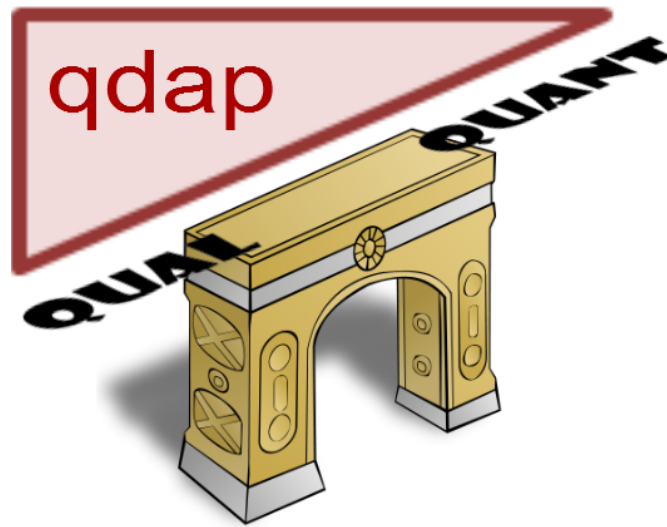


qdap-tm Package Compatibility

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The **qdap** package (Rinker, 2013) is an R package designed to assist in quantitative discourse analysis. The package stands as a bridge between qualitative transcripts of dialogue and statistical analysis and visualization. The **tm** package (Feinerer and Hornik, 2014) is a major R (R Core Team, 2013) package used for a variety of text mining tasks. Many text analysis packages have been built around the **tm** package's infrastructure (see CRAN Task View: Natural Language Processing). As **qdap** aims to act as a bridge to other R text mining analyses it is important that **qdap** provides a means of moving between the various **qdap** and **tm** data types.

This vignette serves as a guide towards navigating between the **qdap** and **tm** packages. Specifically, the two goals of this vignette are to (1) describe the various data formats of the two packages and (2) demonstrate the use of **qdap** functions that enable the user to move seamlessly between the two packages.

1 Data Formats

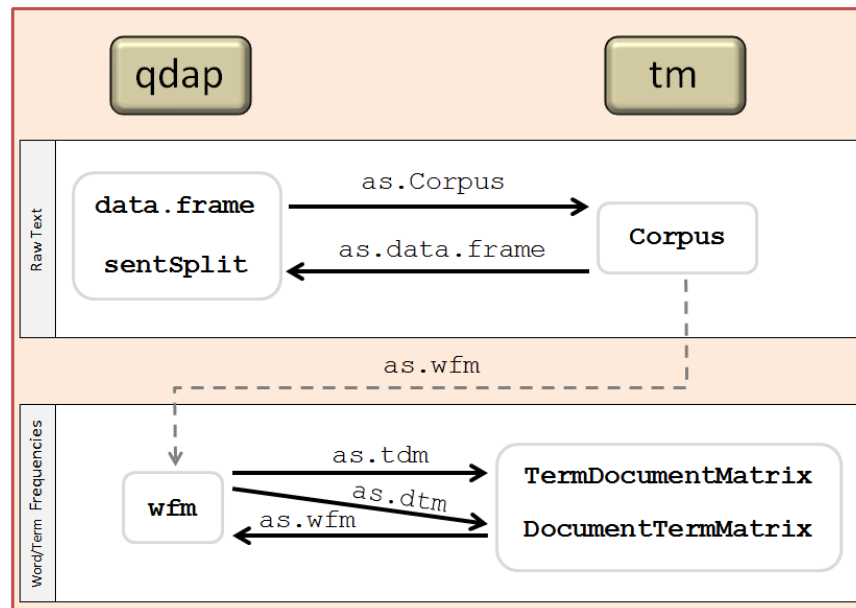
The **qdap** and **tm** packages each have two basic data formats. **qdap** stores raw text data in the form of a `data.frame` augmented with columns of demographic variables whereas **tm** stores raw text as a `Corpus` and annotates demographic information with Meta Data attributes. The structures are both `lists` and are comparable.

The second format both packages use is a matrix structure of word frequency counts. The **qdap** package utilizes the *Word Frequency Matrix* (`wfm` function) whereas the **tm** package utilizes the *Term Document Matrix* or *Document Term Matrix* (`TermDocumentMatrix` and `DocumentTermMatrix` functions). Again the structure is similar between these two data forms. Table 1 lays out the data forms of the two packages.

