

# Package ‘define’

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**Type** Package

**Title** Create FDA-Style Data and Program Definitions

**Version** 0.2.8

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**Description** Creates a directory of archived files with a descriptive 'PDF' document at the root level (i.e. 'define.pdf') containing tables of definitions of data items and relative-path hyperlinks to the documented files. Converts file extensions to 'txt' per FDA expectations and converts 'CSV' files to 'SAS' Transport format. Relies on data item descriptors stored as per R package 'spec'. See 'package?define'. See also '?define'. Requires a compatible installation of 'pdflatex', e.g. <<https://miktex.org/>>.

**License** GPL-3

**LazyData** TRUE

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define-package	<i>Create FDA-style dataset and program definitions.</i>
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### Description

**define** helps you create 'define.pdf' and associated file tree for FDA-style submission of analysis datasets, etc. It converts csv files to SAS Transport V. 5 'xpt' format, using metadata encoded in a specification file. It enforces the 'txt' extension for other (presumably ASCII) files.

### Details

The only function you're likely to need from **define** is [define](#). You may want to learn more about metadata encoding from **encode** and more about specification files from **spec**.

### Author(s)

Tim Bergsma, <bergsmat@gmail.com>

### References

[FDA Study Data Specifications](#)  
[FDA PDF Specifications](#)  
[SAS Transport Format Specification](#)

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as.define	<i>Coerce to Define</i>
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---

### Description

Coerces to class 'define'. Generic, with method for 'spec'.

Coerces to class 'define' from class 'spec'. Extra arguments ignored.

**Usage**

```
as.define(x, ...)

## S3 method for class 'spec'
as.define(x, sep = " = ", collapse = "; ",
  escape = character(0), ...)
```

**Arguments**

x	object
...	passed arguments
sep	separates codes from respective decodes where given
collapse	separates code/decode pairs where given
escape	values to escape for proper latex formatting

**Methods (by class)**

- spec: method for spec

**See Also**

[specification](#)  
[as.spec](#)

---

as.document.define      *Coerce to Document from Define*

---

**Description**

Coerces to class 'document' from class 'define'.

**Usage**

```
## S3 method for class 'define'
as.document(x, morePreamble = command("usepackage", args =
  "longtable"), geoLeft = "1in", geoRight = "1in", geoTop = "1in",
  geoBottom = "1in", pagestyle = command("pagestyle", args = "plain"), ...)
```

**Arguments**

x	passed to <a href="#">as.tabular.define</a>
morePreamble	passed to <a href="#">as.document.character</a>
geoLeft	passed to <a href="#">as.document.character</a>
geoRight	passed to <a href="#">as.document.character</a>

geoTop	passed to <code>as.document.character</code>
geoBottom	passed to <code>as.document.character</code>
pagestyle	passed to <code>as.document.character</code>
...	passed to <code>as.document.character</code> and <code>as.tabular.define</code>

---

as.document.submission

*Coerce a submission object to a document.*

---

## Description

Coerces a submission object to a document.

## Usage

```
## S3 method for class 'submission'
as.document(x, title, short = title, protocol = "~",
  sponsor = "~", program = "~", author = "~",
  date = "\\mydate \\today", lhead1 = short, lhead2 = protocol,
  rhead1 = sponsor, rhead2 = program, lfoot = author, rfoot = date,
  logo = NULL, logoscale = 1, morePreamble = NULL, geoLeft = "1in",
  geoRight = "1in", geoTop = "1in", geoBottom = "1in", pagestyle = NULL,
  thispagestyle = NULL, units = FALSE, ...)
```

## Arguments

x	a list of artifacts each having attributes: x, tag, des, file, spec
title	a title for the document
short	short title
protocol	relevant protocol
sponsor	program sponsor
program	drug development program
author	document author
date	today's date by default
lhead1	left header 1, e.g. short title
lhead2	left header 2, e.g. relevant protocol(s)
rhead1	right header 1, e.g. sponsor
rhead2	right header 2, e.g. development program
lfoot	left footer (italicized), e.g. responsible party
rfoot	right footer, today's date by default
logo	file path for title page logo
logoscale	size adjustment for logo

morePreamble	if NULL, a special value is passed to <code>as.document.character</code> . See function definition for details, and override if necessary.
geoLeft	passed to <code>as.document.character</code>
geoRight	passed to <code>as.document.character</code>
geoTop	passed to <code>as.document.character</code>
geoBottom	passed to <code>as.document.character</code>
pagestyle	passed to <code>as.document.character</code>
thispagestyle	passed to <code>as.document.character</code>
units	Should units for continuous variables be printed in Codes column?
...	passed to <code>as.define</code> , <code>as.tabular</code> , <code>as.document.character</code>

### Details

Makes a pdf-ready character object representing a latex document. Essentially a wrapper for `as.document`. Title, logo, headers, footers, date are placed on the title page. The second page has a menu (table) of defined objects that creates bi-directional links to any defined data tables. Links are also created to the storage locations relative to the (resulting) `define.pdf`. Following pages table the attributes of data items in any datasets.

