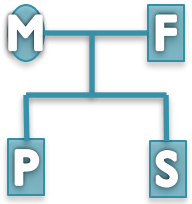
Are there any genetic variants present in affected children, that are not in their parents or unaffected siblings?



SFARI SIMONS FOUNDATION AUTISM RESEARCH INITIATIVE

De novo mutation discovery and validation

De novo mutations:
Sequences not inherited from your parents.




```
Reference:    ...TCAAATCCTTTTAATAAAGAAGAGCTGACA...

Father(1):    ...TCAAATCCTTTTAATAAAGAAGAGCTGACA...
Father(2):    ...TCAAATCCTTTTAATAAAGAAGAGCTGACA...

Mother(1):    ...TCAAATCCTTTTAATAAAGAAGAGCTGACA...
Mother(2):    ...TCAAATCCTTTTAATAAAGAAGAGCTGACA...

Sibling(1):   ...TCAAATCCTTTTAATAAAGAAGAGCTGACA...
Sibling(2):   ...TCAAATCCTTTTAATAAAGAAGAGCTGACA...

Proband(1):   ...TCAAATCCTTTTAATAAAGAAGAGCTGACA...
Proband(2):   ...TCAAATCCTTTTAAT****AAGAGCTGACA...
```

4bp heterozygous deletion at chr15:93524061 CHD2

