**The Transcription Cycle in Bacteria**

A) Bacterial Promoters vary in strength and sequence, but have certain defining features.

- The enzyme **RNA polymerase** catalyzes the process of transcription.
  
  ![DNA-dependent RNA polymerase](because it uses a DNA template for the synthesis of an RNA chain).

- In bacteria, RNA pol. is responsible for unwinding.
  
  - In Euk., unwinding is done by other proteins that bind to DNA near the start point for transcription.
  
  - Unlike DNA polymerases, RNA polymerases can initiate new RNA chains; in other words, no primer is needed.

- Gene

- **Promoter**

- **RNA-coding sequence**

- **Terminator**

- **Transcription initiation site**

- **Transcription termination site**

- **5' Non-template strand**

- **3' Non-template strand**

- **5' template strand**

- **3' template strand**

- The promoter is upstream of the coding sequence, the terminator downstream.

- The coding sequence begins at nucleotide +1.

- Promoter consists of two conserved sequences, each of six nucleotides, are separated by a non-specific stretch of 17-19 nucleotides.
In case of E.coli, the predominant σ-factor is called σ^70.

Vast majority of σ^70 promoters contain recognizable -35 and -10 regions.

The correlation between promoter strength and sequence explains why promoters are so heterogeneous. Some genes need to be expressed more highly than others and the former are likely to have sequences closer to the consensus.

**UP-element**

![Up-element diagram]

An additional DNA element that binds RNA polymerase is found in some strong promoters, for example those directing the expression of the ribosomal RNA (rRNA) genes. This is called the **UP-element**.

It increases polymerase binding by providing an additional specific interaction between the enzyme and the DNA.

![Extending -10 element diagram]

Another class of σ^30 promoters lacks a -35 region and instead has a so-called **extending -10** element. This comprises a standard -10 region with an additional short sequence element at its upstream end.

Extra contacts made by polymerase and this additional sequence element compensate for the absence of a -35 region.