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as.labeled	<i>Coerce to class labeled.</i>
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---

### Description

Coerces to class `labeled`.

Coerces character to a `labeled data.frame`.

### Usage

```
as.labeled(x, ...)
```

```
## S3 method for class 'character'
as.labeled(x, spec, as.is = TRUE, na.strings = c("",
  "."), rename = function(x, ...) x, ...)
```

### Arguments

x	length-one filename for csv-formatted data file
...	passed to <code>as.labeled.dat</code>
spec	length-one file name for spec
as.is	passed to <code>read.csv</code>
na.strings	passed to <code>read.csv</code>
rename	a function with arguments x, ... to pre-process column names

**Methods (by class)**

- character: data.frame method for as.labeled

**See Also**

[as.labeled.data.frame](#)

---

as.labeled.data.frame *Coerce data.frame to labeled.*

---

**Description**

Coerces data.frame to labeled.

**Usage**

```
## S3 method for class 'data.frame'  
as.labeled(x, label, spec, check = TRUE, ...)
```

**Arguments**

x	data.frame
label	a SAS-style label for x
spec	a spec (specification) data.frame containing column labels
check	should the data.frame be required to match its specification?
...	ignored

**Details**

Positive numeric values less than 1e-70 are coerced to zero to solve SAS encoding issues. Column names are forced unique and forced SAS-compliant with `link{makesasnames}`. Labels are added to the data.frame column names, and to the data.frame itself.

**See Also**

[as.labeled.character](#)

---

as.pdf.define	<i>Coerce to PDF from Define</i>
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---

**Description**

Coerces to PDF from class 'define'.

**Usage**

```
## S3 method for class 'define'
as.pdf(x, stem, ...)
```

**Arguments**

x	define object
stem	passed to <a href="#">as.pdf</a>
...	passed to <a href="#">as.pdf</a> and <a href="#">as.document</a>

---

as.submission	<i>Create a submission.</i>
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---

**Description**

Returns a list of vetted artifacts (spec or char corresponding to x) that represent a submission object for further processing.

Converts a character vector of file names to class submission.

**Usage**

```
as.submission(x, ...)

## S3 method for class 'character'
as.submission(x, tag = names(x),
  description = basename(x), dir = ".", subdir = NULL, ...)
```

**Arguments**

x	filenames: xpt, csv, spec, txt, other
...	passed along to handlers
tag	short names for each element of x
description	informative multi-word label for each element of x
dir	parent directory for placement of submission artifacts
subdir	optional subdirectories relative to dir for each submission artifact

**Value**

a list of artifacts each having attributes: x, tag, des, file, spec

**Methods (by class)**

- character: character method for as.submission

---

```
as.submission.submission
```

*Coerce a submission to class submission.*

---

**Description**

Coerces a submission to class submission.

**Usage**

```
## S3 method for class 'submission'
as.submission(x, ...)
```

**Arguments**

x	object of dispatch
...	passed along

---

```
as.tabular.define
```

*Coerce to Tabular from Define*

---

**Description**

Coerces to class 'tabular' from class 'define'.

**Usage**

```
## S3 method for class 'define'
as.tabular(x, caption = "", grid = TRUE, rules = 1,
  colwidth = c("1in", "1in", "0.5in", "1.5in", "1.5in"),
  tabularEnvironment = "longtable", walls = 1, tabnum = FALSE,
  pretable = if (is.null(caption)) "" else paste(if (tabnum) "\\caption{"
  else "\\caption*{", caption,
  "}}\\\"), prepos = 1, headerBold = TRUE, reserve = FALSE, ...)
```



**Arguments**

x	define object
caption	caption for definitions table
grid	passed to <code>as.tabular.data.frame</code>
rules	passed to <code>as.tabular.data.frame</code>
colwidth	passed to <code>as.tabular.data.frame</code>
tabularEnvironment	passed to <code>as.tabular.data.frame</code>
walls	passed to <code>as.tabular.data.frame</code>
tabnum	whether to number the table
pretable	material to include before table, typically a caption
prepos	after which line number should pretable be inserted?
headerBold	whether to use a bold header
reserve	passed to <code>as.tabular</code>
...	passed to <code>as.tabular</code>

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as.xport	<i>Coerce to class xport.</i>
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**Description**

Coerces to class xport.

