Steps in a ChIP-seq analysis

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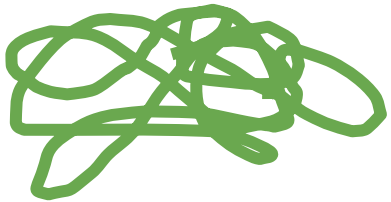
Background on ChIP-seq

DNA ACTGACCTAGATCAGTGTAGCGATCGTATACGAGACCGATTCATCGGCAT

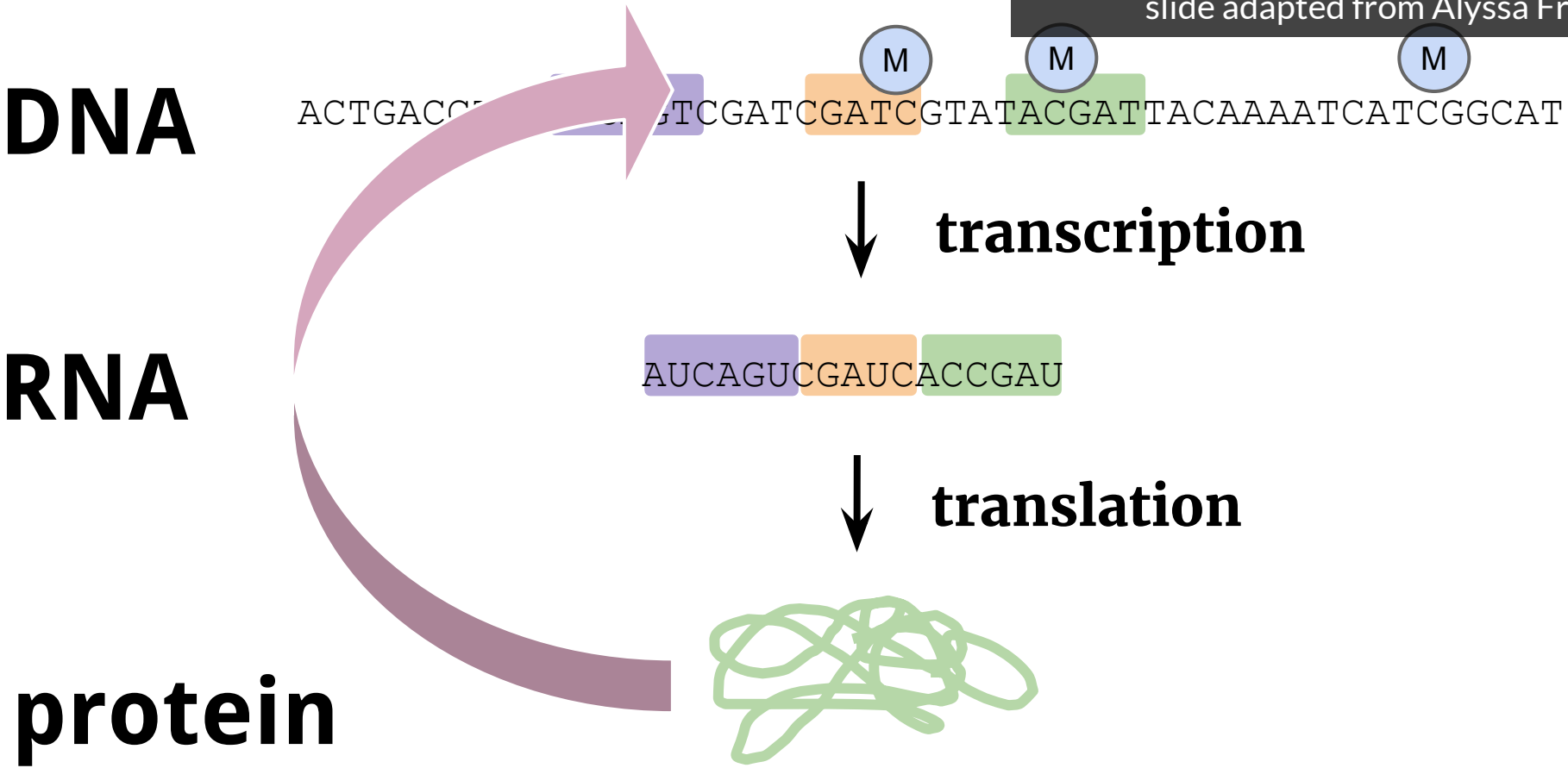
↓ **transcription**

