

Introduction to RNA-seq sequencing: Preprocessing

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Last edited on 31 October, 2022

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1 The study of gene expression

- The first part of this course focussed on proteomics, studying the concentration of proteins in biological samples. We have seen that identification of proteins and measuring their respective concentrations are extremely challenging, leading to many technological and statistical challenges in order to interpret these data.
- In the second part of the course, we will focus on measuring gene expression, i.e., measuring the concentration of mRNA molecules, that may eventually be translated into proteins, but may also have functions on their own.

```
include_graphics("./images_sequencing/centralParadigm.png")
```

- Alternative splicing

```
include_graphics("./images_sequencing/alternative_splicing.png")
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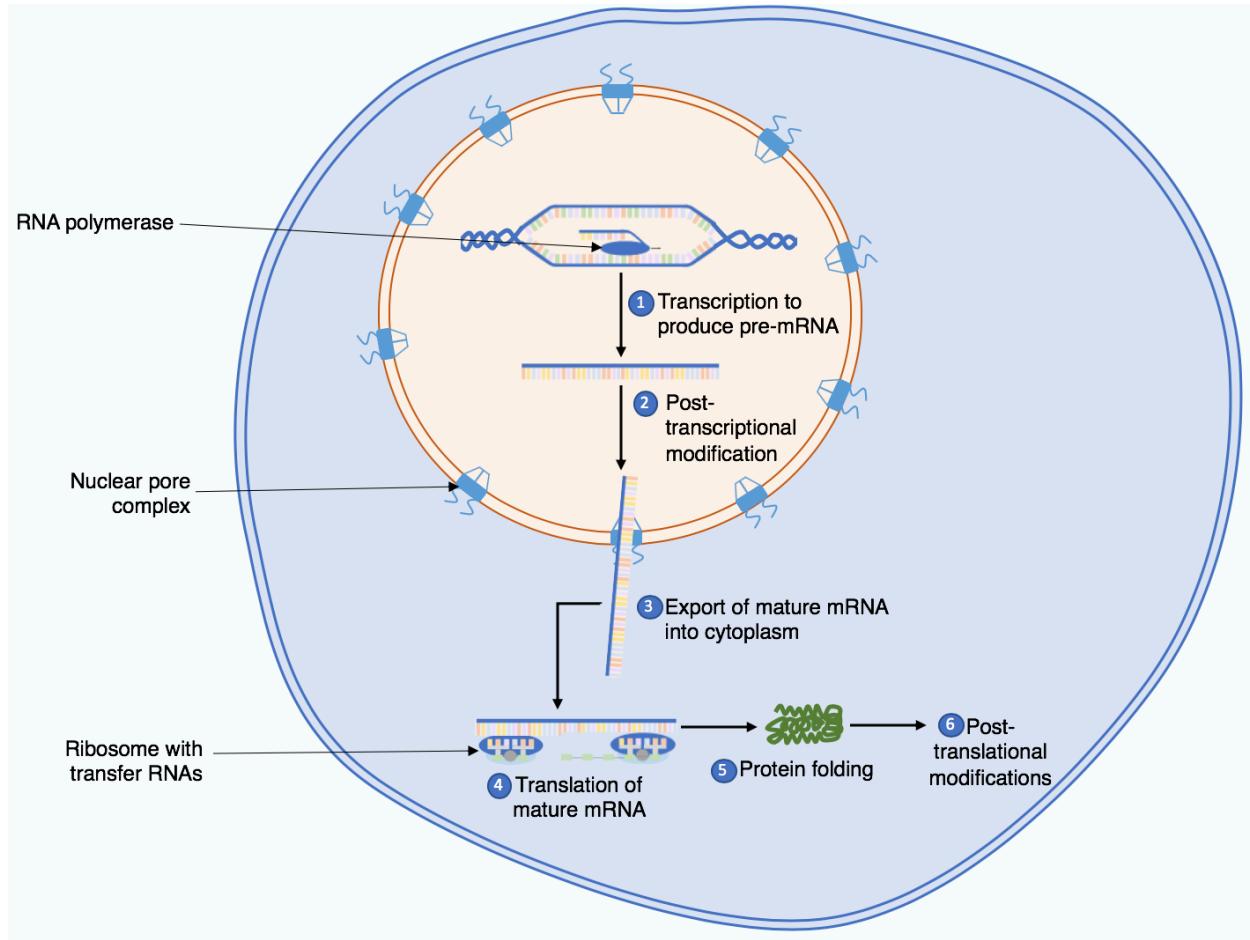


Figure 1: Central Paradigm of Biology: a gene, a specific region in the DNA, is first transcribed into RNA and then into proteins. Note, that for RNA-genes the RNA molecule is the end product itself, which is referred to as non-coding RNA (ncRNA) (Source: Wikipedia)

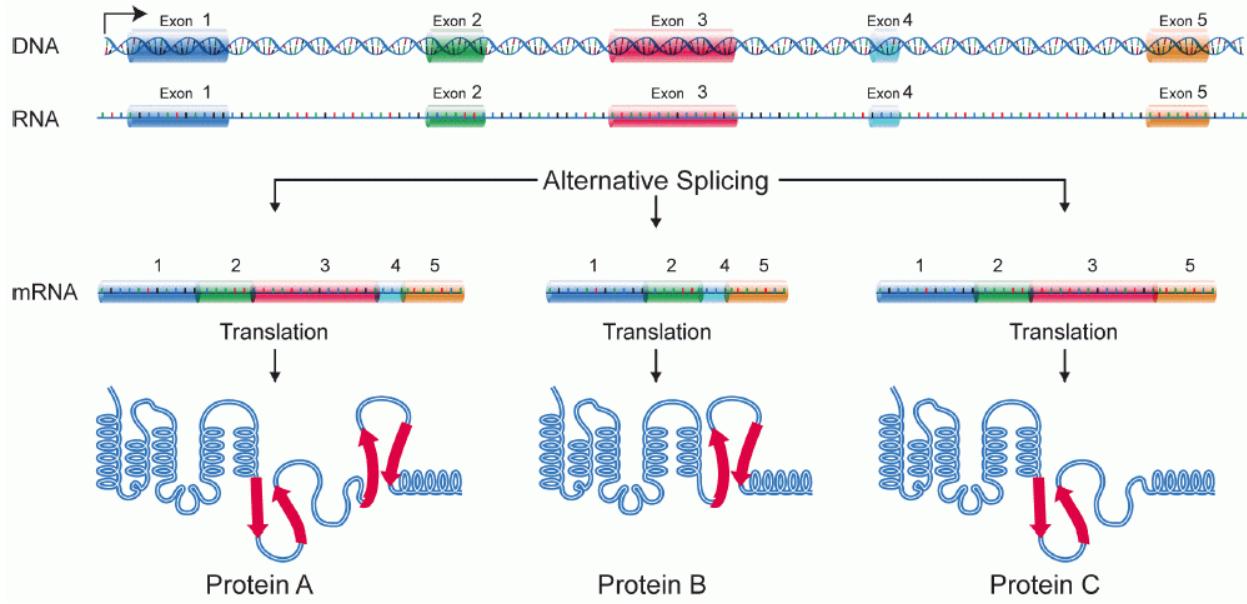


Figure 2: Alternative splicing allows a single gene in Eucaryotes to code for multiple proteins. During alternative splicing particular exons of a gene may be included or excluded from the premature messenger RNA when producing the messenger RNA (mRNA) from that gene. Hence exons can be joined in different combinations, leading to different (alternative) mRNA strands. The proteins translated from alternatively spliced mRNAs thus differ in their amino acid sequence and, often, in their biological functions (Source: Wikipedia)

2 Sequencing technology

- Measuring mRNA molecules typically happens through sequencing.
- The technology continues to evolve at an incredible speed. The data output of so-called ‘next generation’ sequencing machines has more than doubled each year! Simultaneously, the cost of sequencing (in terms of \$ per Gigabase) is dropping. Each year, we’re able to sequence more for less money, providing more information, as well as also computational and statistical challenges.
- This tremendous technological revolution has revolutionized biology, and genomic sequencing is now a core component of the modern-day biologist’s toolkit.
- The large majority of sequencing data is generated using sequencing-by-synthesis using machines produced by the company Illumina. While new players such as Pacific Biosciences and Oxford Nanopore have entered the scene, these are typically most useful for (but not limited to) DNA sequencing rather than gene expression studies, owing to their capability of sequencing long molecules.

- From sample to data analysis

- Illumina Sequencing

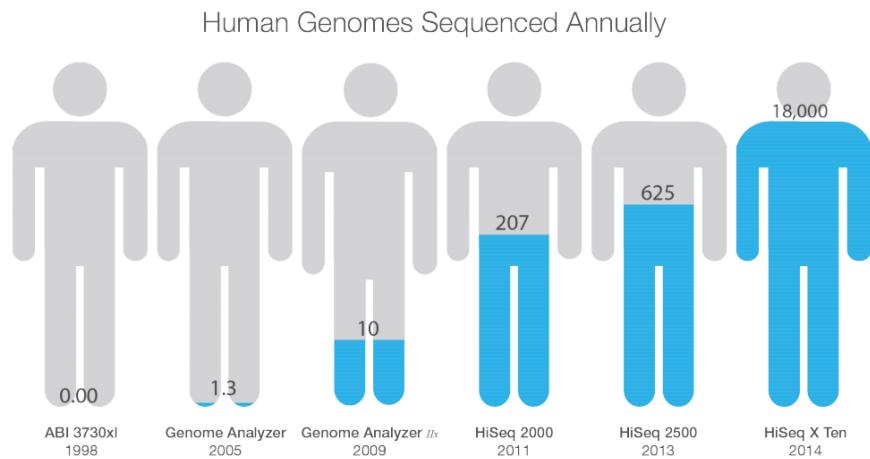


Figure 2: Human Genome Sequencing Over the Decades—The capacity to sequence all 3.2 billion bases of the human genome (at 30 \times coverage) has increased exponentially since the 1990s. In 2005, with the introduction of the Illumina Genome Analyzer System, 1.3 human genomes could be sequenced annually. Nearly 10 years later, with the Illumina HiSeq X Ten fleet of sequencing systems, the number has climbed to 18,000 human genomes a year.

