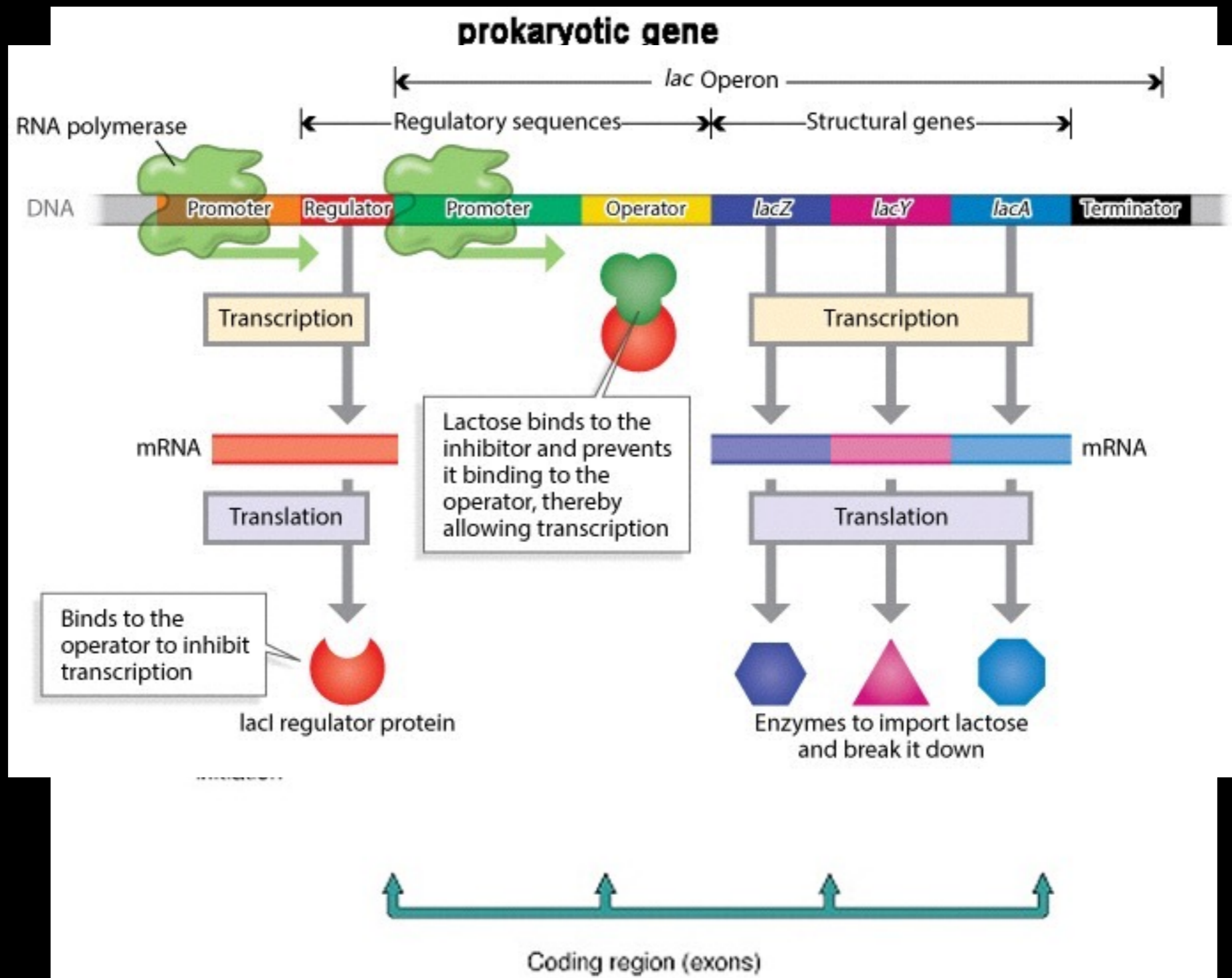


Bacterial RNASeq

Jie (Jessie) Li
PhD

Bioinformatics Core, UC Davis

Prokaryotes vs. Eukaryotes

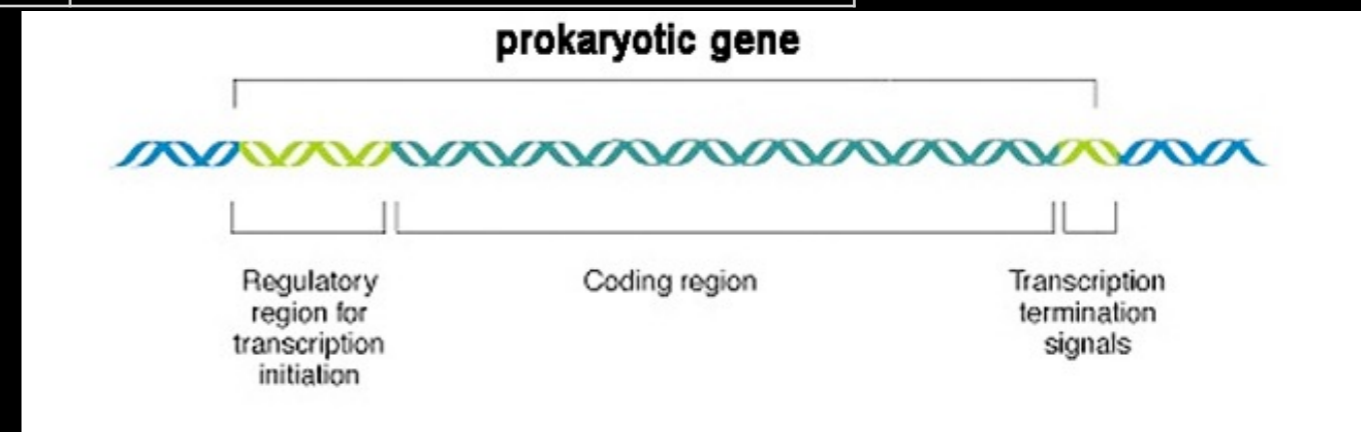


Prokaryotes vs. Eukaryotes in library prep

extract RNA and remove DNA contamination	extract RNA and remove DNA contamination
PolyA selection <i>OR</i> Ribo depletion	Ribo depletion
cDNA synthesis	cDNA synthesis
adding adapters and sequencing	adding adapters and sequencing

Prokaryotes vs. Eukaryotes in Data Analysis

Preprocessing: adapter trimming, quality trimming...	Preprocessing: adapter trimming, quality trimming...
Quantify gene expression: splice aware aligner to genome/ Bowtie2 to transcriptome	Quantify gene expression: no splice (Bowtie2)
Differential expression analysis	Differential expression analysis
	Operon prediction, transcript boundary identification,



