

Week 2

Monday, 2 August 2021 23:33

GENOME ASSEMBLY

ISOLATING DNA FROM ORGANISM
SUBMITTING DNA TO SEQUENCING CENTER
CHROMOSOMES CUTTED INTO READS

ASSEMBLY STICKING RAW READS TOGETHER IN ORDER

→ DE NOVO

→ REFERENCE BASED

PATRIC ONLY OFFERS DE-NOVO
ILLUMINA MOST COMMON SEQUENCERS

HYBRID GENOME ASSEMBLY

USING BOTH SHORT & LONG READS
IF HORIZONTAL GENE TRANSFER (HGT) OR TRANSPOSONS

BUT LONG-READ HAVE LESS COVERAGE

RACON (LONG) : 2 } DEFAULT
PYLON (SHORT) : 2 }

PUBLIC WORKSPACE

MODC_PATRIC_COURSE

UPLOADING FILES (WORKSPACE, UPLOAD MONITOR, APP ITSELF)

SUBMITTING READS TO ASSEMBLY SERVICE

- SINGLE READS
- PAIR READS
- SESSION # FROM SEQUENCE-READ-ARCHIVE

INTERLEAD → R1 & R2 IN THE SAME FILE

MATE PAIRED → LIB THAT ALLOWS YOU TO HAVE PAIRS FAR APART

PLATFORM → ILLUMINA OR IONTOHENT

PAIRED LIBRARY

PLATFORM:

READ 2:
READ 2:

YOU CAN COMBINE PAIRED & SINGLE READS TOGETHER
REPEATING SAMPLE IN MULTIPLE LANES
BACKUP & GREATER COVERAGE

ILLUMINA (PAIRED)
PACBIO (SINGLE)

SRA SEQUENCE READ ARCHIVE
LOADING DATA INTO ASSEMBLER

SELECTING ASSEMBLY STRATEGIES (PARAMETERS)

AUTO

UNICYCLER ILLUMINA ONLY, LONG READ ONLY SETS, HYBRID ASSEMBLY

SPADES

ASSEMBLING SMALL GENOMES (BACTERIAS)

CANU

LONG-READS-ASSEMBLER, NANOPORES, 3RD-4TH

META-SPADES

METAGENOMIC ASSEMBLY

PLASMID-SPADES

ONLY FOR PLASMIDS

MSA

SINGLE CELL ISOLATES

IF SEQUENCE COULD INCLUDE PLASMIDS
THEN SUBMIT SEQUENCE 2 TIMES
FIRST AS "AUTO", SECOND AS "PLASMID"
AND COMPARISON THEM

TRIM READS (TRIM-GALORE FUNCTION)

RAON & PILON ITERATIONS

↓
LONG

PACBIO
NANOPORE

↓
SHORT

ILLUMINA
IONTOMENT

CONTAINS & READS MAPPED
LOOKING FOR DISCREPANCIES

MIN CONTIG COVERAGE
MIN CONTIG LENGTH