# Tutorial 2: Detecting plankton from video.

This tutorial demonstrates how to use LodeSTAR model to detect plankton from video. LodeSTAR is a deep learning framework which uses self-supervised learning to train a fully convolutional neural network for detecting plankton from microscopy video frames. The training is performed with the help of only a *single* plankton crop from any video frame of users choice.

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This tutorial demonstrates how to train LodeSTAR for detecting plankton positions from video frames. It covers information on:

- Loading any experimental video containing plankton
- Selecting plankton crop(s) from any video frame
- Defining and training LodeSTAR model
- Testing the model on the video frames

Run the following cell to install the required packages to run this tutorial.

In [ ]:
```
!pip install deeptrack
!pip install tqdm
```

%matplotlib inline

## 1. Setup

Imports the required python packages needed to run this tutorial.

In [2]:
```
import warnings
warnings.filterwarnings("ignore")
import numpy as np
import skimage.color
import matplotlib.pyplot as plt
import cv2
from tqdm import tqdm
from PIL import Image
import tensorflow as tf
import datetime
import imageio
import deeptrack as dt
```

## 2. Load the video

### 2.1. Define a function to load the video

In the following cell, we write a function to load the microscopy video. The function takes the path to the video file as input and returns the video as a numpy array.

In [3]:
```
def load_video(path, start=0, end=None):
    video= cv2.VideoCapture(path)
    frames=[]
    total_frames = int(video.get(cv2.CAP_PROP_FRAME_COUNT))
    if end:
        end = min(end, total_frames)
    else:
        end = total_frames
    for i in tqdm(range(start, end, 1), desc="loading frames"):
        video.set(1, i)
        ret, frame=video.read()
        gray_frame = frame#[:,:,0]
        frames.append(gray_frame)
    return np.array(frames)
```

## 2.2. Load the video

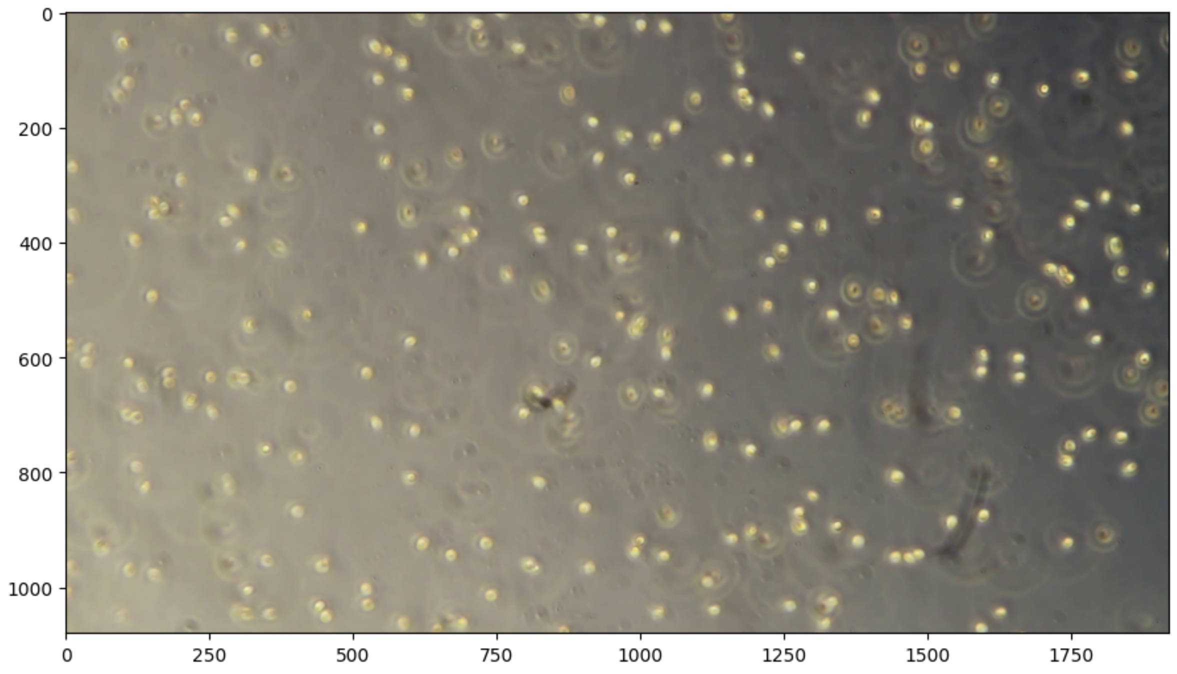
The video for this tutorial is available under the `data/plankton-videos` directory under the name `plankton_video2.mp4`. We use the function defined above to load the video. Adjust the path to the video file if you are using a different video.

