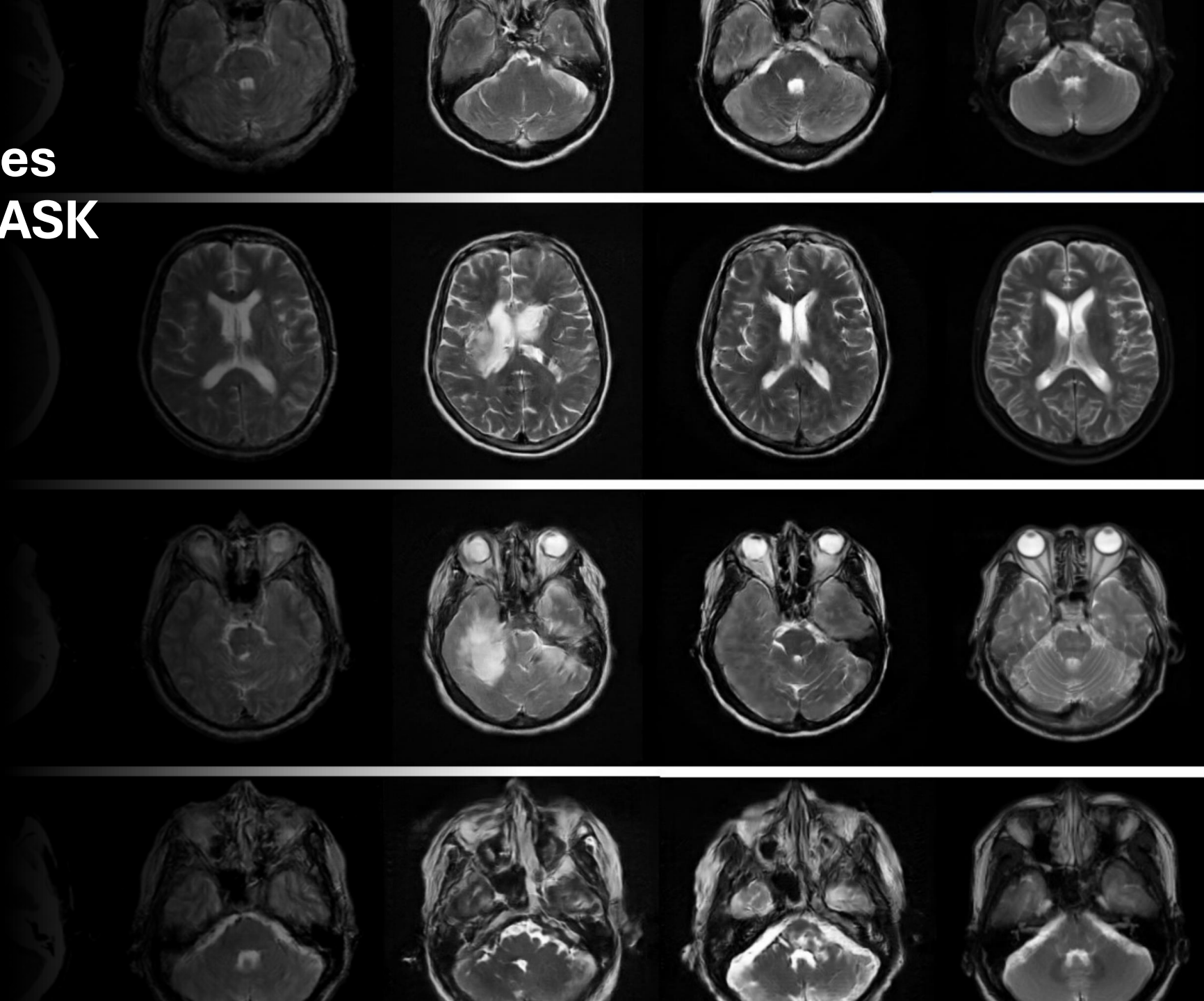
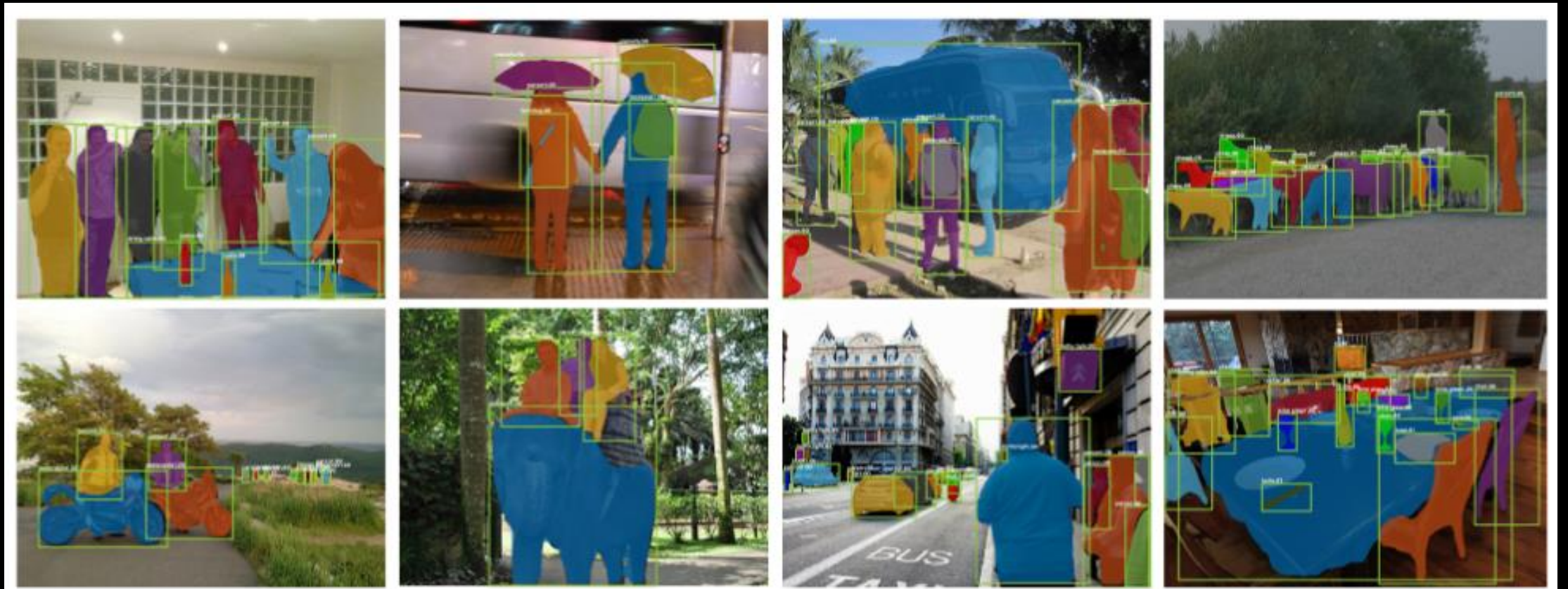
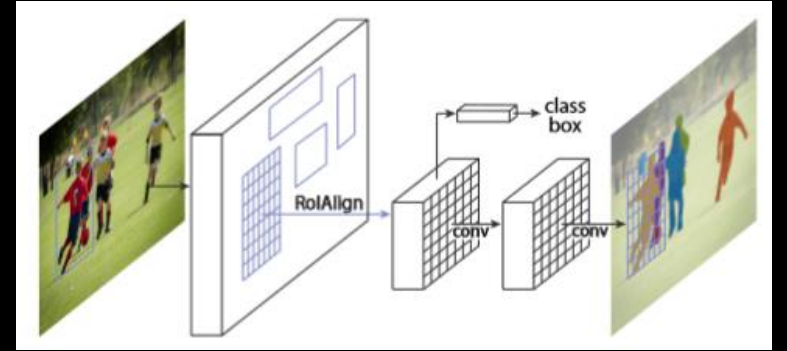


Detección de tumores cerebrales en IRM usando MASK R-CNN

- Expositores:
 - Gonzalo Bello
 - Simón Sánchez

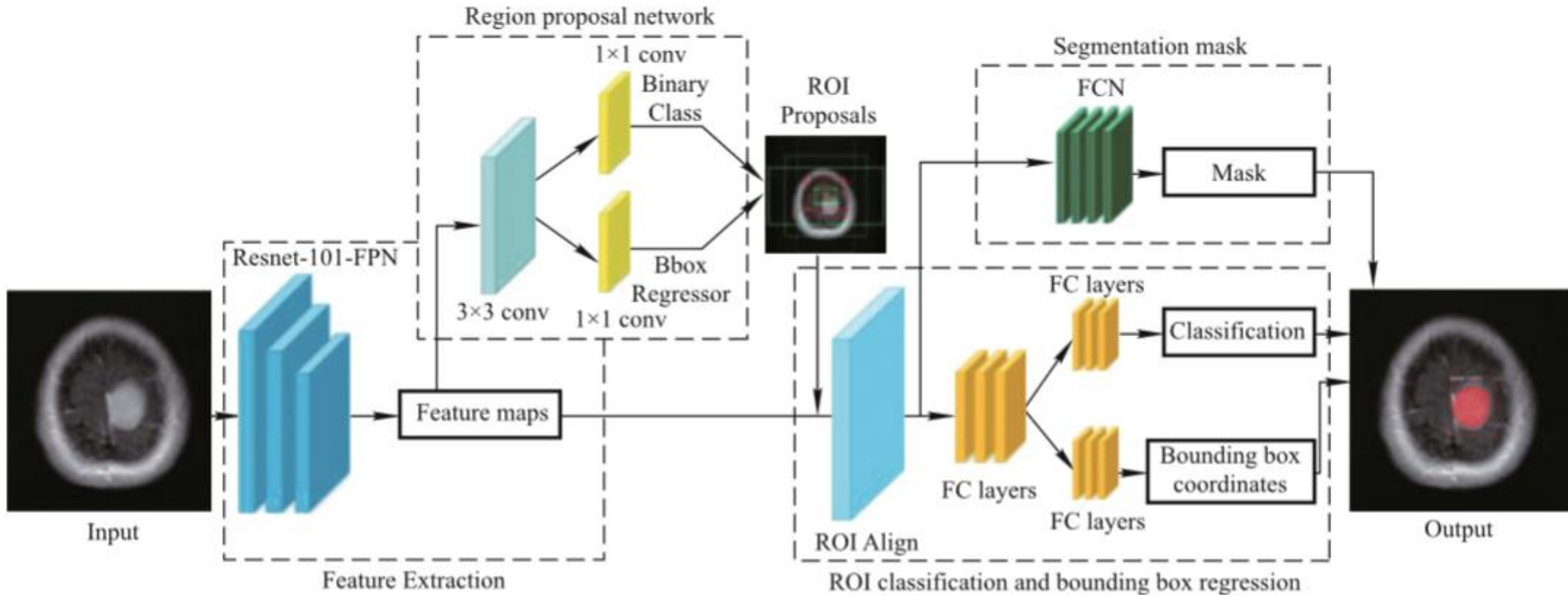


Modelo MASK R-CNN



Modelo MASK R-CNN

Arquitectura:




```

# Cambiar al directorio de trabajo
original_dir = '/content/drive/My Drive/proyecto_dir'
mask_rcnn_dir = os.path.join(original_dir, 'mask-rcnn')
os.chdir(mask_rcnn_dir)

import numpy as np
import json
import skimage.draw
import matplotlib.pyplot as plt
from tensorflow.keras.callbacks import TensorBoard, ModelCheckpoint, ReduceLROnPlateau
from mrcnn.config import Config
from mrcnn import utils
import mrcnn.model as modellib
from mrcnn import visualize

import sys
# Directorio raíz del proyecto
ROOT_DIR = os.path.abspath('.')
print(f"Directorio raíz del proyecto: {ROOT_DIR}")

# Importar Mask RCNN
sys.path.append(ROOT_DIR)

# Importar configuración COCO
sys.path.append(os.path.join(ROOT_DIR, 'implementations'))
import coco
plt.rcParams['figure.facecolor'] = 'white'

