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Mahotas is a computer vision and image processing library for Python.

It includes many algorithms implemented in C++ for speed while operating in numpy arrays and with a very clean Python interface.

Mahotas currently has over 100 functions for image processing and computer vision and it keeps growing. Some examples of mahotas functionality:

- watershed
- convex points calculations.
- hit & miss. thinning
- Zernike & Haralick, local binary patterns, and TAS features.
- morphological processing
- Speeded-Up Robust Features (SURF), a form of local features
- thresholding
- convolution.
- Sobel edge detection.

The release schedule is roughly one release every few months and each release brings new functionality and improved performance. The interface is very stable, though, and code written using a version of mahotas from years back will work just fine in the current version, except it will be faster (some interfaces are deprecated and will be removed after a few years, but in the meanwhile, you only get a warning).

Bug reports with test cases typically get fixed in 24 hours.

See also:

mahotas-imread is side project which includes code to read/write images to files
This is a simple example of loading a file (called test.jpeg) and calling \textit{watershed} using above threshold regions as a seed (we use Otsu to define threshold).

```python
import numpy as np
import mahotas
import pylab

img = mahotas.imread('test.jpeg')
T_otsu = mahotas.thresholding.otsu(img)
seeds, _ = mahotas.label(img > T_otsu)
labeled = mahotas.cwatershed(img.max() - img, seeds)

pylab.imshow(labeled)
```

Computing a distance transform is easy too:

```python
import pylab as p
import numpy as np
import mahotas

f = np.ones((256,256), bool)
f[200:,240:] = False
f[128:144,32:48] = False
# f is basically True with the exception of two islands: one in the lower-right
# corner, another, middle-left

dmap = mahotas.distance(f)
p.imshow(dmap)
p.show()
```
2.1 How To Install Mahotas

The simplest way to install mahotas is to use conda.

If you have conda installed, you can install mahotas using the following pair of commands:

```
conda config --add channels conda-forge
conda install mahotas
```

This relies on the conda-forge project, which builds packages for all major environments (Linux, Mac OS X, and Windows). If you do not want to permanently add the conda-forge channel to your conda configuration, you can also install just mahotas with:

```
conda install -c https://conda.anaconda.org/conda-forge mahotas
```

2.1.1 From source

You can get the released version using pip:

```
pip install mahotas
```

If you prefer, you can download the source from PyPI and run:

```
python setup.py install
```

You will need to have numpy and a C++ compiler.

Visual Studio

For compiling from source in Visual Studio, use:

```
python setup.py build_ext --c msvc
python setup.py install
```
Bleeding Edge (Development)

Development happens on github. You can get the development source there. Watch out that these versions are more likely to have problems.

2.1.2 Packaged Versions

On Windows

On Windows, Christoph Gohlke does an excellent job maintaining binary packages of mahotas (and several other packages).

WinPython

WinPython ships with mahotas as a standard package.

Python(x, y)

If you use Python(x, y), which is often a good solution, then you probably have it already as mahotas is a standard plugin.

Enthought Canopy

Since May 2015, Enthought’s Canopy Package Index includes mahotas.

FreeBSD

Mahotas is available for FreeBSD as graphics/mahotas.

MacPorts

For Macports, mahotas is available as py27-mahotas.

conda

Mahotas is not a part of standard conda packages, but on 64 bit Linux, you can get it from this repository with:

```
conda install -c https://conda.binstar.org/luispedro mahotas
```

Frugalware Linux

Mahotas is available as python-mahotas.
2.2 Finding Wally

This was originally an answer on stackoverflow. We can use it as a simple tutorial example.

The problem is to find Wally (who goes by Waldo in the US) in the following image:

```python
from pylab import imshow, show
import mahotas
import mahotas.demos
wally = mahotas.demos.load('Wally')
imshow(wally)
show()
```

From October 11 2013 onwards (version 1.0.4 or later), you can get the Wally image from mahotas as:

```python
import mahotas.demos
wally = mahotas.demos.load('Wally')
```

Can you see him?

```python
wfloat = wally.astype(float)
r, g, b = wfloat.transpose((2, 0, 1))
w = wfloat.mean(2)
```

Split into red, green, and blue channels. It’s better to use floating point arithmetic below, so we convert at the top.

```python
w is the white channel.
```
Build up a pattern of +1,+1,-1,-1 on the vertical axis. This is Wally’s shirt.

Convolve with red minus white. This will give a strong response where the shirt is.

Look for the maximum value and dilate it to make it visible. Now, we tone down the whole image, except the region of interest:

And we get the following:
2.3 Labeled Image Functions

Labeled images are integer images where the values correspond to different regions. I.e., region 1 is all of the pixels which have value 1, region two is the pixels with value 2, and so on. By convention, region 0 is the background and often handled differently.

2.3.1 Labeling Images

New in version 0.6.5.

The first step is obtaining a labeled function from a binary function:

```
import mahotas as mh
import numpy as np
from pylab import imshow, show

regions = np.zeros((8,8), bool)
regions[:3,:3] = 1
regions[6:,6:] = 1
labeled, nr_objects = mh.label(regions)
```
```python
imshow(labeled, interpolation='nearest')
show()
```

This results in an image with 3 values:

0. background, where the original image was 0
1. for the first region: (0:3, 0:3);
2. for the second region: (6:, 6:).

There is an extra argument to `label`: the structuring element, which defaults to a 3x3 cross (or, 4-neighbourhood). This defines what it means for two pixels to be in the same region. You can use 8-neighbourhoods by replacing it with a square:

```python
labeled, nr_objects = mh.label(regions, np.ones((3,3), bool))
```

New in version 0.7: `labeled_size` and `labeled_sum` were added in version 0.7

We can now collect a few statistics on the labeled regions. For example, how big are they?

```python
sizes = mh.labeled.labeled_size(labeled)
print 'Background size', sizes[0]
print 'Size of first region', sizes[1]
```

This size is measured simply as the number of pixels in each region. We can instead measure the total weight in each area:
```python
array = np.random.random_sample(regions.shape)
sums = mh.labeled_sum(array, labeled)
print 'Sum of first region', sums[1]
```

### 2.3.2 Filtering Regions

New in version 0.9.6: remove_regions & relabel were only added in version 0.9.6

Here is a slightly more complex example. This is in demos directory as nuclear.py. We are going to use this image, a fluorescent microscopy image from a nuclear segmentation benchmark

This image is available as mahotas.demos.nuclear_image()

```python
import mahotas as mh
import mahotas.demos
import numpy as np
from pylab import imshow, show

f = mh.demos.nuclear_image()
f = f[:,:,0]
imshow(f)
show()
```

First we perform a bit of Gaussian filtering and thresholding:


```python
f = mh.gaussian_filter(f, 4)
f = (f > f.mean())
```

(Without the Gaussian filter, the resulting thresholded image has very noisy edges. You can get the image in the demos/ directory and try it out.)

```python
f = mh.gaussian_filter(f, 4)
f = (f > f.mean())
imshow(f)
show()
```

Labeling gets us all of the nuclei:

```python
labeled, n_nucleus = mh.label(f)
print('Found {} nuclei.'.format(n_nucleus))
```

```python
labeled, n_nucleus = mh.label(f)
print('Found {} nuclei.'.format(n_nucleus))
imshow(labeled)
show()
```
42 nuclei were found. None were missed, but, unfortunately, we also get some aggregates. In this case, we are going to assume that we wanted to perform some measurements on the real nuclei, but are willing to filter out anything that is not a complete nucleus or that is a lump on nuclei. So we measure sizes and filter:

```python
sizes = mh.labeled.labeled_size(labeled)
too_big = np.where(sizes > 10000)
labeled = mh.labeled.remove_regions(labeled, too_big)
```

```python
sizes = mh.labeled.labeled_size(labeled)
too_big = np.where(sizes > 10000)
labeled = mh.labeled.remove_regions(labeled, too_big)
imshow(labeled)
show()
```
We can also remove the region touching the border:

```python
labeled = mh.labeled.remove_bordering(labeled)
```

```python
labeled = mh.labeled.remove_bordering(labeled)
imshow(labeled)
show()
```
This array, labeled now has values in the range 0 to \( n_{\text{nucleus}} \), but with some values missing (e.g., if region 7 was one of the ones touching the border, then 7 is not used in the labeling). We can relabel to get a cleaner version:

```python
relabeled, n_left = mh.labeled.relabel(labeled)
print('After filtering and relabeling, there are {} nuclei left.'.format(n_left))
```

Now, we have 24 nuclei and relabeled goes from 0 (background) to 24.

```python
relabeled, n_left = mh.labeled.relabel(labeled)
print('After filtering and relabeling, there are {} nuclei left.'.format(n_left))
imshow(relabeled)
show()
```
In mahotas after version 1.4, we can even make many of the same operations with a single call to `mh.labeled.filter_labeled`:

```python
relabeled, n_left = mh.labeled.filter_labeled(labeled, remove_bordering=True, max_size=1000)
```

### 2.3.3 Borders

A border pixel is one where there is more than one region in its neighbourhood (one of those regions can be the background).

You can retrieve border pixels with either the `borders()` function, which gets all the borders or the `border()` (note the singular) which gets only the border between a single pair of regions. As usual, what neighbour means is defined by a structuring element, defaulting to a 3x3 cross.

### 2.3.4 API Documentation

The `mahotas.labeled` submodule contains the functions mentioned above. `label()` is also available as `mahotas.label`.

`mahotas.labeled.bbox (f, as_slice=False)`

Bounding boxes of all objects in a labeled array.

After:
**bboxes = mh.labeled.bbox(f)**

*bboxes[34]* will contain the bounding box of *(f == 34)*.

**f**: integer ndarray 
**as_slice**: boolean, optional

Whether to return slice objects instead of integer coordinates (default: False).

**Returns**: bboxes : ndarray

**See also**:

mh.bbox the binary version of this function

**mahotas.labeled.borders**(labeled, Bc={3x3 cross}, out={np.zeros(labeled.shape, bool)}

Compute border pixels

A pixel is on a border if it has value *i* and a pixel in its neighbourhood (defined by *Bc*) has value *j*, with *i* ≠ *j*.

**Parameters**

- **labeled**: ndarray of integer type
  - input labeled array

- **Bc**: structure element, optional

- **out**: ndarray of same shape as labeled, dtype=bool, optional
  - where to store the output. If None, a new array is allocated

- **mode**: {'reflect', 'nearest', 'wrap', 'mirror', 'constant' [default], 'ignore'}
  - How to handle borders

**Returns**

- **border_img**: boolean ndarray
  - Pixels are True exactly where there is a border in labeled

**mahotas.labeled.border**(labeled, i, j, Bc={3x3 cross}, out={np.zeros(labeled.shape, bool)}, always_return=True)

Compute the border region between *i* and *j* regions.

A pixel is on the border if it has value *i* (or *j*) and a pixel in its neighbourhood (defined by *Bc*) has value *j* (or *i*).

**Parameters**

- **labeled**: ndarray of integer type
  - input labeled array

- **i**: integer

- **j**: integer

- **Bc**: structure element, optional

- **out**: ndarray of same shape as labeled, dtype=bool, optional
  - where to store the output. If None, a new array is allocated

- **always_return**: bool, optional
  - if false, then, in the case where there is no pixel on the border, returns None. Otherwise (the default), it always returns an array even if it is empty.

**Returns**

- **border_img**: boolean ndarray
  - Pixels are True exactly where there is a border between *i* and *j* in labeled
mahotas.labeled.bwperim($bw, n=4$)
Find the perimeter of objects in binary images.

A pixel is part of an object perimeter if its value is one and there is at least one zero-valued pixel in its neighborhood.

By default the neighborhood of a pixel is 4 nearest pixels, but if $n$ is set to 8 the 8 nearest pixels will be considered.

**Parameters**
- **bw**: ndarray
  A black-and-white image (any other image will be converted to black & white)
- **n**: int, optional
  Connectivity. Must be 4 or 8 (default: 4)
- **mode**: {'reflect', 'nearest', 'wrap', 'mirror', 'constant'} [default], 'ignore'
  How to handle borders

**Returns**
- **perim**: ndarray
  A boolean image

**See also:**
- borders function This is a more generic function

mahotas.labeled.filter_labeled($labeled$, remove_bordering=False, min_size=None, max_size=None)
Filter labeled regions based on a series of conditions
New in version 1.4.1.

**Parameters**
- **labeled**: labeled array
- **remove_bordering**: bool, optional
  whether to remove regions that touch the border
- **min_size**: int, optional
  Minimum size (in pixels) of objects to keep (default is no minimum)
- **max_size**: int, optional
  Maximum size (in pixels) of objects to keep (default is no maximum)

**Returns**
- **filtered**: labeled array
  number of new labels

mahotas.labeled.label($array$, Bc={3x3 cross}, output={new array})
Label the array, which is interpreted as a binary array

This is also called *connected component labeled*, where the connectivity is defined by the structuring element $Bc$.

**See:** http://en.wikipedia.org/wiki/Connected-component_labeling

**Parameters**
- **array**: ndarray
  This will be interpreted as binary array
- **Bc**: ndarray, optional
This is the structuring element to use

```python
out : ndarray, optional
    Output array. Must be a C-array, of type np.int32
```

**Returns**

* **labeled** : ndarray
  Labeled result

* **nr_objects** : int
  Number of objects

```python
mahotas.labeled.labeled_sum(array, labeled, minlength=None)
```

Labeled sum. sum will be an array of size `labeled.max() + 1`, where `sum[i]` is equal to `np.sum(array[labeled == i])`.

**Parameters**

* **array** : ndarray of any type

* **labeled** : int ndarray
  Label map. This is the same type as returned from `mahotas.label()`

* **minlength** : int, optional
  Minimum size of return array. If labeled has fewer than `minlength` regions, 0s are added to the result. (optional)

**Returns**

* **sums** : 1-d ndarray of array.dtype

```python
mahotas.labeled.labeled_max(array, labeled, minlength=None)
```

Labeled minimum. `mins` will be an array of size `labeled.max() + 1`, where `mins[i]` is equal to `np.min(array[labeled == i])`.

**Parameters**

* **array** : ndarray of any type

* **labeled** : int ndarray
  Label map. This is the same type as returned from `mahotas.label()`

**Returns**

* **mins** : 1-d ndarray of array.dtype

```python
mahotas.labeled.labeled_size(labeled)
```

Equivalent to:

```python
for i in range(...):
    sizes[i] = np.sum(labeled == i)
```

but, naturally, much faster.

**Parameters**

* **labeled** : int ndarray

**Returns**

* **sizes** : 1-d ndarray of int

See also:

* `mahotas.fullhistogram` almost same function by another name (the only difference

```python
mahotas.labeled.relabel(labeled, inplace=False)
```

Relabeling ensures that `relabel` is a labeled image such that every label from 1 to `relabel.max()` is used (0 is reserved for the background and is passed through).

**Example:**

2.3. Labeled Image Functions 19
labeled, n = label(some_binary_map)
for region in xrange(n):
    if not good_region(labeled, region + 1):
        labeled[labeled == (region + 1)] = 0
relabeled(labeled, inplace=True)

**Parameters** relabeled : ndarray of int
A labeled array

inplace : boolean, optional
Whether to perform relabeling inplace, erasing the values in labeled (default: False)

**Returns** relabeled: ndarray

nr_objs : int
Number of objects

**See also:**

label function

mahotas.labeled.is_same_labeling(labeled0, labeled1)
Checks whether labeled0 and labeled1 represent the same labeling (i.e., whether they are the same except for a possible change of label values).

Note that the background (value 0) is treated differently. Namely

is_same_labeling(a, b) implies np.all((a == 0) == (b == 0))

**Parameters** labeled0 : ndarray of int
A labeled array

labeled1 : ndarray of int
A labeled array

**Returns** same : bool
True if the labelings passed as argument are equivalent

**See also:**

label function

relabel function

mahotas.labeled.perimeter(bwimage, n=4, mode=\"constant\")
Calculate total perimeter of all objects in binary image.

