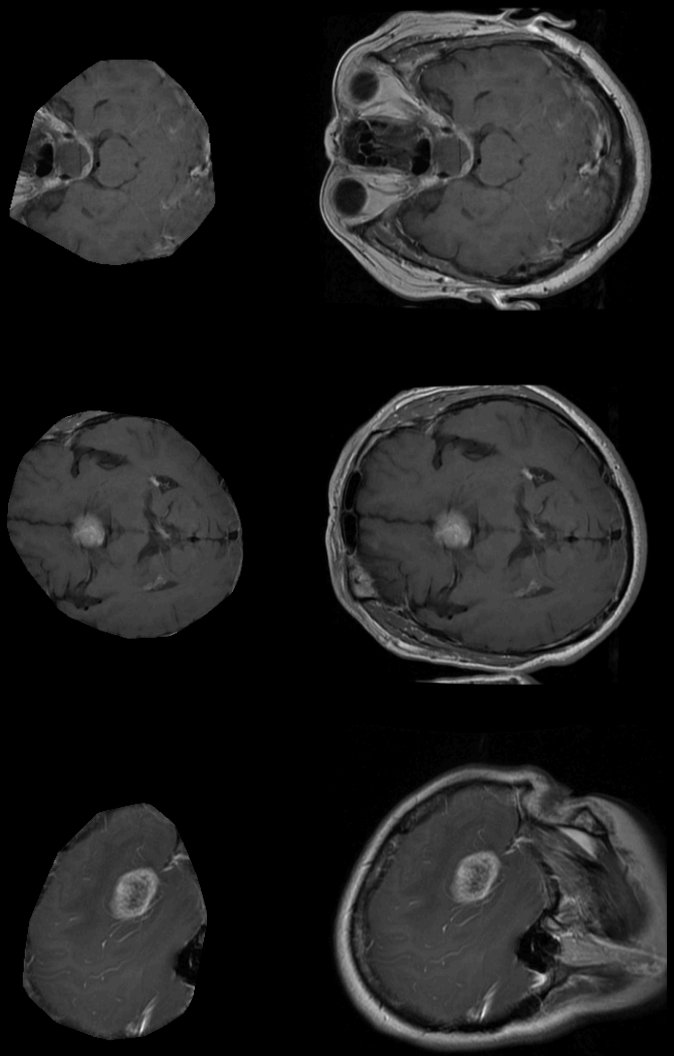
Brain Cancer Segmentation

DAVIDE BELCASTRO - 1962536
LUCIAN DORIN CRAINIC - 1938430

Segmentation

- Skull Stripping
- Mean color of the tumor
- Segmentation of the tumor



Skull Stripping

The goal of this stage is to go and eliminate the edge of the brain and leave only the brain tissue

Mean color of the tumor

In this phase the average color of the brain is analyzed and areas of pixels are sought that have an average color quite distant from the color of the brain

```
'''
this function is used to segment the image using K-Means Clustering.
'''
def KMeansClustering(data, k,img):
    kmeans = KMeans(n_clusters=k, random_state=0)
    kmeans.fit(data)
    labels = kmeans.predict(data)
    segmented_data = np.uint8(kmeans.cluster_centers_[labels])
    segmented_img = segmented_data.reshape(img.shape)
    return segmented_img
```

