

Supplementary Materials

Fractals in pharmacognosy: Linking morphology, metabolites, and pharmacological relevance

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1. Annex 1

In this section, some tools regarding the management of fractal structures are presented. “R” language scripts are suggested to produce theoretical plant-like structures to illustrate the application of fractal dimension in plant world. Additionally, examples of the box-counting method for calculating the fractal dimension D_B starting from pictures are explained in detail.

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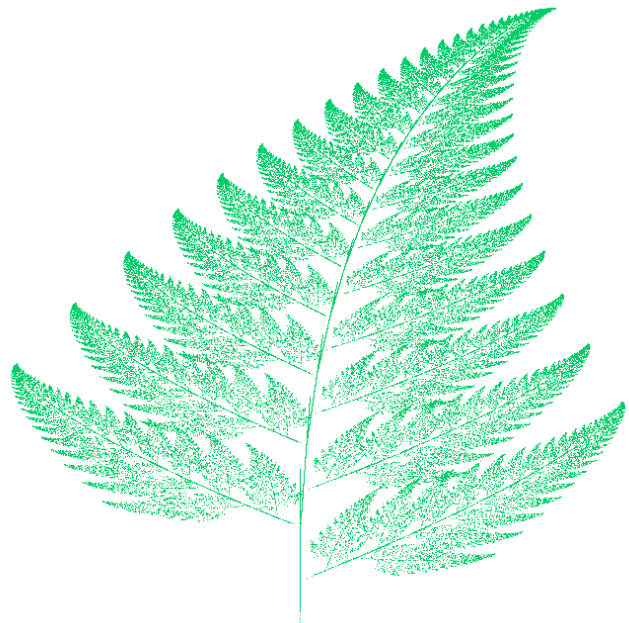
Annex 1.1. "R" script for producing a Barnsley fern.

"R" version 4.5.1 (2025-06-13 ucrt) -- "Great Square Root", Copyright © 2025 The R Foundation for Statistical Computing

The parameters are modified from original Barnsley fern model [1].

```
# Non-standard Barnsley Fern in R
set.seed(123)
n <- 100000
x <- numeric(n)
y <- numeric(n)
x[1] <- 0
y[1] <- 0
# Probabilities (must sum to 1)
p <- c(0.02, 0.80, 0.09, 0.09)
cp <- cumsum(p)
for (i in 2:n) {
  r <- runif(1)
  xi <- x[i - 1]
  yi <- y[i - 1]

  if (r < cp[1]) {
    # Stem
    x[i] <- 0
    y[i] <- 0.25 * yi
  } else if (r < cp[2]) {
    # Main leaf
    x[i] <- 0.85 * xi + 0.03 * yi
    y[i] <- -0.03 * xi + 0.85 * yi + 1
  } else if (r < cp[3]) {
    # Left leaflet
    x[i] <- 0.20 * xi - 0.26 * yi
    y[i] <- 0.23 * xi + 0.22 * yi + 1
  } else {
    # Right leaflet
    x[i] <- -0.15 * xi + 0.28 * yi
    y[i] <- 0.26 * xi + 0.24 * yi + 0.44
  }
}
# Plot
par(bg = "white", mar = c(0,0,0,0))
plot(x, y, pch = ".", col = "springgreen3", axes = FALSE, xlab = "", ylab = "")
```



Alternative way to generate the Barnsley fern is offered by this site:

<https://www.chradams.co.uk/fern/maker.html> (accessed on August 25, 2025)

Annex 1.2. Minimal "R" script for generating a Barnsley fern.

Custom variations can be obtained by modifying the coefficients in the transformation equations for x and y.

```
# Number of points
n <- 100000
x <- numeric(n)
y <- numeric(n)

for (i in 2:n) {
  r <- runif(1)
  if (r <= 0.01) {
    x[i] <- 0
    y[i] <- 0.16 * y[i-1]
  } else if (r <= 0.86) {
    x[i] <- 0.85 * x[i-1] + 0.04 * y[i-1]
    y[i] <- -0.04 * x[i-1] + 0.85 * y[i-1] + 1.6
  } else if (r <= 0.93) {
    x[i] <- 0.20 * x[i-1] - 0.26 * y[i-1]
    y[i] <- 0.23 * x[i-1] + 0.22 * y[i-1] + 1.6
  } else {
    x[i] <- -0.15 * x[i-1] + 0.28 * y[i-1]
    y[i] <- 0.26 * x[i-1] + 0.24 * y[i-1] + 0.44
  }
}

plot(x, y, pch=".", col="darkgreen", axes=FALSE, xlab="", ylab="")
```



Annex 1.3. “R” script to obtain box-counting analysis (D_B method) starting from a .png image.

