FRACLAC FOR IMAGEJ

Using FracLac V 2.0f for ImageJ

FracLac for ImageJ- Fractal, Lacunarity, Multifractal, Morphological - Digital Image Analysis Tools

FracLac for ImageJ

FracLac Advanced User's Manual

These FAQs outline the basic steps to analyze digital images and interpret the results using FracLac. The questions and topics describe how to find the box counting dimension, lacunarity, multifractal spectra, and measures of size and shape (convex hull and bounding circle) metrics for binary images.

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Introduction: How to use this manual

This online document lists questions and answers about how to use FracLac.

FracLac is image analysis software developed as a plugin for ImageJ. A copy of FracLac is included with this manual or can be obtained for free from the ImageJ website at http://rsb.info.nih.gov/ij/plugins/frac-lac.html.

FracLac is also available as a standalone java application. Usually, the plugin is more up-to-date and user-friendly and has more features than the standalone. This manual is written for the ImageJ plugin.

To use this manual browse the table of contents for questions then click on one to view an entry.

- Hyperlinks within each entry connect to additional information. Click a word or phrase in an entry to get more information.

- For references to specific terms, use the online pdf document search function.

- For details of calculations, refer to the FracLac JavaDoc and source code.

- To start analyzing right away, click here for the basic startup FAQ
  or
- To learn fundamental information about using FracLac, read in the order the questions are presented starting with the next page.

If you cannot find help, find errors in this document or bugs in FracLac, or would like to request a feature in this document or FracLac, please notify me at
akarpe@postoffice.csu.edu.au

Set up

How do I set up ImageJ and FracLac?

ImageJ is freely available image analysis software written in Java by Wayne Rasband of the US National Institutes of Health in Bethesda, Maryland. The website (http://rsb.info.nih.gov/ij/) explains how to acquire, setup, and use ImageJ.

To install **FracLac,** copy FracLac_.jar (or a file with a similar name, depending on the version) to the plugins directory of ImageJ. Restart ImageJ if it was open when the file was placed in the directory or else open ImageJ now and FracLac will appear as an option usually under Plugins: Fractal Analysis.

Click for instructions about how to analyze images.

What is FracLac for?

FracLac is used for objectively analyzing complexity and heterogeneity, as well as some other measures of binary digital images.

- Use it to measure difficult to describe geometrical forms where the details of design are as important as gross morphology.
- It is suitable for images of biological cells and other biological structures, including branching structures and textures, as well as known fractals.
- Patterns can be easily extracted from many types of images and converted to binary digital images that can be analyzed with FracLac.

A MONTAGE OF IMAGES ANALYZED USING ONE TYPE OF ANALYSIS, THE SUB SCAN FEATURE, IN FRACLAC.
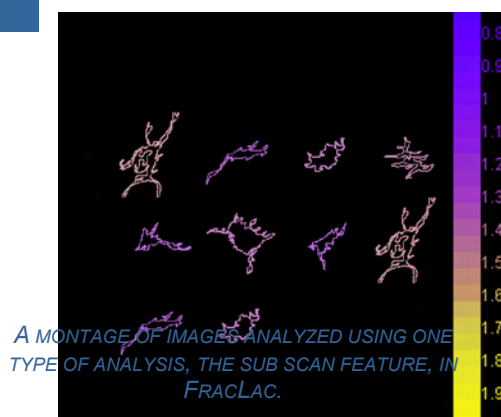
What does FracLac deliver?

FracLac performs different types of analysis to deliver data and graphics for
- *fractal dimensions,*
- *lacunarity, and*
- *multifractal data,*
- *and the shape and size of patterns in binary images.*

What types of scan does FracLac do?

FracLac scans images in different ways:
- *regular box counting,*
- *sub scans,*
- *sliding box lacunarity,*
- *and multifractal scans.*

Analyzing Images with FracLac
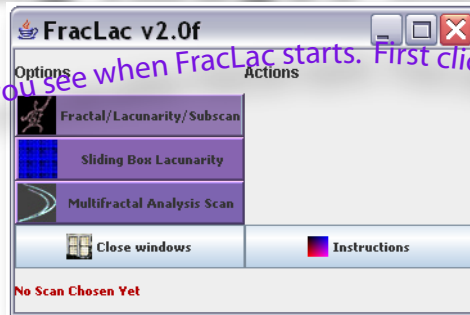
This is what you see when FracLac starts. First click on a purple button, then blue ones.

How do I start using FracLac?

After installing FracLac, select the **Plugins: Fractal Analysis: FracLac** option from the ImageJ menu. A panel of buttons appears, along with a page of basic instructions and a selection tree of colours. *The colour selection tree is for use with subscans and the particle analyzer.*

The basic sequence of events for any analysis is:

1. **CLICK A PURPLE BUTTON TO SELECT A TYPE OF SCAN AND SET ITS OPTIONS.**
   FOR A BASIC SCAN, CLICK THE TOP LEFT PURPLE BUTTON TO BRING UP THE OPTIONS PANEL.

2. **THEN CLICK ONE OF THE RIGHT BLUE BUTTONS TO SCAN IMAGES.**

3. **SAVE or view the different types of RESULTS.**

What is the FracLac Panel for?

The panel is FracLac's user interface.
It first appears with three purple buttons for selecting a scan then three blue ones for starting it.

SCAN TYPES
FRACTAL/LACUNARITY/SUBSCAN
SLIDING BOX LACUNARITY
MULTIFRACTAL ANALYSIS SCAN

ACTIONS
Scan Current Image or ROI
NonRectangular ROI
Select and Scan Files

What are the buttons on the FracLac panel for?

Set up an analysis using the Purple Buttons or perform an analysis using the Blue Buttons.

What are the blue buttons on the FracLac Panel for?

Each of these buttons starts a scan on an ROI or image:
Scan Current Image or ROI
NonRectangular ROI
Select and Scan Files
They appear once options are set and the red text at the bottom of the FracLac button panel shows the type of analysis that is selected.

What do the purple buttons on the FracLac Panel do?

These 3 purple buttons select a scan type.
Fractal/lacunarity/subscan
Sliding box lacunarity
Multifractal analysis scan
They appear on the FracLac panel at start up. One must be

clicked before the blue buttons to perform an analysis will appear. Once this has been done the first time, the new buttons will remain on the panel until FracLac is closed.

What is the Scan Current Image or ROI button for?

This button scans the current image using the current type of analysis and settings. If an ROI is selected, it will scan the ROI as a rectangle. To scan a non-rectangular ROI, use the nonrectangular ROI button.

What is the NonRectangular ROI button for?

This button will scan the currently selected ROI using the current type of analysis and settings. The ROI will be copied and scanned exactly as selected to a new image. To scan a rectangular area, select the top button.

What is the Select and Scan Files button for?

Use this button to select multiple files and analyze them without viewing them, using the current type of analysis and settings.

What does the Close Windows Button on the FracLac Panel do?

Closes all open windows, including images and graphs. This is useful if many graphs or

circularity images were generated.

What does the Red Text on the FracLac Panel mean?

It indicates the type of analysis that is currently set up or else no analysis if one has not yet been selected (by clicking one of the purple buttons).

How do I set up a scan once FracLac is loaded?

Set up a scan using the options panel that appears automatically after a purple button on the FracLac panel has been clicked.

How do I set up a regular box counting scan?

For a standard scan, click the top purple button titled "Fractal/Lacunarity/Subscans". This sets up a fractal analysis that includes lacunarity and other morphometrics This button brings up a gray options panel for setting up the analysis.

How do I scan an image?

After selecting a scan and setting its options, click "OK" and the gray options panel will disappear.The red text at the bottom of the FracLac button panel will show the type of analysis that is selected. Select an image to analyze using the blue buttons on the right of the FracLac panel.

How do I save the results?

The results will appear in the Results Table and if any graphics were selected, on the screen (e.g., multifractal spectra, regression graphs, or bounding circle drawings).
View or save the results using the File/Save As option on the Results Table.
If copying the results table using its Select and Copy functions to import the results directly into a spreadsheet, ensure that the appropriate column headings are recorded as these are not copied by this method.
Multiple images or rois on an image can be recorded in the same Results Table, but results will be lost if the table is closed or other measurements are made.

How do I save graphics?

Graphic results of each scan that appear on the screen (e.g., multifractal spectra, regression graphs, or bounding circle drawings) can be saved. Save graphics as jpg or tif files by selecting the graphic and using the File:Save As option on the ImageJ menu. Data from graphs can be saved using the ImageJ List and Save functions that appear on the graph itself.

How do I do a lacunarity scan?

Lacunarity is calculated automatically in the regular scan (top purple button). A sliding box lacunarity analysis is done separately using the middle purple button.

Images

A stained neuron prepared for fractal analysis using Adobe PhotoShop. Original image (left) was grayscaled, thresholded, and outlined to a single pixel wide binary contour (right).
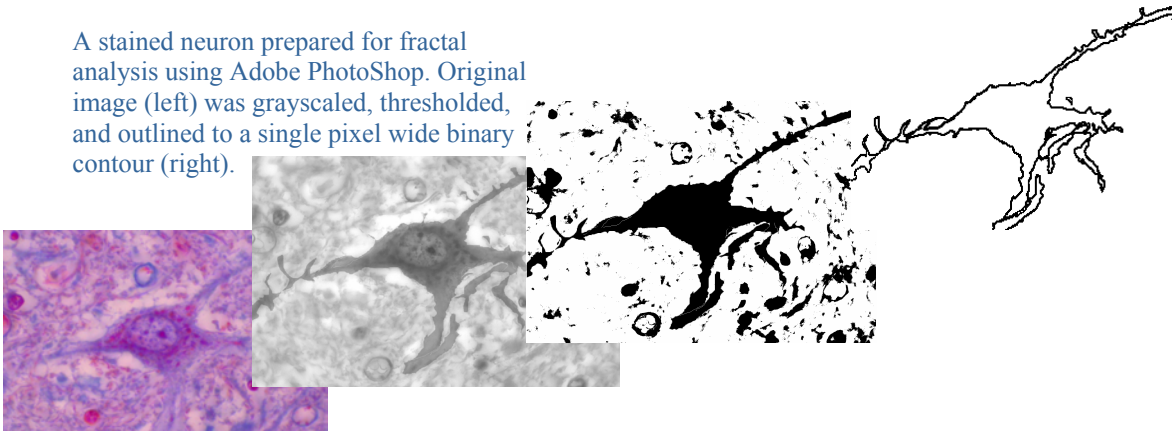
FracLac is suitable for analyzing binary digital images such as contours of biological cells as shown above or **fractals**.

