

RNA-seq解析パイプライン： Transcript-based

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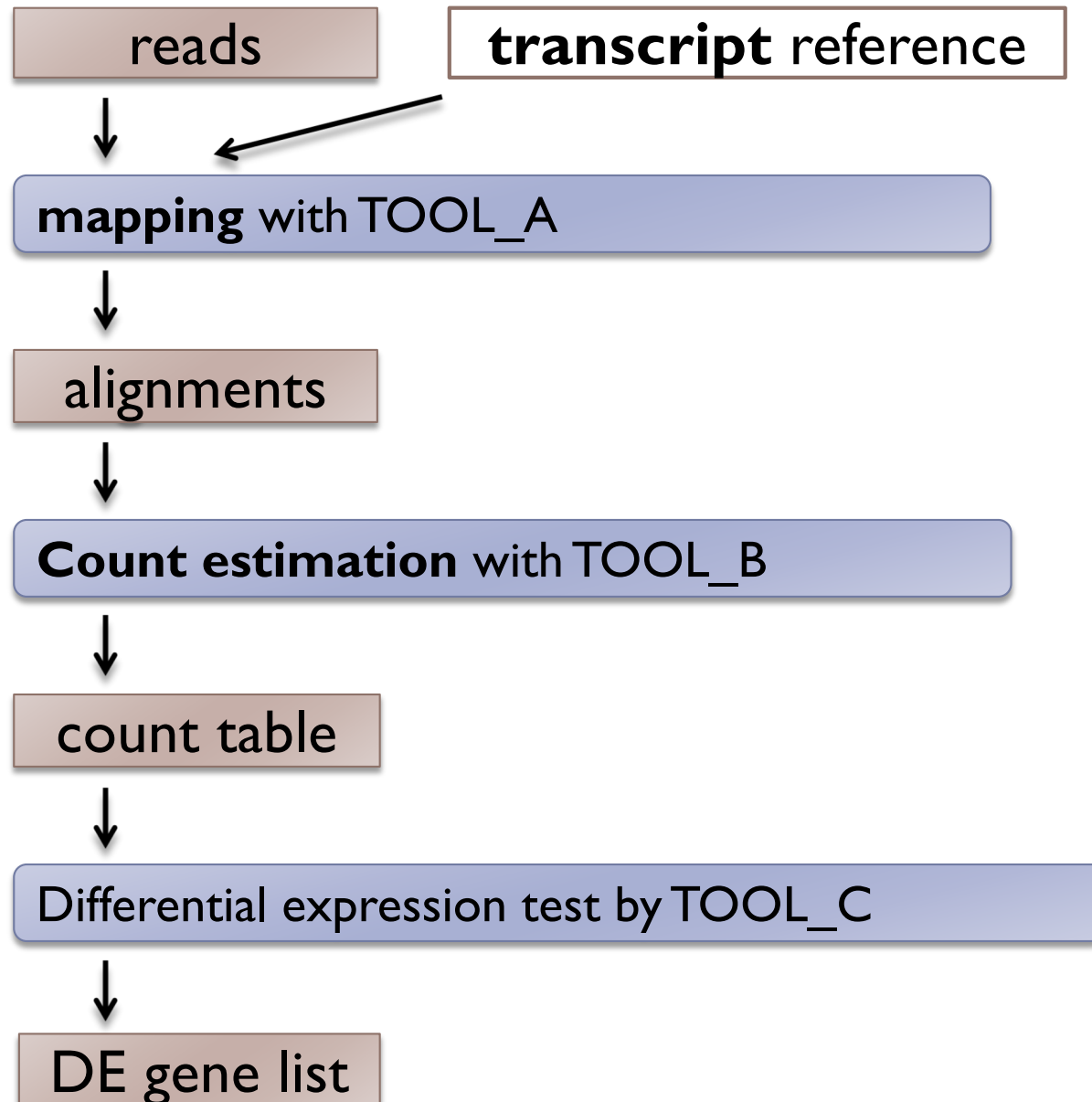
