PeasOnDesk_Solutions

AAB

March 6, 2023

Image Processing

Peas On Desk Practical

10/02/2023, Ver. 1.2

0. Introduction

Image processing/computer vision has evolved a number of techniques that are quite distinct from classical statistical (multivariate) techniques and machine learning for dealing with the special nature of digital images. One set of very successful, fast techniques for computer vision is based on *binary* image processing which we begin to explore in this practical.

You are given an image `croppedpeasondesk.jpg` which is available off the VLE. Load this into *Python* using tools from PIL, and assign the image to variable `X`; display the image.

Note the image type (i.e. paletted or RGB (full colour)); use `np.shape` or other techniques from previous practicals to understand its shape and representation. It is important that you understand how the size and type of the image data – and its representation in *Python*, relate to the display of the image. If you are not sure what this means, ask a demonstrator.

The aim of this exercise is to count and find the locations of the peas using the simplest possible set of operations. From this, even though it will be imperfect, we will create a "database" of pea images.

Whilst this might seem a rather bizarre thing to do, the apparent simplicity of the exercise introduces you to several topics that are usually hidden, such as the statistical characterisation of image data. The ideas we meet here have extensions to object recognition and to methods that are used to statistically characterise images). **Task 3** also implicitly contains an exercise in image registration, although I don't describe it as such.

1. A simple approach to segmentation

Well, we could really complicate this, and train a deep neural network to recognise peas. But this would not give us insight into some of the value of understanding colour-spaces. Secondly, the big headache of pure data driven techniques is that we need to provide training data for such an approach. So, instead, we will try to use some heuristics to detect the locations of peas in the image. Though this will never be perfect, it can be used to bootstrap the acquisition of label data that can then be used to train a network.

We are going to first look at the intensity image, just to see what information it contains. We will use the tools of **PIL** and **scikit-image** to provide the basic functionality. If you have not yet done so, please install **scikit-image** using (if you are using `conda`), entered at the command prompt (PowerShell, `bash` or `zsh` prompt with the appropriate `conda` environment selected.

```
conda install scikit-image
```

or the graphical package installer if you are using it. The user documentation for **scikit-image** is to found here. There are a number of subpackages that are listed here.

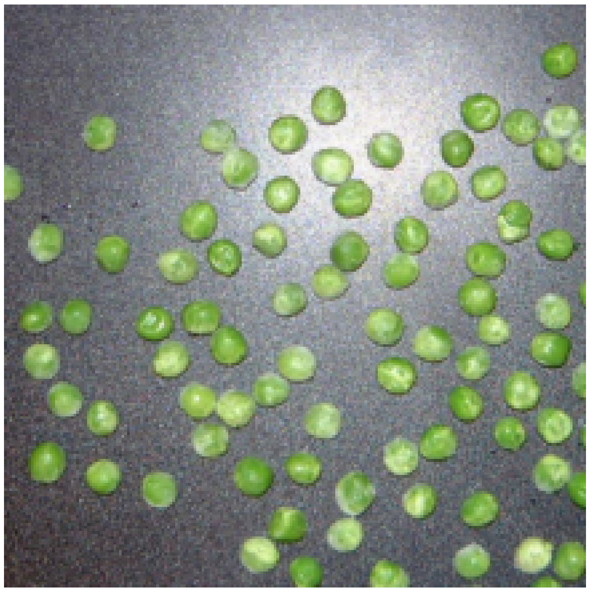
1.1 Getting Started

[1]:
```
from PIL import Image
from skimage import color as skco
import numpy as np
import matplotlib.pyplot as plt
```

[2]:
```
p_image = Image.open('IMGS/croppedpeasondesk.jpg')
plt.imshow(p_image)
plt.axis('off')
plt.title('Fig. 1. Peas On Desk')
```

[2]:
```
Text(0.5, 1.0, 'Fig. 1. Peas On Desk')
```

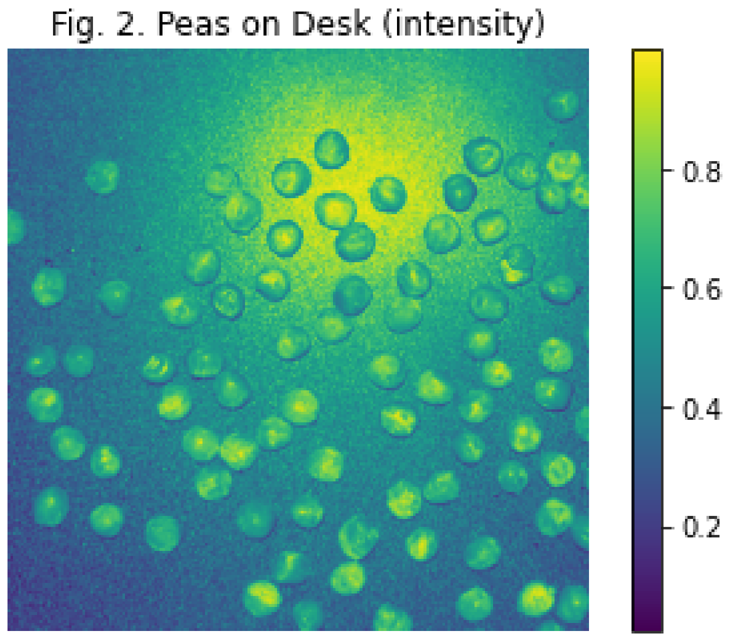
Fig. 1. Peas On Desk



Having seen that intensity-based segmentation works nicely for rice grains, let's have a look at the histogram of *achromatic intensity* first. This is a useful learning experience, showing a *counter example* of the idea shown in the lectures of using intensity-based segmentation.

[3]:
```
na = np.array(p_image)
gr_im = skco.rgb2gray(na)
plt.imshow(gr_im)
plt.axis('off')
plt.colorbar()
plt.title('Fig. 2. Peas on Desk (intensity)')
```

[3]:
```
Text(0.5, 1.0, 'Fig. 2. Peas on Desk (intensity)')
```



[4]:
```
np.shape(gr_im)
```

[4]:
```
(512, 512)
```

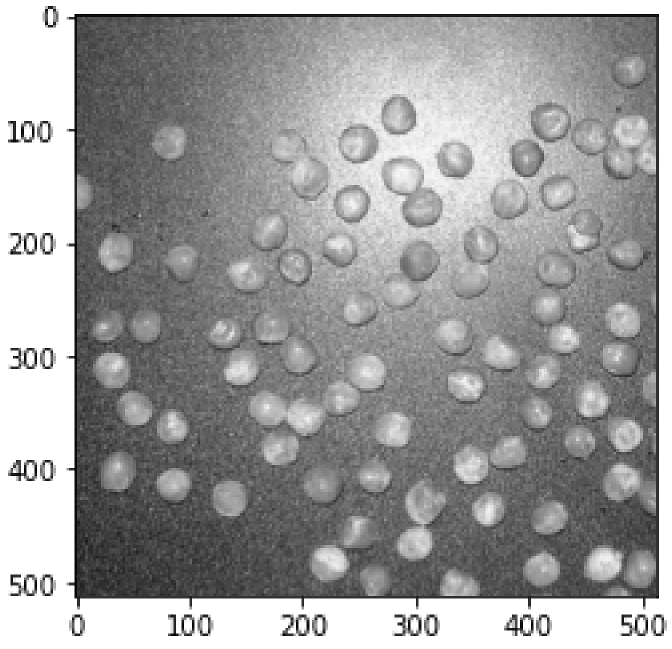
Exercise 1 Using your results from the previous practical, display the image of Fig. 2 with a greyscale colourmap. ■

