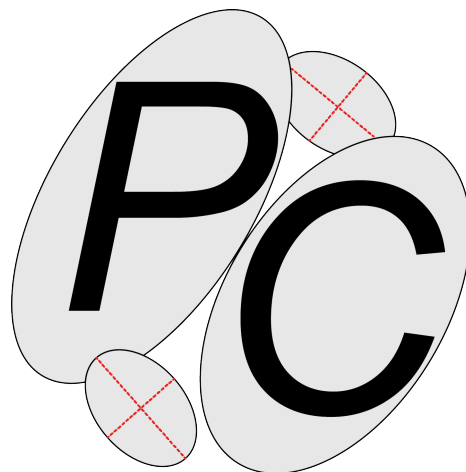

Installing and Running PebbleCounts

Grain-sizing algorithm for gravel-bed river imagery

Ben Purinton (purinton@uni-potsdam.de)



December 2018

Table of Contents

1	Introduction	3
1.1	Disclaimer	3
2	Quick note on imagery and running PebbleCounts	3
3	Installation	4
3.1	For the Pros	4
3.2	For Newbies	4
3.3	For Mac and Linux Users	5
4	Overview	5
5	Detailed Processing Steps	6
6	Command-line Options	9
6.1	Calculate Camera Resolution	9
6.1.1	Example Use	9
6.2	PebbleCounts	10
7	Step-by-Step Example	13
7.1	An important note on clicking!	17
7.2	Ouput	17

1 Introduction

This guide will walk you through the installation and running of PebbleCounts at the command-line. PebbleCounts is a Python based application for the identification and sizing of gravel from either orthorectified, georeferenced (**UTM projected**) images with known resolution or simple non-orthorectified images taken from directly overhead with the image resolution approximated by the camera parameters and shot height. It is a semi-automated program in that edge detection and k-means segmentation are performed automatically, but the user must interactively hand-click the well outlined pebbles and ignore the bad results. The software is extremely useful for area-by-number pebble counts without painstaking field work or the disruption of the natural environment via gravel removal. For the detailed background and validation, check out the publication accompanying the algorithm:

PUBLICATION DOI.

and cite it if you use the results in your own work.

Happy clicking!

1.1 Disclaimer

PebbleCounts is a free (released under GNU General Public License v3.0) and open-source application written by a geologist / amateur programmer. If you have problems installing or running the software contact me purinton@uni-potsdam.de and I can help!

2 Quick note on imagery and running PebbleCounts

Georeferenced ortho-photos should be in a **UTM projection**, providing the scale in meters. You can use the [gdal](#) command line utilities to [translate rasters between various projections](#). Because PebbleCounts doesn't allow you to save work in the middle of clicking it's recommended that you don't use images covering areas of more than 2 by 2 meters or so. Furthermore, the algorithm is most effective on images of 0.8-1.2 mm/pixel resolution, where a lower cutoff of 10-pixels is appropriate. Resampling can also be accomplished quickly in [gdal](#). For higher resolution (< 0.8 mm/pixel) imagery it's recommended not to go above 1 by 1 meter areas, particularly if there are many < 1 cm pebbles, and also to increase the lower cutoff (`-cutoff` flag) value to 25-pixels. If you want to cover a larger area simply break the image into smaller parts and process each individually, so you can give yourself a break. If at anytime you want to end the application simply press `CTRL + C`.

3 Installation

The first step is downloading the [GitHub repository](#) somewhere on your computer. The folder should contain:

1. Three Python scripts:
 - `PebbleCounts.py`
 - `PCfunctions.py`
 - `calculate_camera_resolution.py`
2. An `environment.yml` file containing the Python dependencies and a `install_openCV_env_ubuntu18.sh` shell script for creating an openCV environment with conda on Ubuntu
3. A folder `example_data` with two example images: one orthorectified and the other not
4. A folder `docs` containing this manual

3.1 For the Pros

For those familiar with Python, the best way to install PebbleCounts is by simply downloading the [GitHub repository](#), navigating to the PebbleCounts folder at the command line, ensuring all Python dependencies are installed (see the `environment.yml` file) and getting started by skipping ahead to **Command-line Options**:

3.2 For Newbies

For newcomers to Python, no worries! Installation should be a cinch on most machines and I'll describe it here for Windows. First of all you'll want the [Miniconda](#) Python package manager to setup a new Python environment for running the algorithm ([see this good article on Python package management](#)).

Download either the 32- or 64-bit installer of Python 3.x then follow the installation instructions. It's recommend to add Miniconda to the system `PATH` variable when prompted. PebbleCounts has a number of important dependencies including [gdal](#) for georeferenced raster manipulation, [openCV](#) for image manipulation and GUI operation, [scikit-image](#) for filtering and measuring, [scikit-learn](#) for k-means segmentation, along with a number of standard Python libraries including [numpy](#), [scipy](#), [matplotlib](#), and [tkinter](#).

