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app.triviaAnswers = ["interphase", "prophase", "metaphase", "anaphase", "telophase", "cytokinesis"]
app.brandingColors = ["white", "springGreen", "darkGreen", "lightPink", "deepPink", "green", "black"]
app.background = "skyBlue"

intro = Group(
    Label("Welcome", 200, 125, size = 30, font = "montserrat", bold = True),
    Label("to the cell cycle!", 200, 175, size = 30, font = "montserrat", bold = True),
    Label("Click the button to begin!", 200, 30, size = 15, font = "montserrat", fill = app.brandingColors[0])
)

start = Group(
    Circle(200, 275, 50, fill = app.brandingColors[0], borderWidth = 4, border = app.brandingColors[6]),
    Label("Start", 200, 275, size = 20, font = "montserrat", bold = True)
)

next = Group(
    Polygon(320, 20, 360, 20, 360, 10, 380, 30, 360, 50, 360, 40, 320, 40, fill = "yellow"),
    Label("Next", 340, 30, font = "montserrat", bold = True)
)
next.visible = False

interphase = Group(
    Circle(200, 200, 100, fill = app.brandingColors[1], border = app.brandingColors[2], borderWidth = 4),
    Label("Interphase", 200, 50, size = 30, font = "montserrat", bold = True),
    Circle(210, 210, 65, fill = app.brandingColors[3], borderWidth = 4, border = app.brandingColors[4]),
    Rect(190, 110, 5, 10, fill = app.brandingColors[0], rotateAngle = 15),
    Rect(185, 123, 10, 5, fill = app.brandingColors[0], rotateAngle = 15),
    Rect(170, 111, 5, 10, fill = app.brandingColors[0], rotateAngle = 345),
    Rect(170, 124, 10, 5, fill = app.brandingColors[0], rotateAngle = 345),
    Label("Here, the cell goes through three substages: G1, S, and G2.", 200, 320, font = "montserrat", size = 12),
    Label("In G1, the cell grows, developing organelles needed later on.", 200, 335, font = "montserrat", size = 12),
    Label("In S, the cell duplicates its DNA and centrosomes.", 200, 350, font = "montserrat", size = 12),
    Label("In G2, the cell organizes itself, going through a final check.", 200, 365, font = "montserrat", size = 12),
    Line(190, 180, 200, 200, fill = app.brandingColors[0], lineWidth = 3),
    Line(220, 220, 230, 200, fill = app.brandingColors[0], lineWidth = 3),
    Line(210, 260, 220, 240, fill = app.brandingColors[0], lineWidth = 3),
    Line(180, 210, 190, 230, fill = app.brandingColors[0], lineWidth = 3),
    Line(235, 185, 255, 180, fill = app.brandingColors[0], lineWidth = 3),
    Line(195, 160, 215, 165, fill = app.brandingColors[0], lineWidth = 3),
    Line(160, 195, 180, 185, fill = app.brandingColors[0], lineWidth = 3),
    Line(240, 240, 260, 230, fill = app.brandingColors[0], lineWidth = 3),
    Line(245, 205, 265, 215, fill = app.brandingColors[0], lineWidth = 3),
    Line(170, 250, 190, 245, fill = app.brandingColors[0], lineWidth = 3),
)
interphase.visible = False

prophase = Group(
    Circle(200, 200, 100, fill = app.brandingColors[1], border = app.brandingColors[2], borderWidth = 4),
    Label("Prophase", 200, 50, size = 30, font = "montserrat", bold = True),
    Circle(210, 210, 65, fill = app.brandingColors[3], borderWidth = 4, border = app.brandingColors[4], dashes = True),
    Rect(190, 110, 5, 10, fill = app.brandingColors[0], rotateAngle = 15),
    Rect(185, 123, 10, 5, fill = app.brandingColors[0], rotateAngle = 15),
    Rect(170, 111, 5, 10, fill = app.brandingColors[0], rotateAngle = 345),
    Rect(170, 124, 10, 5, fill = app.brandingColors[0], rotateAngle = 345),
    Label("Here, mitosis starts with chromosomes condensing and the", 200, 320, font = "montserrat", size = 12),
    Label("mitotic spindles forming! Furthermore, the nucleolus and", 200, 335, font = "montserrat", size = 12),
    Label("nuclear envelope break down while microtubules form", 200, 350, font = "montserrat", size = 12),
    Label("the spindles bind to the kinetochores of chromosomes.", 200, 365, font = "montserrat", size = 12),
    Line(190, 180, 200, 200, fill = app.brandingColors[0], lineWidth = 3),
    Line(220, 220, 230, 200, fill = app.brandingColors[0], lineWidth = 3),
    Line(190, 210, 180, 230, fill = app.brandingColors[0], lineWidth = 3),
    Line(180, 210, 190, 230, fill = app.brandingColors[0], lineWidth = 3),
    Line(195, 165, 215, 155, fill = app.brandingColors[0], lineWidth = 3),
    Line(195, 155, 215, 165, fill = app.brandingColors[0], lineWidth = 3),
    Line(190, 200, 200, 180, fill = app.brandingColors[0], lineWidth = 3),
    Line(200, 250, 220, 260, fill = app.brandingColors[0], lineWidth = 3),
    Line(220, 200, 230, 220, fill = app.brandingColors[0], lineWidth = 3),
    Line(200, 260, 220, 250, fill = app.brandingColors[0], lineWidth = 3),
)
prophase.visible = False