**Parameters** bwimage : array
binary image

n : int, optional
passed to bwperim as is

mode : str, optional
passed to bwperim as is
Returns \( p \): float

total perimeter of all objects in binary image

See also:

bwperim function Finds the perimeter region

References

[R1]
mahotas.labeled.remove_bordering(labeled, rsize=1, out=[np.empty_like(im)])

Remove objects that are touching the border.

Pass labeled as out to achieve in-place operation.

Parameters labeled: ndarray

Labeled array

rsize : int or tuple, optional

Minimum distance to the border (in Manhatan distance) to allow an object to survive.
May be int or tuple with len == labeled.ndim.

out : ndarray, optional

If im is passed as out, then it operates inline.

Returns slabeled: ndarray

Subset of labeled

mahotas.labeled.remove_regions(labeled, regions, inplace=False)

removed = remove_regions(labeled, regions, inplace=False):

Removes the regions in regions. If an elementwise in operator existed, this would be equivalent to the following:

\[
labeled[ \text{labeled element-wise-in regions } ] = 0
\]

This function does not relabel its arguments. You can use the relabel function for that:

removed = relabel(remove_regions(labeled, regions))

Or, saving one image allocation:

removed = relabel(remove_regions(labeled, regions), inplace=True)

This is the same, but reuses the memory in the relabeling operation.

Parameters relabeled: ndarray of int

A labeled array

regions : sequence of int

These regions will be removed

inplace : boolean, optional

Whether to perform removal inplace, erasing the values in labeled (default: False)

Returns removed: ndarray
See also:

relabel function After removing unnecessary regions, it is often a good idea to relabel your label image.

mahotas.labeled.remove_regions_where(labeled, conditions, inplace=False)
Remove regions based on a boolean array
A region is removed if conditions[region-id] evaluates true.
This function does not relabel its arguments. You can use the relabel function for that:

    removed = relabel(remove_regions_where(labeled, conditions))

Or, saving one image allocation:

    removed = relabel(remove_regions(labeled, conditions), inplace=True)

This is the same, but reuses the memory in the relabeling operation.
See also:

remove_regions function Variation of this function which uses integer indexing

2.4 Thresholding

The example in this section is present in the source under mahotas/demos/thresholding.py.

We start with an image, a grey-scale image:

import mahotas.demos
photo = mahotas.demos.load('luispedro')
photo = photo.astype(np.uint8)

Before Oct 2013, the mahotas.demos.load function did not exist and you needed to specify the path explicitly:

luispedro_image = '../../mahotas/demos/data/luispedro.jpg'
photo = mahotas.imread(luispedro_image, as_grey=True)

The reason we convert to np.uint8 is because as_grey returns floating point images (there are good reasons for this and good reasons against it, since it’s easier to truncate than to go back, it returns np.uint8).

import mahotas
import mahotas.demos
import numpy as np
from pylab import imshow, gray, show
from os import path

photo = mahotas.demos.load('luispedro', as_grey=True)
photo = photo.astype(np.uint8)

gray()
imshow(photo)
show()
Thresholding functions have a trivial interface: they take an image and return a value. One of the most well-known thresholding methods is Otsu’s method:

```python
T_otsu = mahotas.otsu(photo)
print(T_otsu)
imshow(photo > T_otsu)
show()
```

prints 115.

```python
import mahotas
import mahotas.demos
import numpy as np
from pylab import imshow, gray, show
from os import path

photo = mahotas.demos.load('luispedro', as_grey=True)
photo = photo.astype(np.uint8)

T_otsu = mahotas.otsu(photo)
print(T_otsu)
gray()
imshow(photo > T_otsu)
show()
```
An alternative is the Riddler-Calvard method:

```python
T_rc = mahotas.rc(photo)
print(T_rc)
imshow(photo > T_rc)
show()
```

In this image, it prints almost the same as Otsu: 115.68. The thresholded image is exactly the same:

```python
import mahotas
import mahotas.demos
import numpy as np
from pylab import imshow, gray, show
from os import path

photo = mahotas.demos.load('luispedro', as_grey=True)
photo = photo.astype(np.uint8)
T_rc = mahotas.rc(photo)
print(T_rc)
gray()
imshow(photo > T_rc)
show()
```
See also the labeled documentation which can be very helpful in combination with thresholding.

### 2.4.1 API Documentation

The *mahotas.thresholding* module contains the thresholding functions, but they are also available in the main *mahotas* namespace.

**Thresholding Module**

Thresholding functions.

These functions return the numeric threshold. In order to obtain a thresholded image, you can do the following:

```python
T_otsu = mh.otsu(image)
binarized_image = (image > T_otsu)
```

Functions which have an `ignore_zeros` parameter will only consider non-zero pixels when computing the thresholding.

- `otsu()`: Otsu method
- `rc()`: Riddler-Calvard’s method
- `bernsen`: Bernsen thresholding
- `gbernsen`: Generalized Bernsen thresholding
mahotas.thresholding.**otsu**(*img*, *ignore_zeros=False*)
Calculate a threshold according to the Otsu method.

Example:

```python
import mahotas as mh
import mahotas.demos

im = mahotas.demos.nuclear_image()
# im is stored as RGB, let's convert to single 2D format:
im = im.max(2)

# Now, we compute Otsu:
t = mh.otsu(im)

# finally, we use the value to form a binary image:
bin = (im > t)
```


**Parameters**

- **img**: an image as a numpy array.
  - This should be of an unsigned integer type.

- **ignore_zeros**: Boolean
  - Whether to ignore zero-valued pixels (default: False)

**Returns**

- **T**: integer
  - the threshold

mahotas.thresholding.**rc**(*img*, *ignore_zeros=False*)
Calculate a threshold according to the Riddler-Calvard method.

Example:

```python
import mahotas as mh
import mahotas.demos

im = mahotas.demos.nuclear_image()
# im is stored as RGB, let's convert to single 2D format:
im = im.max(2)

# Now, we compute a threshold:
t = mh.rc(im)

# finally, we use the value to form a binary image:
bin = (im > t)
```

**Parameters**

- **img**: ndarray
  - Image of any type

- **ignore_zeros**: boolean, optional
  - Whether to ignore zero valued pixels (default: False)

**Returns**

- **T**: float
  - threshold

mahotas.thresholding.**soft_threshold**(*f*, *tval*)
Soft threshold function:
Parameters $f$: ndarray

tval: scalar

Returns thresholded: ndarray

```python
mahotas.thresholding.bernsen(f, radius, contrast_threshold, gthresh={128})
```

Bernsen local thresholding

Parameters $f$: ndarray

- input image
- radius: integer
  - radius of circle (to consider “local”)
- contrast_threshold: integer
  - contrast threshold
- gthresh: numeric, optional
  - global threshold to fall back in low contrast regions

Returns thresholded: binary ndarray

See also:

- gbernsen function Generalised Bernsen thresholding

```python
mahotas.thresholding.gbernsen(f, se, contrast_threshold, gthresh)
```

Generalised Bernsen local thresholding

Parameters $f$: ndarray

- input image
- se: boolean ndarray
  - structuring element to use for “locality”
- contrast_threshold: integer
  - contrast threshold
- gthresh: numeric, optional
  - global threshold to fall back in low contrast regions

Returns thresholded: binary ndarray
2.5 Wavelet Transforms

New in version 0.9.1: Wavelet functions were only added in version 0.9.1

We are going to use wavelets to transform an image so that most of its values are 0 (and otherwise small), but most of the signal is preserved.

The code for this tutorial is available from the source distribution as mahotas/demos/wavelet_compression.py.

We start by importing and loading our input image

```python
import numpy as np
import mahotas
import mahotas.demos

from mahotas.thresholding import soft_threshold
from matplotlib import pyplot as plt
from os import path

f = mahotas.demos.load('luispedro', as_grey=True)
f = f[:256,:256]
plt.gray()
# Show the data:
print('Fraction of zeros in original image: {0}'.format(np.mean(f==0)))
plt.imshow(f)
plt.show()
```
There are no zeros in the original image. We now try a baseline compression method: save every other pixel and only high-order bits.

```python
direct = f[::2,::2].copy()
direct /= 8
direct = direct.astype(np.uint8)
print("Fraction of zeros in original image (after division by 8): \{0\}".format(np.mean(direct==0)))
plt.imshow(direct)
plt.show()
```

2.5. Wavelet Transforms
There are only a few zeros, though. We have, however, thrown away 75% of the values. Can we get a better image, using the same number of values, though?

We will transform the image using a Daubechies wavelet (D8) and then discard the high-order bits.

```python
# Transform using D8 Wavelet to obtain transformed image t:
t = mahotas.daubechies(f,'D8')

# Discard low-order bits:
t /= 8

print("Fraction of zeros in transform (after division by 8): {0}".format(np.mean(t==0)))
plt.imshow(t)
plt.show()
```
This has 60% zeros! What does the reconstructed image look like?

```python
# Let us look at what this looks like
r = mahotas.idaubechies(t, 'D8')
plt.imshow(r)
plt.show()
```
This is a pretty good reduction without much quality loss. We can go further and discard small values in the transformed space. Also, let’s make the remaining values even smaller in magnitude.

Now, this will be 77% of zeros, with the remaining being small values. This image would compress very well as a lossless image and we could reconstruct the full image after transmission. The quality is certainly higher than just keeping every fourth pixel and low-order bits.

```python
tt = soft_threshold(t, 12)
print("Fraction of zeros in transform (after division by 8 & soft thresholding): {0}".format(np.mean(tt==0)))
# Let us look again at what we have:
rt = mahotas.idaubechies(tt, 'D8')
plt.imshow(rt)
```
2.5.1 What About the Borders?

In this example, we can see some artifacts at the border. We can use `wavelet_center` and `wavelet_decenter` to handle borders to correctly:

```python
fc = mahotas.wavelet_center(f)
t = mahotas.daubechies(fc, 'D8')
r = mahotas.idaubechies(fc, 'D8')
rd = mahotas.wavelet_decenter(r, fc.shape)
```

Now, `rd` is equal (except for rounding) to `fc` without any border effects.

2.5.2 API Documentation

A package for computer vision in Python.

**Main Features**

- **features**  Compute global and local features (several submodules, include SURF and Haralick features)
- **convolve** Convolution and wavelets
- **morph** Morphological features. Most are available at the mahotas level, include `erode()`, `dilate()`...
**watershed**  Seeded watershed implementation

**imread/imsave**  read/write image

Documentation: https://mahotas.readthedocs.io/

Citation:


```
mahotas.haar(f, preserve_energy=True, inline=False)
```

Haar transform

**Parameters**  

`f` : 2-D ndarray

Input image

`preserve_energy` : bool, optional

Whether to normalise the result so that energy is preserved (the default).

`inline` : bool, optional

Whether to write the results to the input image. By default, a new image is returned. Integer images are always converted to floating point and copied.

See also:

```
inhaar function Reverse Haar transform
```

```
mahotas.inhaar(f, preserve_energy=True, inline=False)
```

Reverse Haar transform

`inhaar(haar(f))` is more or less equal to `f` (equal, except for possible rounding issues).

**Parameters**  

`f` : 2-D ndarray

Input image. If it is an integer image, it is converted to floating point (double).

`preserve_energy` : bool, optional

Whether to normalise the result so that energy is preserved (the default).

`inline` : bool, optional

Whether to write the results to the input image. By default, a new image is returned. Integer images are always converted to floating point and copied.

**Returns**  

`f` : ndarray

See also:

```
haar function Forward Haar transform
```

```
mahotas.daubechies(f, code, inline=False)
```

Daubechies wavelet transform

This function works best if the image sizes are powers of 2!

**Parameters**  

`f` : ndarray

2-D image

`code` : str

One of ‘D2’, ‘D4’, ... ‘D20’
inline : bool, optional

Whether to write the results to the input image. By default, a new image is returned.
Integer images are always converted to floating point and copied.

See also:

haar function Haar transform (equivalent to D2)

mahotas.idaubechies (f, code, inline=False)
Daubechies wavelet inverse transform

Parameters f : ndarray
2-D image
code : str
One of ‘D2’, ‘D4’, ... ‘D20’
inline : bool, optional
Whether to write the results to the input image. By default, a new image is returned.
Integer images are always converted to floating point and copied.

See also:

haar function Haar transform (equivalent to D2)

2.6 Distance Transform

The example in this section is present in the source under mahotas/demos/distance.py.

We start with an image, a black&white image that is mostly black except for two white spots:

```python
import numpy as np
import mahotas

f = np.ones((256,256), bool)
f[200:,240:] = False
f[128:144,32:48] = False

from pylab import imshow, gray, show
import numpy as np

f = np.ones((256,256), bool)
f[200:,240:] = False
f[128:144,32:48] = False

gray()
imshow(f)
show()
```
There is a simple `distance()` function which computes the distance map:

```python
import mahotas
dmap = mahotas.distance(f)
```

Now `dmap[y,x]` contains the squared euclidean distance of the pixel `(y,x)` to the nearest black pixel in `f`. If `f[y,x] == True`, then `dmap[y,x] == 0`.

```python
from __future__ import print_function

import pylab as p
import numpy as np
import mahotas

f = np.ones((256,256), bool)
f[200:,240:] = False
f[128:144,32:48] = False
# f is basically True with the exception of two islands: one in the lower-right
# corner, another, middle-left

dmap = mahotas.distance(f)
p.imshow(dmap)
p.show()
```
2.6.1 Distance Transform and Watershed

The distance transform is often combined with the watershed for segmentation. Here is an example (which is available with the source in the mahotas/demos/ directory as nuclear_distance_watershed.py).

```python
import mahotas
from os import path
import numpy as np
from matplotlib import pyplot as plt

try:
    nuclear_path = path.join(path.dirname(path.abspath(__file__)), 'data', 'nuclear.png')
except NameError:
    nuclear_path = path.join('data', 'nuclear.png')

nuclear = mahotas.imread(nuclear_path)
nuclear = nuclear[:,:,0]
nuclear = mahotas.gaussian_filter(nuclear, 1.)
threshed = (nuclear > nuclear.mean())
distances = mahotas.stretch(mahotas.distance(threshed))
Bc = np.ones((9,9))

```

2.6. Distance Transform
The code is not very complex. Start by loading the image and preprocessing it with a Gaussian blur:

```python
import mahotas
import mahotas.demos

nuclear = mahotas.demos.nuclear_image()
nuclear = nuclear[:,:,0]
nuclear = mahotas.gaussian_filter(nuclear, 1.)
threshed = (nuclear > nuclear.mean())
```

```python
maxima = mahotas.morph.regmax(distances, Bc=Bc)
spots, n_spots = mahotas.label(maxima, Bc=Bc)
surface = (distances.max() - distances)
areas = mahotas.cwatershed(surface, spots)
areas *= threshed

import random
from matplotlib import colors as c

colors = map(plt.cm.jet, range(0, 256, 4))
random.shuffle(colors)
colors[0] = (0., 0., 0., 1.)
rmap = c.ListedColormap(colors)
plt.imshow(areas, cmap=rmap)
plt.show()
```
Now, we compute the distance transform:

```python
distances = mahotas.stretch(mahotas.distance(threshed))
```

We find and label the regional maxima:

```python
Bc = np.ones((9,9))
maxima = mahotas.morph.regmax(distances, Bc=Bc)
spots, n_spots = mahotas.label(maxima, Bc=Bc)
```

Finally, to obtain the image above, we invert the distance transform (because of the way that \texttt{cwatershed} is defined) and compute the watershed:

```python
surface = (distances.max() - distances)
areas = mahotas.cwatershed(surface, spots)
areas *= threshed
```

We used a random colormap with a black background for the final image. This is achieved by:

```python
import random
from matplotlib import colors as c
colors = map(cm.jet, range(0, 256, 4))
random.shuffle(colors)
colors[0] = (0.,0.,0.,1.)
rmap = c.ListedColormap(colors)
imshow(areas, cmap=rmap)
show()
```

## 2.6.2 API Documentation

A package for computer vision in Python.