```

Implementación del Código

Usando Python en Google Colab
con GPU

Librerías y Pre-entrenamiento (COCO: Common Objects in Context)

```
✓ import numpy as np
import json
import skimage.draw
import matplotlib.pyplot as plt
from tensorflow.keras.callbacks import ReduceLROnPlateau, EarlyStopping, ModelCheckpoint, TensorBoard
from mrcnn.config import Config
from mrcnn import utils
import mrcnn.model as modellib
from mrcnn import visualize

import sys
# Directorio raíz del proyecto
ROOT_DIR = os.path.abspath('.')
print(f"Directorio raíz del proyecto: {ROOT_DIR}")

# Importar Mask RCNN
sys.path.append(ROOT_DIR)

# Importar configuración COCO
sys.path.append(os.path.join(ROOT_DIR, 'samples/coco/'))
import coco
```

Configuración del Modelo

```
class TumorConfig(Config):  
    NAME = 'tumor_detector'  
    GPU_COUNT = 1  
    IMAGES_PER_GPU = 1  
    NUM_CLASSES = 1 + 1  
    DETECTION_MIN_CONFIDENCE = 0.85  
    STEPS_PER_EPOCH = 100  
    LEARNING_RATE = 0.001
```

```
config = TumorConfig()  
config.display()
```

```
Configurations:  
BACKBONE                resnet101  
BACKBONE_STRIDES        [4, 8, 16, 32, 64]  
BATCH_SIZE              1  
BBOX_STD_DEV            [0.1 0.1 0.2 0.2]  
COMPUTE_BACKBONE_SHAPE  None  
DETECTION_MAX_INSTANCES 35  
DETECTION_MIN_CONFIDENCE 0.85  
DETECTION_NMS_THRESHOLD 0.3  
FPN_CLASSIF_FC_LAYERS_SIZE 1024  
GPU_COUNT               1  
GRADIENT_CLIP_NORM      5.0  
IMAGES_PER_GPU          1  
IMAGE_CHANNEL_COUNT      3  
IMAGE_MAX_DIM           1024  
IMAGE_META_SIZE         14  
IMAGE_MIN_DIM           1024  
IMAGE_MIN_SCALE         0  
IMAGE_RESIZE_MODE        square  
IMAGE_SHAPE              [1024 1024   3]  
LEARNING_MOMENTUM        0.9  
LEARNING_RATE           0.001  
LOSS_WEIGHTS             {'rpn_class_loss': 1.0, 'rpn_bbox_loss': 1.0, 'mrcnn_class_loss': 1.0, 'mrcnn_bbox_loss': 1.0, 'mrcnn_mask_loss': 1.0}  
MASK_POOL_SIZE          14  
MASK_SHAPE               [28, 28]  
MASK_POOL_SIZE          14  
MASK_SHAPE               [28, 28]  
MAX_GT_INSTANCES         100  
MEAN_PIXEL               [123.7 116.8 103.9]  
MINI_MASK_SHAPE          (56, 56)  
NAME                     tumor_detector  
NUM_CLASSES              2  
POOL_SIZE                7  
POST_NMS_ROIS_INFERENCE  1000  
POST_NMS_ROIS_TRAINING   2000  
PRE_NMS_LIMIT            6000  
ROI_POSITIVE_RATIO       0.33  
RPN_ANCHOR_RATIOS        [0.5, 1, 2]  
RPN_ANCHOR_SCALES        (32, 64, 128, 256, 512)  
RPN_ANCHOR_STRIDE        1  
RPN_BBOX_STD_DEV         [0.1 0.1 0.2 0.2]  
RPN_NMS_THRESHOLD        0.7  
RPN_TRAIN_ANCHORS_PER_IMAGE 256  
STEPS_PER_EPOCH          100  
TOP_DOWN_PYRAMID_SIZE    256  
TRAIN_BN                 False  
TRAIN_ROIS_PER_IMAGE     200  
USE_MINI_MASK            False  
USE_RPN_ROIS             True  
VALIDATION_STEPS         10  
WEIGHT_DECAY             0.0001
```

Implementación del Dataset para Detección y Segmentación de Tumores Cerebrales

```
class BrainScanDataset(utils.Dataset):

    def load_brain_scan(self, dataset_dir, subset):
        """Load a subset of the dataset."""
        self.add_class("tumor", 1, "tumor")

        assert subset in ["train", "val", "test"]
        dataset_dir = os.path.join(dataset_dir, subset)

        annotations_path = os.path.join(dataset_dir, f'annotations_{subset}.json')
        try:
            with open(annotations_path) as f:
                annotations = json.load(f)
        except FileNotFoundError:
            raise FileNotFoundError(f"Annotations file not found: {annotations_path}")
        except json.JSONDecodeError:
            raise ValueError(f"Error decoding JSON from the file: {annotations_path}")

        annotations = list(annotations.values())
        annotations = [a for a in annotations if a['regions']]

        for a in annotations:
            if type(a['regions']) is dict:
                polygons = [r['shape_attributes'] for r in a['regions'].values()]
            else:
                polygons = [r['shape_attributes'] for r in a['regions']]

            image_path = os.path.join(dataset_dir, a['filename'])
            try:
                image = skimage.io.imread(image_path)
            except FileNotFoundError:
                print(f"Warning: Image file not found: {image_path}")
                continue
            except Exception as e:
                print(f"Warning: Error reading image file {image_path}: {e}")
                continue
```

```
        height, width = image.shape[:2]

        self.add_image(
            "tumor",
            image_id=a['filename'],
            path=image_path,
            width=width,
            height=height,
            polygons=polygons
        )

    def load_mask(self, image_id):
        """Generate instance masks for an image."""
        image_info = self.image_info[image_id]
        if image_info["source"] != "tumor":
            return super(self.__class__, self).load_mask(image_id)

        info = self.image_info[image_id]
        mask = np.zeros([info["height"], info["width"], len(info["polygons"])], dtype=np.uint8)

        for i, p in enumerate(info["polygons"]):
            all_points_y = np.array(p['all_points_y'])
            all_points_x = np.array(p['all_points_x'])

            # Validate coordinates
            all_points_y = np.clip(all_points_y, 0, info["height"] - 1)
            all_points_x = np.clip(all_points_x, 0, info["width"] - 1)

            rr, cc = skimage.draw.polygon(all_points_y, all_points_x)
            mask[rr, cc, i] = 1

        # Utilize the function from utils to convert mask to boolean
        return mask.astype(np.bool_), np.ones([mask.shape[-1]], dtype=np.int32)

    def image_reference(self, image_id):
        info = self.image_info[image_id]
        if info["source"] == "tumor":
            return info["path"]
        else:
            return super(self.__class__, self).image_reference(image_id)
```

Datasets y Callbacks

```
# Crear los datasets
dataset_train = BrainScanDataset()
dataset_train.load_brain_scan('brain-tumor/data_cleaned', 'train')
dataset_train.prepare()

dataset_val = BrainScanDataset()
dataset_val.load_brain_scan('brain-tumor/data_cleaned', 'val')
dataset_val.prepare()

dataset_test = BrainScanDataset()
dataset_test.load_brain_scan('brain-tumor/data_cleaned', 'test')
dataset_test.prepare()
```

```
# Crear el directorio para guardar checkpoints
CHECKPOINT_DIR = os.path.abspath('./brain-tumor/checkpoints')

os.makedirs(CHECKPOINT_DIR, exist_ok=True)
os.makedirs('./brain-tumor/logs', exist_ok=True)

# # Configuración de callbacks
tensorboard_callback = TensorBoard(log_dir='./brain-tumor/logs', histogram_freq=0)
✓ checkpoint_callback = ModelCheckpoint(filepath=os.path.join(CHECKPOINT_DIR,
||||| 'weights.{epoch:02d}-{val_loss:.2f}.h5'), save_weights_only=True)
reduce_lr_callback = ReduceLROnPlateau(monitor='val_loss', factor=0.2, patience=5, min_lr=0.001)
early_stopping_callback = EarlyStopping(monitor='val_loss', patience=10)

# # Lista de callbacks
✓ callbacks = [tensorboard_callback,
||||| checkpoint_callback, reduce_lr_callback, early_stopping_callback]
```