metaphase = Group(
    Circle(200, 200, 100, fill = app.brandingColors[1], border = app.brandingColors[2], borderWidth = 4),
    Label("Metaphase", 200, 50, size = 30, font = "montserrat", bold = True),
    Label("Here, chromosomes line up at the metaphase plate with", 200, 320, font = "montserrat", size = 12),
    Label("the two kinetochores of each chromosome being attached", 200, 335, font = "montserrat", size = 12),
    Label("to microtubules extending to opposite ends of the cell!", 200, 350, font = "montserrat", size = 12),
    Label("Also, the spindle checkpoint takes place to ensure quality.", 200, 365, font = "montserrat", size = 12),
    Line(124, 197, 200, 120, fill = app.brandingColors[4]),
    Line(124, 197, 200, 155, fill = app.brandingColors[4]),
    Line(124, 197, 200, 190, fill = app.brandingColors[4]),
    Line(124, 197, 200, 230, fill = app.brandingColors[4]),
    Line(124, 197, 200, 270, fill = app.brandingColors[4]),
    Line(277, 200, 200, 190, fill = app.brandingColors[4]),
)

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Line(277, 200, 200, 120, fill = app.brandingColors[4]),
Line(277, 200, 200, 155, fill = app.brandingColors[4]),
Line(277, 200, 200, 230, fill = app.brandingColors[4]),
Line(277, 200, 200, 270, fill = app.brandingColors[4]),
Rect(110, 195, 10, 5, fill = app.brandingColors[0]),
Rect(123, 192, 5, 10, fill = app.brandingColors[0]),
Rect(275, 195, 5, 10, fill = app.brandingColors[0]),
Rect(283, 198, 10, 5, fill = app.brandingColors[0]),
Line(195, 180, 205, 200, fill = app.brandingColors[0], lineWidth = 3),
Line(195, 280, 205, 260, fill = app.brandingColors[0], lineWidth = 3),
Line(195, 110, 205, 130, fill = app.brandingColors[0], lineWidth = 3),
Line(195, 220, 205, 240, fill = app.brandingColors[0], lineWidth = 3),
Line(195, 165, 205, 145, fill = app.brandingColors[0], lineWidth = 3),
Line(195, 145, 205, 165, fill = app.brandingColors[0], lineWidth = 3),
Line(195, 200, 205, 180, fill = app.brandingColors[0], lineWidth = 3),
Line(195, 260, 205, 280, fill = app.brandingColors[0], lineWidth = 3),
Line(195, 240, 205, 220, fill = app.brandingColors[0], lineWidth = 3),
Line(195, 130, 205, 110, fill = app.brandingColors[0], lineWidth = 3),
)
metaphase.visible = False

