

r2asciidoc

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r2asciidoc is a R package for writing document with embeded R commands.

1 Short example

As you can see, r2asciidoc is simple.

```
<<>>=  
x <- matrix(1:4, 2, 2)  
x  
@
```

gives :

```
> x <- matrix(1:4, 2, 2)  
> x  
      [,1] [,2]  
[1,]    1    3  
[2,]    2    4
```

```
<<results=ascii,echo=FALSE>>=  
ascii(x, caption = "A simple matrix", width = 30)  
@
```

gives :

Table 1 A simple matrix		
	1.00	3.00
	2.00	4.00

2 What r2asciidoc provides

r2asciidoc provided :

- a Sweave driver: `Sweave("yourfile.Rnw", RweaveAscii())` to use it
- a generic method for common R objects: `ascii()`. Default argument depends of R object.

x	R object
include.-	include rownames ? (logical)
rownames	
include.-	include colnames ? (logical)
colnames	
format	equal to "d" (for integers), "f", "e", "E", "g", "G", "fg" (for reals). Default is "f". "f" gives numbers in the usual xxx.xxx format; "e" and "E" give n.ddde+nn or n.dddE+nn (scientific format); "g" and "G" put x[i] into scientific format only if it saves space to do so. "fg" uses fixed format as "f", but <i>digits</i> as the minimum number of <i>significant</i> digits.
digits	the desired number of digits after the decimal point.
decimal.-	the character to be used to indicate the numeric decimal point.
mark	
na.print	the character to be used for NA
caption	the title (character)

width	the desired width of the table
frame	defines the table border. Can take the following values: "topbot" (top and bottom), "all" (all sides), "none" and "sides" (left and right). Default is "all".
grid	defines which ruler lines are drawn between table rows and columns. Can take "none", "cols", "rows" and "all". Default is "all".
valign	vertically align all cells in a table. Can take "top", "bottom" and "middle".
header	emphase the first line of a table (logical).
footer	emphase the last line of a table (logical).
align	column alignment. Can be "r" (right), "l" (left) or "c" (center).
col.width	columns width (integer proportional value).
style	columns styles. Equal to "d" (default), "e" (emphasis), "m" (monospaced), "s" (strong), "a" (cells cans contain any of the <i>AsciiDoc</i> elements that are allowed inside document), "l" (literal), "v" (verse; all line breaks are retained).

3 Gallery

3.1 Vector

```
> ascii(1:4)
|=====
|1.00|2.00|3.00|4.00
|=====
```

1.00	2.00	3.00	4.00
------	------	------	------

3.2 Matrix

```
> ascii(VADeaths, include.rownames = T, include.colnames = T, caption = "VADeaths ←",
+       header = T, width = 50, valign = "middle", align = "lrrrr",
+       frame = "topbot", grid = "none")
.VADeaths
[frame="topbot",grid="none",valign="middle",options="header",cols="<,>,>,>,>", ←
width="50%"]
|=====
|      |Rural Male|Rural Female|Urban Male|Urban Female
|50-54|11.70      |8.70        |15.40     |8.40
|55-59|18.10      |11.70       |24.30     |13.60
|60-64|26.90      |20.30       |37.00     |19.30
|65-69|41.00      |30.90       |54.60     |35.10
|70-74|66.00      |54.30       |71.10     |50.00
|=====
```

3.3 Data Frame

Table 2 VADeaths

	Rural Male	Rural Female	Urban Male	Urban Female
50-54	11.70	8.70	15.40	8.40
55-59	18.10	11.70	24.30	13.60
60-64	26.90	20.30	37.00	19.30
65-69	41.00	30.90	54.60	35.10
70-74	66.00	54.30	71.10	50.00

```
> ascii(iris[1:10, ], include.rownames = F, caption = "iris", width = 50,
+       align = "c", valign = "bottom")
.iris
[valign="bottom",options="header",cols="^,^,^,^,^",width="50%"]
|=====
|Sepal.Length|Sepal.Width|Petal.Length|Petal.Width|Species
|5.10         |3.50        |1.40        |0.20        |setosa
|4.90         |3.00        |1.40        |0.20        |setosa
|4.70         |3.20        |1.30        |0.20        |setosa
|4.60         |3.10        |1.50        |0.20        |setosa
|5.00         |3.60        |1.40        |0.20        |setosa
|5.40         |3.90        |1.70        |0.40        |setosa
|4.60         |3.40        |1.40        |0.30        |setosa
|5.00         |3.40        |1.50        |0.20        |setosa
|4.40         |2.90        |1.40        |0.20        |setosa
|4.90         |3.10        |1.50        |0.10        |setosa
|=====
```

Table 3 iris

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.10	3.50	1.40	0.20	setosa
4.90	3.00	1.40	0.20	setosa
4.70	3.20	1.30	0.20	setosa
4.60	3.10	1.50	0.20	setosa
5.00	3.60	1.40	0.20	setosa
5.40	3.90	1.70	0.40	setosa
4.60	3.40	1.40	0.30	setosa
5.00	3.40	1.50	0.20	setosa
4.40	2.90	1.40	0.20	setosa
4.90	3.10	1.50	0.10	setosa

