

Chromosome sorting

(FACS, microfluidics, ...)

global

StrandSeq

haplotype

cost/labor

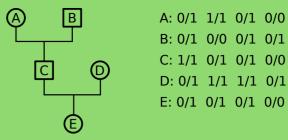
synthetic long reads (TruSeq, 10xGenomics, ...)

3rd-gen. sequencing (PacBio, ONT, ...)

2nd-gen. sequencing (Illumina, ...)

Read-based

## **Genetic Haplotyping**



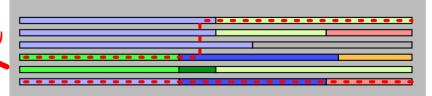
Use genotypes across a pedigree

Supported by most packages for statistical phasing (SHAPEIT, beagle, etc.)

SHAPEIT extension

(Delaneau et al., 2013)

## **Statistical Phasing**



Use genotypes/haplotypes from a reference population