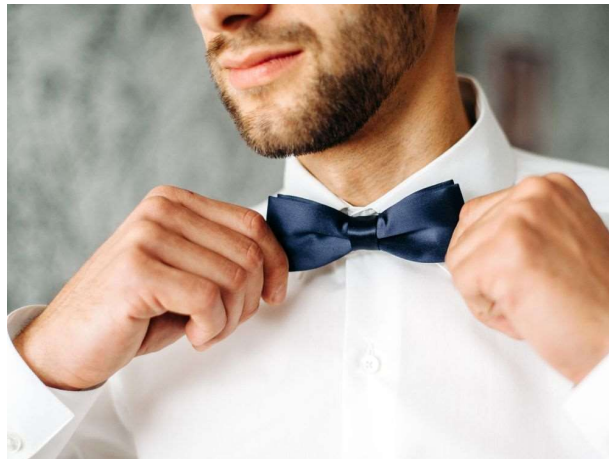
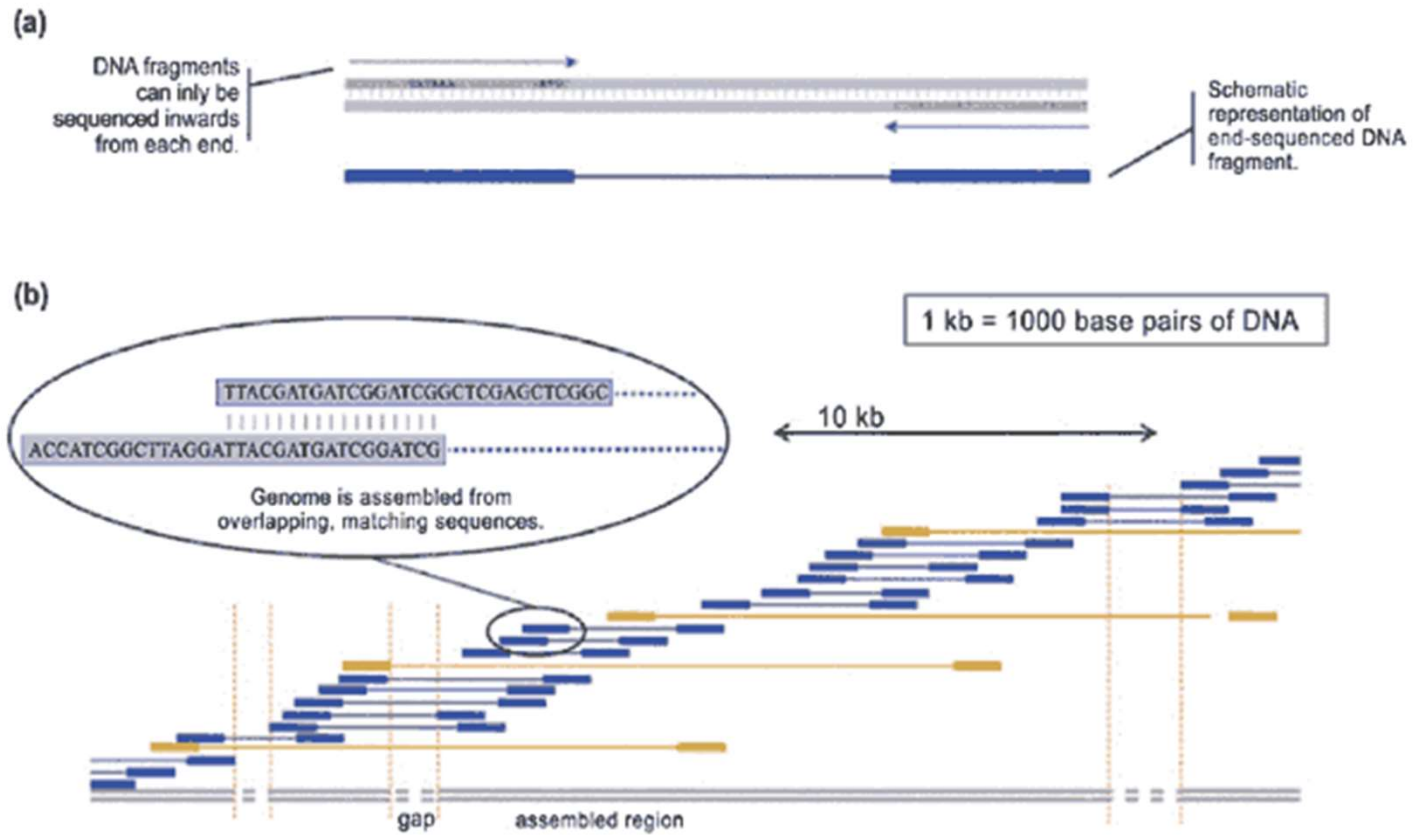


# Bowtie 2



# What is it?



# Bowtie vs Bowtie 2

Both are short read aligners but they are not the same

- better for reads shorter than 50bp
- end-to-end alignments
- upper limit ~1,000 bp
- aligns colorspace reads

- supports gapped alignment
- better for reads longer than 50bp
- end-to-end and local alignment.
- Bowtie2's paired-end alignment is more flexible than Bowtie

Bowtie and Bowtie2 indices and commands are not compatible

# How is it parallel?

- embarrassingly parallel – 1 task per read

- Get the read info
- Align the read to the reference genome
- Write alignment to output



The  
annoying  
parts