

# SPAdesを用いた ゲノムアセンブリの流れ

Raw data

① Raw dataのquality確認 [fastqc / vsearch]

(a)

fastq

(b)

fastq

(c)

fastq

(d)

fastq

② Read1(R1)とRead2 (R2)のmerge [vsearch]

③ Quality control [vsearch]

fastq

fasta

fastq

fasta

④ Assembly [SPAdes]

⑤ Assemblyの評価 [Quast / DFAST]

