

# Digital Grain Size

Version 3, Feb 2012

Quick start guide for MATLAB





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subfunctions



utilities



calibdata.txt



calib\_grainsize.m



dgs.config



dgs.m



dgs\_calib.config



dgs\_minimal.config



magic\_grainsize.m

Start with the folder you downloaded from the web  
which should look a little something like this

```
>> cd /home/daniel/Dropbox/DCS/DCS_website_feb2012
```

Open MATLAB and 'cd' to this directory

```
1 folder = '/home/daniel/Dropbox/SedSimPaper/reanalysis/gravelriver/samples';  
2 verbose = 1;
```

**EXAMPLE 1:**

Using a minimal configuration file (dgs\_minimal.config) which just contains the path to the folder where your sample images are saved, and the option 'verbose' is turned on (1, 0 would mean 'turn off'). The verbose option when turned on means more outputs are printed to screen

```
>> cd /home/daniel/Dropbox/DGS/DGS_website_feb2012  
>> what
```

M-files in the current directory /home/daniel/Dropbox/DGS/DGS\_website\_feb2012

```
calib_grainsize  dgs          magic_grainsize
```

```
/>> [files, GrainSize, GSmat, Settings] = dgs('dgs_minimal.config');
```

Invoke the program using the minimal config file like this

'dgs' is the main callable program

the outputs are 'files', 'GrainSize', 'GSmat', and 'Settings'

the only input the program will take is the config file

seriesC2\_endrun\_16 (2).JPG  
2.0 MBseriesC2\_endrun\_17 (2).JPG  
2.3 MBseriesC2\_endrun\_18 (2).JPG  
2.1 MBseriesC2\_endrun\_19 (1).JPG  
2.0 MBseriesC2\_endrun\_19 (2).JPG  
2.2 MBseriesC2\_endrun\_20 (1).JPG  
2.3 MBseriesC2\_endrun\_20 (2).JPG  
2.3 MBseriesC2\_endrun\_21 (2).JPG  
2.1 MB

This is an example of a folder  
with sample images

dgs will work with any image format  
which is readable by MATLAB  
(type 'help fileformats' in the MATLAB  
command window, without the apostrophes,  
to see what these file formats are



```
Setting to 0 (the filtered, flattened greyscale image will not be returned.  
To change this, input return_used_image=1 in the config file)  
  
No resolution given.  
Setting resolution to 1  $\mu\text{m}/\text{pixel}$  (multiply grain sizes by correct  $\mu\text{m}/\text{pixel}$  value)  
  
No 'use_algo' given.  
Setting to 1 to use the algorithm of Buscoabe et al 2010  
(to change this, input use_algo=2 in the config file to use the calibration approach of Rubin 2004)  
  
No representative autocorrelation vaue (R) given. Setting to 0.5  
  
No algorithm for sorting given. Setting to default  
  
filtering out lighting irregularities ...  
Calculated mean grain-size = 120  
Calculated sorting = 35.9  
filtering out lighting irregularities ...  
Calculated mean grain-size = 182  
Calculated sorting = 59.3  
filtering out lighting irregularities ...  
Calculated mean grain-size = 133  
Calculated sorting = 53.9  
filtering out lighting irregularities ...  
Calculated mean grain-size = 166  
Calculated sorting = 68.8  
filtering out lighting irregularities ...  
Calculated mean grain-size = 180  
Calculated sorting = 69  
filtering out lighting irregularities ...  
Calculated mean grain-size = 146  
Calculated sorting = 62.8  
filtering out lighting irregularities ...  
Calculated mean grain-size = 122  
Calculated sorting = 51.8  
filtering out lighting irregularities ...  
Calculated mean grain-size = 242  
Calculated sorting = 116  
  
>>
```

This is the output screen of running the dgs program with the config file 'dgs\_minimal.config'

```
.....
Calculated mean grain-size = 242
Calculated sorting = 116
```

```
>> whos
```

Name	Size	Bytes	Class	Attributes
CSsat	1x8	64	double	
GrainSize	1x8	239516	cell	
Settings	1x1	1774	struct	
files	1x1	528	cell	

```
>> files
```

```
files =
```

```
 [8x26 char]
```

```
>> files{1}
```

```
ans =
```

```
seriesC2_endrun_16 (2).JPG
seriesC2_endrun_17 (2).JPG
seriesC2_endrun_18 (2).JPG
seriesC2_endrun_19 (1).JPG
seriesC2_endrun_19 (2).JPG
seriesC2_endrun_20 (1).JPG
seriesC2_endrun_20 (2).JPG
seriesC2_endrun_21 (2).JPG
```

```
>> CSsat{1}
```

```
??? Cell contents reference from a non-cell array object.
```

```
>> CSsat
```

```
CSsat =
```

```
119.9169 182.4657 132.8922 165.7560 179.5830 146.3407 122.3855 242.2357
```

```
>> |
```

```
Start
```

dgs is designed to cycle through folders of images so the 'file' and 'GrainSize' outputs are always cellular arrays, one array per folder

'files' contains the list of image names which were processed

GSmat is not a cellular array: it is a numeric array of mean grain sizes corresponding to the images in 'files'. If more than one directory of images was processed, each row of GSmat will correspond to each of the directories in order

'GrainSize' is a cellular array containing the grain size results...

```

files      1x1      S28 cell
>> files
files =
    [8x26 char]
>> files(1)
ans =
seriesC2_endrun_16 (2).JPG
seriesC2_endrun_17 (2).JPG
seriesC2_endrun_18 (2).JPG
seriesC2_endrun_19 (1).JPG
seriesC2_endrun_19 (2).JPG
seriesC2_endrun_20 (1).JPG
seriesC2_endrun_20 (2).JPG
seriesC2_endrun_21 (2).JPG
>> CSwat(1)
??? Cell contents reference from a non-cell array object.
>> CSwat
CSwat =
    119.9169    182.4657    132.8922    165.7560    179.5830    146.3407    122.3855    242.2357
>> GrainSize(1)
ans =
    MeanGrainSize: 119.9169
           srt: [1x1 struct]
           dist: [1x1 struct]

```

The contents of GrainSize will vary depending on the Settings in the config file but an example is shown here. MeanGrainSize is in units as per the input resolution (e.g. mm/pixel) or in pixels, default and if resolution=1

```

    [8x26 char]
>> files(1)
ans =
seriesC2_endrun_16 (2).JPG
seriesC2_endrun_17 (2).JPG
seriesC2_endrun_18 (2).JPG
seriesC2_endrun_19 (1).JPG
seriesC2_endrun_19 (2).JPG
seriesC2_endrun_20 (1).JPG
seriesC2_endrun_20 (2).JPG
seriesC2_endrun_21 (2).JPG

>> GSsat(1)
??? Cell contents reference from a non-cell array object.

>> GSsat
GSsat =
    119.9169    182.4657    132.8922    165.7560    179.5830    146.3407    122.3855    242.2357

>> GrainSize(1)
ans =
    MeanGrainSize: 119.9169
           srt: [1x1 struct]
           dist: [1x1 struct]

>> GrainSize(1).MeanGrainSize
ans =
    119.9169

```

To access data in GrainSize, see examples here

```

seriesC2_endrun_17 (2).JPG
seriesC2_endrun_18 (2).JPG
seriesC2_endrun_19 (1).JPG
seriesC2_endrun_19 (2).JPG
seriesC2_endrun_20 (1).JPG
seriesC2_endrun_20 (2).JPG
seriesC2_endrun_21 (2).JPG

```

```

>> GSmat(1)
??? Cell contents reference from a non-cell array object.

>> GSmat

GSmat =

    119.9169    182.4657    132.8922    165.7560    179.5830    146.3407    122.3855    242.2357

>> GrainSize(1)

ans =

    MeanGrainSize: 119.9169
           srt: [1x1 struct]
           dist: [1x1 struct]

>> GrainSize(1).MeanGrainSize

ans =

    119.9169

>> GrainSize(1).srt

ans =

    srt: 35.8979
    a: [1x133 double]