Figure 3: Figure: The data output revolution of sequencing machines. Image from Illumina documentation.

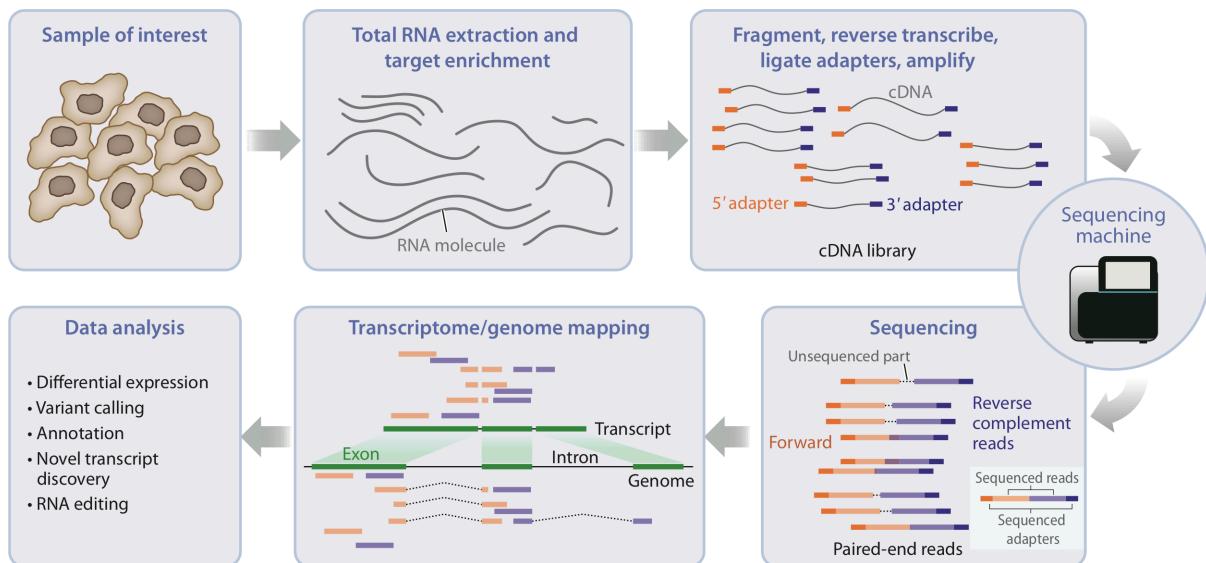
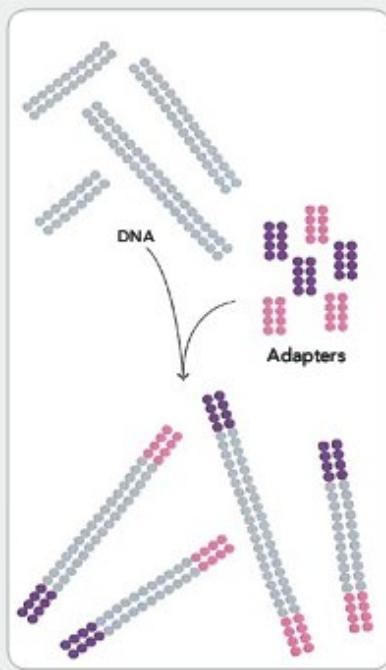
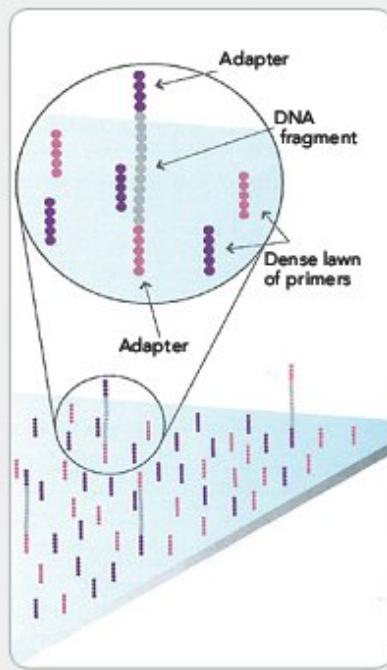


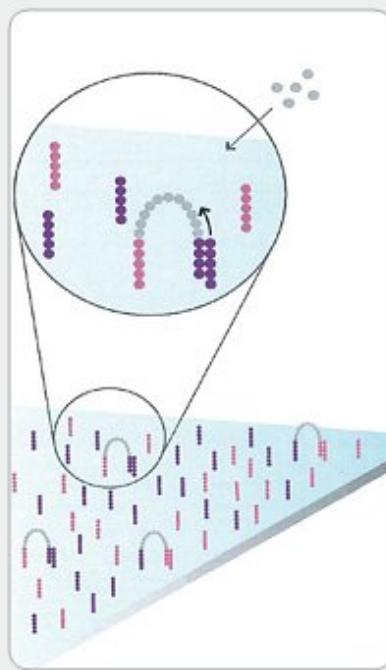
Figure 4: Figure: The sequencing workflow. Image adapted from Van den Berge et al. (2019).

1. PREPARE GENOMIC DNA SAMPLE

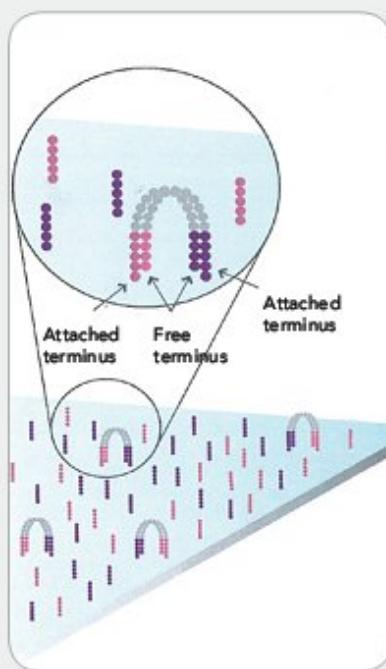
Randomly fragment genomic DNA and ligate adapters to both ends of the fragments.

2. ATTACH DNA TO SURFACE

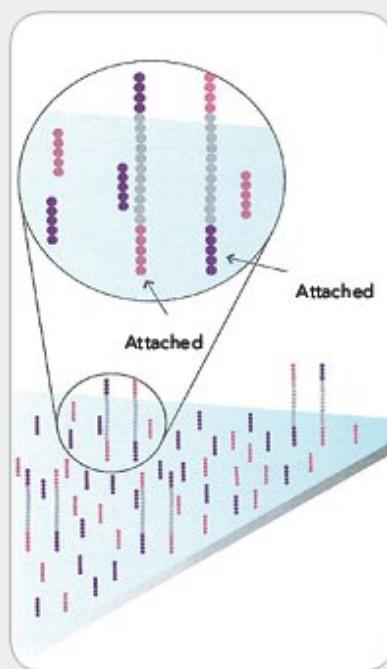
Bind single-stranded fragments randomly to the inside surface of the flow cell channels.

3. BRIDGE AMPLIFICATION

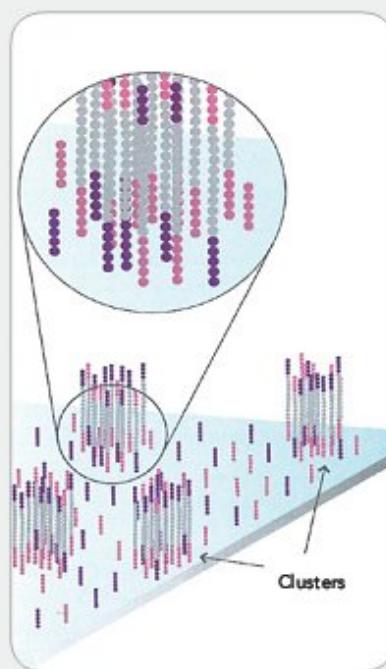
Add unlabeled nucleotides and enzyme to initiate solid-phase bridge amplification.

4. FRAGMENTS BECOME DOUBLE STRANDED

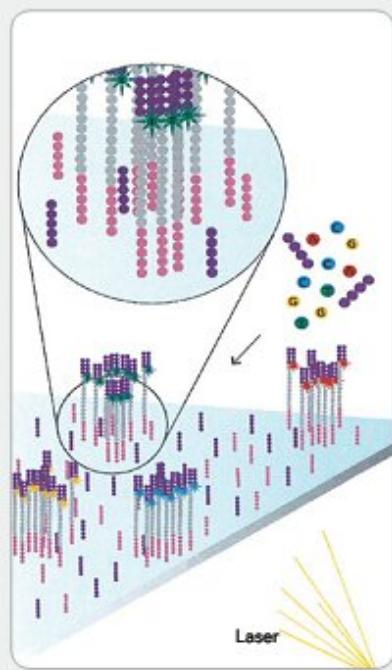
The enzyme incorporates nucleotides to build double-stranded bridges on the solid-phase substrate.

5. DENATURE THE DOUBLE-STRANDED MOLECULES

Denaturation leaves single-stranded templates anchored to the substrate.

6. COMPLETE AMPLIFICATION

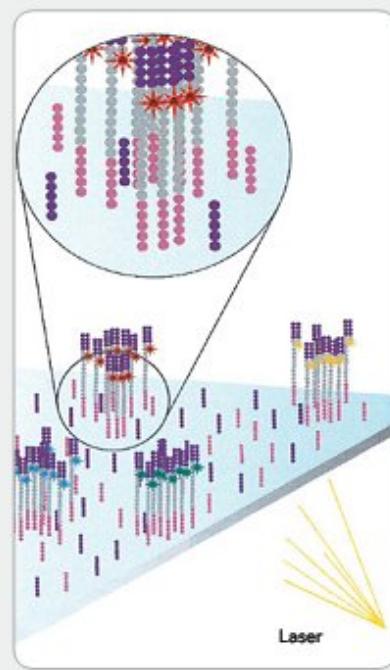
Several million dense clusters of double-stranded DNA are generated in each channel of the flow cell.

7. DETERMINE FIRST BASE

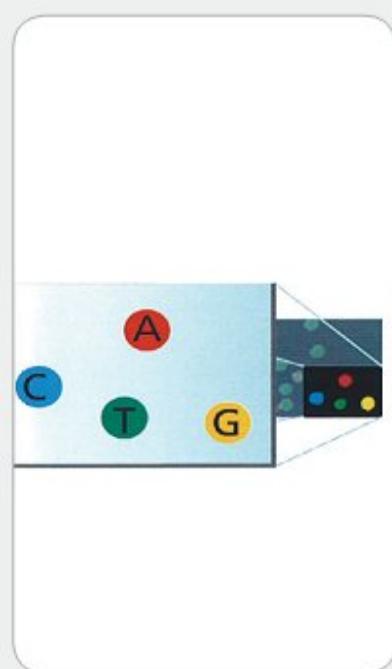
First chemistry cycle: to initiate the first sequencing cycle, add all four labeled reversible terminators, primers and DNA polymerase enzyme to the flow cell.

8. IMAGE FIRST BASE

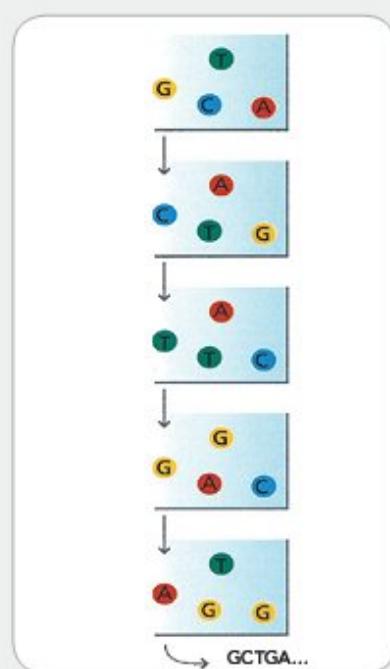
After laser excitation, capture the image of emitted fluorescence from each cluster on the flow cell. Record the identity of the first base for each cluster.

9. DETERMINE SECOND BASE

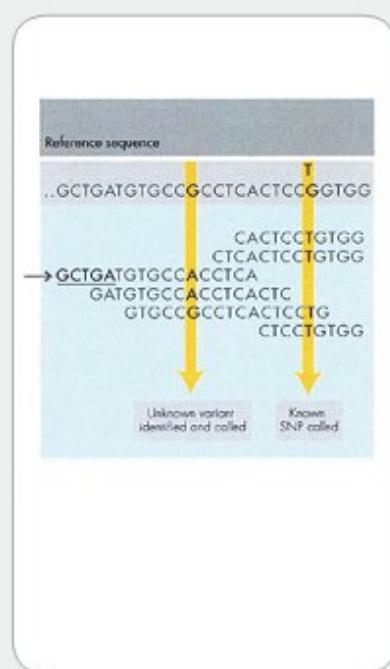
Second chemistry cycle: to initiate the next sequencing cycle, add all four labeled reversible terminators and enzyme to the flow cell.

10. IMAGE SECOND CHEMISTRY CYCLE

After laser excitation, collect the image data as before. Record the identity of the second base for each cluster.

11. SEQUENCE READS OVER MULTIPLE CHEMISTRY CYCLES

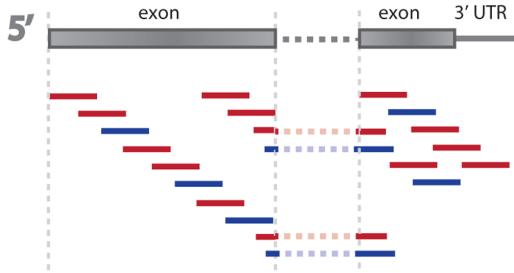
Repeat cycles of sequencing to determine the sequence of bases in a given fragment a single base at time.

12. ALIGN DATA

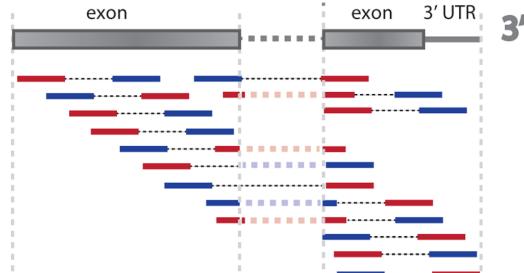
Align data, compare to a reference, and identify sequence differences.

- Single vs paired end

Single-end sequencing



Paired-end sequencing



The sequencing workflow

Library preparation steps

1. First, the biological **samples of interest are collected**. Owing to the maturity of different protocols for sequencing, several types of biological input samples are amenable to sequencing, such as frozen tissues or FFPE-preserved samples.
2. The **mRNA molecules from our sample are captured**. This typically involves cell lysis in order to release the mRNA molecules from within the cells. The mRNA molecules are most often captured using (i) polyA-capture to select for polyadenylated RNA, or (ii) ribosomal depletion, where ribosomal and transfer RNAs are depleted, and so also non-polyA-mRNA molecules may be captured, such as long non-coding RNAs. In the case of ‘targeted sequencing’, where relevant molecules are of main interest (e.g., a gene panel), these targets can be specifically targeted in this step.