In [4]:
```
path = "../original-videos/Plankton2.mp4"
frames = load_video(path, end=200)
```

```
loading frames: 100%|██████████| 200/200 [00:30<00:00,  6.57it/s]
```

Display the fist frame of the video to check if the video is loaded correctly.

In [5]:
```
# %matplotlib tk
# To display image in original colors
dpi = 100
frame = frames[0]
plt.figure(figsize=(frame.shape[0]/dpi, frame.shape[1]/dpi), dpi=dpi)
plt.imshow(cv2.cvtColor(frames[0], cv2.COLOR_BGR2RGB))
plt.show()
```



# 3. Select plankton crop(s) from the video frame

## 3.1. Define plankton positions

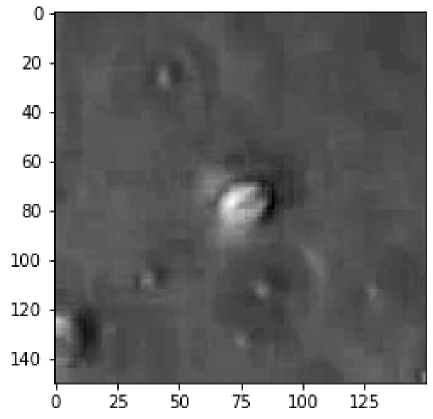
Define approximate plankton positions in the above video frame in the from of coordinates (x, y).

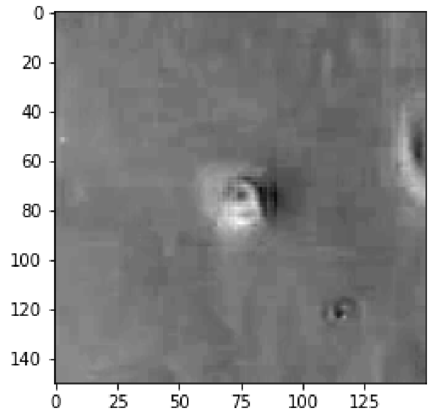
In [6]:
```
plankton_positions = [
    [598, 571],
    [513, 372],
    [1059, 386],
    [1552, 326],
    [1743, 920]
]
```

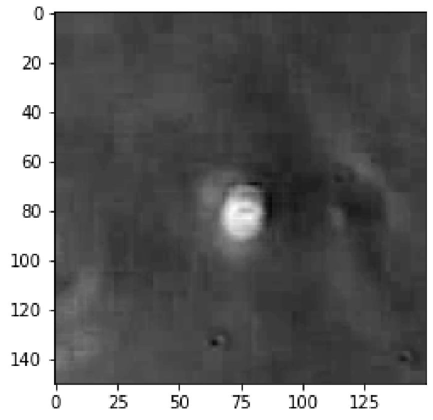
## 3.2. Crop the plankton

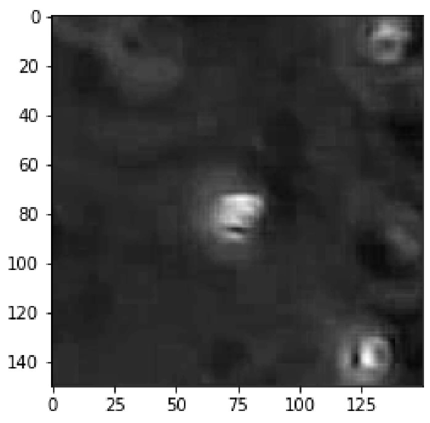
Crop the plankton positions by using the coordinates defined above. The cropped plankton images are stored in a list. The crop size can be adjusted by controlling the `crop_width` parameter. The default value is 150 pixels. This will generate a 150x150 pixel crop around the plankton position.