Entrenamiento del Modelo

```
# # Configurar el modelo para entrenamiento
model = modellib.MaskRCNN(
    mode='training',
    config=config,
    model_dir=CHECKPOINT_DIR
)

model.load_weights(
    os.path.join(ROOT_DIR, "mask_rcnn_coco.h5"),
    by_name=True,
    exclude=["mrcnn_class_logits", "mrcnn_bbox_fc", "mrcnn_bbox", "mrcnn_mask"]
)

# # Entrenar el modelo por 30 época
num_epochs = 30

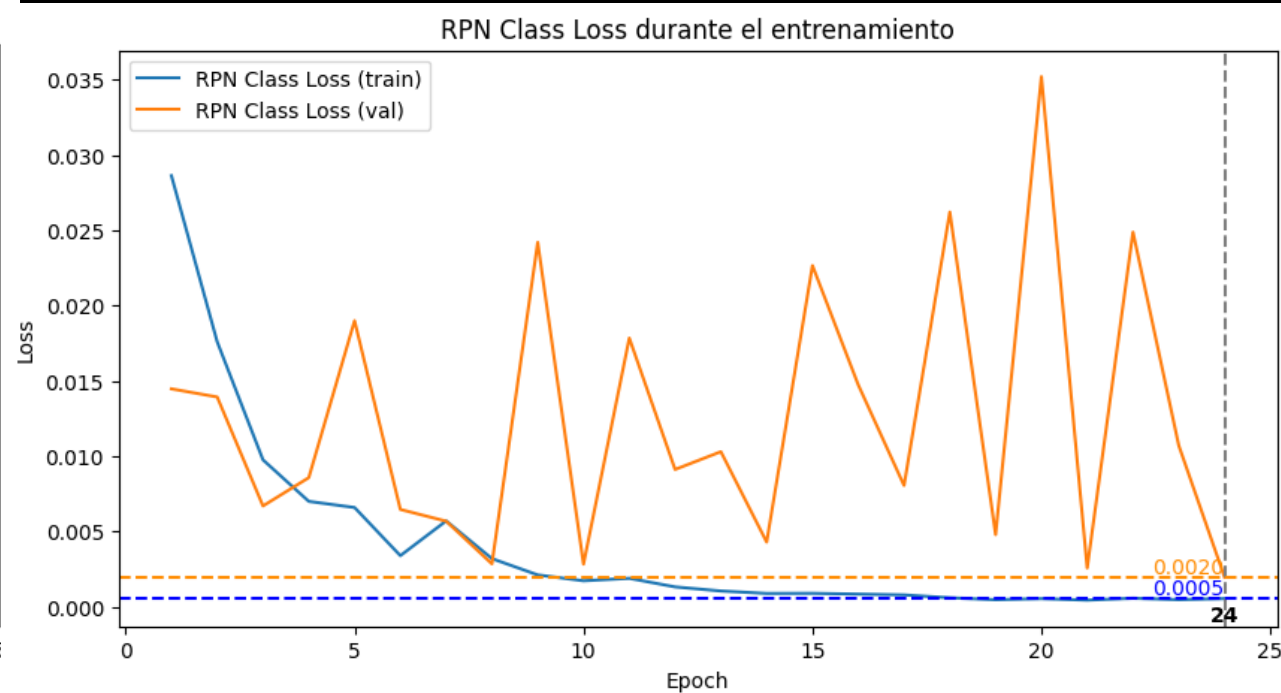
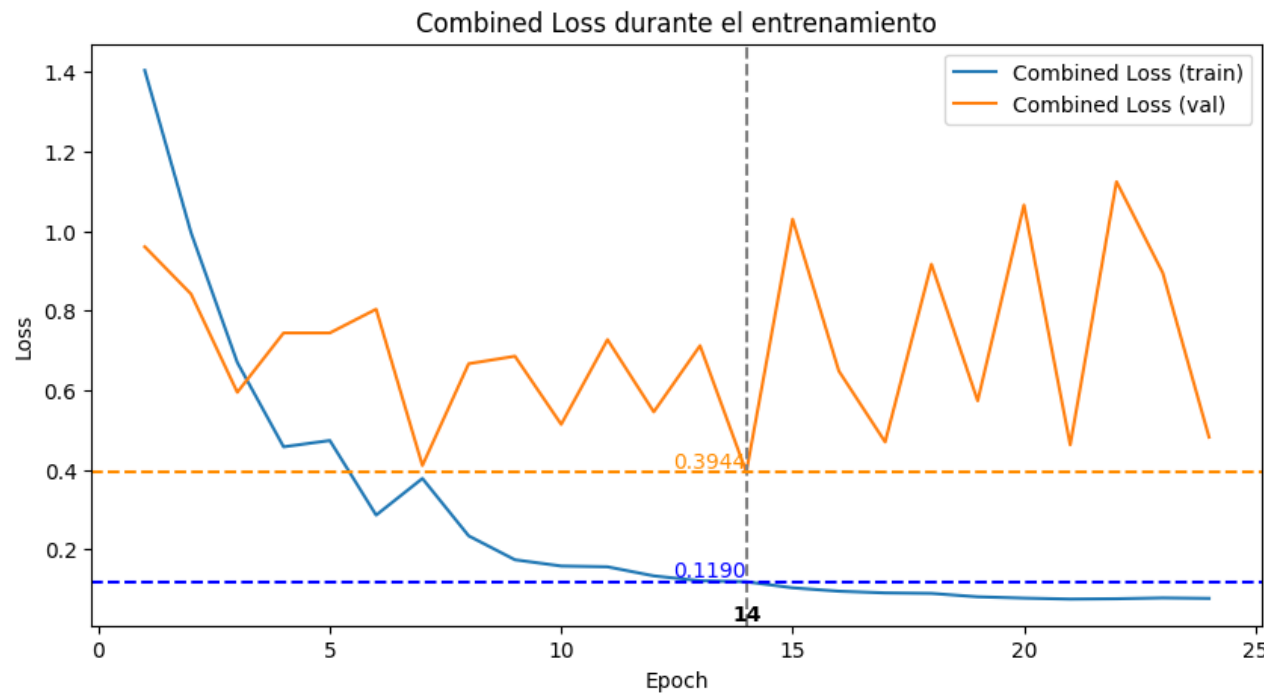
model.train(
    dataset_train,
    dataset_val,
    learning_rate=config.LEARNING_RATE,
    epochs=num_epochs,
    layers='all',
    custom_callbacks=callbacks
)
```

Gráficos de Pérdida durante el entrenamiento

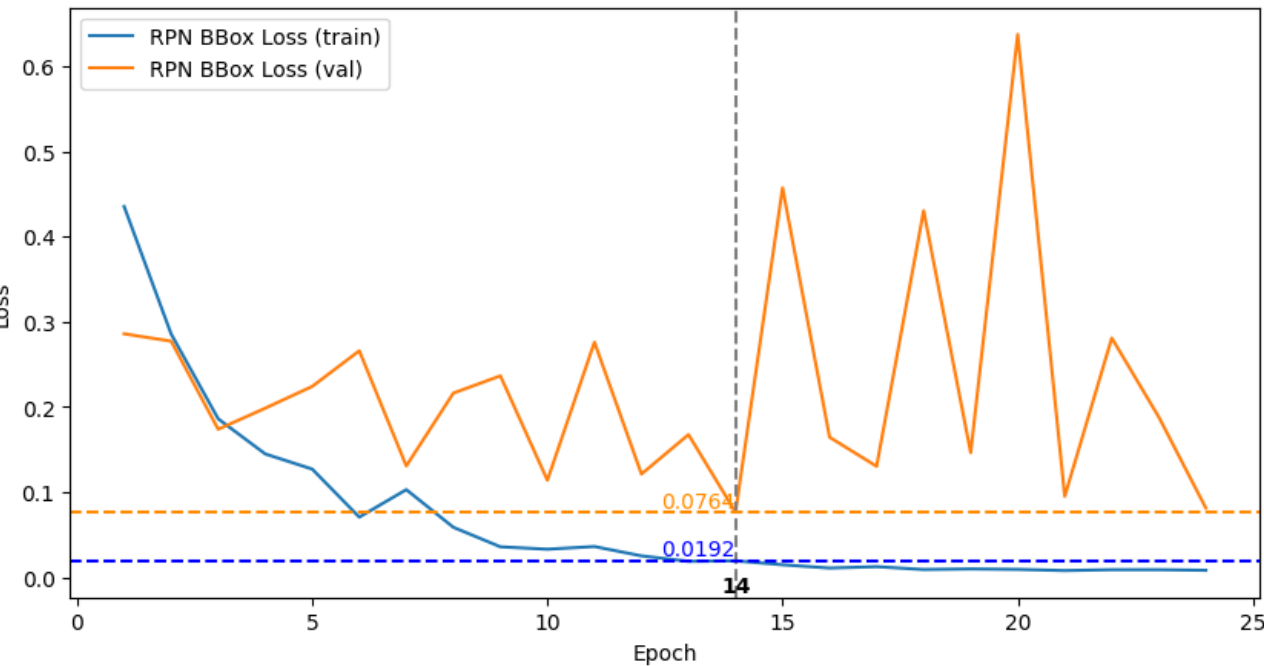
```
# Iterar sobre los pares de tags para generar los gráficos
for train_tag, val_tag, title in tags_pairs:
    # Extraer los datos de las métricas de interés
    epoch_train_steps, epoch_train_values = get_scalar_data(event_acc, train_tag)
    epoch_val_steps, epoch_val_values = get_scalar_data(event_acc, val_tag)

    # Encuentra la época con la pérdida de validación mínima
    epoch_optimal = np.argmin(epoch_val_values)

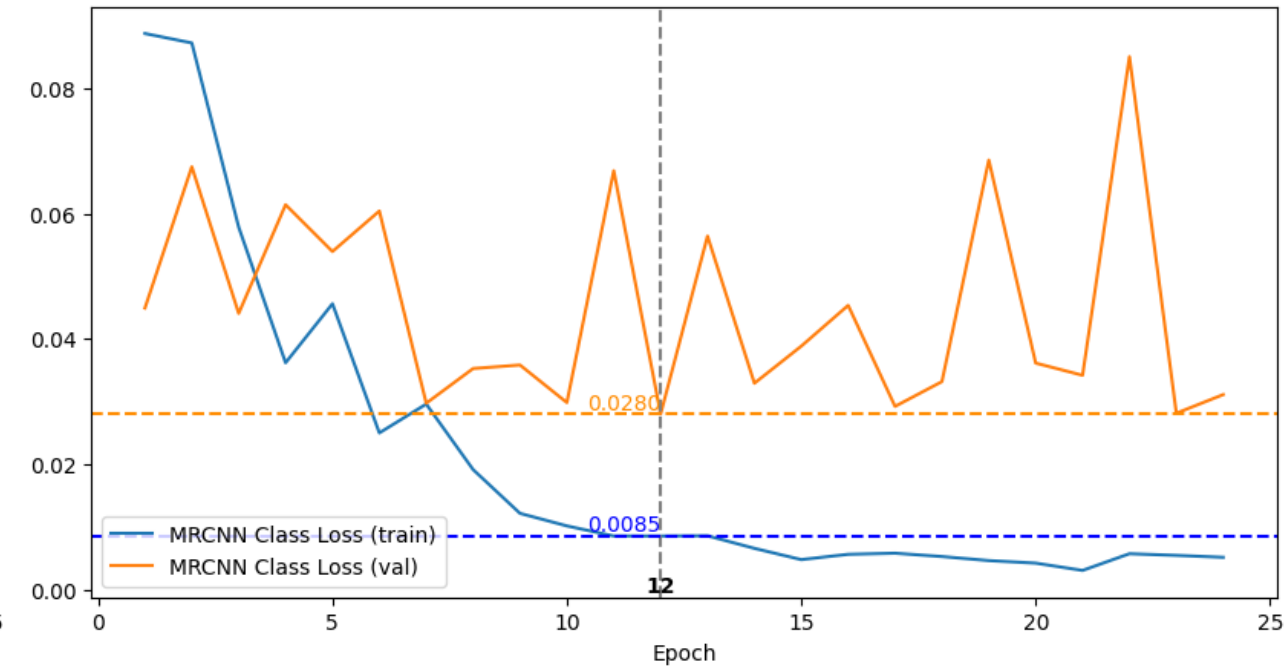
    # Graficar la pérdida
    plt.figure(figsize=(10, 5))
    plt.plot([x + 1 for x in epoch_train_steps], epoch_train_values, label=f'{title} (train)')
    plt.plot([x + 1 for x in epoch_val_steps], epoch_val_values, label=f'{title} (val)')
```