Once you've got `conda` commands installed, you can open a command-line terminal and create a conda environment with:

```
conda create --name pebblecounts python=3.6 opencv \
```

```
scikit-image scikit-learn numpy gdal scipy matplotlib tk
```

Or just use the environment .yml file provided with:

```
conda env create -f environment.yml
```

and once installation is complete (and assuming no errors during the install) activate the new environment to run PebbleCounts by:

```
activate pebblecounts
```

Deactivate the environment to exit anytime by:

```
deactivate
```

3.3 For Mac and Linux Users

Those using Mac OS or Linux shouldn't have much trouble modifying the above commands slightly (just add a leading `source` to the `activate` and `deactivate` commands above). Note that installing openCV and getting it to function properly can be a pain sometimes, especially in the case of Linux. In that case it is recommended to find some instructions for installing openCV's Python API for your specific Linux operating system [online](#). The shell script `install_openCV_env_ubuntu18.sh` should allow for a clean install of an openCV inclusive `pebblecounts` conda environment on an Ubuntu v.18 system.

4 Overview

PebbleCounts can be summed up in the flow chart shown in Figure 1. To briefly summarize, PebbleCounts pre-processes the image by allowing the user to subset the full scene, then interactively mask shadows (interstices between grains) and color (for instance sand). Following this, PebbleCounts windows the scene at three different scales with the window size determined by the input resolution and expected maximum grain size provided by the user. This multi-scale approach allows the algorithm to "burrow" through the grain size distribution beginning by removing the largest grains and ending on the smallest, with the medium sizes in between. At each window the algorithm filters the image, detects edges, and employs [k-means segmentation](#) to get an approximate cleaned-up mask of potential separate pebbles. The window is then shown with the mask overlain and the user is able to click the **good** looking grains and leave out the **bad** ones (see the below sections for the example). These grains are then measured via ellipse fitting to retrieve the long- and short-axis and orientation. This process is

iterated through each window and the output from the counting is provided as a comma separated value (.csv) file for user manipulation.

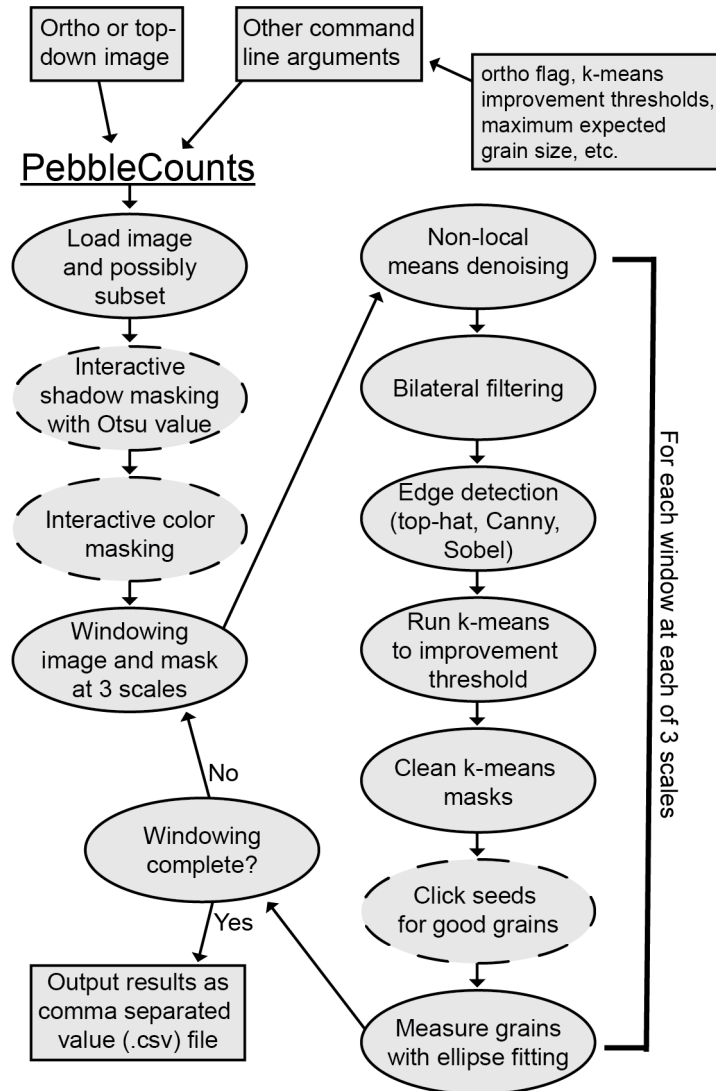


Figure 1: Flowchart of PebbleCounts. The boxes are user supplied input or output from the algorithm. Dashed lines indicate a user input step during processing, either entering and checking values or clicking.