anaphase = Group(
    Label("Anaphase", 200, 50, size = 30, font = "montserrat", bold = True),
    Oval(200, 200, 300, 200, fill = app.brandingColors[1], border = app.brandingColors[2], borderWidth = 4),
    Label("Here, the sister chromatids are separated as the protein ", 200, 320, font = "montserrat", size = 12),
    Label("binding them breaks down. They are pulled to opposite ends", 200, 335, font = "montserrat", size = 12),
    Label("of the cell as the cell's poles elongate using motor proteins ", 200, 350, font = "montserrat", size = 12),
    Label("which carry chromosomes or other microtubules as they walk.", 200, 365, font = "montserrat", size = 12),
    Line(75, 197, 150, 130, fill = app.brandingColors[4]),
    Line(75, 197, 150, 165, fill = app.brandingColors[4]),
    Line(75, 197, 150, 195, fill = app.brandingColors[4]),
    Line(75, 197, 150, 225, fill = app.brandingColors[4]),
    Line(75, 197, 150, 255, fill = app.brandingColors[4]),
    Line(325, 200, 250, 130, fill = app.brandingColors[4]),
    Line(325, 200, 250, 165, fill = app.brandingColors[4]),
    Line(325, 200, 250, 195, fill = app.brandingColors[4]),
    Line(325, 200, 250, 225, fill = app.brandingColors[4]),
    Line(325, 200, 250, 260, fill = app.brandingColors[4]),
    Rect(60, 195, 10, 5, fill = app.brandingColors[0]),
    Rect(72, 192, 5, 10, fill = app.brandingColors[0]),
    Rect(323, 195, 5, 10, fill = app.brandingColors[0]),
    Rect(330, 198, 10, 5, fill = app.brandingColors[0]),
    Line(150, 130, 160, 120, fill = app.brandingColors[0], lineWidth = 3),
    Line(150, 130, 160, 140, fill = app.brandingColors[0], lineWidth = 3),
    Line(150, 165, 160, 155, fill = app.brandingColors[0], lineWidth = 3),
    Line(150, 165, 160, 175, fill = app.brandingColors[0], lineWidth = 3),
    Line(150, 195, 160, 185, fill = app.brandingColors[0], lineWidth = 3),
    Line(150, 195, 160, 205, fill = app.brandingColors[0], lineWidth = 3),
    Line(150, 225, 160, 215, fill = app.brandingColors[0], lineWidth = 3),
    Line(150, 225, 160, 235, fill = app.brandingColors[0], lineWidth = 3),
    Line(150, 255, 160, 245, fill = app.brandingColors[0], lineWidth = 3),
    Line(150, 255, 160, 265, fill = app.brandingColors[0], lineWidth = 3),
    Line(250, 130, 240, 120, fill = app.brandingColors[0], lineWidth = 3),
    Line(250, 130, 240, 140, fill = app.brandingColors[0], lineWidth = 3),
    Line(250, 165, 240, 155, fill = app.brandingColors[0], lineWidth = 3),
    Line(250, 165, 240, 175, fill = app.brandingColors[0], lineWidth = 3),
    Line(250, 195, 240, 185, fill = app.brandingColors[0], lineWidth = 3),
    Line(250, 195, 240, 205, fill = app.brandingColors[0], lineWidth = 3),
    Line(250, 225, 240, 215, fill = app.brandingColors[0], lineWidth = 3),
    Line(250, 225, 240, 235, fill = app.brandingColors[0], lineWidth = 3),
    Line(250, 260, 240, 250, fill = app.brandingColors[0], lineWidth = 3),
    Line(250, 260, 240, 270, fill = app.brandingColors[0], lineWidth = 3),
)
anaphase.visible = False

telophase = Group(
    Label("Telophase", 200, 50, size = 30, font = "montserrat", bold = True),
    Label("Here, the cell splits, creating two separate nuclei", 200, 320, font = "montserrat", size = 12),
    Label("each with its own chromosome set. Furthermore, the nucleoli", 200, 335, font = "montserrat", size = 12),
    Label("and nuclear envelope redevelop as the mitotic spindles break", 200, 350, font = "montserrat", size = 12),
    Label("down and chromosomes begin to decondense!", 200, 365, font = "montserrat", size = 12),
    Circle(125, 200, 105, fill = app.brandingColors[2]),
    Circle(275, 200, 105, fill = app.brandingColors[2]),
    Circle(125, 200, 100, fill = app.brandingColors[1]),
    Circle(275, 200, 100, fill = app.brandingColors[1]),
    Circle(125, 200, 65, fill = app.brandingColors[3], borderWidth = 4, border = app.brandingColors[4]),
    Circle(275, 200, 65, fill = app.brandingColors[3], borderWidth = 4, border = app.brandingColors[4]),
    Rect(30, 195, 10, 5, fill = app.brandingColors[0]),
    Rect(42, 192, 5, 10, fill = app.brandingColors[0]),
    Rect(353, 195, 5, 10, fill = app.brandingColors[0]),
    Rect(360, 198, 10, 5, fill = app.brandingColors[0]),
    Line(80, 180, 90, 200, fill = app.brandingColors[0], lineWidth = 3),
    Line(300, 220, 310, 200, fill = app.brandingColors[0], lineWidth = 3),
    Line(105, 170, 115, 150, fill = app.brandingColors[0], lineWidth = 3),
    Line(125, 210, 135, 230, fill = app.brandingColors[0], lineWidth = 3),