Click here to see the solution to Ex. 1.

```
grey_map=plt.get_cmap('gray')
plt.imshow(gr_im, cmap=grey_map, interpolation=None)
```

[5]:
```
grey_map=plt.get_cmap('gray')
plt.imshow(gr_im, cmap=grey_map, interpolation=None)
```

[5]:
```
<matplotlib.image.AxesImage at 0x117a85d90>
```



You should recognise that you can still see the peas, even with the absence of colour. Despite this, intensity on its own will not be a great cue to use to separate peas from desk: although the peas *generally* have lower pixel values than the background desk (which is a textured black), there is a very bright reflection off a substantial portion of the desk, where the peas actually have almost overlapping intensity with the background.

Looking at and plotting the *histogram* of the pixel values will allow this to be more easily seen.

1.2 Constructing a histogram of intensities Although **matplotlib** has its own histogram routines, I recommend using the `numpy` histograms: you have more control over what you are doing, and you are less likely to get silly autoscaling mistakes, whereby two histograms being compared are constructed using different bins.

You can find the documentation for the histogram function here. But we'll walk you through this to begin with:

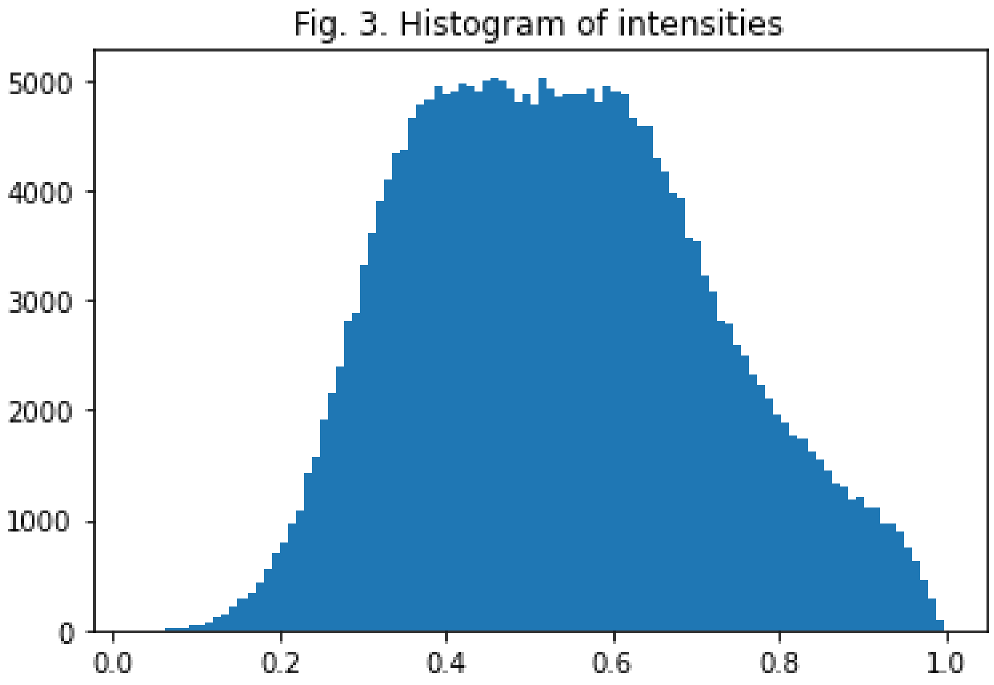
[6]:
```
# First, let's see what range of values we are dealing with
min_intensity = np.min(gr_im)
max_intensity = np.max(gr_im)
print('Min:', min_intensity, ', Max:', max_intensity)
```

```
Min: 0.023827058823529412 , Max: 0.9991666666666668
```

So, we have floating point intensity values. We can form a histogram by simply relying on autoscaling of histogram, and just specify the number of bins. Since we have so many pixels (how many?), we can use *lots* of bins. Let's use 100!

```
[7]: h, bin_edges = np.histogram(gr_im, bins=100)

     # by default, plt.bar is dumb: all bars have a width Of 0.8! Phht....
     barw = bin_edges[1]-bin_edges[0] # Should be the same for all bins.

     plt.bar(bin_edges[:-1], h, width=barw, align='edge') # ...set bar width␣
      ↪properly.
     plt.title('Fig. 3. Histogram of intensities')
```

```
[7]: Text(0.5, 1.0, 'Fig. 3. Histogram of intensities')
```



```
[8]: np.shape(h)
```

```
[8]: (100,)
```

If you try to compute the histogram using `plt.hist()` directly, you may get unpredictable results. I strongly advise not going this route unless you have fully understood the idiosyncracies of automatic scaling.

What do you think `bin_edges` contains? You should examine the shape of `bin_edges`, and its values to make sure you understand where they come from. One thing to be *very* careful with is that the upper and lower limits of the histogram are set automatically *unless* we explicitly set them. So, my preference would be to use this syntax:

```
bin_edges = np.linspace(0, 1.0, 101)
h, _ = np.histogram(gr_im, bins=bin_edges)
```

```
barw = bin_edges[1]-bin_edges[0] # the default bar width is silly
plt.bar(bin_edges[:-1], h, width=barw, align='edge')
plt.title('Fig. 3a. Histogram of approximate intensities')
```

You should compare the figure this produces with the first histogram; the differences are minimal, but can be important, depending on the context and data.

Interlude 1 The important thing to observe is that there is **no** obvious place to set a threshold for this histogram to separate the peas from the desk. But we need to repeat this exercise with the colour information in the image to see what we get.