**Main Features**

- **features**  Compute global and local features (several submodules, include SURF and Haralick features)
- **convolve**  Convolution and wavelets
- **morph**  Morphological features. Most are available at the mahotas level, include erode(), dilate()...
- **watershed**  Seeded watershed implementation
- **imread/imsave**  read/write image

**Documentation:**  [https://mahotas.readthedocs.io/](https://mahotas.readthedocs.io/)

**Citation:**


**mahotas.distance** *(bw, metric=’euclidean’)*

Computes the distance transform of image \texttt{bw}:

```python
dmap[i,j] = min_{i', j'} \{ (i-i')**2 + (j-j')**2 | !bw[i', j'] \}
```

That is, at each point, compute the distance to the background.

If there is no background, then a very high value will be returned in all pixels (this is a sort of infinity).

**Parameters** \texttt{bw} : \texttt{ndarray}
If boolean, `False` will denote the background and `True` the foreground. If not boolean, this will be interpreted as `bw != 0` (this way you can use labeled images without any problems).

**metric** : str, optional

one of ‘euclidean2’ (default) or ‘euclidean’

**Returns**

**dmap** : ndarray

distance map

**References**

For 2-D images, the following algorithm is used:


For n-D images (with n > 2), a slower hand-craft method is used.

## 2.7 Polygon Utilitites

### 2.7.1 Drawing

Mahotas is not a package to generate images, but there are a few simple functions to draw lines and polygons on an image (the target image is known as the *canvas* in this documentation).

The simplest function is `line`: Give it two points and it draws a line between them. The implementation is simple, and in Python, so it will be slow for many complex usage.

The main purpose of these utilities is to aid debugging and visualisation. If you need to generate fancy graphs, look for packages such as matplotlib.

### 2.7.2 Convex Hull

Convex hull functions are a more typical image processing feature. Mahotas has a simple one, called `convexhull`. Given a boolean image (or anything that will get interpreted as a boolean image), it finds the convex hull of all its on points.

The implementation is in C++, so it is fast.

A companion function `fill_convexhull` returns the convex hull as a binary image.

### 2.7.3 API Documentation

```python
mahotas.polygon.line((y0, x0), (y1, x1), canvas, color=1)
```

Draw a line

**Parameters**

**p0** : pair of integers

first point

**p1** : pair of integers
second point

```
canvas : ndarray
    where to draw, will be modified in place

color : integer, optional
    which value to store on the pixels (default: 1)
```

```
mahotas.polygon.fill_polygon([(y0, x0), (y1, x1), ...], canvas, color=1)
```

Draw a filled polygon in canvas

**Parameters**

- **polygon** : list of pairs
  
  a list of (y,x) points

- **canvas** : ndarray
  
  where to draw, will be modified in place

- **color** : integer, optional
  
  which colour to use (default: 1)

```
mahotas.polygon.convexhull(bwimg)
```

Compute the convex hull as a polygon

This is an implementation of the Graham Scan: http://en.wikipedia.org/wiki/Graham_scan

**Parameters**

- **bwimg** : ndarray
  
  input image (interpreted as boolean). Only 2D arrays are supported.

**Returns**

- **hull** : ndarray
  
  Set of (y,x) coordinates of hull corners

```
mahotas.polygon.fill_convexhull(bwimage)
```

Compute the convex hull and return it as a binary mask

**Parameters**

- **bwimage** : input image (interpreted as boolean)

**Returns**

- **hull** : image of same size and dtype as bwimage with the hull filled in.

# 2.8 Features

By features we mean, basically, numerical functions of the image. That is, any method that gives me a number from the image, I can call it a *feature*. Ideally, these should be meaningful.

We can classify features into two types:

- **global** These are a function of the whole image.

- **local** These **have a position** and are a function of a local image region.

Mahotas supports both types.

The classification tutorial illustrates the usefulness of feature computation.

If you simply want to compute features from images (without any further processing), you can also use the mahotas-features.py script, which is installed with mahotas (since version 1.4).
2.8.1 Global features

Haralick features

These are texture features, based on the adjacency matrix (the adjacency matrix stores in position \((i,j)\) the number of times that a pixel takes the value \(i\) next to a pixel with the value \(j\). Given different ways to define next to, you obtain slightly different variations of the features. Standard practice is to average them out across the directions to get some rotational invariance.

They can be computed for 2-D or 3-D images and are available in the `mahotas.features.haralick` module. Only the first 13 features are implemented. The last (14th) feature is normally considered to be unstable, although it is not clear to me why this is. (See this unanswered question on Cross-validated).

Local Binary Patterns

Local binary patterns (LBP) are a more recent set of features. Each pixel is looked at individually. Its neighbourhood is analysed and summarised by a single numeric code. The normalised histogram across all the pixels in the image is the final set of features.

Again, this is an attempt at capturing texture. LBPs are insensitive to orientation and to illumination (scaling).

Threshold Adjacency Statistics

Threshold adjacency statistics (TAS) are a recent innovation too. In the original version, they have fixed parameters, but we have adapted them to parameter-free versions (see Structured Literature Image Finder: Extracting Information from Text and Images in Biomedical Literature by Coelho et al. for a reference). Mahotas supports both.

Zernike Moments

Zernike moments are not a texture feature, but rather a global measure of how the mass is distributed.

2.8.2 Local features

SURF: Speeded-Up Robust Features

Speeded-Up Robust Features (SURF) have both a location (pixel coordinates) and a scale (natural size) as well as a descriptor (the local features).

Read more about SURF.

2.9 Local Binary Patterns

New in version 0.7: LBPs are available before, but an important bug was fixed in 0.7. It is highly recommended that you never use the older version.

Local binary patterns depend on the local region around each pixel. See the diagram below:


The reference pixel is in red, at the centre. A number of points are defined at a distance \(r\) from it. These are the green points. As you go from left to right, the number of green points increases.
The “pattern” in the name is the relationship of the value at the green points when compared to the central red point. We call it a binary pattern because all that is taken into account is whether the value at the green point is greater than the value at the red point.

As you can see, the green points do not necessarily fall exactly on another pixel, so we need to use interpolation to find a value for the green points.

### 2.9.1 API Documentation

The `mahotas.features.lb` module contains the `lbp` function which implements LBPs.

```python
mahotas.features.lbp.lbp(image, radius, points, ignore_zeros=False)
```

Compute Linear Binary Patterns

The return value is a histogram of feature counts, where position \( i \) corresponds to the number of pixels that had code \( i \). The codes are compressed so that impossible codes are not used. Therefore, this is the \( i \)’th feature, not just the feature with binary code ‘\( i \).

**Parameters**
- `image`: ndarray
  - input image (2-D numpy ndarray)
- `radius`: number (integer or floating point)
  - radius (in pixels)
- `points`: integer
  - nr of points to consider
- `ignore_zeros`: boolean, optional
  - whether to ignore zeros (default: False)

**Returns**
- `features`: 1-D numpy ndarray
  - histogram of features. See above for a caveat on the interpretation of these.

```python
mahotas.features.lbp.lbp_transform(image, radius, points, ignore_zeros=False, preserve_shape=True)
```

Compute Linear Binary Pattern Transform

The return value are the transformed pixel values histogram of feature counts, where position \( i \) corresponds to the number of pixels that had code \( i \). The codes are compressed so that impossible codes are not used. Therefore, this is the \( i \)’th feature, not just the feature with binary code ‘\( i \).

**Parameters**
- `image`: ndarray
  - input image (2-D numpy ndarray)
- `radius`: number (integer or floating point)
  - radius (in pixels)
- `points`: integer
  - nr of points to consider
- `ignore_zeros`: boolean, optional
  - whether to ignore zeros. Note that if you set this to True, you will need to set `preserve_shape` to False. (default: False)
- `preserve_shape`: boolean, optional
  - whether to return an array with the same shape as `image`. (default: True)
Returns features: 1-D numpy ndarray

histogram of features. See above for a caveat on the interpretation of these.

References

Gray Scale and Rotation Invariant Texture Classification with Local Binary Patterns Ojala, T. Pietikainen, M. Maenpaa, T. Lecture Notes in Computer Science (Springer) 2000, ISSU 1842, pages 404-420

2.10 Speeded-Up Robust Features

New in version 0.6.1: SURF is only available starting in version 0.6.1, with an important bugfix in version 0.6.2.

New in version 0.8: In version 0.8, some of the inner functions are now in mahotas.features.surf instead of mahotas.surf

Speeded-Up Robust Features (SURF) are a recent innovation in the local features family. There are two steps to this algorithm:

1. Detection of interest points.
2. Description of interest points.

The function `mahotas.features.surf.surf` combines the two steps:

```python
import numpy as np
from mahotas.features import surf

f = ... # input image
spoints = surf.surf(f)
print "Nr points:'", len(spoints)
```

Given the results, we can perform a simple clustering using, for example, milk (we could have used any other system, of course; having written milk, I am most familiar with it):

```python
try:
    import milk
    # spoints includes both the detection information (such as the position
    # and the scale) as well as the descriptor (i.e., what the area around
    # the point looks like). We only want to use the descriptor for
    # clustering. The descriptor starts at position 5:
    descrs = spoints[:,5:]

    # We use 5 colours just because if it was much larger, then the colours
    # would look too similar in the output.
    k = 5
    values, _ = milk.kmeans(descrs, k)
    colors = np.array([(255-52*i,25+52*i,37**i % 101) for i in xrange(k)])
except:
    values = np.zeros(100)
    colors = [(255,0,0)]
```

So we are assigning different colours to each of the possible

The helper `surf.show_surf` draws coloured polygons around the interest points:
Running the above on a photo of Luis Pedro, the author of mahotas yields:

```python
from __future__ import print_function
import numpy as np
import mahotas as mh
from mahotas.features import surf
from pylab import *
from os import path

f = mh.demos.load('luispedro', as_grey=True)
f = f.astype(np.uint8)
spoints = surf.surf(f, 4, 6, 2)
print("Nr points:", len(spoints))

try:
    import milk
    descrs = spoints[:,5:]
k = 5
    values, _ = milk.kmeans(descrs, k)
    colors = np.array([(255-52*i,25+52*i,37**i % 101) for i in range(k)])
except:
    values = np.zeros(100)
    colors = np.array([(255,0,0)])

f2 = surf.show_surf(f, spoints[:100], values, colors)
imshow(f2)
show()
```
2.10.1 API Documentation

The `mahotas.features.surf` module contains separate functions for all the steps in the SURF pipeline.

`mahotas.features.surf.dense(f, spacing, scale=np.sqrt(spacing), is_integral=False, include_interest_point=False)`

**Parameters**

- **f**: image
  - original image
- **spacing**: integer
  - Distance between points
- **scale**: float, optional
  - Scale of interest points. By default, it is set to `np.sqrt(spacing)`
- **is_integral**: boolean, optional
  - Whether `f` is an integral image
- **include_interest_point**: bool, optional
  - Whether to return interest point information. Default is False

**Returns**

- **descriptors**: ndarray
Descriptors at dense points. Note that the interest point is not returned by default.

See also:

- `surf` function Find interest points and then compute descriptors
- `descriptors` function Compute descriptors at user provided interest points

```
import mahotas.features.surf as surf

fi = surf.integral(f, in_place=False, dtype=np.double):
Compute integral image
```

Parameters:
- `f` : ndarray
  input image. Only 2-D images are supported.
- `in_place` : bool, optional
  Whether to overwrite `f` (default: False).
- `dtype` : dtype, optional
  Dtype to use (default: double)

Returns:
- `fi` : ndarray of `dtype` of same shape as `f`
  The integral image

```
points = surf(f, nr_octaves=4, nr_scales=6, initial_step_size=1, threshold=0.1, max_points=1024, descriptor_only=False):
Run SURF detection and descriptor computations
```

Speeded-Up Robust Features (SURF) are fast local features computed at automatically determined keypoints.

Parameters:
- `f` : ndarray
  input image
- `nr_octaves` : integer, optional
  Nr of octaves (default: 4)
- `nr_scales` : integer, optional
  Nr of scales (default: 6)
- `initial_step_size` : integer, optional
  Initial step size in pixels (default: 1)
- `threshold` : float, optional
  Threshold of the strength of the interest point (default: 0.1)
- `max_points` : integer, optional
  Maximum number of points to return. By default, return at most 1024 points. Note that the number may be smaller even in the case where there are that many points. This is a side-effect of the way the threshold is implemented: only `max_points` are considered, but some of those may be filtered out.
- `descriptor_only` : boolean, optional
  If `descriptor_only`, then returns only the 64-element descriptors (default is False).
Returns points: ndarray of double, shape = (N, 6 + 64)

N is nr of points. Each point is represented as (y, x, scale, score, laplacian, angle, D_0,...,D_63) where y, x, scale is the position, angle the orientation, score and laplacian the score and sign of the detector; and D_i is the descriptor

If descriptor_only, then only the *D_i*s are returned and the array has shape (N, 64)

## 2.11 Implementing SURF-ref With Mahotas

This is a companion to the paper Determining the subcellular location of new proteins from microscope images using local features by Coelho et al. (2013).

```python
def surf_ref(f, ref):
    
    features = surf_ref(f, ref)

    Computer SURF-ref features

    Parameters
    ----------
    f : ndarray
        input image
    ref : ndarray
        Corresponding reference image

    Returns
    -------
    features : ndarray
        descriptors
    
    fi = surf.integral(f.copy())
    points = surf.interest_points(fi, 6, 24, 1, max_points=1024, is_integral=True)
    descs = surf.descriptors(fi, points, is_integral=True, descriptor_only=True)
    if ref is None:
        return descs
    descsref = surf.descriptors(ref, points, descriptor_only=True)
    return np.hstack( (descs, descsref) )
```

This function can take any number of reference images.

We now compute all features for all images in widefield dataset:

```python
from glob import glob
import re

basedir = 'rt-widefield'  # Edit as needed

features = []
labels = []

# We need the following to keep track of the proteins:
origins = []
prev_origin = ''
origin_counter = -1 # set to -1 so it will be correctly initialized on the first image

for dir in glob(basedir):
    
```

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if dir == 'README': continue
for f in glob('{}{}/*-protein.tiff'.format(basedir, dir)):
    origin = f[:5]
    if origin != prev_origin:
        origin_counter += 1
        prev_origin = origin

    f = '{}{}{}'.format(basedir, dir, f)
    f = mh.imread(f)
    ref = mh.imread(f.replace('protein', 'dna'))
    features.append(surf_ref(f, ref))
    labels.append(dir)
    origins.append(origin_counter)

2.11.1 Classification

With all the precomputed features, we can now run 10-fold cross-validation on these features.

We will using milk for machine learning:

```python
import milk
```

Milk’s interface is around learner objects. We are going to define a function:

```python
def train_model(features, labels):
```

The first step is to find centroids:

```python
# concatenate all the features:
concatenated = np.concatenate(features)
```

We could use the whole array concatenated for kmeans. However, that would take a long time, so we will use just 1/16th of it:

```python
concatenated = concatenated[:,::16]
_,centroids = milk.kmeans(concatenated, k=len(labels)//4, R=123)
```

The R argument is the random seed. We set it to a constant to get reproducible results, but feel free to vary it.