How do I extract patterns to analyze with FracLac?

Binarize and outline.

For standard box counting, sliding box lacunarity, or multifractal analysis with FracLac, a pattern must be extracted and converted to a binary (black and white) image file that ImageJ can open (e.g., jpg, tiff, png, gif). This is because FracLac detects only black pixels on a white background, or white pixels on a black background.

Processing images for analysis may be simply a matter of converting to black and white. To analyze simple geometric shapes, such as circles, for instance, little preparation is required beyond thresholding then saving an image as a single pixel wide contour. But pattern extraction may, in other cases, involve considerable preparation, depending on the original image. ImageJ and most image processing software can convert images to black and white. Other functions are often available to make outlines using thresholding, background subtraction, automatic or manual tracing, dilation, etc. The images of stained cells shown here demonstrate the conversion of an original image, acquired using a light microscope with digital camera attached, to a binary outline suitable for fractal analysis with FracLac. FracLac can automatically threshold images to binary.

Original image and binary outline created in ImageJ using thresholding, dilation, and outlining.

To choose or develop a method of pattern extraction you first need to decide what features will be analyzed. Outlining, for example, is often most appropriate for cellular morphology as revealed by a cell's contour, but textures, in contrast, are sometimes better extracted using different methods than work for cell contours.

The technique used to prepare an image for analysis ultimately depends on what type of image is analyzed and determines the pattern extracted.

Because of how FracLac is written, the final image must be binary to be used with FracLac.

Should I use control images?

Although theoretical fractal dimensions do not depend on scale, images do. Digital images of patterns are imperfect and limited by resolution and a myriad of factors. Thus, it is important to test images of known fractal dimension and lacunarity that can be used as a benchmark against the images being analyzed. Images of comparable size to the ones to be analyzed, showing circles, squares, triangles, known fractals, and multifractals can be used for this. Testing is explained in the rest of this manual.

Simple contours such as lines or circles are easy to make in most digital imaging software including ImageJ. Theoretical images can be made using software that can specify line width, level of detail, size, etc. MicroMod is one example of freely available software that can generate fractals. Plugins for ImageJ to generate fractals are available, as well.

Benchmark testing with FracLac shows results generally 1-5% from theoretical for standard images ranging from 100 to 900 pixels in diameter.

Larger images tend to be closer to theoretical, and there is a lower limit on size.

Simple contours have a theoretical fractal dimension of 1.0. Circles and angled lines (not horizontal or vertical) are approximated in digital images. Smaller, more detailed lines show the most deviation from theoretical. *Even a perfect square introduces some deviation from theoretical.*

Box Counting

What is the Box Counting Dimension or D_B?

FracLac delivers a measure of complexity- a fractal dimension- called the box counting fractal dimension or D_B. It is measured from the ratio of increasing detail with increasing scale (ε). The ratio quantifies the increase in detail with increasing magnification or resolution seen in fractals but also in microscopy. The basic technique for calculating the D_B used in FracLac is called **box counting.**

The D_B is *the slope of the regression line* for the log-log plot of box size (or scale) and count from a box counting scan.

FracLac calculates different box counting dimensions:

> an unadjusted fractal dimension for scans using one grid position,
> an average fractal dimension over multiple scans,
> a slope-corrected dimension, and a
> most efficient covering dimension.

It also delivers a mass dimension using overlapping grid samples.
In addition, it can do scans over different types of subareas within an image.

What is a box counting scan?

In essence, several grids of decreasing caliber (box size) are placed over an image and the number of boxes that contain pixels is counted for each grid (boxes containing pixels correspond to the number of parts or detail). Data are gathered for each box of every grid (grid size is specified by the user or calculated automatically).

The D_B is based on the calculation of a scaling rule or fractal dimension using.

$D_B = -lim[logN_\varepsilon/log\varepsilon]$ This is read as "the negative limit of the ratio of the log of the number of boxes at a certain scale over the log of that scale".

The D_B is *the slope of the regression line* for the log-log plot of box size (or scale) and count. *(see sliding box scan)*

What is "the count"?

The count usually refers to the number of grid boxes that contained pixels in a box counting scan. For lacunarity, *the number of pixels per box are counted.*

What is epsilon (ε) or scale?

Epsilon is the scale applied to an object. In FracLac, it refers to box size relative to image size, where image size means the boundary containing the pixelated part of an image. That is, scale = box size/image size.

What is box size or grid calibre?

Box size refers to the size of the individual boxes used to measure an object. Grid caliber and box size are the same. For a nonoverlapping box count, grid calibre is the size of boxes in one grid of a series of grids. For sliding box lacunarity, it is the single overlapping box size. The sizes of boxes for all of the grids used in a box count are calculated in a linear series that depends on the minimum and maximum values as well as the number of sizes chosen. *See epsilon*

What is a scan?

Scanning is applying grids or boxes to an image and counting the number of pixels that fell in each box, as well as the number of boxes required to cover an image. Scans gather data for calculation of the fractal dimension, lacunarity, or the generalized dimension. There are global scans and sub scans, grid scans and sliding box scans. Choose a scan using a purple button; start a scan using a blue button on the FracLac panel.

What are global and regular scans?

A global scan is a box counting scan over the entire image or ROI using non-overlapping grids. This scan may be done using multiple positions. Regular scans are not sliding lacunarity scans, which use overlapping boxes instead of grids. Regular scans are set up using the top left purple button. Sub scans do global scans over an area within an image, so are called local. Multifractal analysis uses regular global scans or random subscans.

What is a nonoverlapping scan?

A nonoverlapping scan uses grids of fixed size and position. That is, each box in a grid is the same size, and the grid does not change position until all the boxes are checked.

What is a local scan?

A local scan is a scan over part of an image or ROI. It is usually called a **sub scan.**

What is grid position?
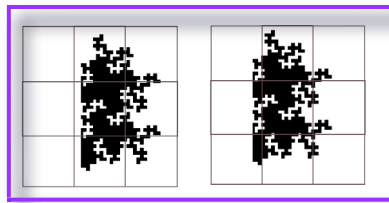
Grid position refers to where a grid is placed on an image in a box count. As shown in the picture, the number of boxes required to cover an image depends on where the grid is laid. *It takes 6 boxes in the left, and 9 in the right.* FracLac scans at multiple grid positions if **the option to do so** is selected. Regular scans assign location randomly within a set area. Multifractal analysis uses a special convention.This grid shown here is nonoverlapping, which means its boxes do not overlap. In a sliding box algorithm, in contrast, the boxes may overlap.

What is an average D_B?

The **average D_B** is the usual box-counting fractal dimension averaged over the number of scans that were done at different grid positions.

What is a slope-corrected D_B?

The **slope-corrected D_B** is corrected for periods of no change in the regression data. These periods arise spuriously as a limitation of pixels and grids. FracLac uses a linear series of box sizes, in order to maximally capture scaling in an image. Using a linear series, after a point, as box size increases relative to image size, the number of boxes required to cover an image stays the same over a long interval of change in size. This causes plateaus in the log-log plot with box counting, but does not necessarily reflect actual features of complexity in a pattern. FracLac removes data points arising from such plateaus to provide the slope-corrected D_B. This value is reported in the results table for a regular scan as the D_B without horizontal intervals

What is a most-efficient cover D_B?

A **most efficient cover D_B** is generated from box counting data over multiple grid positions using the least number of boxes required to cover the image. For each size, only the box count that was most efficient (lowest) is selected from all of the grid positions tried. This value is reported in the results table for a regular scan as the miminum cover D_B.

Lacunarity

What is lacunarity or Λ?

The "lac" in FracLac stands for lacunarity, Λ, which is "gappiness" or "visual texture". Λ is considered a measure of **heterogeneity** (inhomogeneity) or translational or rotational invariance in an image. This measure supplements fractal dimensions in characterizing patterns extracted from digital images.
FracLac automatically calculates some values of lacunarity in a regular scan.

FracLac delivers lacunarity based on
  pixels in standard box counting
  sliding box counting

FracLac delivers different types of lacunarity including:
  CV for pixel distribution
  Prefactor
  CV for occupied/unoccupied
  Probability Density Lacunarity

How is lacunarity calculated for a regular scan over one or multiple locations?

In FracLac, lacunarity is calculated as the variation in pixel density at different box sizes, using the CV for pixel distribution.

First, the number of pixels in each box that was placed on an image at an ε is counted during standard non-overlapping box counting or overlapping box counting. Then, for each ε, the CV^2 is calculated from the standard deviation and mean of pixels per box:

$$\Lambda_\varepsilon = (\sigma/\mu)^2.$$

Lacunarity varies with the size of the sampling unit. Thus, FracLac delivers the mean value of the CV^2 over all ε at a location, or else the data can be looked at directly by plotting ε and Λ. For global scans

using multiple grid positions, the mean lacunarity over all scales is found for each grid position, then the average of this average is found to determine a single value of lacunarity. For sub scans, it is calculated for each subarea.

Prefactor Lacunarity

Another proposed measure of heterogeneity that is reported in a standard scan with multiple locations uses the prefactor A from the scaling rule $y=AX^{D_B}$.

$$\frac{\sum\left[\left(\dfrac{A^{-1}}{\dfrac{\sum A^{-1}}{N}}\right)-1\right]^2}{N}$$

where A = the prefactor and N= the number of grid locations. This value is reported in the results table as the mean y-intercept lacunarity.

CV for occupied/unoccupied

FracLac reports the CV for boxes that contained pixels compared to boxes that did not.

Binned Probability Density Lacunarity

Lacunarity is also calculated using probability densities.

The mean of the probability distribution is: $\sum(i*mprob[i])$ where i is the mass value m[i], and mprob[i] is the weight.

The std dev of the probability distribution is: $\sqrt{\sum(((mprob[i]-meanProb)*(mprob[i]-meanProb))*i)}$;

The Probability Density lacunarity at this epsilon is: $(\sum M^2-(\sum M*\sum M))/(\sum M*\sum M)$;

where $\sum M=\sum(i*mprob[i])$ and $\sum M^2 = \sum(i*i*mprob[i])$;

What are the basic calculations?

HOW IS THE STANDARD ERROR CALCULATED?

$$SE = \sqrt{\frac{\sum C^2 - b\sum C - m\sum SC}{n-2}}$$

S=log of scale or size, C=log of count, n=number of sizes, b = y intercept of the regression line, m = slope of the regression line

HOW IS THE SLOPE OF THE REGRESSION LINE CALCULATED?