```

GrainSize.srt contains the sorting value (same units as MeanGrainSize) and also 'a' which is the radially averaged correlogram for that sample to some determined lag

```
File Edit Debug Parallel Desktop Window Help
Current
Shortcuts How to Add What's New

>> CSsat(1)
??? Cell contents reference from a non-cell array object

>> CSsat
CSsat =
    119.9169    182.4657    132.8922    165.7560

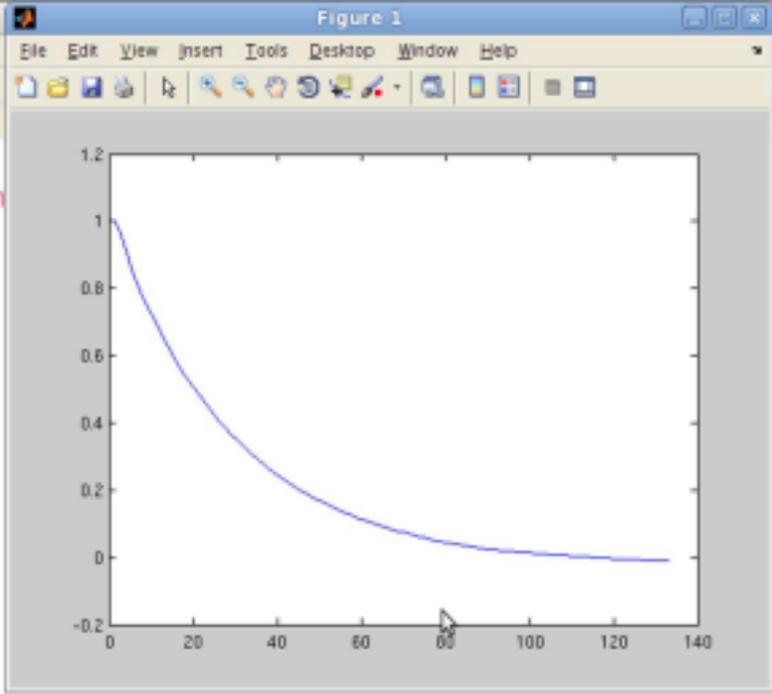
>> GrainSize(1)
ans =
    MeanGrainSize: 119.9169
             srt: [1x1 struct]
             dist: [1x1 struct]

>> GrainSize(1).MeanGrainSize
ans =
    119.9169

>> GrainSize(1).srt
ans =
    srt: 35.8979
    a: [1x133 double]

>> GrainSize(1).srt.srt
ans =
    35.8979

>> plot(GrainSize(1).srt.a)
>>
```



to plot the sample's 1D (radially-averaged) correlogram, do this

```
dist: [1x1 struct]
```

```
>> GrainSize{1}.MeanGrainSize
```

```
ans =
```

```
119.9169
```

```
>> GrainSize{1}.srt
```

```
ans =
```

```
srt: 35.8979
a: [1x133 double]
```

```
>> GrainSize{1}.srt.srt
```

```
ans =
```

```
35.8979
```

```
>> plot(GrainSize{1}.srt.a)
```

```
>> GrainSize.dist
```

```
??? Attempt to reference field of non-structure array.
```

```
>> GrainSize{1}.dist
```

```
ans =
```

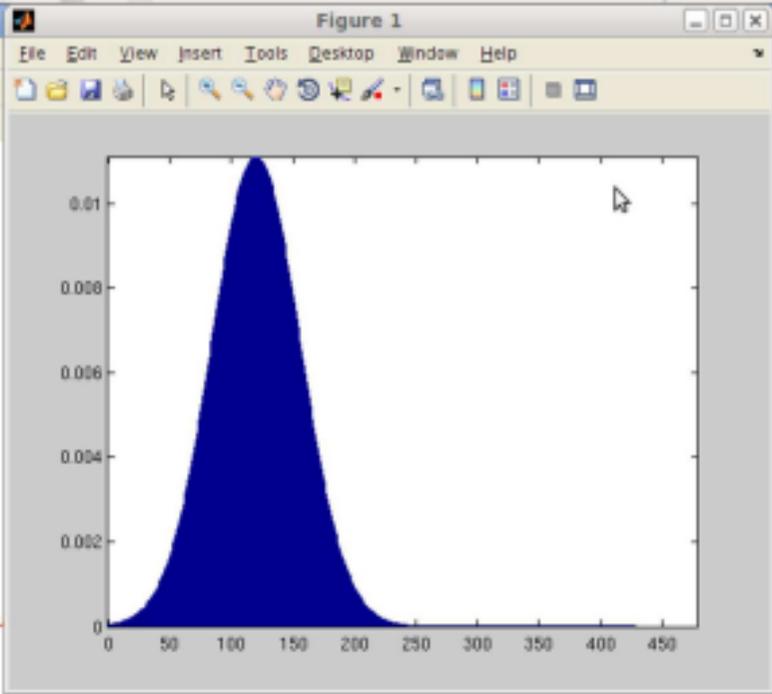
```

    x: [1x480 double]
  normdist: [1x480 double]
  norm_pd: [9x1 double]
    sig: 1.3608
 lognormdist: [1x480 double]
 lognorm_pd: [9x1 double]
  hyperdist: [480x1 double]
  hyperdist_pd: [9x1 double]
```

GrainSize.dist contains many things, including 'x' which is a vector of grain sizes for the estimated histograms 'normdist' (normal/Gaussian distribution), 'lognormdist' (log-normal distribution), and 'hyperdist' (log-hyperbolic distribution).

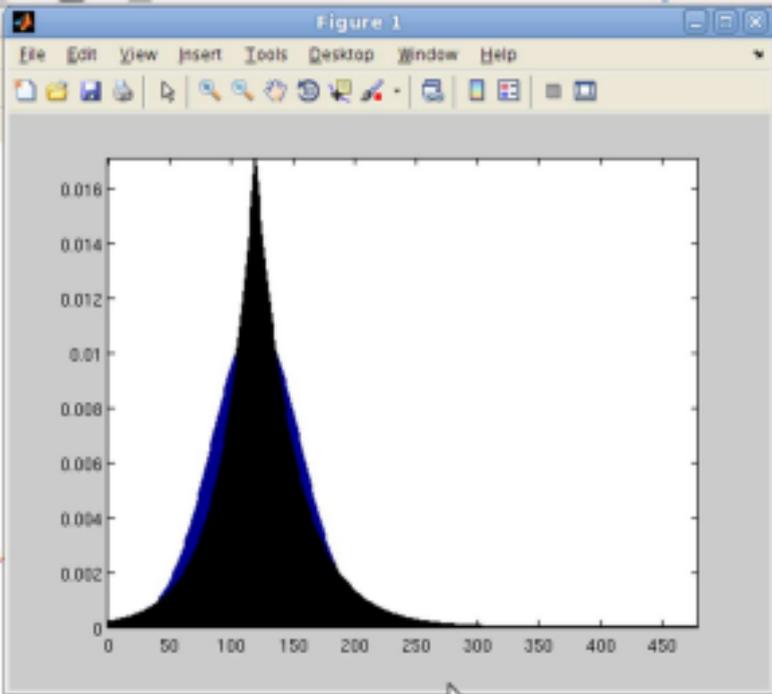
Those variables ended '\_pd' are the 5th, 10th, 16th, 25th, 50th, 75th, 84th, 90th and 95th percentiles associated with the 3 distributions

```
File Edit Debug Parallel Desktop Window Help
Current
Shortcuts How to Add What's New
>> GrainSize(1).MeanGrainSize
ans =
    119.9169
>> GrainSize(1).srt
ans =
    srt: 35.8979
    a: [1x133 double]
>> GrainSize(1).srt.srt
ans =
    35.8979
>> plot(GrainSize(1).srt.a)
>> GrainSize.dist
??? Attempt to reference field of non-struct
>> GrainSize(1).dist
ans =
    x: [1x480 double]
    normdist: [1x480 double]
    norm_pd: [9x1 double]
    sig: 1.3608
    lognormdist: [1x480 double]
    lognorm_pd: [9x1 double]
    hyperdist: [480x1 double]
    hyperdist_pd: [9x1 double]
>> bar(GrainSize(1).dist.x,GrainSize(1).dist.normdist)
>> axis tight
>>
```



Here's an example plot of the normal distribution from a sample

```
File Edit Debug Parallel Desktop Window Help
Current
Shortcuts How to Add What's New
119.9169
>> GrainSize(1).srt
ans =
    srt: 35.8979
     a: [1x133 double]
>> GrainSize(1).srt.srt
ans =
    35.8979
>> plot(GrainSize(1).srt.a)
>> GrainSize.dist
??? Attempt to reference field of non-struct.
>> GrainSize(1).dist
ans =
    x: [1x480 double]
  noradist: [1x480 double]
  nons_pd: [9x1 double]
    sig: 1.3508
 lognoradist: [1x480 double]
 lognons_pd: [9x1 double]
  hyperdist: [480x1 double]
 hyperdist_pd: [9x1 double]
>> bar(GrainSize(1).dist.x,GrainSize(1).dist.noradist)
>> axis tight
>> hold on
>> bar(GrainSize(1).dist.x,GrainSize(1).dist.hyperdist,'r')
>> axis tight
>>
```