5 Detailed Processing Steps

Below is an in-depth description of each processing step applied by PebbleCounts. For those wishing to proceed with counting without the full story, go ahead to the **Command-line Options** and then the

Step-by-Step Example sections below! For the nitty-gritty breakdown, follow along:

1. PebbleCounts begins with the input of georeferenced ortho or simple top-down imagery at the command-line along with a number of variable flags. Most of the 13 variables do not need modification, but see their descriptions below to decide.
2. The image is loaded and the user is given the opportunity to subset with a click-and-drag bounding rectangle.
3. The [Otsu](#) value for gray-scale thresholding is assessed and the user is asked to supply a percentage of this Otsu value for masking out shadows between grains. The resulting mask is then checked by the user and re-evaluated with a new percentage value, for instance if the value is too high thus causing some of the darker grains to also be masked.
4. The image is displayed and the user can click on a color that should be masked (e.g., uniform colored brown sand or vegetation patches). The masking is accomplished via a narrow range applied to the [HSV](#) color-space around the clicked pixel. The user has the opportunity to accept or reject the additional mask and add more color masks if the full range of interest has not been included. Together, the shadow and color mask provide an initial segmentation of the grains in the image.
5. Following these pre-processing steps, the image and shadow/color mask is windowed at three different scales corresponding to approximately 10, 2, and 0.5 times the longest expected grain in the image. Each of these windows is passed through the following steps.
6. [Non-local means denoising](#) on the [CIELab](#) converted image with the color (chromaticity) filtered but the brightness (luminance) un-altered. This provides a more uniform color for mottled grains.
7. [Bilateral filtering](#) on the CIELab chromaticity bands. This filtering technique reduces noise in an image while preserving high gradient edges between grains.
8. Edge detection steps applied to the original gray-scale image. This includes [black top-hat](#) and [Sobel](#) filtering, after which a suggested threshold of 90% is applied to only extract the strongest edges, and [Canny](#) edge detection. At each of these steps the associated edge mask is feature-AND ([see textbook by John C. Russ](#)) operated with the shadow/color mask to add additional segmentation details where there is some overlap to definite inter-granular interstices, while avoiding over segmentation caused by intra-granular noise.
9. Masked pixels are eliminated from the analysis and an $N \times 4$ dimensional vector (N is the number of pixels) is formed with the smoothed CIELab a^* (green-red) and b^* (blue-yellow) chromaticity bands and the X and Y coordinate of the pixel in image space. The chromaticity (a^* and b^*) is rescaled between 0 and 1 and the X and Y is rescaled by a user supplied scaling factor suggested at 0.5. This allows the color information to have a larger influence on clustering in the k-means step, thus avoiding some over-segmentation of larger grains.
10. This $N \times 4$, rescaled vector is passed to the k-means algorithm, which iteratively clusters the pixels by color and spatial location and checks the overall inertia of the clusters then repeats

the clustering with centers shifted until the improvement in subsequent inertia is less than a threshold fractional percentage. This threshold improvement is suggested to be 0.01 for the first, large scale and 0.1 for the medium and fine scale.

11. When the improvement threshold is met, the vector is transformed back into image space, maintaining the k-means labels. Each of these labels is then separately selected and cleaned up via a combination of [binary erosion, dilation, removal of small objects, and clearing of border-touching elements](#). The cleaned label masks are then combined into a final potential grain mask.
12. The potential grain mask is now displayed over the original RGB color image and the user is asked to click labels that contain single, well-defined grains. Here it is suggested that any grain mask that contains the majority of the grain (particularly the edges of the grain) is selected, even if the k-means segmentation led to jagged edges and over-segmentation within the grain. This is because the final ellipse fitting ignores these holes and fits to the largest area covered by the mask label.
13. Each of the labels with a user-selected point clicked inside of it is analyzed for [region properties](#) to extract the grain centroid, average hue and saturation color from HSV space, area of the grain in number of pixels, and the following parameters of an ellipse fit to the region: minor and major axis length and orientation of the ellipse measured from $-\pi/2$ to $\pi/2$ relative to the positive x-axis (orientation=0) in Cartesian coordinates.
14. The clicked regions are then added to the shadow/color mask and the processing is repeated from step 6 on the next window or beginning at the next of the three scales.
15. Following all windowing, the resulting average color for each grain (in hue and saturation) is again passed to a k-means clustering step, however, the number of clusters is user supplied in this case as the number of expected uniquely colored lithologies present in the image. This provides another numbered label for each grain with the estimated lithology. For uniform lithology this value should be 1.
16. The results of each grain are output as a comma separated value text file. The measurements are given in pixel and metric units by multiplying the pixel amounts by the image resolution in meters per pixel. In case of a UTM projected georeferenced image, the UTM X (Easting) and Y (Northing) coordinates of the grain centroid are also provided. Additionally, from the color mask a fractional percentage of the image that was masked by the HSV range is provided in the output file (e.g., the percentage sand) along with the fractional percentage of the image that was not measured (so combined shadows and grains not identified by PebbleCounts).

6 Command-line Options

Great you've got it installed! Hopefully that is, we're about to find out! The first step to running the software is navigating to the directory where the three scripts live. On Windows that might look like:

```
cd C:\Users\YourName\PebbleCounts
```

Just replace everything after `cd` with the path on your computer to the downloaded `PebbleCounts` folder.

