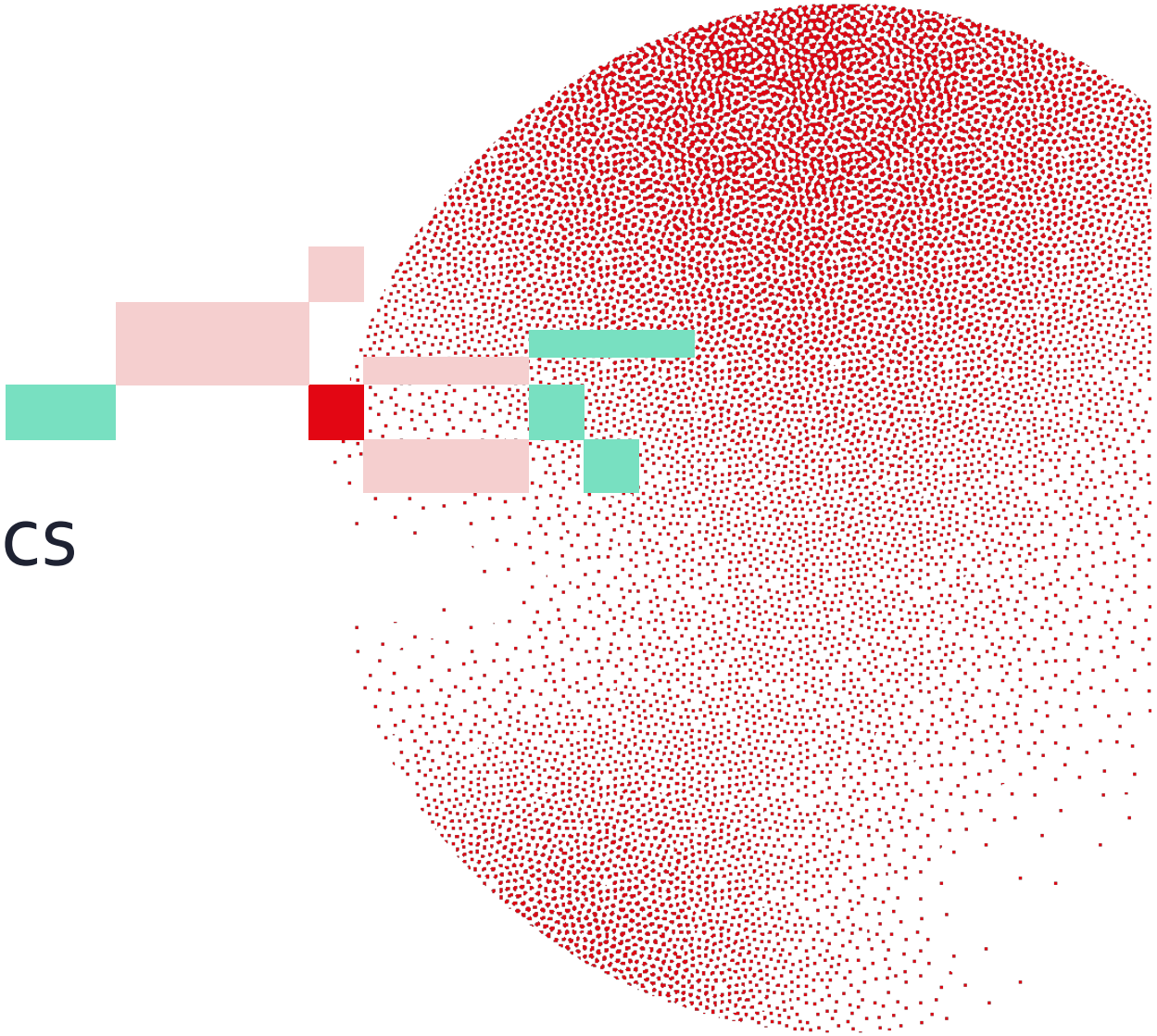
Swiss Institute of Bioinformatics

INTRODUCTION TO BIOINFORMATICS:

Clinical Bioinformatics

V. Barbié, Clinical Bioinformatics

Zürich, 05 December 2023



Outline

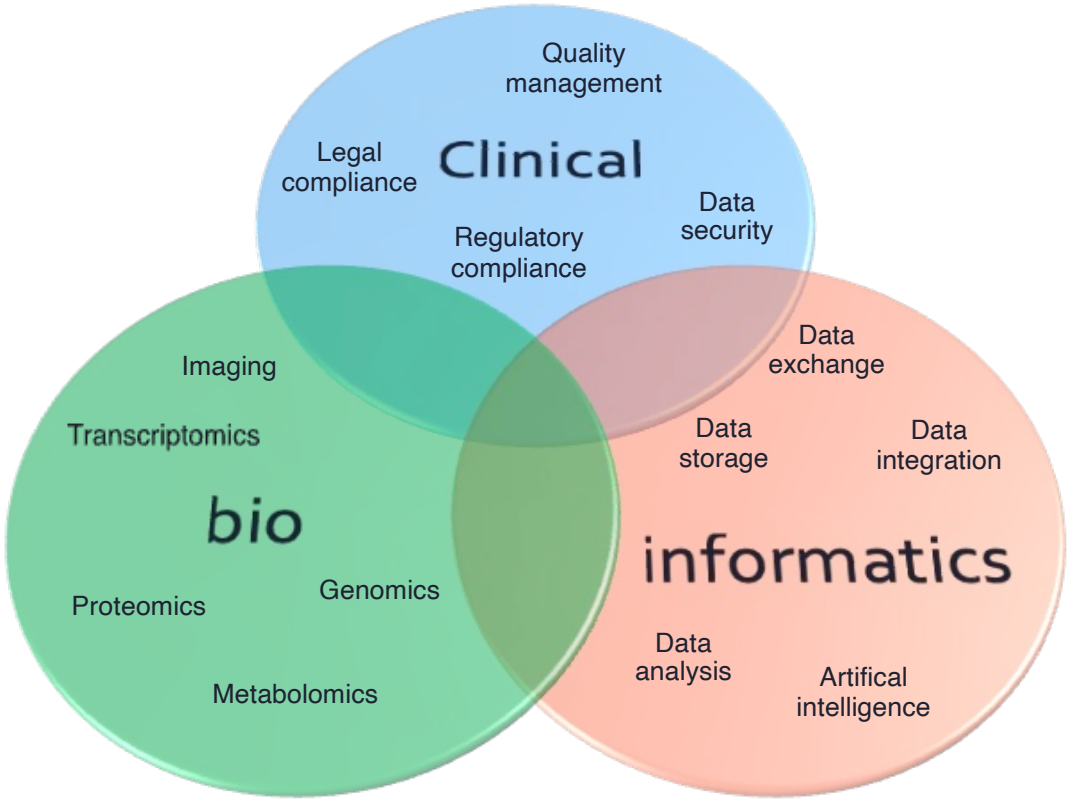
What is
clinical bioinformatics

Why clinical bioinformatics?
Next Generation Sequencing (NGS) in medical diagnosis

Overview of an oncology NGS diagnostic pipeline

Other considerations

What is clinical bioinformatics?



