Package: gaRbage (via r-universe)

September 9, 2024

Type Package

Title `gaRbage` is an R package for that random but sometimes useful
code.

Version 0.1.0

Author Eric Hunt

Maintainer Eric Hunt <52219938+eric-hunt@users.noreply.github.com>

Description `gaRbage` is an R package for that random but sometimes
useful code.

License MIT + file LICENSE

Encoding UTF-8

RoxygenNote 7.3.2.9000

Imports stringr

Repository https://eric-hunt.r-universe.dev

RemoteUrl https://github.com/eric-hunt/gaRbage

RemoteRef HEAD

RemoteSha 9ad478d1dba5f3dbc73b093fadd1e931f6b4d478

Contents

---

seq_gc   *Get the GC content of a nucleic acid sequence*

Description

Get the GC content of a nucleic acid sequence

Usage

```
seq_gc(seq, digits = 4)
```

Arguments

seq   A string - the nucleic acid sequence formatted as a single string

digits   An integer - rounding precision for the result (see [base::round()])

Value

A double, the GC content of *seq*, with precision defined by *digits*

---

seq_revcomp   *Get the reverse complement of a nucleic acid sequence*

Description

Get the reverse complement of a nucleic acid sequence

Usage

```
seq_revcomp(seq)
```

Arguments

seq   A string - the nucleic acid sequence formatted as a single string

Value

A string - the reverse complement of *seq*

Index