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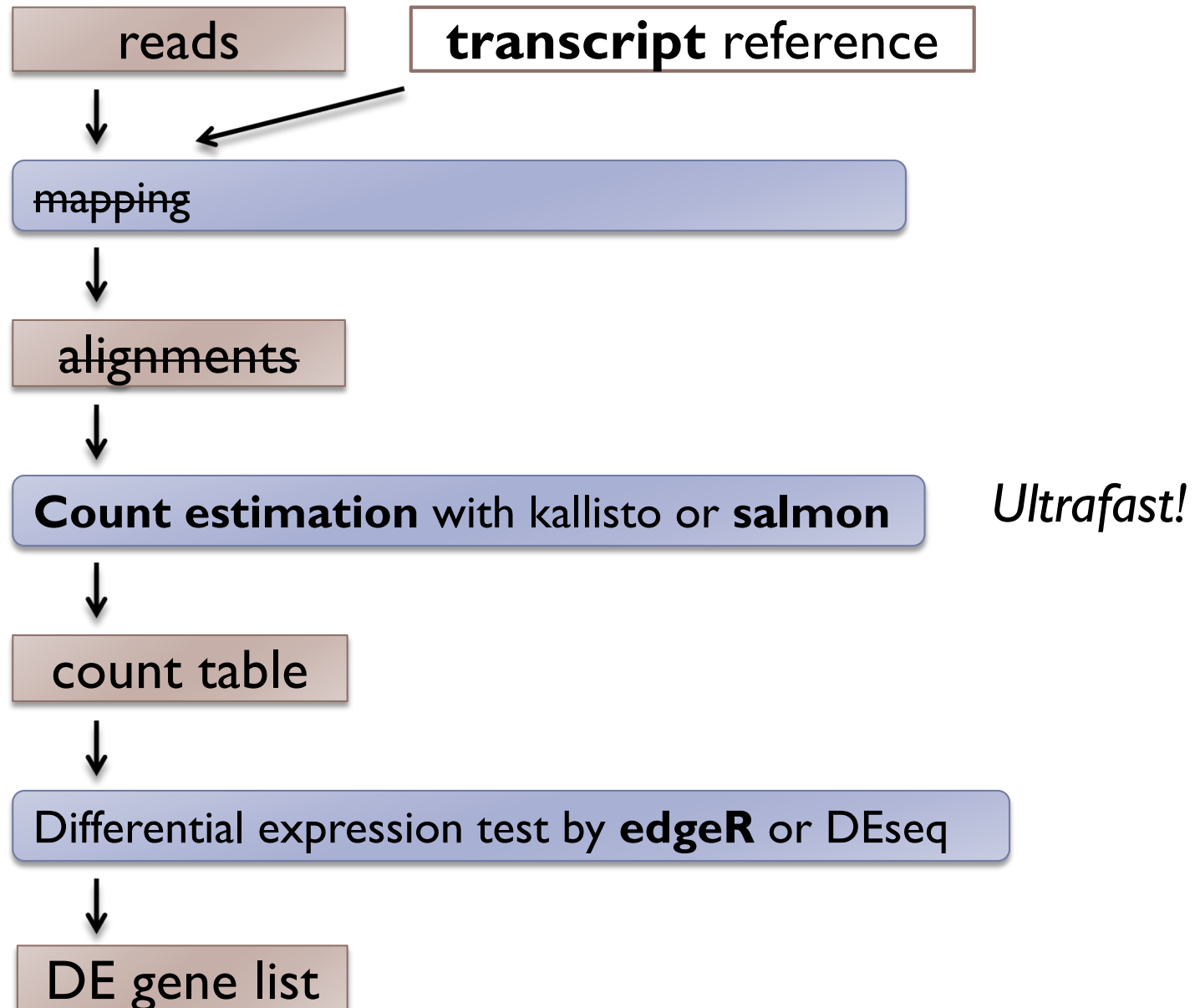
Two Basic Pipelines