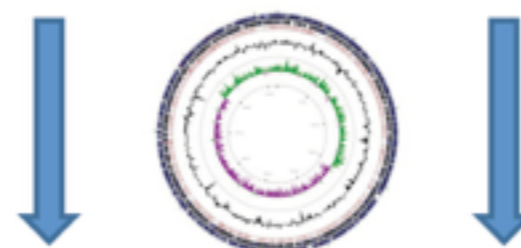
Rockhopper

- <https://cs.wellesley.edu/~btjaden/Rockhopper/>
- A java based program, which can be run in GUI based fashion or on command line.
- It carries out all types of analysis for bacterial RNASeq
 - Differential expression
 - transcript boundary identification
 - operon prediction

Input: Genome, gene annotations, and sequencing reads

>AGTCGTAGCTAGTCGA
>GGATAGCGTGATCTAC
>TTTGTTAGTCTATGCA

>TATGCTTATACGTT
>CGCACGGTAGCATG
>GTAGCGCTAGTACA



1. Align reads to genome

2. Normalize experiments

GACCAT
CCATTG
TAAGACCATTGC

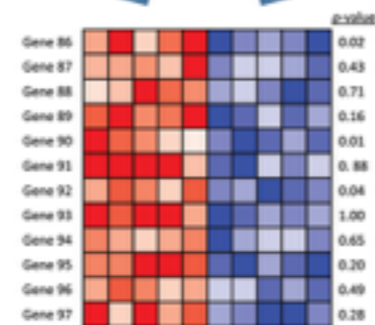
CCAT
AGACC
TAAGACCATTGC

3. Assemble transcripts and identify transcript boundaries

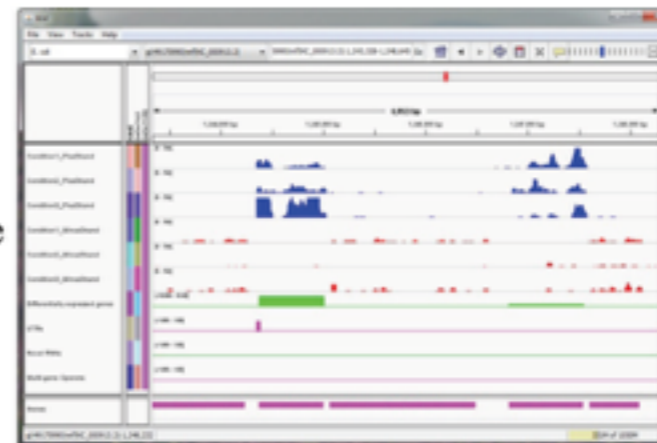
4. Quantify transcript abundance



5. Test for differential gene expression



7. Visualize results in genome browser



6. Characterize operon structures