3. **Fragmentation** of captured molecules. The captured molecules are fragmented, either chemically or mechanically. The appropriate size of fragments depends on the sequencing machines, but is often in the range of 300 - 500bp.
4. **Reverse transcription**. Current dominant sequencing machines only sequence double-stranded DNA molecules. Therefore, in order to measure single-stranded mRNA, we must first reverse transcribe these molecules to a double-stranded complementary (cDNA) molecule.
5. **Adapter ligation**. Adapters are oligonucleotides (short sequences of nucleotides) that are platform-specific sequences for fragment recognition by the sequencing machines. These are added either to the 3' or 5' end of the cDNA molecules or used as primers in the reverse transcription reaction. The final cDNA library consists of cDNA inserts flanked by an adapter sequence on each end.
6. **PCR amplification**. To increase concentration, several PCR reactions are performed.
7. Loading the amplified cDNA library on the **sequencing** machine. Find out how sequencing-by-synthesis works through this video. Note that the video shows paired-end sequencing, where a number of basepairs are sequenced at each end of the fragment. All previous steps together are described as ‘sample prep’ in that video.

Note that several variants of library preparation protocols are available. The most important ones are:

- Single-end vs paired-end sequencing: In single-end sequencing, a single end (3' or 5') of the cDNA fragment is sequenced. In paired-end sequencing, both ends are sequenced, and depending on the size of the fragment, the reads may or may not overlap.
- Strand-specific protocols: Some library preparation protocols allow measuring strand specificity, where the strand information (i.e., sense/antisense) of each read can be preserved.

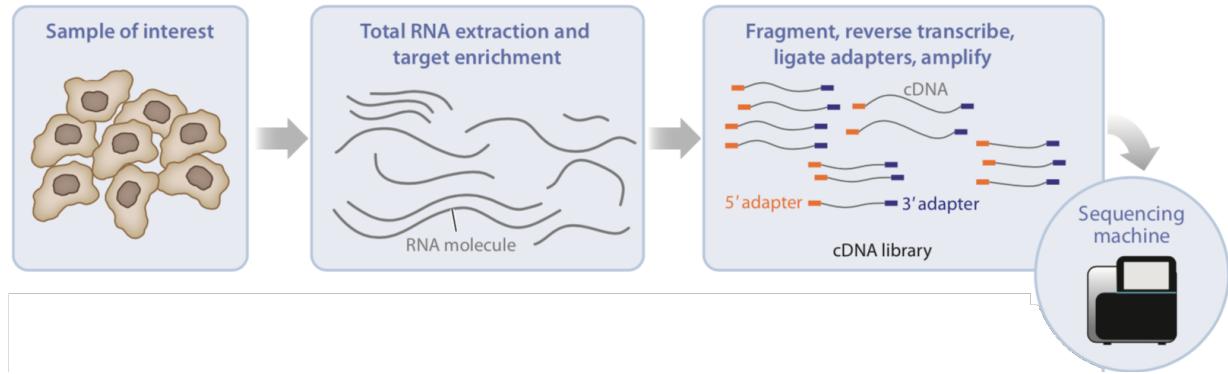


Figure 5: Figure: The sequencing workflow. Image adapted from Van den Berge et al. (2019).

2.1 The sequencing output files

- The typical output of a sequencing machine we will be working with are FASTA or FASTQ files for each sample. Each of these files are several gigabases large and contain millions of sequences, which we will call **reads**. For paired-end sequencing, there are two files for each sample, one for each end of the sequenced fragments.
- The difference between a FASTA file and a FASTQ file, is that while FASTA files only store the results of base calls (sequences), FASTQ files also store the quality score of each base call (i.e., each called nucleotide), which can be useful in downstream analyses such as mapping or variant calling.
- A FASTQ file contains four lines for each sequenced read:
 1. Sequence identifier line, starting with @.
 2. The sequence.
 3. Another sequence identifier line, now starting with +.
 4. Quality scores.

As you'll have noticed, the base call quality scores are encoded as ASCII characters for efficient storage. These ASCII characters can be converted into integers called Phred scores, which are logarithmically related to the probability of an erroneous base call.

2.1.1 Quality score

The Phred Score is a quality score

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

, with p the probability on an incorrect base call

Phred Score	Probability on incorrect base call	Base call accuracy
10	1/10	90%
20	1/100	99%
30	1/1000	99.9%
40	1/10000	99.99%
50	1/100000	99.999%

Phred score encoded as an ASCII letter. E.g. Phred+33:

FASTQ format - sequence ID line