Exercise 2 Using your experience from Practical 1, and in particular, `getchannel()`, extract the individual R, G, B channels from the peas on desk image; display each of the channels as an image, with an appropriate colourmap, and then compute the histogram of each of the channels.
■

Click here to see one solution to Ex. 2

```
R = p_image.getchannel('R')
G = p_image.getchannel('G')
B = p_image.getchannel('B')

# To display the images, we can do this:
plt.figure(figsize=(12,4))
plt.subplot(1,3,1)
plt.imshow(R, cmap='gray')
plt.title('R')

plt.subplot(1,3,2)
plt.imshow(G, cmap='gray')
plt.title('G')

plt.subplot(1,3,3)
plt.imshow(B, cmap='gray')
plt.title('B')

bin_edges = np.linspace(0, 256, 101)
hr, _ = np.histogram(R, bins=bin_edges)
hg, _ = np.histogram(G, bins=bin_edges)
hb, _ = np.histogram(B, bins=bin_edges)

barw = bin_edges[1]-bin_edges[0] # the default bar width is silly

plt.figure(figsize=(12,4))
plt.subplot(2,3,4)
plt.bar(bin_edges[:-1], hr, width=barw, align='edge', color='r')
plt.title('Histogram of red')
plt.subplot(2,3,5)
plt.bar(bin_edges[:-1], hg, width=barw, align='edge', color='g')
plt.title('Histogram of green')


plt.subplot(2,3,6)
plt.bar(bin_edges[:-1], hb, width=barw, align='edge', color='b')
plt.title('Histogram of blue')
```

Quiz Do you think it would be possible to set a threshold on the green channel of the Peas on Desk image, in order to obtain binary regions that correspond to peas? Try it! What do you observe, and what is the explanation?

 Click here if stuck on the quiz.

The answer is no: the best threshold that you could set (from the lectures, where might it be?) is going to leave you with either lots of missed peas, or a massive chunk of the region of the image containing the large specular reflection.

Exercise 3 Using your experience from **Practical 1**, and in particular, the normalised or trichromatic coefficients, calculate and display the spatial fields corresponding to *nR*, *nG* and *nB*.

Hint: You need to be **careful** with numeric representations in doing these calculations. But remember that `numpy` has routines specifically for converting from one numeric representation to another. ■

Click here for one solution to Ex. 3

```
# Start by converting everything to floating point
fR = np.asarray(R, dtype=float)
fG = np.asarray(G, dtype=float)
fB = np.asarray(B, dtype=float)

# Check the shape as you do these calculations
my_eps = 0.001 # Avoids divide by zero!
denominator = (fR+fG+fB+my_eps)

nR = fR/denominator
nG = fG/denominator
nB = fB/denominator

plt.figure(figsize=(12,4))
plt.subplot(1,3,1)
plt.title('nR')
plt.imshow(nR, cmap=grey_map)
plt.subplot(1,3,2)
plt.title('nG')
plt.imshow(nG, cmap=grey_map)
plt.subplot(1,3,3)
plt.imshow(nB, cmap=grey_map)
plt.title('nB')
```

Exercise 4 Calculate and display the histograms corresponding to *nR*, *nG* and *nB*. What do you notice about the histograms of these channels? Which ones can be used to separate the peas from the background? ■

Click here to see one solution to Ex. 4

```
# Assuming that Ex. 3 has been completed!
bin_edges = np.linspace(0, 1, 101) # Why? And can we do better?
hnR, _ = np.histogram(nR, bins=bin_edges)
hnG, _ = np.histogram(nG, bins=bin_edges)
hnB, _ = np.histogram(nB, bins=bin_edges)

barw = bin_edges[1]-bin_edges[0] # the default bar width is silly

plt.figure(figsize=(12,4))
plt.subplot(1,3,1)
plt.bar(bin_edges[:-1], hnR, width=barw, align='edge', color='r')
plt.title('Histogram of nR')


plt.subplot(1,3,2)
plt.bar(bin_edges[:-1], hnG, width=barw, align='edge', color='g')
plt.title('Histogram of nG')


plt.subplot(1,3,3)
plt.bar(bin_edges[:-1], hnB, width=barw, align='edge', color='b')
plt.title('Histogram of nB')
```

2. Creating a Binary Image

The next step in our simple pea analysis exercise is to create a binary image where each pixel is labelled according to whether it belongs to a pea, or the background.

2.1 Examining and Selecting a Threshold As we have discussed in the practicals, one of the most appropriate ways of doing this is to start by *looking* at the histogram. You can always automate later if you really need to: there is no substitute for examining the data!

Exercise 5 Using the material of the lectures, and by carefully examining the histograms you produced in Exercise 4, create a binary image that contains pixels of value 1 if the pixel belongs to a pea, and a value of 0 if the pixel belongs to the background. Call this image-type variable `P_Mask`.

It turns out that more than one channel contains useful information. Which channel do you think is best to use?

Click here to see one solution to Ex. 5.

Assuming that you have `nG` correctly computed as the normalised green channel, then

```
P_Mask = nG > 0.37
```

will do the trick! This will not be a perfect segmentation result, but it gets us started. To see the result, just (then) use: `plt.imshow(P_Mask)`

```
[9]: P_Mask = nG > 0.37
     np.shape(P_Mask)
```

```
---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
Cell In[9], line 1
----> 1 P_Mask = nG > 0.37
      2 np.shape(P_Mask)

NameError: name 'nG' is not defined
```

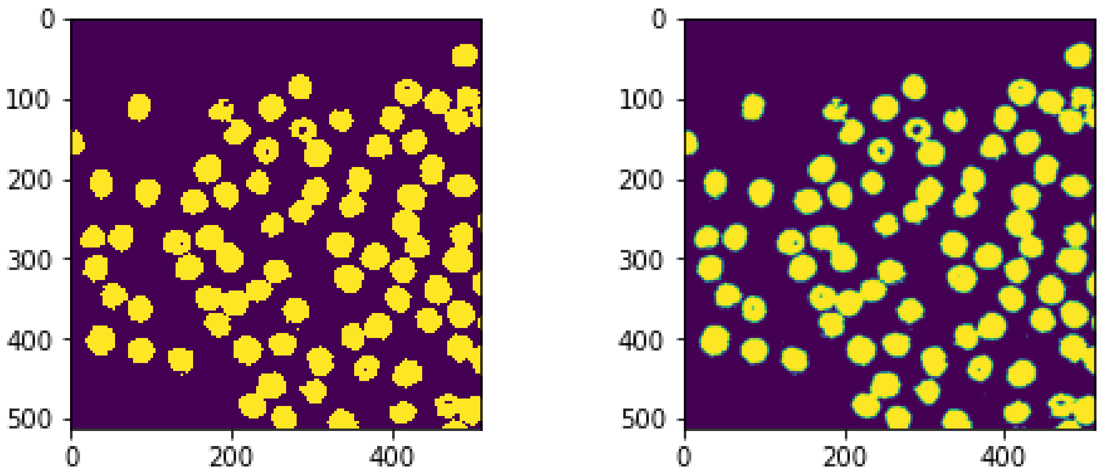
If you are stuck having not completed **Ex. 4**, please speak to a demonstrator. To help you progress whilst/if you are waiting for help on Ex. 3 or Ex. 4 there is a saved binary image stored which is loaded by executing the cell below:

```
[10]: # If stuck, you can load a pre-computed pea mask image by running this cell
      if 'P_Mask' not in globals().keys():
          P_Mask=np.load('IMGS/MaskFromNGreen.npy')
```