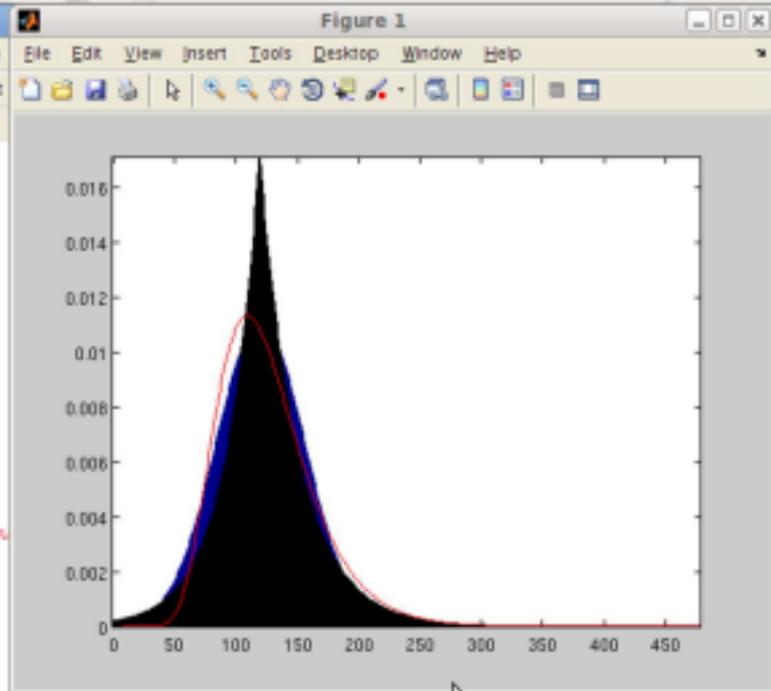
Here's a normal and a log-hyperbolic distribution from a sample overlain

```

119.9169
>> GrainSize(1).srt
ans =
    srt: 35.8979
     a: [1x133 double]
>> GrainSize(1).srt.srt
ans =
    35.8979
>> plot(GrainSize(1).srt.a)
>> GrainSize.dist
??? Attempt to reference field of non-struct.
>> GrainSize(1).dist
ans =
     x: [1x480 double]
  normdist: [1x480 double]
   norm_pd: [9x1 double]
     sig: 1.3608
 lognormdist: [1x480 double]
 lognorm_pd: [9x1 double]
 hyperdist: [480x1 double]
 hyperdist_pd: [9x1 double]

>> bar(GrainSize(1).dist.x,GrainSize(1).dist.normdist)
>> axis tight
>> hold on
>> bar(GrainSize(1).dist.x,GrainSize(1).dist.hyperdist,'r')
>> axis tight
>> plot(GrainSize(1).dist.x,GrainSize(1).dist.lognormdist,'r')
>>

```



Here's all three estimated distributions plotted

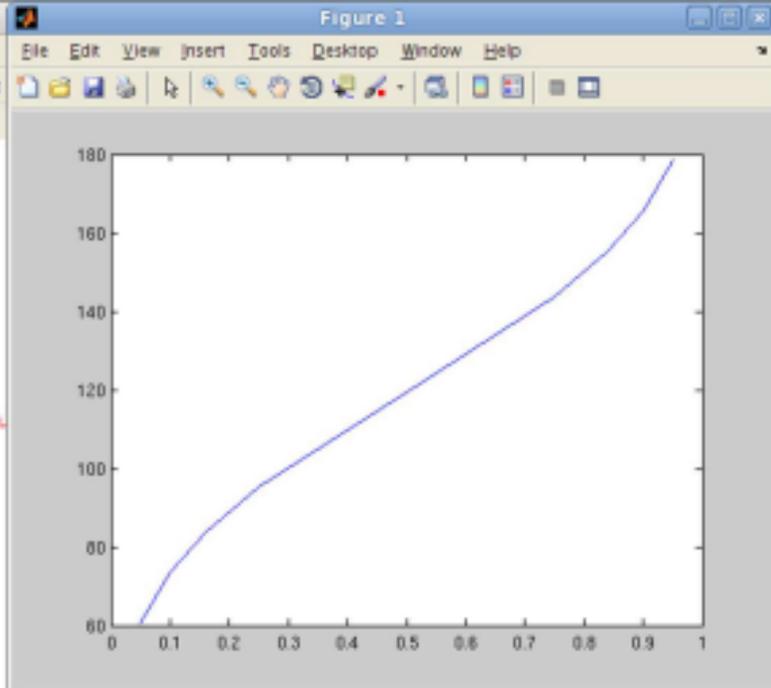
```

File Edit Debug Parallel Desktop Window Help
Current
Shortcuts How to Add What's New

srt: 35.8979
a: [1x133 double]
>> GrainSize(1).srt.srt
ans =
    35.8979
>> plot(GrainSize(1).srt.a)
>> GrainSize.dist
??? Attempt to reference field of non-struct.
>> GrainSize(1).dist
ans =
    x: [1x480 double]
   noradist: [1x480 double]
   norm_pd: [9x1 double]
   sig: 1.3608
  lognoradist: [1x480 double]
  lognorm_pd: [9x1 double]
  hyperdist: [480x1 double]
  hyperdist_pd: [9x1 double]

>> bar(GrainSize(1).dist.x,GrainSize(1).dist.noradist)
>> axis tight
>> hold on
>> bar(GrainSize(1).dist.x,GrainSize(1).dist.hyperdist,'r')
>> axis tight
>> plot(GrainSize(1).dist.x,GrainSize(1).dist.lognoradist,'r')
>> close
>> plot([.05 .1 .16 .25 .5 .75 .84 .9 .95],GrainSize(1).norm_pd)
??? Reference to non-existent field 'norm_pd'.
>> plot([.05 .1 .16 .25 .5 .75 .84 .9 .95],GrainSize(1).dist.norm_pd)
>>

```



Here's a plot of percentiles from the normal distribution estimated from a sample

```

1
2 %% REQUIRED INPUTS
3
4 %% there are two options for pointing the program to the folder(s) on your computer which contains the images to be processed
5 %% option 1 is to hard-wire the full path to the folder. For just 1 directory, create a string e.g.:
6 folder = '/home/daniel/PRAA_MAY/cropped';
7
8 %% if more than 1 folder, create a cellular array with folders, e.g.:
9 %folder{1} = '/home/daniel/PRAA_MAY/Praa_DGS/08052011/s5/cropped';
10 %folder{2} = '/home/daniel/PRAA_MAY/Praa_DGS/08052011/s6/cropped';
11 %folder{3} = '/home/daniel/PRAA_MAY/Praa_DGS/08052011/s7/cropped';
12
13 %% option 3 is to leave the folder option out, or empty, or set to zero, e.g.
14 %folder = 0;
15
16 %res = 1;
17
18 %% 1 = spectral autocorrelation (recommended); 2 = spatial autocorrelation;
19 use_algo = 1;
20
21 %% if use_algo = 2, then you need a calibration file and the grain sizes it represents
22 %calibrationfile='/home/daniel/Desktop/website_nov2011/calibdata.txt';
23 %calibrationsizes=linspace(10,170,7);
24
25 %% FOR 'MAGIC'
26 %R = 0.5;
27
28 % sorting algo
29 % 1 = min of Gauss, expo, and cosine-expo
30 % 2 = expo
31 % 3 = cosine-exp
32 % 4 = Gaussian
33 sort=1;
34
35

```

**EXAMPLE 2:**  
a full config file with specified options





Figure 1

File Edit View Insert Tools Desktop Window Help

File Edit Debug Parallel Desktop Window Help

Current

Shortcuts How to Add What's New

Digital Grain Size  
by Daniel Buscombe, October 2011  
A program to estimate grain size from image

~~~~~

No 'verbose' setting given.  
Setting to 0 (output will not be printed to  
To change this, input verbose=1 in the command

start - end  
> finished!

>> Settings

Settings =

```
folder: '/home/daniel/PRAA_
use_algo: 1
sort: 1
filter: 0
flatten: 1
return_used_image: 1
verbose: 0
res: 1
R: 0.5000
```

>> GrainSize(1)

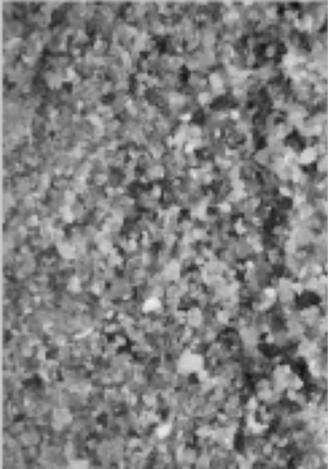
ans =

```
MeanGrainSize: 72.1260
usedImage: [1669x1168 double]
srt: [1x1 struct]
dist: [1x1 struct]
```

>> imagesc(GrainSize(1).usedImage), axis image off  
>> colormap gray

>> |

Start



and here is an example how to view this image. This output option is provided if you want to check what the filter and/or flatten options do to the input sample images

OVF



dgs\_calib.config X