```
@D7MHBFI1:202:D1BUDACXX:4:1101:1340:1967 1:N:0:CATGCA
NATCTTCGGATCACTTGGTCAAATTGAAACGATAACAGAGAAGATTGTAAGTAACAATATTACCAAGGTTCGAGTCATACTAAGTCGTGCTATAGT
+
#1=DDFFFHHHHHJJJJJJJJHIJIIJJIIJGIIIIJJJJIIJIIJJHIIFGIIIIJJJJIIIEHJIHHGFFF@?ADFEDDEDCCDBDDBCDDDEC
```

- D7MHBFI1 - unique instrument name
- 202 - run ID
- D1BUDACXX - flowcell ID
- 4 - flowcell lane
- 1101 - tile number within lane
- 1340 - x-coordinate of cluster within tile
- 1967 - y-coordinate of cluster within tile
- 1 - member of pair (1 or 2). Older versions: /1 and /2
- Y/N - whether the read failed quality control (Y = bad)
- 0 - none of the control bits are on
- CATGCA - index sequence (barcode)

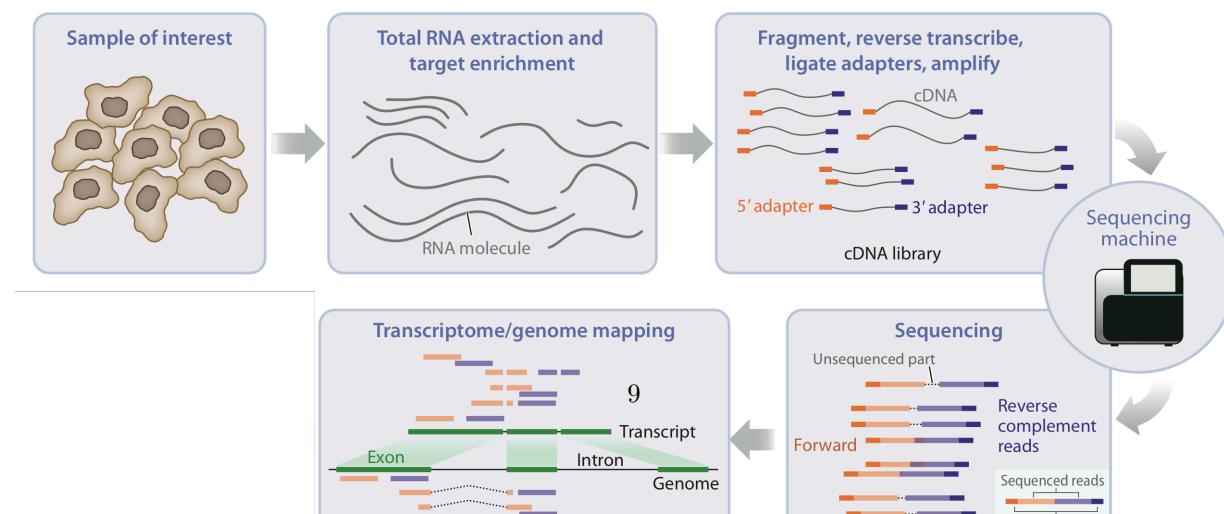
Figure 6: Figure: One read in a FASTQ file. Slide courtesy by Charlotte Soneson.