- ▶ Choice of reference
 - ▶ **Genome** – standard for genome-known species
 - ▶ **Transcript** – the only way for genome-unknown species
 - can be used for genome-known species

A transcript-based pipeline



A transcript-based pipeline (alignment-free method)



Alignment-free RNAseq quantification

- ▶ **Software**

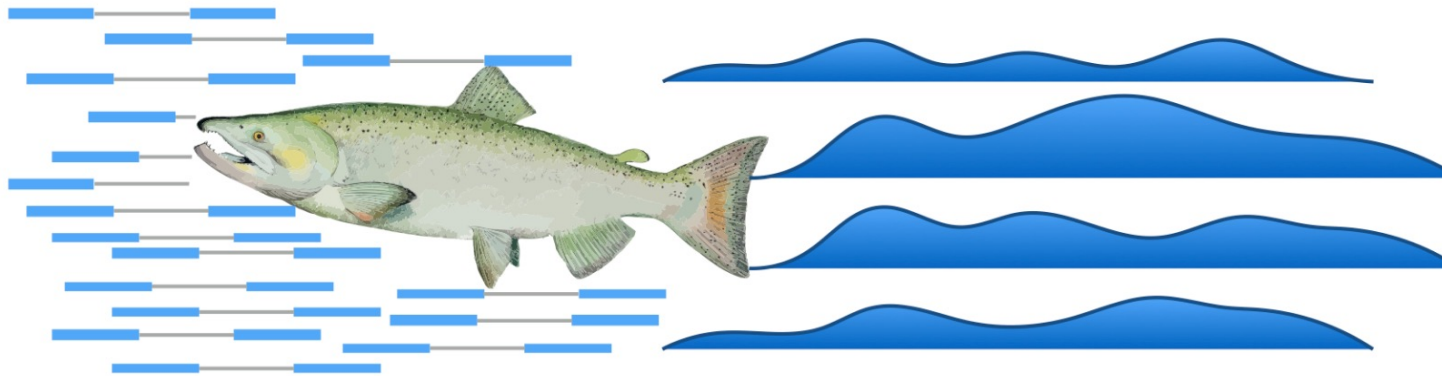
- ▶ Salmon
- ▶ Kallisto
- ▶ Sailfish

- ▶ **Concept**

- ▶ Precise alignments are not required to assign reads to their origins.
- ▶ => “pseudo-alignment” using a de bruijn graph information (kallisto), a k-mer approach (Sailfish old ver.) or a “quasi-mapping” (Salmon)

- ▶ **Benefit**

- ▶ Ultrafast
- ▶ Computationally cheap
- ▶ Accuracy: similar or better than mapping-based methods



Salmon —Don't count . . . quantify!

Overview

- ultra-fast
- stable; sophisticated; well-documented
- Alevin for single-cell RNA-seq

Salmon is a tool for quantifying the expression of transcripts using RNA-seq data. Salmon uses new algorithms (specifically, coupling the concept of *quasi-mapping* with a two-phase inference procedure) to provide accurate expression estimates very quickly (i.e. *wicked-fast*) and while using little memory. Salmon performs its inference using an expressive and realistic model of RNA-seq data that takes into account experimental attributes and biases commonly observed in *real* RNA-seq data.

Citing Salmon

If you find Salmon useful, or have suggestions for improving Salmon in your work, please cite the Salmon paper:

<https://combine-lab.github.io/salmon/>

Salmon

Salmon is a tool for quantifying the expression of transcripts using RNA-seq data. Salmon uses new algorithms to provide accurate expression estimates very quickly.

(example)

```
$salmon index ...    # step 1. build index  
$salmon quant ...    # step 2. quantification
```

► Input

- reference (fasta) and reads (fastq)

► Output

- Count estimation table: **quant.sf**

Let's Try **Salmon**

Map 75-bp Illumina reads to a transcript reference and quantify the abundance.