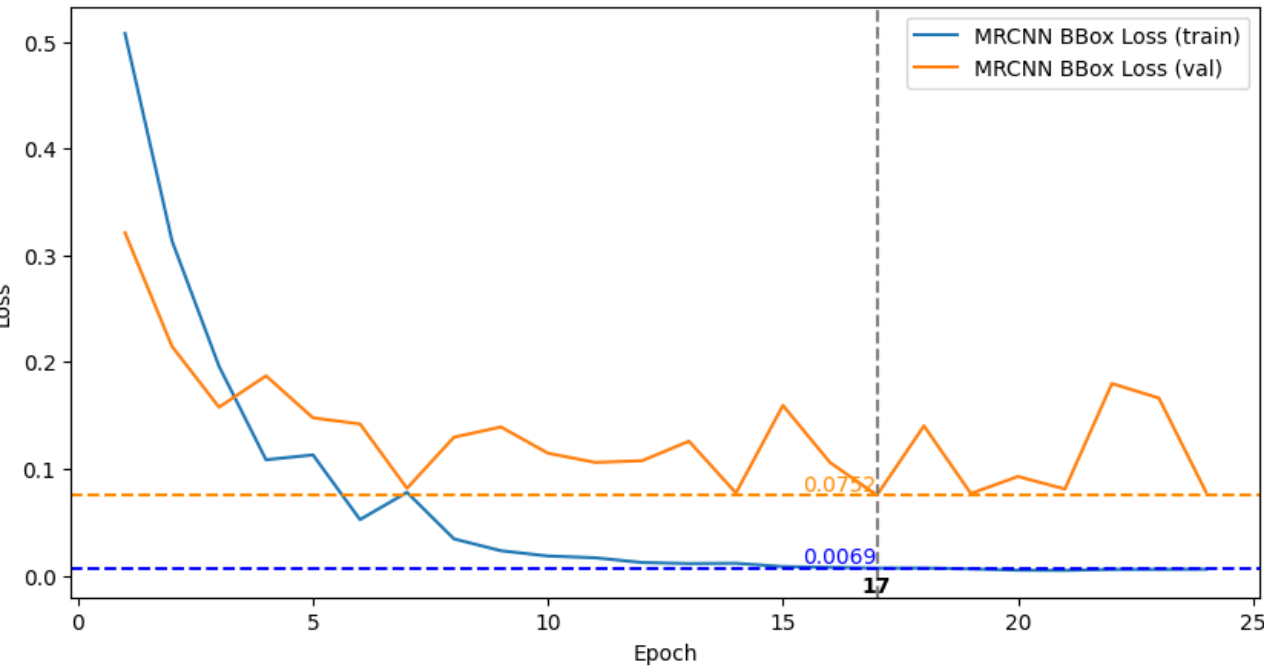
RPN BBox Loss durante el entrenamiento



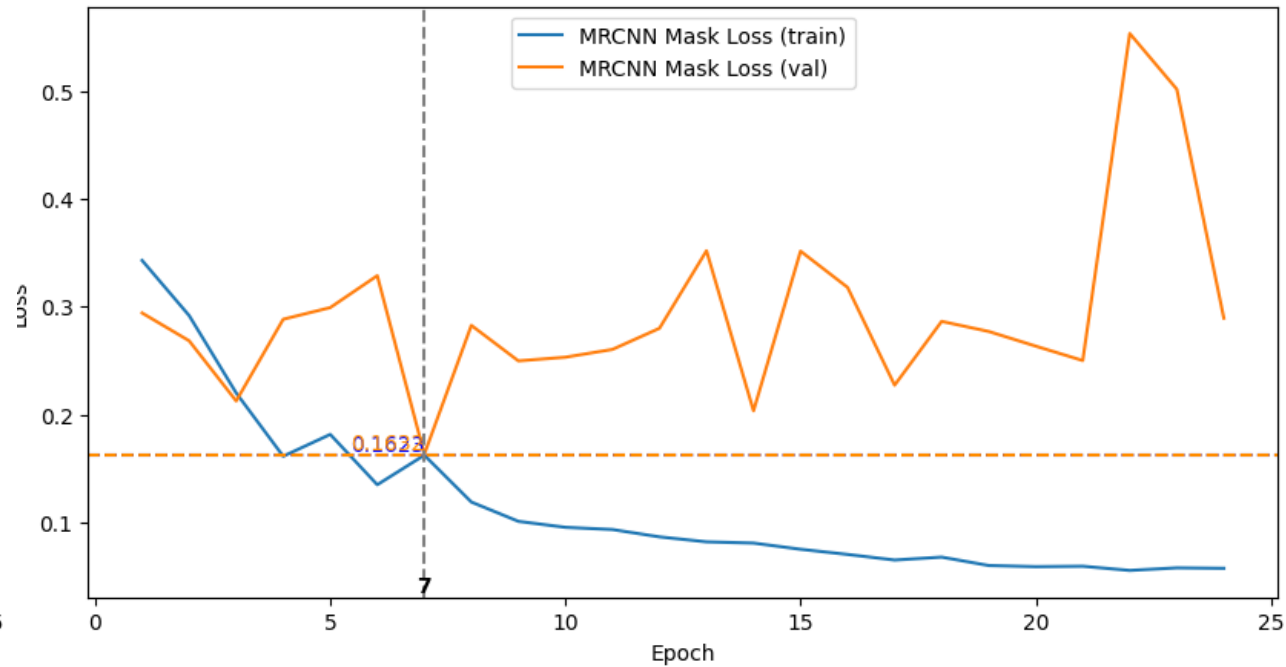
MRCNN Class Loss durante el entrenamiento



MRCNN BBox Loss durante el entrenamiento



MRCNN Mask Loss durante el entrenamiento



Configuración del Modelo en Modo Inferencia

```
# Configurar el modelo para inferencia (desactivar el entrenamiento)
model = modellib.MaskRCNN(
    mode="inference",          # Modo inferencia para realizar predicciones
    config=config,             # Configuración específica para el proyecto
    model_dir=CHECKPOINT_DIR   # Directorio donde se guardan los pesos del modelo
)

# Obtener la ruta a los pesos guardados más recientes (mejor modelo entrenado)
model_path =  '/content/drive/MyDrive/proyecto_dl/brain-tumor/checkpoints/weights.14-0.3944.h5' 

# Cargar los pesos en el modelo utilizando solo los nombres de las capas que coinciden
model.load_weights(model_path, by_name=True)
```


Predicción y Visualización

```
# Definir la función para predecir y visualizar
def get_ax(rows=1, cols=1, size=16):
    _, ax = plt.subplots(rows, cols, figsize=(size*cols, size*rows))
    return ax

def display_image(dataset, ind):
    plt.figure(figsize=(5,5))
    plt.imshow(dataset.load_image(ind))
    plt.xticks([])
    plt.yticks([])
    plt.title('Original Image')
    plt.show()

def predict_and_plot_differences(dataset, img_id):
    original_image, image_meta, gt_class_id, gt_bbox, gt_mask = modellib.load_image_gt(
        dataset, config, img_id, augmentation=None
    )

    results = model.detect([original_image], verbose=0)
    r = results[0]

    visualize.display_instances(
        original_image,
        r['rois'], r['masks'], r['class_ids'],
        dataset.class_names, r['scores'],
        ax=get_ax()
    )
```

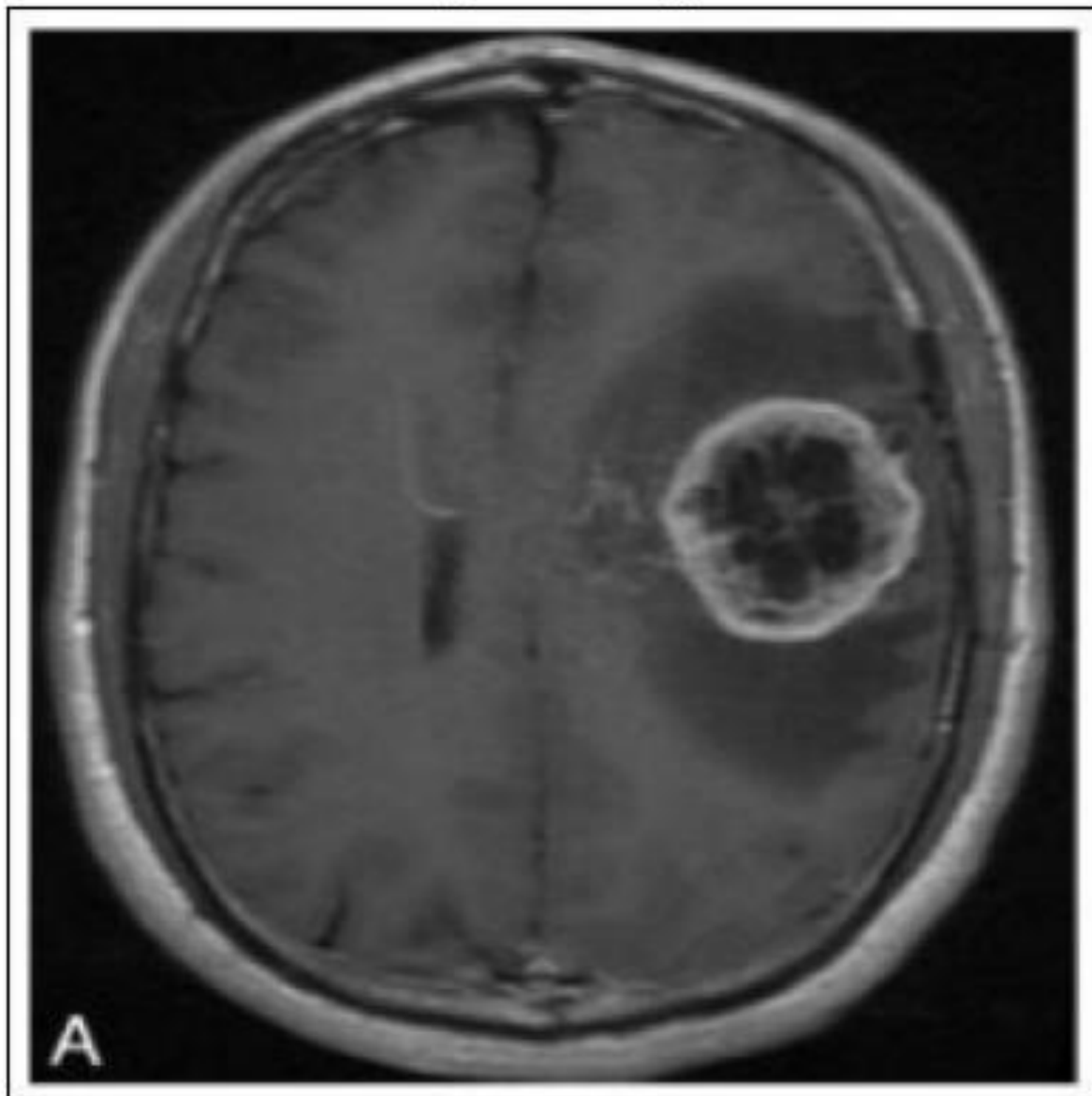
```
# Se define función para ver las anotaciones reales y poder comparar
def display_real_annotations(dataset, img_id):
    # Cargar la imagen y las anotaciones reales
    original_image, image_meta, gt_class_id, gt_bbox, gt_mask = modellib.load_image_gt(
        dataset, config, img_id)

    # Visualizar las anotaciones reales
    visualize.display_instances(
        original_image,
        gt_bbox,
        gt_mask,
        gt_class_id,
        dataset.class_names,
        scores=None, # No scores for ground truth
        title="Ground Truth",
        ax=get_ax()
    )
```

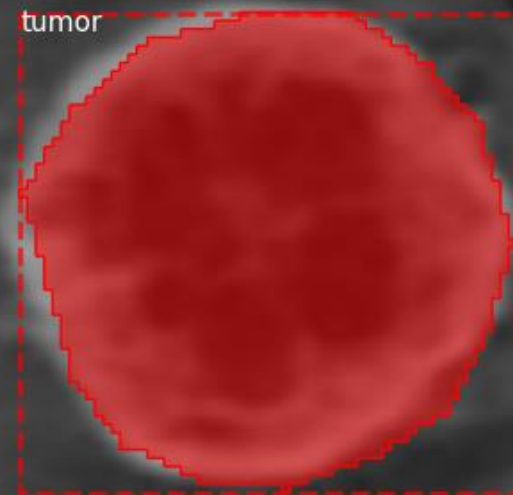
```
# Evaluar y visualizar resultados
ind = 0 # aquí poner el número dentro del rango de las imágenes de evaluación
display_image(dataset_test, ind)
display_real_annotations(dataset_test, ind)
predict_and_plot_differences(dataset_test, ind)
```

