

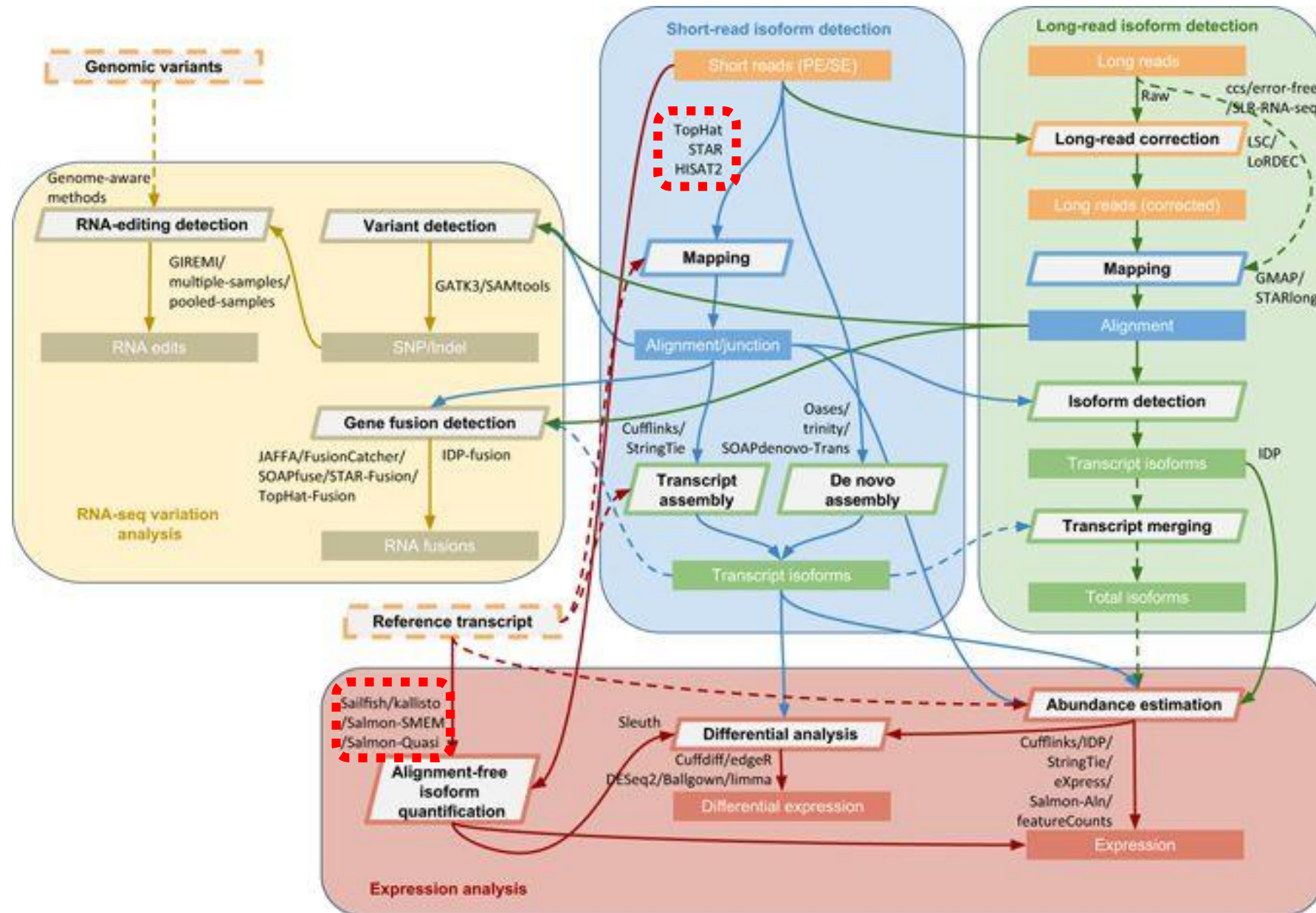


# Overview of RNA-Seq data alignment methods

SPP workshop  
October 2019 | MIPZ Cologne

Yulong Niu

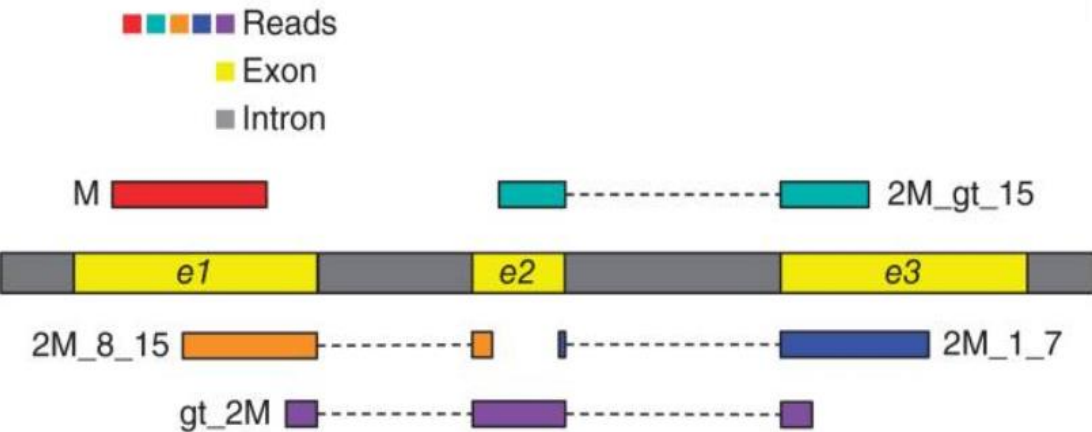
# 1. Modern RNA-Seq alignment methods



## 2. Alignment and pseudo-alignment

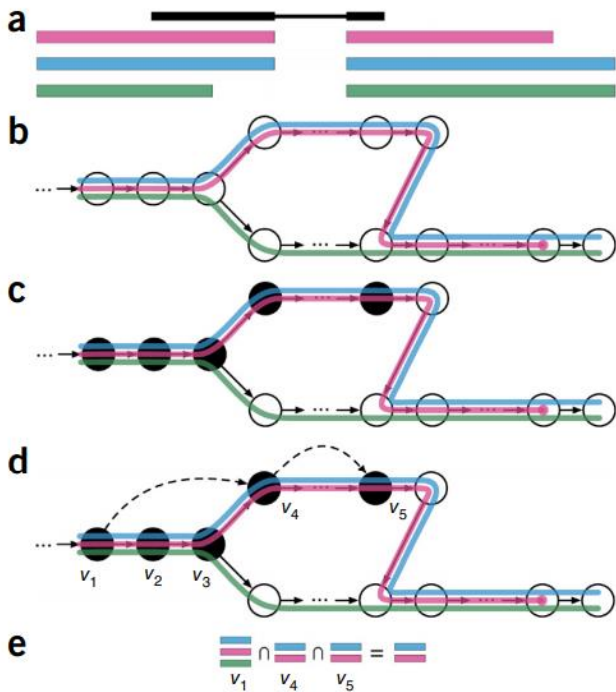
(genome) alignment

**HISAT2**



(transcriptome) alignment

**kallisto**



	HISAT2	kallisto
Reference	genome	transcriptome
Speed	slow	fast
Novel splicing	Yes	No

1. Kim D et. al., 2015  
2. Nicolas L Bray et. al., 2016

### 3. (Pseudo)-alignment workflow



**HISAT2**

*hisat2-build*

*hisat2*

*StringTie and Ballgown*

Pertea M et. al., *Nature Protocol* 2016

**kallisto**

*kallisto index*

*kallisto quant*

*kallisto quant*

# Hands-on session: Read alignment and pseudo-alignment

[https://github.com/YulongNiu/MPIPZ\\_SPP\\_workshop/blob/master/RNA-Seq/tutorials/RNA-Seq\\_alignment.md](https://github.com/YulongNiu/MPIPZ_SPP_workshop/blob/master/RNA-Seq/tutorials/RNA-Seq_alignment.md)