

Source: [\[KBIO101CentralDogma\]](#)

# 1 | DNA Replication

DNA replication is known to be “semi-conservative” — meaning that it is a process that pairs a synthesized half of the DNA with an original half of the DNA (i.e. takes the ORIGINAL template strand + makes the NEW coding strand & takes the ORIGINAL coding strand + makes the NEW template strand.)

Because **polymerases copy uni-directionally** => DNA polymerase move along the 3' to 5' DNA to create a copy 5' to 3'. Meaning, the polymerase is able to add nucleotide onto the 3' end of the DNA.

As mentioned before, **DNA Polymerase** is the enzyme that catalyzes this process of DNA replication.

## 1.1 | The Process of DNA Replication

### 1.1.1 | DNA Unzipping

=> DNA is unzipped at the origin of replication. The parent DNA strand serves as a template for the new strand; when it is unzipped, the nucleotides are exposed for complementary base pairing. **Helicase** is the enzyme that unzips the DNA molecule, breaking the hydrogen bonds between nucleotides to expose them for complementary base pairing.

### 1.1.2 | DNA priming

DNA polymerase will REQUIRE a double-stranded area to begin work from, so **Primase** synthesizes already double-stranded RNA primers that DNA polymerase could bootstrap to the single-stranded DNA to begin the replication process (think: create-react-app).

### 1.1.3 | DNA “flexing” (what’s the actual word?)

The primed DNA is broken and rejoined in order to reduce strain caused by unzipping. Topoisomerase is responsible for relieving unwinding-induced strain.

### 1.1.4 | The actual process of replication

In this step, DNA polymerase does what we came here to do.

Because DNA polymerase could only add nucleotides 5' to 3', there are two types of styles of copying depending on which of the two strands are being copied.

- In the **leading** strand (3' to 5'), polymerase will run alongside the helicase for they are opening and replicating in the same direction.
- In the **lagging** strand (5' to 3'), polymerase will wait until the helix opens a little segment, and rushes forward and moves backwards.

*NOTE: the lagging strand... 1) takes longer to transcribe 2) is done in small chunks (each “rush forward”). Each chunk is called an Okazaki fragment — this is why there was that [\[KBhBIO101mRNAPreprocessing\]](#) process during transcription because that would help correct any errors in joining these fragments*

## DNA replication fork and strand synthesis

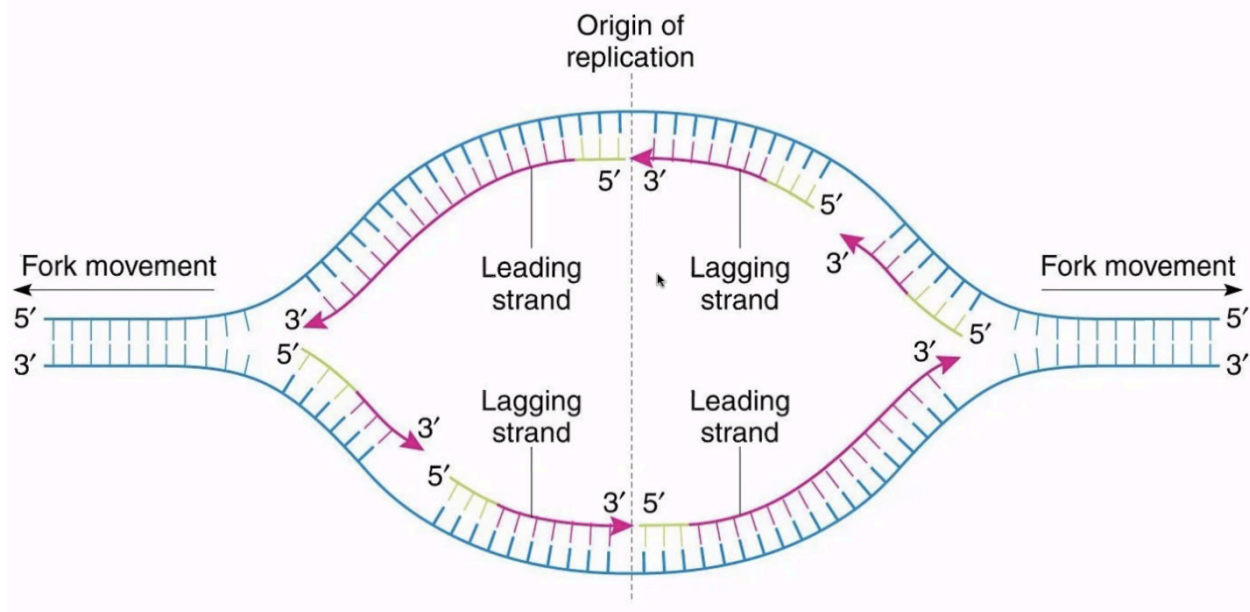


Figure 1: leadinglagging.png

### 1.1.5 | DNA Proofreading

DNA polymerase will detect unfitting bonds and remove leftover RNA primer bootstrap units to repair them in a process called "proofreading." DNA polymerase is assisted with "glue" ligase to help the DNA polymerase pick out and replace problematic/unneeded nucleotides and perhaps their neighbors. This is where the Okazaki fragments get joined.