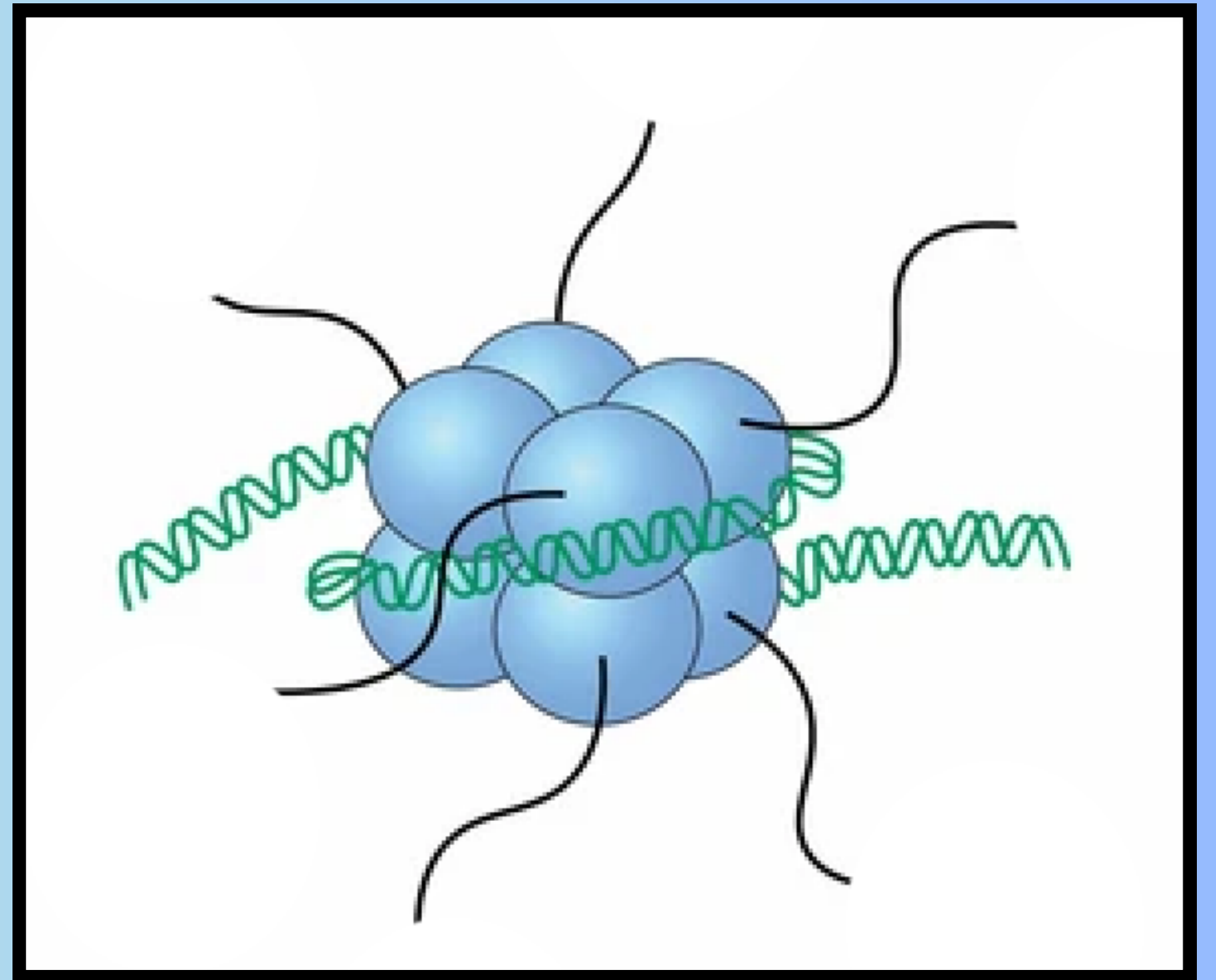


Chromatin Packing & Unpacking

Key Idea: Coiled, tightly-packed DNA is down-regulated;
Unpacked DNA is up-regulated