6.1 Calculate Camera Resolution

First off, if the imagery you intend to use is not orthorectified and georeferenced you'll want to calculate the approximate ground resolution of the photos in millimeters per pixel. To do so you can run the script `calculate_camera_resolution.py` at the command line. Parameters to be provided can be listed with `python calculate_camera_resolution.py -h`. Here they all are:

```
usage: calculate_camera_resolution.py [-h] [-focal FOCAL] [-height HEIGHT]
                                     [-sensorHW SENSORHW [SENSORHW ...]]
                                     [-imageHW IMAGEHW [IMAGEHW ...]]

optional arguments:
  -h, --help            show this help message and exit
  -focal FOCAL          Camera focal length in millimeters
  -height HEIGHT        Photo capture height in meters
  -sensorHW SENSORHW [SENSORHW ...]
                        The height and width of the internal camera sensor in
                        millimeters
  -imageHW IMAGEHW [IMAGEHW ...]
                        The height and width of the photography in pixels
```

6.1.1 Example Use

Let's say I have a photo that I took from a height of 1.5 meters at a camera focal length of 35 mm. The camera has a [sensor size](#) of 15 by 26 mm and was shot at 24 MP resolution, providing a 4000 pixel high by 6000 pixel wide picture. My command would look like this:

```
python calculate_camera_resolution.py -focal 35 -height 1.5 -sensorHW 15 26 -imageHW \
4000 6000
```

And the output printed to the screen would be:

```
Focal length 35.00 mm; Shot from 1.50 m; Sensor size (15.00, 26.00) mm; Image size \
(4000, 6000) pixels:

The field of view is 0.64 by 1.11 m

approximate (x,y) resolution in mm/pixel = (0.1607, 0.1857)
average resolution in mm/pixel = 0.1732
```

And I could then pass this resolution (0.1732) to the `PebbleCounts.py` script.

Note on Shot Height: If you aren't sure exactly what height the image was shot from, use an approximate value. Even for differences of up to 1 m in shot height the ground resolution for most cameras will change by less than 0.2 mm, and thus have a negligible effect on the resulting grain-sizes measured.

6.2 PebbleCounts

The code can be run from the command-line with

```
python PebbleCounts.py ...
```

Parameters to be provided can be listed with `python PebbleCounts.py -h`. Here they all are:

```
usage: PebbleCounts.py [-h] [-im IM] [-ortho ORTHO]
                    [-input_resolution INPUT_RESOLUTION]
                    [-lithologies LITHOLOGIES] [-maxGS MAXGS]
                    [-cutoff CUTOFF]
                    [-min_sz_factors MIN_SZ_FACTORS [MIN_SZ_FACTORS ...]]
                    [-win_sz_factors WIN_SZ_FACTORS [WIN_SZ_FACTORS ...]]
                    [-improvement_ths IMPROVEMENT_THS [IMPROVEMENT_THS ...]]
                    [-coordinate_scales COORDINATE_SCALES [COORDINATE_SCALES ...]]
                    [-overlaps OVERLAPS [OVERLAPS ...]]
                    [-nl_means_chroma_filts NL_MEANS_CHROMA_FILTS \
                    [NL_MEANS_CHROMA_FILTS ...]]
                    [-bilat_filt_szs BILAT_FILT_SZS [BILAT_FILT_SZS ...]]
                    [-tophat_th TOPHAT_TH] [-sobel_th SOBEL_TH]
                    [-canny_sig CANNY_SIG] [-resize RESIZE]

optional arguments:
  -h, --help            show this help message and exit
  -im IM                The image to use including the full path and
                        extension.
```

```

-ortho ORTHO          'y' if geo-referenced ortho-image, 'n' if not. Supply
                      input resolution if 'n'.
-input_resolution INPUT_RESOLUTION
                      If image is not ortho-image, input the calculated
                      resolution from calculate_camera_resolution.py
-lithologies LITHOLOGIES
                      What is the expected number of lithologies with
                      distinct colors? DEFAULT=1
-maxGS MAXGS          Maximum expected longest axis grain size in meters.
                      DEFAULT=0.3
-cutoff CUTOFF        Cutoff factor (minimum b-axis length) in pixels for
                      inclusion of pebble in final count. 10 is good for ~1
                      mm/pixel images, 25 for < 0.8 mm/pixel. DEFAULT=10
-min_sz_factors MIN_SZ_FACTORS [MIN_SZ_FACTORS ...]
                      Factors to multiply cutoff value by at each scale.
                      Used to clean-up the masks for easier clicking. The
                      default values are good for ~1 mm/pixel imagery but
                      should be doubled for < 0.8 mm/pixel or halved for
                      centimeter resolution imagery. DEFAULT=[100, 10, 2]
-win_sz_factors WIN_SZ_FACTORS [WIN_SZ_FACTORS ...]
                      Factors to multiply maximum grain-size (in pixels) by
                      at each scale. The default values are good for
                      millimeter and sub-millimeter imagery, but should be
                      doubled for coarser centimeter imagery. DEFAULT=[10,
                      2, 1]
-improvement_ths IMPROVEMENT_THS [IMPROVEMENT_THS ...]
                      Improvement threshold values for each window scale
                      that tells k-means when to halt. DEFAULT=[0.01, 0.1,
                      0.1]
-coordinate_scales COORDINATE_SCALES [COORDINATE_SCALES ...]
                      Fraction to scale X/Y coordinates by in k-means.
                      DEFAULT=[0.5, 0.5, 0.5]
-overlaps OVERLAPS [OVERLAPS ...]
                      Fraction of overlap between windows at the different
                      scales. DEFAULT=[0.5, 0.3, 0.1]
-nl_means_chroma_filts NL_MEANS_CHROMA_FILTS [NL_MEANS_CHROMA_FILTS ...]
                      Nonlocal means chromaticity filtering strength for the
                      different scales. DEFAULT=[3, 2, 1]
-bilat_filt_szs BILAT_FILT_SZS [BILAT_FILT_SZS ...]
                      Size of bilateral filtering windows for the different
                      scales. DEFAULT=[9, 5, 3]
-tophat_th TOPHAT_TH  Top percentile threshold to take from tophat filter
                      for edge detection. DEFAULT=90