Prepare reads and reference genome

Sequences for this exercise are stored in `~/gitc/data/SS/`.

```
IlluminaReads1.fq : Illumina reads in fastq format  
minimouse_mRNA.fa : a set of transcript sequences
```

Build index of reference sequence

```
$salmon index -t minimouse_mRNA.fa \  
  -i minimouse_mRNA.fa.salmon.idx -k 31
```

Quantification

```
$salmon quant -i minimouse_mRNA.fa.salmon.idx \  
  -l A -o salmon_out -r IlluminaReads1.fq
```


Salmon outputs

NumReads => edgeR

`quant.sf`

Name	Length	EffectiveLength	TPM	NumReads
Icl ENSMUST00000074761	381	132.000	169.095133	5.000
Icl ENSMUST00000136312	2205	1956.000	90.036424	39.451
Icl ENSMUST00000004316	1671	1422.000	0.000000	0.000
Icl ENSMUST00000105465	1665	1416.000	5801.782522	1840.332
Icl ENSMUST00000165878	1656	1407.000	0.000000	0.000
Icl ENSMUST00000177779	1674	1425.000	0.000000	0.000
Icl ENSMUST00000179238	1674	1425.000	136.797600	43.668
Icl ENSMUST00000082402	1545	1296.000	6110.505937	1774.000
Icl ENSMUST00000092163	447	198.000	32984.331687	1463.000
Icl ENSMUST00000092162	447	198.000	0.000000	0.000
Icl ENSMUST00000100497	1128	879.000	328.241125	64.633
Icl ENSMUST00000094434	552	303.000	8390.396792	569.504
Icl ENSMUST00000090860	552	303.000	0.000000	0.000
Icl ENSMUST00000005950	1422	1173.000	4014.976469	1055.000
Icl ENSMUST00000120655	1212	963.000	0.000000	0.000
Icl ENSMUST00000019649	918	669.000	1047.905860	157.043
Icl ENSMUST00000071555	1128	879.000	1271.484978	250.364
Icl ENSMUST00000167721	888	639.000	4172.375467	597.249
Icl ENSMUST00000082405	684	435.000	8599.700325	838.000
Icl ENSMUST00000171419	795	546.000	0.000000	0.000
Icl ENSMUST00000082408	684	435.000	8599.700325	838.000

Salmon to edgeR

Name	Length	EffectiveLength	TPM	NumReads
Ic ENSMUST00000074761	381	132.000	169.095133	5.000
Ic ENSMUST00000136312	2205	1956.000	90.036424	39.451
Ic ENSMUST00000004316	1671	1422.000	0.000000	0.000
Ic ENSMUST00000105465	1665	1416.000	5801.782522	1840.332
Ic ENSMUST00000165878	1656	1407.000	0.000000	0.000
Ic ENSMUST00000177779	1674	1425.000	0.000000	0.000
Ic ENSMUST00000179238	1674	1425.000	136.797600	43.668
Ic ENSMUST00000082402	1545	1296.000	6110.505937	1774.000
Ic ENSMUST00000092163	447	198.000	32984.331687	1463.000
Ic ENSMUST00000092162	447	198.000	0.000000	0.000
Ic ENSMUST00000100497	1128	879.000	328.241125	64.633
Ic ENSMUST00000094434	552	303.000	8390.396792	569.504
Ic ENSMUST00000090860	552	303.000	0.000000	0.000
Ic ENSMUST00000005950	1422	1173.000	4014.976469	1055.000
Ic ENSMUST00000120655	1212	963.000	0.000000	0.000
Ic ENSMUST00000019649	918	669.000	1047.905860	157.043
Ic ENSMUST00000071555	1128	879.000	1271.484978	250.364
Ic ENSMUST00000167721	888	639.000	4172.375467	597.249
Ic ENSMUST00000082405	684	435.000	8599.700325	838.000
Ic ENSMUST00000171419	795	546.000	0.000000	0.000
Ic ENSMUST00000092408	691	422.000	8208.082507	804.000