```
PhoebeI 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40
PhoebeB4 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73
+
33
ASCII # $ % & ' ( ) * + , - . / 0 1 2 3 4 5 6 7 8 9 : ; < = > ? @ A B C D E F G H I
```

3 Preprocessing of raw sequencing data

After sequencing, we typically do a quality control (QC) check to verify the quality of the samples. During QC check, aberrant samples due to e.g. degraded mRNA can be detected.

The sequencing reads on their own contain a lot of information, but are most useful if we would be able to assign sequencing reads to genomic features (genes, exons, transcripts, etc.), i.e., for each sequencing read we will try to derive the (set of) feature(s) that could have plausibly produced the fragment through the process of gene expression. This process is called **mapping**. Most often we map reads to genes.



- Adaptor sequence
- Bar code
- (deteriorating bases at the end of reads)
- often already done by the sequencing provider.
- remaining polyA tails
- Read filtering
 - low quality reads
 - PhiX reads (should be removed already by sequence provider) in
 - RNA-seq never remove duplicates because they can occur for highly expressed transcripts
- Perform fastQC again

3.3 Mapping

- Mapping is a critical step in the interpretation of RNA-seq data, where we are attributing reads to genomic features.
- Allows us to measure how strong a feature such as a gene is expressed: the number of reads mapping to a gene serve as a proxy for how high that gene has been expressed in the sample.
- While this opens the door to many opportunities, mapping is hard.
- We are **typically unable to assign each individual read uniquely** to one specific gene; some reads cannot be unambiguously mapped and are compatible with multiple genes. These reads are said to be ‘multi-mapping’.

Finally, a note on terminology. In this text we will use the words ‘read’ or ‘fragment’ (referring to the fragmented mRNA molecule being sequenced) to designate a datum, note that this could be either a single read (in single-end sequencing) or a read pair (in paired-end sequencing). The literature may also use these words interchangeably, although ‘fragment’ seems better at avoiding ambiguity between single-end reads and paired-end read pairs.

3.3.1 Reference files

- The alignment most often relies on a **reference genome** of the species, which can be considered a ‘representative example’ of the genome sequence of that species. Reference genomes are continuously updated and released periodically.
- Reference genomes can be freely downloaded from several providers, for example Ensembl or Gencode.
- Along with a reference genome, an annotation GFF or GTF file defines the coordinates of specific genomic features.
- While here we will focus on reference-based alignment, i.e., alignment where a reference genome or transcriptome is available, note that a *de novo* construction of a reference transcriptome is also possible, where the reference may be constructed from the observed sequencing reads.
- More recently, mapping of RNA-seq data occurs more often against a **reference transcriptome**, which is a reference file containing the sequences all known isoforms of a particular species, e.g., using kallisto or Salmon.
- The set of spliced transcripts is much smaller than the entire genome, and therefore mapping against a reference transcriptome is typically **fast and memory efficient**.
- However, it has been noted that mapping against a reference transcriptome may also introduce spurious expression for genes that are not expressed. These observations can be explained by **intronic reads** that share some sequence similarity with transcripts, and could map to spliced transcript sequences. Recent methods, such as alevin-fry, avoid this by expanding the reference transcriptome to also include intronic sequences.

The human reference genome

www.ensembl.org/info/data/ftp/index.html

<https://www.gencodegenes.org/human/>

Single species data

Popular species are listed first. You can customise this list via our [home page](#)

Show 10 entries		Show/hide column				
	Species	DNA (FASTA)	cDNA (FASTA)	CDS (FASTA)	ncRNA (FASTA)	Protein sequence (FASTA)
Y	<u>Human</u> <i>Homo sapiens</i>	FASTA				
Y	<u>Mouse</u> <i>Mus musculus</i>	FASTA				
Y	<u>Zebrafish</u> <i>Danio rerio</i>	FASTA				

Content	Regions	Description	Download
Transcript sequences	CHR	<ul style="list-style-type: none"> Nucleotide sequences of all transcripts on the reference chromosomes 	Fasta
Protein-coding transcript sequences	CHR	<ul style="list-style-type: none"> Nucleotide sequences of coding transcripts on the reference chromosomes Transcript biotypes: protein_coding, nonsense_mediated_decay, non_stop_decay, IG_*, gene, TR_*, gene, polymorphic_pseudogene 	Fasta
Protein-coding transcript translation sequences	CHR	<ul style="list-style-type: none"> Amino acid sequences of coding transcript translations on the reference chromosomes Transcript biotypes: protein_coding, nonsense_mediated_decay, non_stop_decay, IG_*, gene, TR_*, gene, polymorphic_pseudogene 	Fasta
Long non-coding RNA transcript sequences	CHR	<ul style="list-style-type: none"> Nucleotide sequences of long non-coding RNA transcripts on the reference chromosomes 	Fasta
Genome sequence (GRCh38.p12)	ALL	<ul style="list-style-type: none"> Nucleotide sequence of the GRCh38.p12 genome assembly version on all regions, including reference chromosomes, scaffolds, assembly patches and haplotypes The sequence region names are the same as in the GTF/GFF3 files 	Fasta
Genome sequence, primary assembly (GRCh38)	PRI	<ul style="list-style-type: none"> Nucleotide sequence of the GRCh38 primary genome assembly (chromosomes and scaffolds) The sequence region names are the same as in the GTF/GFF3 files 	Fasta

 [Homo_sapiens.GRCh38.dna.primary_assembly.fa.gz](#) 840 MB

Figure 8: slide courtesy Charlotte Soneson

Figure 9: Figure: A reference sequence of human chr1.

www.ensembl.org/info/data/ftp/index.html

<https://www.gencodegenes.org/human/>

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Show/hide columns								
DS STA	ncRNA (FASTA)	Protein sequence (FASTA)	Annotated sequence (EMBL)	Annotated sequence (GenBank)	Gene sets	Whole databases	Variab	
TA	FASTA	FASTA	EMBL	GenBank	GTF GFF3	MySQL	G	
TA	FASTA	FASTA	EMBL	GenBank	GTF GFF3	MySQL	G	
TA	FASTA	FASTA	EMBL	GenBank	GTF GFF3	MySQL	G	

GTF / GFF3 files			
Content	Regions	Description	Download
Comprehensive gene annotation	CHR	<ul style="list-style-type: none"> It contains the comprehensive gene annotation on the reference chromosomes only This is the main annotation file for most users 	GTF GFF3
Comprehensive gene annotation	ALL	<ul style="list-style-type: none"> It contains the comprehensive gene annotation on the reference chromosomes, scaffolds, assembly patches and alternate loci (haplotypes) This is a superset of the main annotation file 	GTF GFF3
Comprehensive gene annotation	PRI	<ul style="list-style-type: none"> It contains the comprehensive gene annotation on the primary assembly (chromosomes and scaffolds) sequence regions This is a superset of the main annotation file 	GTF GFF3
Basic gene annotation	CHR	<ul style="list-style-type: none"> It contains the basic gene annotation on the reference chromosomes only This is a subset of the corresponding comprehensive annotation, including only those transcripts tagged as 'basic' in every gene 	GTF GFF3

Figure 10: slide courtesy Charlotte Soneson