Interlude I have previously griped about the buggy nature of `imshow()`. Here is a demonstration of that bugginess.

```
[11]: %matplotlib inline

      # Demonstration of broken imshow() (at least on my machine)
      plt.figure(figsize=(8,3))
      plt.subplot(1,2,1)
      plt.imshow(255*P_Mask, interpolation='none')
      plt.subplot(1,2,2)
      plt.imshow(255*P_Mask, interpolation=None)
```

```
[11]: <matplotlib.image.AxesImage at 0x117d0d0d0>
```

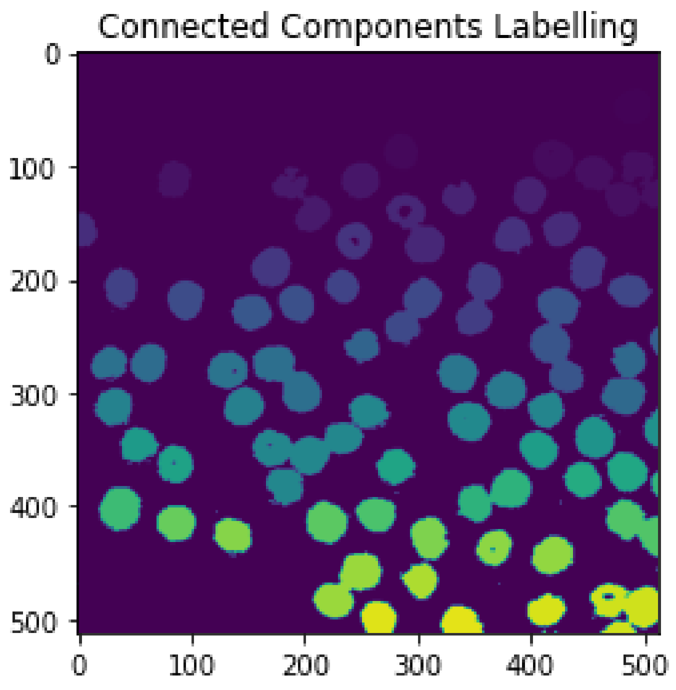


Explanation of the problem that I see on *my* installations: the image on the left has only two visible colours, blue and yellow; the one on the right has a green border around all the peas, if I use the default colourmap. This is because `imshow` is interpolating the image, despite trying to turn it off with the `None` keyword. It does turn it off if I use "none" as a string.... You may see something entirely different in your *Python* environment.

2.2 Labelling each pea Assuming we have a binary image mask assigned, we can apply *connected components labelling* to the task of labelling each region. We **will** have some erroneous regions, but the point is that we can use properties of each region (including moments etc) to reject regions that are unlikely to be single peas.

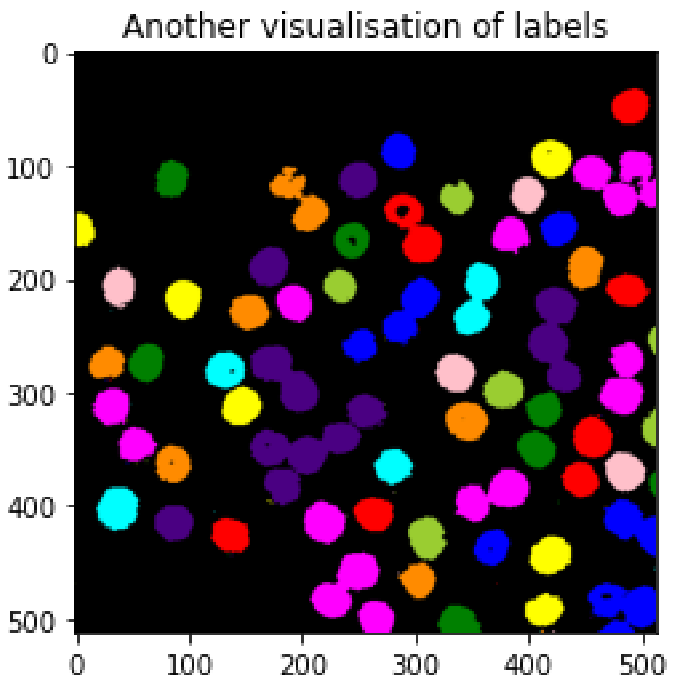
[12]:
```
from matplotlib import colors
from skimage.measure import label, regionprops

P_L = label(P_Mask)
plt.imshow(P_L)
plt.title('Connected Components Labelling')
```

[12]:
```
Text(0.5, 1.0, 'Connected Components Labelling')
```



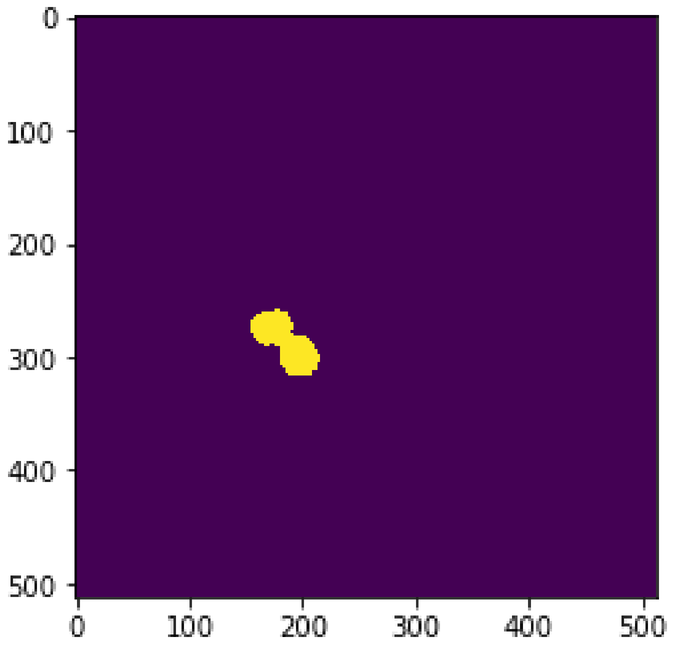
```
[13]: # Funkier option
      plt.imshow(skco.label2rgb(P_L, bg_label=0))
      plt.title('Another visualisation of labels')
```

```
[13]: Text(0.5, 1.0, 'Another visualisation of labels')
```



[14]:
```
plt.imshow(P_L==36, interpolation='none')
```

[14]:
```
<matplotlib.image.AxesImage at 0x1378df100>
```



2.2 Region Properties The **scikit-image** library contains a set of *modules* for analysing binary image regions. We will look at one big fat function called `regionprops()`.