count matrix



Name	Lib-1 NumReads	Lib-2 NumReads	Lib-3 NumReads	Lib-4 NumReads
Ic ENSMUST00000074761	5.000	27.957	15.037	230.000
Ic ENSMUST00000136312	39.451	674.000	61.696	42.809
Ic ENSMUST00000004316	0.000	528.689	0.000	156.235
Ic ENSMUST00000105465	1840.332	521.304	111.396	0.000
Ic ENSMUST00000165878	0.000	148.549	0.000	218.000
Ic ENSMUST00000177779	0.000	470.496	348.508	215.000
Ic ENSMUST00000179238	43.668	0.000	0.000	29.956
Ic ENSMUST00000082402	1774.000	195.495	1.534	192.288
Ic ENSMUST00000092163	1463.000	499.000	260.604	159.365
Ic ENSMUST00000092162	0.000	454.000	104.191	198.000
Ic ENSMUST00000100497	64.633	447.000	0.000	0.000
Ic ENSMUST00000094434	569.504	0.000	0.000	159.985
Ic ENSMUST00000090860	0.000	410.000	1.608	0.000
Ic ENSMUST00000005950	1055.000	332.068	135.311	1.002
Ic ENSMUST00000120655	0.000	266.106	239.000	192.000
Ic ENSMUST00000019649	157.043	406.000	0.000	6.017
Ic ENSMUST00000071555	250.364	0.000	264.000	0.000
Ic ENSMUST00000167721	597.249	4.998	89.000	135.272

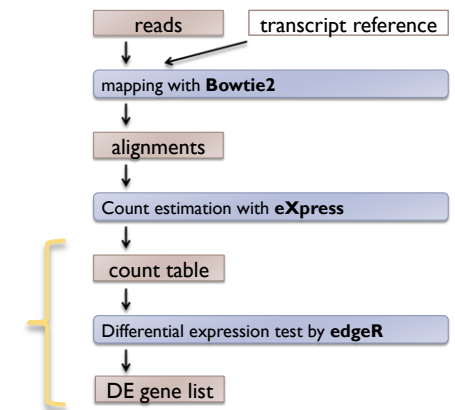
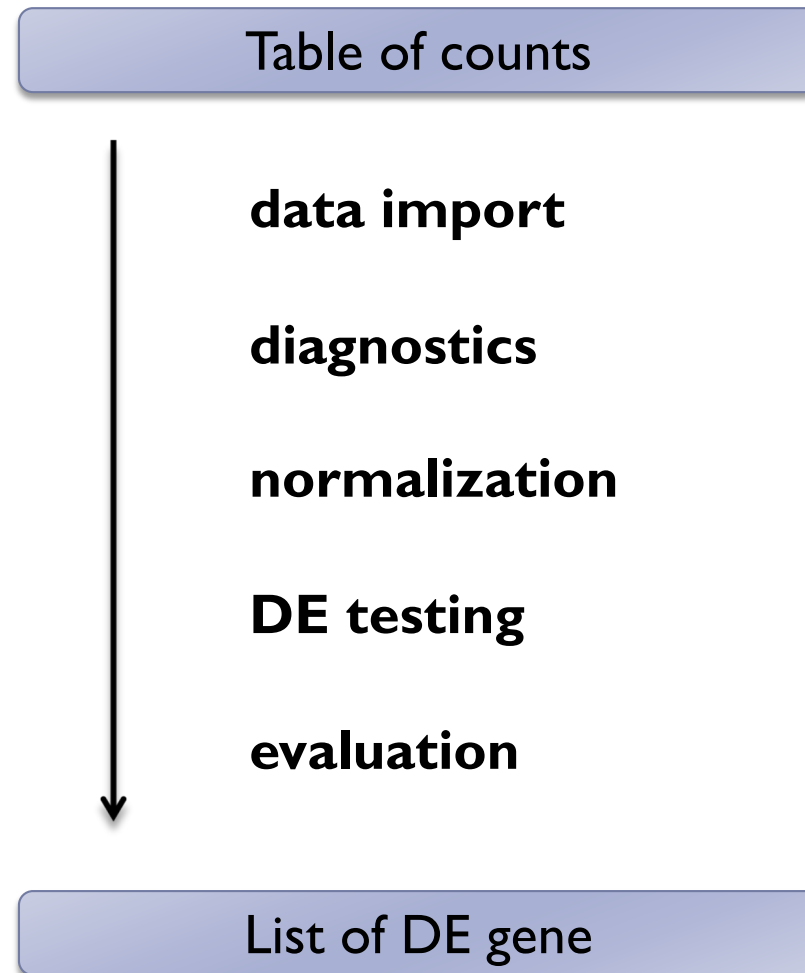
quant1.sf

quant2.sf

quant3.sf

quant4.sf

\$salmon quantmerge ...