```
1
2
3 folder = '/home/daniel/PRAA_MAY/cropped';
4
5 %% 1 = spectral autocorrelation (recommended); 2 = spatial autocorrelation;
6 use_algo = 2;
7
8 %% if use_algo = 2, then you need a calibration file and the grain sizes it represents
9 calibrationfile='calibdata.txt';
10 calibrationsizes=linspace(10,170,7);
11
12
13 %% IMAGE FILTERING
14 filter = 0; % 1 = yes, 0 = no
15
16 %% if filter=1, then you need to specify options
17 %filtoptions.boost = 3;
18 %filtoptions.Cutoff = .2;
19 %filtoptions.order = 2;
20
21 flatten = 1; % 1 = yes, 0 = no
22
23 %% OUTPUTS
24 return_used_image = 0; % 1 = yes, 0 = no
25
26 verbose = 1;
27
28
29
```

**EXAMPLE 3:**

using the algorithm in original mode which requires a calibration to be carried out

in which case:  
use\_algo=2





dgs\_manyfolders.config X

```

1
2 %% REQUIRED INPUTS
3
4 %% there are two options for pointing the program to the folder(s) on your computer which contains the images to be processed
5 %% option 1 is to hard-wire the full path to the folder. For just 1 directory, create a string e.g.:
6 %folder = '/home/daniel/PRAA_MAY/cropped';
7
8 %% if more than 1 folder, create a cellular array with folders, e.g.:
9 folder{1} = '/home/daniel/Dropbox/SedSimPaper/reanalysis/gravelriver/samples';
10 folder{2} = '/home/daniel/Dropbox/SedSimPaper/reanalysis/GC/samples';
11
12 %% option 3 is to leave the folder option out, or empty, or set to zero, e.g.
13 %folder = 0;
14
15 %res = 1;
16
17 %% 1 = spectral autocorrelation (recommended); 2 = spatial autocorrelation;
18 use_algo = 1;
19
20 %% if use algo = 2, then you need a calibration file and the grain sizes it represents
21 %calibrationfile='/home/daniel/Desktop/website_nov2011/calibdata.txt';
22 %calibrationsizes=linspace(10,170,7);
23
24 %% FOR 'MAGIC'
25 %R = 0.5;
26
27 % sorting algo
28 % 1 = min of Gauss, expo, and cosine-expo
29 % 2 = expo
30 % 3 = cosine-exp
31 % 4 = Gaussian
32 sort=1;
33
34
35 %% IMAGE FILTERING

```

**EXAMPLE 3:**  
processing many folders using the cellular  
folder option like this

```

files =
    [ 8x26 char]
    [11x20 char]

GrainSize =

Columns 1 through 9
    [1x1 struct] []
    [1x1 struct] [1x1 struct]

Columns 10 through 11
    [] []
    [1x1 struct] [1x1 struct]

GSmat =

119.9169 182.4657 132.8922 165.7560 179.5830 146.3407 122.3855 242.2357 0 0 0
 68.6232  56.3486  58.7504  65.3360  89.3966  55.0279 104.2541  92.3778 52.4083 63.0985 77.3067

Settings =

    folder: {'/home/daniel/Dropbox/SedSisPaper/reanalysis/gravelriver/samples' '/home/daniel/Dropbox/SedSisPaper/reanalysis/GC/samples'}
    use_algo: 1
    sort: 1
    filter: 0
    flatten: 1
    return_used_image: 0
    verbose: 0
    res: 1
    R: 0.5000

```

Here's the output from the example with many folders which contains results in different cells for 'files' and 'GrainSize' and different rows for GSmat. Note that in GSmat there is a different row per folder of images. Zeros are present where folders contain unequal numbers of images

```
ans =  
S053502.tif_crop.tif  
S082802.tif_crop.tif  
S082803.tif_crop.tif  
S111702.tif_crop.tif  
S115803.tif_crop.tif  
S137302.tif_crop.tif  
S137501.tif_crop.tif  
S137502.tif_crop.tif  
S146801.tif_crop.tif  
S146802.tif_crop.tif  
S147003.tif_crop.tif  
  
>> CSeat  
  
CSeat =  
  
119.9169 182.4657 132.8922 165.7560 179.5890 146.3407 122.3855 242.2357 0 0 0  
68.6232 56.3486 58.7504 65.3360 89.3966 55.0279 104.2541 92.3778 52.4083 63.0985 77.3067  
  
>> GrainSize(1)  
  
ans =  
  
MeanGrainSize: 119.9169  
    srt: [1x1 struct]  
    dist: [1x1 struct]  
  
>> GrainSize(2)  
  
ans =  
  
MeanGrainSize: 68.6232  
    srt: [1x1 struct]  
    dist: [1x1 struct]
```

```

ans =

S053502.tif_crop.tif
S082802.tif_crop.tif
S082803.tif_crop.tif
S111702.tif_crop.tif
S115803.tif_crop.tif
S137302.tif_crop.tif
S137501.tif_crop.tif
S137502.tif_crop.tif
S146801.tif_crop.tif
S146802.tif_crop.tif
S147003.tif_crop.tif

>> CSwat

CSwat =

    119.9169    182.4657    132.8922    165.7560    179.5830    146.3407    122.3855    242.2357         0         0         0
     68.6232     56.3495     58.7504     65.3960     89.3966     55.0279    104.2541     92.3778     52.4083     63.0985     77.3067

>> GrainSize(1)

ans =

    MeanGrainSize: 119.9169
           srt: [1x1 struct]
           dist: [1x1 struct]

>> GrainSize(2)

ans =

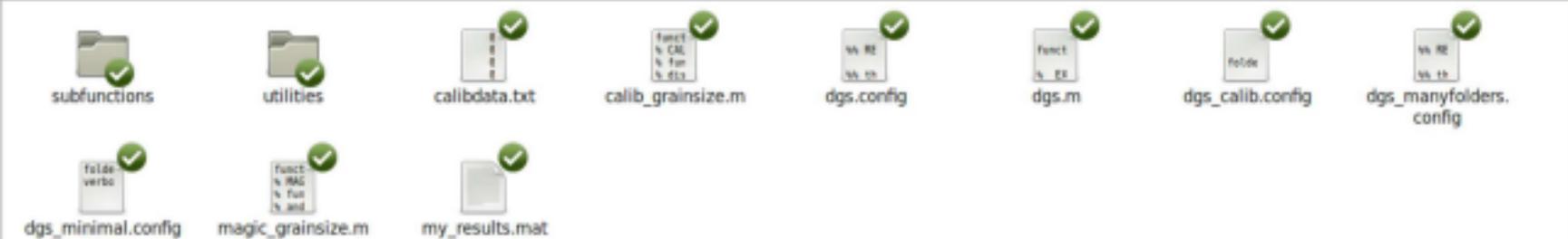
    MeanGrainSize: 68.6232
           srt: [1x1 struct]
           dist: [1x1 struct]