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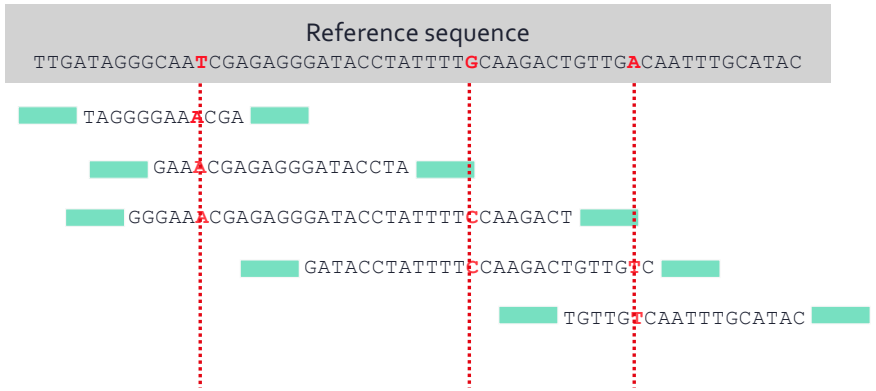
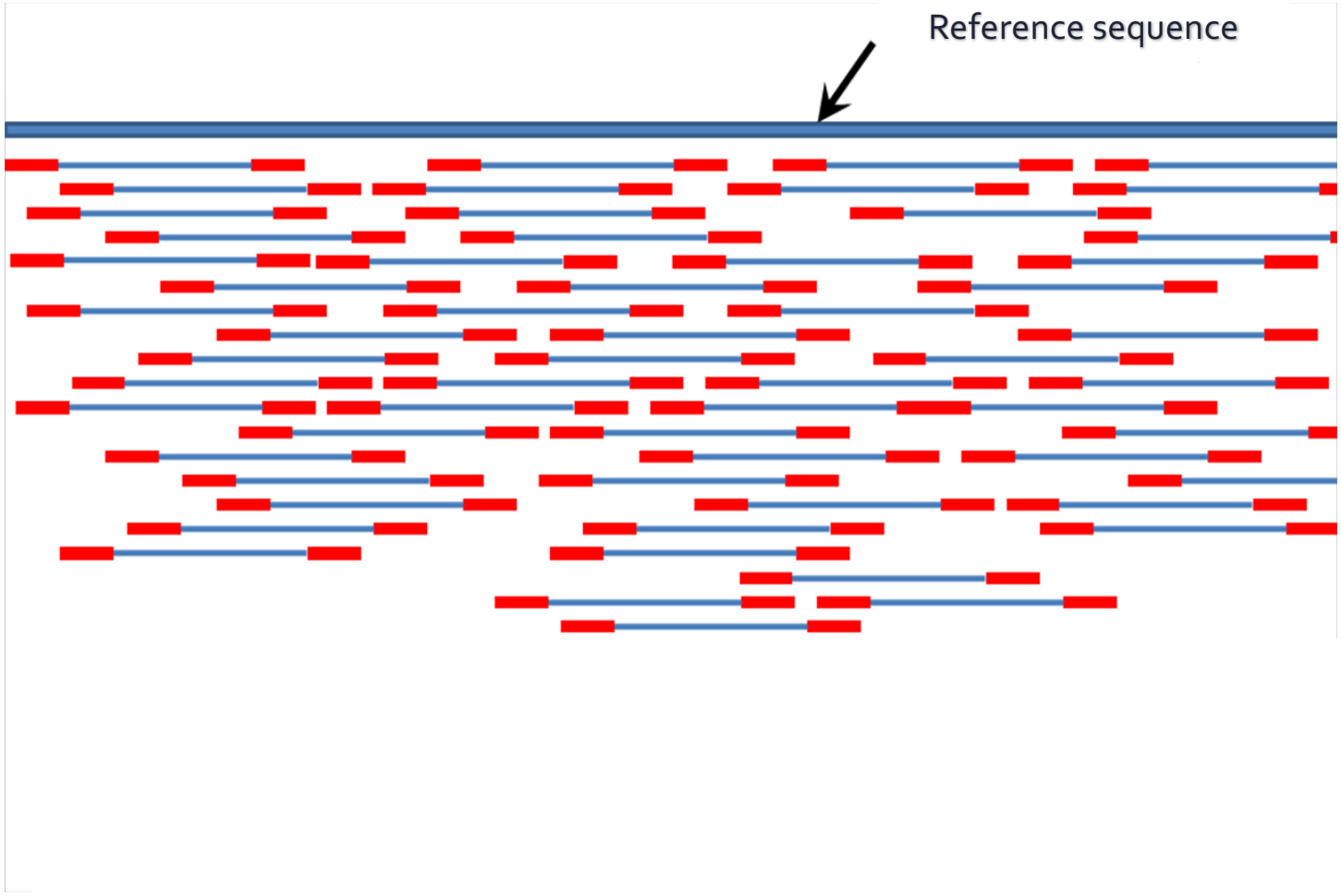
Next Generation Sequencing principle

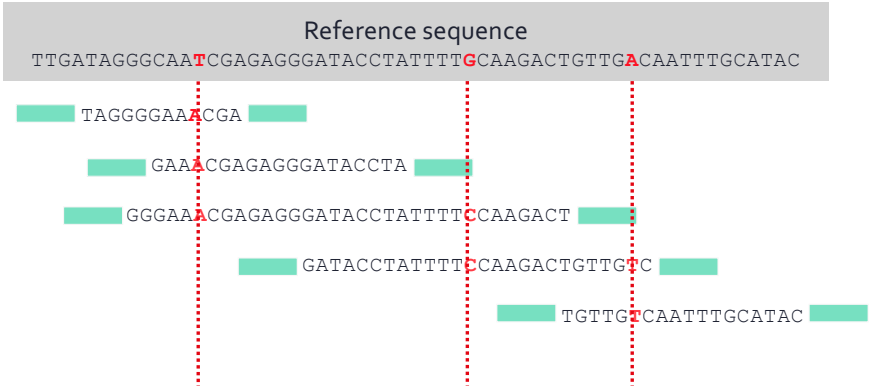


Next Generation Sequencing principle

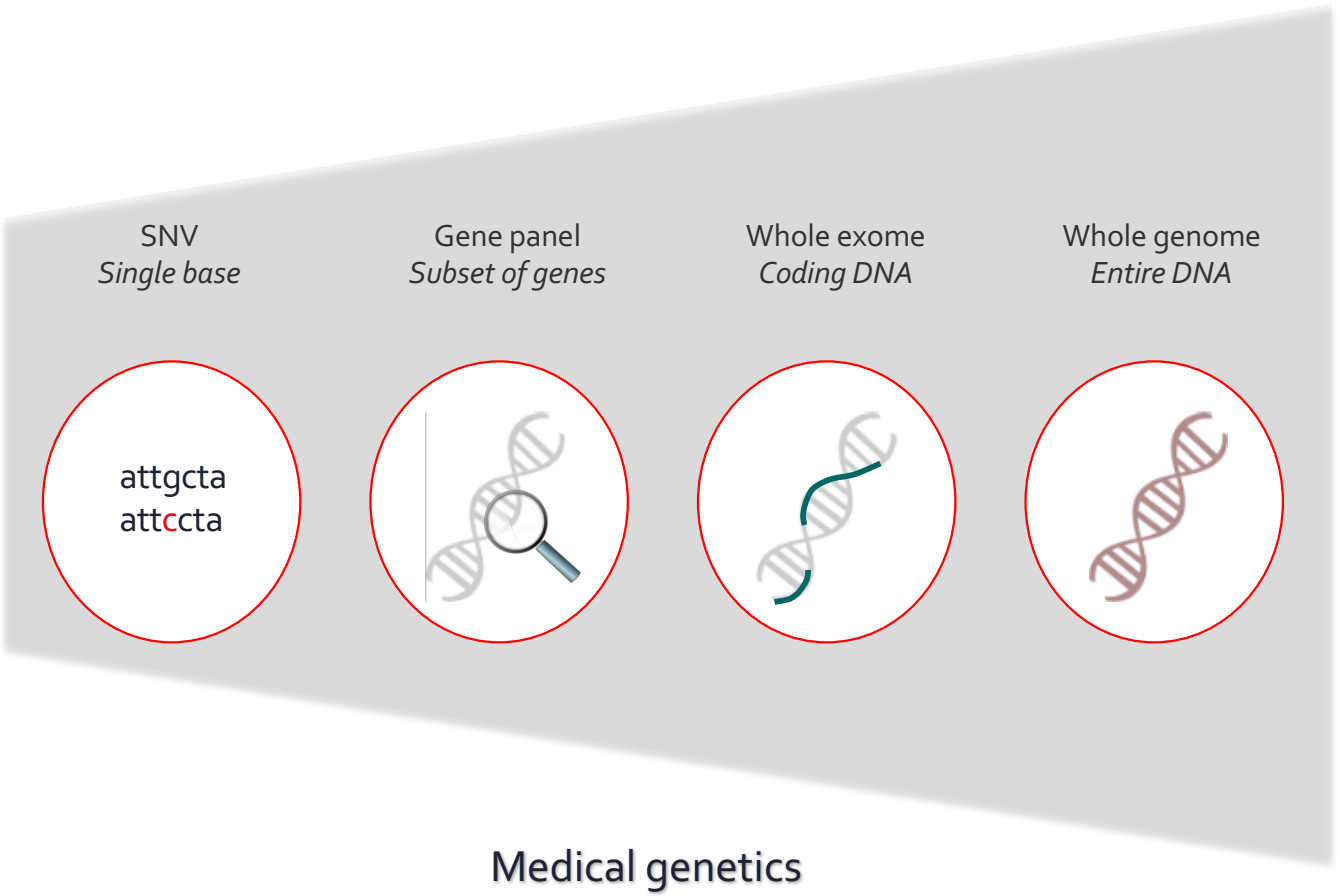


Examples of NGS clinical applications

	Source DNA	Reference DNA
Oncology	Patient tumor or blood	Consensus human genome Germline



Scale matters



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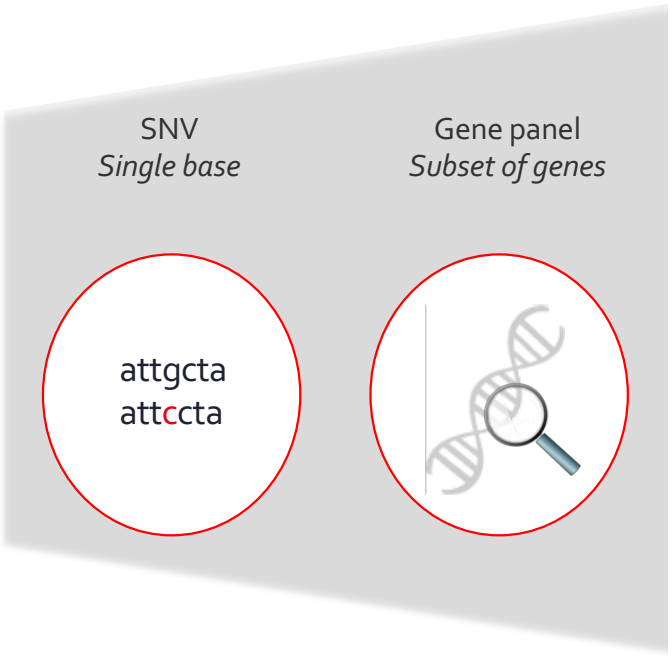

Oncology

Reimbursement is limited

Clinically-actionable variants

Results turn around time

Incidental findings management

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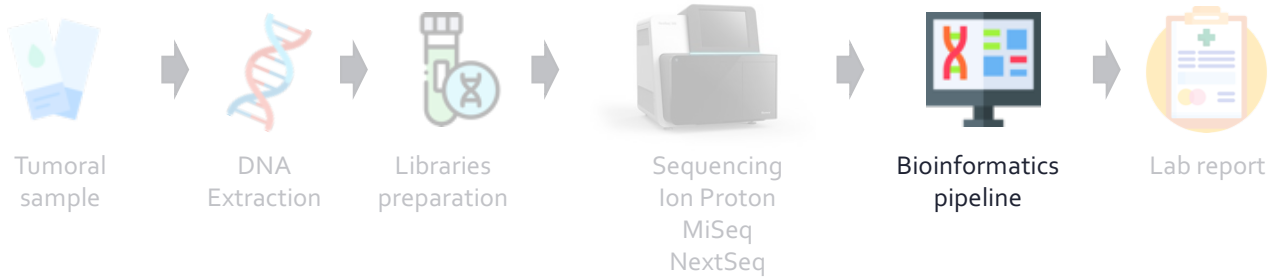
NGS in cancer diagnosis?

