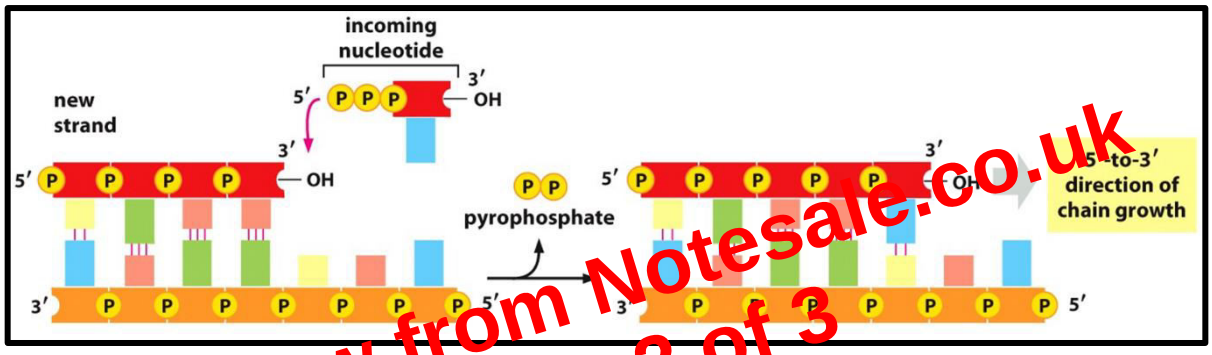
- Now that the **conservative theory was ruled out** (due to **all the DNA sitting in the middle of the ^{14}N and ^{15}N benchmarks**), Meselson and Stahl sought to discover whether the DNA followed semiconservative or dispersive replication:
    - So, they **heated up the hybrid strands** to form single stranded DNA molecules
    - They then **centrifuged these strands on the caesium chloride gradient**
        - This produced a **single light band and a single dark band**, thereby confirming that DNA reproduced via **semiconservation**

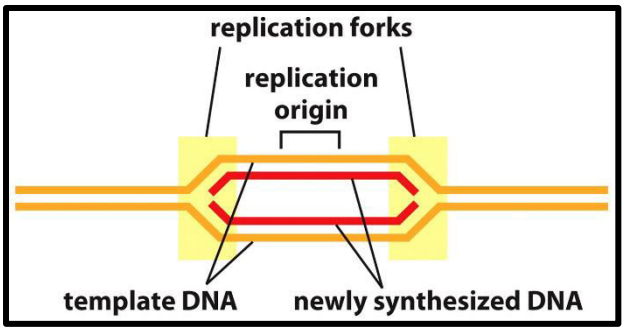
- DNA can replicate faithfully due to the bases on each strand. This is because each base only pairs to their counterpart
    - The new strand created is complementary to the template strand

- One of the main enzymes involved in this replication is **DNA polymerase**
    - This is involved in the polymerisation of **deoxyribonucleotide triphosphates** (d*N*TPs) (see below)
        - The **N can be adenine, cytosine, guanine or thymine**
        - The **polymerase can only add dNTPs to the 3' end** of the new growing DNA strand
            - Hence, the **synthesis is 5' to 3'**
    - The two furthermost phosphates are removed before the nucleotide is added to the 3' end of the strand via the **catalysis of the covalent linkage between the two nucleotides**
        - A **pyrophosphate is released**



- The DNA polymerase makes an **error roughly every 10^7 nucleotides**
    - Fortunately, the **polymerase recognises this**, changes shape and allows another active site on the enzyme to **excise the faulty addition**
        - Every nucleotide is checked
    - **A mistake that goes unrecognised will produce a mutation**

- To begin the synthesis of a new strand of DNA, **an initiator protein must bind to the replicator origin**s
    - These **replicator regions are specific sequences of DNA**
    - The **initiator proteins pull the two strands apart**
        - **Less energy is required to pull a few base pairs apart than to pull the entire helix apart**
        - This produces **two replication forks** (see right)
            - The **forks move in opposite directions**



- This produces a problem however, if the strands run antiparallel and the polymerase only works in the 5' to 3' direction
    - The **leading strand** that runs 5' to 3' is **synthesised continuously**
    - The **lagging strand is synthesised discontinuously**