```
(base) Koens-MacBook-Pro:gtf koenvandenberge$ cat test_ensemble_chr22.gtf
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22 miRNA transcript 13518 13571 . + gene_biotype "miRNA"; gene_id "ENSG00000221160"; gene_name "MIR1281"; gene_source "ensembl"; transcript_id "ENST0000408233"; transcript_name "MIR1281-201"; transcript_source "ensembl"; tss_id "TSS185801";
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22 protein_coding start_codon 14010 14012 . + 0 ccds_id "CCDS14010"; exon_number "1"; gene_biotype "protein_coding"; gene_id "ENSG00000100393"; gene_name "EP300"; gene_source "ensembl_havana"; p_id "P5137"; tag "CCDS"; transcript_id "ENST00000263253"; transcript_name "EP300-001"; transcript_source "ensembl_havana"; tss_id "TSS138009";
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```

Figure 11: Figure: An example GTF file.

3.3.2 Alignment-based workflows

- Traditionally, alignment-based workflows have been used to map reads, where one tries to find the exact coordinates a read maps to on the reference genome or the reference transcriptome.
- Note that due to alternative splicing, reads do not necessarily map contiguously on a reference genome, as a read can overlap with a splicing junction, where an intron has been excised. When mapping against a transcriptome, however, reads should be mapping contiguously.
- A main challenge in spliced alignment against a reference genome is the proper alignment of reads that span a splice junction, especially when these junctions are not annotated a priori. Indeed, in spliced alignment reads can be split at any nucleotide, and the corresponding subsequences can map several thousands of basepairs apart. Meanwhile, the main challenge in unspliced alignment to a transcriptome is the redundant sequence among related transcripts in the transcriptome, which often leads to a high multi-mapping rate (i.e., reads that cannot be unambiguously assigned to a single transcript).
- Spliced alignment against a genome is therefore computationally a much harder task. Since the transcript sequences are already spliced when aligning to a reference transcriptome, reads should align contiguously, and many of the computationally expensive steps and heuristics can be avoided, there.

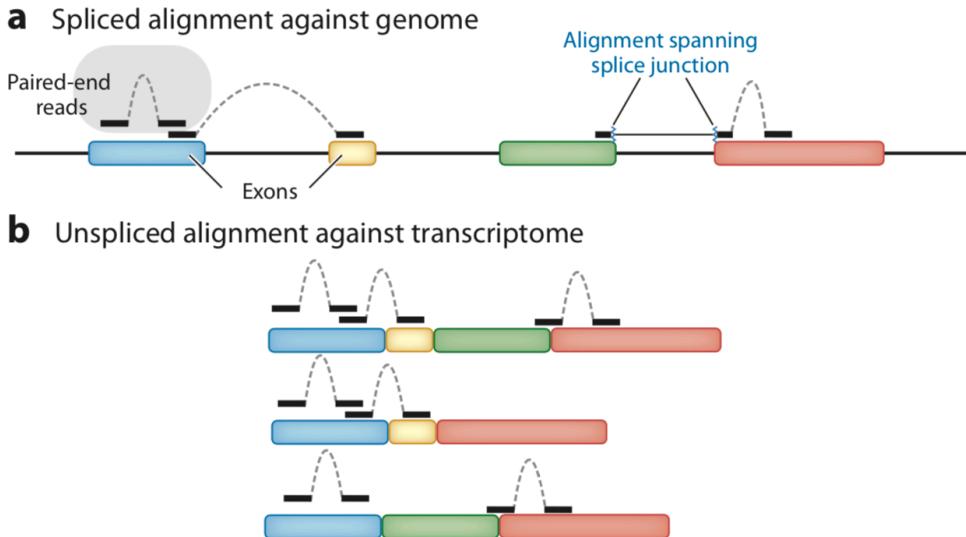


Figure 4

An illustration of spliced alignment of RNA sequencing (RNA-seq) fragments to a genome (*a*) and direct alignment to a transcriptome (*b*). Reads are designated by thick solid lines, while dashed arcs represent the pairing relationship between paired-end reads. This illustration depicts alignment to a single four-exon gene consisting of three distinct transcripts. In the spliced alignment (*a*), the left read of the rightmost pair is a junction-spanning alignment to the red-green exon boundary. In the direct alignment to the transcriptome (*b*), one observes how the same alignment (e.g., the alignment to the blue exon) is repeated for each transcript.

Figure 12: Figure: Unspliced and spliced alignment. Figure from Van den Berge et al. (2019).

3.3.3 Alignment-free workflows

- Modern approaches avoid mapping each fragment individually (i.e., do not attempt to find the exact coordinates of a read's origin), and instead posit a probabilistic model where transcript abundances are typically defined using its constituent k -mers. These methods are sometimes referred to as *lightweight*.

- A k -mer is a short sequence of nucleotides of length k . The space of possible k -mers and the corresponding transcripts can be precomputed in advance using the reference transcriptome, providing a computational advantage as it only needs to be computed once.
- For each fragment, the transcripts its k -mers are compatible with is searched for using an indexed (efficiently searchable) transcriptome. The set of compatible transcripts is called the ‘ k -compatibility class’, ‘equivalence class’ or ‘transcript compatibility class’ of the fragment.