- Identify single nucleotide variants (SNVs), insertions-deletions (indels) to inform clinical management

Overview of a NGS bioinformatics pipeline

- Gene panels analysis in clinical routine
  - Identify **differences**
  - Identify **artifacts**: quality control
  - Identify **somatic** vs. germline variants
  - Variant **annotation**: does it provide clinically-useful information?

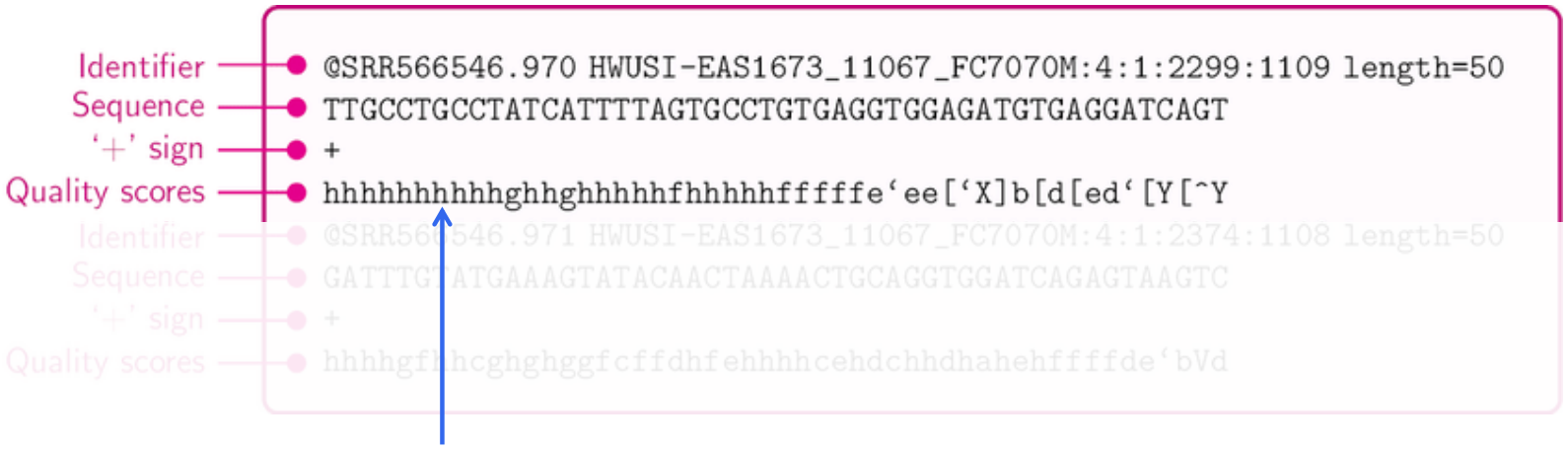
Overview of a NGS bioinformatics pipeline



Reads filtering

Quality control

Out of the sequencer: FASTQ file

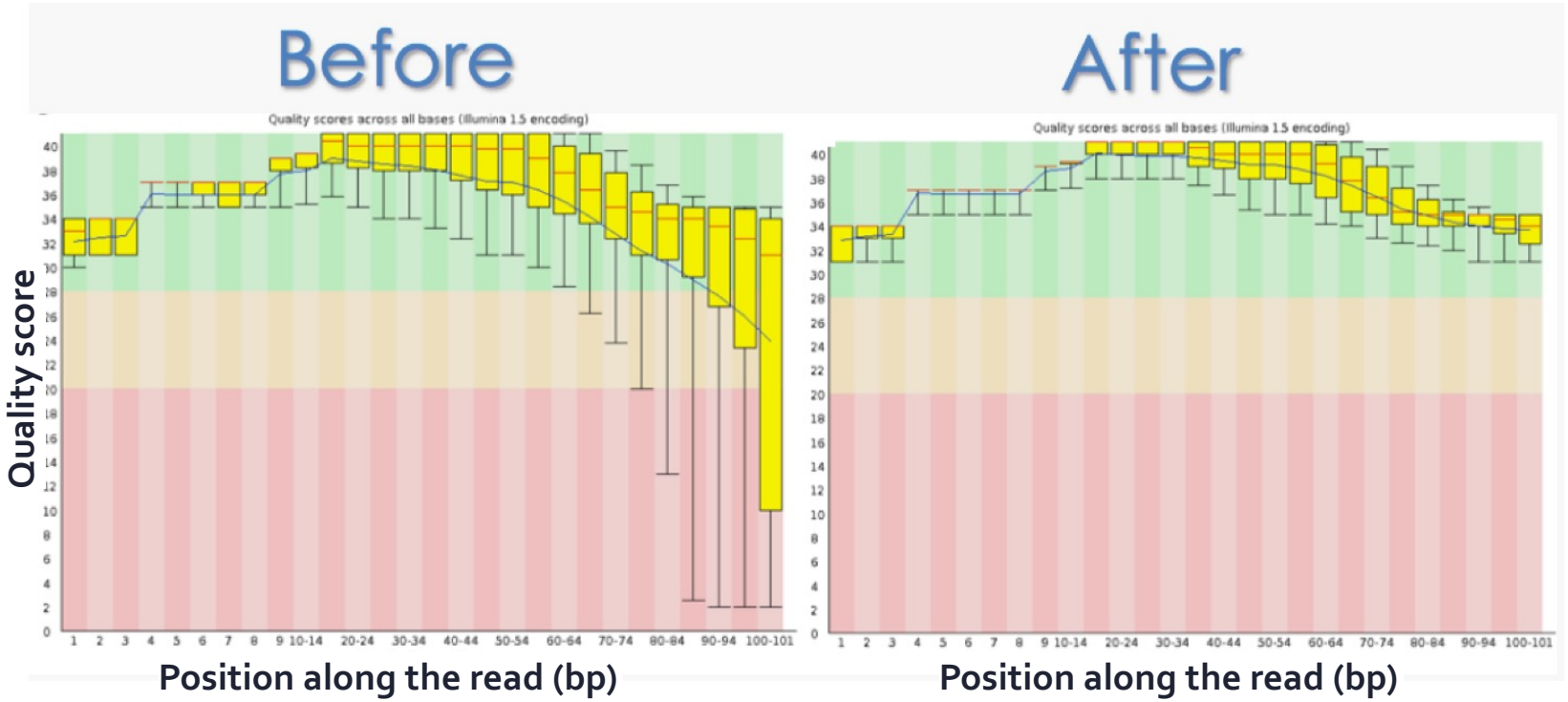


Each nucleotide has a **quality score (Phred score)**
representing the probability that a base was miscalled by the sequencer

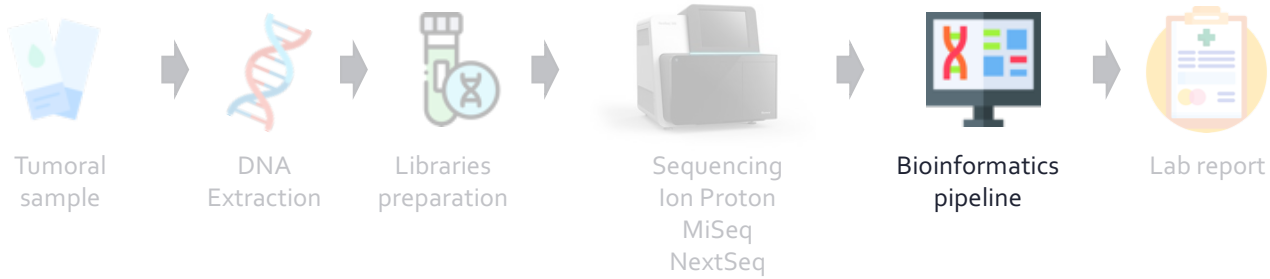
$$Q = -10 \log_{10} P$$

Phred Score	Prob. of incorrect base call	Base call accuracy	Code
10	1 in 10	90%	J
20	1 in 100	99%	T
30	1 in 1'000	99.9%	^
40	1 in 10'000	99.99%	h

Quality-based reads trimming



Overview of a NGS bioinformatics pipeline

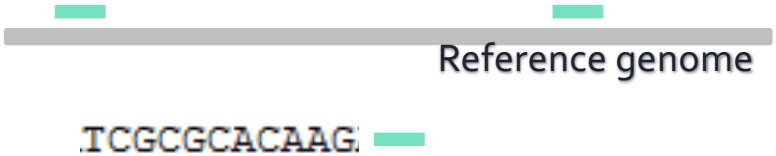


Reads filtering → Reads mapping

Quality control

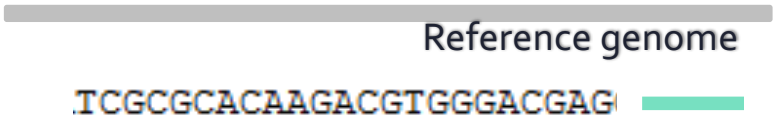
Variant identification

Let's align the reads



! **Short reads** are likely to map at several positions along the reference genome