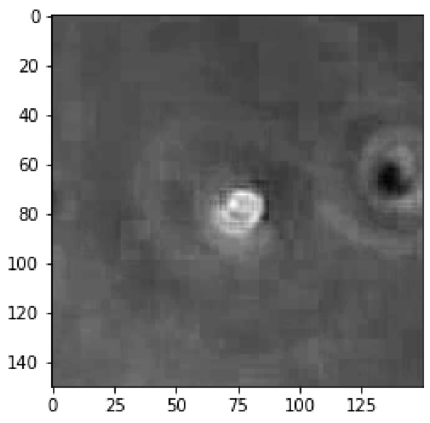
In [7]:
```
crop_width = 150
crops = []
for pos in plankton_positions:
    crop = frame[int(pos[1] - crop_width/2) :int(pos[1] + crop_width/2), int(pos[0] - cro
    crops.append(crop)
    plt.imshow(crop, cmap="gray")
    plt.show()
crops = np.expand_dims(crops, axis=-1)
```









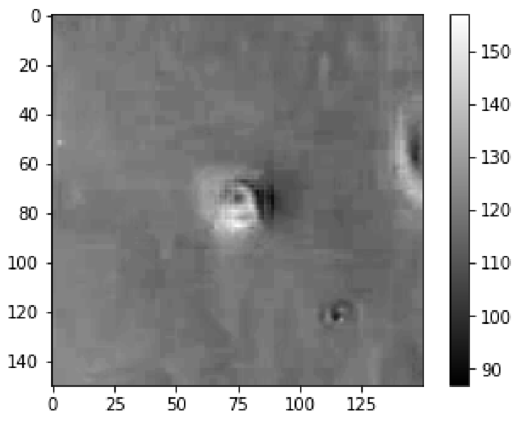


## 3.3. Select a random crop

Select a random crop from the list of cropped plankton images. This will be used for training the LodeSTAR model. Having multiple good crops will give us a choice to select the best crop for training. In this case, we have randomly select a crop from the list of good crops we have generated above.

In [9]:
```python
import random
# random.seed(20)
crop = random.choice(crops)
plt.imshow(crop, cmap="gray")
plt.colorbar()
```

Out[9]:
```
<matplotlib.colorbar.Colorbar at 0x7fa517e2afa0>
```



In [10]:
```python
random_crop = dt.Value(lambda: random.choice(crops))
```

Define a downsampling parameter to control the size of the cropped plankton image. The default value is 2. This will downsample the cropped plankton image by a factor of 2. This will generate a 75x75 pixel crop around the plankton position. By having this we need not generate multiple crops for different crop sizes.

In [11]:
```
downsample = 2
```

## 4. Train the LodeSTAR model

In the following code, we define and train the LodeSTAR model. Set the parameter, `TRAIN` to `True` to train the model from scratch. If you want to use the pre-trained model, set the parameter to `False`.

The pre-trained models are located in directory `data/pre-trained-models`. The pre-trained model is named as `lodestar-model-plankton2.h5`.

