



*Better lives through livestock*

# Consensus Genome Assembly

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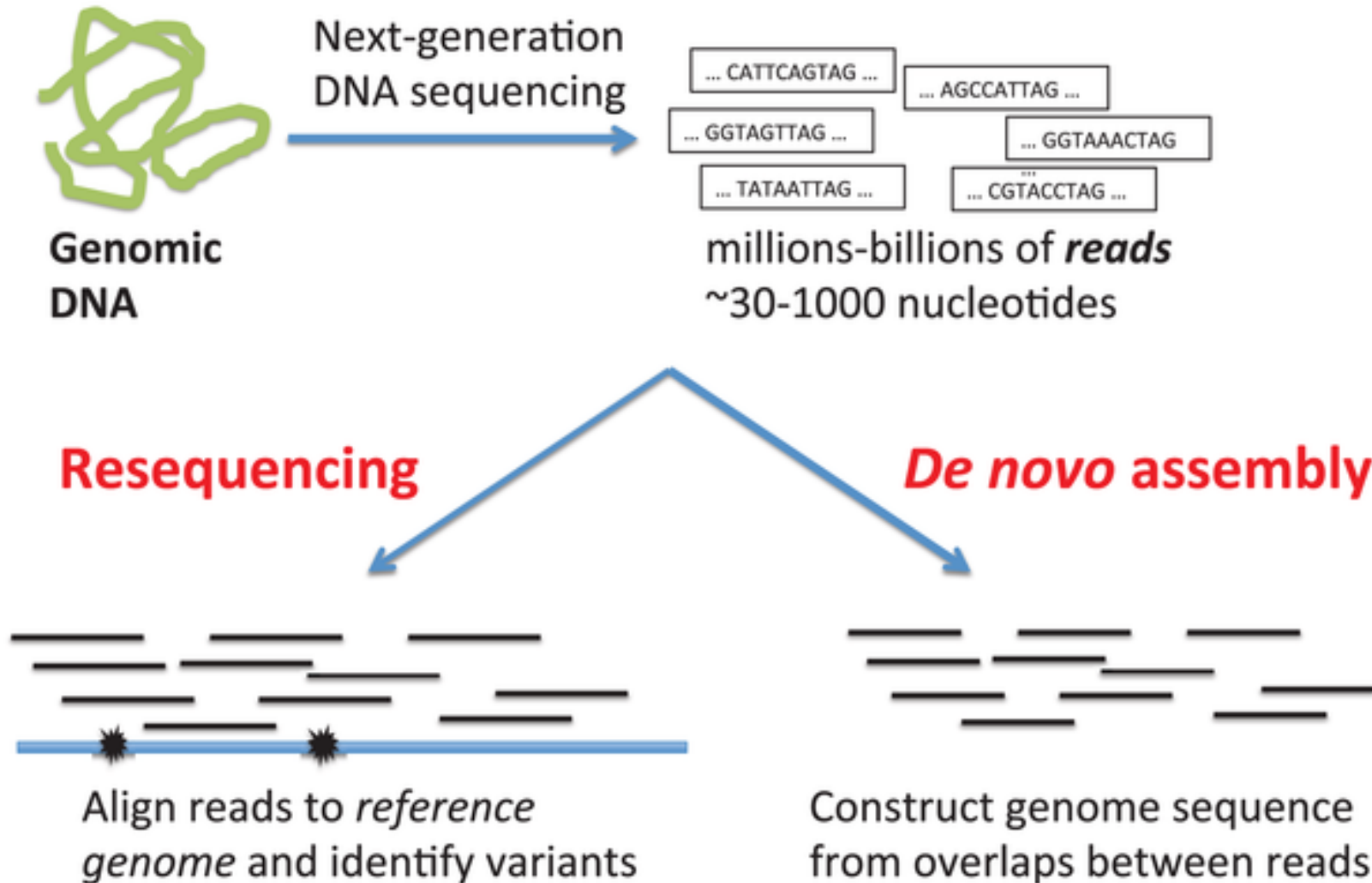
International Livestock Research Institute (ILRI)

Viral Pathogen Genome Sequencing and Bioinformatics Analysis Training Workshop  
6<sup>th</sup> – 17<sup>th</sup> May, 2024

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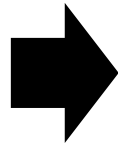
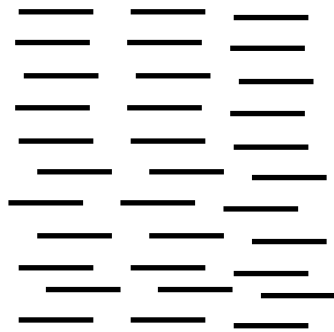