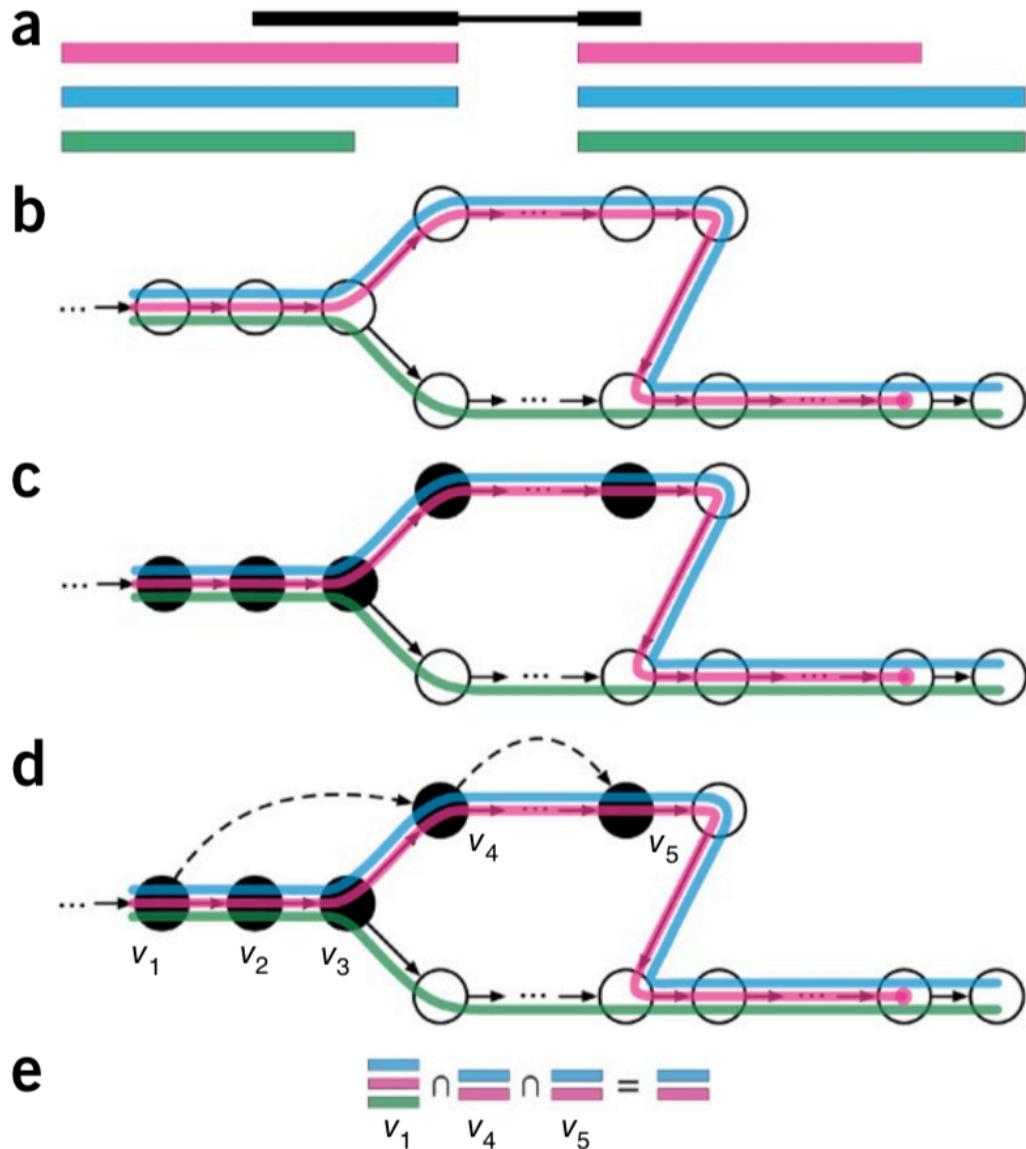


Figure 1 Overview of kallisto. The input consists of a reference transcriptome and reads from an RNA-seq experiment. (a) An example of a read (in black) and three overlapping transcripts with exonic regions as shown. (b) An index is constructed by creating the transcriptome de Bruijn Graph (T-DBG) where nodes (v_1, v_2, v_3, \dots) are k -mers, each transcript corresponds to a colored path as shown and the path cover of the transcriptome induces a k -compatibility class for each k -mer. (c) Conceptually, the k -mers of a read are hashed (black nodes) to find the k -compatibility class of a read. (d) Skipping (black dashed lines) uses the information stored in the T-DBG to skip k -mers that are redundant because they have the same k -compatibility class. (e) The k -compatibility class of the read is determined by taking the intersection of the k -compatibility classes of its constituent k -mers.

3.4 Abundance quantification

Given a set of mappings, using either alignment-based or alignment-free workflows, the estimation of expression of a gene/transcript/exon may occur in several ways.

Counting:

- In alignment-based workflows, one could do a direct counting of fragments at the gene-level, counting the number fragments mapping to each gene. This has been the dominant approach for the first decade of RNA-seq data, often obtained using reference genome alignments.
- Many heuristic choices need to be made: Do we count a fragment as soon as it intersects with the gene's coordinates, or do we require the full fragment to map to the gene? Do we count intronic reads? Do we count multi-mapping reads?

Estimation:

- Abundance quantification is more recently starting to shift from counting towards using statistical models to estimate the expression counts for a feature, which in this case is typically a transcript.
- This approach is amenable to alignment-free workflows, since the number of fragments in each equivalence class are sufficient statistics for the abundance quantification, meaning that they contain all information needed to estimate the parameters of the statistical model, and hence the feature-level abundances. Since the expression counts in this case are estimated, they are not necessarily integer counts, and will be referred to as 'estimated counts'.
- In order to derive these, the EM-algorithm is often used, although other approaches have been used by tools like Salmon. A big advantage of the estimation approach is that it probabilistically assigns fragments to transcripts, thereby automatically dealing with multi-mapping reads. The total number of fragments mapping to each transcript is then the sum of all fragment-level probabilities to be assigned to that respective transcript.

3.4.1 Abundance metrics

- For simplicity, we have only been talking about feature-level counts as in sums of fragments. However, this is merely one metric that can be used as a proxy for expression, and several others exist.

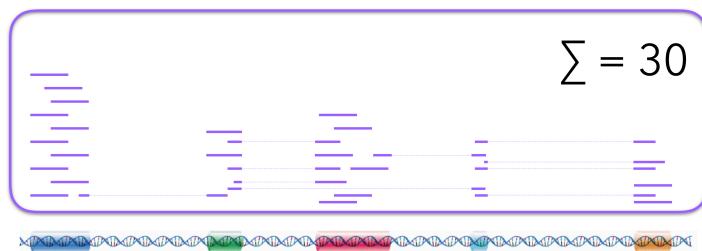
Gene and transcripts



Reads



Gene-level quantification:



Exon-level quantification:

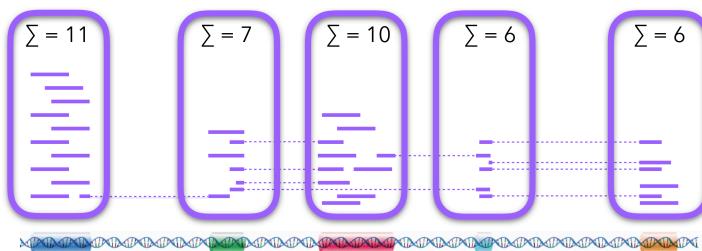


Figure 13: Figure: Gene- and exon-level read counting. Image adapted from Charlotte Soneson.