>> save('my_results','files','CSwat','GrainSize','Settings')
>>

```

THE PROGRAM DOES NOT SAVE THE OUTPUTS AUTOMATICALLY

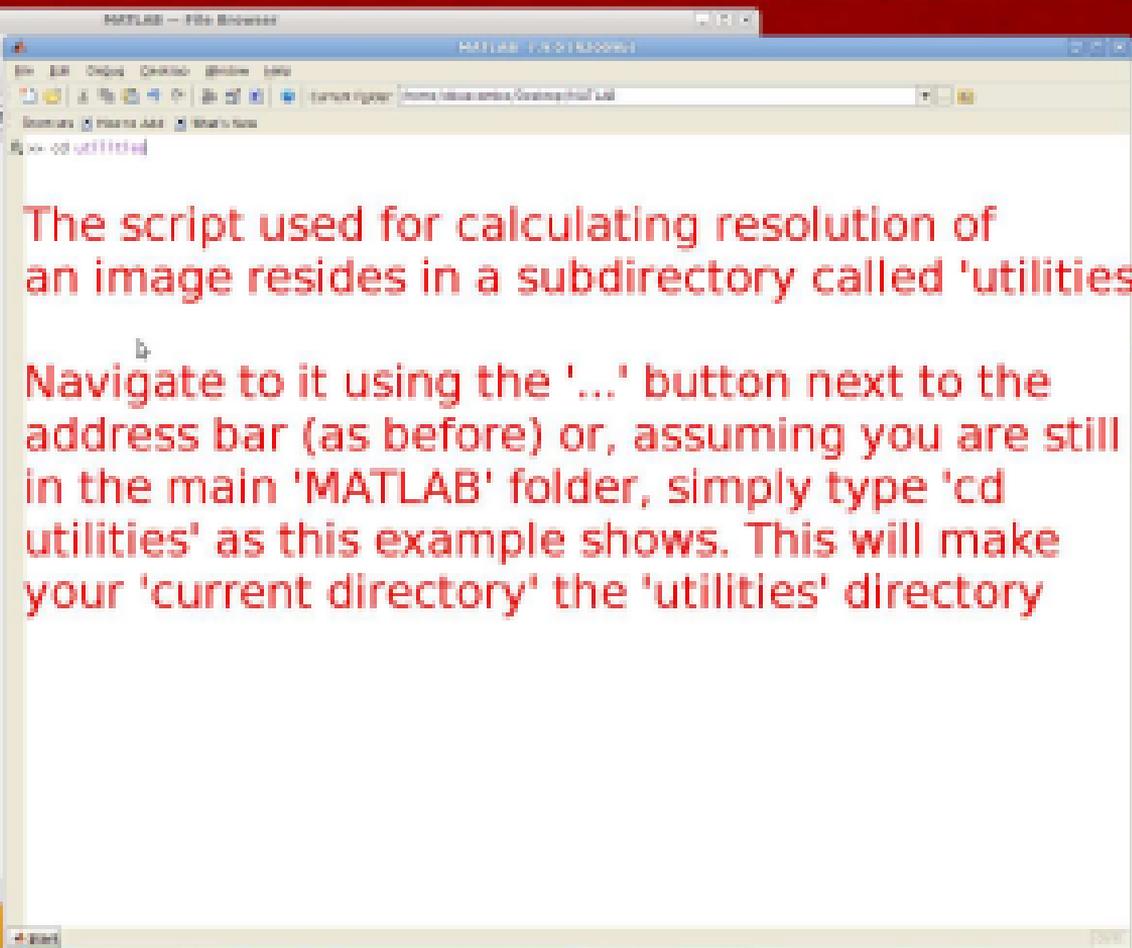
In order to save the data in matlab (.mat) format, use this as an example

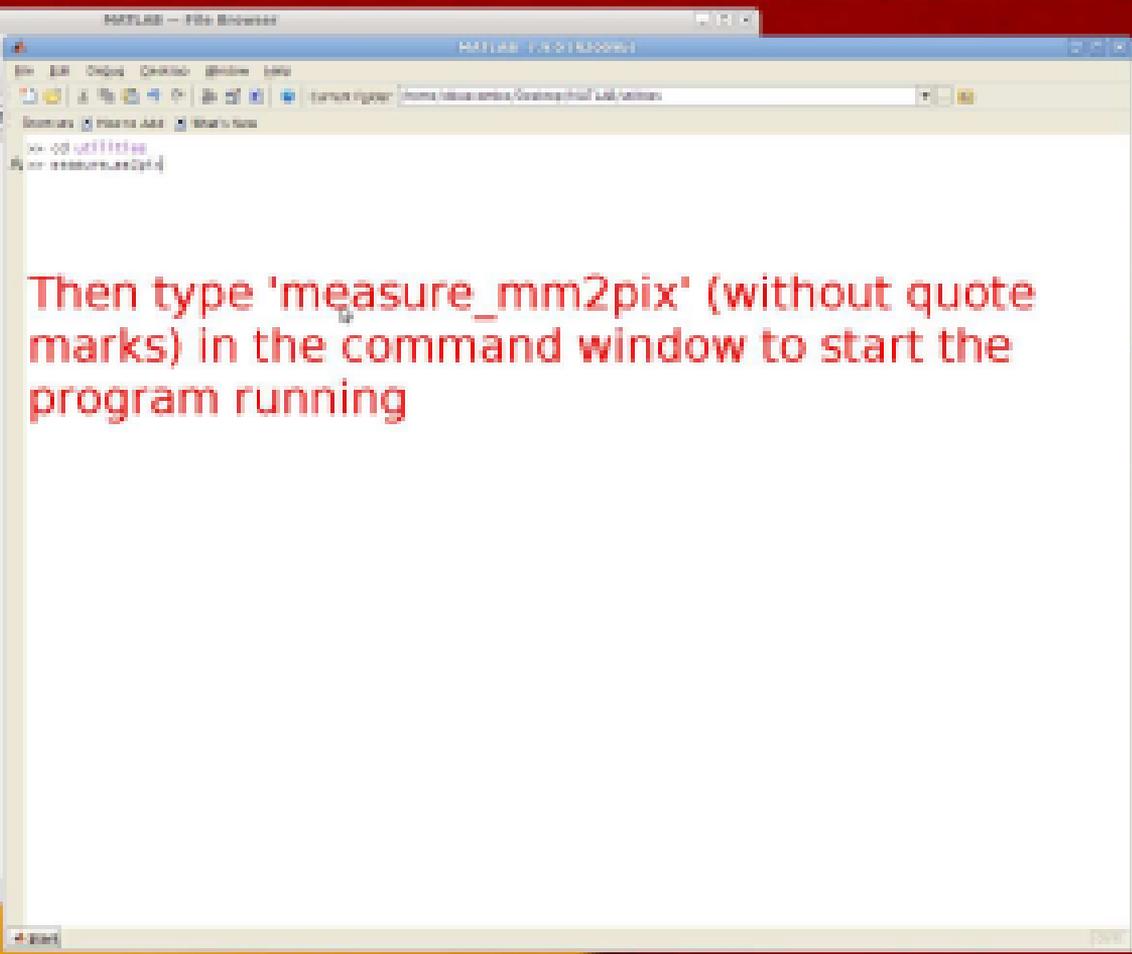


The saved results file is saved in your directory

In order to calculate the pixel (spatial) resolution you need an image with something for scale inside. Here's an example. There's a script in this toolbox which makes calculating the resolution easy. Typically, each image in a folder has the same resolution (if the same camera was used, taken from the same height above the sediment surface). In that case, the calculated resolution can be applied to all grain size results that have been calculated in pixels. Otherwise, a separate resolution is required per image which requires something for scale in each sediment image









MATLAB — File Browser

MATLAB T.L.O (R2009a)

File Edit Debug Desktop Window Help

Current folder: C:\Users\user\Documents\DevApp\MAT\utils

Details Home Add Share

Go to: [utils](#)  
or: [utils\utils](#)

The program will prompt you to select the folder on your computer which contains the 'scale image' - the image which contains something of

Select Directory to Open

Look in:

Files of type: All files

OK Cancel

known length (such as a ruler or coin or pen) which you can use to work out the length of 1 pixel represented in the image

0 items, Free space: 50 / 100





File Edit View Go Bookmarks Help Help

Location: /home/username/Desktop/MATLAB

subfunctions utilities README.txt

0 items, Free space: 59.2 GB

MATLAB T.I.O. (Task Input Output)