# Overview of assembly techniques

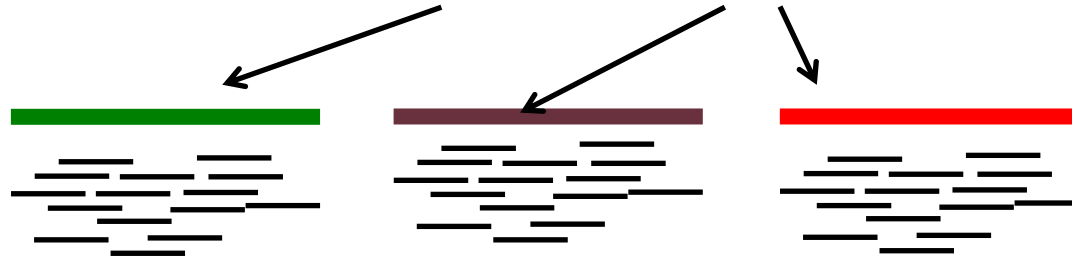


# De-novo assembly basics

## 1. Shotgun reads

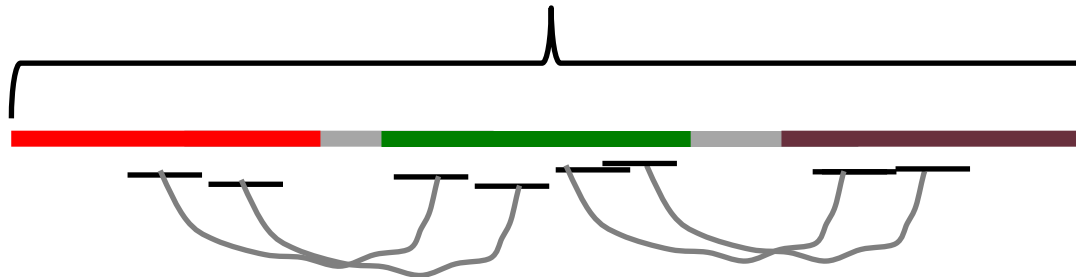


## 2. Assemble reads into contigs

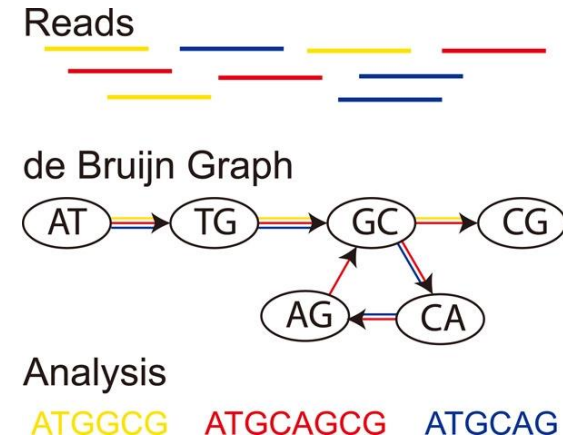


## 3. Order contigs onto a scaffold

Use paired-end info to determine order of (and distance between) contigs