edgeR

- ▶ A Bioconductor package for differential expression analysis of digital gene expression data
- ▶ **Model:** An over dispersed Poisson model, negative binomial (NB) model, is used
- ▶ **Normalization:** TMM method (trimmed mean of M values) to deal with composition effects
- ▶ **DE test:** exact test and generalized linear models (GLM)

edgeR (classic)

- ▶ input: **count data** (not RPKM or TPM)
- ▶ output: gene table with DE significance statistics (FDR)

(example)

```
$ R
> library(edgeR) #load edgeR library
> dat <- read.delim("count_data.txt", ...) #import count table to R
> group <- c(rep("M", 3), rep("H", 3)) #assign groups
> D <- DGEList(dat, group=group) #import data to edgeR
> D <- calcNormFactors(D) #normalization (TMM)
> D <- estimateCommonDisp(D) #estimate common dispersion
> D <- estimateTagwiseDisp(D) #estimate tagwise dispersion
> de <- exactTest(D, pair=c("M", "H")) #DE test
> topTags(de)
```

Comparison of groups: H-M

	logConc	logFC	P.Value	FDR
AT5G48430	-15.36821	6.255498	9.919041e-12	2.600872e-07
AT5G31702	-15.88641	5.662522	3.637593e-10	4.083773e-06
AT3G55150	-17.01537	5.870635	4.672331e-10	4.083773e-06
...				

edgeR (GLM)

- ▶ input: **count data** (not RPKM or TPM)
- ▶ output: gene table with DE significance statistics (FDR)

(example)

```
$ R
> library(edgeR) #load edgeR library
> dat <- read.delim("count_data.txt", ...) #import count table to R

> treat <- factor(c("M", "M", "M", "H", "H", "H"))
> treat <- relevel(treat, ref="M")
> design <- model.matrix(~treat)
> rownames(design) <- colnames(y)

> D <- DGEList(dat, group=treat) #import data to edgeR
> D <- calcNormFactors(D, method="TMM") #normalization (TMM)
> D <- estimateDisp(D, design) #estimate dispersion
> fit <- glmFit(D, design) #fitting to model
> lrt <- glmLRTt(D, coef=2) #DE test
> topTags(lrt)
> ...
```

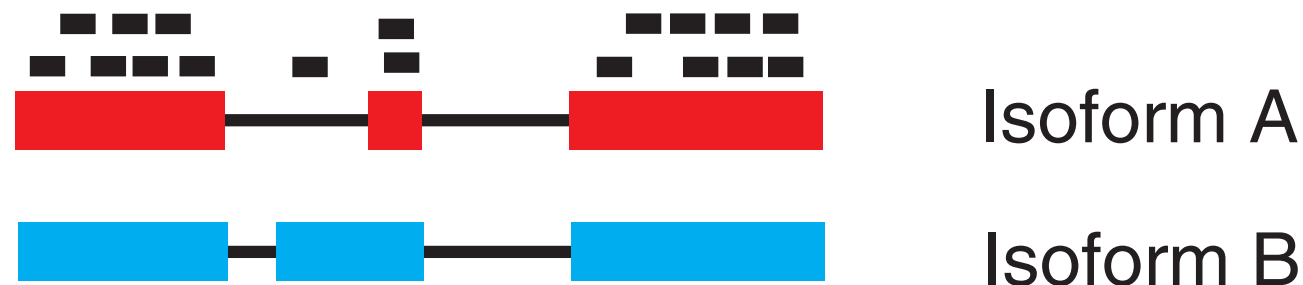
Let's try edgeR

- ▶ edgeR classic
 - ▶ ex402: Differential expression analysis with edgeR (pairwise)
- ▶ edgeR linear model [advanced]
 - ▶ ex403-1: Differential expression analysis with edgeR (GLM)
 - ▶ ex403-2: Differential expression analysis with edgeR (GLM; considering batch effect)

Estimate Abundance

► **Multimapping issues**

- Isoforms
 - Very similar paralogs
 - Repetitive sequences
 - => cannot align reads uniquely
- Mapping ambiguity should be taken into consideration.



- Critical for RNA-seq de novo analysis
- Software: RSEM and eXpress (EM algorithm)