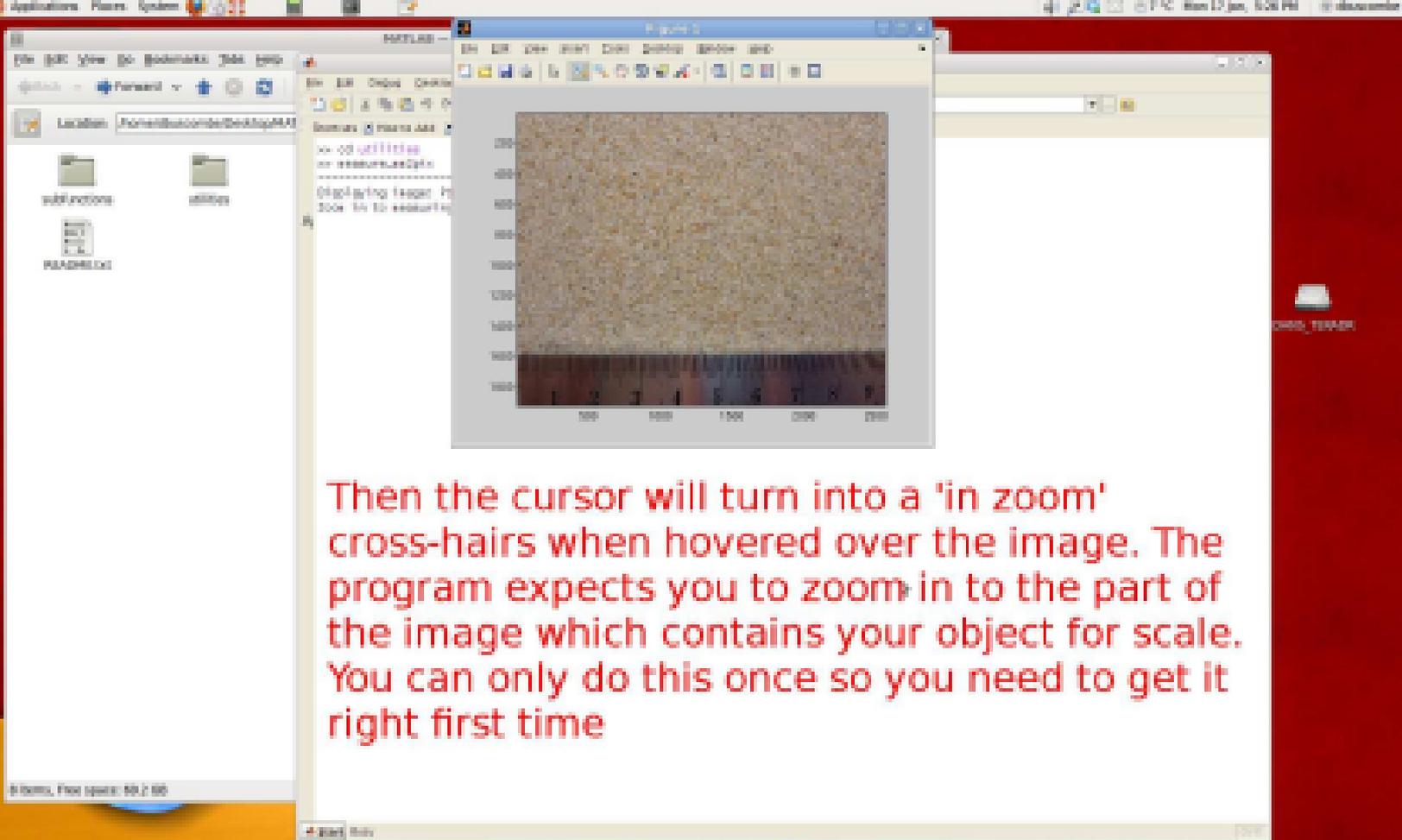
Save to: images

File name: [Empty]

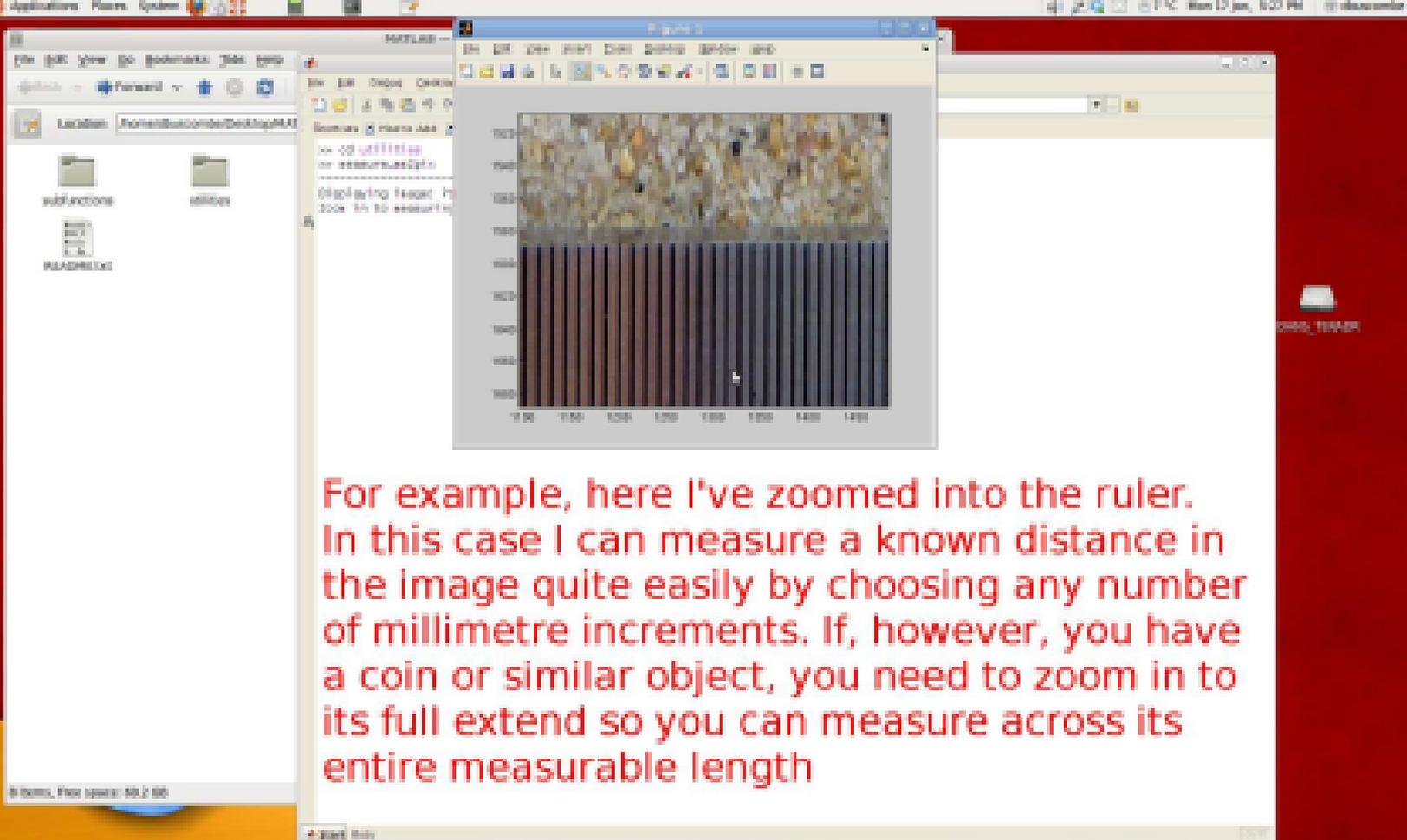
File type: Text file

OK Cancel

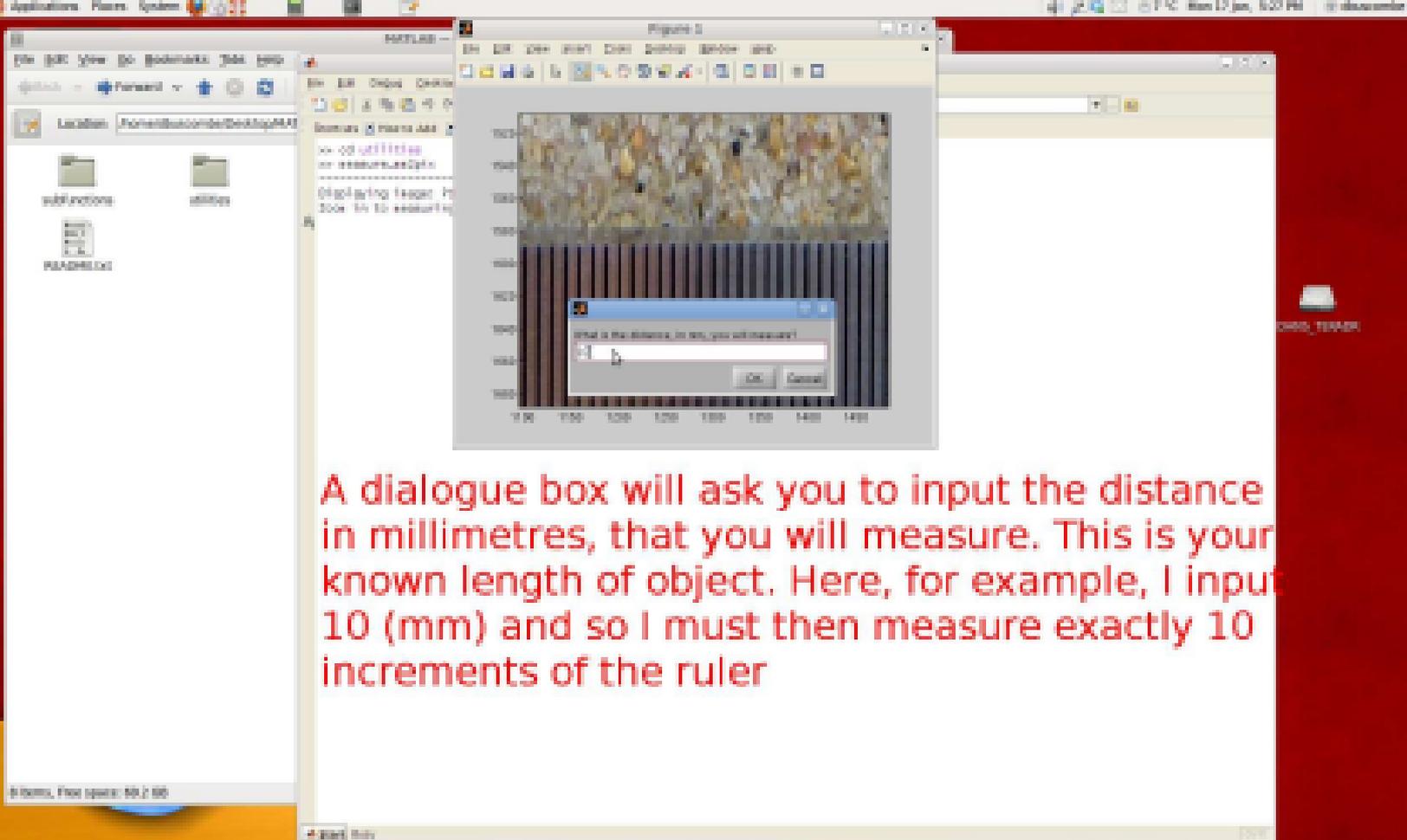
The program will then prompt you to give it a name of the file it will write to contain the result. The program will automatically create this file. By default, it's called 'mm\_pix.txt' which you could leave as it is, or modify if you wish.



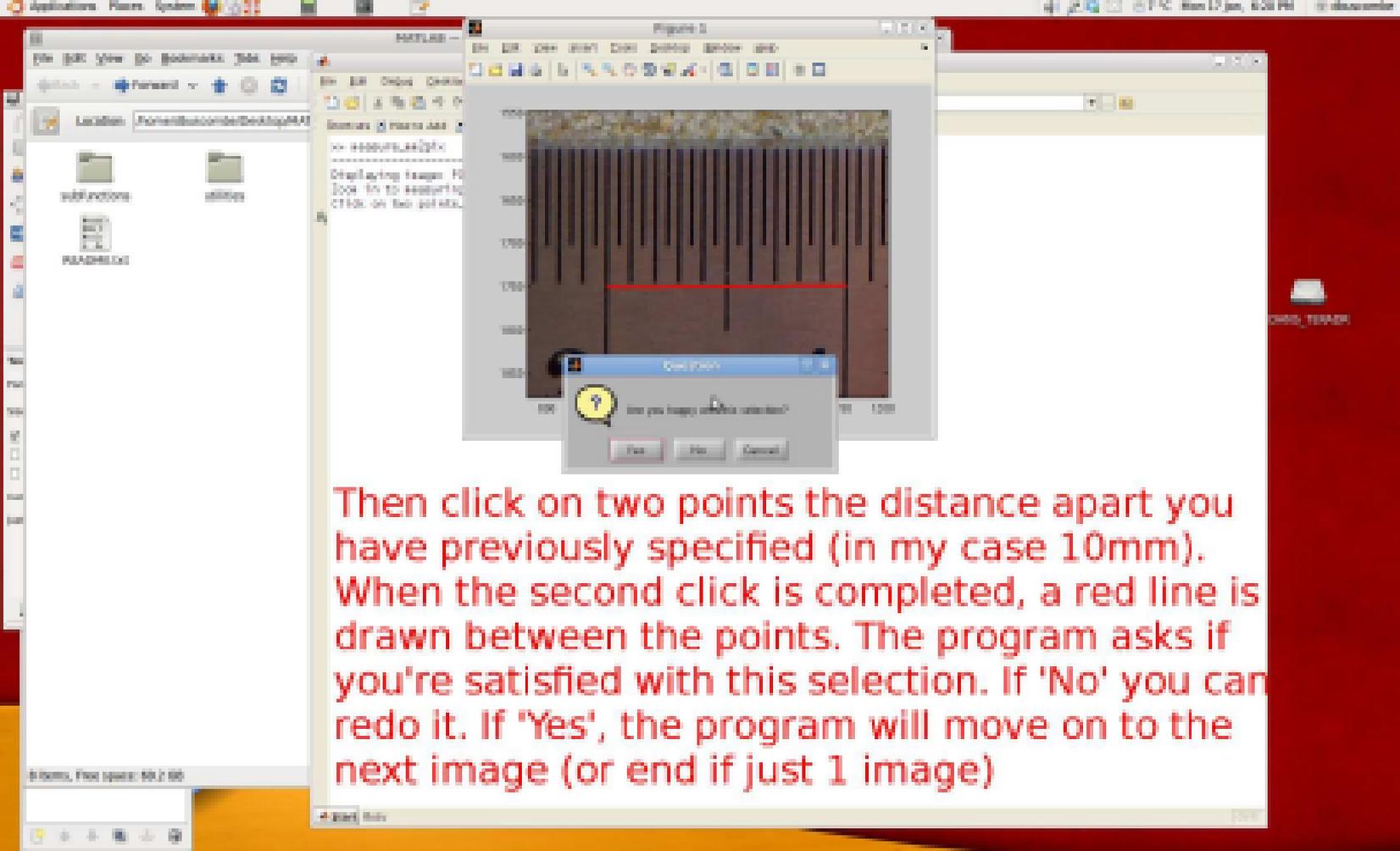
Then the cursor will turn into a 'in zoom' cross-hairs when hovered over the image. The program expects you to zoom in to the part of the image which contains your object for scale. You can only do this once so you need to get it right first time



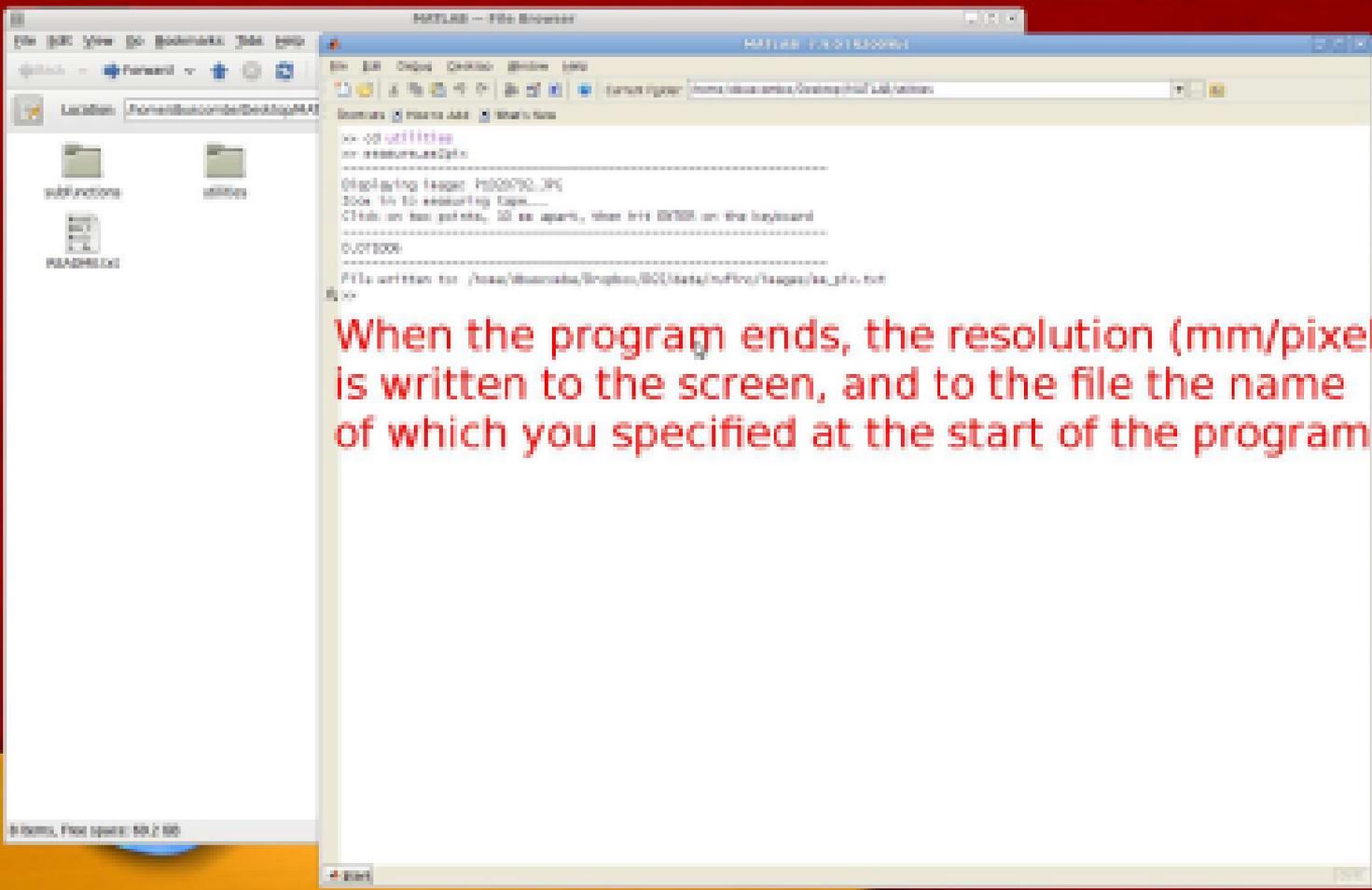
For example, here I've zoomed into the ruler. In this case I can measure a known distance in the image quite easily by choosing any number of millimetre increments. If, however, you have a coin or similar object, you need to zoom in to its full extent so you can measure across its entire measurable length



A dialogue box will ask you to input the distance in millimetres, that you will measure. This is your known length of object. Here, for example, I input 10 (mm) and so I must then measure exactly 10 increments of the ruler



Then click on two points the distance apart you have previously specified (in my case 10mm). When the second click is completed, a red line is drawn between the points. The program asks if you're satisfied with this selection. If 'No' you can redo it. If 'Yes', the program will move on to the next image (or end if just 1 image)



The screenshot shows a MATLAB File Browser window with the following content:

```
File Edit View Go Bookmarks Help Help  
Forward  
Location: /home/luowenbin/Desktop/MATLAB  
subfunctions  
utilities  
README.txt  
9 items, Free space: 50 / 100
```

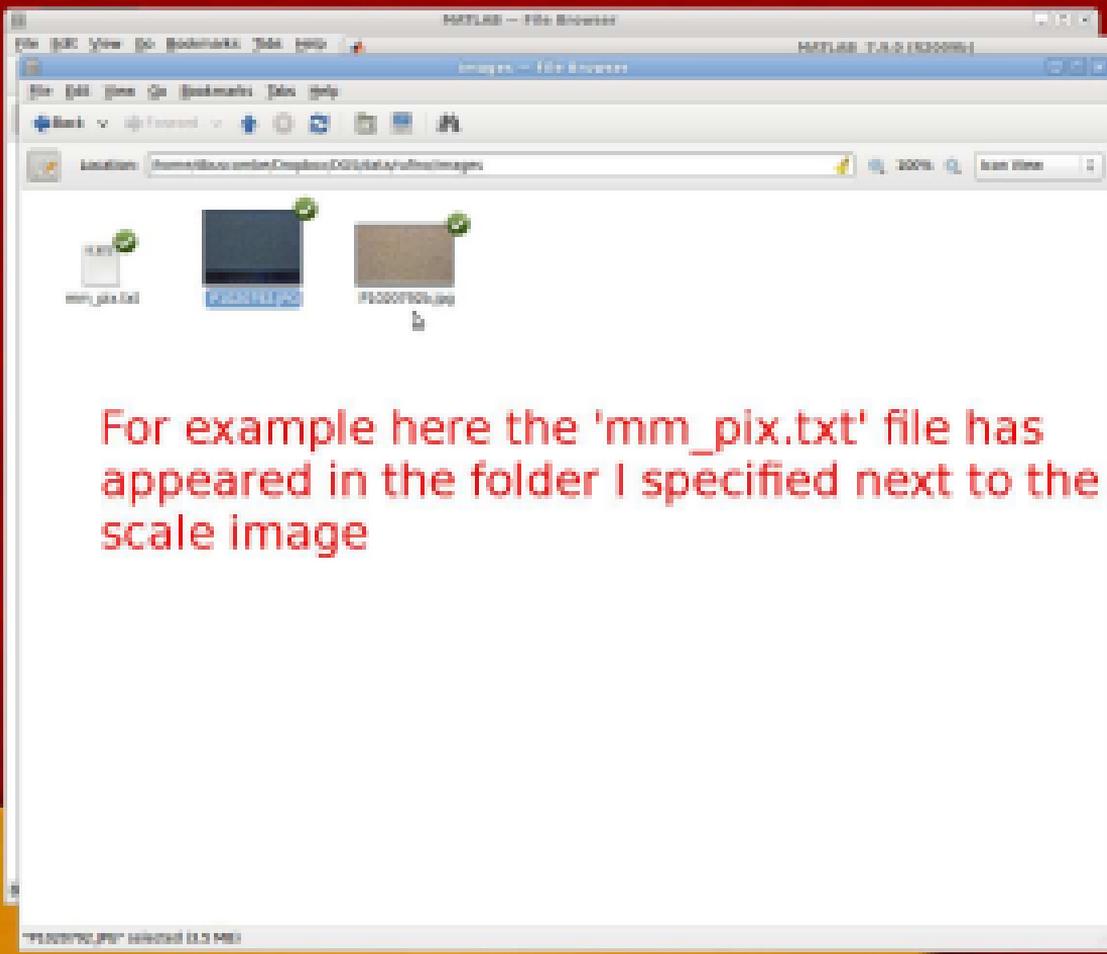
Execution log:

```
MATLAB: File Browser  
MATLAB: File Browser  
current folder: /home/luowenbin/Desktop/MATLAB  
Scripts Home Add Share  
in: cd util/1111.m  
or: edit util/1111.m  
-----  
Executing script: util/1111.m  
Now in the executing loop...  
Click on the graph, or its parts, then hit ENTER on the keyboard  
-----  
OUTPUT  
-----  
File written to: /home/luowenbin/Desktop/MATLAB/data/utf1111/figures/aa_gf1.m  
^
```

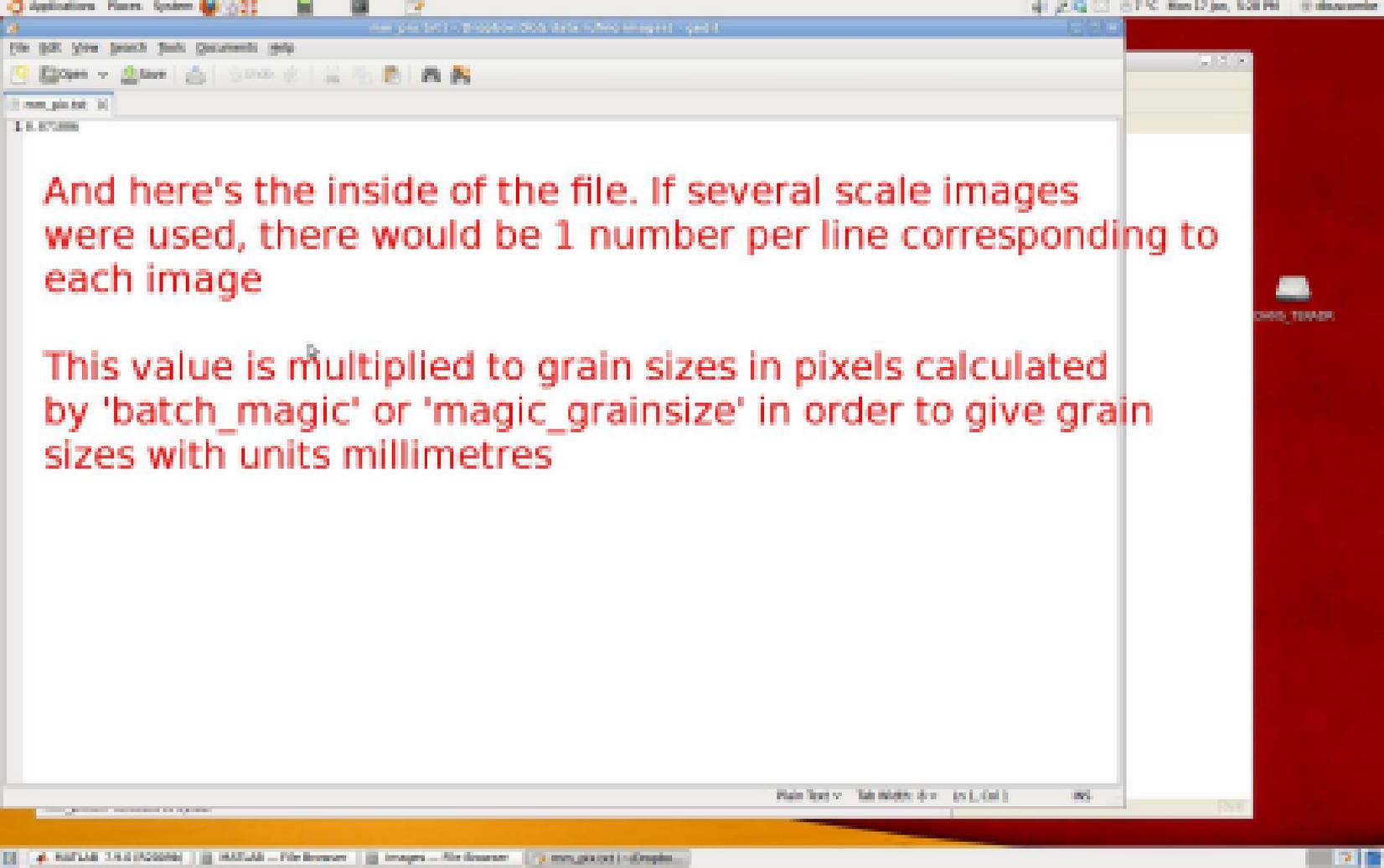
When the program ends, the resolution (mm/pixel) is written to the screen, and to the file the name of which you specified at the start of the program



01-10-17-11-11



For example here the 'mm\_pix.txt' file has appeared in the folder I specified next to the scale image



And here's the inside of the file. If several scale images were used, there would be 1 number per line corresponding to each image

This value is multiplied to grain sizes in pixels calculated by 'batch\_magic' or 'magic\_grainsize' in order to give grain sizes with units millimetres

Feedback, Questions and Comments? Email Dan Buscombe:

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Digital Grain Size

Version 3, Feb 2012