[15]:
```
from skimage.measure import regionprops

Regions = regionprops(P_L)

# Examine the type of the return
print(type(Regions))
```

```
<class 'list'>
```

So, let's look at the length of the list, and also grab one item from this list and probe it:

[16]:
```
print(len(Regions))
```

```
99
```

And let's also look at **one** of the items from the list and see what it contains:

[17]:
```
print(type(Regions[0]))
```

```
<class 'skimage.measure._regionprops.RegionProperties'>
```

So, this is an object. Let's see what it contains:

[18]:
```
dir(Regions[0])
```

[18]:
```
['__class__',
 '__delattr__',
 '__dict__',
 '__dir__',
 '__doc__',
 '__eq__',
 '__format__',
 '__ge__',
 '__getattr__',
 '__getattribute__',
 '__getitem__',
 '__gt__',
 '__hash__',
 '__init__',
 '__init_subclass__',
 '__iter__',
 '__le__',
 '__lt__',
 '__module__',
 '__ne__',
 '__new__',
 '__reduce__',
 '__reduce_ex__',
 '__repr__',
 '__setattr__',
 '__sizeof__',
 '__str__',
 '__subclasshook__',
 '__weakref__',
 '_cache',
 '_cache_active',
 '_extra_properties',
 '_image_intensity_double',
 '_intensity_image',
 '_label_image',
 '_multichannel',
 '_ndim',
 '_slice',
 '_spatial_axes',
 'area',
 'area_bbox',
 'area_convex',
 'area_filled',
 'axis_major_length',
 'axis_minor_length',
 'bbox',
 'centroid',
 'centroid_local',
 'centroid_weighted',
 'centroid_weighted_local',
 'coords',
 'eccentricity',
 'equivalent_diameter_area',
 'euler_number',
 'extent',
 'feret_diameter_max',
 'image',
 'image_convex',
 'image_filled',
 'image_intensity',
 'inertia_tensor',
 'inertia_tensor_eigvals',
 'intensity_max',
 'intensity_mean',
 'intensity_min',
 'label',
 'moments',
 'moments_central',
 'moments_hu',
 'moments_normalized',
 'moments_weighted',
 'moments_weighted_central',
 'moments_weighted_hu',
 'moments_weighted_normalized',
 'orientation',
 'perimeter',
 'perimeter_crofton',
 'slice',
 'solidity']
```

Ooh! Lots of either methods (object-specific functions) or attributes; let's look further at the first of these intended for us to play with (those with `__xxxx__` are usually internal variables/attributes of the object):

```
[19]: print(dir(Regions[0].area))
```

```
['T', '__abs__', '__add__', '__and__', '__array__', '__array_interface__',
'__array_priority__', '__array_struct__', '__array_wrap__', '__bool__',
'__class__', '__class_getitem__', '__copy__', '__deepcopy__', '__delattr__',
'__dir__', '__divmod__', '__doc__', '__eq__', '__float__', '__floordiv__',
'__format__', '__ge__', '__getattribute__', '__getitem__', '__gt__', '__hash__',
'__index__', '__init__', '__init_subclass__', '__int__', '__invert__', '__le__',
'__lshift__', '__lt__', '__mod__', '__mul__', '__ne__', '__neg__', '__new__',
'__or__', '__pos__', '__pow__', '__radd__', '__rand__', '__rdivmod__',
'__reduce__', '__reduce_ex__', '__repr__', '__rfloordiv__', '__rlshift__',
'__rmod__', '__rmul__', '__ror__', '__round__', '__rpow__', '__rrshift__',
'__rshift__', '__rsub__', '__rtruediv__', '__rxor__', '__setattr__',
'__setstate__', '__sizeof__', '__str__', '__sub__', '__subclasshook__',
'__truediv__', '__xor__', 'all', 'any', 'argmax', 'argmin', 'argsort', 'astype',
'base', 'bit_count', 'byteswap', 'choose', 'clip', 'compress', 'conj',
'conjugate', 'copy', 'cumprod', 'cumsum', 'data', 'denominator', 'diagonal',
'dtype', 'dump', 'dumps', 'fill', 'flags', 'flat', 'flatten', 'getfield',
'imag', 'is_integer', 'item', 'itemset', 'itemsize', 'max', 'mean', 'min',
'nbytes', 'ndim', 'newbyteorder', 'nonzero', 'numerator', 'prod', 'ptp', 'put',
'ravel', 'real', 'repeat', 'reshape', 'resize', 'round', 'searchsorted',
'setfield', 'setflags', 'shape', 'size', 'sort', 'squeeze', 'std', 'strides',
'sum', 'swapaxes', 'take', 'tobytes', 'tofile', 'tolist', 'tostring', 'trace',
'transpose', 'var', 'view']
```

So this looks like a variable that is a number or array. Let's see what it has:

```
[20]: print(Regions[0].area)
```

```
803
```

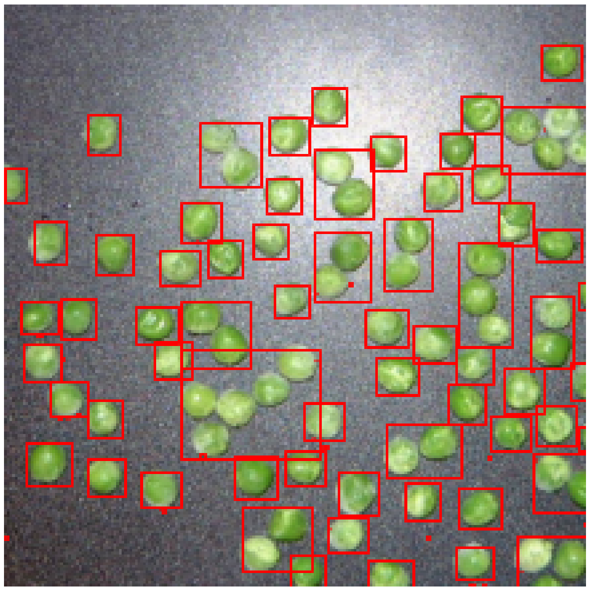
So, this is just a number. Looking at the documentation of **scikit-image** (named, rather stupidly, `skimage` as a module), we can see that this should tell us the number of pixels in the region. Let's look at another property of the same region:

```
[21]: print(Regions[0].bbox)
```

```
(33, 473, 64, 507)
```

So, these are (m, n) coordinates that correspond to an enclosing box in the coordinate space of the image: the box encloses the pixels of the particular region we are considering. Be careful, as – generally speaking – they might be in either an (x, y) coordinate system or an (m, n) coordinate system, in which case we may have to swap coordinates around when plotting or when trying to relate a position in a classical (x, y) coordinate system to a position in the image array!

```
[22]: # We get hold of a rectangle drawing routine...
from matplotlib.patches import Rectangle as drawrect

# Let's collect all the bounding box information to try
# to visualise it; below, we are using List Comprehension
BBs = [thisRegion.bbox for thisRegion in Regions]

# And let's try to plot it; to do this, we will need to
# make sure that the command used to do plotting of the
# lines representing the boxes that bound each
# region is consistent with the coordinate system of
# the image. In a concrete sense, we want to use the
# same AXIS for plotting both. Hence, our plotting needs
# to be a bit more sophisticated than we have done before...

# Create a figure and return an axis object
fig, ax = plt.subplots() # no argument to subplots means just 1

ax.imshow(p_image) # rather than plt.imhsow(), we explicitly
                   # draw it on the axis of the figure window
ax.axis('off')

for bb in BBs:
    r = drawrect((float(bb[1]),float(bb[0])),
                 bb[3]-bb[1],bb[2]-bb[0],
                 edgecolor='r', facecolor='none')
    ax.add_patch(r)
```



Well, that looks like it worked, but as we can see, there are some regions that actually contain multiple peas. You can see the problem if you have a look at the original connected components results, where there are as many as 5 peas that, when labelled, are treated as one cluster (region). We will learn how to deal with this in Chapter 4. But for now, our main goal is to identify the boxes corresponding to valid *single pea* regions. How can we do this?