Package	Raw Text	Word Counts
qdap	Dataframe	Word Frequency Matrix
tm	Corpus	Term Document Matrix/Document Term matrix

Table 1: **qdap**-**tm** Data forms

Figure 1 provides a visual overview of the **qdap** functions used to convert between data structures. Many of these conversion could be achieved via the **tm** package as well.



*Note: `as.tdm` & `as.dtm` are short hand for `as.TermDocumentMatrix` & `as.DocumentTermMatrix`

Figure 1: Converting Data between **qdap** and **tm**

One of the most visible differences between **qdap-tm** data forms is that **qdap** enables the user to readily view the data while the **tm** utilizes a print method that provides a summary of the data. The `tm::inspect` function enables the user to view **tm** data forms. The **qdap** package provides `qdap::qview` and `qdap::htruncdf` functions to view more digestible amounts of the data. Let's have a look at the different data types. We'll start by loading both packages:

```
library(qdap); library(tm)
```

Now let us have a look at the raw text storage of both packages.

1.1 Raw Text

1.1.1 qdap's Raw Text

```
DATA
qview(DATA)
htruncdf(DATA)
```

```
## > DATA
##
##      person sex adult                                state code
## 1      sam   m     0      Computer is fun. Not too fun.  K1
## 2      greg   m     0                No it's not, it's dumb.  K2
## .
## .
## .
## 9      sally  f     0      What are you talking about?  K9
## 10 researcher f     1      Shall we move on? Good then.  K10
## 11      greg   m     0 I'm hungry. Let's eat. You already? K11
```

```
## > qview(DATA)
##
## =====
## nrow = 11          ncol = 5          DATA
## =====
##      person sex adult          state code
```

```
## 1      sam  m    0 Computer i  K1
## 2      greg  m    0 No it's no  K2
## .
## .
## .
## 8      sam  m    0 I distrust  K8
## 9      sally f    0 What are y  K9
## 10 researcher f    1 Shall we m  K10
```

```
## > htruncdf(DATA)
##
##      person sex adult      state code
## 1      sam  m    0 Computer i  K1
## 2      greg  m    0 No it's no  K2
## .
## .
## .
## 8      sam  m    0 I distrust  K8
## 9      sally f    0 What are y  K9
## 10 researcher f    1 Shall we m  K10
```

1.1.2 tm's Raw Text

```
data("crude")
crude
inspect(crude)
```

```
## > crude
## A corpus with 20 text documents
##
## > crude[[1]]
## Diamond Shamrock Corp said that
## effective today it had cut its contract prices for crude oil by
## 1.50 dlrs a barrel.
##      The reduction brings its posted price for West Texas
```

```
## Intermediate to 16.00 dlrs a barrel, the copany said.
##     "The price reduction today was made in the light of falling
## .
## .
## .
##     Diamond is the latest in a line of U.S. oil companies that
## have cut its contract, or posted, prices over the last two days
## citing weak oil markets.
## Reuter
```

1.2 Word/Term Frequency Counts

Now we'll look at how the two packages handle word frequency counts. We'll start by setting up the raw text forms the two packages expect.

```
tm_dat <- qdap_dat <- DATA[1:4, c(1, 4)]
rownames(tm_dat) <- paste("docs", 1:nrow(tm_dat))
tm_dat <- Corpus(DataframeSource(tm_dat[, 2, drop=FALSE]))
```

Both `qdap_dat` and `tm_dat` are storing this basic information:

```
##   person          state
## 1   sam Computer is fun. Not too fun.
## 2   greg      No it's not, it's dumb.
## 3 teacher      What should we do?
## 4   sam      You liar, it stinks!
```

1.2.1 qdap's Frequency Counts

```
with(qdap_dat, wfm(state, person))
```

```
##           greg sam teacher
## computer    0  1     0
## do          0  0     1
## dumb        1  0     0
## fun         0  2     0
## is          0  1     0
## it          0  1     0
## it's        2  0     0
## liar        0  1     0
## no          1  0     0
## not         1  1     0
## should      0  0     1
## stinks      0  1     0
## too         0  1     0
## we          0  0     1
## what        0  0     1
## you         0  1     0
```

1.2.2 tm's Frequency Counts

```
TermDocumentMatrix(tm_dat,
  control = list(
    removePunctuation = TRUE,
    wordLengths=c(0, Inf)
  )
)
```

```
## <<TermDocumentMatrix (terms: 16, documents: 4)>>
## Non-/sparse entries: 17/47
## Sparsity           : 73%
## Maximal term length: 8
```

```
## Weighting          : term frequency (tf)
```

