

Package ‘SobolSequence’

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Type Package

Title Sobol Sequences with Better Two-Dimensional Projections

Version 1.0

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Description R implementation of S. Joe and F. Y. Kuo(2008)
<[DOI:10.1137/070709359](https://doi.org/10.1137/070709359)>.
The implementation is based on the data file new-joe-kuo-6.21201
<<http://web.maths.unsw.edu.au/~fkuo/sobol/>>.

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Imports Rcpp (>= 0.12.9)

LinkingTo Rcpp

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

URL <http://web.maths.unsw.edu.au/~fkuo/sobol/>

RoxygenNote 6.0.1

NeedsCompilation yes

Repository CRAN

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SobolSequence-package *Sobol Sequence*

Description

R implementation of S. Joe and F. Y. Kuo, "Constructing Sobol sequences with better two-dimensional projections", SIAM J. Sci. Comput. 30, 2635-2654 (2008).

Details

The implementation is based on the data file new-joe-kuo-6.21201 <<http://web.maths.unsw.edu.au/~fkuo/sobol/>>. Porting to R by Mutsuo Saito. The R version does not returns coordinate value zero, but returns value very near to zero, 2^{-64} .

Acknowledgments

I, Mutsuo Saito, wish to thank Frances Kuo and Stephen Joe for their research, and agreement to use thier source code.

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Reference

S. Joe and F. Y. Kuo, "Constructing Sobol sequences with better two-dimensional projections", SIAM J. Sci. Comput. 30, 2635-2654 (2008).

Examples

```
srange <- sobolSequence.dimMinMax()
mrange <- sobolSequence.dimF2MinMax(srange[1])
points <- sobolSequence.points(dimR=srange[1], dimF2=mrange[1], count=10000)
points <- sobolSequence.points(dimR=srange[1], dimF2=mrange[1], count=10000,
                              digitalShift=TRUE)
```

sobolSequence.dimF2MinMax

get minimum and maximum F2 dimension number.

Description

get minimum and maximum F2 dimension number.

Usage

```
sobolSequence.dimF2MinMax(dimR)
```

Arguments

dimR dimation.

Value

supportd minimum and maximum F2 dimension number.

sobolSequence.dimMinMax *get minimum and maximum dimension number of Sobol Sequence*

Description

get minimum and maximum dimension number of Sobol Sequence

Usage

sobolSequence.dimMinMax()

Value

supportd minimum and maximum dimension number.

sobolSequence.points *get points from SobolSequence*

Description

This R version does not returns cordinate value zero, but returns value very near to zero, 2^{-64} .

Usage

sobolSequence.points(dimR, dimF2 = 10, count, digitalShift = FALSE)

Arguments

dimR dimation.
dimF2 F2-dimation of each element.
count number of points.
digitalShift use digital shift or not.

Value

matrix of points where every row contains dimR dimensional point.

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