Structure

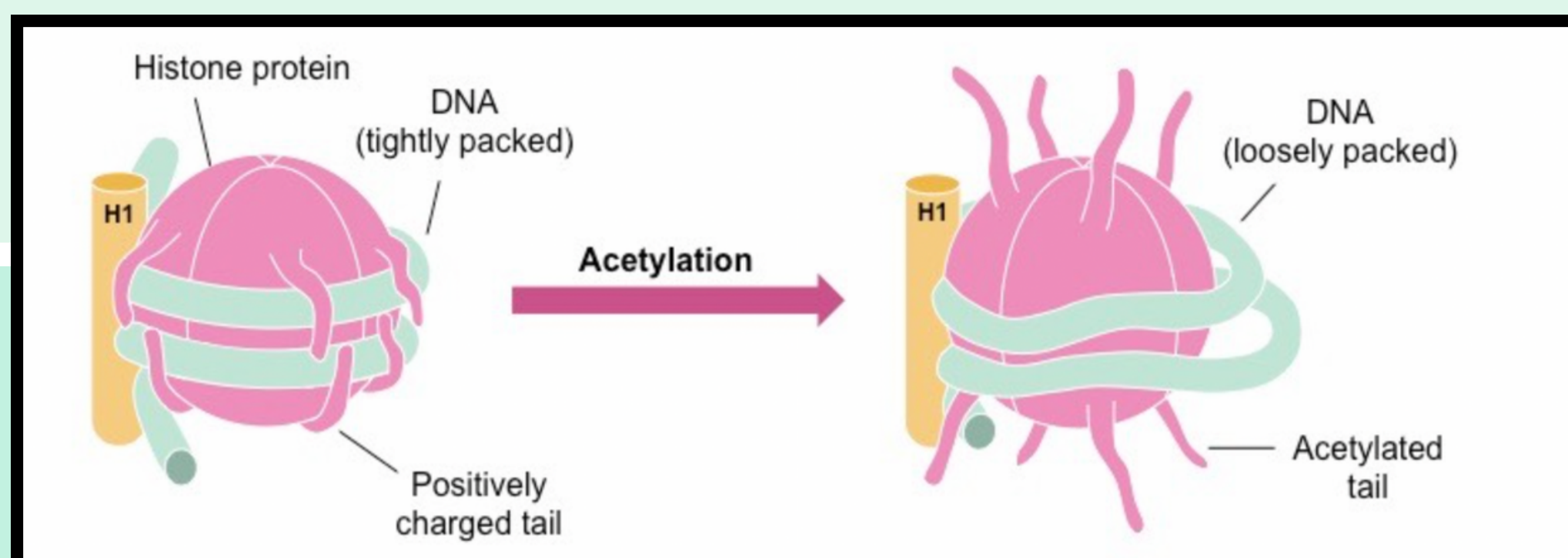
- Role is to condense DNA to fit inside the nucleus
- Two main types of DNA packing:
 - **heterochromatin:** Densely packed and transcriptionally inactive DNA
 - **euchromatin:** Less dense, transcriptionally active DNA
- Histone Tails protrude outwards from the histones, making themselves available to enzymes



Nucleosome pictured with histones and their protruding tails

Acetylation

- **Acetylation** enhances transcription by making histones looser (upregulating)
- Histone Modifications
 - **Reversible:** does not change the DNA sequence
 - **Histone Acetylation** is when acetyl groups are attached to lysines in histone walls, via the **histone acetyltransferase** enzyme.
 - This neutralizes the lysines charge, promoting a looser chromatin structure
 - Facilitates transcription because of easier access of RNA polymerase to genes and recruitment of transcription factors.
 - **Histone Deacetylation**
 - Histone acetylation is reversible by the enzyme **histone deacetylase** that removes acetyl groups.