Based on these centroids, we project the features to histograms. Now, we are using all of the features:

```python
features = np.array([project_centroids(centroids, fs, histogram=True)
                     for fs in features])
```

Finally, we can use a traditional milk learner (which will perform feature selection, normalization, and SVM training):

```python
learner = milk.defaultlearner()
model = learner.train(features, labels)
```

We must return both the centroids that were used and the classification model:

```python
return centroids, model
```

To classify an instance, we define another function, which uses the centroids and the model:

```python
def apply_many(centroids, model, features):
    features = np.array([project_centroids(centroids, fs, histogram=True)
                          for fs in features])
```
In fact, while the above will work well, milk already provides a learner object which will perform all of those tasks!

```python
import milk
from milk.supervised.precluster import frac_precluster_learner
learner = frac_precluster_learner(kfrac=4, sample=16)
cmatrix, names = milk.nfoldcrossvalidation(features, labels, origins=origins, learner=learner)
acc = cmatrix.astype(float).trace()/cmatrix.sum()
print('Accuracy: {:.1}%'.format(100.*acc))
```

### 2.12 Morphological Operators

New in version 0.8: open() & close() were added in version 0.8

Morphological operators were the first operations in mahotas (back then, it was even, briefly, just a single C++ module called morph). Since then, mahotas has grown a lot. This module, too, has grown and acquired more morphological operators as well as being optimised for speed.

Let us first select an interesting image

```python
import mahotas
import mahotas.demos
from pylab import gray, imshow, show
import numpy as np

luispedro = mahotas.demos.load('luispedro')
luispedro = luispedro.max(2)
T = mahotas.otsu(luispedro)
lpbin = (luispedro > T)
gray()
眼 = ~lpbin[112:180, 100:190]
imshow(眼)
show()
```
After Oct 2013, you can get this image with mahotas as:

```python
import mahotas.demos
luispedro = mahotas.demos.load('luispedro')
luispedro = luispedro.max(2)
```

### 2.12.1 Dilation & Erosion

Dilation and erosion are two very basic operators (mathematically, you only need one of them as you can define the erosion as dilation of the negative or vice-versa).

These operations are available in the `mahotas.morph` module:

```python
mahotas.morph.dilate(eye)
```

Dilation is, intuitively, making positive areas “fatter”:

```python
imshow(mahotas.morph.dilate(eye))
show()
```
mahotas.morph.erode(eye)

Erosion, by contrast, thins them out:

```python
import mahotas

display = imshow(mahotas.morph.erode(eye))
show()
```
Mahotas supports greyscale erosion and dilation (depending on the `dtype` of the arguments) and you can specify any structuring element you wish (including non-flat ones). By default, a 1-cross is used:

```python
# if no structure-element is passed, use a cross:
se = np.array(
    [[0, 1, 0],
     [1, 1, 1],
     [0, 1, 0]], bool)
```

However, you can use whatever structuring element you want:

```python
se = np.array(
    [[1, 1, 0],
     [1, 1, 1],
     [0, 1, 1]], bool)
dilated = mahotas.morph.dilate(eye, se)
eroded = mahotas.morph.erode(eye, se)
```

Note that when you pass it a non-boolean array as the first argument, you will get greyscale erosion. Mahotas supports full greyscale erosion, including arbitrary, flat or non-flat, structuring elements).

### 2.12.2 Close & Open

Closing and opening are based on erosion and dilation. Again, they work in greyscale and can use an arbitrary structure element.

**2.12. Morphological Operators**
Here is closing:

```python
mahotas.morph.close(eye)

imshow(mahotas.morph.close(eye))
show()
```

And here is opening:

```python
mahotas.morph.open(eye)

imshow(mahotas.morph.open(eye))
show()
```
Both `close` and `open` take an optional structuring element as a second argument:

```
mahotas.morph.open(eye, se)
```

## 2.13 Color Space Conversions

New in version 0.9.6.

### 2.13.1 Red-green-blue images

An RGB image is represented as a 3-dimensional array of shape `(h, w, 3)`, where each pixel is represented by three values, red/green/blue.

For example, the classic lena image is a `(512, 512, 3)` array:

```
import mahotas as mh
lena = mh.demos.load('lena')
print lena.shape
```

We can convert it to greyscale as using `rgb2grey` (or `rgb2gray` if you prefer, both work). This conversion uses a visually realistic method (which weighs the green channel more heavily as human eyes are more sensitive to it). For example:

```
import mahotas as mh
lena = mh.demos.load('lena')
```

```
print lena.shape
```
We can also convert to sepia with \texttt{rgb2sepia}:

\begin{verbatim}
lenas = mh.colors.rgb2sepia(lena)
\end{verbatim}

\begin{verbatim}
from pylab import imshow
import mahotas as mh
lena = mh.demos.load('lena')
lenas = mh.colors.rgb2sepia(lena)

imshow(lenas)
\end{verbatim}
2.13.2 Other Colour Spaces

Mahotas can also convert to XYZ space and to the Lab space with rgb2xyz and rgb2lab, respectively.

2.14 Input/Output with Mahotas

Mahotas does not have any builtin support for input/output. However, it wraps a few other libraries that do. The result is that you can do:

```python
import mahotas as mh
image = mh.imread('file.png')
mh.imsave('copy.png', image)
```

It can use the following backends (it tries them in the following order):

1. It prefers mahotas-imread, if it is available. Imread is a native C++ library which reads images into Numpy arrays. It supports PNG, JPEG, TIFF, WEBP, BMP, and a few TIFF-based microscopy formats (LSM and STK).

2. It also looks for freeimage. Freeimage can read and write many formats. Unfortunately, it is harder to install and it is not as well-maintained as imread.

3. Finally, it tries to load pillow.
Thus, to use the `imread` or `imsave` functions, you need to install one of the packages above. At one point, mahotas supported wrapping matplotlib, but their image loading methods are unreliable as it uses other packages itself. Thus, depending on what you had installed, the resulting images would be different.

If you are running on Windows, you may wish to try Christoph Gohlke’s packages.

### 2.15 Tutorial: Classification Using Mahotas

New in version 0.8: Before version 0.8, texture was under mahotas, not under mahotas.features

Here is an example of using mahotas and milk for image classification (but most of the code can easily be adapted to use another machine learning package). I assume that there are three important directories: positives/ and negatives/ contain the manually labeled examples, and the rest of the data is in an unlabeled/ directory.

Here is the simple algorithm:

1. Compute features for all of the images in positives and negatives
2. learn a classifier
3. use that classifier on the unlabeled images

In the code below I used jug to give you the possibility of running it on multiple processors, but the code also works if you remove every line which mentions TaskGenerator.

We start with a bunch of imports:

```python
from glob import glob
import mahotas
import mahotas.features
import milk
from jug import TaskGenerator
```

Now, we define a function which computes features. In general, texture features are very fast and give very decent results:

```python
@TaskGenerator
def features_for(imname):
    img = mahotas.imread(imname)
    return mahotas.features.haralick(img).mean(0)
```

`mahotas.features.haralick` returns features in 4 directions. We just take the mean (sometimes you use the spread `ptp()` too).

Now a pair of functions to learn a classifier and apply it. These are just milk functions:

```python
@TaskGenerator
def learn_model(features, labels):
    learner = milk.defaultclassifier()
    return learner.train(features, labels)

@TaskGenerator
def classify(model, features):
    return model.apply(features)
```

We assume we have three pre-prepared directories with the images in jpeg format. This bit you will have to adapt for your own settings:
Finally, the actual computation. Get features for all training data and learn a model:

```python
positives = glob('positives/*.jpg')
negatives = glob('negatives/*.jpg')
unlabeled = glob('unlabeled/*.jpg')

features = map(features_for, negatives + positives)
labels = [0] * len(negatives) + [1] * len(positives)
model = learn_model(features, labels)
labeled = [classify(model, features_for(u)) for u in unlabeled]
```

This uses texture features, which is probably good enough, but you can play with other features in `mahotas.features` if you’d like (or try `mahotas.surf`, but that gets more complicated).

(This was motivated by a question on Stackoverflow).

## 2.16 Tutorial: Extended Depth of Field

This is an example of how to use mahotas to implement an algorithm that it does not have built-in: *extended depth of field.*

The idea is that you have a stack of images, taken at different focal points, and you build a single image so that you get everything in focus.

Start with standard imports:

```python
import numpy as np
import mahotas as mh
```

We are going to assume that you have an `image` object, which has three dimensions: the stack, height, and width:

```python
stack, h, w = image.shape
```

We use `mh.sobel` as the measure of “in focusness” for each pixel:

```python
focus = np.array([mh.sobel(t, just_filter=True) for t in image])
```

Now, we select the best slice at each pixel location:

```python
best = np.argmax(focus, 0)
```

So far, very easy. The next part is the hard part. We want to do the following:

```python
r = np.zeros((h, w))-1
for y in xrange(h):
    for x in xrange(w):
        r[y, x] = image[best[y, x], y, x]
```

But this is very slow (never run nested loops in Python if you can avoid it). We get the same result with a slightly less legible, but faster manipulation:

```python
r = np.zeros((h, w))-1
for y in xrange(h):
    for x in xrange(w):
        r[y, x] = image[best[y, x], y, x]
```

---

1. Other methods simply use a different measure here.
2. I am not 100% convinced that this is the best. After all we create an array of size `len(image)` just to index. I would be happy to find an alternative.
Et voilà!

Here is an example, from a stack of microbes imaged. This is is the maximum intensity projection:

This is the most in-focus slice (using the sobel operator as the measure):

And this is the extended depth of field result:
It is clearly sharper, perhaps at the expense of some possible noise. I actually played around with blurring the image a little bit and it did improve things ever so slightly.

2.17 mahotas-features.py

New in version 1.4.0: The mahotas-features.py script appeared in version 1.4.0 (July 2015)

With the installation of mahotas, a script called mahotas-features.py is installed, which can be used to compute features from a set of files.

2.17.1 Usage

You call the script with a set of flags specifying which features you want to compute, followed by a list of files. For example:

```bash
$ mahotas-features.py --haralick --lbp image-file1.tiff image-file2.tiff
```

This will output to the file features.tsv (this default can be changed with the --output option)

2.17.2 Full Usage Information

You can obtain help on all the options by running mahotas-features.py --help:

If you use mahotas in a scientific publication, please cite Coelho, LP (2013). http://dx.doi.org/10.5334/jors.ac

```bash
usage: mahotas-features.py [-h] [--output OUTPUT] [--clobber]
[--convert-to-bw CONVERT_TO_BW] [--no-color]
[--haralick] [--lbp] [--lbp-radius LBP_RADIUS]
[--lbp-points LBP_POINTS]
input_file_name [input_file_name ...]
```

Compute features using mahotas
<table>
<thead>
<tr>
<th>positional arguments:</th>
</tr>
</thead>
<tbody>
<tr>
<td>input_file_name  Image files names</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>optional arguments:</th>
</tr>
</thead>
<tbody>
<tr>
<td>-h, --help                       show this help message and exit</td>
</tr>
<tr>
<td>--output OUTPUT                  Output file for feature files</td>
</tr>
<tr>
<td>--clobber                       Overwrite output file (if it exists)</td>
</tr>
<tr>
<td>--convert-to-bw CONVERT_TO_BW   Convert color images to greyscale. Acceptable values:</td>
</tr>
<tr>
<td>no: raises an error (default) max: use max projection</td>
</tr>
<tr>
<td>yes: use rgb2gray</td>
</tr>
<tr>
<td>--no-color                       Do not print in color (for error and warning messages)</td>
</tr>
<tr>
<td>--haralick                       Compute Haralick features</td>
</tr>
<tr>
<td>--lbp                            Compute LBP (linear binary patterns) features</td>
</tr>
<tr>
<td>--lbp-radius LBP_RADIUS          Radius to use for LBP features</td>
</tr>
<tr>
<td>--lbp-points LBP_POINTS          Nr of points to use for LBP features</td>
</tr>
</tbody>
</table>

2.18 Frequently Asked Questions

2.18.1 How do I install mahotas with anaconda?

If you are using conda, you can install mahotas from conda-forge using the following commands:

```bash
conda config --add channels conda-forge
conda install mahotas
```

2.18.2 Who uses mahotas?

In June 2016, there were 34 papers citing the mahotas paper.

2.18.3 Why did you not simply contribute to scipy.ndimage or scikits.image?

When I started this project (although it wasn’t called mahotas and it was more of a collection of semi-organised routines than a project), there was no scikits.image.

In the meanwhile, all these projects have very different internal philosophies. ndimage is old-school scipy, in C, with macros. scikits.image uses Cython extensively, while mahotas uses C++ and templates. I don’t want to use Cython as I find that it is not yet established enough and at the time it could not be used to write functions that run on multiple types (like with C++ templates). The scipy community does not want to use C++.

I have, on the other hand, taken code from ndimage and ported it to C++ for use in mahotas. In the process, I feel it is much cleaner code (because you can use RAII, exceptions, and templates) and I want to keep it that way.

In any case, we all use the same data format: numpy arrays. It is very easy (trivial, really) to use all the packages together and take whatever functions you want from each. All the packages use function based interfaces which make it easy to mix-and-match.
2.18.4 I ran out of memory computing Haralick features on 16 bit images. Is it not supported?

Yes, it is supported, but your machine may not be big enough to do the computation. In order to compute Haralick features, first a cooccurrence matrix is computed. This matrix has the size \((\text{ngrey}, \text{ngrey})\) where \(\text{ngrey}\) is the largest grey value in the input. Thus, if your image has a very high dynamic range (i.e., \(\text{ngrey}\) is large), you may not have the resources to compute the cooccurrence matrix.

It is often a good idea to contrast stretch your images. For example, using the following code, stretches your images to the 0-255 range:

```python
im_stretched = mh.stretch(im)
features = mh.features.haralic(im_stretched)
```

16 bit images where the dynamic range is not too large (for example, some imaging equipment can only really produce 12 bits, \(\text{so ngrey < 4096}\)) are not a problem.

2.18.5 What are the parameters to Local Binary Patterns?

Read the documentation on local binary patterns.

2.18.6 I am using mahotas in a scientific publication, is there a citation?

If you use mahotas in a scientific publication, please cite:


In BibTeX format:

```latex
@article{coelho:mahotas,
  title = {Mahotas: Open source software for scriptable computer vision},
  author = {Luis Pedro Coelho},
  journal = {Journal of Open Research Software},
  year = {2013},
  volume = {1},
  doi = {10.5334/jors.ac},
  url = {http://dx.doi.org/10.5334/jors.ac}
}
```

This is accessible in Python using `mahotas.citation()`.

2.18.7 Imread cannot find FreeImage

Mahotas itself does not have the functionality to read in images (see the I/O section.

Functions such as `imread` are just a wrapper around one of 2 backends:

1. mahotas-imread (i.e., https://pypi.python.org/pypi/imread)
2. FreeImage

Thus, you need to install one of the packages above. At one point, mahotas supported wrapping matplotlib, but their image loading methods are unreliable as it uses other packages itself. Thus, depending on what you had installed, the resulting images would be different.

If you are running on Windows, you may wish to try Christoph Gohlke’s packages.
2.19 Mahotas Internals

This section is of interest if you are trying to understand how mahotas works in order to fix something, extend it (patches are always welcome), or use some of its technology in your projects.

2.19.1 Philosophy

Mahotas should not suck.

This is my main development goal and, if I achieve it, this alone should put mahotas in the top ten to one percent of software packages.

Mahotas should have no bugs. None. Ever.

Of course, some creep in. So, we settle for the next best thing: \textit{Mahotas should have no **known bugs**}. Whenever a bug is discovered, the top priority is to squash it.

Read the principles of mahotas

2.19.2 C++/Python Division

Mahotas is, for the most part, written in C++, but almost always, you call a Python function which checks types and then calls the internal function. This is slightly slower, but it is easier to develop this way (and, for all but the smallest image, it will not matter).

So each module.py will have its associated _module.cpp.

2.19.3 C++ Templates

The main reason that mahotas is in C++ (and not in pure C) is to use templates. Almost all C++ functions are actually 2 functions:

1. A \texttt{py\_function} which uses the Python C/API to get arguments, &c. This is almost always pure C.

2. A template \texttt{function\!<\!\texttt{dtype}\!\>} which works for the \texttt{dtype} performing the actual operation.