Imagen 1

Original Image



Ground Truth Tumor



Predicted Tumor

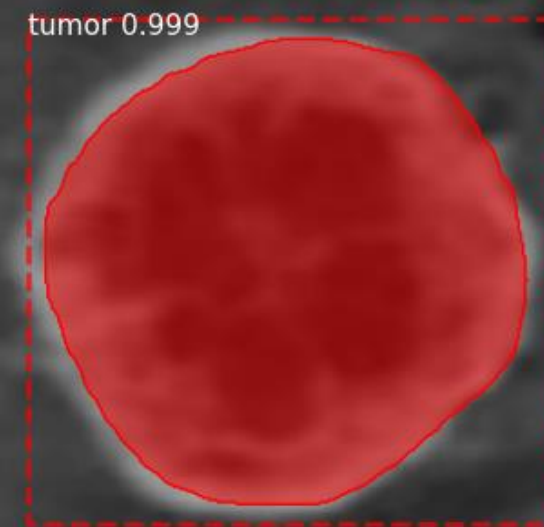
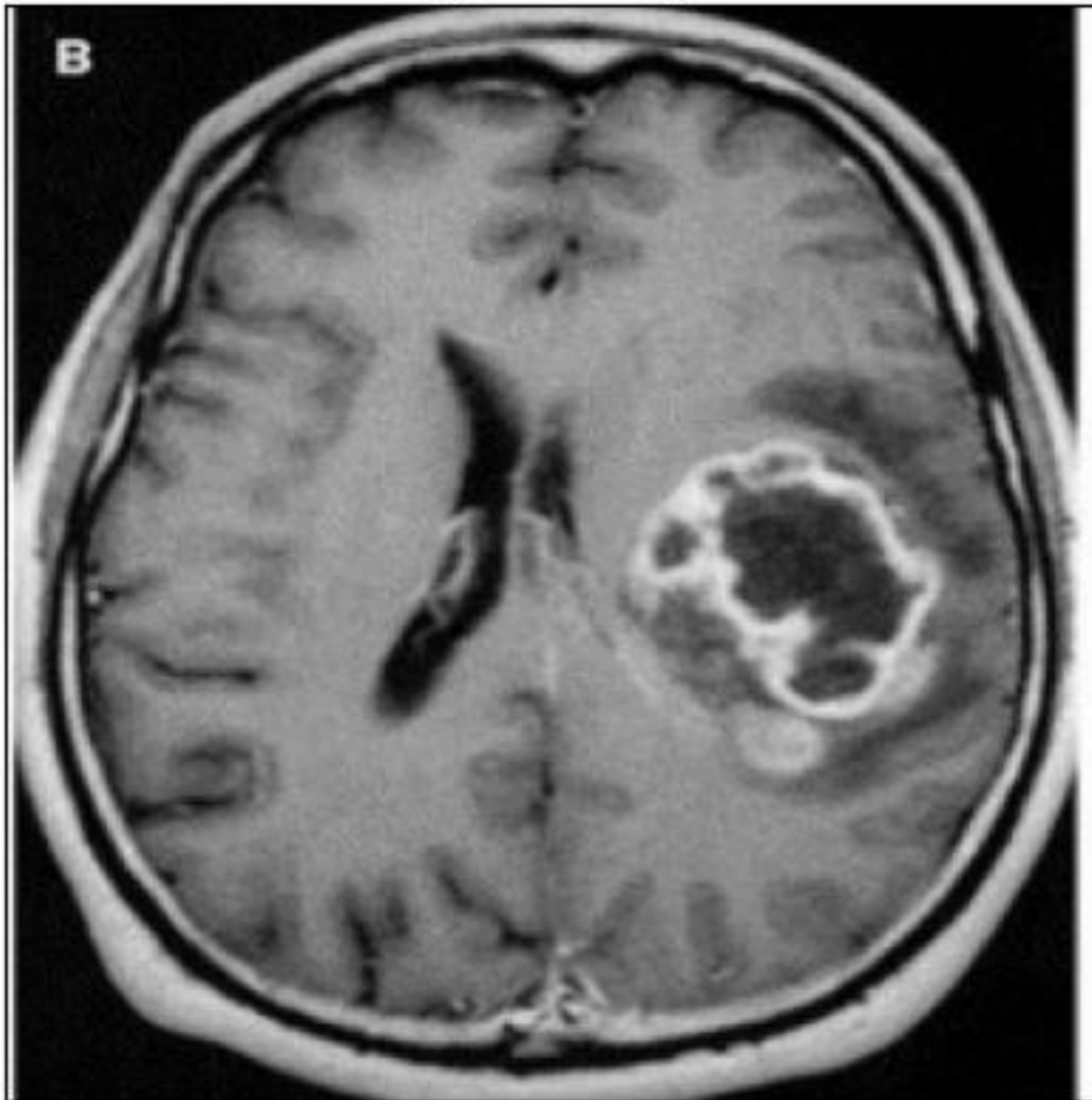
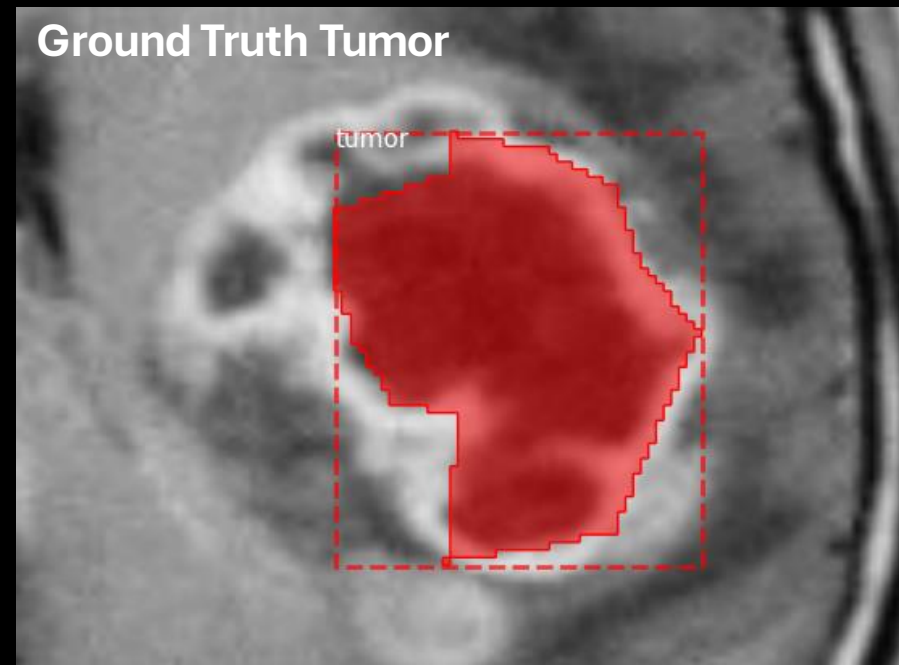


