# Package: dnafractal (via r-universe)

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**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>, Hill, Schisler, and Singh (1992) <doi:10.1007/BF00178602>, and Löchel and Heider (2021) <doi: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** https://cran.r-universe.dev

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**RemoteUrl** https://github.com/cran/dnafractal

**RemoteRef** HEAD

**RemoteSha** 57df746d35d5feb25379f1cdda3b245b47c4773b

# Contents

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## `coordinates2sequence` *Generates a DNA Sequence Based on an X and Y Coordinate over several iterations*

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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")
```

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## `human_mitogenome` *Human Mitochondrial Genome Sequence*

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### Description

Human Mitochondrial Genome Sequence

### Usage

```
human_mitogenome
```

### Format

## ‘human_mitogenome‘ Human Mitochondrial Genome Sequence

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## `sign2base` *Returns a DNA base based on the sign value of an X and Y coordinate*

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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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