Coerces labeled to xport.

**Usage**

```
as.xport(x, ...)
```

```
## S3 method for class 'labeled'
```

```
as.xport(x, name, file, autogen.formats = FALSE, ...)
```

**Arguments**

x	a labeled data.frame
...	passed to write.xport
name	a name for the data.frame
file	where to write the data.frame
autogen.formats	passed to write.xport

**Methods (by class)**

- labeled: labeled method for as.xport

---

define *Define objects per FDA guidance.*

---

## Description

Defines (documents) a set of files in a manner intended to comply with FDA guidance on submission of study data and related documentation. In particular, files in csv format are converted to SAS Transport (xpt), extensions for other files (presumably ASCII) are coerced to txt, files are copied to a directory tree, and define.pdf is created at the top level to describe the files in more detail.

Define a set of files per FDA guidance.

tag is taken by default as the names of x, but may be supplied explicitly. The following should have the same length as x: tag, description, subdir. subdir may also be length one. Other arguments have length one.

The function iterates across the elements of x to create a 'submission' object, a side effect of which is to copy (conditionally, transformed) each corresponding file to (subdir of) dir. The 'submission' object is then converted to a pdf, written directly to dir as '<stem>.pdf'.

Arguments short, protocol, sponsor, program, author, and date are length-one character that define attributes of the pdf title page. Alternatively, they may be specified by names that reflect position rather than semantics: lhead1, lhead2, rhead1, rhead2, lfoot, rfoot (respectively).

## Usage

```
define(x, ...)
```

```
## S3 method for class 'character'
define(x, stem = "define", tag = names(x),
       description = basename(x), title = dirname(x[[1]]), short = title,
       protocol = "~", sponsor = "~", program = "~", author = "~",
       date = "\\mydate \\today", logo = NULL, logoscale = 1,
       dir = "./define", subdir = ".", clear = TRUE, units = FALSE, ...)
```

## Arguments

x	paths to existing files to be documented; possibly a named character vector
...	passed to as.submission and as.pdf
stem	the base of the file name for the pdf to be created
tag	short object names for each element of x; appears in pdf menu, and as table name in XPT file
description	informative labels for each element of x
title	a title to appear in the pdf
short	short title a.k.a. lhead1 (upper left pdf header)
protocol	relevant protocols a.k.a. lhead2 (lower left pdf header)
sponsor	study sponsor a.k.a. rhead1 (upper right pdf header)

program	drug development program a.k.a. rhead2 (lower right pdf header)
author	document author a.k.a. lfoot left pdf footer, italicized)
date	date format string a.k.a. rfoot (right footer) today's date by default
logo	file path for logo to include on cover page
logoscale	size adjustment for logo
dir	path to directory in which to place pdf and copied (transformed) files
subdir	path to subdirectories to which to copy each (transformed) file represented by x; use NULL to suppress archiving
clear	should dir be deleted if it exists?
units	should units for continuous variables be printed in Codes column?

**Value**

invisible result of as.pdf. Used for side effects.

**Methods (by class)**

- character: character method for define

**See Also**

<http://tinyurl.com/fda-pdf-spec-4-0>

<http://tinyurl.com/fda-study-data-spec-2-0>

**Examples**

```
library(spec)           # read and write data specifications
library(latexpdf)      # make dummy logo for pdf
library(encode)        # encode factor levels for spec file

dir <- tempdir()        # a place to experiment
dir <- gsub('\\', '/', dir) # clean up windows path
outdir <- file.path(dir, 'out') # where to put the define archive
csv <- file.path(dir, 'theoph.csv') # path to data
script <- file.path(dir, 'theoph.R') # path to script making data
spec <- file.path(dir, 'theoph.spec') # path to data specification

# make dummy logo
## Not run:
as.pdf('{\\huge \\em Pharma, Inc.}', wide = 50, long = 8, stem = 'logo', dir = dir)

## End(Not run)
# browseURL(system.file(package = 'define', 'logo.pdf')) # cached
logo <- system.file(package = 'define', 'logo.pdf') # path to dummy logo

# make data more interesting
Theoph$renal <- 0
```

```

# create script
code <- "write.csv(x = Theoph, file = csv, row.names = FALSE, quote = FALSE)"
writeLines(code, script)

# 'run' the script
eval(parse(text = code))

# make data specification
s <- specification(Theoph)
renalcat <- c(
  'GFR >= 90 mL/min/1.73m^2',
  '60 <= GFR < 90 mL/min/1.73m^2',
  '45 <= GFR < 60 mL/min/1.73m^2',
  '30 <= GFR < 45 mL/min/1.73m^2',
  'GFR < 30 mL/min/1.73m^2'
)
codes <- encode(0:4, renalcat)
codes
s$guide[s$column == 'renal'] <- codes

write.spec(s, spec)

file.exists(csv)
file.exists(spec)
define(c(theoph = csv), stem = 'minimal', dir = outdir, clean=FALSE)
# browseURL(file.path(outdir, 'minimal.pdf'))
# browseURL(system.file(package = 'define', 'minimal.pdf')) # cached

## Not run:
define(
  x = c(
    theodat = csv,
    theoprgr = script
  ),
  subdir = c(
    'm5/datasets/analysis/datasets',
    'm5/datasets/analysis/programs'
  ),
  description = c(
    'Theophylline PK Dataset',
    'Theophylline PK Script'
  ),
  title = 'Pharmacokinetics of Theophylline',
  short = 'Theophylline PK',
  protocol = 'Protocol tpk-001',
  sponsor = 'Pharma, Inc.',
  program = 'Theophylline',
  author = 'define package for R',
  logo = logo,
  logoscale = 2,
  clear = FALSE,
  dir = outdir
)