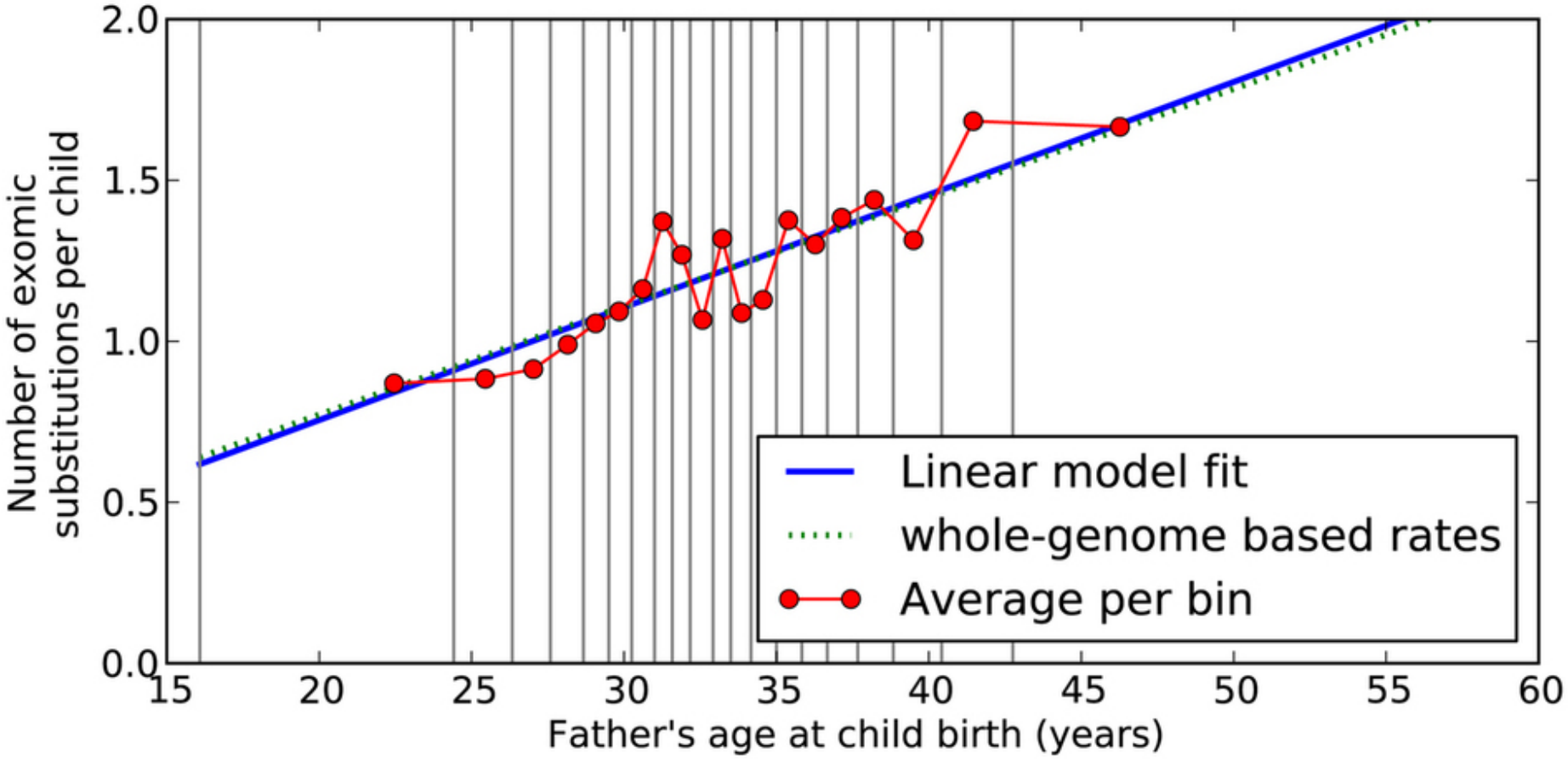
De novo Genetics of Autism

- In 593 family quads so far, we see significant enrichment in de novo ***likely gene killers*** in the autistic kids
  - Overall rate basically 1:1
  - 2:1 enrichment in nonsense mutations
  - 2:1 enrichment in frameshift indels
  - 4:1 enrichment in splice-site mutations
  - Most de novo originate in the paternal line in an age-dependent manner (56:18 of the mutations that we could determine)

- Observe strong overlap with the 842 genes known to be associated with fragile X protein FMPR
  - Related to neuron development and synaptic plasticity
  - Also strong overlap with chromatin remodelers

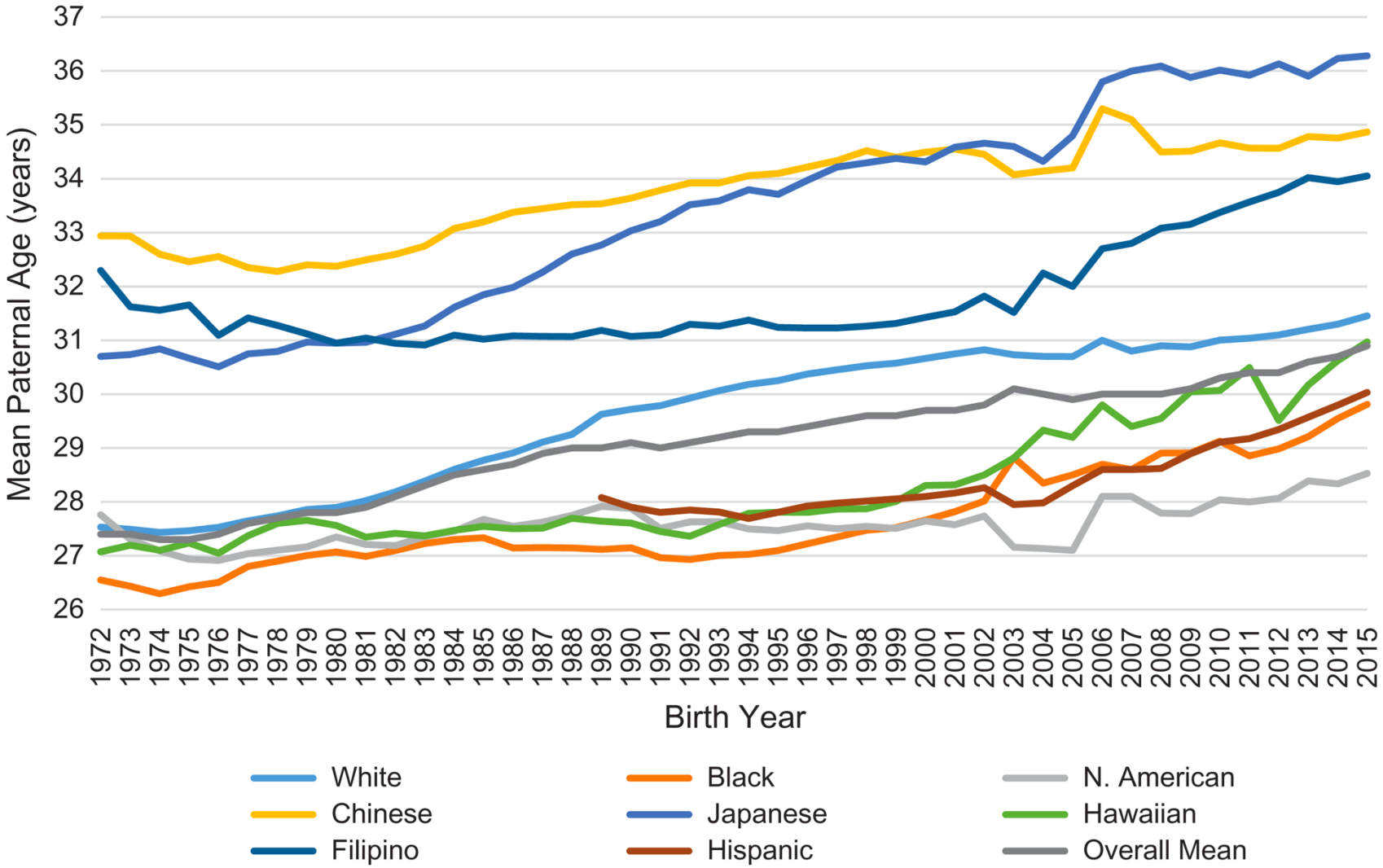
Accurate de novo and transmitted indel detection in exome-capture data using microassembly.
Narzisi *et al* (2014) Nature Methods doi:10.1038/nmeth.3069