! **Mismatches** and **gaps** allowed
→ algorithms have scoring functions

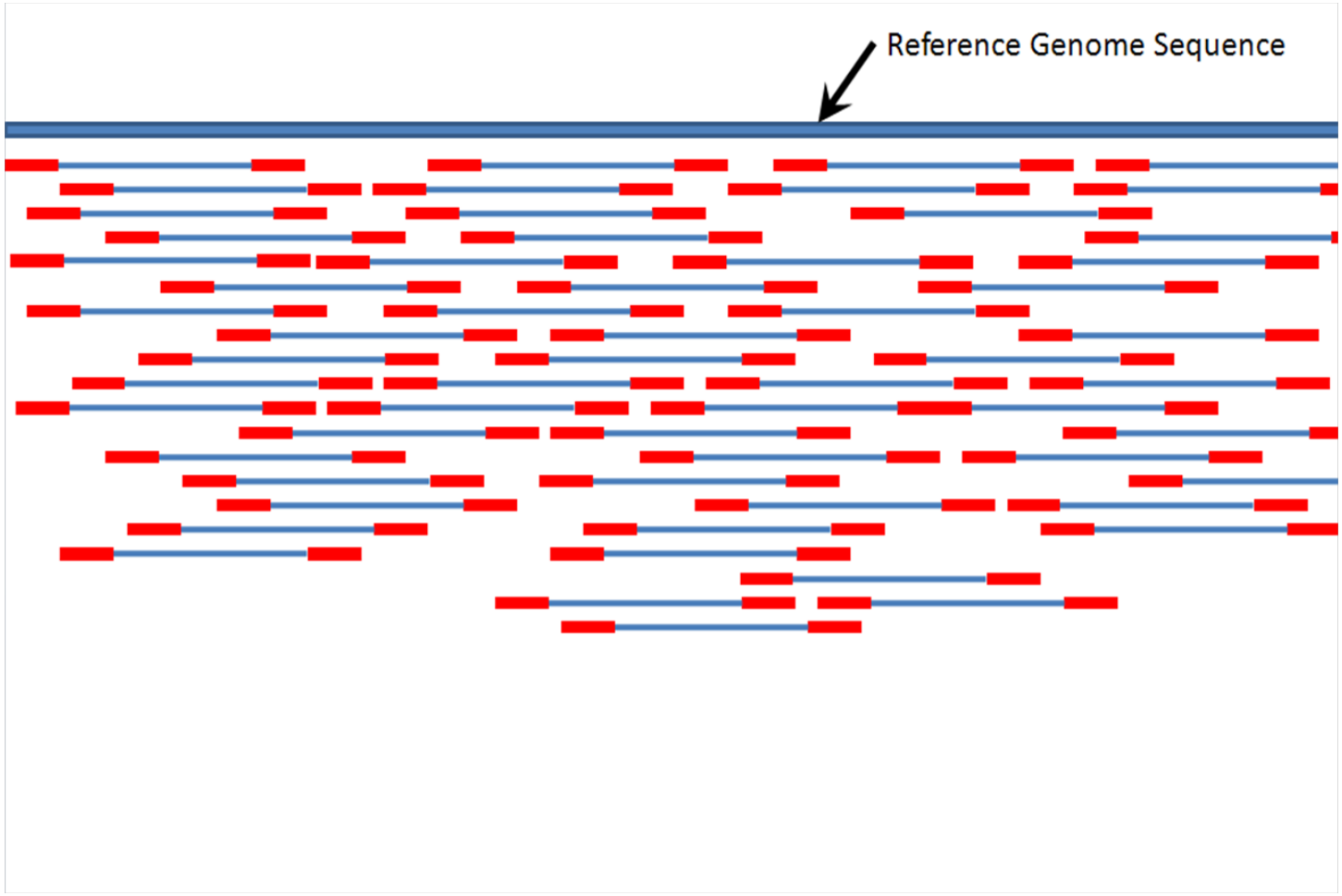


! **Longer reads** are less ambiguous
→ but computationally more expensive

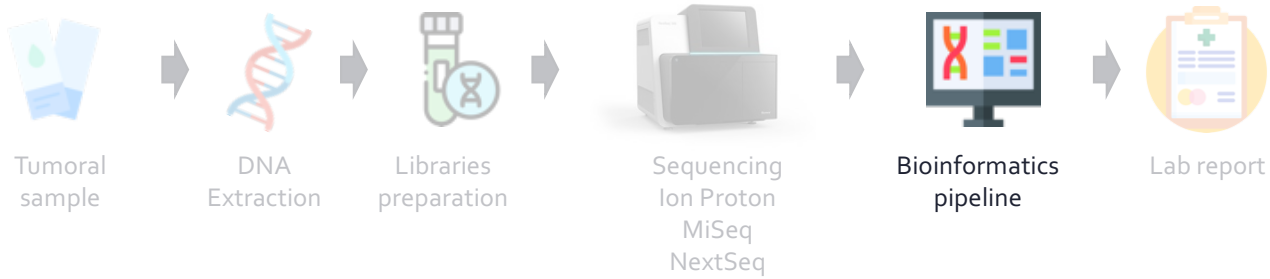
Paired-end sequencing

Much better alignment on across regions difficult to sequence (e.g. repetitive regions)

Mapping: finding the best position for each read



Overview of a NGS bioinformatics pipeline



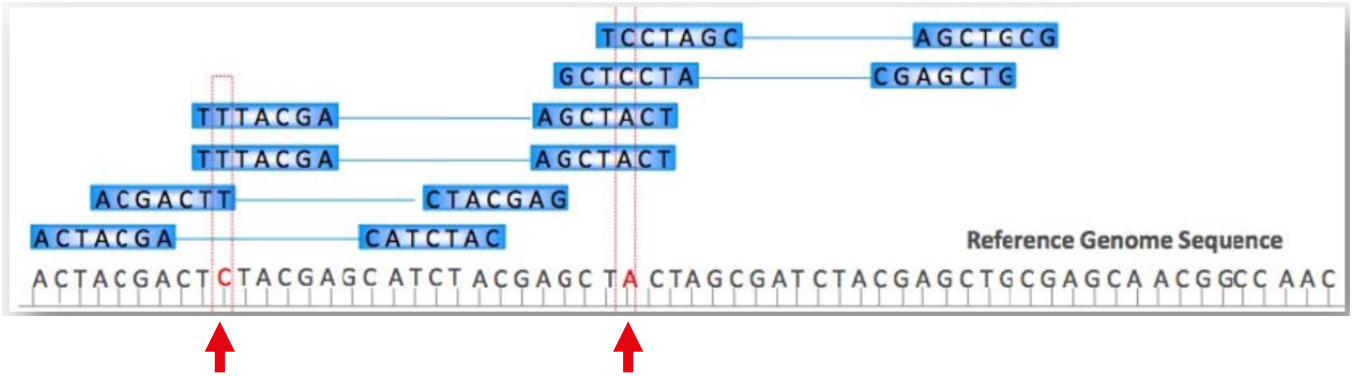
Reads filtering → **Reads mapping** → **Variant calling**

