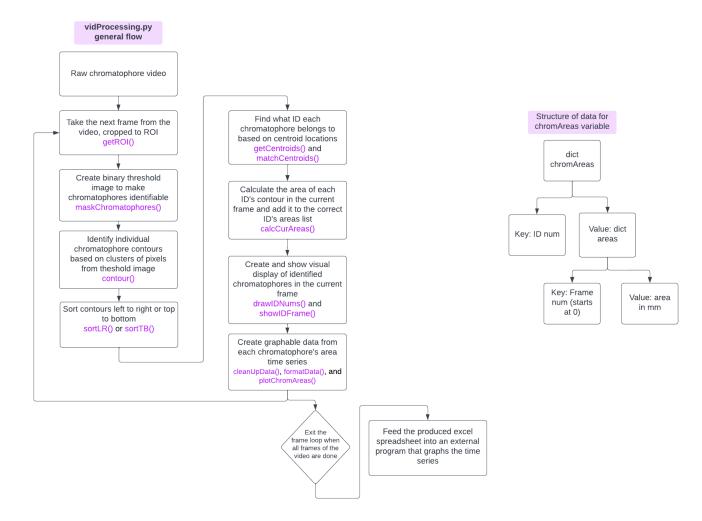
vidProcessing.py

Processing raw video data for chromatophore experiments in the Gilly lab at Hopkins Marine Station -- code by Elisabeth Holm, undergrad ML/CV intern

Versions:
Python 3.10.4
imutils 0.5.4
opency-python 4.6.0.66
numpy 1.22.4
scipy 1.8.1
matplotlib 3.5.2
argparse 1.4.0
xlwt 1.3.0

General flow:



Function breakdown:

- setGlobalNums()
 - Sets the global constants for window width and chromatophore pixel diameter based on command line arguments
- getROI(frame)
 - Sets ROI (region of interest) from command line or the user manually choosing takes in the first frame of the video and returns ROI coordinates/dimensions
- maskChromatophores(curFrame)
 - Masks the current frame from the video to identify only the chromatophores
 - Returns the masked frame
- contour(threshold, origing)
 - Defines and draws the contour lines based on the masked frame
 Takes in the binary masked image and original image
 - o Returns the list of chromatophores
- createRotatedBRects(contours)
 - Creates rotated bounding rectangles for each contour in contours
 - Returns a list of bounding rects
- drawRotatedRect(rect, img)
 - Draws rotated rectangle
 - Takes in a rotated rectangle and image to draw it on
 - Returns the image with the rectangle drawn on it
- sortLR(contours)
 - Sorts the given contours from left to right
 - Returns the sorted contours and sorted bounding boxes
- sortTB(contours)
 - Sorts the given contours from top to bottom
 - Returns the sorted contours and bounding boxes
- createAreasDict(ff_contours)
 - Takes in the chromatophore contours found in the first frame (ff) of the video
 - Builds the chromAreas list of chromatophores (setting up to later add area data for each chromatophore)
 - Only called during the first frame of the video
- createMatchedCentroids(curCentroids)
 - Populate the matchedCentroids dictionary with {objectID: centroid} in the first frame of the video when there is no previous frame to compare to
 - Only called during the first frame of the video
- getCentroids(bBoxes, contours)
 - Put the centroids of each bounding box in a list with the center of each bounding box in the same index as the original bounding box
 - Takes in the list of bounding boxes and contours
 - Note: index of bBoxes and contours must correspond
 - Returns centroids and a dict that maps each centroid to its contour

- register(centroid)
 - Register a new chromatophore
- deregister(objectID)
 - Deregister given chromatophore in matchedCentroids and disappeared dicts
- matchCentroids(curCentroids)
 - Compare current centroids with previous centroids to determine the closest matches
 - Returns the calculated IDs of each current centroid.
 - Takes in the list of current centroids and dict of previous matched centroids
 - o Returns dict of ID num:current centroids matched
 - Code based on

https://pyimagesearch.com/2018/07/23/simple-object-tracking-with-opency/

- calcCurAreas(centroidsToContours, curFrameIndex)
 - Takes in chromatophore contours, calculates area for each chromatophore
 - Adds area to appropriate area time series (the dict of areas under the chrom w/ the correct ID num) in chromAreas
- drawIDNums(boundingRects, frame)
 - o Draw ID numbers, bounding boxes, and centroids for each object in the frame
 - Returns frame with everything drawn in it
- getStdDev(areas)
 - o Takes in a 1D list of areas, returns the standard deviation
- cleanUpData()
 - Filter out irrelevant data entries (ex: chrom that was only identified in a few frames)
- formatData(numFrames, ROI)
 - Formats final dataset into a spreadsheet and saves it to the same folder as the video
 - Takes in the number of frames in the video and the ROI coordinates/dimensions
 - Important note: the xlwt library currently only supports up to 256 columns, so the number of chromatophores in the selected ROI must be < 256
- plotChromAreas()
 - Plots chrom areas over time (each chromatophore is one line) and then shows the graph. Commented out: saving the graph to the computer
- showIDFrame(curFrameIndex, ID frame)
 - Shows the current frame with chromatophore IDs, adjusting for mac and windows systems (running on windows caused an error with displaying the frame)
- showAllImages(curFrameIndex, original, gray, threshold, contours, ID labeled)
 - Show images from each step of the process
- saveIndividualImages(curFrameIndex, original, gray, threshold, contours, ID_labeled)
 - Saves each generated image individually in the frame_cap folder, showing each step of the process for the current frame
 - To use, call at the end of the while True loop in processData() instead of saveImages()
- saveImages(curFrameIndex, original, gray, threshold, contours, ID_labeled)

- Saves one image that shows each step of the process for the current frame.
 Saves to the frame_cap folder
- To use, call at the end of the while True loop in processData()
- processData(vidPath)
 - Summary function of the entire program
 - Takes in filepath to raw video, goes through the entire identification process, and saves the time series of each chromatophores' change in area as .xls files – one for cleaned data and one for uncleaned data