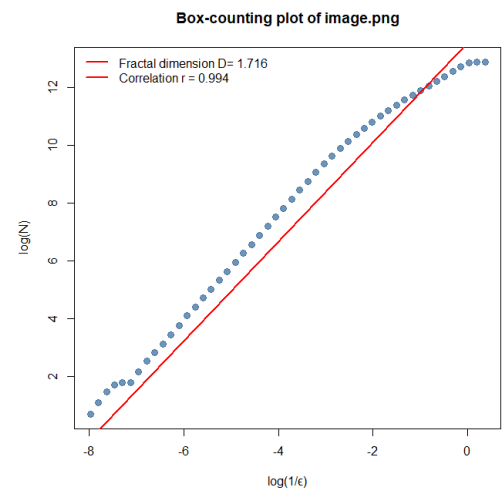
The box-counting analysis and plot were produced using the *Rdimtools* package [2].

To run the below reported script in “R”, just write the desired “image.png” file name.

```
# install & load required packages
install.packages("Rdimtools")
install.packages("png") # read, write and display bitmap images stored in the PNG format

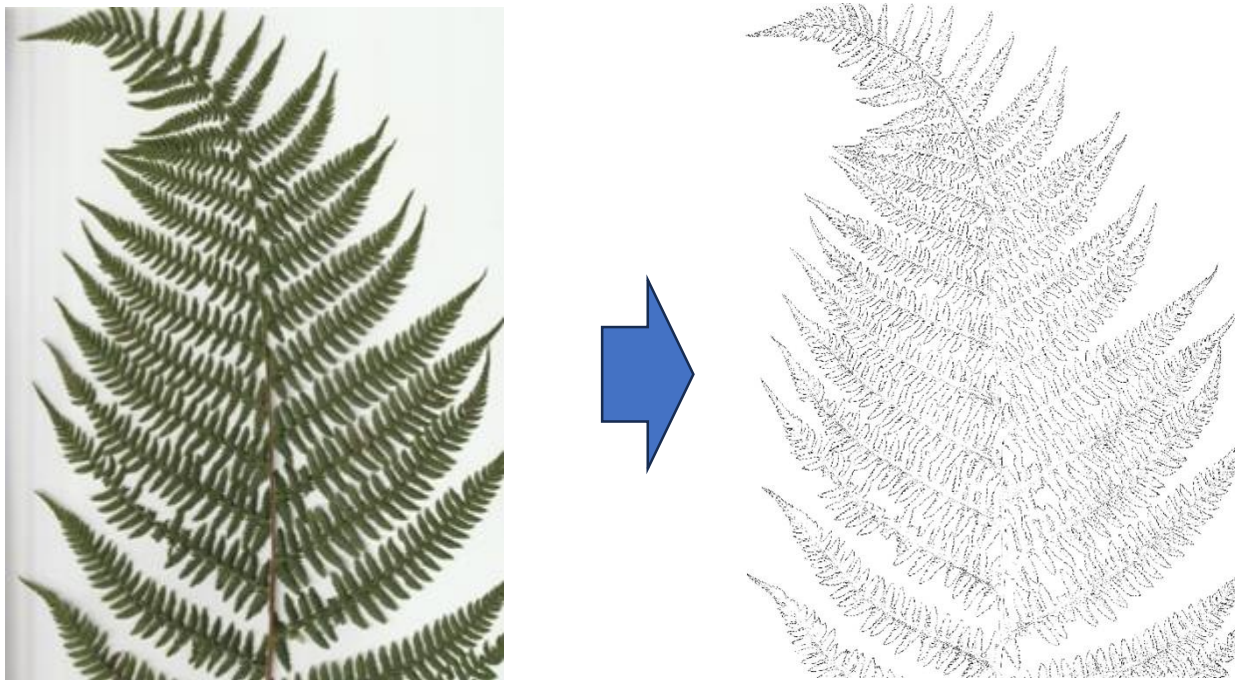
library(Rdimtools)
library(png) # to read PNG images

# Step 1: Upload image
img <- readPNG("image.png")
# Step 2: Convert into grey scale if the image is RGB
if (length(dim(img)) == 3) {
  img_gray <- 0.2989*img[,1] + 0.5870*img[,2] + 0.1140*img[,3]
} else {
  img_gray <- img
}
# Step 3: make image binary-coded
threshold <- 0.5
img_bin <- ifelse(img_gray < threshold, 1, 0) # image = 1, background = 0
# Step 4: Extract white pixel coordinates
coords <- which(img_bin == 1, arr.ind = TRUE)
# Step 5: Calculate fractal dimension using est.boxcount()
res <- est.boxcount(X = coords, nlevel = 50, cut = c(0.1, 0.9))
# Step 6: Show result
print(res$estdim)
# Step 7: Show log-log plot
# Prepare log-log data
log_r <- log(1 / res$r)
log_N <- log(res$Nr)
# Compute correlation coefficient
r_value <- cor(log_r, log_N)
# Plot points
plot(log_r, log_N, pch=19, col=rgb(0.2,0.4,0.6,0.7),
      main="Box-counting plot of image.png",
      xlab="log(1/ε)", ylab="log(N)", cex=1.2)
# Add fitted line using slope = fractal dimension and intercept
slope <- res$estdim
intercept <- coef(lm(log_N ~ log_r))[1] # calculate proper intercept
abline(a = intercept, b = slope, col="red", lwd=2)
# Add legend with fractal dimension and correlation coefficient
legend("topleft",
       legend=c(paste("Fractal dimension D=", round(res$estdim,3)),
                paste("Correlation r =", round(r_value,3))),
       col="red", lwd=2, bty="n")
```