Quality control

Variant identification

Variant identification

Variant calling: putting it all together

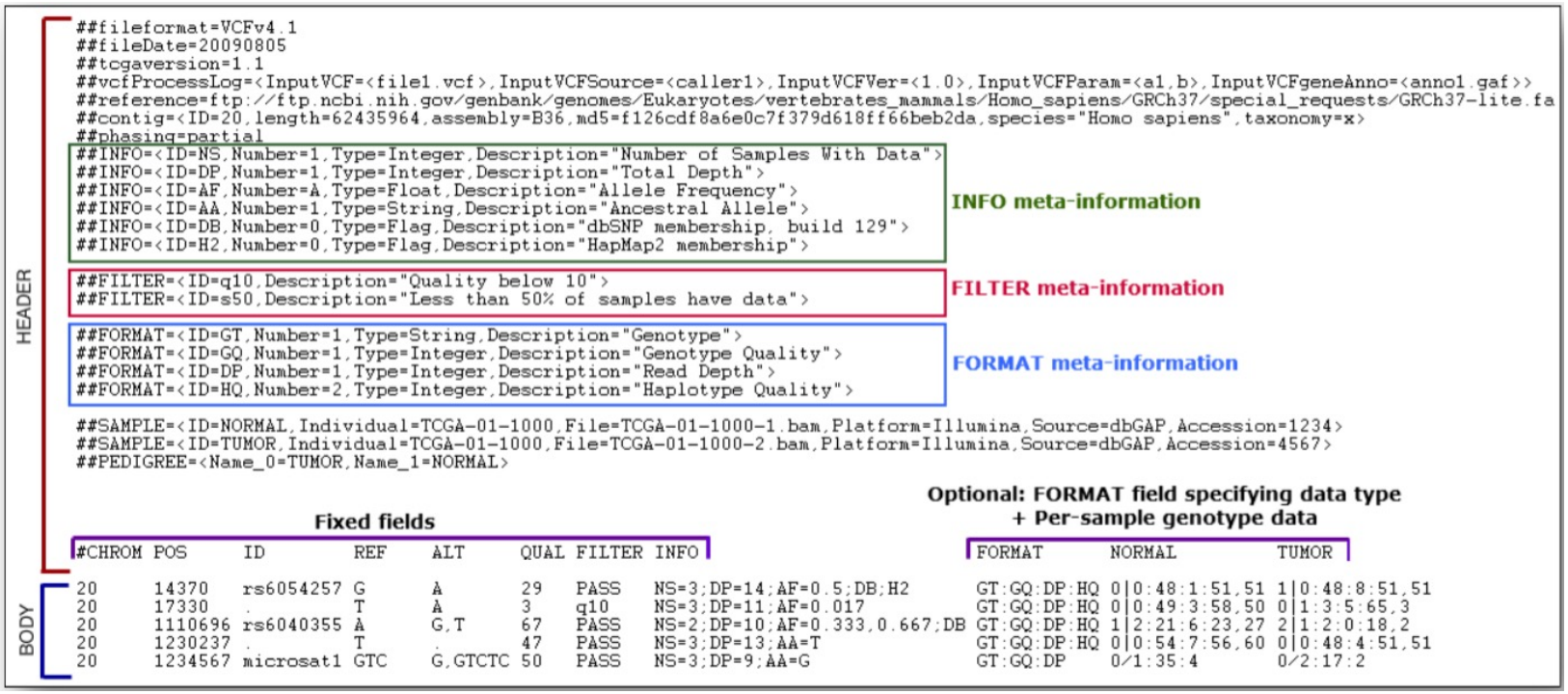


True variant or technical error?

- Performed by the sequencer software or the bioinformatician
- Germline vs somatic calling
  - Germline: constitutional genome analysis, where variants occur in 50% (heterozygous) or 100% (homozygous) of the reads.
  - Somatic: no ploidy assumption, low frequency alleles.

Output of the variant caller: VCF

VCF: Variant Call Format



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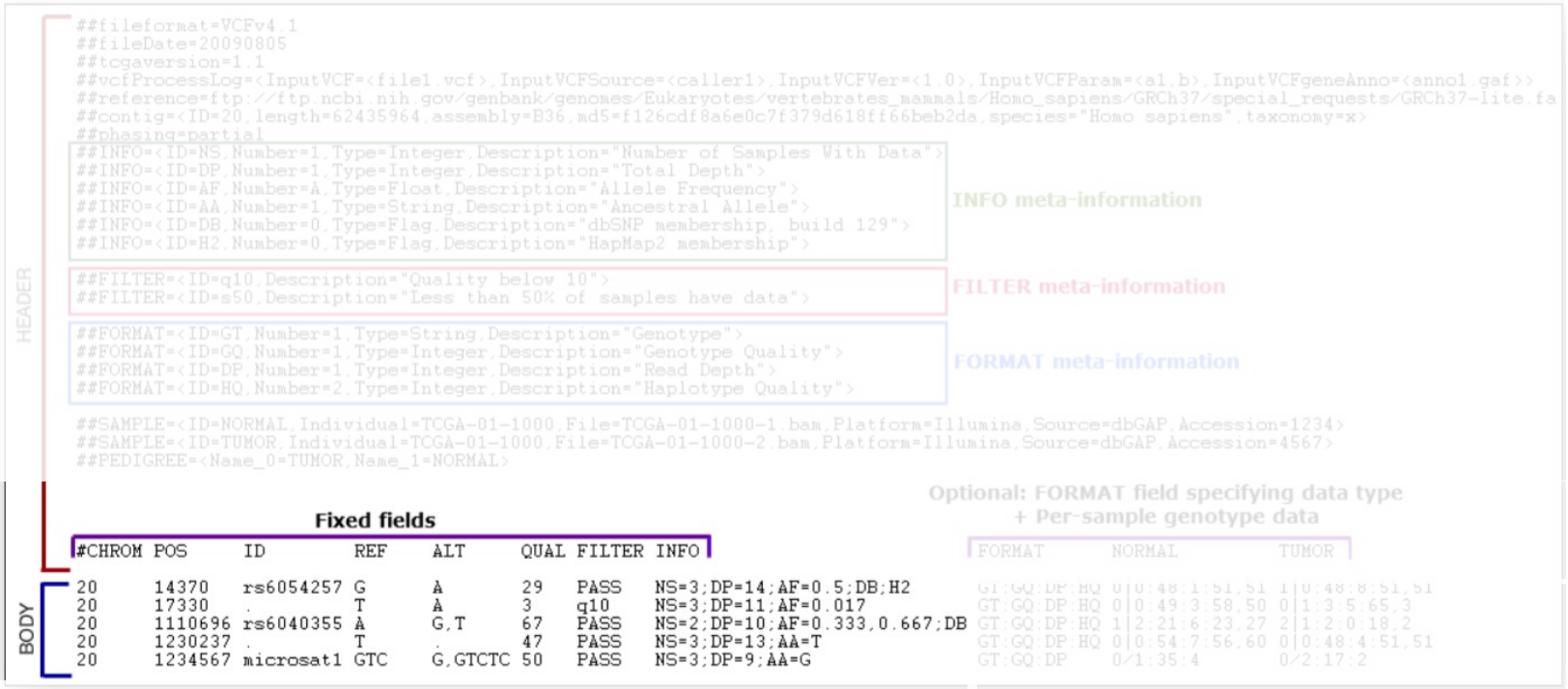

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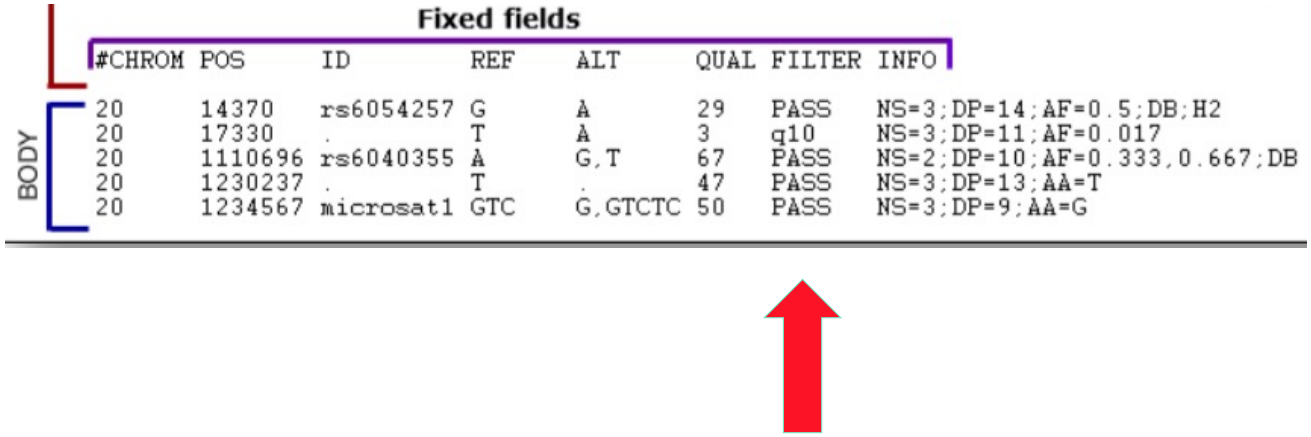
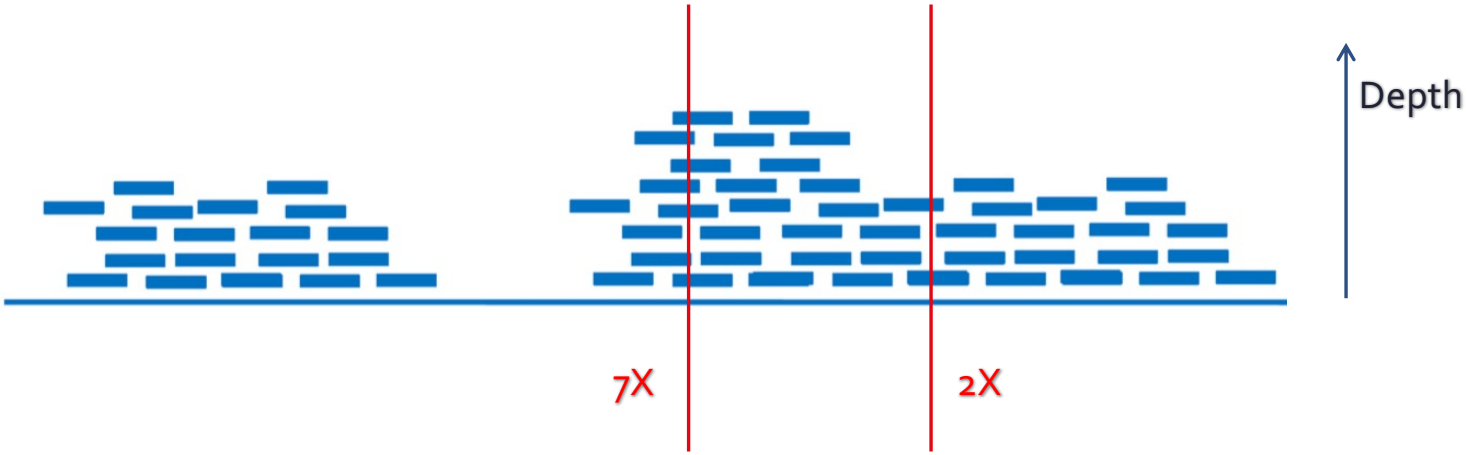