```

<code>-sobel_th SOBEL_TH</code>	Top percentile threshold to take from sobel filter for edge detection. DEFAULT=90
<code>-canny_sig CANNY_SIG</code>	Canny filtering sigma value for edge detection. DEFAULT=2
<code>-resize RESIZE</code>	Value to resize windows by should be between 0 and 1. DEFAULT=0.8

Here's a bit more detail on some of the less obvious inputs to clarify:

- `-resize` controls the pop-up window size for the GUI. If you notice the window is too small to see the grains then use a high value like 0.9, but if the image is partially off-screen you should try lowering the value to around 0.8.
- `-lithologies` is the expected number of different rock types in the image with distinct coloration differences. It defaults to 1, meaning the lithology is uniform or the color differences between lithologies are minimal and therefore difficult to discern from the image alone.
- `-maxGS` is the expected size in meters of the largest rock in the image based on some field knowledge. This value is used during the windowing to set the appropriate sizes at the three scales in conjunction with the `-win_sz_factors` input.
- `-cutoff` is the algorithm's lower limit on b-axis measurement given in pixels. The default value of 10 is what we found to be reliable for accurate distribution measurement using ~1 mm/pixel imagery. A value of 25-pixels is more appropriate for higher resolutions (e.g., < 0.8 mm/pixel). This value is also used by the `-min_sz_factors` input to cleanup the mask at each of the three window scales and should also be scaled depending on the imagery resolution (sub-mm, mm, cm).
- `-improvement_ths` is the fractional percentage (from 0-1) that k-means uses to assess convergence and stopping. The default values are probably good here.
- `-coordinate_scales` is the fractional percentage (from 0-1) to scale the x,y coordinates of each pixel compared with the color information in the k-means segmentation. Since we want to allow for anisotropic grains covering large areas if they have semi-uniform color, we want to scale the relative importance of pixel location by approximately 50% of the color, hence the default values of 0.5 at each scale.
- `-nl_means_chroma_filts` is the level of chromaticity filtering to apply during **non-local means denoising**, which should be reduced at each scale. Higher values lead to more smoothing of the image and a cartoonish appearance. The default values should again be good here.
- `-bilat_filt_szs` is the square window size to apply for **bilateral filtering**, with the aim of further smoothing the image while preserving interstices between the grains. The size of this filter window should be reduced with the windowing scale. The default values are also good here.
- `-tophat_th`, `-sobel_th`, and `-canny_sig` are the **tophat** filter percentile threshold, **Sobel**

filter percentile threshold, and [Canny](#) edge detection smoothing standard deviation. These are the values used on edge detection from the gray-scale image and are probably good at the default value. The same value is used for each scale.

7 Step-by-Step Example

1. Depending on whether you're going to use an ortho or non-ortho image (and default or modified arguments) run one of the following commands (**Note:** While all of the default arguments can be modified at the command line, it is recommended to stick mostly to the default values. In most cases, only the expected lithologies and maximum expected grain-size need to be modified for different images given 0.8-1.2 mm/pixel imagery. For < 0.8 mm/pixel resolution imagery, it is necessary to double the `-min_sz_factors` default values and to use a `-cutoff` value of 25-pixels.):

- **Ortho With Default Arguments:** (Be sure to set the `-ortho` flag to `y` and the resolution will be automatically read by [gdal](#))

```
python PebbleCounts.py -im example_data\ortho_resolution_1.2mmPerPix.tif -ortho y
```

- **Ortho With Modified Arguments:** (Increase number of expected lithologies and the maximum grain size)

```
python PebbleCounts.py -im example_data\ortho_resolution_1.2mmPerPix.tif -ortho y \
-lithologies 3 -maxGS 0.4
```