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Line(235, 185, 255, 180, fill = app.brandingColors[0], lineWidth = 3),
Line(275, 160, 295, 165, fill = app.brandingColors[0], lineWidth = 3),
Line(140, 175, 160, 165, fill = app.brandingColors[0], lineWidth = 3),
Line(260, 240, 280, 230, fill = app.brandingColors[0], lineWidth = 3),
Line(245, 205, 265, 215, fill = app.brandingColors[0], lineWidth = 3),
Line(125, 250, 145, 245, fill = app.brandingColors[0], lineWidth = 3),
)
telophase.visible = False

cytokinesis = Group(
    Label("Cytokinesis", 200, 50, size = 30, font = "montserrat", bold = True),
    Label("Finally, the cytoplasm is divided between the two cells", 200, 320, font = "montserrat", size = 12),
    Label("while a cleavage furrow made of actin is formed!", 200, 335, font = "montserrat", size = 12),
    Label("The cleavage furrow pinches completely, creating", 200, 350, font = "montserrat", size = 12),
    Label("two identical daughter cells as a result!", 200, 365, font = "montserrat", size = 12),
    Circle(100, 200, 90, fill = app.brandingColors[1], border = app.brandingColors[2], borderWidth = 4),
    Circle(300, 200, 90, fill = app.brandingColors[1], border = app.brandingColors[2], borderWidth = 4),
    Circle(100, 200, 60, fill = app.brandingColors[3], borderWidth = 4, border = app.brandingColors[4]),
    Circle(300, 200, 60, fill = app.brandingColors[3], borderWidth = 4, border = app.brandingColors[4]),
    Line(80, 180, 90, 200, fill = app.brandingColors[0], lineWidth = 3),
    Line(300, 220, 310, 200, fill = app.brandingColors[0], lineWidth = 3),
    Line(105, 190, 115, 170, fill = app.brandingColors[0], lineWidth = 3),
    Line(125, 210, 135, 230, fill = app.brandingColors[0], lineWidth = 3),
    Line(255, 200, 265, 180, fill = app.brandingColors[0], lineWidth = 3),
    Line(85, 160, 105, 150, fill = app.brandingColors[0], lineWidth = 3),
    Line(285, 235, 265, 225, fill = app.brandingColors[0], lineWidth = 3),
    Line(310, 240, 330, 230, fill = app.brandingColors[0], lineWidth = 3),
    Line(295, 185, 315, 175, fill = app.brandingColors[0], lineWidth = 3),
    Line(75, 230, 95, 225, fill = app.brandingColors[0], lineWidth = 3),
)
cytokinesis.visible = False

triviaIntro = Group(
    Label("Now, it's time to stretch your brain!", 200, 150, size = 18, font = "montserrat", bold = True),
    Label("Match the trivia to its stage", 200, 200, size = 18, font = "montserrat", bold = True),
    Label("by clicking the stage's label!", 200, 250, size = 18, font = "montserrat", bold = True)
)
triviaIntro.visible = False

stages = Group(
    Label("", 100, 57, size = 18, font = "montserrat"),
    Label("", 100, 114, size = 18, font = "montserrat"),
    Label("", 100, 171, size = 18, font = "montserrat"),
    Label("", 100, 228, size = 18, font = "montserrat"),
    Label("", 100, 285, size = 18, font = "montserrat"),
    Label("", 100, 342, size = 18, font = "montserrat")
)

trivia = Group(
    Label("In this phase, due to ", 280, 150, size = 17, font = "montserrat", bold = True),
    Label("the type of cell, a cell", 280, 200, size = 17, font = "montserrat", bold = True),
    Label("plate may form as well!", 280, 250, size = 17, font = "montserrat", bold = True),
    Label("Click the name of a stage to see if you are correct!", 200, 380, font = "montserrat", fill = app.brandingColors[0])
)
trivia.visible = False