RNA AUCAGUCGAUCACCGAU

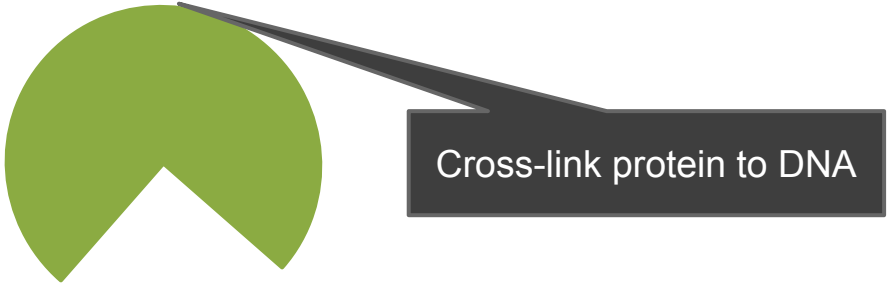
↓ **translation**

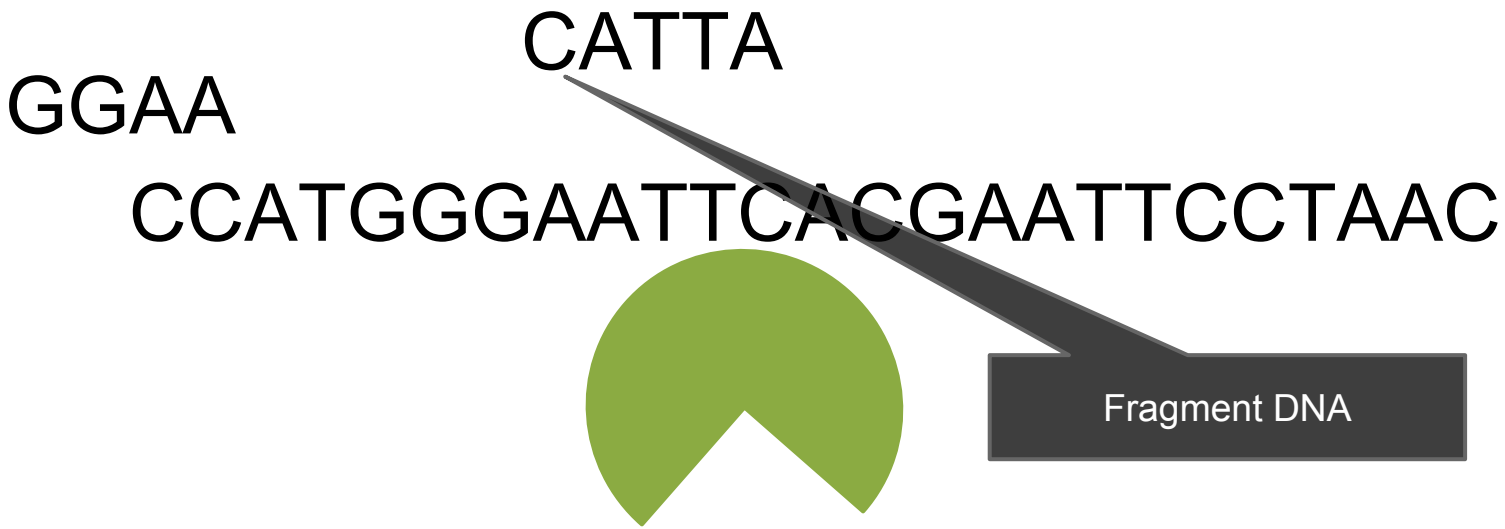


protein


DNA
ACTGACC
GTCGATCGATCGTATACGATTACAAAATCATCGGCAT
M
M
M
transcription
RNA
AUCAGUCGAUCACCGAU
translation
protein