- **Non-ortho Imagery With Default Arguments:** (Be sure to set the `-ortho` flag to `n` and also provide the `-input_resolution` in mm/pixel, which can be found as in the above section **Calculate Camera Resolution**. Also, for < 0.8 mm/pixel imagery we recommend changing the lower cutoff to 25-pixels)

```
python PebbleCounts.py -im example_data\nonortho_resolution_0.63mmPerPix.tif -ortho n \
-input_resolution 0.63 -cutoff 25
```

- **Non-ortho Imagery With Modified Arguments:** (Increase number of expected lithologies and decrease the maximum grain size. Also, since the resolution of this image is < 0.8 mm/pixel, I've doubled the default values for `-min_sz_factors`)

```
python PebbleCounts.py -im example_data\nonortho_resolution_0.63mmPerPix.tif -ortho n \
-input_resolution 0.63 -cutoff 25 -lithologies 2 -maxGS 0.2 -min_sz_factors 200 20 4
```

- Interactively subset the image by typing *y* or don't by typing *n*. If you do subset, click and drag a box on the pop-up window and press the *spacebar* to close the window again.
- Input a percentage (0-100) of the *Otsu* shadow threshold value, then press enter. This will open a pop-up window displaying the image with the Otsu mask in white. On the keyboard press *r* to flash the original un-masked image, *y* to accept the mask and move on, and *n* to close the window and enter a new value (Figure 2).

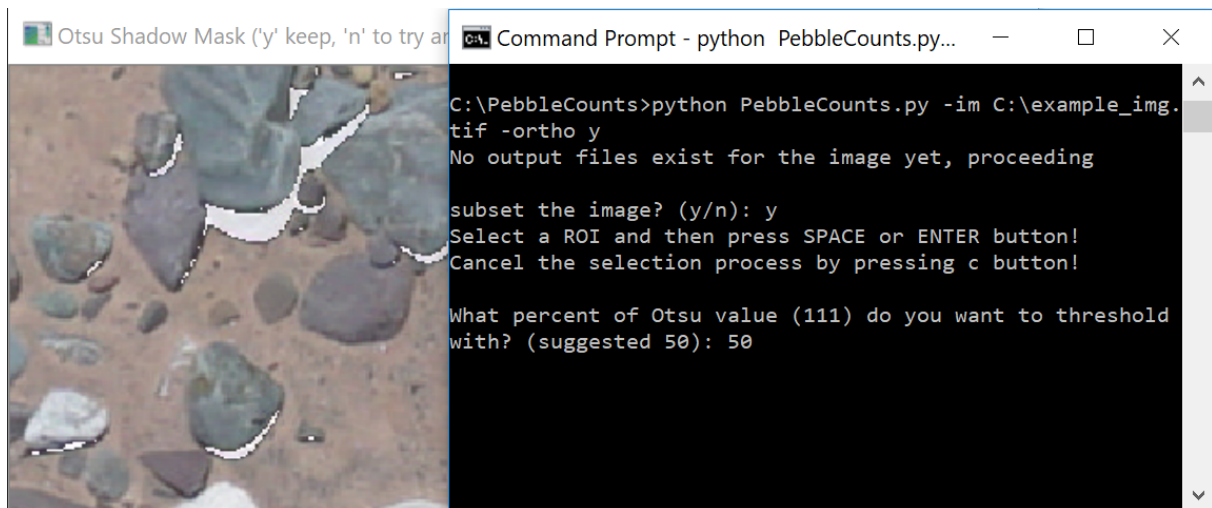


Figure 2: Otsu thresholding of the image with an entered value 0-100. Press *r* to flash the original image, *y* to accept the mask, or *n* to try a different value.

- Is there a color you want to mask out in the scene? Maybe the sand is a uniform color distinct from the pebbles. If so, then in the next step enter *y*, which will bring up another pop-up window. With the window active, you can press *q* to close it if you decide not to color mask and *r* to flash the original image (Figure 3). Once you click a point in the window with a color you'd like to mask a second pop-up will open displaying the result of applying a mask to this color. Press *y* to accept the mask or *n* to close it and try another click in the first window (Figure 3). Pressing *y* here will return you to the command prompt where you can finish color masking by entering *n* or adding additional color masks by entering *y*.

