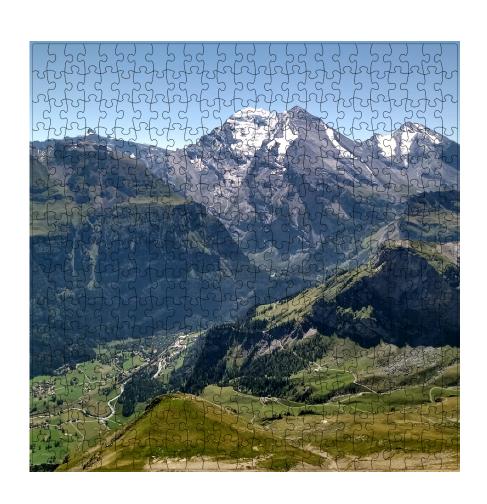
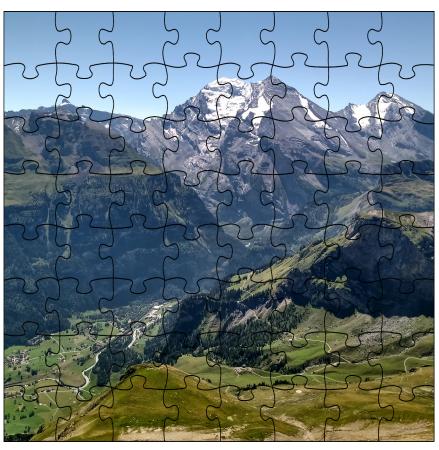
Long-read sequence analysis

Applications

Why long reads?





Applications

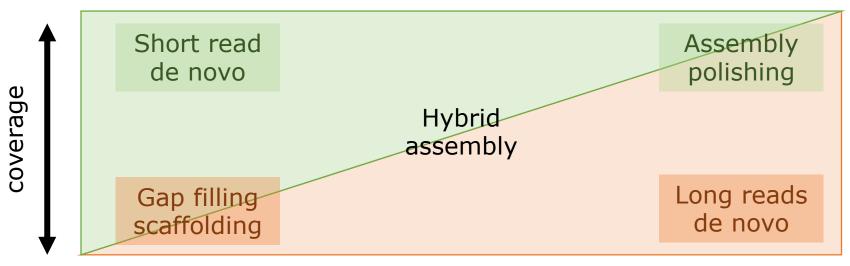
- (Genome) assembly
- Variant analysis
- Transcriptome analysis
- Epigenetics
- Metagenomics

Assembly

- Reconstructing a DNA sequence out of fragmented sequences:
 - Better understand variations between and within species
 - Reduces resources and increases accuracy for many applications
- Longer reads:
 - Less assembly errors
 - Higher contiguity (longer contigs)
 - Lower computational resources required

Assembly

Illumina short reads



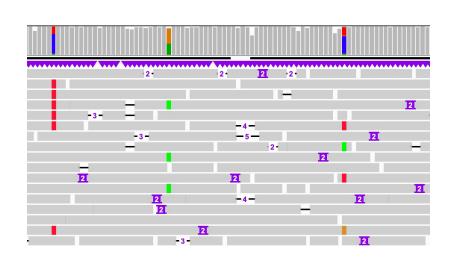
Long reads

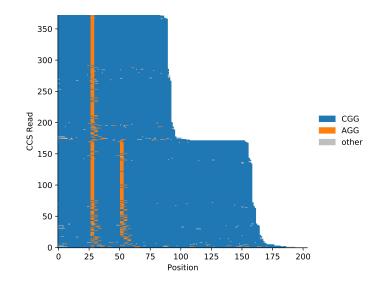
LR assembly software

- Microbial:
 - HGAP
 - Trycycler
- Large(r) genomes:
 - Shasta (ONT only)
 - Raven
 - wtdbg2
 - Falcon (PacBio only)
 - Canu
 - Flye

Variant analysis

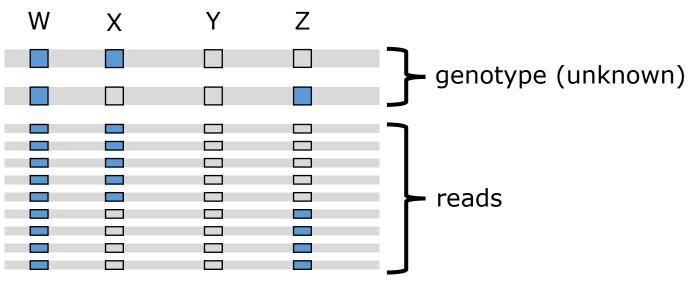
- Low accuracy long reads: not particularly good at variant analysis
- Major applications
 - Structural variation/large repeats
 - Phasing of variants