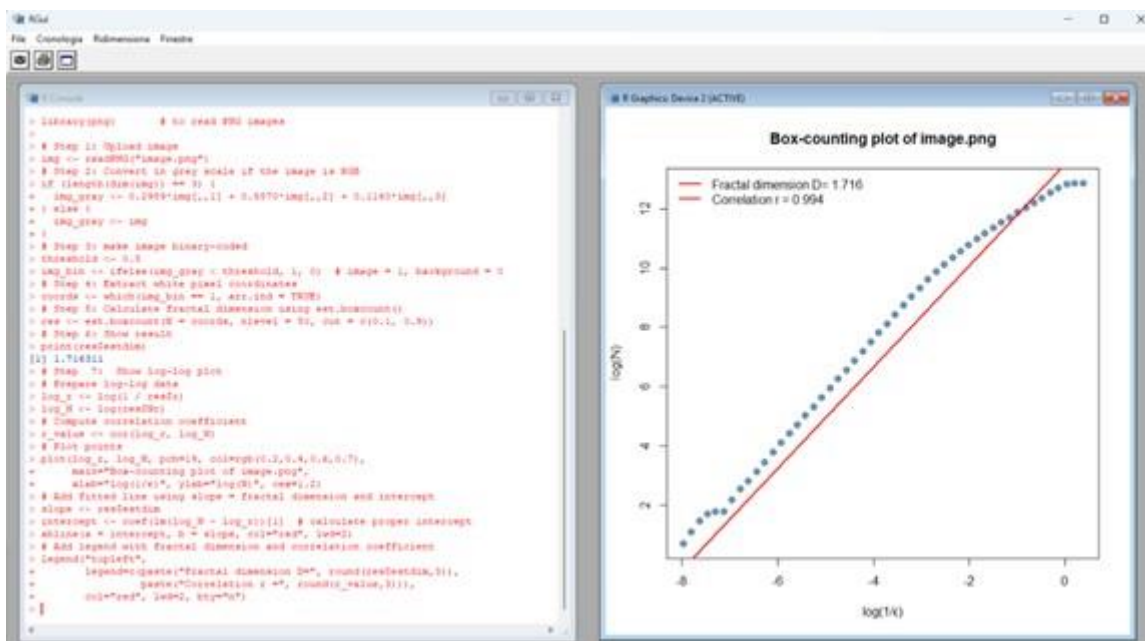


Annex 1.4. How to obtain a box-counting analysis (D_B method) starting from a photo or a scan.

1. Use an image editor (e.g., *Photofiltre* or *GIMP*) to preprocess the image prior to fractal analysis. To optimize the performance of the script, the colored image is first converted to grayscale and then thresholded to obtain a binary silhouette (edge representation). The resulting binary image is subsequently used for box-counting estimation of the fractal dimension. In this study, images were saved in *.png* format.