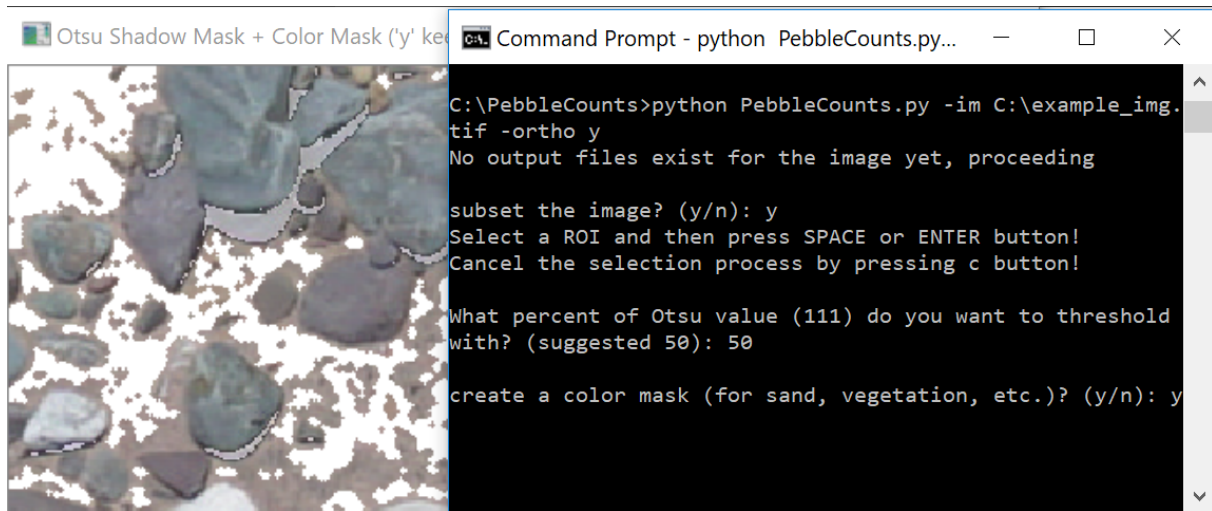


Figure 3: Color masking clicking window. Click on a color you want to mask to open a second window and check it. Press *q* to close window or *r* to flash the original image. Press *y* to accept or *n* to try a different click in the previous window.

5. After these couple interactive steps, PebbleCounts will take over the automated windowing, filtering, edge detection, and k-means segmentation at each window, after which a new window with the mask will open (Figure 4). The command prompt should look something like this:

```
Beginning k-means segmentation
Scale 1 of 3
Window 1 of 1
Non-local means filtering
Bilateral filtering
Black tophat edge detection
Canny edge detection
Sobel edge detection
Running k-means
Current number of clusters: 2, total inertia: 59896.391
Current number of clusters: 3, total inertia: 48804.694
.
Current number of clusters: X, total inertia: XXXX
Cleaning up k-means mask
```

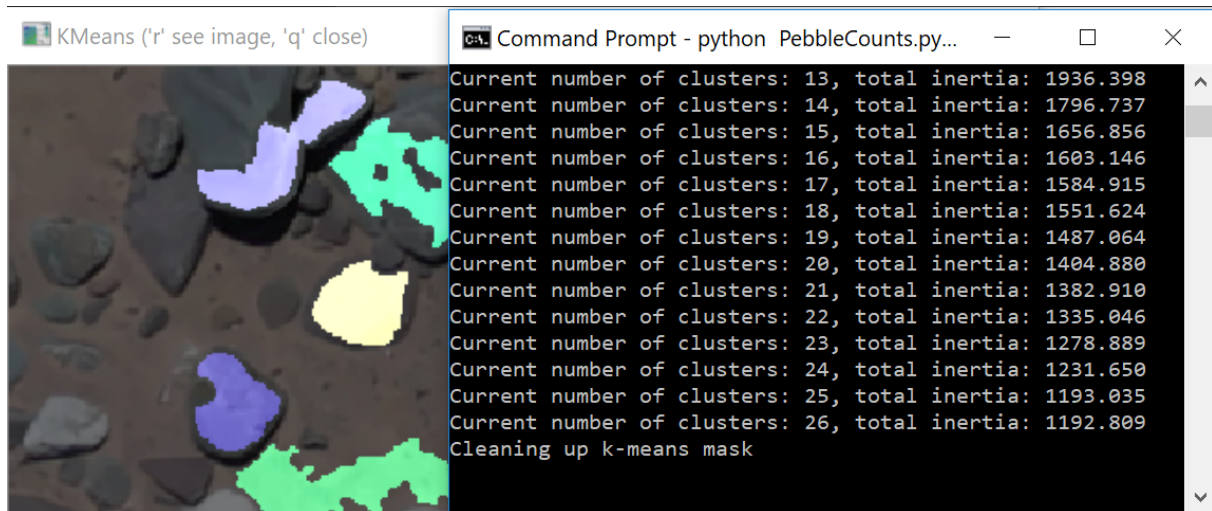


Figure 4: Automated segmentation via edge detection and k-means clustering and pop-up window.

6. After the mask is cleaned a new window will open where you need to click the good looking grains and ignore the bad ones (Figure 5). Left clicking anywhere on the image will produce a black circle at that point, meaning that you've selected all the pixels in this connected region as one grain. A right click anywhere on the image will remove the last click and exchange the black circle for a red one, indicating this area will not be considered (unless of course you add another left click to the region). Overlay the original image to help decide what is and is not a well delineated grain by pressing *r* once to open the image and *r* again to close the image and return to the mask. Once you are satisfied with your clicks press *q* to close the window and automatically move on to the next window and/or scale. The clicked grains will be automatically measured and added to the final output.