app.cycleStage = 0

def changeStages(stage):
    app.cycleStage = stage
    if app.cycleStage == 1:
        interphase.visible = True
        prophase.visible = False
    if app.cycleStage == 2:
        prophase.visible = True
        interphase.visible = False
    if app.cycleStage == 3:
        prophase.visible = False
        metaphase.visible = True
    if app.cycleStage == 4:
        metaphase.visible = False
        anaphase.visible = True
    if app.cycleStage == 5:
        anaphase.visible = False
        telophase.visible = True
    if app.cycleStage == 6:
        telophase.visible = False
        cytokinesis.visible = True
    if app.cycleStage == 7:
        cytokinesis.visible = False
        triviaIntro.visible = True
    if app.cycleStage == 8:
        triviaIntro.visible = False
        for index in range(len(app.triviaAnswers)):
            if index % 6 == 0:

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        stages.children[0].value = app.triviaAnswers[0]
    if(index % 6 == 1):
        stages.children[1].value = app.triviaAnswers[1]
    if(index % 6 == 2):
        stages.children[2].value = app.triviaAnswers[2]
    if(index % 6 == 3):
        stages.children[3].value = app.triviaAnswers[3]
    if(index % 6 == 4):
        stages.children[4].value = app.triviaAnswers[4]
    if(index % 6 == 5):
        stages.children[5].value = app.triviaAnswers[5]
trivia.visible = True
next.visible = False

def onMousePress(mouseX, mouseY):
    if(start.children[0].hits(mouseX, mouseY)):
        app.cycleStage += 1
        changeStages(app.cycleStage)
        intro.visible = False
        start.visible = False
        next.visible = True
    if(next.children[0].hits(mouseX, mouseY)):
        app.cycleStage += 1
        changeStages(app.cycleStage)
    if(trivia.visible == True):
        if(stages.children[5].hits(mouseX, mouseY)):
            next.visible = False
            trivia.visible = False
            stages.visible = False
            Label("Correct!", 200, 200, size = 30, font = "montserrat", bold = True)
            Label("Thank you for learning about the cell cycle!", 200, 250, size = 15, font = "montserrat")
        if(stages.children[4].hits(mouseX, mouseY)):
            next.visible = False
            Label("Incorrect!", 200, 200, size = 30, font = "montserrat", bold = True)
            Label("The correct answer is cytokinesis!", 200, 250, size = 15, font = "montserrat", fill = app.brandingColors[5])
            Label("Thank you for learning about the cell cycle!", 200, 300, size = 15, font = "montserrat")
            trivia.visible = False
            stages.visible = False
        if(stages.children[3].hits(mouseX, mouseY)):
            next.visible = False
            Label("Incorrect!", 200, 200, size = 30, font = "montserrat", bold = True)
            Label("The correct answer is cytokinesis!", 200, 250, size = 15, font = "montserrat", fill = app.brandingColors[5])
            Label("Thank you for learning about the cell cycle!", 200, 300, size = 15, font = "montserrat")
            trivia.visible = False
            stages.visible = False
        if(stages.children[2].hits(mouseX, mouseY)):
            next.visible = False
            Label("Incorrect!", 200, 200, size = 30, font = "montserrat", bold = True)
            Label("The correct answer is cytokinesis!", 200, 250, size = 15, font = "montserrat", fill = app.brandingColors[5])
            Label("Thank you for learning about the cell cycle!", 200, 300, size = 15, font = "montserrat")
            trivia.visible = False
            stages.visible = False
        if(stages.children[1].hits(mouseX, mouseY)):
            next.visible = False
            Label("Incorrect!", 200, 200, size = 30, font = "montserrat", bold = True)
            Label("The correct answer is cytokinesis!", 200, 250, size = 15, font = "montserrat", fill = app.brandingColors[5])
            Label("Thank you for learning about the cell cycle!", 200, 300, size = 15, font = "montserrat")
            trivia.visible = False
            stages.visible = False
        if(stages.children[0].hits(mouseX, mouseY)):
            next.visible = False
            Label("Incorrect!", 200, 200, size = 30, font = "montserrat", bold = True)
            Label("The correct answer is cytokinesis!", 200, 250, size = 15, font = "montserrat", fill = app.brandingColors[5])
            Label("Thank you for learning about the cell cycle!", 200, 300, size = 15, font = "montserrat")
            trivia.visible = False
            stages.visible = False

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