So, for example, this is how \texttt{erode} is implemented. \texttt{py\_erode} is generic:

```python
PyObject* py_erode(PyObject* self, PyObject* args) {
    PyArrayObject* array;
    PyArrayObject* Bc;
    if (!PyArg_ParseTuple(args, "OO", &array, &Bc)) return NULL;
    PyArrayObject* res_a = (PyArrayObject*)PyArray_SimpleNew(array->nd, array->dimensions, PyArray_TYPE(array));
    if (!res_a) return NULL;
    PyArray_FILLWBYTE(res_a, 0);
    #define HANDLE(type) 
        erode<type>(numpy::aligned_array<type>(res_a), numpy::aligned_array<type>(array), numpy::aligned_array<type>(Bc));
        SAFE_SWITCH_ON_INTEGER_TYPES_OF(array)
    #undef HANDLE
    ...
}
```

These functions normally contain a lot of boiler-plate code: read the arguments, perform some sanity checks, perhaps a bit of initialisation, and then, the switch on the input type with the help of the \texttt{SAFE\_SWITCH\_ON\_INTEGER\_TYPES\_OF()} and friends, which call the right specialisation of the template that does the actual work. In this example \texttt{erode} implements (binary) erosion:
template<typename T>
void erode(numpy::aligned_array<T> res, numpy::aligned_array<T> array, numpy::aligned_array<T> Bc) {
    gil_release nogil;
    const unsigned N = res.size();
    typename numpy::aligned_array<T>::iterator iter = array.begin();
    filter_iterator<T> filter(res.raw_array(), Bc.raw_array());
    const unsigned N2 = filter.size();
    T* rpos = res.data();

    for (int i = 0; i != N; ++i, ++rpos, filter.iterate_with(iter), ++iter) {
        for (int j = 0; j != N2; ++j) {
            T arr_val = false;
            filter.retrieve(iter, j, arr_val);
            if (filter[j] && !arr_val) goto skip_this_one;
        }
        *rpos = true;
    }
    skip_this_one: continue;
}

The template machinery is not that complicated and the functions using it are very simple and easy to read. The only downside is that there is some expansion of code size. Given the small size of these functions however, this is not a big issue.

In the snippet above, you can see some other C++ machinery:

**gil_release** This is a RAII object that release the GIL in its constructor and gets it back in its destructor. Normally, the template function will release the GIL after the Python-specific code is done.

**array** This is a thin wrapper around `PyArrayObject` that knows its type and has iterators. Relying on these objects has the further advantage that in debug mode, it checks bounds for many memory accesses. While this is very costly for everyday usage, it can catch bugs faster than the alternatives.

**filter_iterator** This is taken from `scipy.ndimage` and it is useful to iterate over an image and use a centered filter around each pixel (it keeps track of all of the boundary conditions).

The inner loop is as direct an implementation of erosion as one would wish for: for each pixel in the image, look at its neighbours. If all are true, then set the corresponding output pixel to true (else, skip it as it has been initialised to zero).

Most of the functions follow this architecture.

### 2.20 The Why of mahotas

#### 2.20.1 Principles of Mahotas

Here are the principles of mahotas, in decreasing order of importance:

1. Just work
2. Well documented
3. Fast code
4. Simple code
5. Minimal dependencies
2.20.2 Just work

The first principle is that things should just work. This means two things: (1) there should be no bugs, and (2) interfaces should be flexible or fail well.

To avoid bugs, tests are extensively used. Every reported bug leads to a new test case, so that it never happens again. New features should at least have a smoke test (test that runs the feature and verifies some basic properties of the output).

Interfaces are designed to be as flexible as possible. No specific types are required unless it is really needed or in performance-enhancing features (such as using out parameters).

The user should never be able to crash the Python interpreter with mahotas.

2.20.3 Well documented

No public function is without a complete docstring. In addition to that hard documentation (i.e., information with complete technical detail of every nook and cranny of the interface), there is also soft documentation (tutorial-like documentation with examples and higher level reasoning).

2.20.4 Fast code

Performance is a feature.

The code should be as fast as possible without sacrificing generality (see just work above). This is why C++ templates are used for type independent code.

2.20.5 Simple code

The code should be simple.

2.20.6 Minimal dependencies

Mahotas tries to avoid dependencies.

Right now, building mahotas depends on a C++ compiler, numpy. These are unlikely to ever change. To run mahotas, we need numpy. In order to read images, we need one of (1) imread or (2) FreeImage.

The imread/freeimage dependency is a soft dependency: everything, except for imread works without it. The code is written to ensure that import-ing mahotas without an IO backend will not trigger an error unless the imread() function is used.

Therefore, once mahotas is compiled, all you really need is numpy. This is unlikely to ever change.

2.21 Contributing

Development happens on github and the preferred contribution method is by forking the repository and issuing a pull request. Alternatively, just sending a patch to luis@luispedro.org will work just as well.

If you don’t know git (or another distributed version control system), which is a fantastic tool in general, there are several good git and github tutorials. You can start with their official documentation.

If you want to work on the C++ code, you can read the chapter in the internals before you start. Also, read the principles declaration.
2.21.1 Debug Mode

If you compile mahotas in debug mode, then it will run slower but perform a lot of runtime checks. This is controlled by the \texttt{DEBUG} environment variable.

There are two levels:

1. \texttt{DEBUG=1} This turns on assertions. The code will run slower, but probably not noticeably slower, except for very large images.

2. \texttt{DEBUG=2} This turns on the assertions and additionally uses the debug version of the C++ library (this is probably only working if you are using GCC). Some of the internal code also picks up on this and adds even more sanity checking. The result will be code that runs \textbf{much slower} as all operations done through iterators into standard containers are now checked (including many inner loop operations).

The Makefile that comes with the source helps you:

\begin{verbatim}
make clean
make debug
make test
\end{verbatim}

will rebuild in debug mode and run all tests. When you are done testing, use the \texttt{fast} Make target to get the non-debug build:

\begin{verbatim}
make clean
make fast
\end{verbatim}

Using make will not change your environment. The \texttt{DEBUG} variable is set internally only.

If you don’t know about it, check out \texttt{ccache} which is a great tool if you are developing in compiled languages (this is not specific to mahotas or even Python). It will allow you to quickly perform \texttt{make clean; make debug} and \texttt{make clean; make fast} so you never get your builds mixed up.

2.22 Possible Tasks

Here are a few ideas for improving mahotas.

2.22.1 New Features

- HOG
- BRISK
- Canny edge detection
- Hough Transform
- bilateral filtering
- Non Local Filtering
- Wiener filtering

2.22.2 Small Improvements

- something like the \texttt{overlay} function from \texttt{pymorph} (or even just copy it over and adapt it to mahotas style).
- H-maxima transform (again, pymorph can provide a basis)
• entropy thresholding

2.22.3 Internals

These can be very complex as they require an understanding of the inner workings of mahotas, but that does appeal to a certain personality.

• special case 1-D convolution on C-Arrays in C++. The idea is that you can write a tight inner loop in one dimension:

```c
void multiply(floating* r, const floating* f, const floating a, const int n, const int r_step, const int f_step) {
    for (int i = 0; i != n; ++i) {
        *r += a * *f;
        r += r_step;
        f += f_step;
    }
}
```

to implement:

```plaintext
r[row] += a * f[row+offset]
```

and you can call this with all the different values of a and offset that make up your filter. This would be useful for Gaussian filtering.

2.22.4 Tutorials

Mahotas has very good API documentation, but not so many start to finish tutorials which touch several parts of it (and even other packages, the ability to seamlessly use other packages in Python is, of course, a good reason to use it).

2.23 History

2.23.1 Version 1.4.3 (Oct 3 2016)

• Fix distribution (add missing README.md file)

2.23.2 Version 1.4.2 (Oct 2 2016)

• Fix resize\_to return exactly the requested size
• Fix hard crash when computing texture on arrays with negative values (issue #72)
• Added distance argument to haralick features (pull request #76, by Guillaume Lemaitre)

2.23.3 Version 1.4.1 (Dec 20 2015)

• Add filter\_labeled function
• Fix tests on 32 bit platforms and older versions of numpy
2.23.4 Version 1.4.0 (July 8 2015)

• Added mahotas-features.py script
• Add short argument to citation() function
• Add max_iter argument to thin() function
• Fixed labeled.bbox when there is no background (issue #61, reported by Daniel Haehn)
• bbox now allows dimensions greater than 2 (including when using the as_slice and border arguments)
• Extended croptobbox for dimensions greater than 2
• Added use_x_minus_y_variance option to haralick features
• Add function lbp_names

2.23.5 Version 1.3.0 (April 28 2015)

• Improve memory handling in freeimage.write_multipage
• Fix moments parameter swap
• Add labeled.bbox function
• Add return_mean and return_mean_ptp arguments to haralick function
• Add difference of Gaussians filter (by Jianyu Wang)
• Add Laplacian filter (by Jianyu Wang)
• Fix crash in median_filter when mismatched arguments are passed
• Fix gaussian_filter1d for ndim > 2

2.23.6 Version 1.2.4 (December 23 2014)

• Add PIL based IO

2.23.7 Version 1.2.3 (November 8 2014)

• Export mean_filter at top level
• Fix to Zernike moments computation (reported by Sergey Demurin)
• Fix compilation in platforms without npy_float128 (patch by Gabi Davar)

2.23.8 Version 1.2.2 (October 19 2014)

• Add minlength argument to labeled_sum
• Generalize regmax/regmin to work with floating point images
• Allow floating point inputs to cwatershed()
• Correctly check for float16 & float128 inputs
• Make sobel into a pure function (i.e., do not normalize its input)
• Fix sobel filtering
2.23.9 Version 1.2.1 (July 21 2014)

- Explicitly set numpy.include_dirs() in setup.py [patch by Andrew Stromnov]

2.23.10 Version 1.2 (July 17 2014)

- Export locmax|locmin at the mahotas namespace level
- Break away ellipse_axes from eccentricity code as it can be useful on its own
- Add find() function
- Add mean_filter() function
- Fix cwatershed() overflow possibility
- Make labeled functions more flexible in accepting more types
- Fix crash in close_holes() with nD images (for n > 2)
- Remove matplotlibwrap
- Use standard setuptools for building (instead of numpy.distutils)
- Add overlay() function

2.23.11 Version 1.1.1 (July 4 2014)

- Fix crash in close_holes() with nD images (for n > 2)

2.23.12 1.1.0 (February 12 2014)

- Better error checking
- Fix interpolation of integer images using order 1
- Add resize_to & resize_rgb_to
- Add coveralls coverage
- Fix SLIC superpixels connectivity
- Add remove_regions_where function
- Fix hard crash in convolution
- Fix axis handling in convolve1d
- Add normalization to moments calculation

2.23.13 1.0.4 (2013-12-15)

- Add mahotas.demos.load()
- Add stretch_rgb() function
- Add demos to mahotas namespace
- Fix SLIC superpixels
2.23.14 1.0.3 (2013-10-06)

- Add border & as_slice arguments to bbox()
- Better error message in gaussian_filter
- Allow as_rgb() to take integer arguments
- Extend distance() to n-dimensions
- Update to newer Numpy APIs (remove direct access to PyArray members)

2.23.15 1.0.2 (July 10 2013)

- Fix requirements filename

2.23.16 1.0.1 (July 9 2013)

- Add lbp_transform() function
- Add rgb2sepia function
- Add mahotas.demos.nuclear_image() function
- Work around matplotlib.imsave’s implementation of greyscale
- Fix Haralick bug (report & patch by Tony S Yu)
- Add count_binary1s() function

2.23.17 1.0 (May 21 2013)

- Fix a few corner cases in texture analysis
- Integrate with travis
- Update citation (include DOI)

2.23.18 0.99 (May 4 2013)

- Make matplotlib a soft dependency
- Add demos.image_path() function
- Add citation() function

This version is 1.0 beta.

2.23.19 0.9.8 (April 22 2013)

- Use matplotlib as IO backend (fallback only)
- Compute dense SURF features
- Fix sobel edge filtering (post-processing)
- Faster 1D convolutions (including faster Gaussian filtering)
- Location independent tests (run mahotas.tests.run() anywhere)
• Add labeled.is_same_labeling function
• Post filter SLIC for smoother regions
• Fix compilation warnings on several platforms

2.23.20  0.9.7 (February 03 2013)

• Add haralick_features function
• Add out parameter to morph functions which were missing it
• Fix erode() & dilate() with empty structuring elements
• Special case binary erosion/dilation in C-Arrays
• Fix long-standing warning in TAS on zero inputs
• Add verbose argument to tests.run()
• Add circle_se to morph
• Allow loc(max|min) to take floating point inputs
• Add Bernsen local thresholding (bernsen and gbernsen functions)

2.23.21  0.9.6 (December 02 2012)

• Fix distance() of non-boolean images (issue #24 on github)
• Fix encoding issue on PY3 on Mac OS (issue #25 on github)
• Add relabel() function
• Add remove_regions() function in labeled module
• Fix median_filter() on the borders (respect the mode argument)
• Add mahotas.color module for conversion between colour spaces
• Add SLIC Superpixels
• Many improvements to the documentation

2.23.22  0.9.5 (November 05 2012)

• Fix compilation in older G++
• Faster Otsu thresholding
• Python 3 support without 2to3
• Add cdilate function
• Add subm function
• Add tophat transforms (functions tophat_close and tophat_open)
• Add mode argument to euler() (patch by Karol M. Langner)
• Add mode argument to bwperim() & borders() (patch by Karol M. Langner)
2.23.23 0.9.4 (October 10 2012)

- Fix compilation on 32-bit machines (Patch by Christoph Gohlke)

2.23.24 0.9.3 (October 9 2012)

- Fix interpolation (Report by Christoph Gohlke)
- Fix second interpolation bug (Report and patch by Christoph Gohlke)
- Update tests to newer numpy
- Enhanced debug mode (compile with DEBUG=2 in environment)
- Faster morph.dilate()
- Add labeled.labeled_max & labeled.labeled_min (This also led to a refactoring of the labeled_* code)
- Many documentation fixes

2.23.25 0.9.2 (September 1 2012)

- Fix compilation on Mac OS X 10.8 (reported by Davide Cittaro)
- Freeimage fixes on Windows by Christoph Gohlke
- Slightly faster _filter implementation

2.23.26 0.9.1 (August 28 2012)

- Python 3 support (you need to use 2to3)
- Haar wavelets (forward and inverse transform)
- Daubechies wavelets (forward and inverse transform)
- Corner case fix in Otsu thresholding
- Add soft_threshold function
- Have polygon.convexhull return an ndarray (instead of a list)
- Memory usage improvements in regmin/regmax/close_holes (first reported as issue #9 by thanasi)

2.23.27 0.9 (July 16 2012)

- Auto-convert integer to double on gaussian_filter (previously, integer values would result in zero-valued outputs).
- Check for integer types in (reglloc)(maximin)
- Use name out instead of output for output arguments. This matches Numpy better
- Switched to MIT License
2.23.28 0.8.1 (June 6 2012)

- Fix gaussian_filter bug when order argument was used (reported by John Mark Agosta)
- Add morph.cerode
- Improve regmax() & regmin(). Rename previous implementations to locmax() & locmin()
- Fix erode() on non-contiguous arrays

2.23.29 0.8 (May 7 2012)

- Move features to submodule
- Add morph.open function
- Add morph.regmax & morph.regmin functions
- Add morph.close function
- Fix morph.dilate crash

2.23.30 0.7.3 (March 14 2012)

- Fix installation of test data
- Greyscale erosion & dilation
- Use imread module (if available)
- Add output argument to erode() & dilate()
- Add 14th Haralick feature (patch by MattyG) — currently off by default
- Improved zernike interface (zernike_moments)
- Add remove_bordering to labeled
- Faster implementation of bwperim
- Add roundness shape feature

2.23.31 0.7.2 (February 13 2012)

There were two minor additions:

- Add as_rgb (especially useful for interactive use)
- Add Gaussian filtering (from scipy.ndimage)

And a few bugfixes:

- Fix type bug in 32 bit machines (Bug report by Lech Wiktor Piotrowski)
- Fix convolve1d
- Fix rank_filter
2.23.32 0.7.1 (January 6 2012)

The most important change fixed compilation on Mac OS X

Other changes:

- Add convolve1d
- Check that convolution arguments have right dimensions (instead of crashing)
- Add descriptor_only argument to surf.descriptors
- Specify all function signatures on freeimage.py

For version 0.7 (Dec 5 2011):

The big change was that the dependency on scipy was removed. As part of this process, the interpolate submodule was added. A few important bug fixes as well.