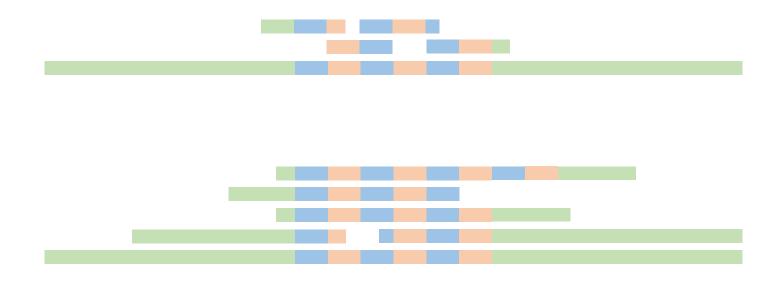


Phasing

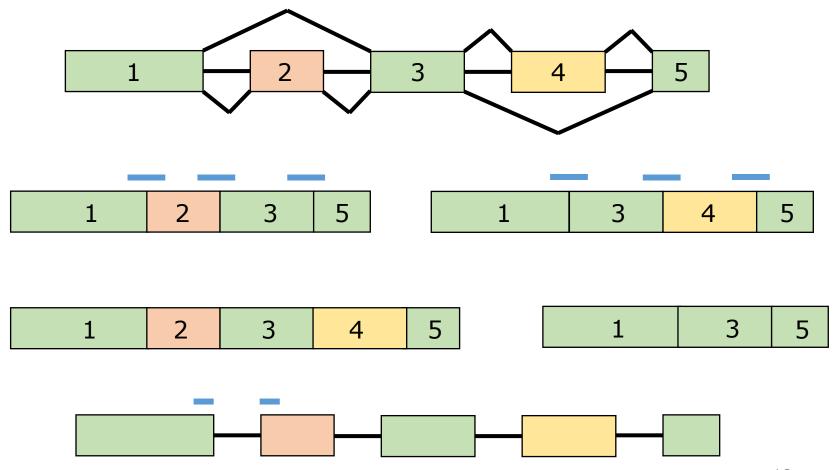
- Variant calling:
 - DeepVariant (Pacbio + ONT)
 - Medaka (ONT)
- Phasing: Whatshap



Repeat expansion - project 2



Transcriptome analysis



Transcriptome analysis

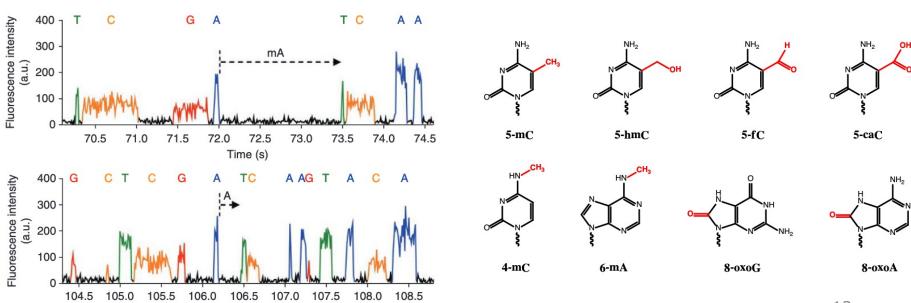
- Full transcripts: less ambiguous identification + quantification of transcript isoforms
- Better gene model prediction (e.g. for genome annotation)
- ONT direct RNA-seq:
 - No PCR amplification
 - No reverse transcription
 - Base modification identification

Epigenetics

- Base modification in non-amplified libraries (Pacbio and ONT)
- No multiplexing

Time (s)

Also possible in direct RNA-seq (ONT)



2

Metagenomics

- Full length 16S genes: better classification (PacBio CCS)
- Metagenome Assembled Genomes (MAGs) -> flye --meta

New possibilities

- Cas9 based targeting (both PacBio & ONT): also base modifications
- Adaptive sampling (ONT)