In [12]:
```
TRAIN = False

if TRAIN:
    model = dt.models.LodeSTAR(input_shape=(None, None, 1))
    train_set =    (
        dt.Value(random_crop)
        >> dt.AveragePooling(ksize=(downsample, downsample, 1))
        # >> dt.Affine(rotate=lambda: np.random.rand()*np.pi*2, scale=lambda:np.random.ur
        # >> dt.Add(lambda: np.random.randn() * 0.2)
        # >> dt.Gaussian(sigma=lambda:np.random.uniform(0, 0.01))
        # >> dt.Multiply(lambda: np.random.uniform(0.3, 1.6))
    )

    model.fit(
        train_set,
        epochs=30,
        batch_size=8,
        verbose=1
    )

    model.model.model.save_weights("lodestar-model-plankton2.h5")

else:
    model = dt.models.LodeSTAR(input_shape=(None, None, 1))
    model.model.model.load_weights("../data/pre-trained-models/lodestar-model-plankton2.h
```

```
Metal device set to: AMD Radeon Pro 5300M

systemMemory: 16.00 GB
maxCacheSize: 1.99 GB
```

```
2022-10-18 14:20:27.752109: I tensorflow/core/platform/cpu_feature_guard.cc:193] This Te
nsorFlow binary is optimized with oneAPI Deep Neural Network Library (oneDNN) to use the
following CPU instructions in performance-critical operations:  AVX2 FMA
To enable them in other operations, rebuild TensorFlow with the appropriate compiler fla
gs.
2022-10-18 14:20:27.754392: I tensorflow/core/common_runtime/pluggable_device/pluggable_
device_factory.cc:305] Could not identify NUMA node of platform GPU ID 0, defaulting to
0. Your kernel may not have been built with NUMA support.
2022-10-18 14:20:27.755525: I tensorflow/core/common_runtime/pluggable_device/pluggable_
device_factory.cc:271] Created TensorFlow device (/job:localhost/replica:0/task:0/devic
e:GPU:0 with 0 MB memory) -> physical PluggableDevice (device: 0, name: METAL, pci bus i
d: <undefined>)
Generating 175 / 160 samples before starting training
Epoch 1/30
2022-10-18 14:20:35.746022: I tensorflow/core/grappler/optimizers/custom_graph_optimizer
_registry.cc:113] Plugin optimizer for device_type GPU is enabled.
```

```
175/175 [==============================] - 10s 36ms/step - total_loss: 4.4349 - consiste
ncy_loss: 2.8347
Epoch 2/30
175/175 [==============================] - 6s 37ms/step - total_loss: 4.1382 - consisten
cy_loss: 2.1741
Epoch 3/30
175/175 [==============================] - 7s 38ms/step - total_loss: 3.2562 - consisten
cy_loss: 1.7422
Epoch 4/30
175/175 [==============================] - 6s 37ms/step - total_loss: 2.4335 - consisten
cy_loss: 1.2226
Epoch 5/30
175/175 [==============================] - 7s 40ms/step - total_loss: 2.1601 - consisten
cy_loss: 1.1146
Epoch 6/30
175/175 [==============================] - 7s 41ms/step - total_loss: 0.5781 - consisten
cy_loss: 0.2153
Epoch 7/30
175/175 [==============================] - 7s 37ms/step - total_loss: 0.2133 - consisten
cy_loss: 0.0543
Epoch 8/30
175/175 [==============================] - 7s 41ms/step - total_loss: 0.1653 - consisten
cy_loss: 0.0420
Epoch 9/30
175/175 [==============================] - 8s 43ms/step - total_loss: 0.1374 - consisten
cy_loss: 0.0403
Epoch 10/30
175/175 [==============================] - 7s 39ms/step - total_loss: 0.1496 - consisten
cy_loss: 0.0391
Epoch 11/30
175/175 [==============================] - 8s 44ms/step - total_loss: 0.1278 - consisten
cy_loss: 0.0354
Epoch 12/30
175/175 [==============================] - 8s 43ms/step - total_loss: 0.1101 - consisten
cy_loss: 0.0314
Epoch 13/30
175/175 [==============================] - 7s 39ms/step - total_loss: 0.1214 - consisten
cy_loss: 0.0293
Epoch 14/30
175/175 [==============================] - 7s 41ms/step - total_loss: 0.1087 - consisten
cy_loss: 0.0260
Epoch 15/30
175/175 [==============================] - 7s 43ms/step - total_loss: 0.1019 - consisten
cy_loss: 0.0255
Epoch 16/30
175/175 [==============================] - 6s 37ms/step - total_loss: 0.1108 - consisten
cy_loss: 0.0273
Epoch 17/30
175/175 [==============================] - 7s 40ms/step - total_loss: 0.1132 - consisten
cy_loss: 0.0246
Epoch 18/30
175/175 [==============================] - 7s 42ms/step - total_loss: 0.0986 - consisten
cy_loss: 0.0228
Epoch 19/30
175/175 [==============================] - 7s 38ms/step - total_loss: 0.1046 - consisten
cy_loss: 0.0222
Epoch 20/30
175/175 [==============================] - 8s 43ms/step - total_loss: 0.1000 - consisten
cy_loss: 0.0217
Epoch 21/30
175/175 [==============================] - 8s 46ms/step - total_loss: 0.0999 - consisten
cy_loss: 0.0213
Epoch 22/30
175/175 [==============================] - 7s 42ms/step - total_loss: 0.0841 - consisten
cy_loss: 0.0198
Epoch 23/30
175/175 [==============================] - 8s 45ms/step - total_loss: 0.0848 - consisten
cy_loss: 0.0182
Epoch 24/30
175/175 [==============================] - 8s 44ms/step - total_loss: 0.0881 - consisten
```

```
cy_loss: 0.0175
Epoch 25/30
175/175 [==============================] - 8s 43ms/step - total_loss: 0.0919 - consisten
cy_loss: 0.0170
Epoch 26/30
175/175 [==============================] - 8s 44ms/step - total_loss: 0.0878 - consisten
cy_loss: 0.0167
Epoch 27/30
175/175 [==============================] - 8s 45ms/step - total_loss: 0.0949 - consisten
cy_loss: 0.0162
Epoch 28/30
175/175 [==============================] - 7s 42ms/step - total_loss: 0.0956 - consisten
cy_loss: 0.0150
Epoch 29/30
175/175 [==============================] - 8s 45ms/step - total_loss: 0.0740 - consisten
cy_loss: 0.0139
Epoch 30/30
175/175 [==============================] - 8s 46ms/step - total_loss: 0.0744 - consisten
cy_loss: 0.0144
```