The slope of the regression line, used for calculating the D_B, is:

$$m- = \frac{n\sum SC - \sum S \sum C}{n\sum S^2 - \left(\sum S\right)^2} = -D_B$$

S=log of scale or size, C=log of count, n=number of sizes, slope of the regression line

For other regression lines, S=the value along the x-axis, and y = the value along the y-axis.

HOW IS THE CORRELATION (R^2) FOR THE REGRESSION LINE CALCULATED?

$$r^2 = \left[\frac{n\sum SC - \sum S \sum C}{\sqrt{\left(n\sum S^2 - \left(\sum S\right)^2\right)\left(n\sum C^2 - \left(\sum C\right)^2\right)}}\right]^2$$

S=log of scale or size, C=log of count, n=number of sizes,

HOW IS THE Y-INTERCEPT OF THE REGRESSION LINE CALCULATED?

$$y\,\text{int} = \frac{\sum C - m\sum S}{n}$$

S=log of scale or size, C=log of count, n=number of sizes, m = slope of the regression line

HOW IS THE PREFACTOR FOR THE SCALING RULE CALCULATED?

The prefactor A = Euler's e$^{\text{y-int}}$
Where for y = AX^{D_B}, -D_B = slope of the regression line, and y-int = the y-intercept of the regression line.

WHAT IS A CV?

CV stands for coefficient of variation=σ/μ.

In FracLac, it is used to calculate lacunarity (Λ) as a measure of variation in pixel distribution for regular box counting and sliding box lacunarity.

It measures variation in a set of data and is calculated as the standard deviation over the mean (σ/μ) for the data. It can be multiplied by 100 or squared, depending on the usage.

These panels automatically appear after a purple button is clicked to select a scan type. They are what the user sets scan options with.

Standard Options
Sliding Lacunarity Options
Multifractal Options

After options are set, click "OK" and the gray panel will disappear and red text at the bottom of the FracLac button panel will display the type of analysis selected.

How do I set the standard FracLac options?

The standard scan is a regular box counting scan.

AUTOTHRESHOLD

Leave autothreshold unselected for binary images. Check autothreshold to automatically threshold images using ImageJ's built-in function. It is unselected by default and recommended only when it is certain that only the pixels of interest will be thresholded. The threshold settings cannot be changed within FracLac.

QUICK SCAN

Select quick scan to scan using a faster but slightly less accurate algorithm. Unselecting this box is slower and it is recommended to leave it selected as the default.

GLOBAL SCAN POSITIONS

Type a number for the number of scans at different locations. FracLac does multiple scans if this is set to more than one, otherwise the grid is laid at the top left corner of the pixelated part of the image. The box counting dimension depends on grid location, so using multiple locations lets FracLac determine dimensions using average and most-efficient coverings rather than just one fixed location.

The higher the number, the more accurate the result, to a point, but also the slower the scan, especially for very large images.

The default is set to 4 locations for standard and multifractal analyses. In a regular scan, sampling is random. *Setting this value to 4 for a multifractal analysis ensures that* **sampling** *is optimum.* Note that this setting is for scans over the entire image, not *subscans* . The number of positions used is reported in the results table.

BOX SIZES PER SCAN

Type a number for the number of box sizes or different calibers of grid that will be used in a scan. The series increases in size linearly by a fixed increment from the **minimum** to the **maximum**. The increment is set by dividing this range by the number of sizes requested. **Set the number of sizes to 0 for the default optimized value.** Or, using the slider, set any number of box sizes to use. Leaving this to 0 is recommended as it sets an optimum value according to the image size. The number of box sizes used is reported in the results table.

SMALLEST GRID

Type a number to set the smallest grid size in the series.

The smallest size possible is 1 pixel, but this lower limit should match the resolution of the image.

LARGEST GRID

Type a number for the largest grid in the series of grids used in box counting. This number is a percentage of image size rather than a number of pixels, because when box size goes beyond about 50% of the image size, errors are introduced.

The default value of 45% is generally optimal for standard box counting scans.

For multifractal analysis, the default is 100%.

SUMMARIZE FRACTAL AND LACUNARITY STATISTICS

Select summarize to print final values for the D_B in the Results Table, and not print data for each pixel count. By unselecting this option, raw data are printed, from which the fractal dimension and lacunarity can be determined.

SLIP GRID AT EACH POSITION

Selecting this option adds a random factor. Grid position is selected randomly within an area then if this option is set further adjusted at scan time.

Check this box to print raw data showing the frequency of different numbers of pixels appearing in a box at each box size for calculating lacunarity.

Type a number for the number of frequency distributions to use for the mass vs. frequency distribution. Actual data are included in addition to a frequency distribution.

Check this option to analyze individual areas within an image. This is suitable to see variation within an image or for images that are easily segmented using ImageJ's Particle Analyzer (e.g., images with several cells that are separated by the Particle Analyzer).

To see the raw data for box counts graphically, select Graph Regression Line. A graph like the one shown here is generated, plotting the log of box size and the log of pixel count.

The graph can be saved using File:Save As on the ImageJ menu.

Note that when analyzing many files at once, this will produce a potentially unwieldy number of on screen graphs.

The numbers reported on the graph for the regression lines are explained in Interpreting the Results Table.
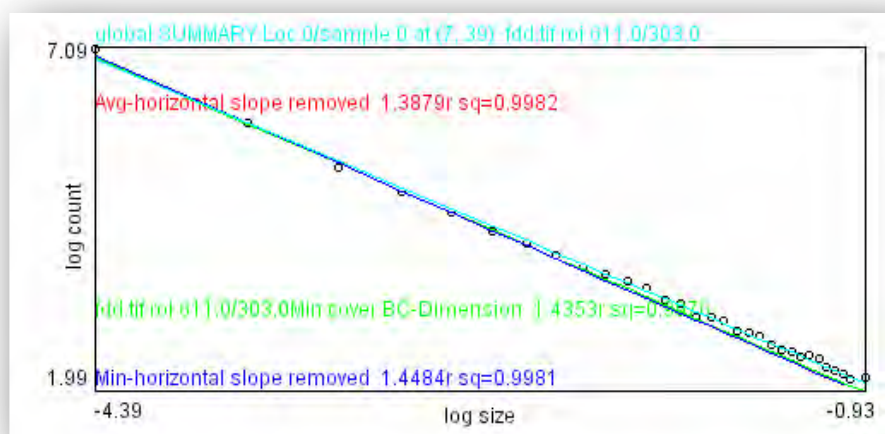
Select Include Circularity Data to analyze other features of images. This function is designed for binary contours but will work on other types of patterns. It calculates the convex hull enclosing the pixelated part of an image and various measures based on the hull and the smallest bounding circle enclosing the hull. (See Interpreting Circularity and Morphometrics).

Convex hull of neuron shown earlier.

If circularity is selected, select this option to see the convex hull and bounding circle on a copy of the original image, as shown in the diagram here. The new image can be saved. Note that if you are analyzing many files at once, this will produce a potentially unwieldy number of new images so is most suitable for single analyses.

Interpreting the Results

Each scan is interpreted differently. Click below to learn how to interpret the different results.

Standard box counting may return a standard results table, a raw data results table, a subscans results table, a convex hull graphic, a regression line graphic, and a subscan graphic.

How do I interpret a standard box counting analysis?
How do I interpret a sliding lacunarity analysis?
How do I interpret a multifractal analysis?
How do I interpret a sub scan analysis?

How do I read the data in the results table from a standard box counting analysis?

Using the defaults for a basic fractal analysis at 4 origins, the results table lists a row of values for complexity, heterogeneity, size, shape, image features, etc., for each image. Each column in the Results Table is briefly described here. Details of data gathering and analysis are outlined in the JavaDoc and source code.

FRACLAC2004
Filename or ROI location within the image

FOREGROUND PIXELS
The total pixels counted that were the foreground colour in a scan. Images analyzed with FracLac are assumed to have only white and black pixels. Only pixels that are the colour that is considered foreground are analyzed. The foreground colour is set automatically according to the relative numbers of pixels in an image. The foreground is black and the background is white if there are more white than black pixels; otherwise the foreground colour is white and the background is black. *See autothreshold*

TOTAL PIXELS
The number of pixels counted that were the foreground colour or the background colour.

MEAN BOX COUNTING FRACTAL DIMENSION (D_B)
The D_B or box counting fractal dimension averaged over all locations.

CORRELATION (R^2)
The r^2 value for the regression line showing the relationship between the log of count and size. *This value appears beside each fractal dimension in the results table.*
This is one test of the regression line. Strictly speaking, a value of 1.0 shows perfect correlation in the data.

STANDARD ERROR
The standard error for the regression line. *This value appears beside each fractal dimension in the results table.* This is a test of the validity of the regression line from which the D_B is calculated

COEFFICIENT OF VARIATION (CV) OVER ALL LOCATIONS
The coefficient of variation measures variation in the D_B over all locations. This can be used along with lacunarity to measure heterogeneity and dependence of the D_B on grid position.

MEAN D_B WITHOUT HORIZONTAL INTERVALS
The average D_B over all locations, **corrected for periods of no change** in box count with change in size.

MINIMUM COVER D_B

The D_B calculated from a **most efficient grid covering**.

MINIMUM COVER D_B WITHOUT HORIZONTAL INTERVALS

The most efficient-covering D_B corrected for periods of no change in the regression data.

MEAN Y-INTERCEPT OF REGRESSION LINE

The average value for all y-intercepts of all regression lines at all locations.

MEAN Y-INTERCEPT LACUNARITY

This is an alternative measure of lacunarity calculated using the prefactor in the relationship $y = Ax^{D_B}$.

CV FOR Y-INTERCEPT

The coefficient of variation for the y-intercepts is a measure of heterogeneity or lacunarity. The standard deviation for all y-intercepts of all regression lines at all locations divided by the mean.

MEAN BINNED PROBABILITY DENSITY LACUNARITY

The average value for lacunarity calculated using probability distributions

MEAN CV FOR BPDL

The coefficient of variation for the above measure

MEAN CV^2 FOR PIXELS PER BOX OVER ALL LOCATIONS

Lacunarity: the usual measure of lacunarity or Λ calculated as the average coefficient of variation in pixels per box over all grid locations.

CV FOR MEAN CV^2

The coefficient of variation in lacunarity as it depends on grid location.

EMPTIES MEAN CV OVER ALL LOCATIONS

A measure of heterogeneity using the variation in the number of empty boxes.