GGAACCATGGGAATTCACGAATTCCTAACCATTA

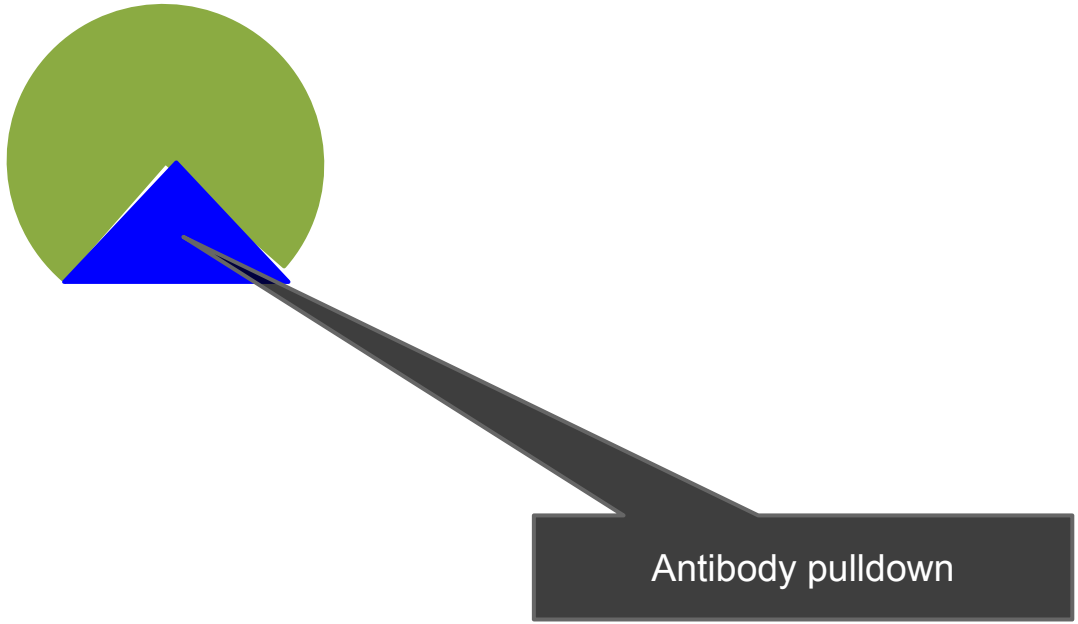



CATTA
GGAA
CCATGGGAATTCACGAATTCCTAAC
Fragment DNA

CATTAG

GGAA

CCATGGGAATTCACGAATTCCTAAC



CCATGGGAATTCACGAATTCCTAAC

Steps

1. Align
2. Peak detection
3. Counting
4. Normalization
5. Statistical tests
6. Annotation/Motif analysis

Step 1: Align

Software:

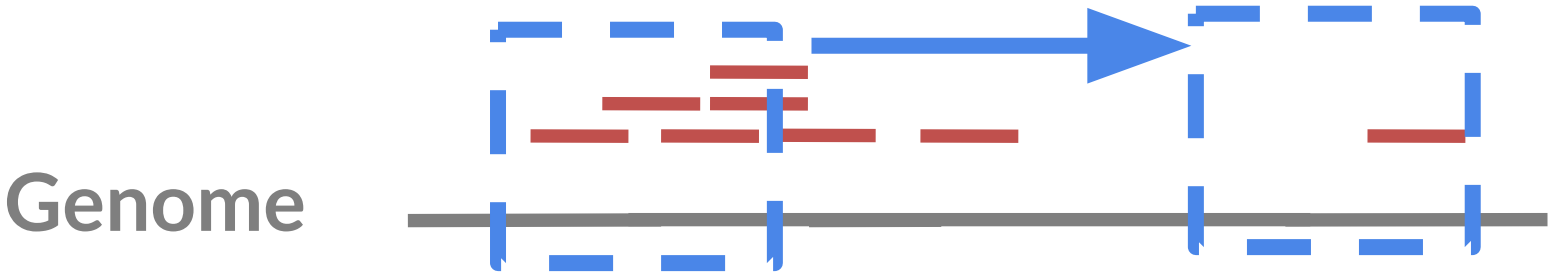
- Bowtie2
- BWA

Slide adapted from Hongkai Ji

Step 2: Peak detection

Software:

- CisGenome
- MACS
- PICS

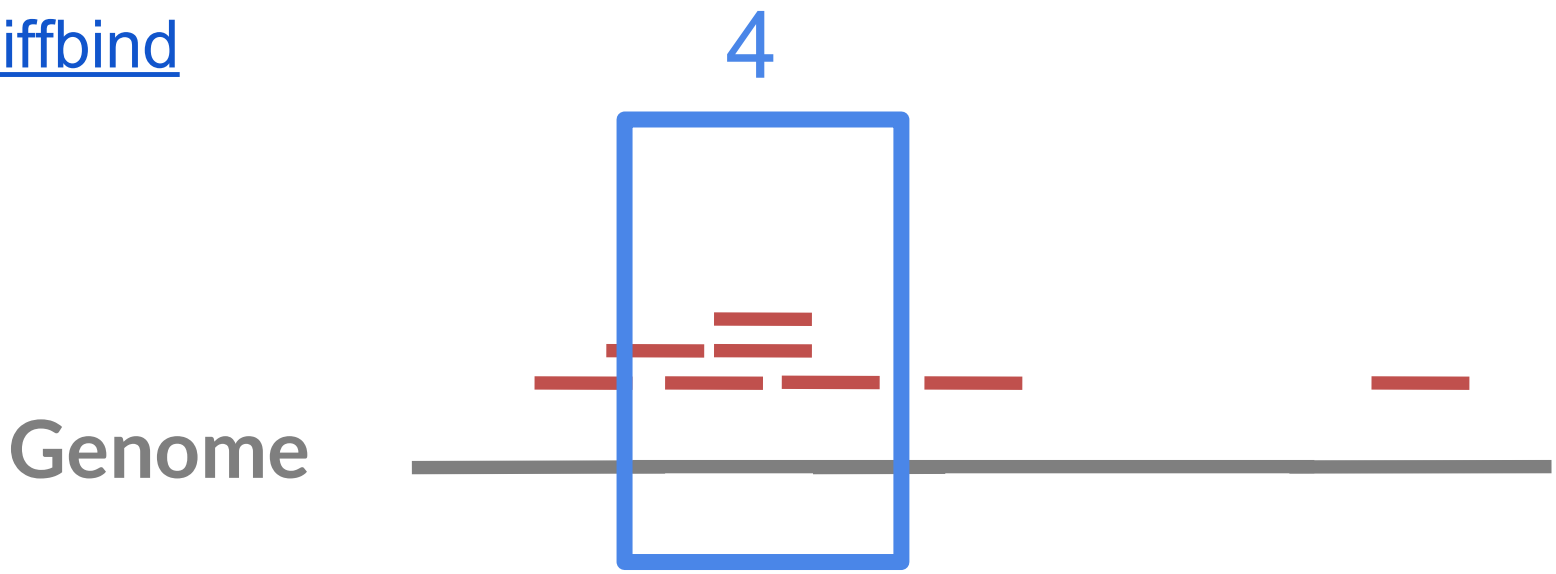


Slide adapted from Hongkai Ji

Step 3: Counting

Software:

- CisGenome
- MACS
- diffbind

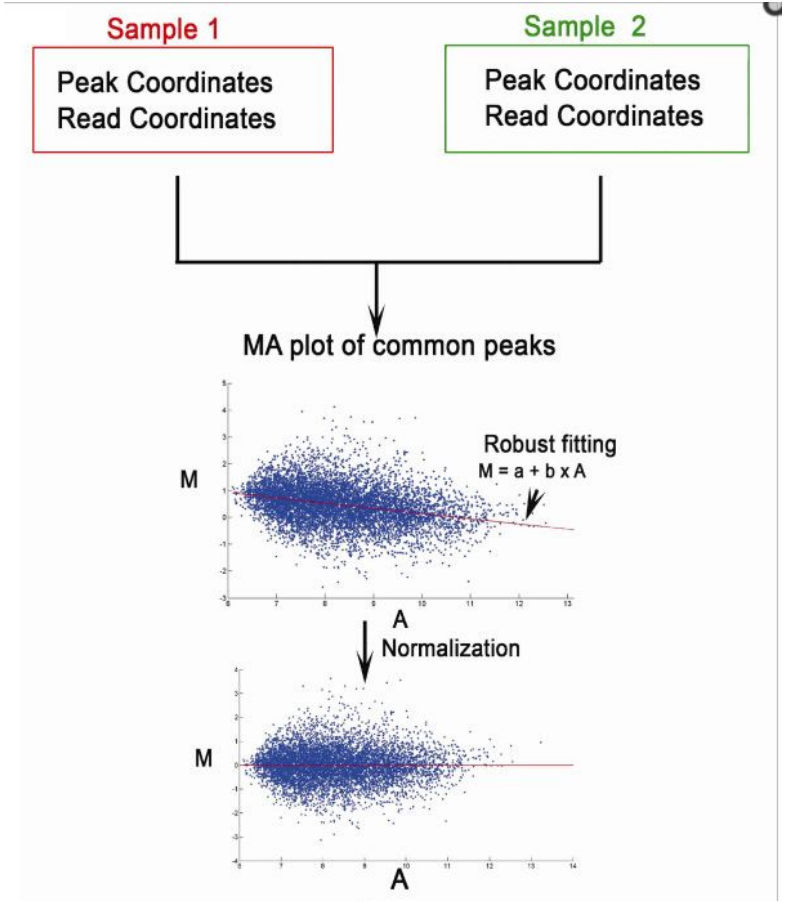


Slide adapted from Hongkai Ji

Step 4: Normalization

Software:

- diffbind
- MAnorm

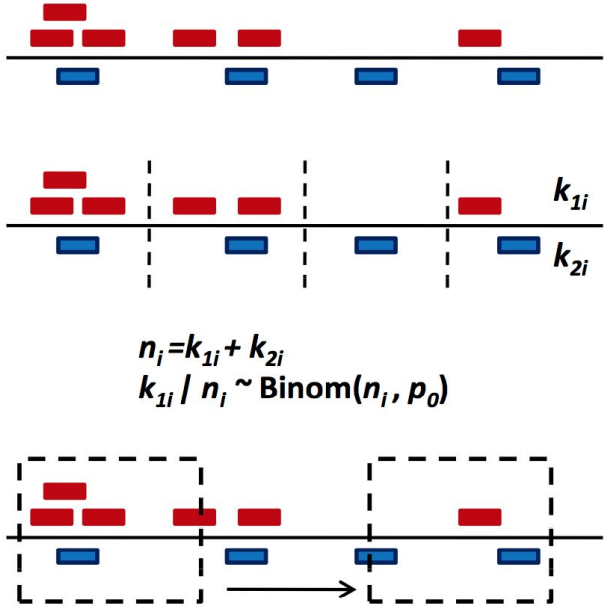


Slide adapted from Hongkai Ji

Step 5: Statistical tests

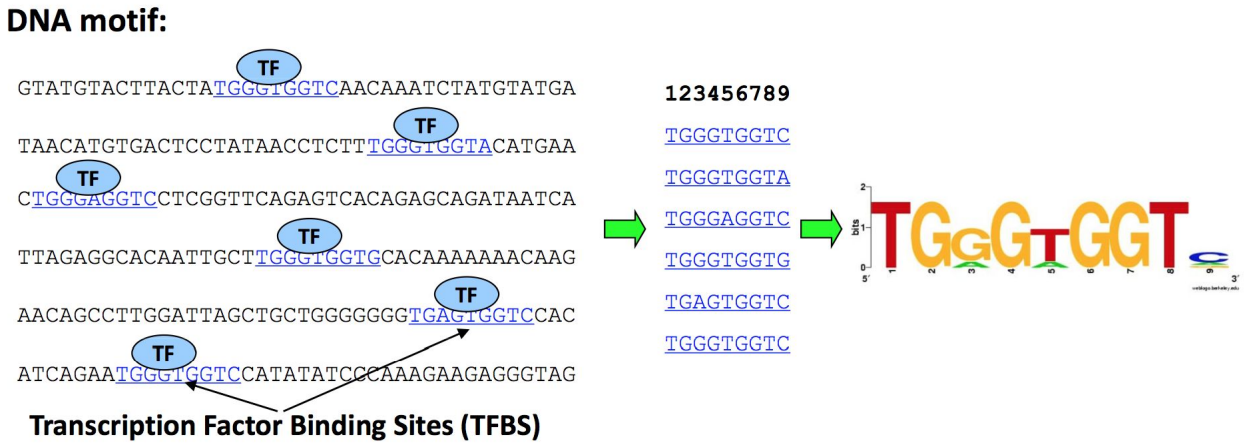
Software:

- CisGenome
- MACS
- diffbind



Slide adapted from Hongkai Ji

Step 6: Sequence motifs & Annotation

Software:

- CisGenome
- meme-suite
- BioC Annotation Workflow