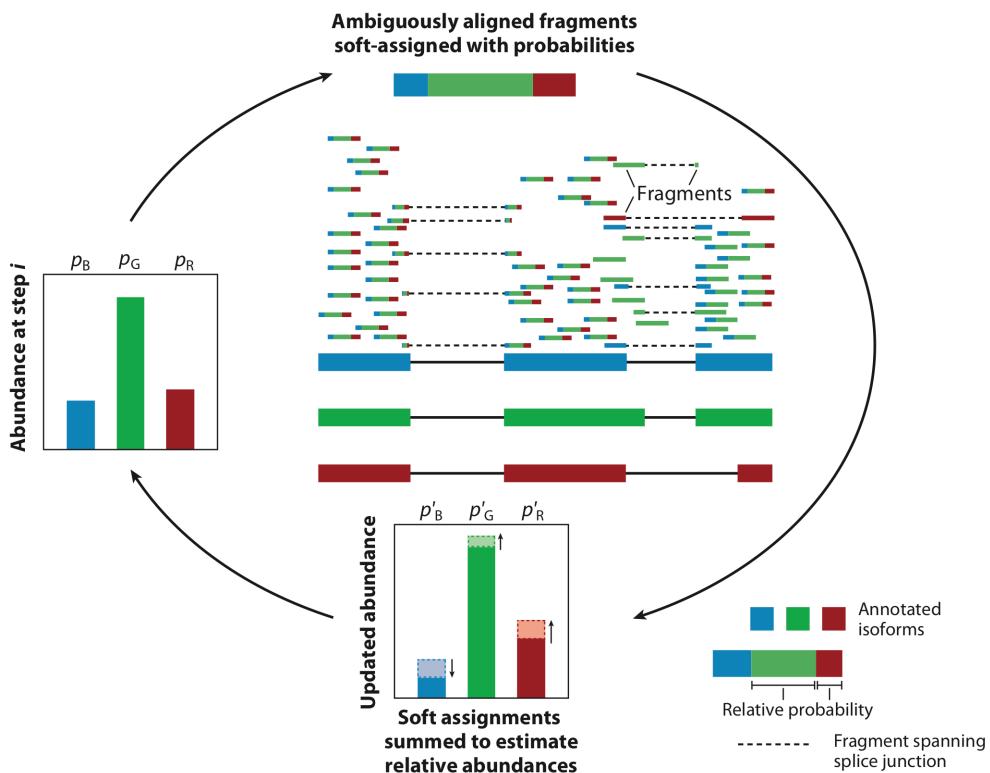


Figure 5

An illustration of the alignment of various reads to a gene with three isoforms: blue (B), green (G), and red (R). In this example, we wish to estimate the abundances of these isoforms, but most reads have ambiguous origins and need to be probabilistically assigned to the transcripts (relative probabilities for each read are shown by the magnitudes of the three colors). Some reads are consistent only with the B and G transcripts, and a few reads uniquely align to a single transcript (single color). In the expectation-maximization (or related) algorithm, given the current abundance estimates, fragments are probabilistically assigned to transcripts, and then estimated abundances are updated by summarizing the (proportional) allocations over all fragments; transcript abundance estimates are determined by iterating the procedure until convergence.

Figure 14: Figure: Abundance quantification using the EM algorithm. Figure from Van den Berge et al. (2019).

- Most of these were introduced to attempt to make the abundances more comparable across samples or features, as compared to the simple counts. These mainly serve to correct for technical biases such as transcript length and sequencing depth, both of which have significant impact on the observed counts.
- Indeed, for a gene with the same mRNA concentration in two samples, sequencing one sample deeper, will on average result in a higher count.
- Likewise, for two transcripts with the same mRNA concentration but different transcript lengths, one will tend to observe more fragments from the longer transcript due to the fragmentation step in the RNA-seq protocol, where longer transcripts can be split into more fragments of appropriate length.

Below we introduce several relevant abundance metrics, but note that most data analysis methods we will discuss in this course will work with (estimated) counts. In what follows, let Y_{fi} denote the random variable representing the expression counts of feature f in sample i (obtained either as a simple sum of fragments or estimated using lightweight approaches), and let $N_i = \sum_f Y_{fi}$ denote the sequencing depth of sample i .

- **Counts per million (CPM)** are the counts one could expect to observe if the sample was sequenced to a depth of one million.

$$CPM_{fi} = \frac{Y_{fi}}{N_i} 10^6$$

- **Transcripts per million (TPM)** refers to the concentration or proportion of your feature in the sample. TPMs take into account the length of the feature, which is often reformulated into an *effective length* $l_{fi}^{(eff)}$, relating to the number of possible start sites that a feature may have in order to generate fragments of a typical length observed in your dataset. This typical length is often calculated using the observed fragment length distribution from the data and defined as

$$l_{fi}^{(eff)} = l_f - \hat{\bar{F}}_i + 1,$$

where l_f is the total length of a feature in terms of number of nucleotides, and $\hat{\bar{F}}_i$ is the estimated average fragment length in sample i . We can use this to define

$$TPM_{fi} = \frac{Y_{fi}}{l_{fi}^{(eff)}} \left(\frac{1}{\sum_f \frac{Y_{fi}}{l_{fi}^{(eff)}}} \right) 10^6.$$

Note that the first part of the right-hand-side (RHS), $\frac{Y_{fi}}{l_{fi}^{(eff)}}$ is the expression counts normalized for the length of the feature. This measure, however, is still affected by the sequencing depth, which is then alleviated by dividing by the sum of the length-normalized counts across all features, i.e., $\sum_f \frac{Y_{fi}}{l_{fi}^{(eff)}}$. TPMs hence normalize for the feature length as well as sequencing depth.

3.4.2 The final countdown

Once abundances have been quantified, the (estimated) counts are typically stored in a count matrix, with genes spanning the rows and samples spanning the columns. This count matrix forms the basis of most downstream analyses to interpret RNA-seq data, and it will be the main object we will be working with in the following lectures.

4 References

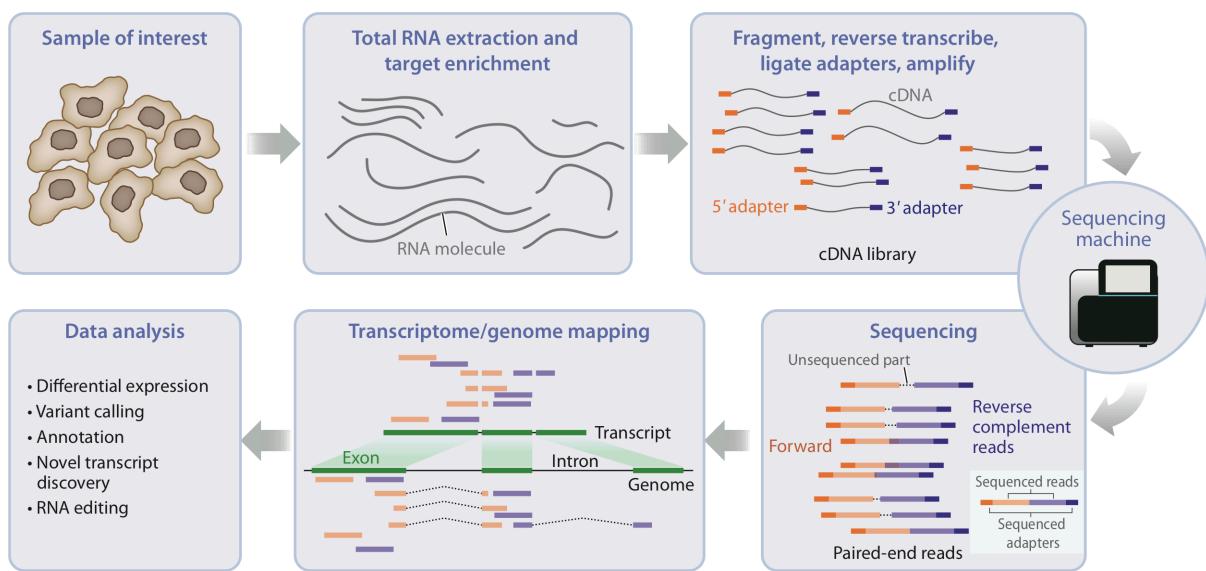


Figure 15: Figure: An updated sequencing workflow. Image adapted from Van den Berge et al. (2019).