Now we'll Look at the tm output using inspect.

```
inspect(TermDocumentMatrix(tm_dat,  
  control = list(  
    removePunctuation = TRUE,  
    wordLengths=c(0, Inf)  
  )  
))
```

```
##           Docs  
## Terms      1 2 3 4  
## computer  1 0 0 0  
## do        0 0 1 0  
## dumb     0 1 0 0  
## fun      2 0 0 0  
## is       1 0 0 0  
## it       0 0 0 1  
## its     0 2 0 0  
## liar    0 0 0 1  
## no     0 1 0 0  
## not    1 1 0 0  
## should 0 0 1 0  
## stinks 0 0 0 1  
## too    1 0 0 0  
## we     0 0 1 0  
## what  0 0 1 0  
## you   0 0 0 1
```

The two matrices are essentially the same, with the exception of column order and names. Notice that by default **tm** removes words with fewer characters (word length) and does not discard punctuation (we made the matrices equal by specifying `removePunctuation = TRUE` and `wordLengths=c(0, Inf)` for **tm**'s `control` argument). **qdap** takes the opposite approach, removing punctuation and utilizing all words, by default. Likewise, the **tm** package stores demographic information as meta data within the Corpus, whereas, **qdap** incorporates the demo-

graphics with the text into a single `data.frame` structure. These differences arise out of the intended uses, audiences, and philosophies of the package authors. Each has strengths in particular situations. The **qdap** output is an ordinary matrix whereas the **tm** output is a more compact `simple_triplet_matrix`. While the storage is different, both packages can be made to mimic the default of the other.

Also note that the **qdap** summary method for `wfm` provides the user with information similar to the `TermDocumentMatrix/DocumentTermMatrix` functions' default print method.

```
summary(with(qdap_dat, wfm(state, person)))
```

```
## <<A word-frequency matrix (16 terms, 3 groups)>>
##
## Non-/sparse entries      : 17/31
## Sparsity                 : 65%
## Maximal term length     : 8
## Less than four characters : 56%
## Hapax legomenon         : 13(81%)
## Dis legomenon           : 3(19%)
## Shannon's diversity index : 2.73
```

Now we'll look at some **qdap** functions that enable the user to move between packages, gaining the flexibility and benefits of both packages.

2 Converting Data Forms

We'll again use the following preset data:

```
tm_dat <- qdap_dat <- DATA[1:4, c(1, 4)]
rownames(tm_dat) <- paste("docs", 1:nrow(tm_dat))
tm_dat <- Corpus(DataframeSource(tm_dat[, 2, drop=FALSE]))

qdap_wfm <- with(qdap_dat, wfm(state, person))
tm_tdm <- TermDocumentMatrix(tm_dat,
  control = list(
    removePunctuation = TRUE,
    wordLengths = c(0, Inf)
  )
)
```



```
)
```

1. `qdap_dat` – is a **qdap** raw text form
2. `tm_dat` – is a **tm** raw text format
3. `qdap_wfm` – is a **qdap** word frequencies count
4. `tm_tdm` – is a **tm** word frequencies count

The reader is encouraged to view each of the data formats:

```
qdap_dat; qview(qdap_dat)
tm_dat; inspect(tm_dat)
qdap_wfm; summary(qdap_wfm)
tm_tdm; inspect(tm_tdm)
```

2.1 Corpus to data.frame

To move from a `Corpus` to a `data.frame` the `as.data.frame` function is used as follows:

```
as.data.frame(tm_dat)
```

```
##   docs          text
## 1 doc 1 Computer is fun. Not too fun.
## 2 doc 2      No it's not, it's dumb.
## 3 doc 3          What should we do?
## 4 doc 4      You liar, it stinks!
```

2.2 data.frame to Corpus

To move from a `data.frame` to a `Corpus` the `as.Corporus` function is used as follows:

```
with(qdap_dat, as.Corporus(state, person))
```

```
## <<VCorpus>>
## Metadata: corpus specific: 0, document level (indexed): 3
## Content: documents: 3
```

*Note the 3 text documents; one for each grouping variable. To get one for each row use:

```
with(qdap_dat, as.Corporus(state, id(person)))
```

2.3 TermDocumentMatrix/DocumentTermMatrix to wfm

To move from a TermDocumentMatrix to a wfm the `as.wfm` function is used as follows:

```
as.wfm(tm_tdm)
```

```
##      1 2 3 4
## computer 1 0 0 0
## do      0 0 1 0
## dumb    0 1 0 0
## fun     2 0 0 0
## is      1 0 0 0
## it      0 0 0 1
## its     0 2 0 0
## liar    0 0 0 1
## no      0 1 0 0
## not     1 1 0 0
## should  0 0 1 0
## stinks  0 0 0 1
## too     1 0 0 0
## we      0 0 1 0
## what    0 0 1 0
## you     0 0 0 1
```