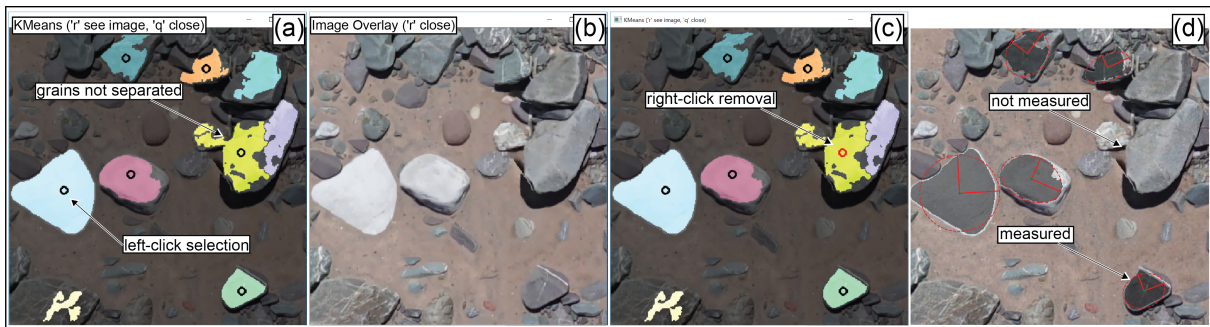


Figure 5: (a) Interactive k-means mask clicking window. A left click adds a pebble region and black circle. Pressing *q* will close the image and continue segmentation on the next window. (b) Pressing *r* opens the original image to check the mask against, *r* again to close the original image. (c) Right click anywhere on the image to remove the last clicked point and replace the black circle with a red one. (d) Shows the final ellipses fit to each of the clicked regions.

7. Repeat the clicking on each window that pops up (see the command window for what number window out of the full number you are on). With a little practice this will go quickly. After the windows are done the results will be saved out and you can repeat from step 1 with another image.

7.1 An important note on clicking!

As shown in Figure 5, PebbleCounts does not provide a perfect segmentation. Two errors you will commonly note are:

1. Under-segmentation of overlapping grains. Avoid clicking these regions or the resulting ellipse will be fit to many grains.
2. Over-segmentation of single grains. Here it is up to the user to decide which part of the segmented grain (if any) to select. If the mask covers the majority of the grain despite some holes or shrinkage, then it is advisable to select the grain, since the final ellipse will be fit to the full region covered. Even if the center of a grain is entirely missing from the mask, if the ends of the grain are in the same mask then the fit ellipse will approximate the grain well.

7.2 Output

PebbleCounts saves out a few outputs in the same folder that the image resides:

- csv: `filename_PebbleCounts_CSV.csv`
- label image (georeferenced if original is): `filename_PebbleCounts_LABELS.tif`

- figure showing results: `filename_PebbleCounts_FIGURE.png`

The results .csv has an entry for each grain (Figure 6) showing the fraction of the scene not measured (combined background shadow and unmeasured grains) the fraction of the scene that was selected by the color mask as background color (e.g., sand) and each grains' characteristics including a- and b-axis of the fit ellipse in pixels and in meters, the area covered by the grain mask in pixels and square meters, the orientation of the fit ellipse measured from $-\pi/2$ to $\pi/2$ relative to the positive x-axis (orientation=0) in cartesian coordinates. If the input imagery is georeferenced the UTM Northing (Y) and Easting (X) coordinates of the pebble's centroid are be provided.

	A	B	C	D	E	F	G	H	I	J	K	L
1	<i>perc. not meas.</i>	<i>perc. background color</i>	<i>UTM X (m)</i>	<i>UTM Y (m)</i>	<i>a (px)</i>	<i>b (px)</i>	<i>a (m)</i>	<i>b (m)</i>	<i>area (px)</i>	<i>area (m2)</i>	<i>orientation</i>	<i>lithology</i>
2	0.59361996281	0.017379832734566	833597.627	7245222.312	54.2856	29.8832	0.0626	0.0344	1146	0.0015225	-0.7914827	1
3	0.59361996281	0.017379832734566	833597.563	7245222.305	19.5576	12.3652	0.0225	0.0143	168	0.0002232	-1.4709456	0
4	0.59361996281	0.017379832734566	833597.603	7245222.289	38.4725	24.9816	0.0443	0.0288	565	0.0007506	-0.9672299	1
5	0.59361996281	0.017379832734566	833597.774	7245222.292	32.8349	29.368	0.0378	0.0339	710	0.0009433	-1.2299834	2

Figure 6: Example .csv file output by PebbleCounts for a georeferenced image. *perc. not meas.* is the fractional percentage of the image that was either shadows or not measured by PebbleCounts and *perc. background color* is the fractional percentage of the image that was masked during interactive HSV color selection (e.g., for sand).