Things to watch out when assessing variant quality

Depth

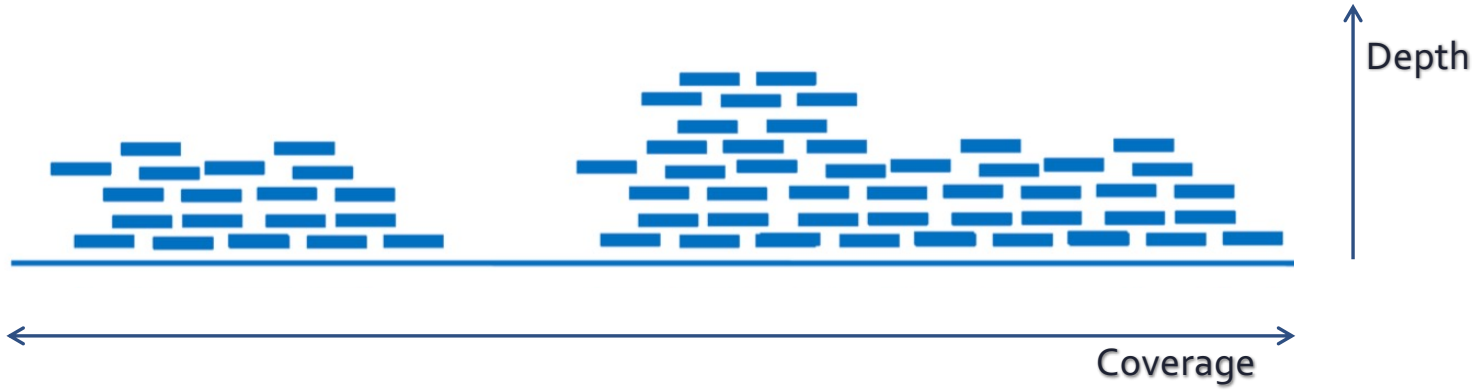
Depth: nb of reads that include a given nucleotide, at a given position



- Diagnosis: gene panel at 1500X, whole exome at 100X
- In oncology, impossible to detect low frequency clones with exome analyses

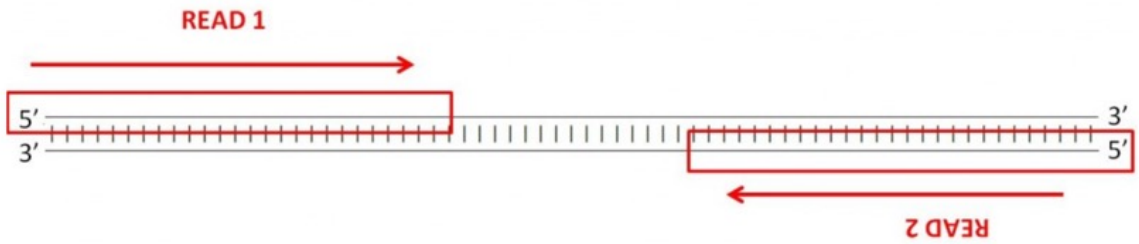
Coverage

Coverage: % or nb of bases of a reference genome that are covered with a certain depth, e.g. 90% at 5X



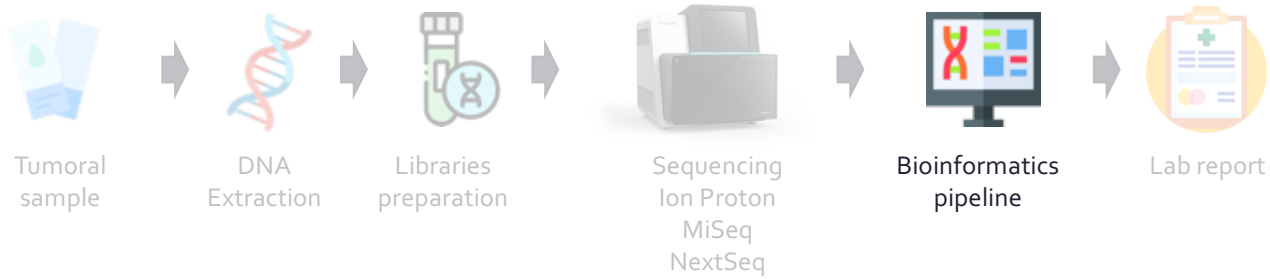
Strand bias in paired-end sequencing

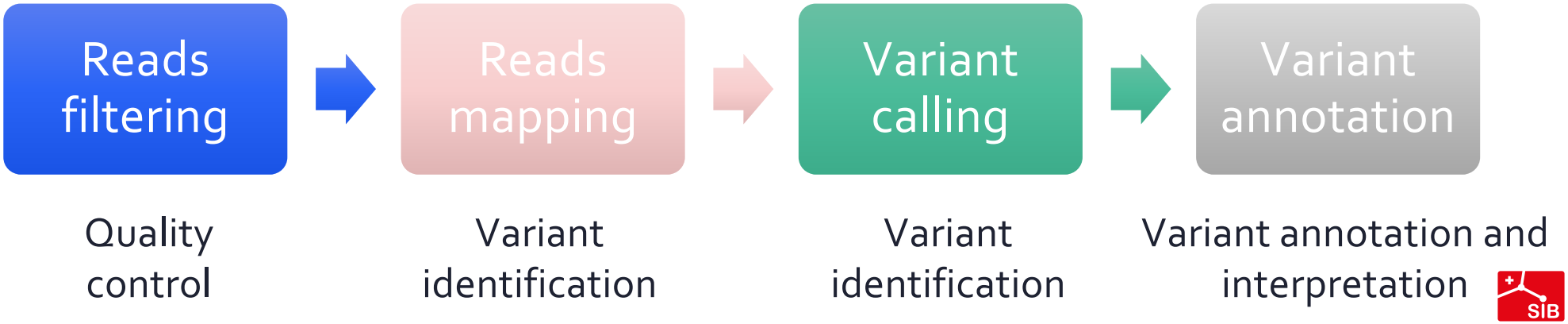
- Both DNA strands are sequenced
- Normal mutations should occur on both with equal frequencies



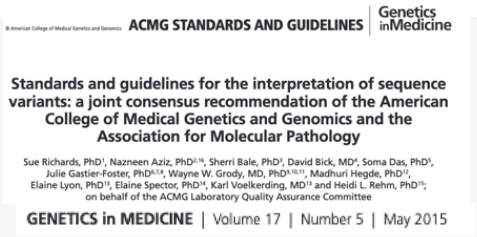
http://www.cureffi.org/2012/12/19/forward-and-reverse-reads-in-paired-end-sequencing/

Overview of a NGS bioinformatics pipeline





Medical genetics: focus on pathogenicity


ACMG STANDARDS AND GUIDELINES | Genetics inMedicine

Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology

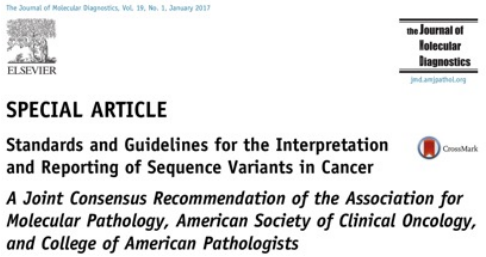
Sue Richards, PhD[1], Nazneen Aziz, PhD[2,16], Sherri Bale, PhD[3], David Bick, MD[4], Soma Das, PhD[5], Julie Gastier-Foster, PhD[6,7,8], Wayne W. Grody, MD, PhD[9,10,11], Madhuri Hegde, PhD[12], Elaine Lyon, PhD[13], Elaine Spector, PhD[14], Karl Voelkerding, MD[13] and Heidi L. Rehm, PhD[15]; on behalf of the ACMG Laboratory Quality Assurance Committee

GENETICS in MEDICINE | Volume 17 | Number 5 | May 2015

Find pathogenic variants

i.e. genetic alterations increasing an individual's susceptibility or predisposition to a certain disorder

Oncology: focus on clinical significance



The Journal of Molecular Diagnostics, Vol. 19, No. 1, January 2017

ELSEVIER

the Journal of Molecular Diagnostics

jmd.amjpathol.org

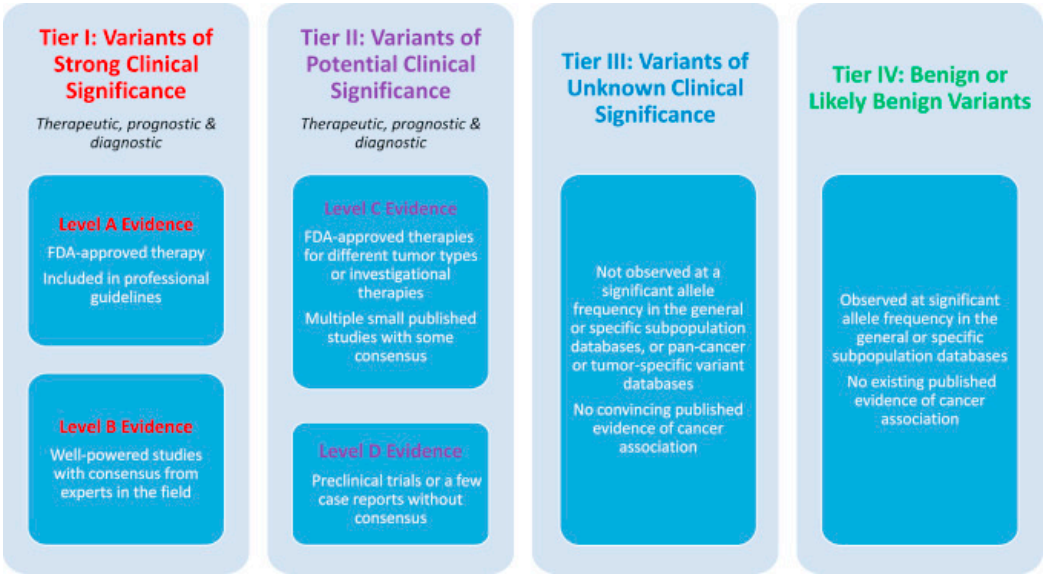
SPECIAL ARTICLE

Standards and Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer

A Joint Consensus Recommendation of the Association for Molecular Pathology, American Society of Clinical Oncology, and College of American Pathologists

