Package ‘asciiruler’

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Type Package
Title Render an ASCII Ruler
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Description An ASCII ruler is for measuring text and is especially useful for sequence analysis. Included in this package are methods to create ASCII rulers and associated GenBank sequence blocks, multi-column text displays that make it easy for viewers to locate nucleotides by position.
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Depends R (>= 2.14)
Imports stringr
Collate 'asciiruler.R'
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Suggests testthat
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R topics documented:

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Generate an ascii ruler

Description

<table>
<thead>
<tr>
<th>v borders</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
</tr>
<tr>
<td></td>
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<tr>
<td>+-----------------------------------------------------------------</td>
</tr>
</tbody>
</table>

Usage

asciirule(low = 0L, high = 50L, sparse_ticks = 5L, dense_ticks = TRUE, block_space = 0L, borders = FALSE, numbers_down = TRUE, line_break = "\n", strict_width = FALSE)

default.asciiruler(x)

Arguments

low the range start, can be negative
high the range end, can be negative
sparse_ticks intermittent ticks appear every sparse_ticks, set to 0 to hide row
dense_ticks display a row of ticks at every position
block_space break up the ruler with a space every block_space blocks encountered, a multiple of sparse_ticks, set to 0 to disable
borders display borders
numbers_down display the ruler so the numbers are below the ticks
line_break the line break character(s)
strict_width hide numbers whose display would force the ruler to be wider than width(high-low)

Value

asciiruler object with the following slots:

output delimited ruler string ready to cat
content vector of lines comprising the ruler
width width of ruler
leftmargin position of the first tick relative to the left edge of the ruler
**References**

Inspired by [http://codegolf.stackexchange.com/questions/4910/ascii-ruler-generation](http://codegolf.stackexchange.com/questions/4910/ascii-ruler-generation)

**Examples**

```python
asciiruler(low=-30, high=30, borders=True)
```

---

**genbank_seqblock**

*Generate a GenBank sequence block*

**Description**

```
  1  6 11  16  21  26  31  36  41  46  51  56
  |   |   |   |   |   |   |   |   |   |   |
  1 GATCACAGGT CTATCACCCCT ATTAACACT CACGGAGAGCT CTTGATATTT
  61 GTTCTGAGGG GTTGCACCGC GATAGCATTG CGAGACGCTG GAGCCGGAGC ACCCTATGTC
  121 GCAGTATCTG CTCTCGAATC CTGCCCATCT ATTTATTTC TCGCACCCT ACCTAATTT
  181 ACAGGCAATG ATACTTACAT AAGTGTGTAT ATTAATATG GTTTATAGGA CATAATATA
  241 ACAATTGAACT GTCTGACAGC CCGCTTATCA CACAGACATC ATAACAAAAA ATTTCCACCA
  301 AACCCCCCAT CCCCGGCTTC TGGCGACAGC ACCTAAACAC ATCTCTGC
```

**Usage**

```python
genbank_seqblock(string, start = 1L, end = 0L, blocksize = 10L,
                 width = 60L, sep = " ", line_break = "\n", ruler = TRUE, ...)
```

**Arguments**

- `string`: the sequence string to display
- `start`: the substring start, should be 1 or greater
- `end`: substring end, should be > start, negative to trim
- `blocksize`: number of characters in each block
- `width`: width of the sequence block
- `sep`: space character between blocks
- `line_break`: the line break character(s)
- `ruler`: display an ascii ruler
- `...`: additional arguments passed to asciiruler

**Value**

delimited GenBank block string ready to cat
Examples

```r
my_sequence <- 'GATCACAGGTCTATCACCTATTAACCACTCACGGAAGCTCTCCATTCATTTTGTTGATTTTCTGTGCGGG
GTATGCAAGGATGATCTGCTGAGAGCTCCATCGGACAGCTGGAGCCGACCCCTATATGCGATATGTACCTTGAATTC
CTGCTTCACTCTATTATTCTGCGACTGTTCAATATTACAGGCAACATATTACATACATTAAAGTGTGTA
ATTATTTATGCTGACATAAATAAATAATTGATGTGCTGACAGGCCACTTTCCGACAGACATC'
my_seqblock <- genbank_seqblock(my_sequence)
cat(my_seqblock)
```

---

**print.asciiruler**  
*Print an asciiruler*

**Description**

Print an asciiruler

**Usage**

```r
## S3 method for class 'asciiruler'
print(x, ...)
```

**Arguments**

- `x`  
  the asciiruler

- `...`  
  additional arguments

---

**width**  
*Get the total width of an asciiruler*

**Description**

Get the total width of an asciiruler

**Usage**

```r
width(x, ...)
```

**Arguments**

- `x`  
  the asciiruler

- `...`  
  additional arguments
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