





# Informatics on High-throughput Sequencing Data

(Summer Course 2020)

**Day 17** 



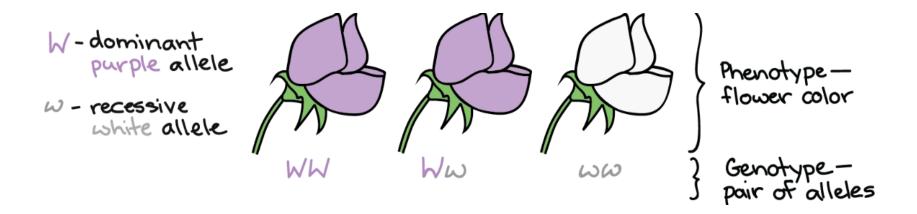
# **Variant Calling**

- Variant calling is the process by which we identify variants from sequence data.
  - 1. Carry out whole genome or whole exome sequencing to create FASTQ files.
  - 2. Align the sequences to a reference genome, creating BAM files.
  - Identify where the aligned reads differ from the reference genome and write to a VCF file.

https://www.ebi.ac.uk/training-beta/online/courses/human-genetic-variation-introduction/variant-identification-and-analysis/

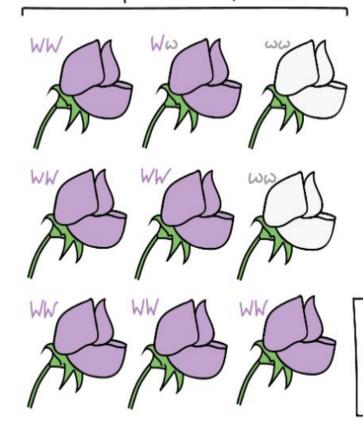
# Notes!

- A genotype is an individual's collection of genes. The term also can refer to the two alleles inherited for a particular gene.
- Allele is a variant form of a given gene. a heritable unit that controls a particular feature of an organism.



# Notes!

## Population of peas



GENOTYPE FREQUENCY:  $\longrightarrow$  How often we see each allele combo Freq; of  $W\omega = 6/9 = 0.67$  allele combo  $W\omega$ ,  $W\omega$ , or  $\omega\omega$  Freq; of  $\omega\omega = 2/9 = 0.22$ 

PHENOTYPE FREQUENCY: 2 How often we see white Freq; of purple = 7/9 = 0.78 vs. purple Freq; of white = 2/9 = 0.22

ALLELE FREQUENCY: Thow often we see each allele  $\rho = Freq$  of W = 13/18 = 0.72 Were  $\omega$  g = Freq of  $\omega = 5/18 = 0.28$ 

# Notes!

- Unphased data are simply the genotypes without regard to which one of the pair of chromosomes holds that allele.
- /: genotype unphased
- Phased data are ordered along one chromosome and so from these data you know the haplotype.
- |: genotype phased
- A haplotype can refer to a combination of alleles or to a set of single nucleotide polymorphisms (SNPs) found on the same chromosome.
- Information about haplotypes is being collected by the International HapMap Project and is used to investigate the influence of genes on disease.

## **VCF/BCF** format

- VCF is the standard file format for storing variation data.
- VCF files are tab delimited text files.

## **Types of variants**

#### **SNPs**

Alignment	VCF representation		
ACGT	POS	REF	ALT
ATGT	2	C	T

### **Deletions**

Alignment	VCF I	repres	sentation
ACGT	P <sub>0</sub> S	REF	ALT
AT	1	ACG	Α

## Large structural variants

```
VCF representation
POS REF ALT INFO
100 T <DEL> SVTYPE=DEL; END=300
```

### **Insertions**

Alignment	VCF I	repres	sentation
AC-GT	P <sub>0</sub> S	REF	ALT
ACTGT	2	C	CT

## **Complex events**

Alignment	<b>VCF</b>	repres	sentation
ACGT	P <sub>0</sub> S	REF	ALT
A-TT	1	ACG	AT

# Thanks! // |?