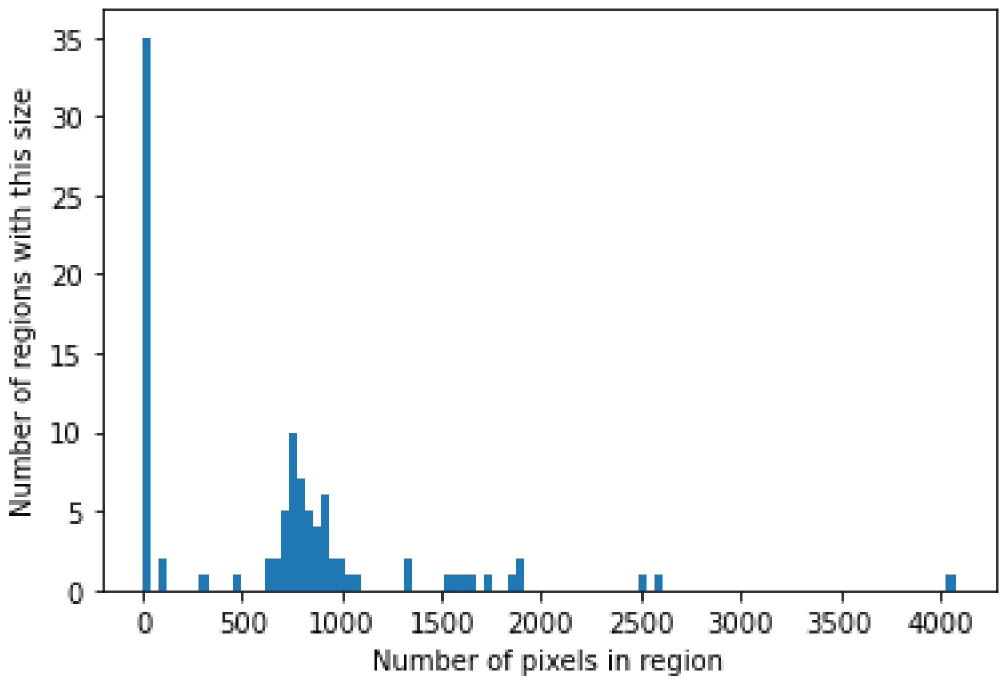
2.3 Filtering Regions All pattern recognition algorithms will, at some point, fail. So, it is important to be able to use simple heuristics to identify implausible results in the simplest way possible.

Looking at properties of binary regions is one of the things that we can do to easily improve results, rejecting regions that do not fit the criteria that we expect.

First, let's look at a simple heuristic based on the sizes of regions found by our thresholding and connected components labelling. We will start by collecting and forming a histogram of the region areas (i.e. number of pixels in each region) that have been detected.

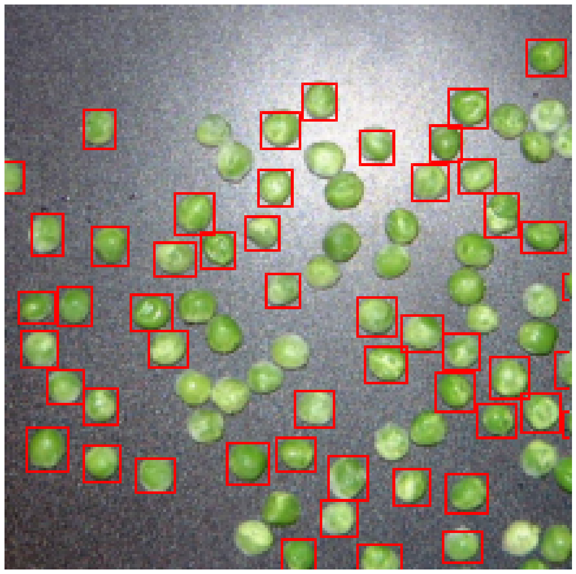
```
[23]: Areas = [thisRegion.area for thisRegion in Regions]

      # I am taking the lazy option here! Compare with
      # previous use of np.hist.
      HistogramOfPeaSize = plt.hist(Areas, 100)
      plt.xlabel('Number of pixels in region')
      plt.ylabel('Number of regions with this size')
```

```
[23]: Text(0, 0.5, 'Number of regions with this size')
```



Exercise 6 Interpret the reason for the appearance of the histogram, paying particular attention to the locations of peaks. Can you determine an appropriate criterion to apply to the regions to remove those that are unlikely to correspond to single whole peas?

Hint After filtering, your bounding boxes should look something like that shown below, and you will have somewhere between 50 and 65 regions:



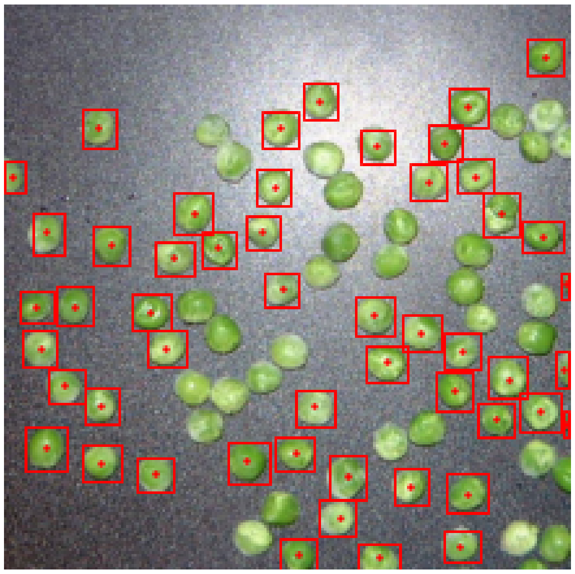
Hint Figure (above): Shows the bounding boxes **after** a simple region filtering.

Click here for one solution to Ex. 6.

```
# One Solution, using list comprehension
ValidRegions = [region for region in Regions if
                         (region.area>50 and region.area<1200)]
```

Exercise 7 Using the `centroid` attribute of the bounding boxes, plot the centroid as a small circle on each pea region using the **matplotlib** `scatter` method. Adjust the plotting using the size of the marker until you get the plot looking about right.