- Allow specification of centre in Zernike moment computation
- Fix Local Binary Patterns
- Remove dependency on scipy
- Add interpolate module (from scipy.ndimage)
- Add labeled_sum & labeled_sizes
- gvoronoi no longer depends on scipy
- mahotas is importable without scipy
- Fix bugs in 2D TAS (reported by Jenn Bakal)
- Support for 1-bit monochrome image loading with freeimage
- Fix GIL handling on errors (reported by Gareth McCaughan)
- Fix freimage for 64-bit computers

For version 0.6.6 (August 8 2011):
- Fix fill_polygon bug (fix by joferkington)
- Fix Haralick feature 6 (fix by Rita Simões)
- Implement `morph.getstructuring_element` for ndim > 2. This implies that functions such as `label()` now also work in multiple dimensions
- Add median filter & `rank_filter` functions
- Add template_match function
- Refactor by use of mahotas.internal
- Better error message for when the compiled modules cannot be loaded - Update contact email. All docs in numpydoc format now.

For version 0.6.5:
- Add `max_points` & `descriptor_only` arguments to mahotas.surf
- Fix haralick for 3-D images (bug report by Rita Simões)
- Better error messages
- Fix hit&miss for non-boolean inputs
- Add `label()` function

For version 0.6.4:

- Fix bug in `cwatershed()` when using return_lines=1
- Fix bug in `cwatershed()` when using equivalent types for image and markers
- Move tests to mahotas.tests and include them in distribution
- Include ChangeLog in distribution
- Fix compilation on the Mac OS
- Fix compilation warnings on gcc

For version 0.6.3:

- Improve `mahotas.stretch()` function
• Fix corner case in surf (when determinant was zero)
• threshold argument in mahotas.surf
• imreadfromblob() & imsavetoblob() functions
• max_points argument for mahotas.surf.interest_points()
• Add mahotas.labeled.borders function

For version 0.6.2:

Bugfix release:
• Fix memory leak in _surf
• More robust searching for freeimage
• More functions in mahotas.surf() to retrieve intermediate results
• Improve compilation on Windows (patches by Christoph Gohlke)

For version 0.6.1:
• Release the GIL in morphological functions
• Convolution
• just_filter option in edge.sobel()
• mahotas.labeled functions
• SURF local features

For version 0.6:
• Improve Local Binary patterns (faster and better interface)
• Much faster erode() (10x faster)
• Faster dilate() (2x faster)
• TAS for 3D images
• Haralick for 3D images

2.24 Full API Documentation

A package for computer vision in Python.

2.24.1 Main Features

features Compute global and local features (several submodules, include SURF and Haralick features)
convolve Convolution and wavelets
morph Morphological features. Most are available at the mahotas level, include erode(), dilate()...
watershed Seeded watershed implementation
imread/imsave read/write image

Documentation: https://mahotas.readthedocs.io/
Citation:
mahotas.as_rgb(r, g, b)

Returns an RGB image with r in the red channel, g in the green, and b in the blue. The channels are contrast stretched.

If any of the channels is None, that channel is set to zero. The same can be achieved by passing 0 as that channels value. In fact, passing a number as a channel value will set the whole channel to that value.

**Parameters**

- r, g, b : array-like or int, optional
  The channels can be of any type or None. At least one must be not None and all must have the same shape.

**Returns**

- rgb : ndarray
  RGB ndarray

mahotas.bbox(img, border=[0], as_slice=[False])

Calculate the bounding box of image img.

**Parameters**

- img : ndarray
  Any integer image type

**Returns**

- min1, max1, min2, max2 : int, int, int
  These are such that img[min1:max1, min2:max2] contains all non-zero pixels.
  Returned when as_slice is false (the default)

- s : slice
  A slice representation of the bounding box. Returned when as_slice is true

mahotas.border(labeled, i, j, Bc={3x3 cross}, out={np.zeros(labeled.shape, bool)}, always_return=True)

Compute the border region between i and j regions.

A pixel is on the border if it has value i (or j) and a pixel in its neighbourhood (defined by Bc) has value j (or i).

**Parameters**

- labeled : ndarray of integer type
  input labeled array

- i : integer

- j : integer

- Bc : structure element, optional

- out : ndarray of same shape as labeled, dtype=bool, optional
  where to store the output. If None, a new array is allocated

- always_return : bool, optional
  if false, then, in the case where there is no pixel on the border, returns None. Otherwise (the default), it always returns an array even if it is empty.

**Returns**

- border_img : boolean ndarray
  Pixels are True exactly where there is a border between i and j in labeled

mahotas.borders(labeled, Bc={3x3 cross}, out={np.zeros(labeled.shape, bool)})

Compute border pixels

A pixel is on a border if it has value i and a pixel in its neighbourhood (defined by Bc) has value j, with i != j.
Parameters labeled : ndarray of integer type
    input labeled array
    Bc : structure element, optional
    out : ndarray of same shape as labeled, dtype=bool, optional
        where to store the output. If None, a new array is allocated
    mode : {'reflect', 'nearest', 'wrap', 'mirror', 'constant' [default], 'ignore'}
        How to handle borders

Returns border_img : boolean ndarray
    Pixels are True exactly where there is a border in labeled

mahotas.bwperim(bw, n=4)
Find the perimeter of objects in binary images.

A pixel is part of an object perimeter if its value is one and there is at least one zero-valued pixel in its neighbor-
borhood.

By default the neighborhood of a pixel is 4 nearest pixels, but if n is set to 8 the 8 nearest pixels will be con-
considered.

Parameters bw : ndarray
    A black-and-white image (any other image will be converted to black & white)
    n : int, optional
        Connectivity. Must be 4 or 8 (default: 4)
    mode : {'reflect', 'nearest', 'wrap', 'mirror', 'constant' [default], 'ignore'}
        How to handle borders

Returns perim : ndarray
    A boolean image

See also:

borders function This is a more generic function

mahotas.cdilate(f, g, Bc={3x3 cross}, n=1)
Conditional dilation
cdilate creates the image y by dilating the image f by the structuring element Bc conditionally to the image g.
This operator may be applied recursively n times.

Parameters f : Gray-scale (uint8 or uint16) or binary image.
    g : Conditioning image. (Gray-scale or binary).
    Bc : Structuring element (default: 3x3 cross)
    n : Number of iterations (default: 1)

Returns y : Image

mahotas.center_of_mass(img, labels=None)
Returns the center of mass of img.

If labels is given, then it returns L centers of mass, one for each region identified by labels (including region 0).
Parameters img : ndarray

labels : ndarray, optional

A labeled array (i.e., an array of integers of the same shape as img such that each “object” is identified by areas with different values).

Returns coords : ndarray

The exact shape of the output depends on whether the labels argument was used. If labels is None, then the return value is a 1-ndarray of coordinates (size = len(img.shape)); otherwise, the return value is a 2-ndarray of coordinates (shape = (labels.max()+1, len(img.shape)).

mahotas.cerode(f, g, Bc={3x3 cross}, out={np.empty_as(A)})

Conditional morphological erosion.

The type of operation depends on the dtype of A! If boolean, then the erosion is binary, else it is greyscale erosion. In the case of greyscale erosion, the smallest value in the domain of Bc is interpreted as -Inf.

Parameters f : ndarray

input image

g : ndarray

conditional image

Bc : ndarray, optional

Structuring element. By default, use a cross (see getstructuring_elem for details on the default).

Returns conditionally_eroded : ndarray

eroded version of f conditioned on g

See also:

erode function Unconditional version of this function
dilate

mahotas.close(f, Bc={3x3 cross}, out={np.empty_like(f)})

Morphological closing.

close creates the image y by the morphological closing of the image f by the structuring element Bc. In the binary case, the closing by a structuring element Bc may be interpreted as the intersection of all the binary images that contain the image f and have a hole equal to a translation of Bc. In the gray-scale case, there is a similar interpretation taking the functions umbra.

Parameters f : ndarray

Gray-scale (uint8 or uint16) or binary image.

Bc : ndarray, optional

Structuring element. (Default: 3x3 elementary cross).

out : ndarray, optional

Output array

output : deprecated

Do not use
Returns y : ndarray

See also:

open function

mahotas.close_holes(ref, Bc=None)
closed = close_holes(ref, Bc=None):

Close Holes

Parameters ref : ndarray

Reference image. This should be a binary image.

Bc : structuring element, optional

Default: 3x3 cross

Returns closed : ndarray

superset of ref (i.e. with closed holes)

mahotas.convolve(f, weights, mode='reflect', cval=0.0, out={new array})

Convolution of f and weights

Convolution is performed in doubles to avoid over/underflow, but the result is then cast to f.dtype. This conversion may result in over/underflow when using small integer types or unsigned types (if the output is negative). Converting to a floating point representation avoids this issue:

\[
c = \text{convolve}(f.\text{astype}(float), \text{kernel})
\]

Parameters f : ndarray

input. Any dimension is supported

weights : ndarray

weight filter. If not of the same dtype as f, it is cast

mode : {'reflect' [default], 'nearest', 'wrap', 'mirror', 'constant', 'ignore'}

How to handle borders

cval : double, optional

If mode is constant, which constant to use (default: 0.0)

out : ndarray, optional

Output array. Must have same shape and dtype as f as well as be C-contiguous.

Returns convolved : ndarray of same dtype as f

mahotas.convolve1d(f, weights, axis, mode='reflect', cval=0.0, out={new array})

Convolution of f and weights along axis axis.

Convolution is performed in doubles to avoid over/underflow, but the result is then cast to f.dtype.

Parameters f : ndarray

input. Any dimension is supported

weights : 1-D ndarray

weight filter. If not of the same dtype as f, it is cast
axis : int
Axis along which to convolve

mode : {'reflect' [default], 'nearest', 'wrap', 'mirror', 'constant', 'ignore'}
How to handle borders
cval : double, optional
If mode is constant, which constant to use (default: 0.0)
out : ndarray, optional
Output array. Must have same shape and dtype as f as well as be C-contiguous.

Returns convolved : ndarray of same dtype as f

See also:

convolve function generic convolution

mahotas.croptobbox(img, border=0)
Returns a version of img cropped to the image’s bounding box

Parameters img : ndarray
Integer image array

border : int, optional
whether to add a border (default no border)

Returns nimg : ndarray
A subimage of img.

mahotas.cwatershed(surface, markers, Bc=None, return_lines=False) W, WL = cwatershed(surface, markers, Bc=None, return_lines=True)
Seeded watershed in n-dimensions
This function computes the watershed transform on the input surface (which may actually be an n-dimensional volume).
This function requires initial seed points. A traditional way of initializing watershed is to use regional minima:

```python
minima = mh.regmin(f)
markers, nr_markers = mh.label(minima)
W = cwatershed(f, minima)
```

Parameters surface : image

markers : image
initial markers (must be a labeled image, i.e., one where 0 represents the background and higher integers represent different regions)

Bc : ndarray, optional
structuring element (default: 3x3 cross)

return_lines : boolean, optional
whether to return separating lines (in addition to regions)

Returns W : integer ndarray (int64 ints)
Regions image (i.e., \( W_{i,j} == \text{region for pixel } (i,j) \))

\( WL \) : Lines image (if \( \text{return\_lines}==\text{True} \))

\texttt{mahotas.daubechies}(f, code, inline=False)

Daubechies wavelet transform

This function works best if the image sizes are powers of 2!

**Parameters**
\( f \) : ndarray
2-D image

\( code \) : str
One of ‘D2’, ‘D4’, ... ‘D20’

\( inline \) : bool, optional
Whether to write the results to the input image. By default, a new image is returned. Integer images are always converted to floating point and copied.

**See also:**

\texttt{haar} function Haar transform (equivalent to D2)

\texttt{mahotas.dilate}(A, Bc=None, out=None, output=None)

Morphological dilation.

The type of operation depends on the \( \text{dtype} \) of \( A \)! If boolean, then the dilation is binary, else it is greyscale dilation. In the case of greyscale dilation, the smallest value in the domain of \( Bc \) is interpreted as +Inf.

**Parameters**
\( A \) : ndarray of bools
input array

\( Bc \) : ndarray, optional
Structuring element. By default, use a cross (see \texttt{get\_structuring\_elem} for details on the default).

\( out \) : ndarray, optional
output array. If used, this must be a C-array of the same \( \text{dtype} \) as \( A \). Otherwise, a new array is allocated.

\texttt{output} : deprecated
Do not use

**Returns**
\( \text{dilated} \) : ndarray
dilated version of \( A \)

**See also:**

\texttt{erode}

\texttt{mahotas.disk}(radius, dim=2)

Return a binary disk structuring element of radius \( \text{radius} \) and dimension \( \text{dim} \)

**Parameters**
\( \text{radius} \) : int
Radius (in pixels) of returned disk

\( \text{dim} \) : int, optional
mahotas Documentation, Release 1.4.3

Dimension of returned array (default: 2)

**Returns** D : boolean ndarray

```
mahotas.distance(bw, metric='euclidean2')
```

Computes the distance transform of image `bw`:

```
dmap[i, j] = min_{i', j'} { (i-i')**2 + (j-j')**2 | !bw[i', j'] }
```

That is, at each point, compute the distance to the background.

If there is no background, then a very high value will be returned in all pixels (this is a sort of infinity).

**Parameters**

- **bw** : ndarray
  
  If boolean, **False** will denote the background and **True** the foreground. If not boolean, this will be interpreted as `bw != 0` (this way you can use labeled images without any problems).

- **metric** : str, optional
  
  one of 'euclidean2' (default) or 'euclidean'

**Returns**

- **dmap** : ndarray
  
  distance map

**References**

For 2-D images, the following algorithm is used:


For n-D images (with n > 2), a slower hand-craft method is used.

```
mahotas.dog(img, sigma1 = 2, thresh= None, just_filter = False)
```

Compute edges using the Difference of Gaussian (DoG) operator.

`edges` is a binary image of edges.

**Parameters**

- **img** : Any 2D-ndarray

  - **sigma1** : the sigma value of the first Gaussian filter. The second filter will have sigma value 1.001*sigma1

  - **multiplier** : the multiplier to get sigma2. sigma2 = sigma1 * multiplier

  - **just_filter** : boolean, optional

    If true, then return the result of filtering the image with the DoG filters, no zero-crossing is detected (default is False).

**Returns**

- **edges** : ndarray

  Binary image of edges, unless `just_filter`, in which case it will be an array of floating point values.

```
mahotas.erode(A, Bc={3x3 cross}, out={np.empty_as(A)})
```

Morphological erosion.

The type of operation depends on the `dtype` of `A`. If boolean, then the erosion is binary, else it is greyscale erosion. In the case of greyscale erosion, the smallest value in the domain of `Bc` is interpreted as -Inf.
Parameters  

**A**: ndarray  
input image  

**Bc**: ndarray, optional  
Structuring element. By default, use a cross (see `getstructuringelem` for details on the default).  

**out**: ndarray, optional  
output array. If used, this must be a C-array of the same `dtype` as `A`. Otherwise, a new array is allocated.  

