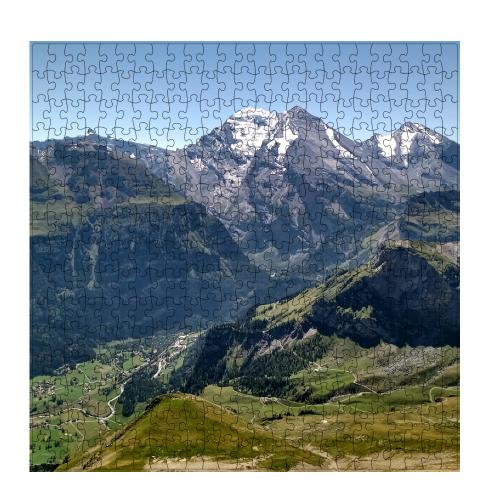
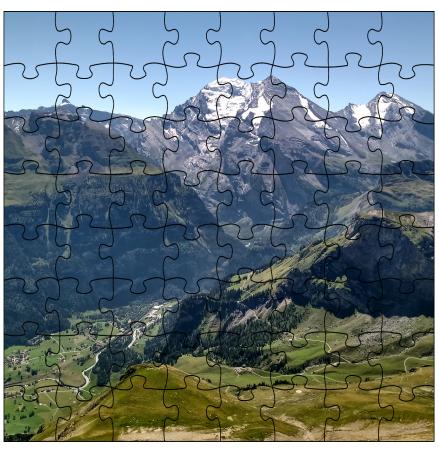
## Long-read sequence analysis

**Applications** 

### Why long reads?





#### Applications

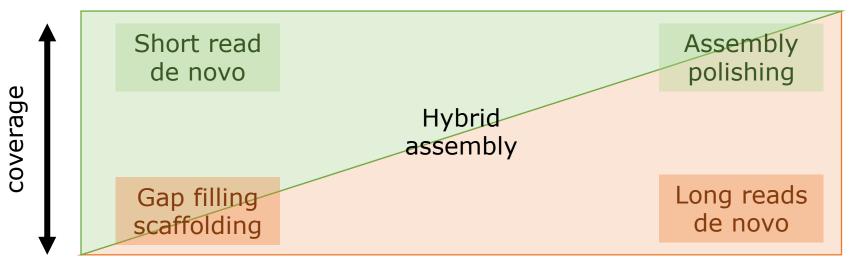
- (Genome) assembly
- Variant analysis
- Transcriptome analysis
- Epigenetics
- Metagenomics

#### 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

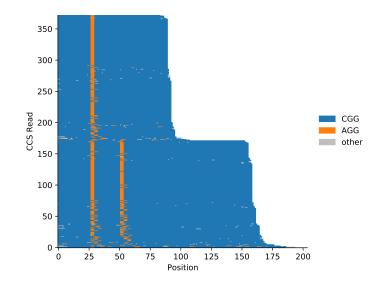
#### LR assembly software

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

#### Variant analysis

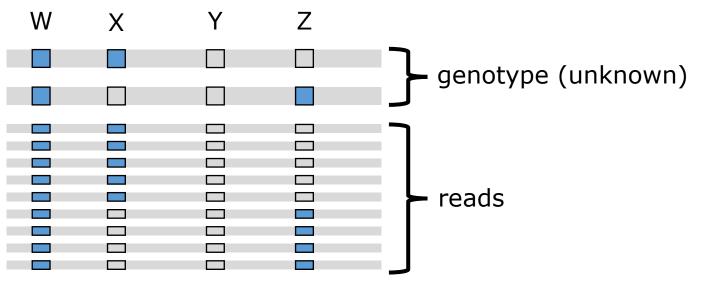
- Low accuracy long reads: not particularly good at variant analysis
- Major applications
  - Structural variation/large repeats
  - Phasing of variants



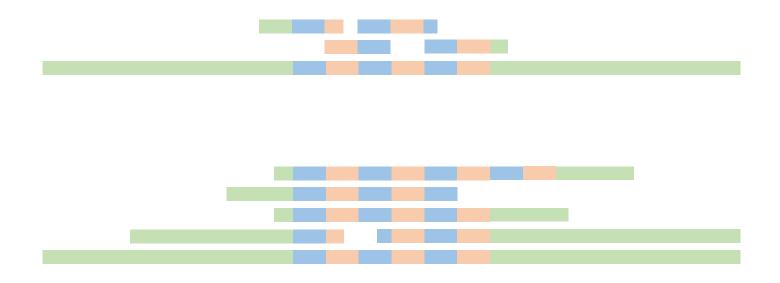


#### Phasing

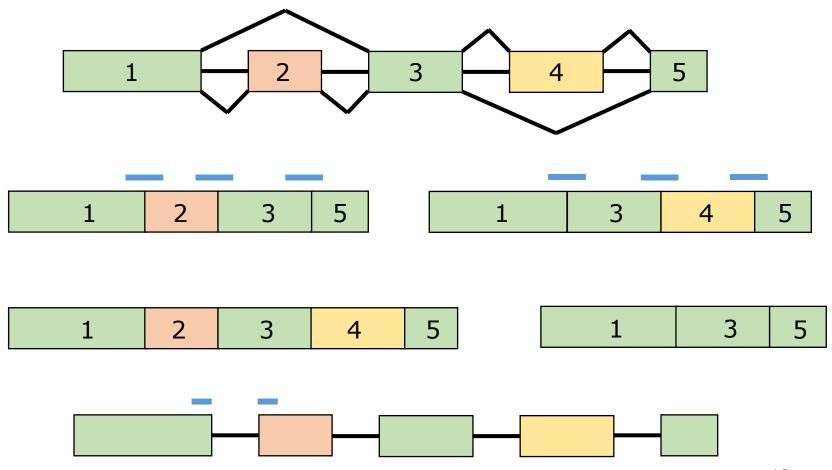
- Variant calling:
  - DeepVariant (Pacbio + ONT)
  - Medaka (ONT)
- Phasing: Whatshap



# Repeat expansion - project 2



#### Transcriptome analysis



#### Transcriptome analysis

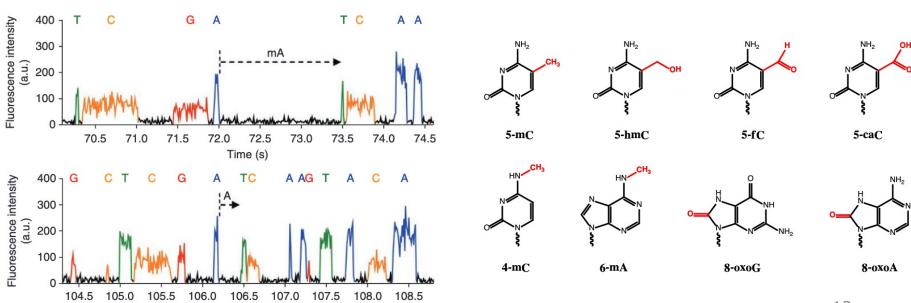
- Full transcripts: less ambiguous identification + quantification of transcript isoforms
- Better gene model prediction (e.g. for genome annotation)
- ONT direct RNA-seq:
  - No PCR amplification
  - No reverse transcription
  - Base modification identification

#### 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
- Metagenome Assembled Genomes (MAGs)

#### New possibilities

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