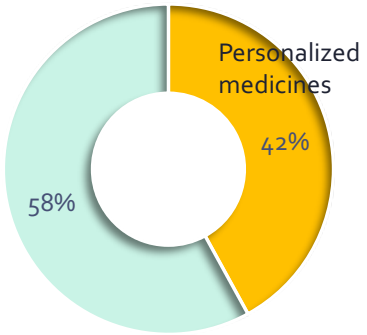
Find actionable variants

i.e. genetic alterations possibly having an impact on clinical care

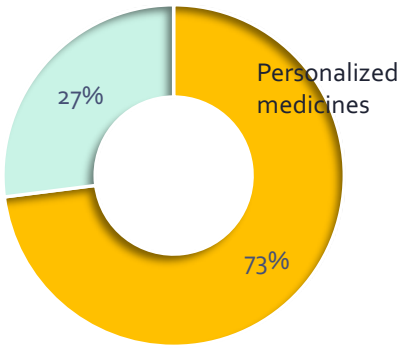


Categories of markers

Predisposition	Indicates risk to develop a disease
Diagnostic	Supports disease characterization
Prognostic	Indicates disease evolution
Predictive	Supports treatment decisions



All drugs in development



Oncology drugs in development

Bioinformatics to the rescue…

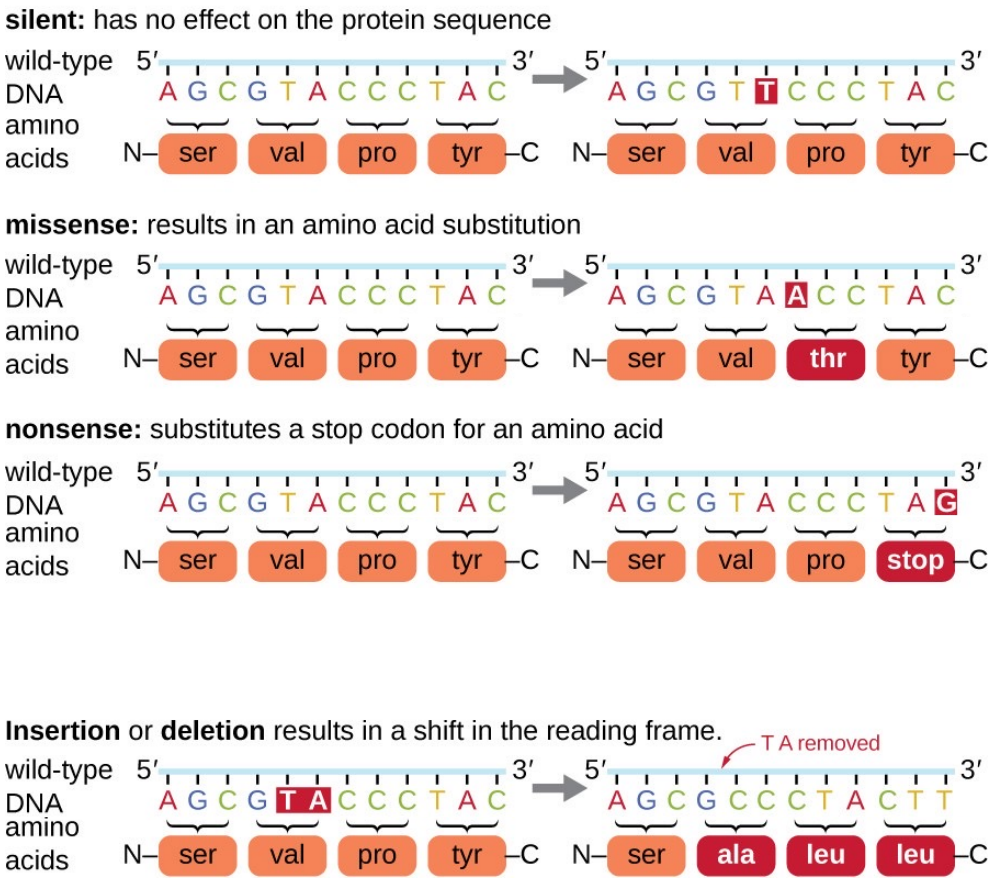
- Location of the variant (e.g. intron, exon, regulatory region…)
- Genes and transcripts affected by the variant
- Predict variant effect (e.g. stop gained, missense…)

http://www.ensembl.org/info/docs/tools/vep/index.html

Locating variants

- Convert genomic coordinates (chromosome, position) to the corresponding cDNA/amino-acid coordinates
- HGVS nomenclature (http://varnomen.hgvs.org)
  - Substitution c.76A>T
  - Deletion c.76delA
  - Insertion c.76_77insG
  - Genomic sequence g.476A>T
  - Protein sequence p.Lys76Asn
- Important to store for tracking
  - Version of the human genome assembly
  - Accession and version of the mRNA transcripts

Predicting variants effect on the protein



Point mutations (single base substitution)

Frameshift mutations (insertion or deletion of one or several bases)

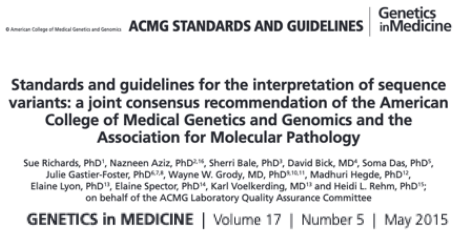
https://courses.lumenlearning.com/microbiology/chapter/mutations/

Bioinformatics to the rescue…

- Location of the variant (e.g. intron, exon, regulatory region…)
- Genes and transcripts affected by the variant
- Predict variant effect (e.g. stop gained, missense…)
- Predict variant impact on protein function, splicing

Predicting variants impact: examples of tools

TOOLS	SnpEff (ClinEff)	VEP	SIFT	PolyPhen-2	FATHMM
Variant effect and location (sequence ontology)	✓	✓			
Prediction of impact (score or category)	✓	←	✓	✓	✓
Features used for impact prediction	Rules based on variant effect (stop gained, lost…)		AA conservation in related seq.	AA conservation and structural features	AA conservation and protein tolerance to mutations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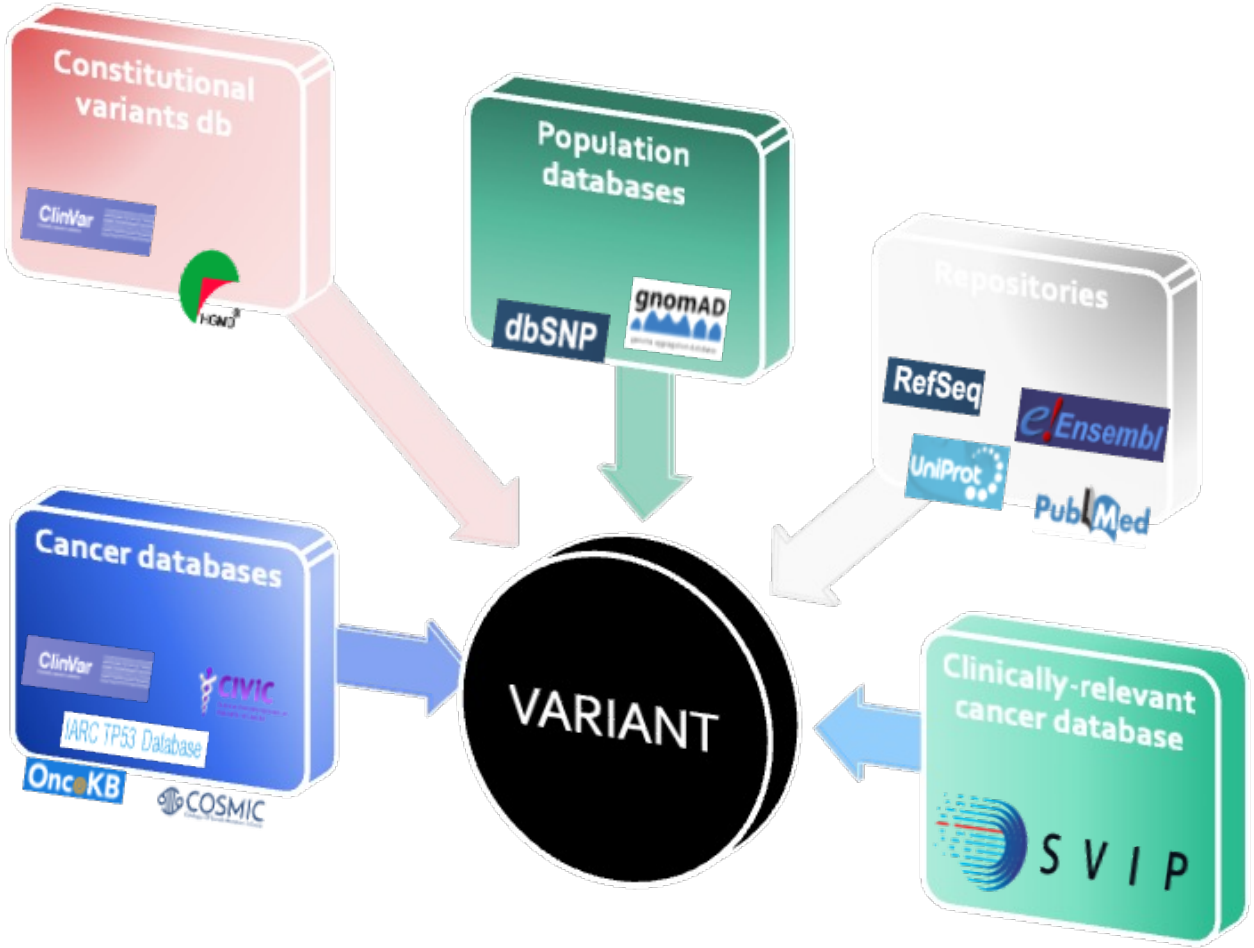
Use a combination of tools and keep variants with consensus prediction.