Hint Your result should look something like that shown in the figure below.



Click here for one solution to Ex 7.

```
Areas = [thisRegion.area for thisRegion in ValidRegions]
BBs = [thisRegion.bbox for thisRegion in ValidRegions]
Centroids = [thisRegion.centroid for
            thisRegion in ValidRegions]

fig, ax = plt.subplots()
ax.imshow(p_image)
ax.axis('off')

# The zip thing is not needed, you can instead use
# enumerate and grab the corresponding indexed
# value from each list, but this is more readable...
for (bb,area,centroid) in zip(BBs,Areas,Centroids):
    r = drawrect((float(bb[1]-1),float(bb[0]-1)),
        bb[3]-bb[1],bb[2]-bb[0],
        edgecolor='r', facecolor='none')

    ax.add_patch(r)
    plt.scatter(centroid[1]-1, centroid[0]-1, c='r', s=2)
```

3. Creating an Ensemble of Peas!

In order to make explicit the concept of what an “average” pea is, we will stack individual peas into an experimental space. However, before we do this, there are some things to take into consideration. These details do not alter the concept of averaging across experimental (or observation) space, but they are nevertheless important, because they involve practical issues. These issues will be present in whatever programming language you use, so this has not much to do with *Python*, specifically.

3.1 2D, 3D and 4D arrays We can view a 2D array as consisting of a set of 1D arrays which are stacked together, row by row, or column by column. In the same way, we can view a 3D array as a series of 2D arrays which are stacked one after the other into the third dimension.

However, in all cases (i.e. 1D->2D or 2D->3D) each d-dimensional array being constructed by stacking (d-1) dimensional arrays should be of the same size. What we have seen so far is that the bounding boxes around each pea are of different sizes.

So, how do we arrange these peas into a third dimension (experimental space in our case, or pea-space if you are so inclined). If we go back to the colour pea image, we'd actually be placing each three-dimensional patch into one "hyperslice" in the 4th dimension, which will be the experimental space.

3.2 A recipe for how to stack the peas into a 4D array NB: You may try to do this yourself, with no hints. But before you start, I suggest thinking about the problem carefully, sketching, as best you can, what is involved in this exercise.

- First, eliminate all regions that are not likely to be peas, because of their size. In order to construct the 4 dimensional array of peas (we have width, height, colour channels and then pea "instance"), we need to place all the pea regions into one array, preferably so that all their centres are aligned. Since the bounding boxes around the peas will be of different sizes, we need a bit of work to place all pea regions into a four-dimensional array by making sure each pea patch is of the same size.
- Why is this necessary? From a programming point of view, all rows of a digital image have the same number of columns, and all slices of a 3D matrix should be of the same number of elements. Thus, one solution is to take the largest practical patch size that contains all peas which can then be used as the "common" dimensions for all images in the pea array.
- Find the **largest bounding** box amongst the peas that you have detected. The aim here is to find a common size that can be used to generate the four dimensional pea array. This should not be too large compared to the size of most peas, so be careful in estimating this. Once you have a rough idea of what size the common bounding box size around each centroid should be, you would then extract, from the original image, the pixels within the bounding box, and stack them into a 4D array. **Convey this to a demonstrator**.
- In stacking the peas into a 4D array, we want to do this so that all of the pea centres are aligned in (*row*,*column*) space, or aligned with the centre of each "slice" of the 4D array as closely as possible. The most convenient way to do this and to first write a function (`def getsquareregion()`), that takes in the whole image, and extracts the region that you specify through passing in the centroid and width/length of the square box size as arguments. Making it a square is sensible, as there is no particular reason (in this data) that there should be any isotropy in the average pea. If the extracted region might fall partly outside the image, reject the region (return nothing, or `None`). Do this in **Exercise 8.**

Exercise 8 Create a *Python* function to extract a square region from an input image. The inputs should be the image, the centroid of the desired region and its width/height. You should return a `numpy array`. ■

Click here for one solution to Ex. 8

```
def getsquareregionfromimage(image, centroid, LW):

    # This should work, if it does not speak to a demonstrator
    image = np.asarray(p_image)

    # Get number of rows/columns and channels
    ImageSize = np.shape(image)

    NRows = ImageSize[0]
    NCols = ImageSize[1]
    if len(ImageSize)>2:
        NChannels = ImageSize[2]
    else:
        NChannels = 1

    HalfLW = float(LW)/2.0

    # Upper left coordinate
    UL = (round(centroid[0] - HalfLW), round(centroid[1] - HalfLW))
    LR = (round(centroid[0] + HalfLW), round(centroid[1] + HalfLW))

    # Avoid returning an array if the coordinates would take us outside
    # the image array

    if UL[0] < 0 or UL[1] < 0 or LR[0] > NRows or LR[1] > NCols:
        # region = np.asarray([], dtype=image.dtype)
        return None
    else:
        if NChannels==1:
            region = image[UL[0]:LR[0],UL[1]:LR[1]]
        else:
            # The "ellipses" argument in nparray slices a variable number of dims
            region = image[UL[0]:LR[0],UL[1]:LR[1],...]

    return region
```

Exercise 9 Create your 4-dimensional stack of single peas! Make sure you eliminate any empty regions before making the stack. Use `subplot()` (from `matplotlib.pyplot`) with appropriate argument to loop over and display each pea region. ■

Click here for some solutions to Ex. 9.

Solution 1 Definitely non-Pythonic, and rather inelegant.

```
counter = 0
```

```
for C in Centroids:
    arr=getsquareregionfromimage(p_image, C, 41)
    # We only try to stack the results if
    if not (arr is None):
        counter += 1
        if counter==1: # We place our first pea into the empty stack
            PeaStack=arr
        elif counter==2: # We already have one pea in, but we want to add another
            PeaStack = np.append(PeaStack[:,:,:,np.newaxis], arr[:,:,:,np.newaxis], axis=3)
        else: # PeaStack is already 4 dimensional; just append new 4D data
            PeaStack = np.append(PeaStack, arr[:,:,:,np.newaxis], axis=3)

np.shape(PeaStack)
```

Solution 2 Quite *Pythonic*

```
# Collect all regions
RegionsAsList = [getsquareregionfromimage(p_image, C, 41) for C in Centroids]
#Eliminate empty regions (which were too close to border)
PeaRegionsAsList = [Region for Region in RegionsAsList if not (Region is None)]
PeaStack = np.concatenate([arr[...,np.newaxis] for arr in PeaRegionsAsList], axis=3)

np.shape(PeaStack)
```

Solution 3 Pointlessly *Pythonic* ...