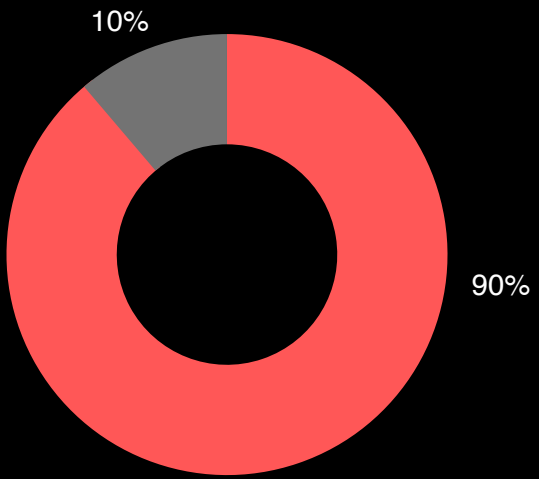
```python
def get_tumor(color_tumor,brain,segm,mylist,area_contorno_esterno,colore_cervello):
    lista_contorni = []
    for value in mylist:
        mask = np.zeros(brain.shape[:2], np.uint8)
        mask[segm == value] = 255
        contours, hierarchy = cv2.findContours(mask, cv2.RETR_TREE, cv2.CHAIN_APPROX_SIMPLE)
        for el in contours:
            el = cv2.convexHull(el)
            area = cv2.contourArea(el)
            circumference = cv2.arcLength(el, True)
            if circumference == 0:
                continue
            circularity = 4 * np.pi * (area / (circumference * circumference))
            if (circularity >= 0.3 and area >= 0.005*area_contorno_esterno and area <=
0.15*area_contorno_esterno) or(circularity >= 0.45 and area > 0.15 * area_contorno_esterno and area <=
0.20 * area_contorno_esterno) or (circularity >= 0.55 and area > 0.20 * area_contorno_esterno and area
<= 0.22 * area_contorno_esterno) :
                mask2 = np.zeros(brain.shape[:2], dtype="uint8")
                diz = {}
                cv2.drawContours(mask2, [el], -1, 255, -1)
                for i in range(0, brain.shape[0]):
                    for j in range(0, brain.shape[1]):
                        if mask2[i][j] == 255:
                            if brain[i][j] in diz:
                                diz[brain[i][j]] += 1
                            else:
                                diz[brain[i][j]] = 1
                somma = 0
                for k,v in diz.items():
                    somma+=k
                media = somma/len(diz)
                lista_contorni.append((el, media,area,circularity))
```

```python
    diz_contorni = []
    for tup in lista_contorni:
        media_pesata = get_media_pesata(tup,color_tumor,area_contorno_esterno,colore_cervello)
        diz_contorni.append(media_pesata)
    brain = cv2.cvtColor(brain, cv2.COLOR_GRAY2BGR)
    index = 0
    diz_appoggio = {}
    for el in lista_contorni:
        r_random = np.random.randint(0, 255)
        g_random = np.random.randint(0, 255)
        b_random = np.random.randint(0, 255)
        cl = (r_random, g_random, b_random)
        diz_appoggio[(diz_contorni[index],cl)] = (el[0],el[1])
        cv2.drawContours(brain, [el[0]], -1, cl, 2)
        index+=1
    dizionario_2 = {}
    for k,v in diz_appoggio.items():
        if k[0] >= 1.15:
            dizionario_2[k] = v
    diz_appoggio = dizionario_2
    diz_appoggio = dict(sorted(diz_appoggio.items(), key=lambda item: item[0][0]))
    diz_appoggio = dict(reversed(list(diz_appoggio.items())))
    if len(diz_appoggio) == 0:
        return "no tumor",0
    my_tumor = diz_appoggio[list(diz_appoggio.keys())[0]][0]
    color = diz_appoggio[list(diz_appoggio.keys())[0]][1]
    area = cv2.contourArea(my_tumor)
    circumference = cv2.arcLength(my_tumor, True)
    if circumference == 0:
        return "no tumor",0
    circularity = 4 * np.pi * (area / (circumference * circumference))
    percentuale_area_tumore = (area / area_contorno_esterno) * 100
    if circularity >=0.75:
        probability =
get_probability_of_tumor(area,circularity,color,colore_cervello,area_contorno_esterno)
        return my_tumor,probability
    else:
        return "no tumor",0
```

Segmentation

In this part we analyze the image returned from phase 1 and the value returned from phase 2, the k-mean algorithm is applied and the "best" contour is found