Imagen 2

Original Image



Ground Truth Tumor



Predicted Tumor

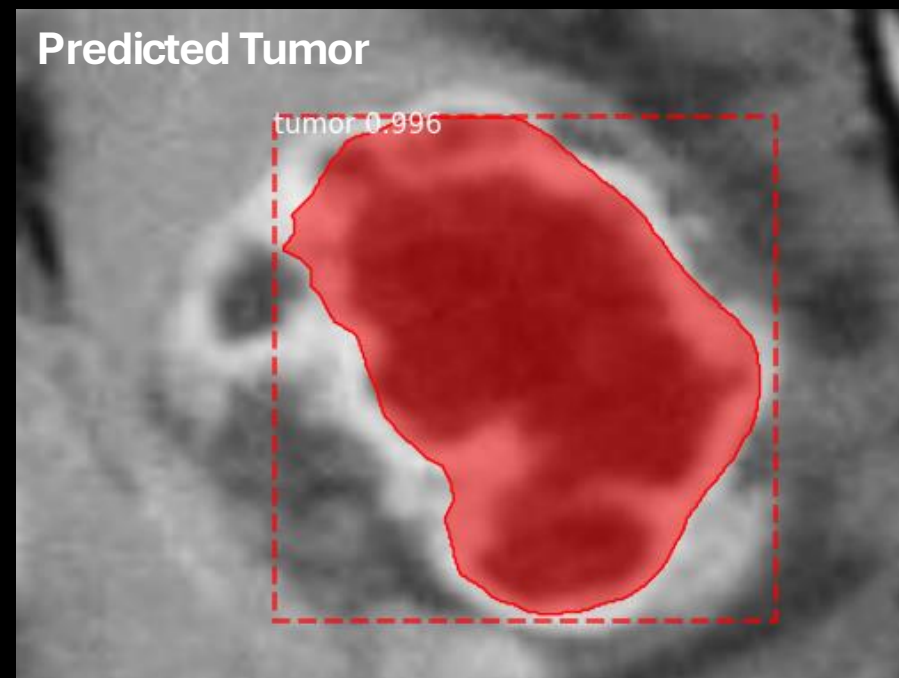
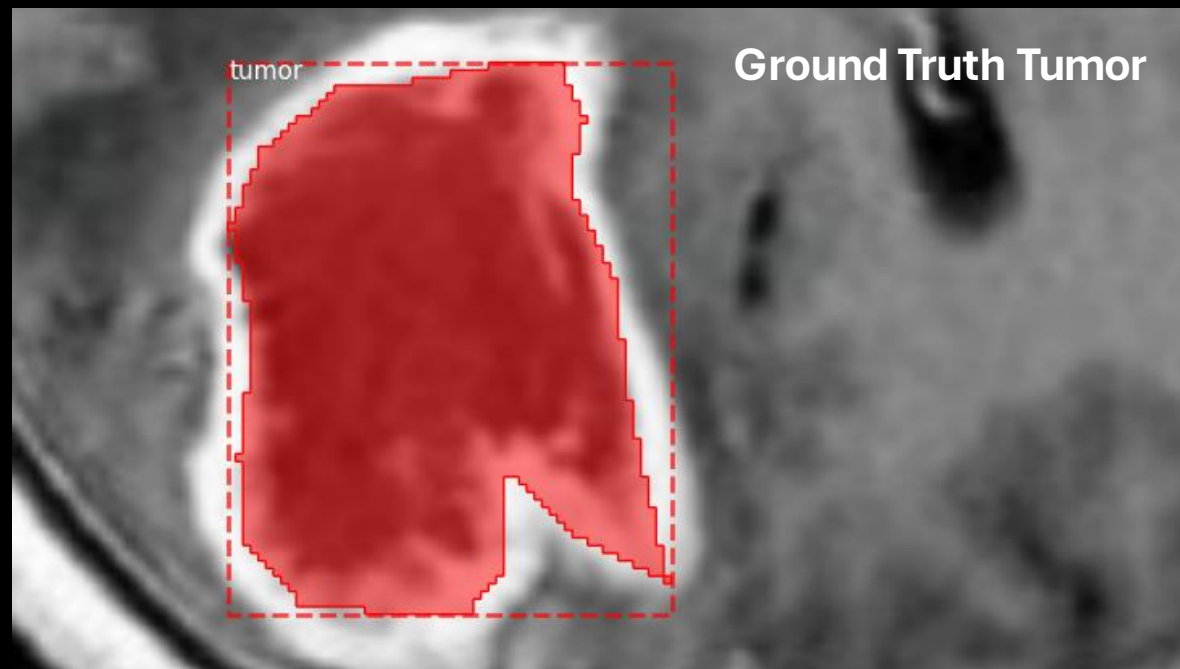
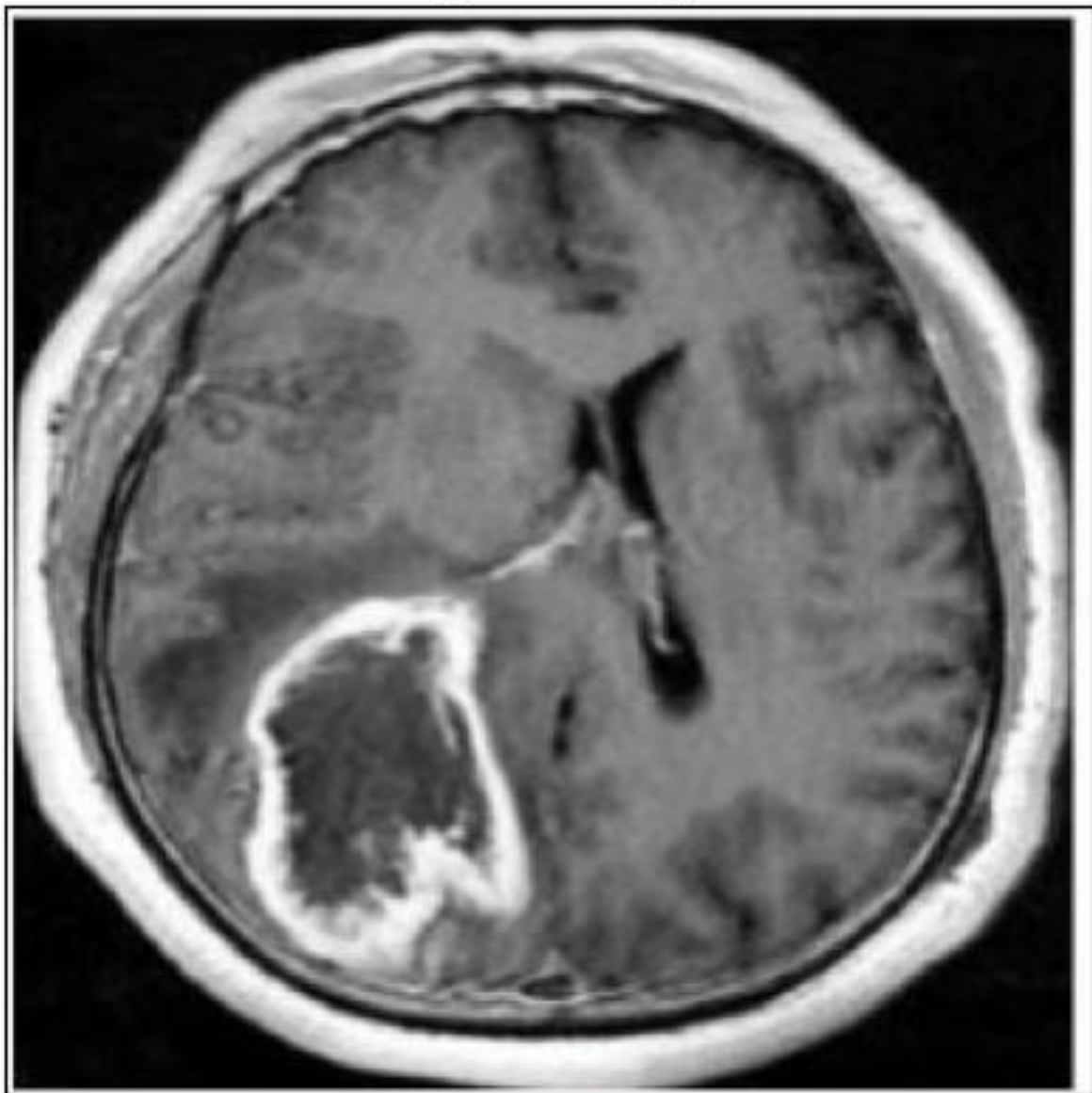
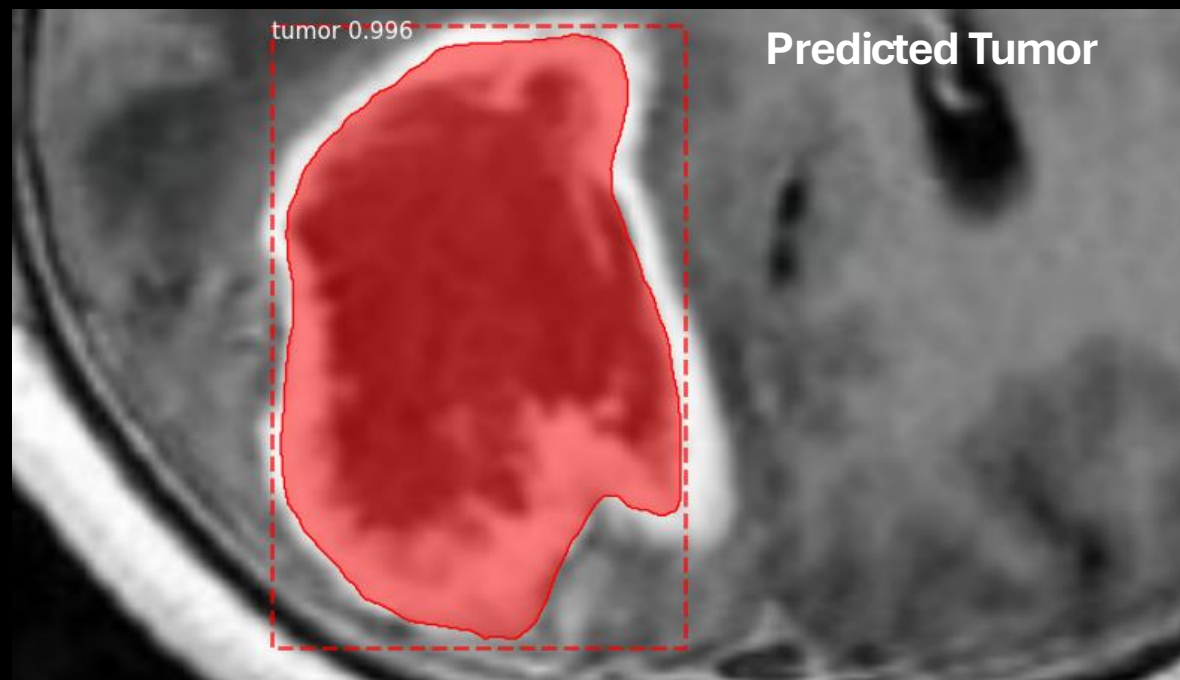