COUNTS CV

The coefficient of variation for the count of boxes having pixels; A measure of heterogeneity using the number of filled boxes.

MEAN CV FOR BPDL

The mean coefficient of variation for binned probability density lacunarity

CV FOR UNOCCUPIED/ CV OCCUPIED

Heterogeneity in the ratio of empty to non-empty boxes with box size and location.

HULL AREA

The area in pixels of the convex hull enclosing the pixelated part of an image

HULL PERIMETER

The perimeter in pixels of the convex hull enclosing the pixelated part of an image

BOUNDING CIRCLE DIAMETER

The diameter in pixels of the smallest circle enclosing the convex hull enclosing the pixelated part of an image. This is a measure of cell size for biological cells. Compare the area of this circle (area=πr^2) with the area of the convex hull.
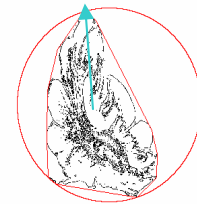
Convex Hull , Bounding Circle, and Maximum Radius of Hull for Image of Cerebellum

HULL CIRCULARITY

A measure of shape of the convex hull = (area/perimeter^2)*4π. Compare this number to a circle, for which the ratio is 1.00.

WIDTH

The width of the rectangle enclosing the image oriented horizontally/vertically.

HEIGHT

The height of the rectangle enclosing the image oriented horizontally/vertically.

MAXIMUM RADIUS

The greatest distance from the centre of mass of the convex hull to its boundary. This measure is different from the smallest bounding circle, because the convex hull's centre of mass is not necessarily centred on the bounding circle.

MAXIMUM RADIUS/MINIMUM RADIUS

The ratio of the maximum to the minimum distances across the image from the centre of mass to the boundary of the convex hull.

CENTRE

x,y coordinate pair for the circle's centre and x,y coordinate pair for the convex hull's centre of mass

NUMBER OF BOX SIZES USED IN TOTAL ANALYSIS

The number of box sizes that were tested

ADJUSTED NUMBER OF BOX SIZES

The number of box sizes considered for the **slope-corrected** D_B

NUMBER OF ORIGINS

The number of times a complete scan was done, each at a different randomly generated grid position.

MAXIMUM BOX SIZE

the largest grid caliber that was used in the series of box sizes that were tested

MINIMUM BOX SIZE

the smallest grid caliber that was used in the series of box sizes that were tested

MAX V OR H SPAN

The largest span across the pixelated part of the image based on horizontal and vertical boundaries; This is used in determining ε. See Bounding Circle Diameter and Maximum Radius

DENSITY

Usually an image feature. The number of pixels of foreground colour divided by the total number of pixels in the convex hull.

SPAN RATIO

A measure of shape as the ratio of major and minor (orthogonal) axes for the convex hull.; intended for biological cells as a measure of overall shape based on the convex hull.

How do I read the results table for raw data for a standard scan?

If raw data are listed, the results table contains different data than otherwise:

First the results for each scan are summarized at each location as in the standard results table

Then results summarized over all locations are listed.

Then the raw data are listed. There is one row for each box size, and several columns, each listing data from the headings outlined below. If more than one location is used, then each column is repeated consecutively for each location before the next column heading is used.

The column headings from left to right are:

Box size

grid calibre in pixels

Scale (ε)

1/image size

Count

Number of boxes that had any pixels at that size and position

Empties

Number of boxes with no pixels at that size and position

Mean pixels per box

μ-the average number of pixels in a box at that size and position

Standard Deviation for pixels per box

σ-the standard deviation for the number of pixels in a box at that size and position

cv^2 for pixels per box

Λ- lacunarity for the distribution of pixels in an image. It is the CV for the number of pixels that were found in a box at that size and position. The CV at each size can be averaged to get a value of lacunarity over the image. These averages can be further averaged over all locations to get the lacunarity using multiple locations. (See Results Table)

Binned Probability Density Lacunarity

This is an alternative method of calculating lacunarity, which also uses the pixel distribution. The number of pixels per box is binned into categories then the same values are calculated as for the CV described above.

Measures of Size and Shape

In addition to fractal and lacunarity data, FracLac returns measures based on the convex hull and bounding circle, as well as the pixels and pixel density in an image. The convex hull and bounding circle are calculated only if selected on the options panel. The circle's diameter and the convex hull's area, perimeter, radii, circularity, vertical and horizontal dimensions, and span ratio are measured.

What is a convex hull?

The convex hull is a boundary enclosing the foreground pixels of an image using straight line segments to each outermost point, as shown in the figure to the right. This boundary defines some aspects of the size and shape of the two dimensional space occupied by a biological cell in cellular morphology. In FracLac, it is calculated using Roy's convex hull algorithm, which is outlined in the source code and JavaDoc for FracLac. *It is calculated using the circularity option in the options panel.*
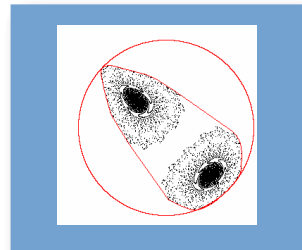
Convex hull and bounding circle of Henon multifractal

What is a bounding circle?

The bounding circle is the smallest circle enclosing the foreground pixels of an image, as shown in the figure. This measure describes the size occupied by a pattern. It is supplemented by the convex hull and other measures. The bounding circle is calculated using three points on the convex hull. *It is calculated using the circularity option in the options pane; see bounding circle*

Sub Scans

What is a sub scan?

A subscan is a regular scan applied to individual areas of an image. It is set up using the subscan option.

How do I do a subscan?

To scan areas of an image separately in a standard analysis:

1. **Click the top** purple button **on the FracLac Panel**

2. **Select DoSubs from the FracLac Options panel.**

3. **Set Sub Scan options using the panel that appears after clicking "OK" on the options panel.**

4. **View or save the results and graphics.**

To scan areas of an image separately in a multifractal analysis, select Do Random Mass Sample from the Multifractal Analysis Options Panel.

How do I set the Sub Scan Options?

If **DoSubs** is selected on the standard Options Panel, after clicking "OK" at the bottom, another panel will appear requesting options for a sub scan.
1. **Set the sub scan options on this panel, then click "OK" or click "Cancel" to cancel the sub scan.**
2. **To perform the sub area scan, click one of the blue buttons on the FracLac panel.**
3. **View or save the graphics and results table.**

Doing subscans takes considerably more time for large images. It also depends on the size of subscan areas (smaller areas take longer).
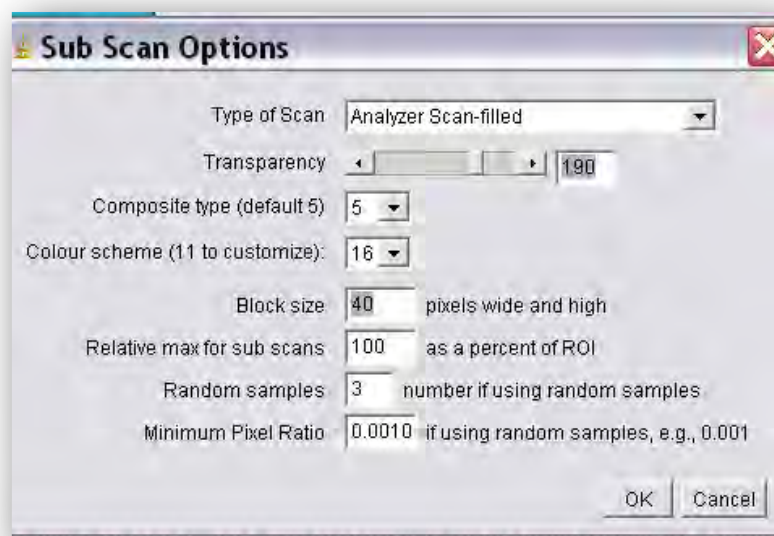
Type of Subscan

Subscans find local fractal dimensions over an image. This can show how the dimension depends on the sample size and how its distribution over an image can change. Images can be scanned in systematic or random blocks, or as particles. Graphics are colour coded by pixel, block, or particle.

DISPLAY DIMENSION

Select a scan that says "display dimension" to display the fractal dimension as a number on each subarea.

FILLED

Select a scan that says "filled" to draw a colour-coded graphic representing the fractal dimension as a filled area covering each subarea with a colour representing the fractal dimension according to the colour code scheme selected.

PIXELS

Select a scan that says "pixels" to replace each foreground pixel with a colour-coded pixel representing the fractal dimension by a colour

according to the colour code scheme selected.

RANDOM

The areas sampled can be chosen randomly or be part of a systematic sample. For random samples, each position is randomly chosen. For nonrandom (systematic) samples, the entire image is sampled from left to right and top to bottom. In both cases, the same series of grids of decreasing caliber is used at each location.

ANALYZER

Analyzer options use ImageJ's built-in particle analyzer to analyze only areas identified by the Particle Analyzer. Use these scans for images of multiple cells, for instance, or wherever particles are adequately separated using the analyzer. In contrast, rectangular scans scan rectangular areas, and block scans scan squares over the entire image.

ANALYZER CONTOUR

Use this option to display contours of the Particle Analyzer's particles coloured

according to the fractal dimension of each particle.

ANALYZER FILLED

Use this option to display filled contours of the Particle Analyzer's particles filled with colour according to the fractal dimension of each particle.

ANALYZER DIPLAY DIMENSION

Use this option to display the fractal dimension directly on each particle of the image using the Particle Analyzer.

TRANSPARENCY/OPAQUENESS

Set the transparency for the colour coded image. Use lower values to reveal the image underneath the colour coding, higher to cover it with colour.

COMPOSITE TYPE

Set the composite type for the image. This function is best left at the default value of 5.
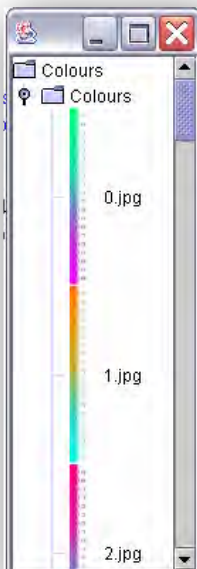
COLOUR SCHEME

Choose the colour scheme. This is also available through the colour selector tree (left) that appears when FracLac is started. Type a number or select an option on the colour selector to determine how images will be colour coded. A separate scale image appears with each colour coded image.