PE reads with known distances

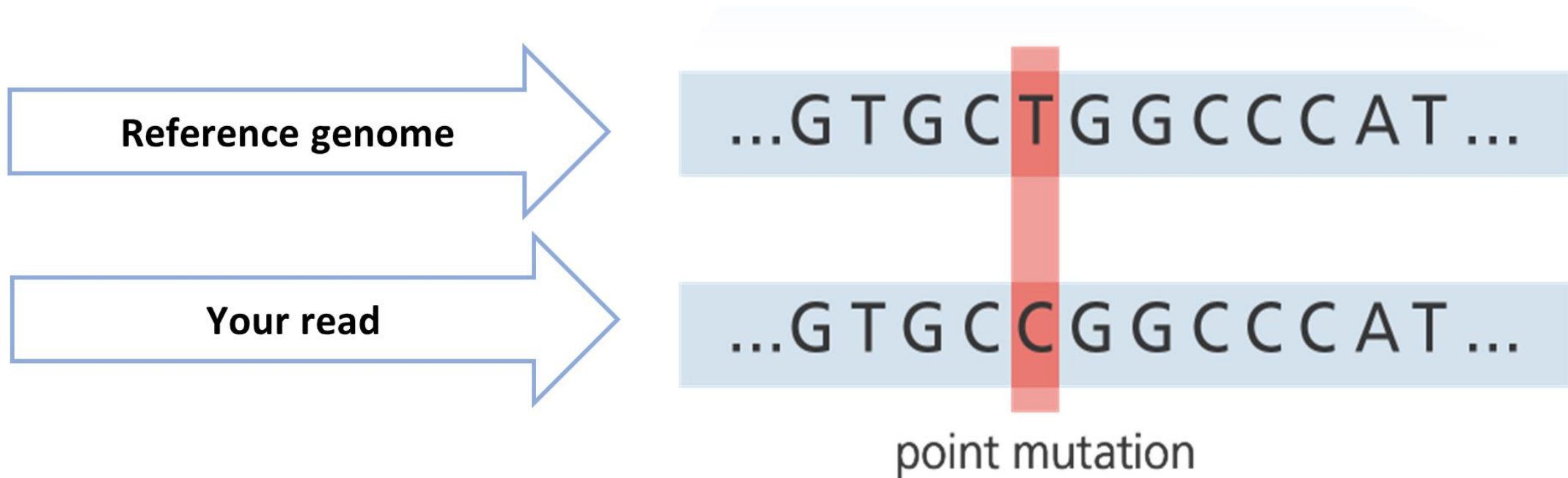


## 4. (optional) gaps between contigs are filled in by mapping reads back to the scaffolds

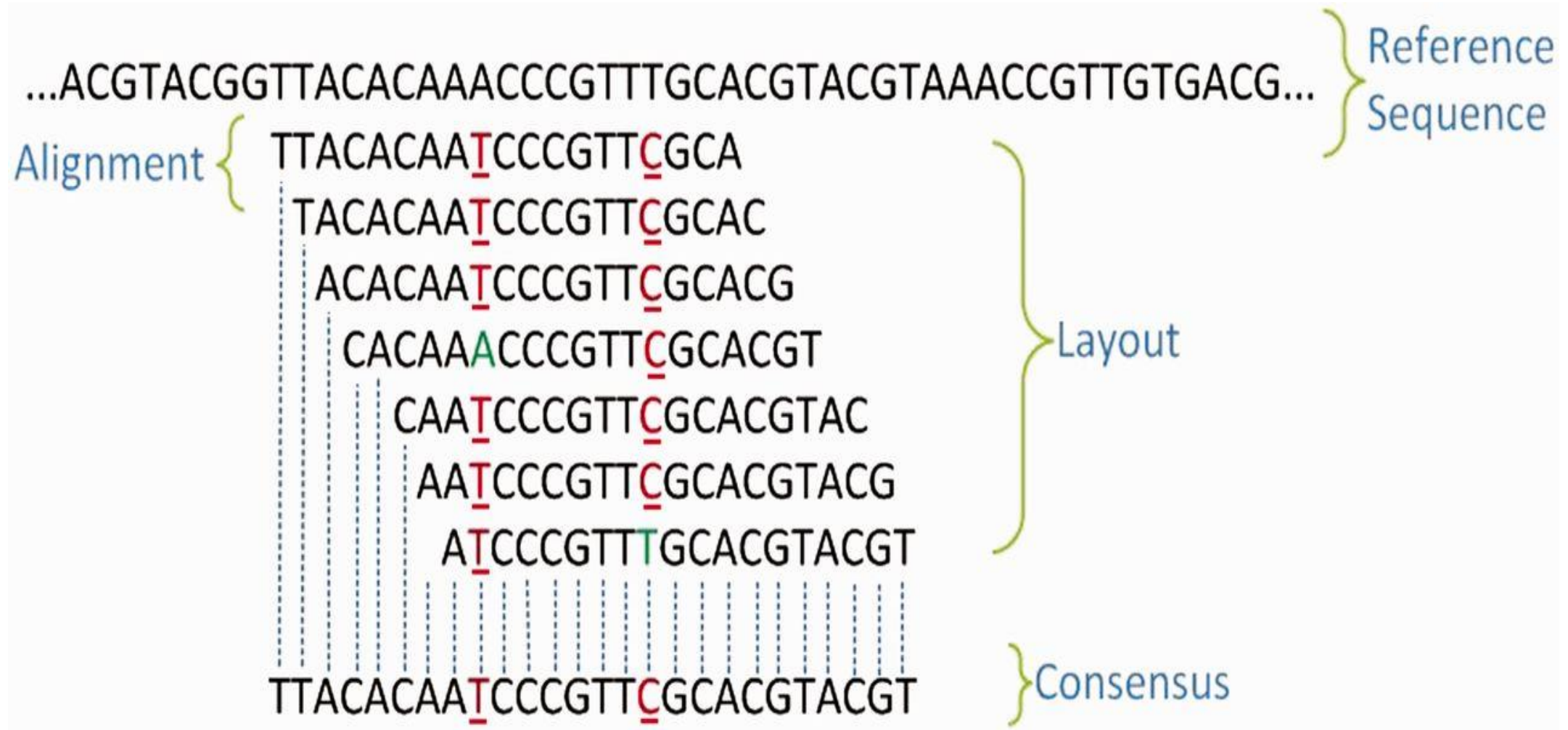
# Reference-based assembly



# Why perform reference-based assembly?



# Generate the consensus genome



# Acknowledgments