Imagen 3

Original Image



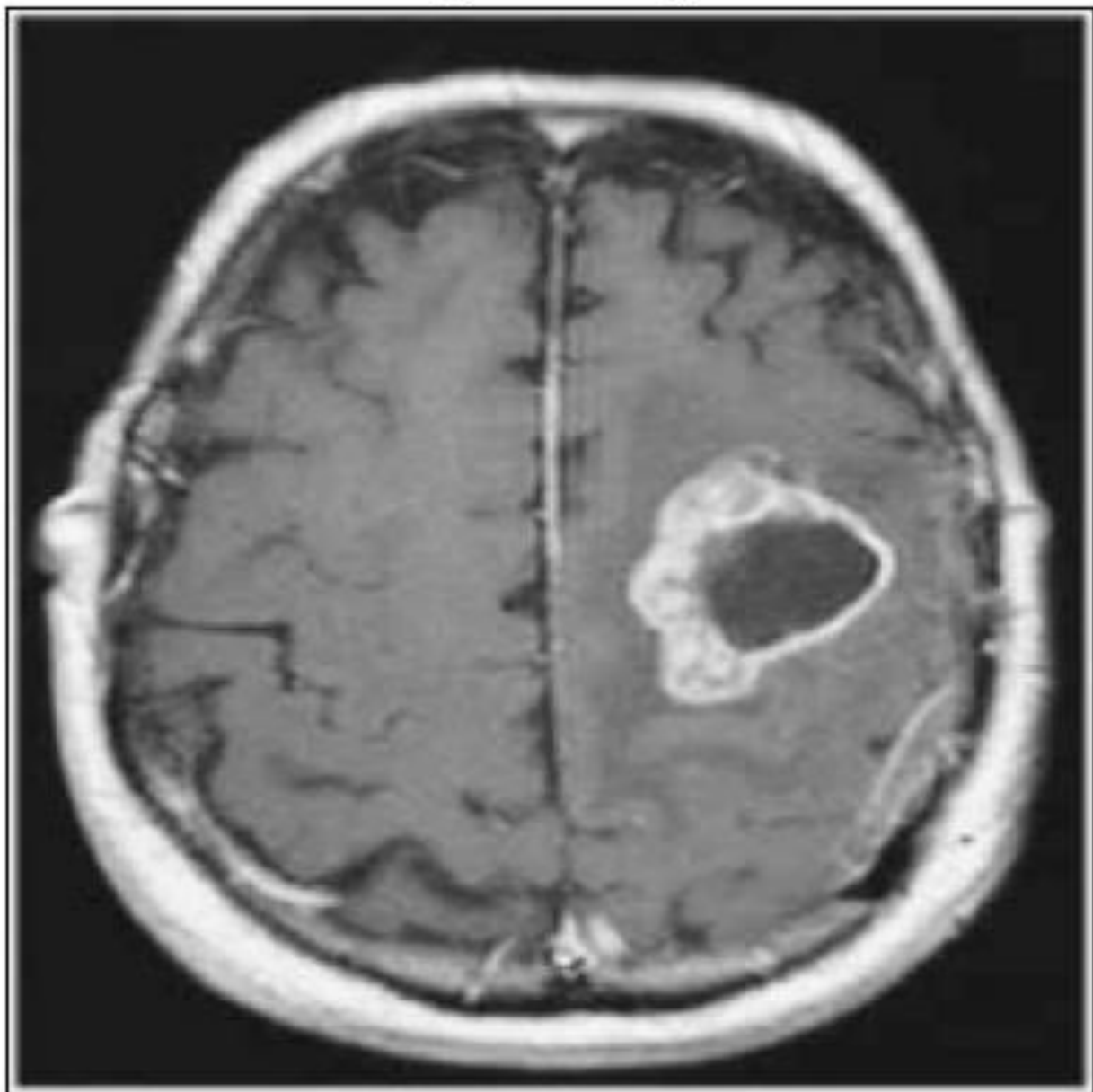
Ground Truth Tumor



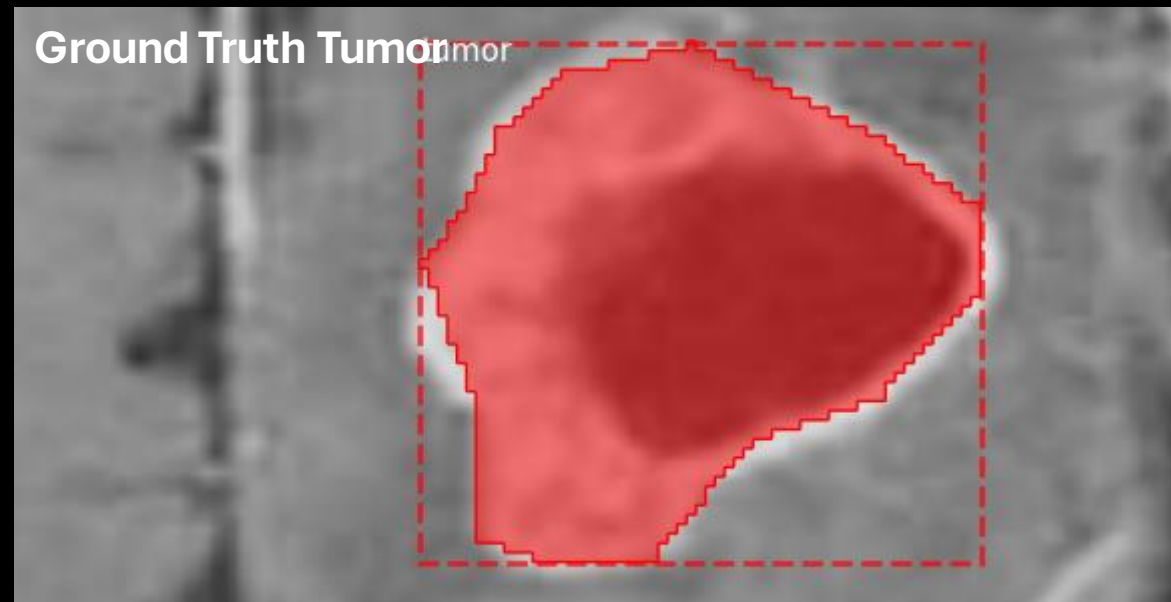
Predicted Tumor

Imagen 4

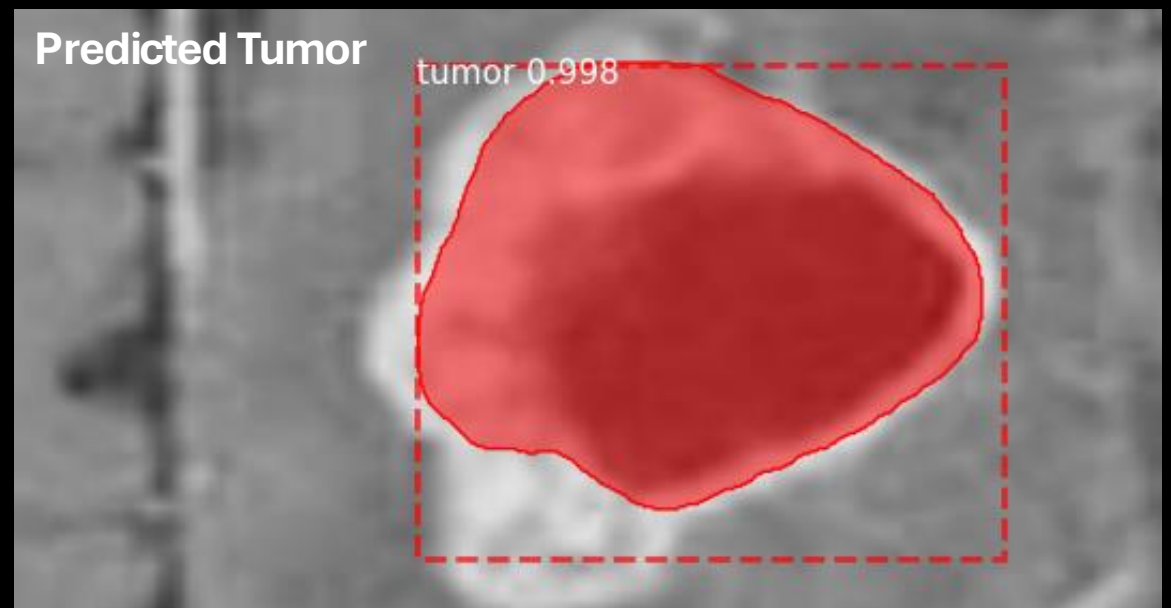
Original Image



Ground Truth Tumor



Predicted Tumor



Métricas de Desempeño

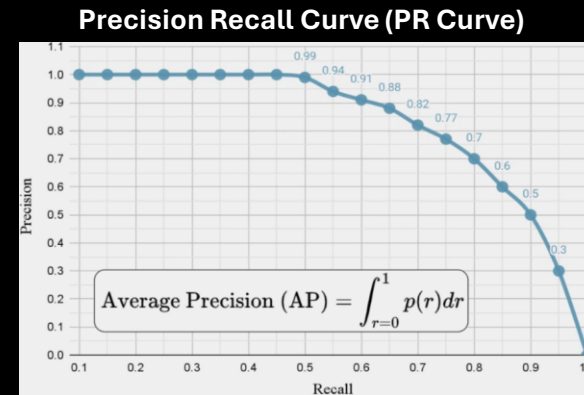
- **Precision:** La precisión mide la proporción de verdaderos positivos entre todos los casos que se predijo como positivo.
- **Recall:** Mide la proporción de verdaderos positivos entre todos los casos que realmente son positivos.
- **F1-Score:** Es la media armónica entre precisión y recall.

$$\text{Precision} = \frac{TP}{TP + FP}$$

$$\text{Recall} = \frac{TP}{TP + FN}$$

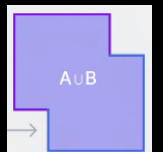
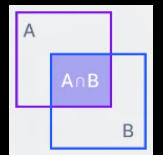
$$\text{F1-Score} = 2 \cdot \frac{\text{Precision} \cdot \text{Recall}}{\text{Precision} + \text{Recall}}$$

- **Average Precision (AP):** Área bajo la curva de Precisión-Recall para un valor específico de IoU, típicamente 0.5.



- **Intersection over Union (IoU):** mide la superposición entre la región predicha por el modelo y la región real

$$\text{IoU} = \frac{\text{Área de Intersección}}{\text{Área de la unión}} =$$



Métricas de Desempeño

```
def evaluate_image_metrics(dataset, model, config, image_id, curve_PR=False):
    """
    Calcula las métricas y muestra los resultados para una imagen específica.
    """

    # Cargar la imagen y las anotaciones de ground truth
    image, image_meta, gt_class_id, gt_bbox, gt_mask = \
        modellib.load_image_gt(dataset, config, image_id)

    # Realizar la predicción en la imagen usando el modelo
    results = model.detect([image], verbose=0)

    # Extraer las predicciones
    r = results[0]
    pred_class_id = r['class_ids']
    pred_bbox = r['rois']
    pred_mask = r['masks']
    pred_scores = r['scores'] # Puntuaciones de confianza

    # Calcular las métricas
    AP, precisions, recalls, overlaps = utils.compute_ap(
        gt_bbox, gt_class_id, gt_mask,
        pred_bbox, pred_class_id, pred_scores, pred_mask,
        iou_threshold=0.5)

    # Plot de la curva Precision-Recall
    if curve_PR:
        visualize.plot_precision_recall(AP, precisions, recalls)
        plt.show() # Forzar la visualización del gráfico
        plt.close() # Cerrar la figura para liberar memoria

    # Quitar el primer y último valor de las listas de precisions y recalls
    precisions = precisions[1:-1]
    recalls = recalls[1:-1]

    # Calcular F1-Score y IoU promedio
    f1_score = calculate_f1_score(precisions, recalls)
    iou_avg = calculate_iou_average(overlaps)
```

```
# Imprimir los resultados
print(f"\nImagen ID: {image_id}")
print("AP:", AP)
print("Precisions:", precisions)
print("Recalls:", recalls)
print("Overlaps:", overlaps)
print("Scores:", pred_scores) # Imprime las puntuaciones de confianza
print("F1-Score:", f1_score) # Promedio del F1-Score
print("IoU Promedio:", iou_avg)

return AP, precisions, recalls, f1_score, iou_avg

# Iterar sobre todas las imágenes en el conjunto de datos
all_aps = []
all_precisions = []
all_recalls = []
all_f1_scores = []
all_iou_avgs = []

for image_id in range(len(dataset_test.image_ids)):
    AP, precisions, recalls,
    f1_score, iou_avg = evaluate_image_metrics(dataset_test,
                                              model, config, image_id, curve_PR=True)

    # Guardar los resultados en las listas
    all_aps.append(AP)
    all_precisions.append(np.mean(precisions)) # Promedio de precisiones para cada imagen
    all_recalls.append(np.mean(recalls)) # Promedio de recalls para cada imagen
    all_f1_scores.append(f1_score)
    all_iou_avgs.append(iou_avg)

# Calcular y mostrar el promedio de las métricas
print("\nPromedios generales:")
print("mAP @ IoU=50:", np.mean(all_aps))
print("Precisión Promedio:", np.mean(all_precisions))
print("Recall Promedio:", np.mean(all_recalls))
print("F1-Score Promedio:", np.mean(all_f1_scores))
print("IoU Promedio General:", np.mean(all_iou_avgs))
```

Métricas de Desempeño

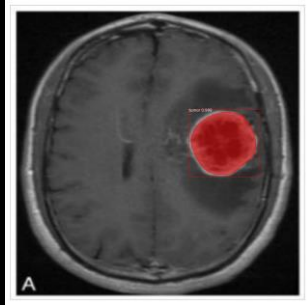


Imagen ID: 0
AP: 1.0
Precisions: [1.]
Recalls: [1.]
Overlaps: [[0.93148404]]
Scores: [0.9991941]
F1-Score: 1.0
IoU Promedio: 0.93148404

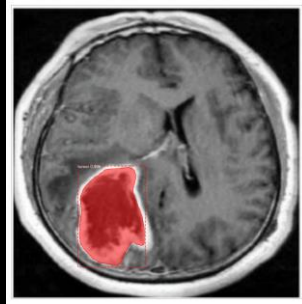


Imagen ID: 2
AP: 1.0
Precisions: [1.]
Recalls: [1.]
Overlaps: [[0.8097122]]
Scores: [0.9958521]
F1-Score: 1.0
IoU Promedio: 0.8097122

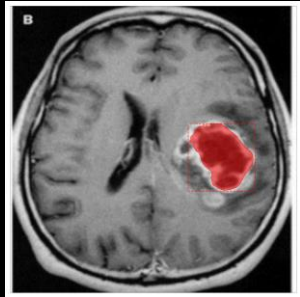


Imagen ID: 1
AP: 1.0
Precisions: [1.]
Recalls: [1.]
Overlaps: [[0.7673453]]
Scores: [0.996202]
F1-Score: 1.0
IoU Promedio: 0.7673453

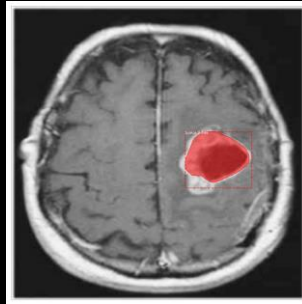
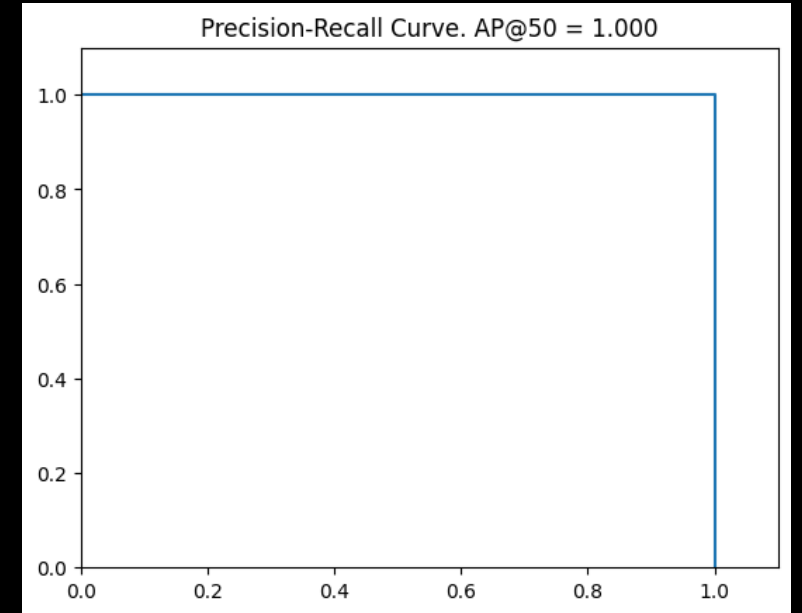