2. Place the *.png* file in the working directory of “R” and run the script. The analysis outputs the box-counting plot together with the main parameters, namely the fractal dimension (D_B) and the correlation coefficient (r).



Annex 1.5. How a complex image can be resolved in terms of fractal complexity.

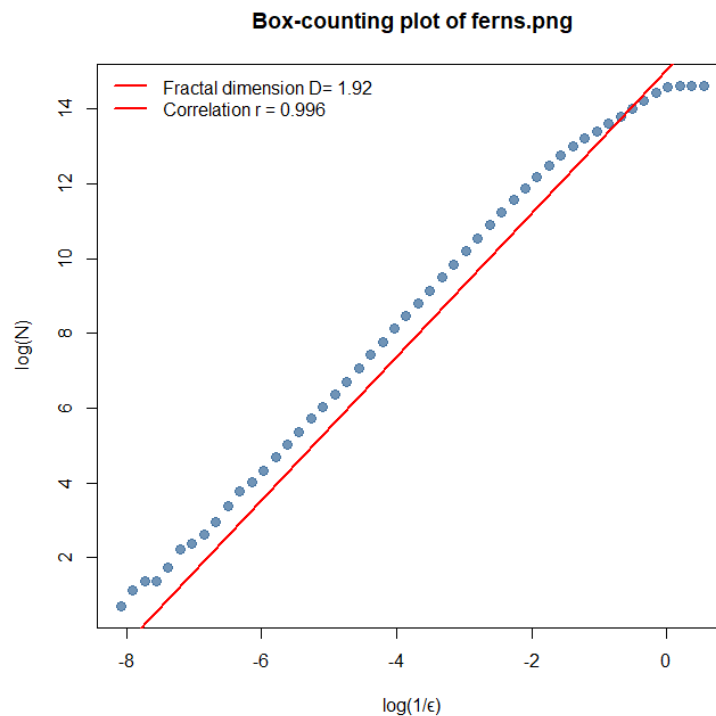
To illustrate how a complex image can be characterized in terms of fractal dimension, a photograph of a group of ferns with multiple branching structures is analyzed:



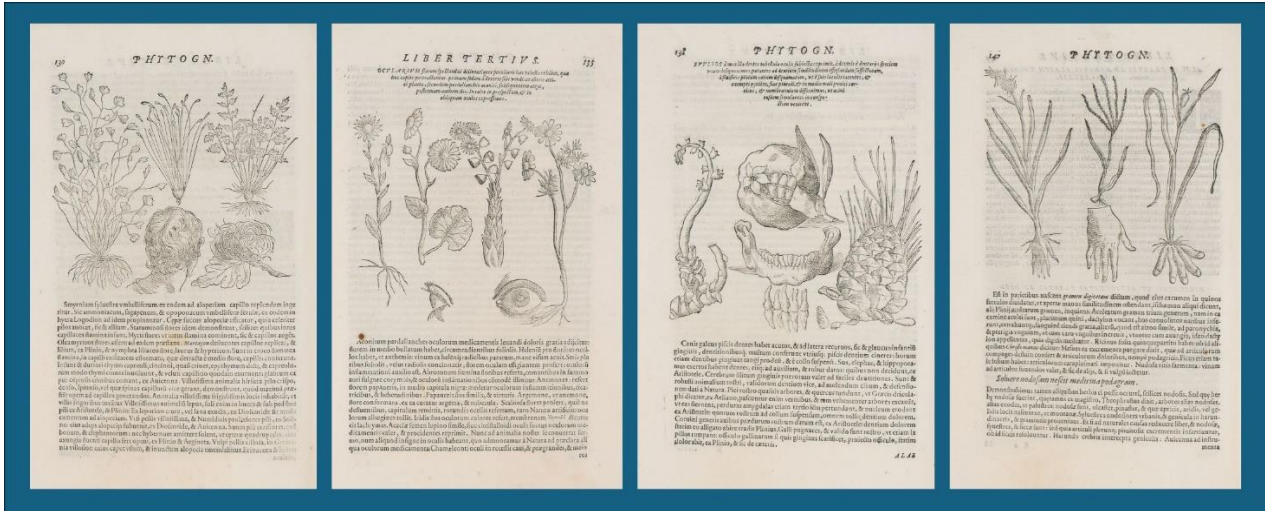
The image is preprocessed (conversion to grayscale and thresholding) to obtain a binary silhouette suitable for fractal analysis:



Fractal dimension D_B is then estimated using the standard box-counting method implemented in the “R” routines described above. The resulting box-counting plot and parameters are reported:

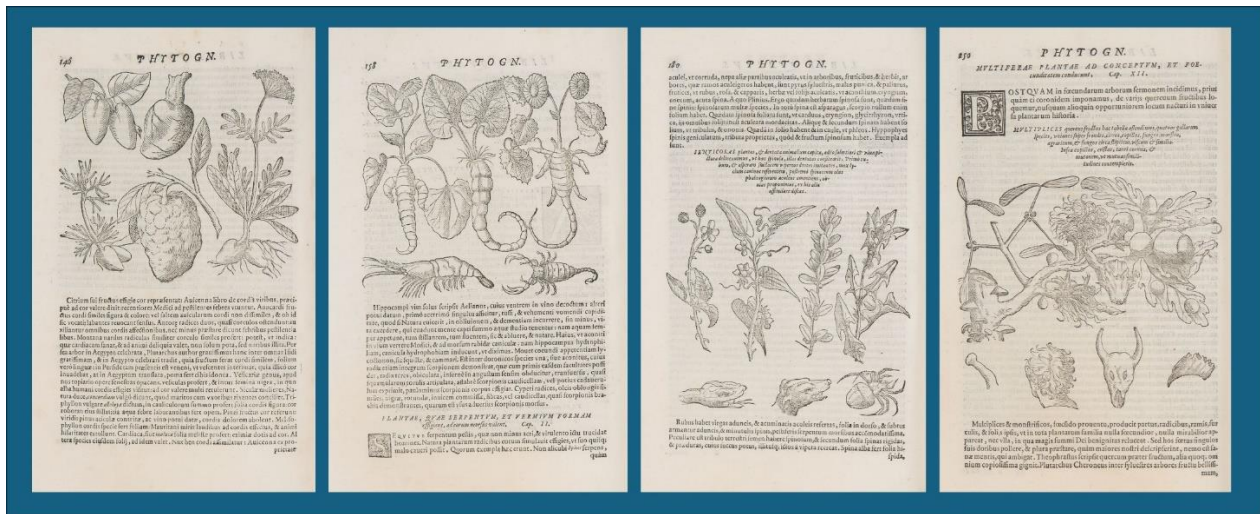


Note: The fern is a commonly cited example of fractality, and here is used as typical pattern. However, it has been reported that fern leaves, as well as cauliflower curds (another frequently cited example), are not truly fractal [3]. While Barnsley’s fractal representation of fern leaves [1] and similar depictions of cauliflower are visually appealing, they are biologically misleading. In reality, fern leaves and cauliflower curds contain only a small number of anatomically variable, non-iterating bifurcations, which may superficially appear self-similar but do not exhibit true fractal scaling. Moreover, their development occurs inside-out through biological growth processes, unlike the purely mathematical iterative procedures used in fractal drawings. This critique highlights the limitations of applying abstract mathematical fractals to biological structures without realistic modeling of their developmental processes. Nevertheless, fractal analysis of leaf shapes using methods such as box-counting can still provide useful quantitative descriptors of complexity, allowing comparative studies of morphology even if the structures are not true mathematical fractals.



Annex 2: Figure S1. A. Representative pages of Della Porta treatise on “Phytognomica” [4], referring to the signature theory. Part 1.

Images taken from the digitalized book available at Phaidra Digital Collections of University of Padova (<https://phaidra.cab.unipd.it/view/o:387612>, accessed August 31, 2025; licensed under a Creative Commons CC BY-NC-SA 4.0 License).



Annex 2: Figure S1. B. Representative pages of Della Porta treatise on “Phytognomica” [4], referring to the signature theory. Part 2.

Images taken from the digitalized book available at Phaidra Digital Collections of University of Padova (<https://phaidra.cab.unipd.it/view/o:387612>, accessed August 31, 2025; licensed under a Creative Commons CC BY-NC-SA 4.0 License).

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3. Lev-Yadun, S. Fern leaves and cauliflower curds are not fractals. Plant Signal Behav. 2012;7(5):533-4. <https://doi.org/10.4161/psb.19796>
4. Della Porta, G.B. Phytognomica; Horatium Saluianum: Napoli, Italy, 1588