## 5. Check the model performance

The following few cells of code are not important. You can directly jump to step 6.

This next few lines of code is just to cross-check whether the trained model is able to process a given crop or not. If the model is able to process the crop, you will be able to see a shadow of the plankton like the shown in the second image plotted below.

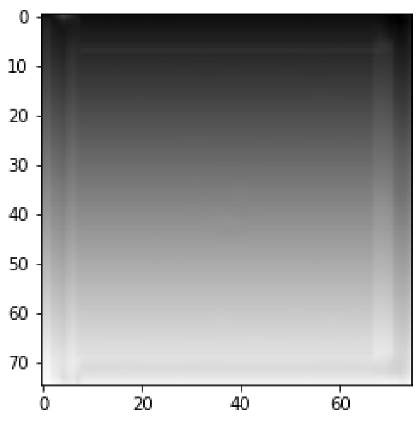
In [13]:
```
crop2 = np.expand_dims(crop, axis=0)
```

In [14]:
```
p, w = model.predict(crop2)
```

```
2022-10-18 14:30:32.555874: I tensorflow/core/grappler/optimizers/custom_graph_optimizer
_registry.cc:113] Plugin optimizer for device_type GPU is enabled.
1/1 [==============================] - 0s 316ms/step
```

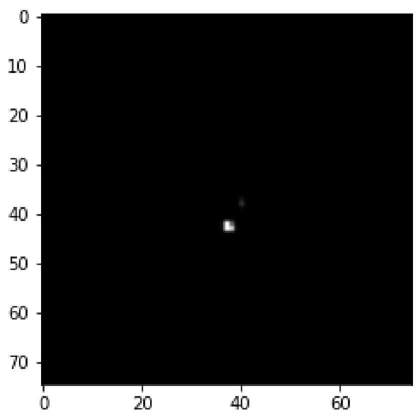
In [15]:
```
plt.imshow(p[0,:,:,0], cmap="gray")
```

Out[15]:
```
<matplotlib.image.AxesImage at 0x7fa5225b0a90>
```



In [16]:
```
plt.imshow(w[0,:,:,0], cmap="gray")
```

Out[16]:
```
<matplotlib.image.AxesImage at 0x7fa532a97d60>
```



## 6. Test the model of a video frame

### 6.1. Predict the plankton position

Here we test the model on a video frame. We use the same video frame we used for training the model. The model is able to detect the plankton position in the video frame.

Adjust the `starting_frame` and `ending_frame` parameters to select the range of video frames you want to test the model on. By default, the model is tested on the full video. This will take some time to process.

In [21]:
```
#May need to tune these to get optimal performance!
alpha = 1
cutoff = 0.1

starting_frame = 0
ending_frame = len(frames)

frames2 = np.expand_dims(frames[:,:,:,0], axis=-1)
detections = model.predict_and_detect(frames2[starting_frame:ending_frame, ::downsample,
```

