**Central Dogma as a Rest API (CDaaR API)**

**When digital technology is united with biology to build a computational translation of biology it supports genomic research and bioinformatics workflows. CDaaR API automate mRNA, cDNA, and DNA oligonucleotide conversions**

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As genomic data becomes increasingly central to both biomedical research and clinical diagnostics, it’s essential to have intuitive tools that simulate biological processes in silico. The **Central Dogma as a REST (CDaaR) API** was developed to address this need by allowing educators to explain key molecular transformations between DNA and RNA sequences during **transcription**, **reverse transcription**, and **complementary strand synthesis**. These operations, grounded in fundamental molecular biology, and are not only useful for teaching but also for validating experimental data, simulating sequencing pipelines, and generating synthetic test datasets.

A dna strand with colorful bars

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The CDaaR API exposes four endpoints — each of which models a distinct biological mechanism.

The first endpoint **/DNA/v2/**, **DNA reverse complement**, captures how DNA polymerase reads DNA strands in a 5’ to 3’ direction. This API function reverses a DNA coding strand and generates its reverse complement, producing the antisense strand used during DNA replication. In data visualizations, this can help display relationships between coding regions and their antisense counterparts or map reverse complement usage across genomic regions.

The second endpoint **/RNA/v2/**, **RNA transcription**, mimics the action of RNA polymerase. When a DNA coding strand is submitted, the API calculates its reverse complement to simulate the template strand, then transcribes this sequence into pre-mRNA using canonical base-pairing rules. This process illustrates how genomic coding regions ultimately lead to protein synthesis via the central dogma: DNA → RNA → Protein.

The third endpoint **/CDNA/v2/** models **reverse transcription**, wherein mRNA sequence is translated back into a complementary double-stranded DNA (cDNA) molecule — a crucial process in molecular diagnostics, especially for synthesizing DNA libraries from RNA templates. The API returns both strands of the synthesized cDNA in proper 5’ to 3’ and 3’ to 5’ orientations.

A diagram of a strand

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The fourth endpoint **/Polypeptide/v2/** depict theTranslation of mRNA into a polypeptide chain of amino acids (via codon decoding).

A screenshot of a computer

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Each of these endpoints enforces input validation using **Pydantic models**, ensuring that sequences are biologically accurate and under 10,000 nucleotides. This provides clean, structured data for loading into dashboards, where sequence inputs and their transformed outputs can be aggregated, filtered, and compared across projects, labs, or use cases.

By integrating the CDaaR API with , a student can tell a compelling data story: how base-level changes in DNA sequences propagate through transcription and reverse transcription, ultimately shaping the information that flows through a biological system. This not only aids in scientific understanding but also enhances the reproducibility and visualization of complex molecular processes.