Choose 11 to customize the colours. If 11 is selected on the selection tree or on the option panel, after clicking "OK", a new panel appears with seven sliders (right) representing 7 colour groups. Each slider sets the limit for one colour category. Set each slider to the limit of a fractal dimension times 100 for each category of interest. Thus, the lowest value goes at index 7 and the highest at Index 1. Manage the size of each interval to best frame the range of fractal dimensions relevant to your analysis.

How do I interpret a sub scan analysis?

A sub scan generates results and graphics. The graphics differ for random, systematic, or particle scans.

How do I interpret the Results Table from a subscan?

The results table for images scanned using sub areas is interpreted the same as the results table for a standard analysis. The only difference is that there is a row of data for each subarea scanned, as well as a row for the global scan over the entire image.

How do I interpret the graphics from a subscan?

RECTANGULAR AND BLOCK SCANS

Scan areas of an image using the sub-box size setting.

A-C were scanned using a rectangular sub scan, but the results are displayed differently.

- **A** was made using a pixel replacing strategy.
- **B** was made using a block filling strategy.
- **C** was made using the "display dimension" strategy. Each block in **C** is colour-coded in outline for the D_B of that portion of the image, and the D_B is printed in the block.

A colour-coded legend is also generated with each image for interpreting the results. The legend can be saved separately. It lists the colour with the corresponding fractal dimension beside it.
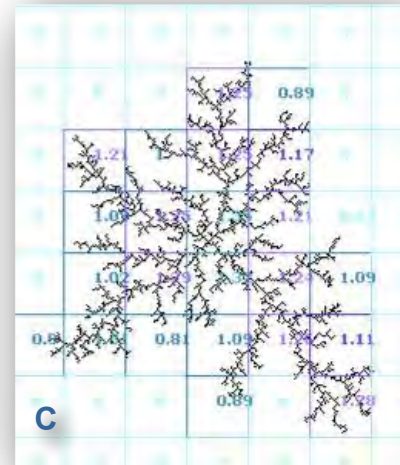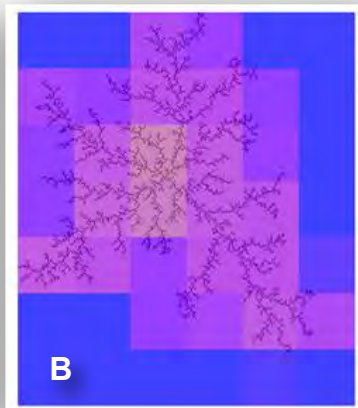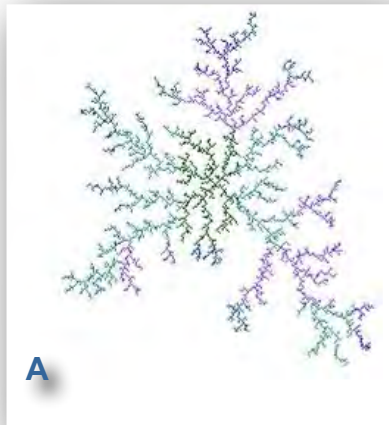
- Images are coded as particles rather than arrays.
- D was analyzed using the Particle Analyzer with contour pixels replaced.
- The original image showed binary contours arranged as shown.
- Each cell within the image was automatically identified and analyzed.
- The fractal dimension is printed on the colour-coded contour. Selecting a different setting would fill the particle or not print the value and just colour in the pixels of the automatically identified particle.
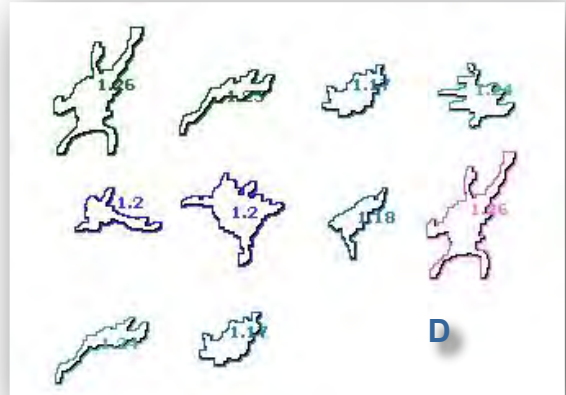
A colour-coded legend is also generated with each image for interpreting the results. The legend can be saved separately. It lists the colour with the corresponding fractal dimension beside it.
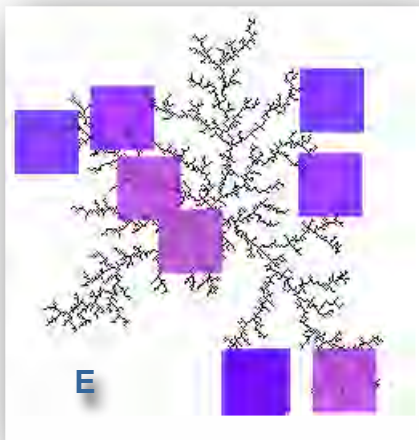
- **E** is an image scanned using a random sampling method.
- Each colour block is coded to show the fractal dimension over that area.

A colour-coded legend is also generated with each image for interpreting the results. The legend can be saved separately. It lists the colour with the corresponding fractal dimension beside it.

Sliding box lacunarity

What is sliding box lacunarity?

Sliding box lacunarity is a measure of heterogeneity in a digital image. The value reported by FracLac is calculated from the number of pixels found in an area and how it depends on the size of the area. The data are the number of pixels per box, where $\Lambda = \sigma^2/\mu^2$. It depends on scale, so can be interpreted by looking at the log-log plot of Λ vs. ε. This is similar to the standard box counting value for lacunarity that FracLac reports.

What is a sliding box lacunarity scan?

A sliding box lacunarity scan places a box of fixed size on an image, counts pixels that fall on the box, slides the box horizontally a fixed number of pixels (x), then counts again. At the end of each row, the box is slid down some fixed amount of pixels (y), and the row is scanned again in the same way until the entire image has been scanned. This process is repeated for each box size. This differs from a regular box counting scan in which all boxes at one size are laid as a nonoverlapping grid, because for a sliding box scan, boxes at the same size can overlap.

How do I do sliding box lacunarity analysis?

1. Open the FracLac panel
2. Click the purple Sliding Box Lacunarity button to set up its options.

3. Click a blue button to run the scan.
4. View or save the results.

How do I use the sliding box lacunarity options?
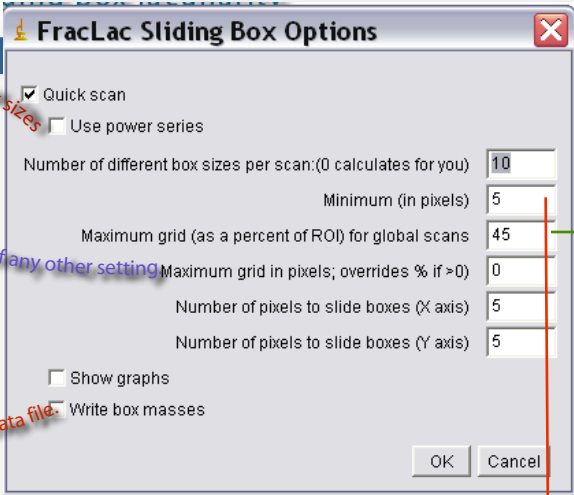
*Calculates an exponential series of box sizes*

Sets the largest box size in the series as a number of pixels, regardless of any other setting

Lists raw data for each box size; produces a large data file.

FracLac Sliding Box Options

☑ Quick scan
☐ Use power series
Number of different box sizes per scan:(0 calculates for you) `10`
Minimum (in pixels) `5`
Maximum grid (as a percent of ROI) for global scans `45`
Maximum grid in pixels; overrides % if >0) `0`
Number of pixels to slide boxes (X axis) `5`
Number of pixels to slide boxes (Y axis) `5`
☐ Show graphs
☐ Write box masses

OK   Cancel

AUTOTHRESHHOLD
See autothreshold

QUICKSCAN
See quick scan

NUMBER OF DIFFERENT BOX SIZES PER SCAN
Type a number for the number of box sizes or different calibers of grid that will be used to gather data. The series increases in size linearly by a fixed increment from the minimum to the maximum unless a power series is used.

The increment is set by dividing this range by the number of sizes requested.

Set the number of sizes to 0 for the default optimized value. The number of box sizes used affects processing time significantly with sliding boxes. Small series (e.g., 10 sizes) generally produce good results.

MINIMUM BOX SIZE IN PIXELS
Type a number in pixels to set the smallest grid size in the series. The smallest size possible is 1 pixel, but this lower limit should match the resolution of the image. Using 1 increases time significantly.

MAXIMUM GRID AS PERCENTAGE OF IMAGE SIZE
Type a percentage (as a number, e.g., 50) for the largest

grid size in the series. This number is a percentage of image size.

NUMBER OF PIXELS TO SLIDE BOXES (X)
Type a number for the distance to move the grid horizontally for each sliding box scan.

NUMBER OF PIXELS TO SLIDE BOXES (Y)
Type a number for the distance to move the grid vertically for each sliding box scan.

WRITE BOX MASSES
Select this option to print pixels per box for all box sizes (large data file).

SAMPLE ONLY WITHIN CONTOUR
Select this option to sample only boxes that fall within the convex hull.

SHOW GRAPHS
Select this option to show graphs of the data for a sliding box lacunarity analysis.

How do I interpret the sliding box lacunarity results table?

The sliding box results table lists the image name, the values for x and y, and the box count data. Each row of data lists statistics for the corresponding box size. The headings for the columns of statistics are explained below. Lacunarity is calculated using two data gathering methods. The mass fractal dimension is included from the log/log plot of box count and mean pixels per box.

BOX SIZE
The size of each box that was slid overlappingly by x and y across the image.

EPSILON
Scale = 1/image dimension

MEAN (μ)
The mean number of pixels that were in a box at that size.

STANDARD DEVIATION (σ)
The standard deviation of the number of pixels that were in a box at that size.

LACUNARITY (Λ) AS (σ^2/μ^2) See Coefficient of Variation
A value for sliding box lacunarity. It is calculated as (σ^2/μ^2) for pixels per box.
Lac 1:3 is based on the pixel distribution counting only boxes having pixels. Lac 2:4 is based on all boxes tested, so increases more steeply than 1:3.

What are the results of a sliding box lacunarity scan?

A sliding box lacunarity scan generates a results table and graphics.

How do I interpret the sliding box lacunarity graphics?

