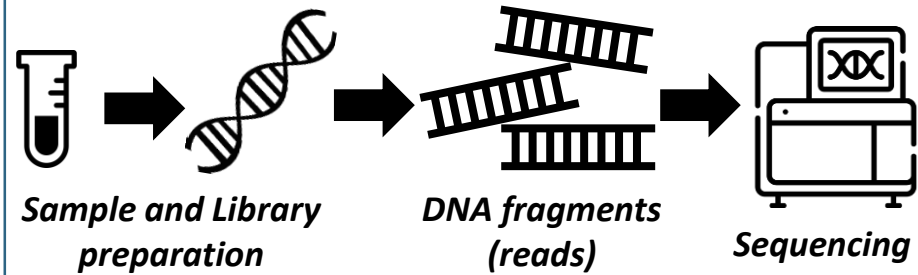


## Sequencing method



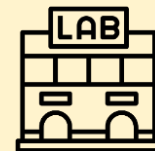
## Source domain

*e.g., publicly available  
aligned reads with variant labels*



## Target domain

*e.g., aligned reads produced via  
individual lab sequencing method*



*Bioinformatics pipeline (e.g., read alignment)*

## Data generation in RUN-DVC

*Select sequencing data that has candidate variants*

*Summarize sequencing data to 3D tensors*

**Labeled dataset  
(3D tensor)**

**Unlabeled dataset  
(3D tensor)**

## Sequencing data

*More Read Features ...*

*Read Base Quality*

*Reference Genome*

`..TCCCATAACAAGTAGACAGAAGCATTCTCAGAAA..`

*Aligned Reads*

`TCCCATAACAAGTAGAAA`

`AACTATAAGAAGCAATCTCAGAAA`

`TAGAAAGCAGCATTCTCAGAAA`

`CAGAAG-ATTCTCAGAAA`