Histone pictured before and after acetylation

DNA METHYLATION

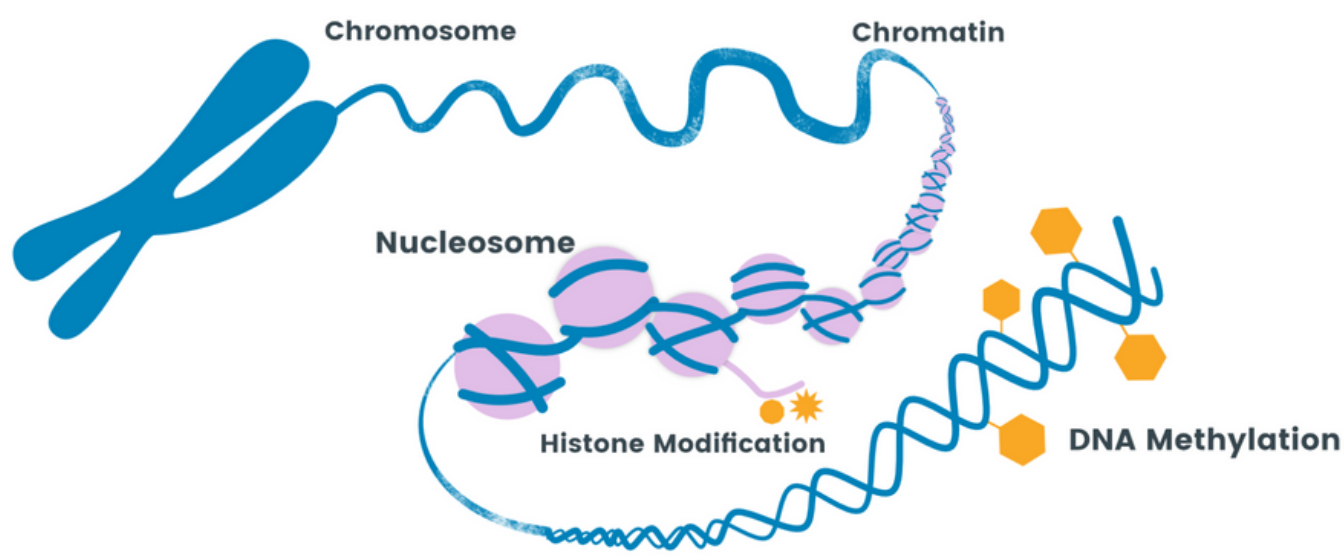


Diagram shows how methyl groups can attach to both histone tails and DNA nucleotides

Methylation

- Methylation can both increase and decrease gene expression
- **Methylation**
 - Methyl groups added to histone and/or DNA by the enzyme **methyltransferase**, resulting in condensed DNA, making the gene silently transcribed
- **Demethylation**
 - Removal of methyl groups, via added phosphate
- DNA Methylation: **Permanent**
 - Because the methyl group is added to cytosine nucleotides
- Histone Methylation: **Reversible**
 - By demethylation

Epigenetics

- **Epigenome** is a collection of DNA, RNA, proteins, and their chemical modifications that regulate gene expression, without changing the actual DNA sequence
 - Regulated by modifications to histone tails
- Epigenetic modification patterns of chromatin change during development, can respond to environmental factors
 - When cells are exposed to outside stimuli, the patterns of chromatin modification can become unregulated
- Epigenetics are **driven by modifications at the DNA level, pre-transcription**

Real Applications

- Epigenetic Inheritance:
 - **the inheritance of changes** due to environmental factors
 - if these modifications are present in the germ cells, they can be passed down through generations
 - Example: Obesity
 - Methylated food intake can cause obese individuals to have different methylation patterns
 - **methylation changes influence the gene expression of metabolic dysregulation and fat accumulation**
 - **environmental factors can disrupt enzyme activity that is responsible for histone acetylation and deacetylation**
- X-chromosome inactivation
 - Males have XY chromosomes, while females have XX chromosomes
 - 1 X chromosome is the “normal amount”, so to make up for this, females **silence one of the X chromosomes** in embryonic development
 - By random selection, one of the X chromosomes coils up compactly, making a **Barr Body structure**
 - Compacts because of methylation
 - **Barr Body genes are inactive = not transcribed**

X-inactivation

XX female	
XY male	

X-inactivation exemplified by comparing XX chromosomes to XY chromosomes