```

```
# browseURL(file.path(outdir,'define.pdf'))

## End(Not run)
# browseURL(system.file(package = 'define','define.pdf')) # cached
# browseURL(system.file(package = 'define','poster.pdf')) # earlier work

# Alternatively, supply aesthetics by position:
## Not run:
define(
  x = c(
    theodat = csv,
    theoprgr = script
  ),
  subdir = c(
    'm5/datasets/analysis/datasets',
    'm5/datasets/analysis/programs'
  ),
  description = c(
    'Theophylline PK Dataset',
    'Theophylline PK Script'
  ),
  title = 'Pharmacokinetics of Theophylline',
  lhead1 = 'Theophylline PK',
  lhead2 = 'Protocol tpk-001',
  rhead1 = 'Pharma, Inc.',
  rhead2 = 'Theophylline',
  lfoot = 'define package for R',
  rfoot = '\\mydate \\today',
  logo = logo,
  logoscale = 2,
  clear = FALSE,
  dir = outdir
)

## End(Not run)

# Tags for elements of x can be given explicitly rather than as names:
## Not run:
define(
  x = c(csv, script),
  tag = c('theodat','theoprgr'),
  subdir = c(
    'm5/datasets/analysis/datasets',
    'm5/datasets/analysis/programs'
  ),
  description = c(
    'Theophylline PK Dataset',
    'Theophylline PK Script'
  ),
  title = 'Pharmacokinetics of Theophylline',
  lhead1 = 'Theophylline PK',
  lhead2 = 'Protocol tpk-001',
  rhead1 = 'Pharma, Inc.',
```

```

rhead2 = 'Theophylline',
lfoot = 'define package for R',
rfoot = '\\mydate \\today',
logo = logo,
logoscale = 2,
clear = FALSE,
dir = outdir
)

## End(Not run)

# If the title is short, no need to supply a short version.
# Most arguments have suitable defaults. But be sure to
# supply tags, or names for elements of x.
## Not run:
define(
  x = c(
    theodat = csv,
    theoprgr = script
  ),
  description = c(
    'Theophylline PK Dataset',
    'Theophylline PK Script'
  ),
  title = 'Theophylline PK',
  dir = outdir
)

## End(Not run)

```

---

makesasnames

*Make names for a dataset that are unique and follow SAS naming conventions.*

---

### Description

Makes names for a dataset that are unique and follow SAS naming conventions. Modeled after SASxport::makeSasNames, but handling special cases.

### Usage

```
makesasnames(names, nchar = 8, maxPasses = 10, quiet = FALSE)
```

### Arguments

names	existing column names
nchar	limit on number of characters

maxPasses	limit on number of reconciliation attempts
quiet	should messages be suppressed?

**Value**

character

---

recode	<i>Recode an encoded object.</i>
--------	----------------------------------

---

**Description**

Recodes an encoded object.

Recodes an encoded character vector.

**Usage**

```
recode(x, ...)
```

```
## S3 method for class 'character'
recode(x, ...)
```

**Arguments**

x	vector of strings that represent encodings
...	passed to supply

**Details**

[specification](#) creates a template spec object corresponding to a data frame. Not able to guess factor level decodes (labels) or column descriptions (e.g. SAS labels) it supplies defaults by repeating the argument values. These have value for development, but not for reporting. This function drops non-informative decodes.

**Value**

character

**Methods (by class)**

- character: character method for recode

**See Also**

[encode](#)

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