The graphs of Λ vs. ε show typical patterns that generally distinguish multifractal scaling from other types of scaling. The graphs along the bottom in this image, showing ln Λ +1 vs ln ε are shown with the same scales along the x- and y-axes. As illustrated, multifractals typically show humped graphs with higher lacunarity overall, whereas mono- and non-fractals have flatter curves with lower values, nonfractals being generally flatter than monofractals.

Multifractal Henon   Non fractal oval   32-segment quadric fractal
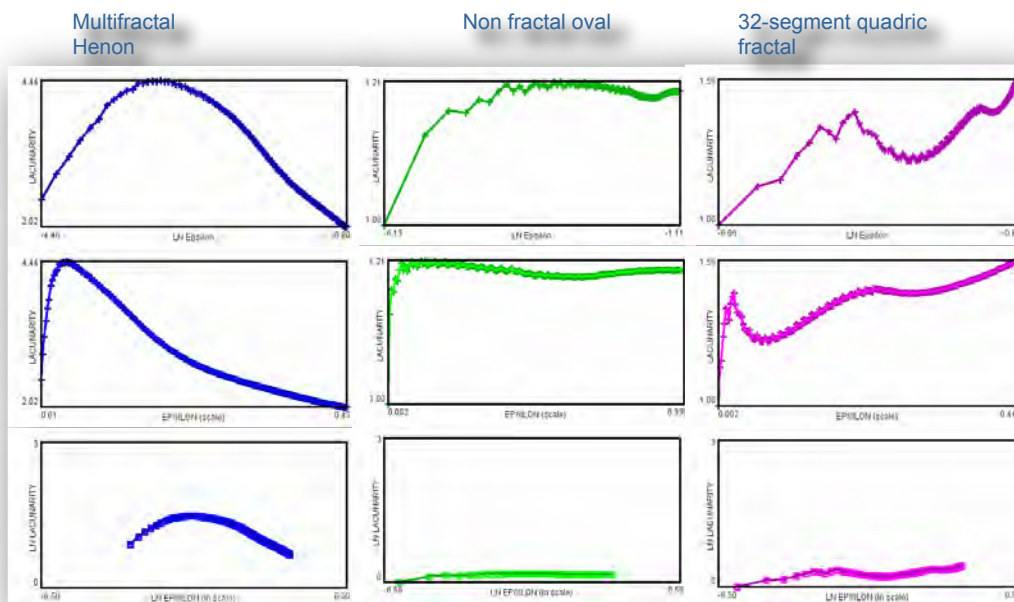
Multifractality

1.   Select multifractal analysis on the purple buttons on the FracLac panel.
2.   Set the options on the Multifractal Analysis Options panel that appears.
3.   View or save the multifractal graphics and multifractal results table.

How do I do use the multifractal analysis options?

DATA PROCESSING: Select Standard to use all box sizes as counted. Select slope-corrected from the drop-down box to calculate using only the series of boxes for which the count of consecutive boxes was not the same (i.e., this series has periods of horizontal slope removed. Select Most Efficient Cover to calculate using the series of box sizes that most efficiently covered the image (i.e., a series made from the box size at whichever grid position had the lowest count).

Set the number of sizes to 0 for the default optimized value based on each image's size. The series increases in size linearly by a fixed increment from the minimum to the maximum. The increment is set by dividing this range by the number of sizes requested. The sizes used depend on the minimum and maximum values as well as the number of sizes chosen, unless a power series is being used..

MINIMUM (IN PIXELS) Type a number for the minimum size of grid caliber to use. The minimum practical value is 1 pixel, but this may not match the resolution of images being analyzed.

Type a number for the maximum percent of image size to set as the maximum for grid caliber.   For multifractal analysis, this value should usually be set to 100%. Alternatively, set the maximum in pixels.

Select power series to calculate the grid calibres as an exponential series. Otherwise, use the following options.

Select Quick Scan to scan using a quicker but less random algorithm.

Multifractal Analysis Options

Data Processing Standard

Number of global scan positions: 4

☑ Quick scan   ☐ Use Power Series

Number of box sizes per scan:(0 calculates for you) 20

Minimum grid (pixels) 10

Maximum grid (as a percent of ROI) for global scans 45

Maximum (in pixels overrides % if >0) 0

Type a number for the number of grid positions. In a multifractal analysis, the first four grids are oriented to have the last box in each size of each scan fall at the four corners of the image, similar to rotating by 90° each time. Scans after these are randomly chosen based on the top left corner.

☑ Omit box count data   ☐ Include all box masses   ☐ Probability Distributions ☐ Slip grid at epsilon

Show Graphs:

☐ D(Q) vs Q   ☐ alpha vs Q   ☐ F vs Q   ☐ F vs alpha   ☐ Regression ☐ Tau

☐ Show Location with Highest CV

☐ Print Slope and CV for D(Q)vsQ

Number of bins for Frequency Distributions 40

Maximum Q for Generalized Dimension Spectrum: 10.00

Minimum Q: -10.00

Increment between Qs: 0.250

Select mass method None

Subarea (percent of image size) 100

Maximum grid (as a percent of ROI) for sub scans 100

Number of samples: 3

Minimum pixel ratio to accept in samples 0.0100

OK   Cancel

OMIT BOX COUNT DATA

Select this box to print one row of summarized data for box counting only. Leave it unselected to omit the raw data for box count and size.

PROBABILITY DISTRIBUTIONS

Select this box to print the raw data for probability distributions.

SLIP GRID

Select this option to randomly move the grid, in addition to the initial random selection of grid locations, at the beginning of each scan.

STAY WITHIN CONVEX HULL

Select this option to sample only within the convex hull.

Graphs

There are several graphs for multifractal data. Click on each name to see a sample and notes on interpreting the graph.

$D_{(Q)}$ vs Q
f(α) vs α
Regression
Tau τ

SHOW LOCATION WITH HIGHEST CV

Select this option to restrict the shown graphics and printed data to the grid location that is the "most multifractal" in that is

has the highest coefficient of variation for the $D_{(Q)}$.

PRINT SLOPE AND CV FOR D(Q) VS Q

To print only one line of data, select this option and select SHOW LOCATION WITH HIGHEST CV.
Unselect this option to print a row of data for each value of Q, including $D(Q)$, f, f(α), and τ.

NUMBER OF BINS FOR FREQUENCY DISTRIBUTION

The number of bins to categorize frequencies of numbers of pixels.

MAXIMUM Q FOR GENERALIZED DIMENSION SPECTRUM

The maximum value of Q, an arbitrary exponent.

MINIMUM Q

The maximum value of Q, an arbitrary exponent.

INCREMENT BETWEEN QS

The increment between values of Q.

DO RANDOM MASS SAMPLE

Select this option to sample the image randomly using areas of fixed size. *(see Results)*

SUBAREA

Type a number to specify the size of the area to sample as a percent of the image's size.

MAXIMUM GRID

Type a number for the maximum grid size to use as a percent of the subarea.

NUMBER OF SAMPLES

Type a number for the number of overlapping samples to take.

MINIMUM PIXEL RATIO

Type a number for the minimum ratio of foreground to background pixels. A lower number makes successful scans less likely; a higher number ensures that areas with very low number of pixels are not included.

INCLUDE CIRCULARITY

See Circularity

What does FracLac do about Multifractality?

FracLac generates a mass distribution for an image.
From this, a spectrum of values for the GENERALIZED DIMENSION (D_Q) is calculated.
The range of Q values is specified by the user.
FracLac delivers the multifractal measures outlined in the calculations shown here,
and graphs the typical multifractal spectra of f(α) versus α, and D_Q versus Q.

What is Q and how is it specified in FracLac?

Each value of Q is an exponent used in calculating the multifractal spectra. The Maximum, Minimum, and Increment between Qs are set on the multifractal analysis options panel. These are arbitrary values the user sets. The default range is from -20 to 20, incremented by .5. Experiment with these values to see how the multifractal spectra are affected for different images and ranges.

What are Multifractal Spectra?

Simply put, multifractal spectra are graphs of how a pattern behaves if amplified in certain ways. FracLac makes graphs of D_Q versus Q and *f*(α) versus α, or of τ, which are all variously called *multifractal spectra*. The generalized dimension is used along with the other multifractal measures, generally *f*(α) over a range of diverging exponents, α. These measures help characterize the variety within a pattern inasmuch as it depends on the scale at which the pattern is observed. Simple or *mono*fractals show less variation than so-called multifractals in the *f*(α) vs α multifractal spectrum. The simple monofractal spectrum converges on a value whereas the multifractal is typically humped. Also, for a non- or mono-fractal the plot of D_Q versus Q tends to be horizontal or non-increasing, but for a multifractal, it is generally sigmoidal and decreasing.

What is D(Q)?

The generalized dimension, D_Q, addresses how mass varies with ε (resolution or box size) in an image. To distill its calculation into a describable form, it is, in essence, a distortion of the mean (μ) of the probability distribution for pixels at some ε. That is, it is μ exaggerated by being raised to some arbitrary exponent, Q, then compared again to how the exaggeration varies with ε.

How do I interpret the graphics from a multifractal analysis?

Multifractal spectra graphs tells different stories. Click one below to see its explanation. (See Calculations for explanations of individual variables shown on each graph)

$D_{(Q)}$ vs Q
$f_{(α)}$ vs α
Regression
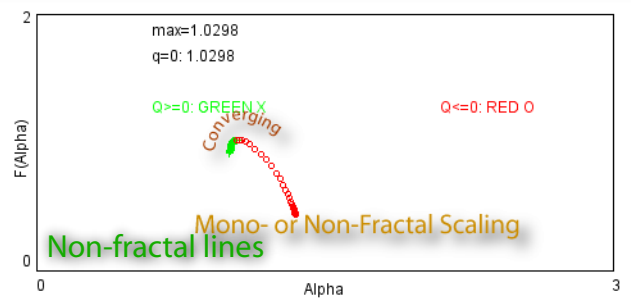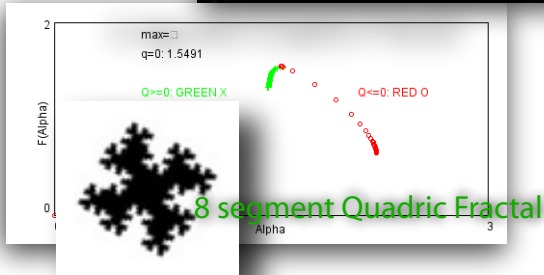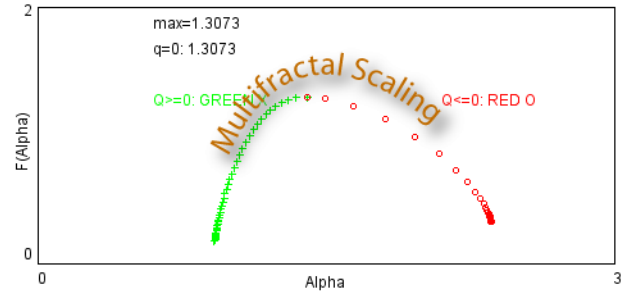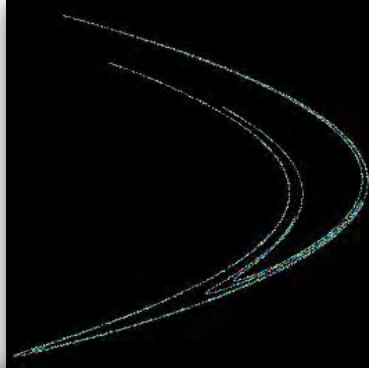Tau τ

The graph of f(α) vs α shows a multifractal spectrum. If the graph is humped as in the lower figure, the scaling is considered multifractal. If the graph converges, as in the top figure, the scaling is considered mono- or non-fractal. The maximum and value at Q=0 are listed on the graph.