Returns  

**erosion**: ndarray  
eroded version of `A`  

See also:  

dilate  

mahotas.euler(`f`, `n=8`)  
Compute the Euler number of image `f`  
The Euler number is also known as the Euler characteristic given that many other mathematical objects are also known as Euler numbers.  

Parameters  

**f**: ndarray  
A 2-D binary image  

**n**: int, optional  
Connectivity, one of (4,8). default: 8  

**mode**: {'reflect', 'nearest', 'wrap', 'mirror', 'constant' [default]}  
How to handle borders  

Returns  

**euler_nr**: int  
Euler number  

References  
The following algorithm is used:  

*A Fast Algorithm for Computing the Euler Number of an Image and its VLSI Implementation*, doi: 10.1109/ICVD.2000.812628  

mahotas.find(`f`, `template`)  
Match template to image exactly  
coordinates = find(`f`, `template`)  
The output is in the same format as the `np.where` function.  

Parameters  

**f**: ndarray  
input. Currently, only 2-dimensional images are supported.  

**template**: ndarray  
Template to match. Must be explicitly passed, no default.
Returns match : np.array
coordinates : np.array

These are the coordinates of the match. The format is similar to the output of np.where, but in an ndarray.

mahotas.fullhistogram(img)
Return a histogram with bins 0, 1, ..., “img.max()“.
After calling this function, it will be true that hist[i] == (img == i).sum(), for all i.

Parameters img : array-like of an unsigned type
input image.

Returns hist : an ndarray of type np.uint32
This will be of size img.max() + 1.

mahotas.gaussian_filter(array, sigma, order=0, mode='reflect', cval=0., out={np.empty_like(array)})
Multi-dimensional Gaussian filter.

Parameters array : ndarray
input array, any dimension is supported. If the array is an integer array, it will be converted to a double array.
sigma : scalar or sequence of scalars
standard deviation for Gaussian kernel. The standard deviations of the Gaussian filter are given for each axis as a sequence, or as a single number, in which case it is equal for all axes.
order : {0, 1, 2, 3} or sequence from same set, optional
The order of the filter along each axis is given as a sequence of integers, or as a single number. An order of 0 corresponds to convolution with a Gaussian kernel. An order of 1, 2, or 3 corresponds to convolution with the first, second or third derivatives of a Gaussian. Higher order derivatives are not implemented
How to handle borders
cval : double, optional
If mode is constant, which constant to use (default: 0.0)
out : ndarray, optional
Output array. Must have same shape as array as well as be C-contiguous. If array is an integer array, this must be a double array; otherwise, it must have the same type as array.

Returns filtered : ndarray
Filtered version of array

Notes

The multi-dimensional filter is implemented as a sequence of one-dimensional convolution filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a limited precision, the results may be imprecise because intermediate results may be stored with insufficient precision.
mahotas.gaussian_filter1d(array, sigma, axis=-1, order=0, mode='reflect', cval=0.,
out={np.empty_like(array)})

One-dimensional Gaussian filter.

Parameters
array : ndarray
    input array of a floating-point type

sigma : float
    standard deviation for Gaussian kernel (in pixel units)

axis : int, optional
    axis to operate on

order : {0, 1, 2, 3}, optional
    An order of 0 corresponds to convolution with a Gaussian kernel. An order of 1, 2, or
    3 corresponds to convolution with the first, second or third derivatives of a Gaussian.
    Higher order derivatives are not implemented

mode : {'reflect' [default], 'nearest', 'wrap', 'mirror', 'constant', 'ignore'}
    How to handle borders

cval : double, optional
    If mode is constant, which constant to use (default: 0.0)

out : ndarray, optional
    Output array. Must have same shape and dtype as array as well as be C-contiguous.

Returns
filtered : ndarray
    Filtered version of array

mahotas.get_structuring_elem(A, Bc)

Retrieve appropriate structuring element

Parameters
A : ndarray
    array which will be operated on

Bc : None, int, or array-like
    None Then Bc is taken to be 1
    An integer

There are two associated semantics:

    connectivity Bc[y,x] = [[ is |y - 1| + |x - 1| <= Bc_i
                      ]]

    count Bc.sum() == Bc_i This is the more traditional meaning (when
one writes that “4-connected”, this is what one has in mind).

Fortunately, the value itself allows one to distinguish between the two semantics
and, if used correctly, no ambiguity should ever occur.

An array This should be of the same nr. of dimensions as A and will be passed
through if of the right type. Otherwise, it will be cast.

Returns Bc_out : ndarray
    Structuring element. This array will be of the same type as A, C-contiguous.
mahotas.haar (f, preserve_energy=True, inline=False)
Haar transform

Parameters f : 2-D ndarray
Input image

preserve_energy : bool, optional
Whether to normalise the result so that energy is preserved (the default).

inline : bool, optional
Whether to write the results to the input image. By default, a new image is returned. Integer images are always converted to floating point and copied.

See also:
ihaar function Reverse Haar transform

mahotas.hitmiss (input, Bc, out=np.zeros_like(input))
Hit & Miss transform

For a given pixel position, the hit&miss is True if, when Bc is overlaid on input, centered at that position, the $1$ values line up with "$1$"s, while the "$0$"s line up with "$0$"s ($2$'s correspond to don't care).

Parameters input : input ndarray
This is interpreted as a binary array.

Bc : ndarray
hit & miss template, values must be one of (0, 1, 2)

out : ndarray, optional
Used for output. Must be Boolean ndarray of same size as input

output : deprecated
Do not use

Returns filtered : ndarray

Examples

```python
print(hitmiss(np.array(
    [[0,0,0,0,0],
     [0,1,1,1,1],
     [0,0,1,1,1]],
    np.array([[
     [0,0,0],
     [2,1,1],
     [2,1,1]])
))
```

prints::

```
[[ 0  0  0  0  0]
 [ 0  0  1  1  0]
 [ 0  0  0  0  0]]
```

mahotas.idaubechies (f, code, inline=False)
Daubechies wavelet inverse transform

Parameters f : ndarray
2-D image

code : str
    One of ‘D2’, ‘D4’, ... ‘D20’
inline : bool, optional
    Whether to write the results to the input image. By default, a new image is returned. Integer images are always converted to floating point and copied.

See also:
    haar function Haar transform (equivalent to D2)

mahotas.ihaar(f, preserve_energy=True, inline=False)
Reverse Haar transform

ihaar(haar(f)) is more or less equal to f (equal, except for possible rounding issues).

Parameters f : 2-D ndarray
    Input image. If it is an integer image, it is converted to floating point (double).
preserve_energy : bool, optional
    Whether to normalise the result so that energy is preserved (the default).
inline : bool, optional
    Whether to write the results to the input image. By default, a new image is returned. Integer images are always converted to floating point and copied.

Returns f : ndarray

See also:
    haar function Forward Haar transform

mahotas.imread(filename, as_grey=False)
Read an image into a ndarray from a file.

This function depends on PIL (or Pillow) being installed.

Parameters filename : str
    filename
as_grey : boolean, optional
    Whether to convert to grey scale image (default: no)

mahotas.imresize(img, nsize, order=3)
Resizes image

This function works in two ways: if nsize is a tuple or list of integers, then the result will be of this size; otherwise, this function behaves the same as mh.interpolate.zoom

Parameters img : ndarray
    nsize : float or tuple(float) or tuple(integers)
      Size of return. Meaning depends on the type float:  img’.shape[i] = nsize *
      img.shape[i] tuple of float:  img’.shape[i] = nsize[i] * img.shape[i] tuple of
      int:  img’.shape[i] = nsize[i]

order : integer, optional
    Spline order to use (default: 3)

Returns img’ : ndarray

See also:
**zoom** Similar function

**scipy.misc.pilutil.imresize** Similar function

`mahotas.imsave(filename, array)`

Writes array into file filename

This function depends on PIL (or Pillow) being installed.

**Parameters**
- `filename`: str
  - path on file system
- `array`: ndarray-like

`mahotas.label(array, Bc={3x3 cross}, output={new array})`

Label the array, which is interpreted as a binary array

This is also called connected component labeled, where the connectivity is defined by the structuring element Bc.


**Parameters**
- `array`: ndarray
  - This will be interpreted as binary array
- `Bc`: ndarray, optional
  - This is the structuring element to use
- `output`: ndarray, optional
  - Output array. Must be a C-array, of type np.int32

**Returns**
- `labeled`: ndarray
  - Labeled result
- `nr_objects`: int
  - Number of objects

`mahotas.labeled_sum(array, labeled, minlength=None)`

Labeled sum. sum will be an array of size labeled.max() + 1, where sum[i] is equal to np.sum(array[labeled == i]).

**Parameters**
- `array`: ndarray of any type
- `labeled`: int ndarray
  - Label map. This is the same type as returned from mahotas.label()
- `minlength`: int, optional
  - Minimum size of return array. If labeled has fewer than minlength regions, 0s are added to the result. (optional)

**Returns**
- `sums`: 1-d ndarray of array.dtype

`mahotas.laplacian_2D(array, alpha = 0.2)`

2D Laplacian filter.

**Parameters**
- `array`: ndarray
  - input 2D array. If the array is an integer array, it will be converted to a double array.
- `alpha`: scalar or sequence of scalars
  - controls the shape of Laplacian operator. Must be 0-1. A larger values makes the operator empahsize the diagonal direction.
mahotas Documentation, Release 1.4.3

Returns filtered : ndarray
Filtered version of array

mahotas.locmax (f, Bc={3x3 cross}, out={np.empty(f.shape, bool)})
Local maxima
Parameters f : ndarray
    Bc : ndarray, optional
        structuring element
    out : ndarray, optional
        Used for output. Must be Boolean ndarray of same size as f
output : deprecated
        Do not use
Returns filtered : ndarray
    boolean image of same size as f.

See also:

regmax function Regional maxima. This is a stricter criterion than the local maxima as it takes the whole object into account and not just the neighbourhood defined by Bc:

0 0 0 0 0 0 0 2 0 0 0 0 2 0 0 0 0 3 0 0 0 3 0 0 0 0 0 0 0 0
0 0 3 0 0 0 0 0 0 The top 2 is a local maximum because it has the maximal value in its neighbourhood, but it is not a regional maximum.

locmin function Local minima

mahotas.locmin (f, Bc={3x3 cross}, out={np.empty(f.shape, bool)})
Local minima
Parameters f : ndarray
    Bc : ndarray, optional
        structuring element
    out : ndarray, optional
        Used for output. Must be Boolean ndarray of same size as f
output : deprecated
        Do not use
Returns filtered : ndarray
    boolean image of same size as f.

See also:

locmax function Regional maxima

mahotas.majority_filter (img, N=3, out={np.empty(img.shape, np.bool)})
Majority filter
filtered[y,x] is positive if the majority of pixels in the squared of size N centred on (y,x) are positive.
Parameters img : ndarray
    input img (currently only 2-D images accepted)
    N : int, optional
        size of filter (must be odd integer), defaults to 3.
    out : ndarray, optional
Used for output. Must be Boolean ndarray of same size as img

**output** : deprecated
Do not use

**Returns** filtered : ndarray
boolean image of same size as img.

```python
mahotas.mean_filter(f, Bc, mode='ignore', cval=0.0, out=None)
```
Mean filter. The value at mean[i, j] will be the mean of the values in the neighbourhood defined by Bc.

**Parameters**
- **f**: ndarray
  - input. Any dimension is supported
- **Bc**: ndarray
  - Defines the neighbourhood. Must be explicitly passed, no default.
- **mode**: {'reflect', 'nearest', 'wrap', 'mirror', 'constant', 'ignore' [ignore]}
  - How to handle borders. The default is to ignore points beyond the border, so that the means computed near the border include fewer elements.
- **cval**: double, optional
  - If mode is constant, which constant to use (default: 0.0)
- **out**: ndarray, optional
  - Output array. Must be a double array with the same shape as f as well as be C-contiguous.

**Returns** mean : ndarray of type double and same shape as f

See also:

- **median_filter** An alternative filtering method

```python
mahotas.median_filter(f, Bc={square}, mode='reflect', cval=0.0, out={np.empty(f.shape, f.dtype})
```
Median filter

**Parameters**
- **f**: ndarray
  - input. Any dimension is supported
- **Bc**: ndarray or int, optional
  - Defines the neighbourhood, default is a square of side 3.
- **mode**: {'reflect' [default], 'nearest', 'wrap', 'mirror', 'constant', 'ignore'}
  - How to handle borders
- **cval**: double, optional
  - If mode is constant, which constant to use (default: 0.0)
- **out**: ndarray, optional
  - Output array. Must have same shape and dtype as f as well as be C-contiguous.

**Returns** median : ndarray of same type and shape as f
median[i,j] is the median value of the points in f close to (i,j)

```python
mahotas.moments(img, p0, p1, cm=(0, 0), convert_to_float=True)
```
Returns the p0-p1 moment of image img
The formula computed is
\[ \sum_{ij} \{ \text{img}[i,j] \cdot (i - c_0)^{p_0} \cdot (j - c_1)^{p_1} \} \]

where \(\text{cm} = (c_0,c_1)\). If \(\text{cm}\) is not given, then \((0,0)\) is used.

If image is of an integer type, then it is internally converted to np.float64, unless `convert_to_float` is False. The reason is that, otherwise, overflow is likely except for small images. Since this conversion takes longer than the computation, you can turn it off in case you are sure that your images are small enough for overflow to be an issue. Note that no conversion is made if \(\text{img}\) is of any floating point type.

**Parameters**

- `img` : 2-ndarray
  - An 2-d ndarray
- `p0` : float
  - Power for first dimension
- `p1` : float
  - Power for second dimension
- `cm` : (int,int), optional
  - center of mass (default: 0,0)
- `convert_to_float` : boolean, optional
  - whether to convert to floating point (default: True)
- `normalize` : boolean, optional
  - whether to normalize to size of image (default: False)

**Returns**

- `moment` : float
  - floating point number

**Example**

```python
mahotas.open(f, Bc={3x3 cross}, out={np.empty_like(f)})
```

Morphological opening.

`open` creates the image \(y\) by the morphological opening of the image \(f\) by the structuring element \(Bc\).

In the binary case, the opening by the structuring element \(Bc\) may be interpreted as the union of translations of \(b\) included in \(f\). In the gray-scale case, there is a similar interpretation taking the functions umbra.

**Parameters**

- `f` : ndarray
  - Gray-scale (uint8 or uint16) or binary image.
- `Bc` : ndarray, optional
  - Structuring element (default: 3x3 elementary cross).
- `out` : ndarray, optional
  - Output array
- `output` : deprecated
  - Do not use

**Returns**

- `y` : ndarray

**See also:**

- `open` function

**Example**

```python
mahotas.otsu(img, ignore_zeros=False)
```

Calculate a threshold according to the Otsu method.

Example:
import mahotas as mh
import mahotas.demos

im = mahotas.demos.nuclear_image()
# im is stored as RGB, let's convert to single 2D format:
im = im.max(2)

# Now, we compute Otsu:
t = mh.otsu(im)

# finally, we use the value to form a binary image:
bin = (im > t)


Parameters img:
an image as a numpy array.

    This should be of an unsigned integer type.

    ignore_zeros : Boolean

        whether to ignore zero-valued pixels (default: False)

Returns T:

    the threshold

mahotas.overlay(gray, red=None, green=None, blue=None, if_gray_dtype_not_uint8='stretch')

Create an image which is greyscale, but with possible boolean overlays.

Parameters gray:

    ndarray of type np.uint8

        Should be a greyscale image of type np.uint8

    red, green, blue : ndarray, optional

        boolean arrays

    if_gray_dtype_not_uint8 : str, optional

        What to do if gray is not of type np.uint8, must be one of 'stretch' (default): the function stretch is called. 'error': in this case, an error is raised

Returns overlaid:

    Colour image

mahotas.rank_filter(f, Bc, rank, mode='reflect', cval=0.0, out=None)

Rank filter. The value at ranked[i, j] will be the rank’th largest in the neighbourhood defined by ‘‘Bc.