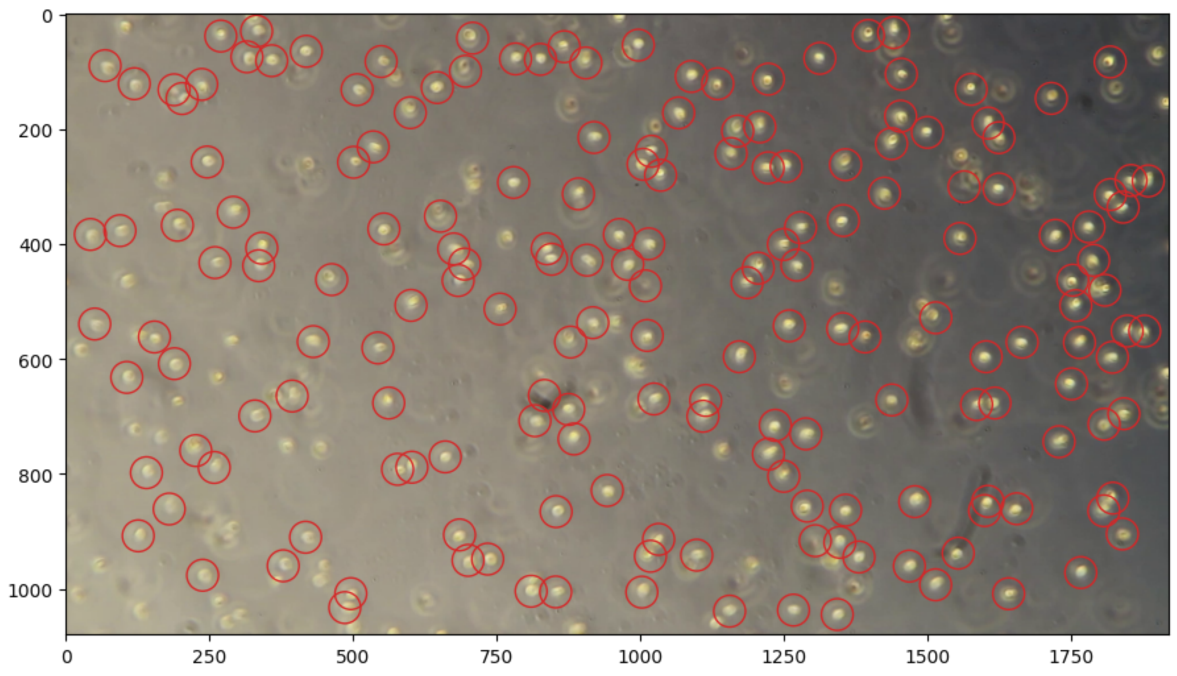
```
7/7 [==============================] - 35s 5s/step
```

### 6.2. Plot the results

Here we overlay the predicted plankton position on the video frame. The plankton position is plotted as a red circle. As you can see, the model is able to detect the plankton position in the video frame. The above process can be repeated for any microscopy video.

In [22]:
```
frame_no = 10
plt.figure(figsize=(frame.shape[0]/dpi, frame.shape[1]/dpi), dpi=dpi)
plt.imshow(cv2.cvtColor(frames[frame_no], cv2.COLOR_BGR2RGB))
plt.scatter(detections[frame_no][:,1] * downsample , detections[frame_no][:,0] * downsamp
```

Out[22]:
```
<matplotlib.collections.PathCollection at 0x7fa4c3e77c10>
```



## 6.3. Save the results

The following code will save the results as a video file. Please adjust the path by changing the `path` parameter accordingly.

In [24]:
```python
_dpi = 200
images = []
path = "../detection-videos/Detection-Plankton2.mp4"

for i in range(len(frames)):
    fig, ax = plt.subplots(
        figsize=(frame.shape[1]/ _dpi, frame.shape[0] / _dpi), dpi=_dpi, frameon=False
    )
    ax.set_axis_off()
    plt.subplots_adjust(left=0, right=1, bottom=0, top=1, hspace=0, wspace=0)
    plt.margins(0, 0)
    plt.imshow(cv2.cvtColor(frames[i], cv2.COLOR_BGR2RGB), origin="upper")
    plt.scatter(
        detections[i][:, 1] * downsample,
        detections[i][:, 0] * downsample,
        s=300,
        facecolors="none",
        edgecolors="tab:red",
    )
    fig.canvas.draw()
    arr = np.array(fig.canvas.renderer.buffer_rgba())
    images.append(arr)

    fig.clear()
    plt.close(fig)
    plt.show()

imageio.mimsave(path, images, fps=30)
```

```
IMAGEIO FFMPEG_WRITER WARNING: input image is not divisible by macro_block_size=16, resi
zing from (1920, 1080) to (1920, 1088) to ensure video compatibility with most codecs an
d players. To prevent resizing, make your input image divisible by the macro_block_size
or set the macro_block_size to 1 (risking incompatibility).
```