**Central Dogma Animation Google Colab Workflow**

**1. Open Google Colab**

* Go to https://colab.research.google.com

**2. Create a New Notebook**

* Click **File → New Notebook**

**3. Install Required Libraries**

* Run this in the first cell:

!pip install matplotlib ipython

**4. Upload or Paste Your Code**

* Either upload central\_dogma\_animation.py
* Or copy-paste this code into a Colab cell:

import matplotlib.pyplot as plt

import matplotlib.patches as patches

import matplotlib.animation as animation

from IPython.display import HTML

# Example DNA sequence

DNA\_seq = "ATGGCCATTGTAATGGGCCGCTGAAAGGGTGCCCGATAG"

# Transcription: DNA -> mRNA

mRNA\_seq = DNA\_seq.replace('T', 'U')

codons = [mRNA\_seq[i:i+3] for i in range(0, len(mRNA\_seq), 3)]

# Translation: simple codon table

codon\_table = {

"AUG": "M", "GCC": "A", "AUU": "I", "GUA": "V", "UGG": "W",

"GCU": "A", "GAA": "E", "AGG": "R", "GUG": "V", "CCC": "P", "GAU": "D", "AG": "\*"

}

amino\_acids = [codon\_table.get(codon, "?") for codon in codons]

fig, ax = plt.subplots(figsize=(10,5))

plt.close(fig)

ax.axis('off')

def animate(frame):

ax.clear()

ax.axis('off')

ax.text(0.1, 0.85, "DNA:", fontsize=15, color='#223388', fontweight='bold')

ax.text(0.28, 0.85, " ".join(DNA\_seq), fontsize=13, color='#223388', fontfamily='monospace')

ax.plot([0.225, 0.8], [0.83, 0.83], color='#4477AA', lw=6, alpha=0.2)

if frame < len(mRNA\_seq):

ax.text(0.1, 0.65, "Transcription (DNA → mRNA)", fontsize=14, color='purple', fontweight='bold')

mRNA\_partial = mRNA\_seq[:frame+1]

ax.text(0.18, 0.60, "mRNA: " + mRNA\_partial, fontsize=13, color='purple', fontfamily='monospace')

ax.add\_patch(patches.FancyBboxPatch((0.18+frame\*0.014, 0.56), 0.03, 0.04, boxstyle="round,pad=0.12",

linewidth=1.2, edgecolor='purple', facecolor='violet', alpha=0.9))

else:

ax.text(0.1, 0.65, "Translation (mRNA → Protein)", fontsize=14, color='green', fontweight='bold')

ax.text(0.18, 0.60, "mRNA: " + mRNA\_seq, fontsize=13, color='purple', fontfamily='monospace')

codon\_idx = min((frame-len(mRNA\_seq))//2, len(codons)-1)

ribo\_x = 0.18 + codon\_idx\*0.042

ax.add\_patch(patches.Circle((ribo\_x+0.018, 0.56), 0.03, color='limegreen', ec='k', lw=1.2, alpha=0.9))

mRNA\_display = ""

for idx,codon in enumerate(codons):

if idx == codon\_idx:

mRNA\_display += f"[{codon}] "

else:

mRNA\_display += codon+" "

ax.text(0.18, 0.53, "Reading: " + mRNA\_display.strip(), fontsize=12, color='darkgreen', fontfamily='monospace')

aa\_seq = "".join(amino\_acids[:codon\_idx+1])

ax.text(0.1, 0.40, "Protein: " + aa\_seq, fontsize=15, color='brown', fontweight='bold')

for i in range(codon\_idx+1):

ax.add\_patch(patches.Circle((0.25 + i\*0.04, 0.35), 0.017, color='orange', alpha=0.75, lw=0.7, ec='k'))

ax.set\_title("Central Dogma Animation: Transcription to Translation", fontsize=16, fontweight='bold', pad=20)

return ax,

frames = len(mRNA\_seq) + 2\*len(codons)

ani = animation.FuncAnimation(fig, animate, frames=frames, interval=600, blit=False)

HTML(ani.to\_jshtml())

**5. Run the Notebook**

* Execute the cells one by one
* Interactive animation will appear in Colab

**6. Customize**

* Change DNA sequence or codon table
* Adjust colors, animation speed, or text labels