3.4 Summary table

```
> ascii(summary(table(1:4, 1:4)))
- Number of cases in table: 4
- Number of factors: 2
- Test for independence of all factors:
* Chisq = 12, df = 9, p-value = 0.2133
* Chi-squared approximation may be incorrect
```

- Number of cases in table: 4
- Number of factors: 2
- Test for independence of all factors:
 - Chisq = 12, df = 9, p-value = 0.2133
 - Chi-squared approximation may be incorrect

3.5 Glm

```

> counts <- c(18, 17, 15, 20, 10, 20, 25, 13, 12)
> outcome <- gl(3, 1, 9)
> treatment <- gl(3, 3)
> d.AD <- data.frame(treatment, outcome, counts)
> glm.D93 <- glm(counts ~ outcome + treatment, family = poisson())
> glm.D93
Call:  glm(formula = counts ~ outcome + treatment, family = poisson())

Coefficients:
(Intercept)      outcome2      outcome3  treatment2  treatment3
  3.045e+00   -4.543e-01   -2.930e-01    8.717e-16    4.557e-16

Degrees of Freedom: 8 Total (i.e. Null);  4 Residual
Null Deviance:      10.58
Residual Deviance:  5.129      AIC: 56.76
> ascii(glm.D93, caption = "glm.D93")
.glm.D93
[options="header"]
|=====
|      |Estimate|Std. Error|z value|Pr(>|z|)|
| (Intercept) |3.04    |0.17     |17.81  |0.00
| outcome2    |-0.45   |0.20     |-2.25  |0.02
| outcome3    |-0.29   |0.19     |-1.52  |0.13
| treatment2  |0.00    |0.20     |0.00   |1.00
| treatment3  |0.00    |0.20     |0.00   |1.00
|=====
> ascii(summary(glm.D93), caption = "summary glm.D93")
.summary glm.D93
[options="header"]
|=====
|      |Estimate|Std. Error|z value|Pr(>|z|)|
| (Intercept) |3.04    |0.17     |17.81  |0.00
| outcome2    |-0.45   |0.20     |-2.25  |0.02
| outcome3    |-0.29   |0.19     |-1.52  |0.13
| treatment2  |0.00    |0.20     |0.00   |1.00
| treatment3  |0.00    |0.20     |0.00   |1.00
|=====
> ascii(anova(glm.D93), caption = "anova glm.D93", include.rownames = T)
.anova glm.D93
[options="header"]
|=====
|      |Df  |Deviance|Resid. Df|Resid. Dev
| NULL  |    |        |         |
| outcome |2.00|5.45   |6.00     |5.13
| treatment|2.00|0.00   |4.00     |5.13
|=====

```

Table 4 glm.D93

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.04	0.17	17.81	0.00
outcome2	-0.45	0.20	-2.25	0.02
outcome3	-0.29	0.19	-1.52	0.13
treatment2	0.00	0.20	0.00	1.00
treatment3	0.00	0.20	0.00	1.00

3.6 Survdiff

Table 5 summary glm.D93

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.04	0.17	17.81	0.00
outcome2	-0.45	0.20	-2.25	0.02
outcome3	-0.29	0.19	-1.52	0.13
treatment2	0.00	0.20	0.00	1.00
treatment3	0.00	0.20	0.00	1.00

Table 6 anova glm.D93

	Df	Deviance	Resid. Df	Resid. Dev
NULL			8.00	10.58
outcome	2.00	5.45	6.00	5.13
treatment	2.00	0.00	4.00	5.13

```
> library(survival)
> survdiff.aml <- survdiff(Surv(time, status) ~ x, data = aml)
> ascii(survdiff.aml, caption = "survdiff.aml", digits = c(0, 0,
+ 2, 2, 2, 0, 5), format = c(rep("f", 6), "E"))
.survdiff.aml
[options="header"]
|=====
|          |N |Observed|Expected| (O-E)^2/E| (O-E)^2/V|df|p
|x=Maintained |11|7      |10.69   |1.27     |3.40     |1 |6.53393E-02
|x=Nonmaintained|12|11     |7.31    |1.86     |3.40     | |
|=====
```

Table 7 survdiff.aml

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V	df	p
x=Maintained	11	7	10.69	1.27	3.40	1	6.53393E-02
x=Nonmaintained	12	11	7.31	1.86	3.40		

4 Convert

Sweave process creates a `yourdocument.txt` file from `yourdocument.Rnw`.

You can convert it to html format with the following command:

```
asciidoc yourdocument.txt
```

or to docbook format with:

```
asciidoc -b docbook yourdocument.txt
```

For example, you can see the source of [this documentation](#), the file [generated by Sweave](#), the same file in [docbook format](#), the same file [converted to pdf](#) with `dblatex`, and the same file [converted to odf](#) with `docbook2odf`.