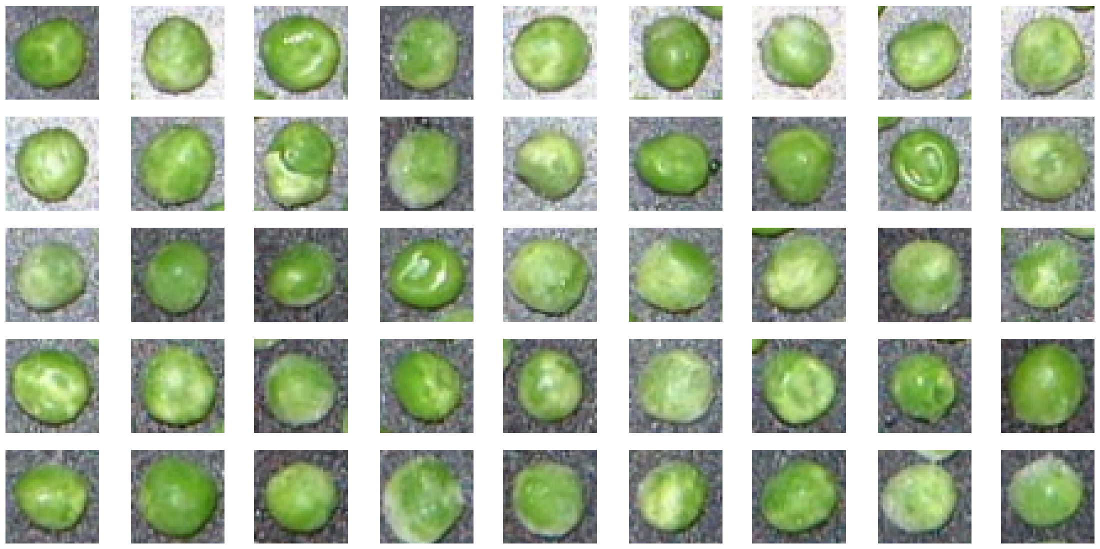
```
PeaRegionsAsList = [Region for Region
                    in [getsquareregionfromimage(p_image, C, 41) for C
                        in Centroids] if not (Region is None)]
PeaStack = np.concatenate([P[...,np.newaxis] for P in PeaRegionsAsList], axis=3)

np.shape(PeaStack)
```

And if you have run any of the possible `PeaStack` solutions, then following (hidden) code displays a montage of peas:

[24]:
```
# If stuck, you can load a pre-computed pea mask image by running this cell
if 'PeaStack' not in globals().keys():
    PeaStack=np.load('IMGS/PeaStack.npy')

DisplayCols=9
DisplayRows=5

fig = plt.figure()
```

```
_,axs = plt.subplots(DisplayRows,DisplayCols,figsize=(8,4))
slice_no = 0
for r in range(DisplayRows):
    for c in range(DisplayCols):
        axs[r,c].imshow(np.squeeze(np.asarray(PeaStack[...
 ↪,slice_no],dtype=int)))
        axs[r,c].axis('off')
        slice_no += 1
```

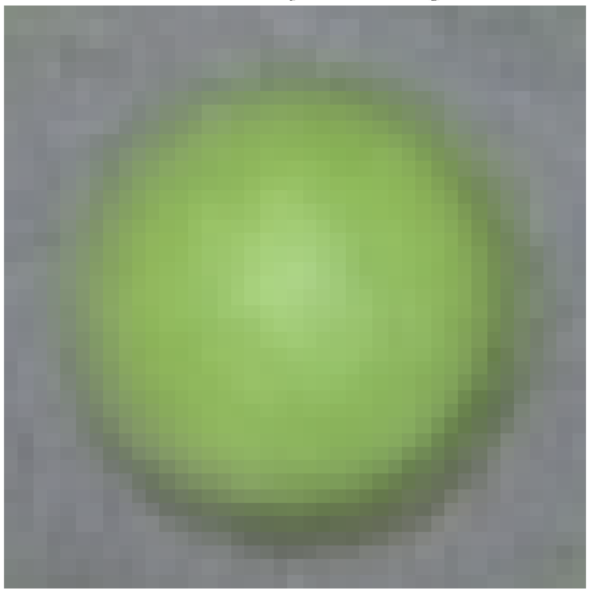
```
<Figure size 432x288 with 0 Axes>
```



Finally, we can compute the *average* pea; you can see this as being the **expected** pea as well, where the observation space is constructed over a single image, but averaging over what we might call pea *instances*:

```
[25]: mPea = np.mean(PeaStack, axis=3)
      plt.imshow(np.asarray(np.round(mPea), dtype=int))
      plt.axis('off')
      plt.title('Yum - into the pot with you....!')
```

```
[25]: Text(0.5, 1.0, 'Yum - into the pot with you…!')
```



4.0 Learning Outcomes

It is important not to get lost in, or worry about, the *Python* syntax of this exercise. From the perspective of learning outcomes, these are the points that you should be taking home.

1. (Major) In the same way that we discussed the setting of a threshold on intensities in the lectures, you can also set thresholds on channels of colour space to create a simple binary image. In fact, any property at all, calculated at each pixel, can be used for this purpose to label pixels according to whether they belong to one type of structure or another.
2. (Minor) It is nice to have histograms all packaged up for you into routines that you can apply to your own data. But beware of the bins that are used. Many histogram routines/libraries will set the bins according to the minimum and maximum values in the sample data that is input to compute the histograms. The number of bins can also make a difference. There usually should be a way to override this, and that can be a good idea, particularly if you want to compare the histograms of two different samples of data. If the bins are not in the same place for both samples, comparison can be difficult, and can lead to incorrect conclusions about how similar two distributions are.
3. (Minor) The spikiness of the histograms is not really noise, but more a consquence of the bin locations of the histogram when the data are quantised (in this case, to integer values).
4. (Major) An alternative colour space (in this case, normalised green and/or normalised blue) can yield separation of pixels that is more in agreement with a human's perception of colour difference than the "raw" RGB colour channels. This can be seen through the ability to find a threshold that separates, reasonably well, the pea pixels from those of the background. Other colour spaces might be similarly effective, but nR,nG,nB is easy to understand/calculate yourself.

5. (Major) Connected components labelling gives you the ability to address individual objects in a binary image.
6. (Minor) Plotting overlays on top of images – handy to check results of calculations.
7. (Major) You can use properties of binary regions to go back into the image and pull out examples (with full colour) of those regions. Simple region rejection criteria can be used to get objects that are more likely to correspond to the ones you are really interested in.
8. (Major) Creation of a stack of examples, representing “instances” of an object is a comon operation, and particularly so in data-driven approaches to image processing. Acquiring the stack requires some idea of how to align the reference examples. Here, we use centroids, but for other objects, we might use something else. For example, for human faces, the tip of the nose is a common reference point! We can study the stack to calculate the average object or structure (done), and also to quantify variations from the average appearance (beyond the scope of this lab, but for example, PCA/KL can be used to find eigenmodes of variation).
9. (Minor) Some 3D/4D array handling examples, and associated syntax.