

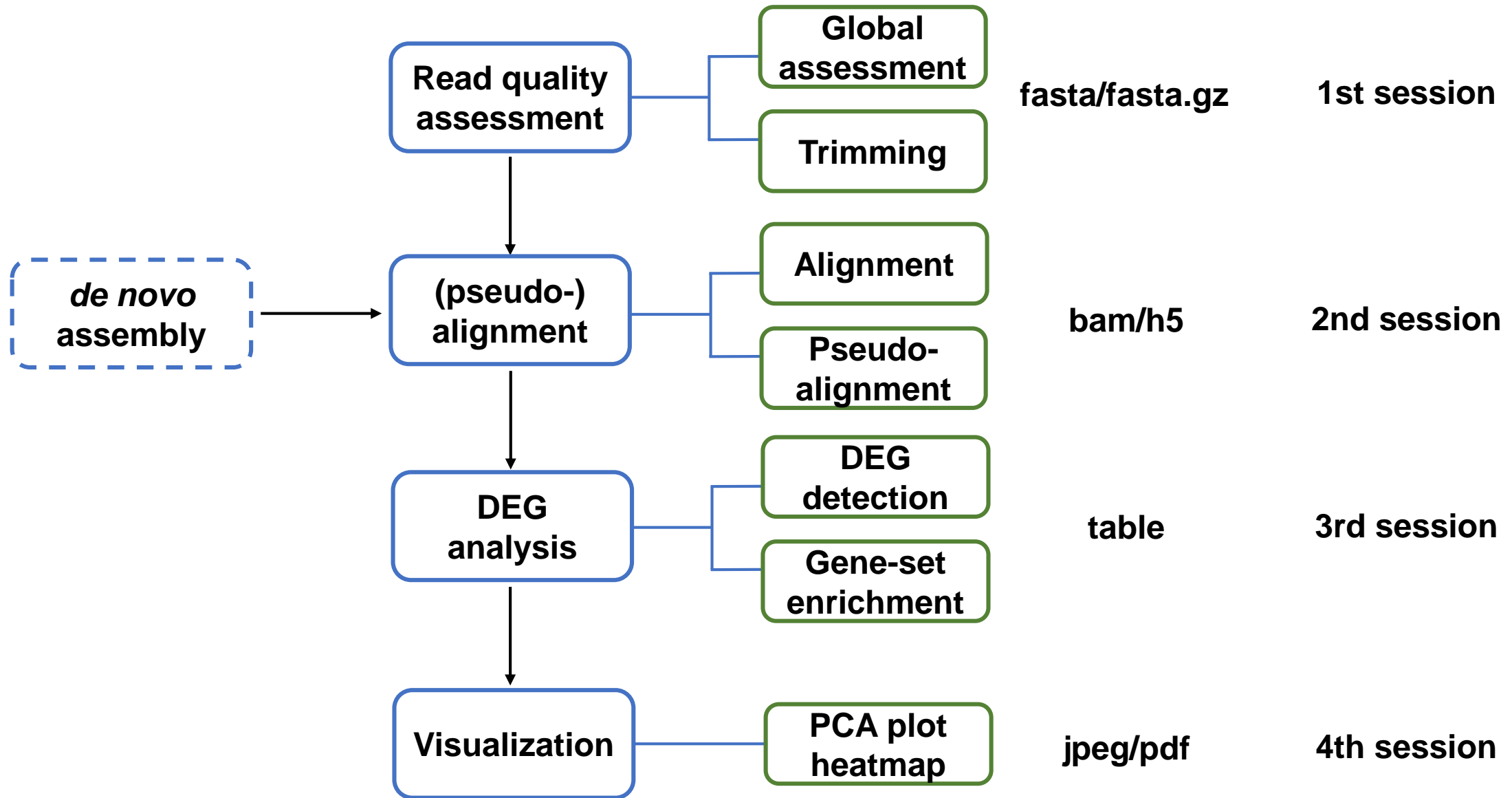


Overview of RNA-Seq data analysis workflows

SPP workshop
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1. RNA-Seq analysis workflow



The workflow is designed for **short reads mRNA sequencing**, not appropriate for **microRNA**, **circular RNA**, **single-cell RNA**, **long reads** analysis.

2. RNA-Seq data sets

pair-end RNA-Seq

```
Col0_p_rep1_R1.fq.gz  
Col0_p_rep1_R2.fq.gz  
Col0_p_rep2_R1.fq.gz  
Col0_p_rep2_R2.fq.gz  
Col0_p_rep3_R1.fq.gz  
Col0_p_rep3_R2.fq.gz  
flg22_p_rep1_R1.fq.gz  
flg22_p_rep1_R2.fq.gz  
flg22_p_rep2_R1.fq.gz  
flg22_p_rep2_R2.fq.gz  
flg22_p_rep3_R1.fq.gz  
flg22_p_rep3_R2.fq.gz
```

Two conditions (three replicates)

Col0

Col0 treated with flg22

single-end RNA-Seq

```
Col0_s_rep1.fq.gz  
Col0_s_rep2.fq.gz  
Col0_s_rep3.fq.gz  
flg22_s_rep1.fq.gz  
flg22_s_rep2.fq.gz  
flg22_s_rep3.fq.gz  
MeJA_s_rep1.fq.gz  
MeJA_s_rep2.fq.gz  
MeJA_s_rep3.fq.gz
```

Three conditions (three replicates)

Col0

Col0 treated with flg22

Col0 treated with methyl jasmonate (MeJA)

Hands-on session: Read quality assessment and *de novo* transcriptome assembly

https://github.com/YulongNiu/MPIPZ_SPP_workshop/blob/master/RNA-Seq/tutorials/RNA-Seq_quality_assessment.md

https://github.com/YulongNiu/MPIPZ_SPP_workshop/blob/master/RNA-Seq/tutorials/RNA-Seq_devo_assembly.md