Multifractal Henon Map

max=1.3073
q=0: 1.3073
Q>=0: GREEN +   Q<=0: RED O
Multifractal Scaling

max=□
q=0: 1.5491
Q>=0: GREEN X   Q<=0: RED O

8 segment Quadric Fractal

max=1.0298
q=0: 1.0298
Q>=0: GREEN X   Q<=0: RED O
Converging
Mono- or Non-Fractal Scaling
Non-fractal lines

What does the graph of D(Q) vs Q show?

32 Segmentbin.jpg roi 160.0/83.0:Loc 3/sample 0 at (12, 85)(slope=-.0048 R^2=0.59)
Slope=-0.0048 Y-int=1.5967

Henon Map.tif roi 276.0/215.0:Loc 0/sample 0 at (192, 187)(slope=-0.0221 R^2=0.9079)
Slope=-0.0221 Y-int=1.349
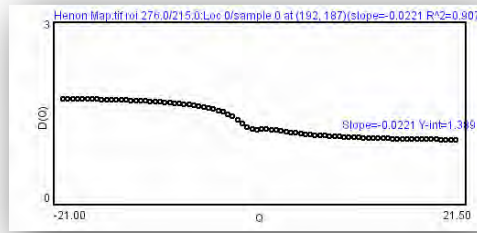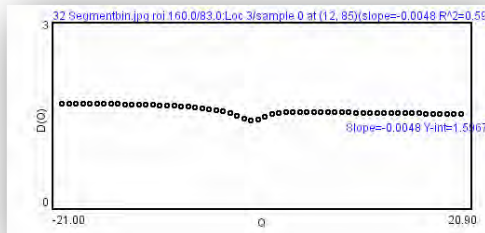
The graph of D(Q) vs Q is decreasing for multifractals, but non-decreasing for mono-- or non-fractals.

What does the graph of τ (Tau) show?

ROIDiffusion:Loc 3/sample 0 at (44, 89)(slope=-1.0491 R^2=0.9989)
Tau (slope=-1.0491)
D(Q)
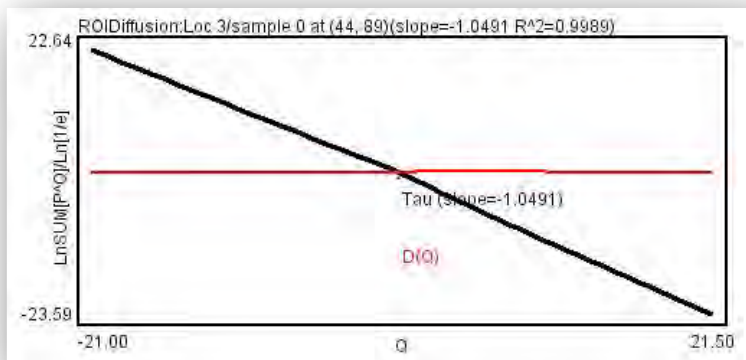
The slope of this graph is equivalent to the box counting dimension. The line for $D_{(Q)}$ vs. Q is also shown (the graph shown here is for a square, with theoretical fractal dimension of 1.00, and non-multifractal scaling as shown by the non-decreasing D(Q) vs. Q.)

How do I interpret the results table from a multifractal analysis?

The results table for a multifractal analysis lists statistics in the Results Table as for a general analysis followed by multifractal data. The last columns of the list are:

OPTIMIZED LOCATION FOR MULTIFRACTAL ANALYSIS
The grid position that had the lowest slope and best coefficient of variation for $D_{(Q)}$ vs. Q.

CV FOR $D_{(Q)}$ VS Q
The coefficient of variation for the regression line for $D_{(Q)}$ vs. Q.

SLOPE FOR $D_{(Q)}$ VS Q
The slope for the regression line for $D_{(Q)}$ vs. Q..

R^2 FOR $D_{(Q)}$ VS Q
The correlation coefficient (r^2) for the regression line for the $D_{(Q)}$ vs. Q.

Q
A column of the arbitrary exponent, Q, set in the options panel. Note the values at Q=0 and 1. *See multifractal calculations*

D(Q)
$D(Q)=\tau/(1-Q)$
The value of the generalized dimension at the corresponding value of Q.
See multifractal calculations

TAU (τ)
$\tau=\lim[\ln(I_{(Q,E)})/\ln(1/\varepsilon)]$
$\tau_{(Q)}=(Q-1)*D_{(Q)}$

$I_{(Q,\varepsilon)}=\sum P(i)^Q$, where

$\sum P(i)=1$ $P(i)$=density for all boxes (i) at this ε
See multifractal calculations

MEAN τ
The mean value of τ.
See multifractal calculations

α
$\mu=P_{(i)}^Q/\sum P(i)^Q$

$\alpha = \sum [\mu_{(i)}*\ln P_{(i)}]/\ln \varepsilon$

for each Q in the row.
$P(i)^Q$=the probability of pixels at the ith box, raised to the exponent Q.

$P(I, \text{epsilon}) = \text{pixels}(I, ep)/\text{sum pixels}(I,e)$
$P(i)$=density for all boxes (i) at this ε
See multifractal calculations

F(α)
$f(\alpha_Q)=\sum [\mu*\ln \mu]/\ln \varepsilon$

for each Q in the row,

where $\mu=P_{(i)}^Q/\sum P_{(i)}^Q$

and $P_{(i)}^Q$=the probability of pixels at the ith box, raised to the exponent Q.

The maximum value of $f(\alpha)$ is listed on the graphic for $f(\alpha)$ vs. α. *See multifractal calculations*

Probability distributions

If print probability distributions is selected, several rows of data appear in the Results Table after the heading *Frequencies and Masses*. The data under the headings *BOX SIZE*, *EPSILON*, and *MEAN PROBABILITY* can be used to calculate the fractal dimension. Epsilon is 1/box size. *MEAN PROBABILITY* refers to the mean pixels per box at a box size. The columns for FREQUENCY and MASS should be correlated as rows by matching BOX SIZES. MASS is a number of pixels; FREQUENCY is the frequency of that number of pixels being in a box at the BOX SIZE. The first rows are for binned probabilities that use ranges of frequencies. Unbinned probabilities use actual number of pixels per box and generate many columns.

Box Count Raw Data

If the option to omit box count data was not selected, the results table will include this data at the end of the multifractal spectra data. There are three columns of data for calculating the fractal dimension. The BOX SIZE column lists each box size at the beginning of each row. The column for SCALE lists box size relative to image size. The column for COUNT lists the number of boxes containing pixels.

How do I interpret the results table from a random mass multifractal analysis?

The random mass sample analysis lists data in the results table according to the headings below:

TOTAL FOREGROUND PIXELS SAMPLED
The number of foreground pixels sampled, combining all samples. This number may exceed the total number of pixels in the image.

MINIMUM RATIO OF FOREGROUND TO BACKGROUND PIXELS
The value set for minimum pixel ratio.

MEAN RATIO OF FOREGROUND TO BACKGROUND PIXELS SAMPLED
The actual ratio of pixels analyzed.

SIZE IN PIXELS OF EACH SAMPLE
The size of each sample area, measured in total pixels.

TOTAL SAMPLES
The number of samples that were analysed.

TOTAL PIXELS SAMPLED
The number of pixels from all samples that were analysed.

MASS FRACTAL DIMENSION USING MEAN MASS AT EPSILON
The fractal dimension calculated from the regression line for the log-log plot using the mean number of pixels and each box size.

Y-INTERCEPT
The y-intercept of the regression line for the **mass fractal dimension**.

MEAN CV^2
The mean coefficient of variation

CV FOR D$_{(Q)}$
The coefficient of variation for all values of D$_{(Q)}$.

Q
A column of the arbitrary exponent, Q, set in the options panel.

See multifractal calculations

D(Q)

D$_{(Q)}$=τ/(1-Q)
The value of the generalized dimension at the corresponding value of Q in the row. *See multifractal calculations*

TAU (τ)

τ=lim[ln(I$_{(Q,E)}$)/ln(1/ε)]

I$_{(Q,\varepsilon)}$= $\sum$P$_{(i)}^Q$, where $\sum$P$_{(i)}$=1

P$_{(i)}$=density for all boxes (i) at this ε *See multifractal calculations*

MEAN τ

The mean value of τ.

See multifractal calculations

α

μ=P$_{(i)}^Q$/$\sum$P$_{(i)}^Q$

α = $\sum$ [$\mu_{(i)}$*lnP$_{(i)}$]/ln ε

for each Q in the row.
P$_{(i)}^Q$=the probability of pixels at the ith box, raised to the exponent Q.
P$_{(i)}$=density for all boxes (i) at this ε
See multifractal calculations

F(α)

f(α)=$\sum$ [μ*ln μ]/ln ε

for each Q in the row,

where μ=P$_{(i)}^Q$/$\sum$P$_{(i)}^Q$

and P$_{(i)}^Q$=the probability of pixels at the ith box, raised to the exponent Q.

See multifractal calculations

What about sampling for multifractal spectra?