(not exhaustive)

Bioinformatics to the rescue…

- Location of the variant (e.g. intron, exon, regulatory region…)
- Genes and transcripts affected by the variant
- Predict variant effect (e.g. stop gained, missense…)
- Predict variant impact on protein function, splicing
- Retrieve annotations from public databases

Knowledge bases



Non exhaustive

Important questions

- Is it prevalent in the cancer subtype of interest?
- Is it known in other cancer subtypes or diseases?
- Is it present in the general population?
- Is it related to an ongoing clinical trial?
- What is the evidence level? Observed vs. predicted
- Are there other known variants in the same gene?

Important questions

- Is the mutation in an evolutionarily conserved region accross species?

Front Pharmacol. 2015 Mar 10;6:1. doi: 10.3389/fphar.2015.00001

I found a damaging mutation: is it always bad?

- Keep the mutation in context: what is the gene function?
  - **Tumor suppressor gene**
    Damaging mutations are pathogenic.

  - **Oncogene**
    Activating mutations are pathogenic.
    (beware: damaging mutation can be activating!)

Keep the gene function in mind
when interpreting its deleteriousness

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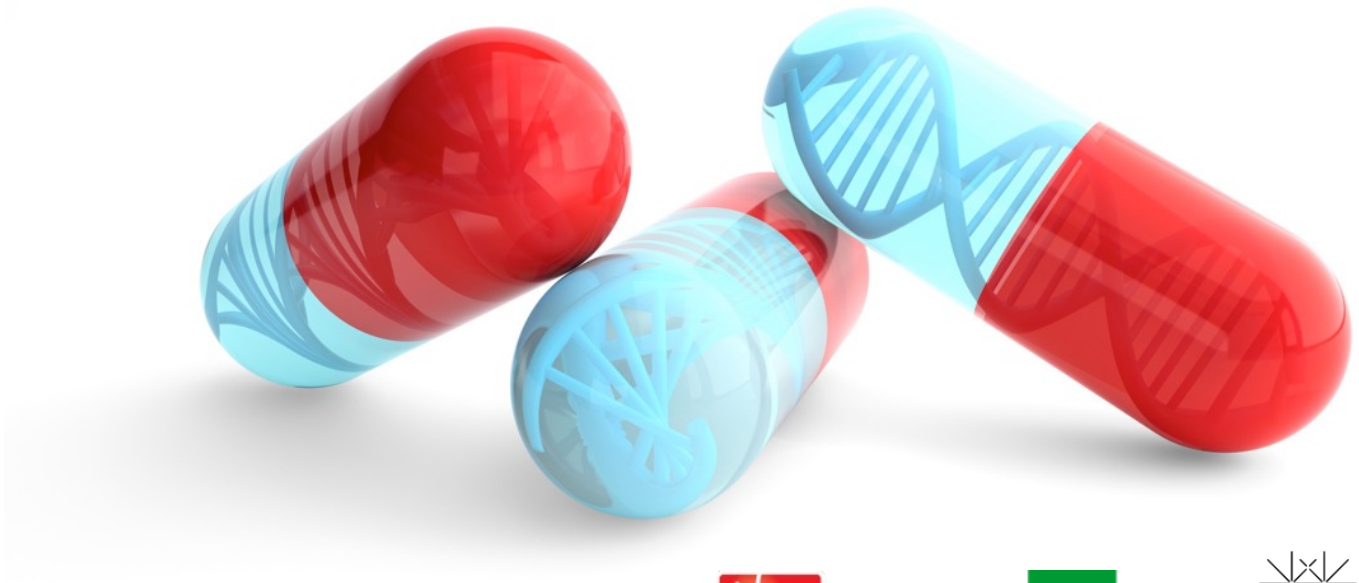
Real-life constraints in the clinics

Certificate of Advanced Studies (CAS) in Personalized molecular oncology

pmo.unibas.ch



Universitätsspital Basel

SIB Swiss Institute of Bioinformatics

CHUV

UNI BASEL

CAS PMO: 4 modules and a mini-thesis

Tumor biology & Genetics
4 days

Lausanne

- Cytogenetics and molecular genetics
- Genetic modifications
- Tumor biology: solid and hematological
- Tumor genetics

Molecular Pathology
4 days

Basel

- Omics technologies
- From sample to data: extraction, sequencing, panels
- Quality control and accreditation
- Molecular profile interpretation, reports

Clinical Bioinformatics
4 days

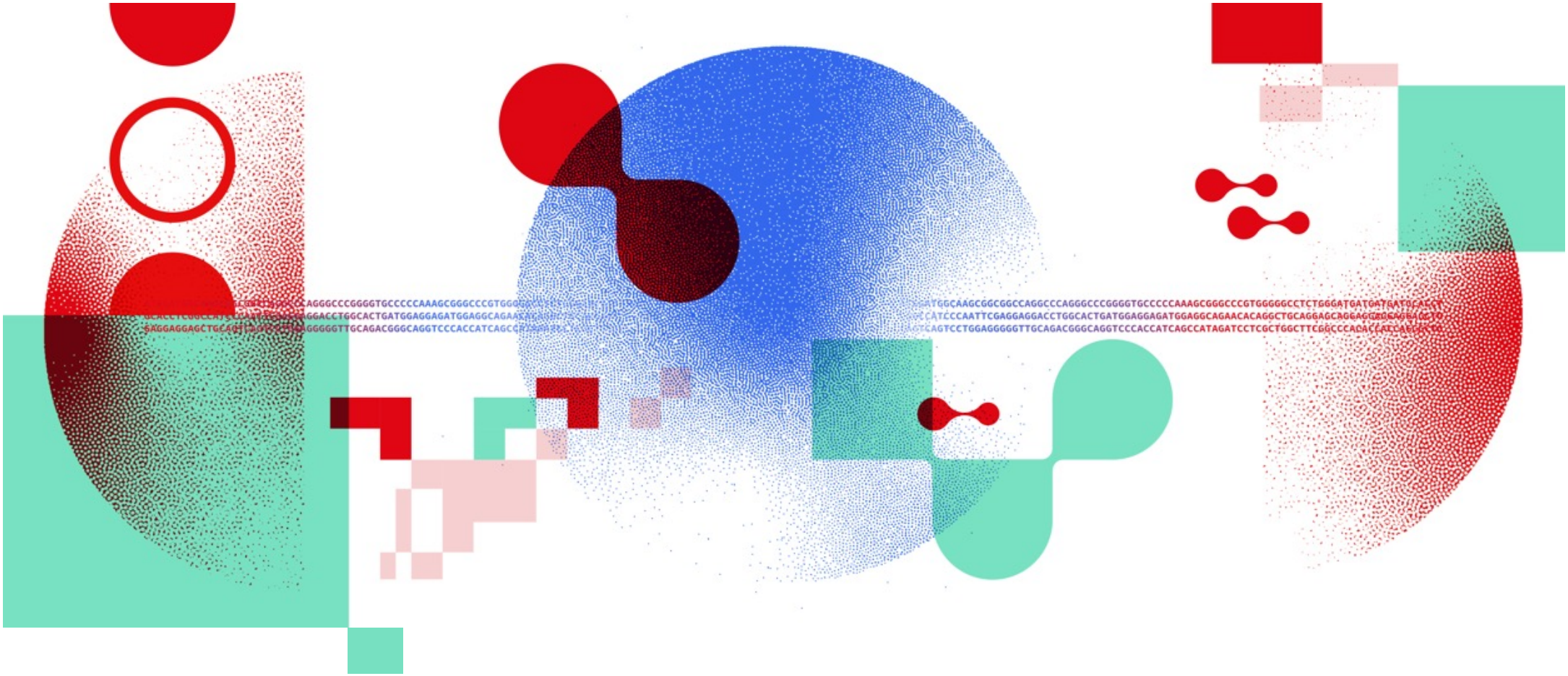
Lausanne

- NGS data processing: mapping, calling, annotation
- Data quality control
- Hardware, security, privacy
- Artificial intelligence applications

Clinical Oncology
4 days

Basel

- Tumor physiology & immunology
- Prognostic and predictive markers
- Interpretation of genetic results
- Clinical trials and tumor board



Thank you

DATA SCIENTISTS FOR LIFE

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