De novo Mutations in Men



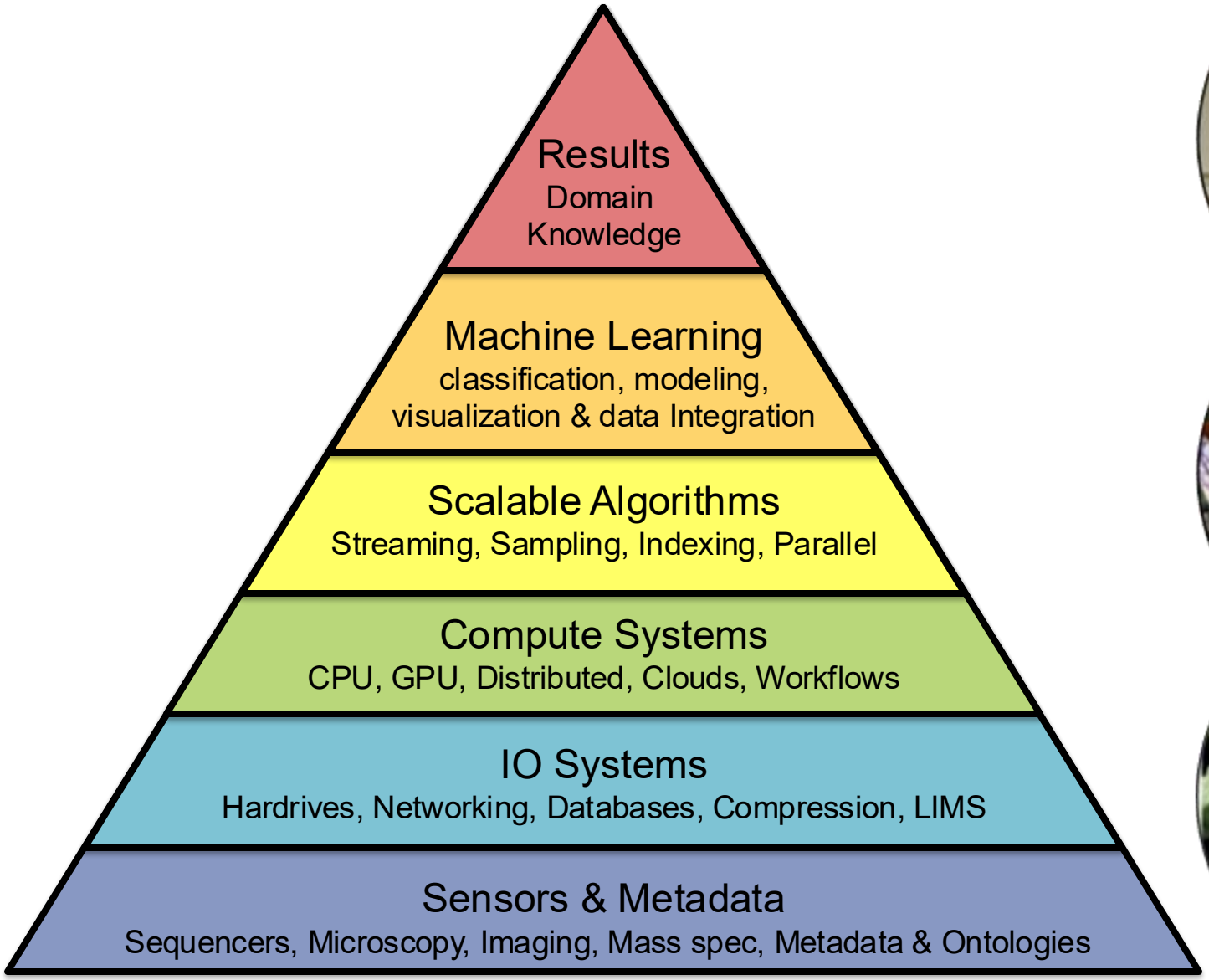
The contribution of de novo coding mutations to autism spectrum disorder
Iossifov *et al* (2014) *Nature*. doi:10.1038/nature13908

Age of Fatherhood



The age of fathers in the USA is rising: an analysis of 168 867 480 births from 1972 to 2015
Khandwala *et al* (2017) *Human Reproduction. https://doi.org/10.1093/humrep/dex267*

Applied Genomics



Next Steps

1. Reflect on the magic and power of DNA ☺
2. Check out the course webpage
3. Register on Piazza
4. Get Ready for assignment 1
    1. Set up conda
    2. Set up Dropbox for yourself!
    3. Get comfortable on the command line