Multifractal spectra from box counting depend on the extracted pixel distribution, which, in turn, depends on how it is extracted. Thus, multifractal data depend (even more than monofractal analysis data) on the grid's position when the data are gathered. One approach to this problem is to randomly sample a pattern to infer the distribution, an approach possible with FracLac but subject to several limitations in acquiring an adequate sample. Alternatively, FracLac's default behaviour for a multifractal analysis is to scan with the grid anchored at each of the four corners of the rectangle enclosing an image, to provide four different spectra similar to what are obtained by rotating the image 90° and reapplying the same series of εs. This strategy can be important when interpreting odd results that sometimes occur with density distributions that attribute too

much importance to very small probabilities that appear in the distribution at some, but not all, grid positions.

More Multifractal Spectra

The image shows data from a multifractal analysis of a Henon Map. Data from four scans are shown together in the first two frames and from only the scan with the optimal probability distribution in the last two frames. The humped curves are the $f(\alpha)$ spectra, and the decreasing curves are the D_Q vs Q spectra. (Note that the $D_{Q=0}$ is the capacity dimension, in this case approximately 1.26).
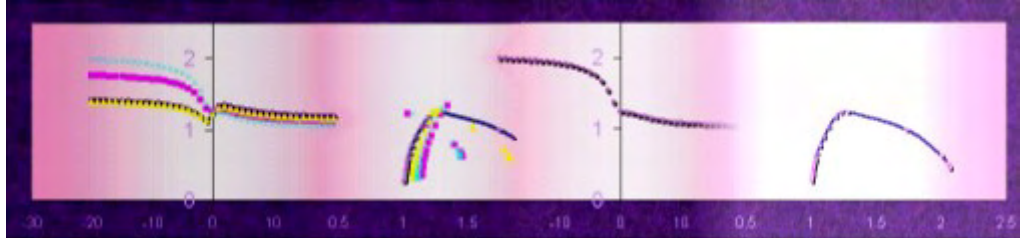
What are the calculations for the multifractal spectra?
GENERALIZED DIMENSION AT Q

- $D_Q = \lim[\ln I_{Q\varepsilon}/\ln\varepsilon^{-1}]/(1-Q)$
- $I_{Q,\varepsilon} = \sum[P_i^Q]$,

  - For Q=1, let ε approach 1, and $D_Q = -\lim[\sum P_i*\ln[P_i]/\ln\varepsilon]$
  - The probability distribution is found from the number of pixels, M, that were contained in each ith element of a size (ε) required to cover an object: $P_{i,\varepsilon} = M_{i,\varepsilon}/\sum M_\varepsilon$
  - Thus, P_i is from the probability distribution of mass for all boxes (i) at this ε where $\sum P_i = 1$

According to the method of Chhabra and Jensen (Phys. Rev . Lett. 62: 1327, 1989):

$$\mu_i = P_i^Q/\sum P_i^Q$$
$$\alpha = \sum[\mu*\ln P_i]/\ln\varepsilon$$
$$f(\alpha_Q) = \sum[\mu_i*\ln\mu_i]/\ln\varepsilon$$
$$\tau_Q = (Q-1)*D_Q$$
$$\text{and } f(\alpha_Q) = Q\alpha_Q - \tau_Q$$

$$D_Q = \lim_{\varepsilon \to 0} \left(\frac{\ln\left(I_{(Q,\varepsilon)}\right)}{\ln \varepsilon^{-1}} \right) \Big/ (1 - Q)$$

N_ε = boxes containing pixels at ε

c = box size

i = the ith box in a scan at ε

$$I_{(Q,\varepsilon)} = \sum_{i=1}^{N_s} P_{(i,\varepsilon)}^Q$$

$$P_{(i,\varepsilon)} = \frac{pixels_{(i,\varepsilon)}}{\sum_{i=1}^{N_s} pixels_{(i,\varepsilon)}} \quad and$$

$$\sum_{i=1}^{N_s} P_{(i,\varepsilon)}^1 = 1 \quad and \quad \sum_{i=1}^{N_s} P_{(i,\varepsilon)}^0 = N_\varepsilon$$

$$\tau_Q = (Q - 1) \bullet D_Q$$

$$\mu_{i(Q,\varepsilon)} = \frac{P_i^Q}{\sum_{i=1}^{N_\varepsilon} P_i^Q}$$

$$\alpha_{(Q,\varepsilon)} = \frac{\sum_{i=1}^{N_\varepsilon} u_{i(Q,\varepsilon)} \bullet \ln P_i}{\ln \varepsilon}$$

$$F(Q) = \frac{\sum_{i=1}^{N_\varepsilon} u_{i(Q,\varepsilon)} \bullet \ln u_{i(Q,\varepsilon)}}{\ln \varepsilon}$$

$$F(\alpha_Q) = Q \bullet \alpha_Q - \tau_Q$$

References for the method of calculating the multifractal spectrum:

A. Chhabra and R.V. Jensen, Direct Determination of the f(α) singularity spectrum, Phys. Rev. Lett. 62: 1327, 1989.
A. N. D. Posadas, D. Gime´nez, M. Bittelli, C. M. P. Vaz, and M. Flury, Multifractal Characterization of Soil Particle-Size Distributions, Soil Sci. Soc. Am. J. 65:1361–1367 2001

Fractals

What are fractals?

Fractals are, in essence, patterns with nonlinear scaling rules. A simple line, such as a circle, scales to 3 pieces 1/3 its size when scaled by 1/3. That is, it scales as N (number of parts) = scale^{-1}. For a fractal, however, the number of new pieces scales nonlinearly with the scale applied. A Koch fractal, for instance, scales into 4 pieces each 1/3 the size of the original.

Koch Fractal scales
as log 4/log 3 ≈ 1.26
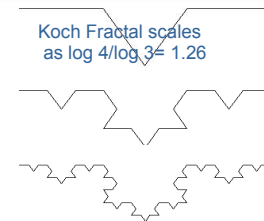
What is a Fractal Dimension?

A fractal dimension is a measure of complexity expressed as a scaling rule comparing the number of new parts and scale. The box counting dimension is a type of fractal dimension.
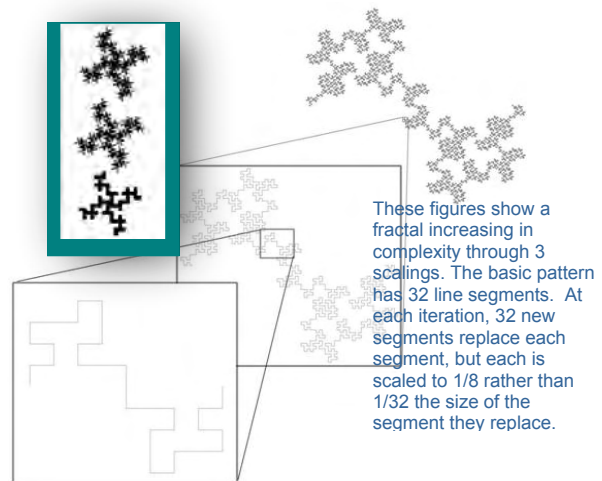
How is a fractal dimension calculated?

Using a scaling rule, N=AC^{-DB}, the fractal dimension, D_B, is calculated from the ratio of the log of the number of new parts N, to the log of scale, C.
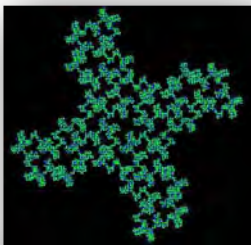
$$D = \lim_{c \to 0} \left[\frac{\ln N_C}{\ln C^{-1}} \right]$$

For a line, the fractal dimension is log N/log N^1 = 1. For this 32-segment quadric fractal contour, it is log 32/log 8 = 1.67.

Using FracLac for digital images, the box counting fractal dimension is found from the slope of the regression line for the log-log plot of box size or scale and count.

These figures show a fractal increasing in complexity through 3 scalings. The basic pattern has 32 line segments. At each iteration, 32 new segments replace each segment, but each is scaled to 1/8 rather than 1/32 the size of the segment they replace.

What kind of fractals can be analyzed with FracLac?

Use FracLac to analyze binary images of monofractals or multifractals.

The image shown here is a 32-segment quadric monofractal contour with a known fractal dimension. The same contour is shown coloured (left) and as a 1 pixel wide binary contour suitable for analysis (right). Generated with MicroMod.

A coloured 32-segment quadric fractal generated with MicroMod.

**A binary 32-segment quadric fractal generated with MicroMod.**

Images not generated as one pixel wide contours can be converted to binary using digital image editing programs such as ImageJ.

Where can I find simple fractals and multifractals to analyze?

Download MicroMod or another freely available fractal generator, to generate images of multifractals and monofractals. All images shown here were generated with MicroMod and can be generated as binary images suitable for analysis. MicroMod generates:

- Sierpinski Triangles
- Menger Sponges/Carpets
- Quadric Fractals
- Koch Fractals
- Diffusion Limited Aggregates
- Branching Structures
- Henon Maps
- And more
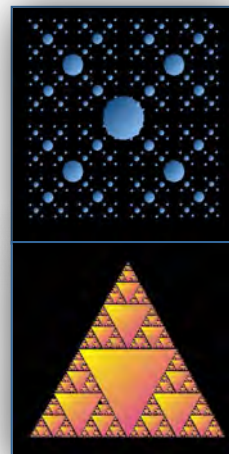
Contact the author to obtain a copy of MicroMod: mailto:akarpe01@postoffice.csu.edu.au

What are monofractals?

Monofractals are fractals with a global scaling rule, such as the 32-segment quadric fractal. They contrast with multifractals. They are usually analyzed using a standard scan.

What are multifractals?

To simplify, multifractals are patterns that scale with multiple scaling rules rather than one global scaling rule. As evidenced by the Henon multifractal shown below, they are not necessarily recognized visually as multifractals. They are analyzed using the Multifractal Scan.

What is a Henon Map?

A Henon Map is an iterated multifractal. This is an example of one generated using MicroMod.
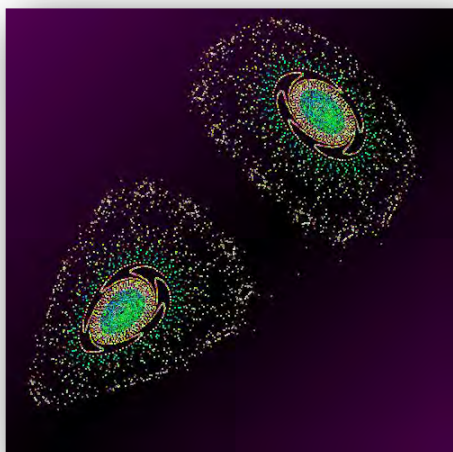
Henon Multifractal generated with MicroMod