Trustworthiness of the program



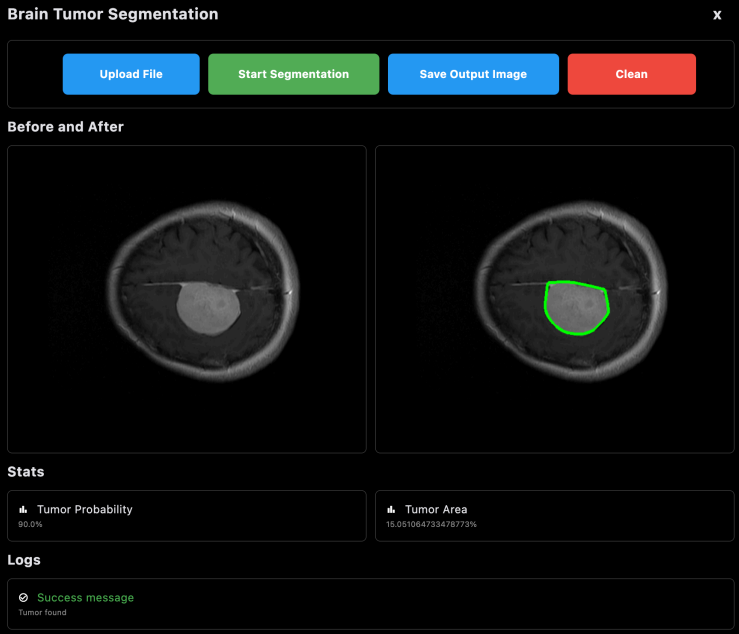
To get an estimate of how reliable the program was, tests were carried out by comparing the segment returned by the program with the "true" segment taken from the dataset.

Interface (GUI)

- Brain Cancer Segmentation
- Segmentation Filters

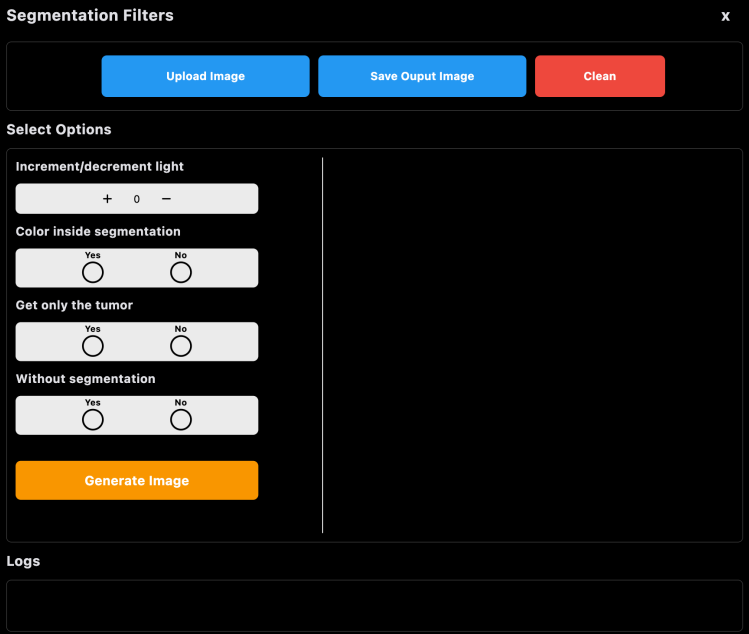
Brain Cancer Segmentation

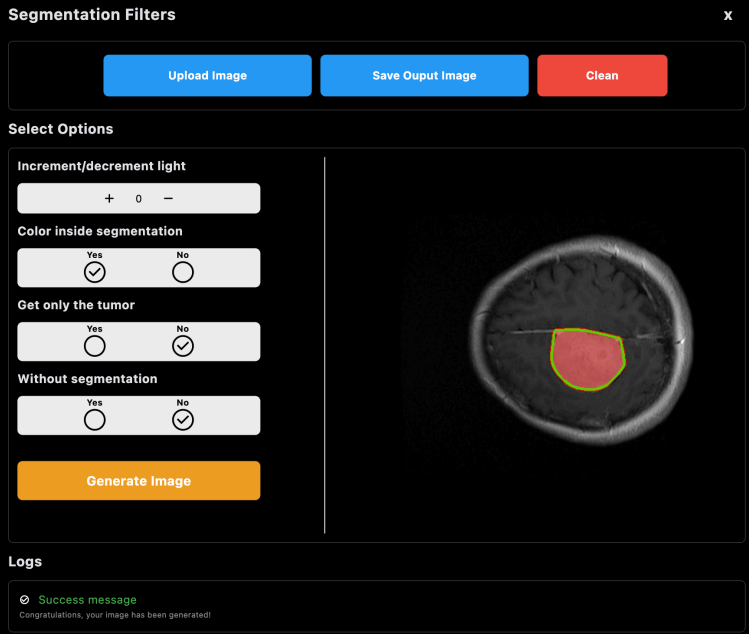
The user can choose an MRI image of a patient's brain and begin segmentation



Segmentation Filters

The user can select at his choice different filters to apply to the image returned from the segmentation





Let's take a look at an example