

Package ‘dnafractal’

July 22, 2025

Version 0.0.2

Date 2025-05-09

Title Generates a Fractal Image of a DNA Sequence

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Description The function takes a DNA sequence, a start point, an end point in the sequence, dot size and dot color and draws a fractal image of the sequence. The fractal starts in the center of the canvas. The image is drawn by moving base by base along the sequence and dropping a midpoint between the actual point and the corner designated by the actual base. For more details see Jeffrey (1990) <[doi:10.1093/nar/18.8.2163](https://doi.org/10.1093/nar/18.8.2163)>, Hill, Schisler, and Singh (1992) <[doi:10.1007/BF00178602](https://doi.org/10.1007/BF00178602)>, and Löchel and Heider (2021) <[doi:10.1016/j.csbj.2021.11.008](https://doi.org/10.1016/j.csbj.2021.11.008)>.

License GPL (>= 3)

Encoding UTF-8

LazyData true

RoxygenNote 7.3.2

Imports stringr, DescTools

NeedsCompilation no

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Depends R (>= 3.5.0)

Repository CRAN

Date/Publication 2025-05-09 22:50:07 UTC

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coordinates2sequence	<i>Generates a DNA Sequence Based on an X and Y Coordinate over several iterations</i>
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Description

The function takes an X and Y coordinate and a number of bases to be represented in the DNA sequence. The function starts at the provided X and Y coordinates and then works backward, calculating every preceding base in the DNA sequence that led to that particular point in the fractal. Based on the actual X, Y point's coordinate, the base pair corresponding to that coordinate is inferred, and the DNA string will be built up and returned as the product of the function.

Version 0.0.1. Author: Dr. Matthew Cserhati Email: matthew.cserhati@cui.edu May 5, 2025

Arguments

xstart	the starting x coordinate in the fractal image
ystart	the starting y coordinate in the fractal image
n	the number of bases to be calculated in the DNA sequence

Value

The DNA sequence

References

- Jeffrey, H. J. (1990) Chaos game representation of gene structure. *Nucleic Acids Research* 18(8):2163-70.
- Hill, K. A., Schisler, N. J., and Singh, S. M. (1992) Chaos game representation of coding regions of human globin genes and alcohol dehydrogenase genes of phylogenetically divergent species. *Journal of Molecular Evolution* 35:261-269.
- Löchel, H. F., and Heider, D. (2021) Chaos game representation and its applications in bioinformatics. *Computational and Structural Biotechnology Journal* 19(2021): 6263-6271.

Examples

```
coordinates2sequence(-10,90,25)
```

dnafractal*Generates a Fractal Image of a DNA Sequence*

Description

The function takes a DNA sequence up to 100 Kbp, a start point, an end point in the sequence, dot size and dot color and draws a fractal image of the sequence. The fractal starts in the center of the canvas. The image is drawn by moving base by base along the sequence and dropping a midpoint between the actual point and the corner designated by the actual base.

Version 0.0.1. Author: Dr. Matthew Cserhati Email: matthew.cserhati@cui.edu May 5, 2025

Arguments

mx	a DNA sequence
start	the starting position in the sequence to be fractalized
end	the ending position in the sequence to be fractalized
cex	the size of the dots in the fractal image
dotcol	the color of the fractal image dots

Value

nil

References

Jeffrey, H. J. (1990) Chaos game representation of gene structure. *Nucleic Acids Research* 18(8):2163-70.

Hill, K. A., Schisler, N. J., and Singh, S. M. (1992) Chaos game representation of coding regions of human globin genes and alcohol dehydrogenase genes of phylogenetically divergent species. *Journal of Molecular Evolution* 35:261-269.

Löchel, H. F., and Heider, D. (2021) Chaos game representation and its applications in bioinformatics. *Computational and Structural Biotechnology Journal* 19(2021): 6263-6271.

Examples

```
dnafractal(human_mitogenome)
dnafractal(human_mitogenome, start=100, end=1000)
dnafractal(human_mitogenome, cex=1, dotcol="blue")
```

human_mitogenome	<i>Human Mitochondrial Genome Sequence</i>
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Description

Human Mitochondrial Genome Sequence

Usage

human_mitogenome

Format

'human_mitogenome' Human Mitochondrial Genome Sequence

sign2base	<i>Returns a DNA base based on the sign value of an X and Y coordinate</i>
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Description

The function takes the sign of an X and Y value and returns the corresponding DNA base.

Version 0.0.1. Author: Dr. Matthew Cserhati Email: matthew.cserhati@cui.edu May 5, 2025

Arguments

sx	sign of X coordinate
sy	sign of Y coordinate

Value

The corresponding base

References

- Jeffrey, H. J. (1990) Chaos game representation of gene structure. *Nucleic Acids Research* 18(8):2163-70.
- Hill, K. A., Schisler, N. J., and Singh, S. M. (1992) Chaos game representation of coding regions of human globin genes and alcohol dehydrogenase genes of phylogenetically divergent species. *Journal of Molecular Evolution* 35:261-269.
- Löchel, H. F., and Heider, D. (2021) Chaos game representation and its applications in bioinformatics. *Computational and Structural Biotechnology Journal* 19(2021): 6263-6271.

Examples

```
sign2base(-1,1)
```

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