Imagen ID: 3
AP: 1.0
Precisions: [1.]
Recalls: [1.]
Overlaps: [[0.8023705]]
Scores: [0.99790215]
F1-Score: 1.0
IoU Promedio: 0.8023705



Promedios generales:

mAP @ IoU=50: 1.0

Precisión Promedio: 1.0

Recall Promedio: 1.0

F1-Score Promedio: 1.0

IoU Promedio General: 0.82772803

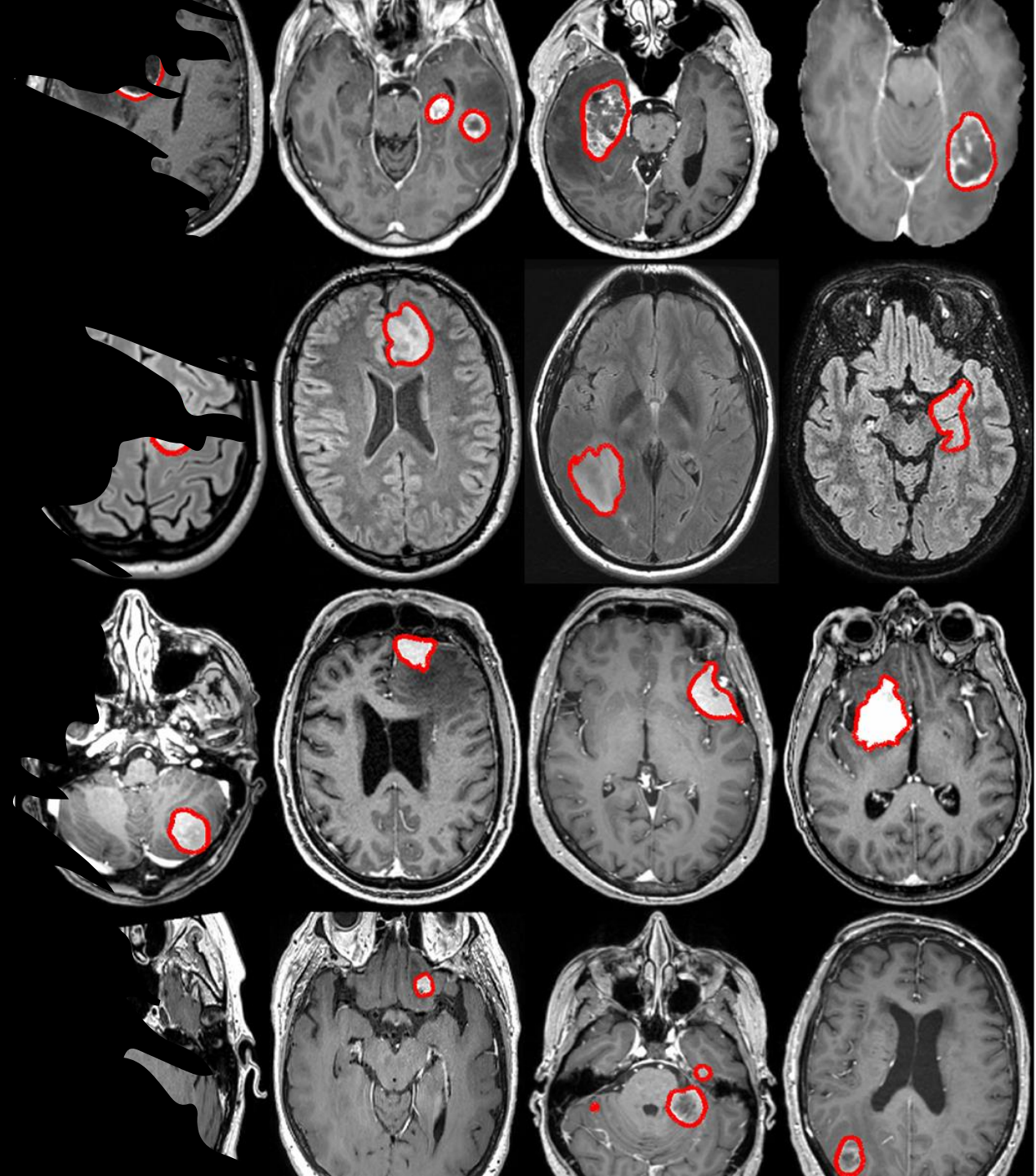
Comparación con otros estudios

* "Brain Tumor Localization and Segmentation Using Mask RCNN" by Masood et al. (2021)

Método	Accuracy	mAP	IoU promedio
R-CNN	0,92	0,91	-
Faster R-CNN	0,94	0,94	-
Masood et al. (2021)*	0,95	0,94	0,95
Nuestro método	1.0	1.0	0,83

Conclusiones

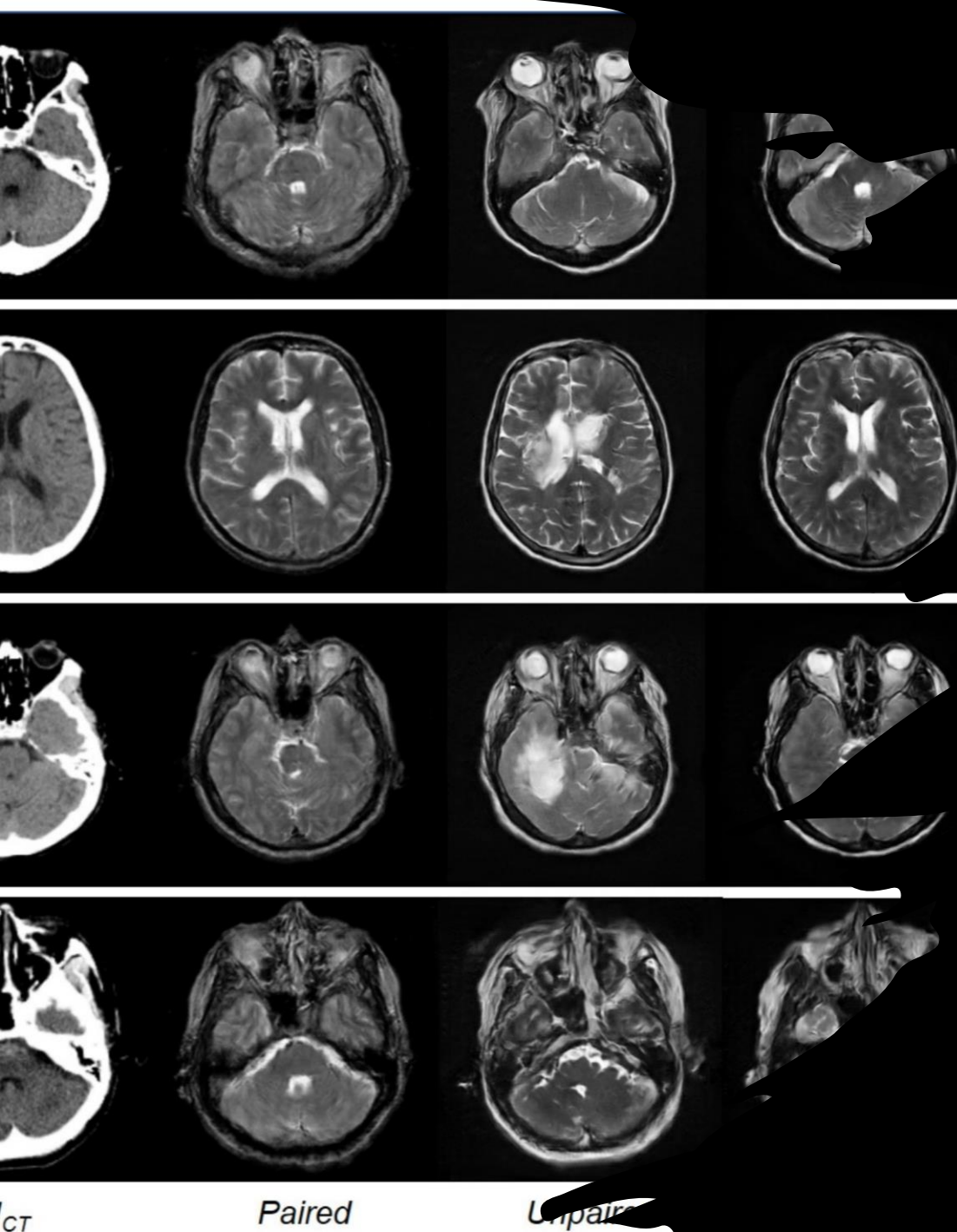
- **Objetivos Cumplidos:**
 - Implementación exitosa del modelo MASK R-CNN y una CNN convencional.
 - Uso efectivo de GPU para acelerar el proceso.
- **Resultados:**
 - Verificación visual de que el modelo identifica tumores y genera máscaras de segmentación.
- **Desempeño:**
 - Desempeño general bueno, aunque con espacio para mejorar el cálculo de métricas para una mejor comparación con otros métodos.





Trabajo futuro

- **Limpieza de Imágenes:** Eliminar letras y símbolos que interfieren con la detección de tumores.
- **Data Augmentation:** Aumentar la diversidad de imágenes con diferentes ángulos y transformaciones.
- **Mayor Volumen de Datos:** Incrementar el número de imágenes en los conjuntos de entrenamiento, validación y testeo para mejorar la generalización del modelo.



Referencias

- Fukushima, K. (1980). "Neocognitron: A self-organizing neural network model for a mechanism of pattern recognition unaffected by shift in position." URL: <https://link.springer.com/article/10.1007/BF00344251>
- Girshick, R., Donahue, Darrell, T., & Malik, J. (2014). "Rich feature hierarchies for accurate object detection and semantic segmentation." URL: <https://arxiv.org/pdf/1311.2524>
- Girshick, R. (2015). "Fast R-CNN." URL: <https://arxiv.org/pdf/1504.08083>
- Ren, S., He, K., Girshick, R., & Sun, J. (2015). "Faster R-CNN: Towards Real-Time Object Detection with Region Proposal Networks." URL: <https://arxiv.org/abs/1506.01497>
- Ren, S., He, K., Girshick, R., & Sun, J. (2015). "Faster R-CNN: Towards Real-Time Object Detection with Region Proposal Networks." URL: <https://arxiv.org/pdf/1506.01497>
- He, K., Gkioxari, G., Dollar, P., & Girshick, R. (2017). "Mask R-CNN." URL: <https://arxiv.org/pdf/1703.06870>
- "Brain Tumor Localization and Segmentation Using Mask RCNN" by Masood et al. (2021). URL: <https://link.springer.com/article/10.1007/s11704-020-0105-y>
- "Brain Tumor Segmentation Using Non-local Mask R-CNN and Single Model Ensemble" by Dai et al. (2021). URL: https://link.springer.com/chapter/10.1007/978-3-031-08999-2_19