Parameters f:

    input. Any dimension is supported

    Bc:

        Defines the neighbourhood. Must be explicitly passed, no default.

    rank:

        integer

    mode : {‘reflect’ [default], ‘nearest’, ‘wrap’, ‘mirror’, ‘constant’, ‘ignore’}

        How to handle borders

    cval : double, optional
If mode is constant, which constant to use (default: 0.0)

out : ndarray, optional
Output array. Must have same shape and dtype as f as well as be C-contiguous.

Returns ranked : ndarray of same type and shape as f
ranked[i,j] is the “rank”th value of the points in f close to (i,j)

See also:
median_filter A special case of rank_filter

mahotas.rc(img, ignore_zeros=False)
Calculate a threshold according to the Riddler-Calvard method.

Example:

import mahotas as mh
import mahotas.demos

im = mahotas.demos.nuclear_image()
# im is stored as RGB, let's convert to single 2D format:
im = im.max(2)

# Now, we compute a threshold:
t = mh.rc(im)

# Finally, we use the value to form a binary image:
bin = (im > t)

Parameters img : ndarray
Image of any type

ignore_zeros : boolean, optional
Whether to ignore zero valued pixels (default: False)

Returns T : float
threshold

mahotas.regmax(f, Bc={3x3 cross}, out={np.empty(f.shape, bool)})
Regional maxima. This is a stricter criterion than the local maxima as it takes the whole object into account and not just the neighbourhood defined by Bc:

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</tr>
</tbody>
</table>

The top 2 is a local maximum because it has the maximal value in its neighbourhood, but it is not a regional maximum.

Parameters f : ndarray

Bc : ndarray, optional
structuring element

out : ndarray, optional
Used for output. Must be Boolean ndarray of same size as f

output : deprecated
Do not use

Returns filtered : ndarray
boolean image of same size as f.

See also:

locmax function Local maxima. The local maxima are a superset of the regional maxima

mahotas.regmin (f, Bc={3x3 cross}, out={np.empty(f.shape, bool)})
Regional minima. See the documentation for regmax for more details.

Parameters f : ndarray

Bc : ndarray, optional
    structuring element

out : ndarray, optional
    Used for output. Must be Boolean ndarray of same size as f

output : deprecated
Do not use

Returns filtered : ndarray
boolean image of same size as f.

See also:

locmin function Local minima

mahotas.sobel (img, just_filter=False)
Compute edges using Sobel’s algorithm
edges is a binary image of edges computed according to Sobel’s algorithm.
This implementation is tuned to match MATLAB’s implementation.

Parameters img : Any 2D-ndarray

just_filter : boolean, optional
    If true, then return the result of filtering the image with the sobel filters, but do not
    threshold (default is False).

Returns edges : ndarray
    Binary image of edges, unless just_filter, in which case it will be an array of
    floating point values.

mahotas.stretch (img, arg0=None, arg1=None, dtype=<type 'numpy.uint8'>)
img’ = stretch(img, [dtype=np.uint8]) img’ = stretch(img, max, [dtype=np.uint8]) img’ = stretch(img, min, max, [dtype=np.uint8])
Contrast stretch the image to the range [0, max] (first form) or [min, max] (second form). The method is simple
linear stretching according to the formula:

\[ p’ = \text{max} \times \frac{(p - \text{img.min()})}{\text{img.ptp()}} + \text{min} \]

Parameters img : ndarray
input image. It is not modified by this function
**min**: integer, optional
- minimum value for output [default: 0]

**max**: integer, optional
- maximum value for output [default: 255]

**dtype**: dtype of output, optional
- [default: np.uint8]

**Returns**
- `img`: ndarray
  - resulting image. ndarray of same shape as *img* and type *dtype*.

```
mahotas.stretch_rgb(img, arg0=None, arg1=None, dtype=<type 'numpy.uint8'>)
```
- Variation of `stretch()` function that works per-channel on an RGB image

**Parameters**
- **img**: ndarray
  - input image. It is *not modified* by this function
- **min**: integer, optional
  - minimum value for output [default: 0]
- **max**: integer, optional
  - maximum value for output [default: 255]
- **dtype**: dtype of output, optional
  - [default: np.uint8]

**Returns**
- `img`: ndarray
  - resulting image. ndarray of same shape as *img* and type *dtype*.

**See also:**
- `stretch` function

```
mahotas.template_match(f, template, mode='reflect', cval=0.0, out=None, output=None)
```
- Match template to image

  ```
  match = template_match(f, template, mode='reflect', cval=0.0, out={np.empty_like(f)})
  ```

- The value at `match[i, j]` will be the difference (in squared euclidean terms), between `template` and a same sized window on `f` centered on that point.

- Note that the computation is performed using the same dtype as `f`. Thus may overflow if the template is large.

**Parameters**
- **f**: ndarray
  - input. Any dimension is supported
- **template**: ndarray
  - Template to match. Must be explicitly passed, no default.
- **mode**: {'reflect' [default], 'nearest', 'wrap', 'mirror', 'constant', 'ignore'}
  - How to handle borders
- **cval**: double, optional
  - If *mode* is constant, which constant to use (default: 0.0)
- **out**: ndarray, optional
  - Output array. Must have same shape and dtype as `f` as well as be C-contiguous.
Returns match : ndarray of same type and shape as f
match[i,j] is the squared euclidean distance between
f[i-s0:i+s0, j-s1:j+s1] and template (for appropriately defined
s0 and s1).

mahotas.thin(binimg)
Skeletonisation by thinning

Parameters binimg : ndarray
Binary input image

max_iter : int, optional
Maximum number of iterations (set to a negative number, the default, to run full
skeletonization)

Returns skel : Skeletonised version of binimg

mahotas.wavelet_center(f, border=0, dtype=float, cval=0.0)
f_c is a centered version of f with a shape that is composed of powers of 2.

Parameters f : ndarray
input image

border : int, optional
The border to use (default is no border)

dtype : type, optional
Type of f_c

cval : float, optional
Which value to fill the border with (default is 0)

Returns f_c : ndarray

See also:

wavelet_decenter function Reverse function

mahotas.wavelet_decenter(w, oshape, border=0)
Undoes the effect of wavelet_center

Parameters w : ndarray
Wavelet array

oshape : tuple
Desired shape

border : int, optional
The desired border. This must be the same value as was used for
wavelet_center

Returns f : ndarray
This will have shape oshape

See also:

wavelet_center function Forward function

mahotas.features.eccentricity(bwimage)
Compute eccentricity

Parameters bwimage : ndarray
Interpreted as a boolean image

Returns r : float

Eccentricity measure

```
mahotas.features.ellipse_axes(bwimage)
```

Parameters of the ‘image ellipse’

```
semimajor, semiminor = ellipse_axes(bwimage)
```

Returns the parameters of the constant intensity ellipse with the same mass and second order moments as the original image.

Parameters bwimage : ndarray

Interpreted as a boolean image

Returns semimajor : float

semiminor : float

References

Prokop, RJ, and Reeves, AP. 1992. CVGIP: Graphical Models and Image Processing 54(5):438-460

```
mahotas.features.haralick(f, ignore_zeros=False, preserve_haralick_bug=False, compute_14th_feature=False)
```

Compute Haralick texture features

Computes the Haralick texture features for the four 2-D directions or thirteen 3-D directions (depending on the dimensions of f).

ignore_zeros can be used to have the function ignore any zero-valued pixels (as background). If there are no-nonzero neighbour pairs in all directions, an exception is raised. Note that this can happen even with some non-zero pixels, e.g.:

```
0 0 0 0
0 1 0 0
0 1 0 0
0 0 0 0
```

would trigger an error when ignore_zeros=True as there are no horizontal non-zero pairs!

Parameters f : ndarray of integer type

input image. 2-D and 3-D images are supported.

distance: int, optional (default=1)

The distance to consider while computing the cooccurrence matrix.

ignore_zeros : bool, optional

Whether to ignore zero pixels (default: False).

Returns feats : ndarray of np.double

A 4x13 or 4x14 feature vector (one row per direction) if f is 2D, 13x13 or 13x14 if it is 3D. The exact number of features depends on the value of compute_14th_feature. Also, if either return_mean or return_mean_pnt is set, then a single dimensional array is returned.

Other Parameters preserve_haralick_bug : bool, optional
whether to replicate Haralick’s typo (default: False). You probably want to always set this to `False unless you want to replicate someone else’s wrong implementation.

**compute_14th_feature**: bool, optional

whether to compute & return the 14-th feature

**return_mean**: bool, optional

When set, the function returns the mean across all the directions (default: False).

**return_mean_ptp**: bool, optional

When set, the function returns the mean and ptp (point-to-point, i.e., difference between max() and min()) across all the directions (default: False).

**use_x_minus_y_variance**: bool, optional

Feature 10 (index 9) has two interpretations, as the variance of $|x-y|$ or as the variance of $P(|x-y|)$. In order to achieve compatibility with other software and previous versions of mahotas, mahotas defaults to using $\text{VAR}[P(|x-y|)]$; if this argument is True, then it uses $\text{VAR}[|x-y|]$ (default: False)

**Notes**

Haralick’s paper has a typo in one of the equations. This function implements the correct feature unless `preserve_haralick_bug` is True. The only reason why you’d want the buggy behaviour is if you want to match another implementation.

**References**

Cite the following reference for these features:

```python
@article{Haralick1973,
    author = {Haralick, Robert M. and Dinstein, Its'hak and Shanmugam, K.},
    journal = {Ieee Transactions On Systems Man And Cybernetics},
    number = {6},
    pages = {610--621},
    publisher = {IEEE},
    title = {Textural features for image classification},
    url = {http://ieeexplore.ieee.org/lpdocs/epic03/wrapper.htm?arnumber=4309314},
    volume = {3},
    year = {1973}
}
```

mahotas.features.**lbp** *(image, radius, points, ignore_zeros=False)*

Compute Linear Binary Patterns

The return value is a histogram of feature counts, where position $i$ corresponds to the number of pixels that had code $i$. The codes are compressed so that impossible codes are not used. Therefore, this is the $i$’th feature, not just the feature with binary code ‘‘i.

**Parameters**

- **image**: ndarray
  
  input image (2-D numpy ndarray)

- **radius**: number (integer or floating point)
  
  radius (in pixels)
**mahotas Documentation, Release 1.4.3**

**points**: integer

*nr of points to consider*

**ignore_zeros**: boolean, optional

*whether to ignore zeros (default: False)*

**Returns features**: 1-D numpy ndarray

*histogram of features. See above for a caveat on the interpretation of these.*

```python
mahotas.features.pftas(img, T=mahotas.threshold.otsu(img))
```

**Compute parameter free Threshold Adjacency Statistics**

TAS were presented by Hamilton et al. in “Fast automated cell phenotype image classification” (http://www.biomedcentral.com/1471-2105/8/110)

The current version is an adapted version which is free of parameters. The thresholding is done by using Otsu’s algorithm (or can be pre-computed and passed in by setting \(T\)), the margin around the mean of pixels to be included is the standard deviation. This was first published by Coelho et al. in “Structured Literature Image Finder: Extracting Information from Text and Images in Biomedical Literature” (http://www.springerlink.com/content/60634778710577t0/)

Also returns a version computed on the negative of the binarisation defined by Hamilton et al. Use tas() to get the original version of the features.

**Parameters**

*img*: ndarray, 2D or 3D

*input image*

*T*: integer, optional

*Threshold to use (default: compute with otsu)*

**Returns**

*values*: ndarray

*A 1-D ndarray of feature values*

```python
mahotas.features.roundness(bw)
```

**Roundness**

**Parameters**

*bw*: ndarray

*Interpreted as a boolean image*

**Returns**

*r*: float

```python
mahotas.features.tas(img)
```

**Compute Threshold Adjacency Statistics**

TAS were presented by Hamilton et al. in “Fast automated cell phenotype image classification” (http://www.biomedcentral.com/1471-2105/8/110)

Also returns a version computed on the negative of the binarisation defined by Hamilton et al. See also pftas() for a variation without any hardcoded parameters.

**Parameters**

*img*: ndarray, 2D or 3D

*input image*

**Returns**

*values*: ndarray

*A 1-D ndarray of feature values*

**See also:**

*pftas* Parameter free TAS
mahotas.features.zernike(im, degree, radius, cm=center_of_mass(im))

mahotas.features.zernike_moments(im, radius, degree=8, cm=center_of_mass(im))

Zernike moments through degree. These are computed on a circle of radius radius centered around cm (or the center of mass of the image, if the cm argument is not used).

Returns a vector of absolute Zernike moments through degree for the image im.

Parameters

im : 2-ndarray
    input image

radius : integer
    the maximum radius for the Zernike polynomials, in pixels. Note that the area outside the circle (centered on center of mass) defined by this radius is ignored.

degree : integer, optional
    Maximum degree to use (default: 8)

cm : pair of floats, optional
    the centre of mass to use. By default, uses the image’s centre of mass.

Returns

zvalues : 1-ndarray of floats
    Zernike moments

### mahotas.colors.rgb2gray(rgb_image, dtype=np.float)

Convert an RGB image to a grayscale image

The interpretation of RGB and greyscale values is very much object dependent (as anyone who has used an overhead projector which mangled their colour figures will have experienced). This function uses a typical method for conversion and will work acceptably well for typical use cases, but if you have strict requirements, consider implementing the conversion by yourself for fine control.

Parameters

array : ndarray of shape (a,b,3)
    dtyp e: dtype, optional
        dtype of return

Returns

grey : ndarray of dtype

### mahotas.colors.rgb2grey(rgb_image, dtype=np.float)

Convert an RGB image to a grayscale image

The interpretation of RGB and greyscale values is very much object dependent (as anyone who has used an overhead projector which mangled their colour figures will have experienced). This function uses a typical method for conversion and will work acceptably well for typical use cases, but if you have strict requirements, consider implementing the conversion by yourself for fine control.

Parameters

array : ndarray of shape (a,b,3)
    dtyp e: dtype, optional
        dtype of return

Returns

grey : ndarray of dtype

### mahotas.colors.rgb2lab(rgb, dtype=float)

Convert sRGB to L*a*b* coordinates

http://en.wikipedia.org/wiki/CIELAB

Parameters

rgb : ndarray
    Must be of shape (h,w,3)
mahotas Documentation, Release 1.4.3

**dtype** : dtype, optional

What dtype to return. Default will be floats

**Returns lab** : ndarray

mahotas.colors.rgb2sepia(rgb)

**Parameters rgb** : ndarray

Must be of shape (h,w,3)

**Returns sepi**a : ndarray

Output is of same shape as rgb

mahotas.colors.rgb2xyz(rgb, dtype=float)

Convert RGB to XYZ coordinates

The input is interpreted as sRGB. See Wikipedia for more details:

http://en.wikipedia.org/wiki/SRGB

**Parameters rgb** : ndarray

**dtype** : dtype, optional

What dtype to return

**Returns xyz** : ndarray

See also:

xyz2rgb function The reverse function

mahotas.colors.xyz2lab(xyz, dtype=float)

Convert CIE XYZ to L*a*b* coordinates

http://en.wikipedia.org/wiki/CIELAB

**Parameters xyz** : ndarray

**dtype** : dtype, optional

What dtype to return. Default will be floats

**Returns lab** : ndarray

See also:

xyz2rgb function The reverse function

mahotas.colors.xyz2rgb(xyz, dtype=float)

Convert XYZ to sRGB coordinates

The output should be interpreted as sRGB. See Wikipedia for more details:

http://en.wikipedia.org/wiki/SRGB

**Parameters xyz** : ndarray

**dtype** : dtype, optional

What dtype to return. Default will be floats

**Returns rgb** : ndarray

See also:

rgb2xyz function The reverse function
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