2.4 wfm to TermDocumentMatrix/DocumentTermMatrix

To move from a wfm to a TermDocumentMatrix or DocumentTermMatrix the `as.tdm` and `as.dtm` functions can be used as follows:

```
as.tdm(qdap_wfm)
as.dtm(qdap_wfm)
```

```
## <<TermDocumentMatrix (terms: 16, documents: 3)>>
## Non-/sparse entries: 17/31
## Sparsity          : 65%
## Maximal term length: 8
## Weighting         : term frequency (tf)
```

```
## <<DocumentTermMatrix (documents: 3, terms: 16)>>
## Non-/sparse entries: 17/31
## Sparsity          : 65%
## Maximal term length: 8
## Weighting         : term frequency (tf)
```

2.5 Corpus to wfm

One can also move directly from a **tm** Corpus to a **qdap wfm** with the `as.wfm` function.

```
as.wfm(tm_dat)
```

```
##      doc 1 doc 2 doc 3 doc 4
## computer  1   0   0   0
## do        0   0   1   0
## dumb      0   1   0   0
## fun       2   0   0   0
## is        1   0   0   0
## it        0   0   0   1
## it's      0   2   0   0
## liar      0   0   0   1
## no        0   1   0   0
## not       1   1   0   0
## should    0   0   1   0
## stinks    0   0   0   1
## too       1   0   0   0
```

```
## we      0    0    1    0
## what   0    0    1    0
## you    0    0    0    1
```

3 Stemming, Stopwords, and Choosing n-Character Words/Terms from a wfm

Many of the **qdap** and **tm** functions have means of stemming, removing stopwords, and bounding, that is filtering rows (greater than, equal to or less than) meeting min/max criteria. **qdap** also offers two external functions to address these issues directly.

3.1 stemming

qdap takes the approach that the user stems the dataframe upon creation (using `sentSplit(..., stem = TRUE)`) or after (using the `stem2df` function), maintaining a column of stemmed and unstemmed text for various analyses.

```
sentSplit(qdap_dat, "state", stem = TRUE)
```

```
##   person tot                state      stem.text
## 1   sam 1.1      Computer is fun.  Comput is fun.
## 2   sam 1.2           Not too fun.   Not too fun.
## 3   greg 2.1 No it's not, it's dumb. No it not it dumb.
## 4 teacher 3.1   What should we do? What should we do?
## 5   sam 4.1   You liar, it stinks! You liar it stink!
```

3.2 Filtering: Stopwords and Bounding

qdap's `Filter` function allows the user to remove stopwords and bound a Word Frequency Matrix (wfm). First we'll construct a minimal Word Frequency Matrix:

```
qdap_wfm <- with(qdap_dat, wfm(state, person))
```

```
##           greg sam teacher
## computer   0  1    0
## do         0  0    1
## dumb       1  0    0
## fun        0  2    0
## is         0  1    0
## it         0  1    0
## it's       2  0    0
## liar       0  1    0
## no         1  0    0
## not        1  1    0
## should     0  0    1
## stinks     0  1    0
## too        0  1    0
## we         0  0    1
## what       0  0    1
## you        0  1    0
```

Now we'll move through a series of examples demonstrating the usage of `Filter` on a `wfm` object.

```
Filter(qdap_wfm, min = 5)
```

```
##           greg sam teacher
## computer   0  1    0
## should     0  0    1
## stinks     0  1    0
```

```
Filter(qdap_wfm, min = 5, max = 7)
```

```
##           greg sam teacher
## should     0  0    1
## stinks     0  1    0
```

```
Filter(qdap_wfm, 4, 4)
```

```
##      greg sam teacher
## dumb   1  0     0
## it's   2  0     0
## liar   0  1     0
## what   0  0     1
```

```
Filter(qdap_wfm, 4, 4, count.apostrophe = FALSE)
```

```
##      greg sam teacher
## dumb   1  0     0
## liar   0  1     0
## what   0  0     1
```

```
Filter(qdap_wfm, 3, 4)
```

```
##      greg sam teacher
## dumb   1  0     0
## fun    0  2     0
## it's   2  0     0
## liar   0  1     0
## not    1  1     0
## too    0  1     0
## what   0  0     1
## you    0  1     0
```

```
Filter(qdap_wfm, 3, 4, stopwords = Top200Words)
```

```
##      greg sam teacher
## dumb   1  0     0
## fun    0  2     0
## it's   2  0     0
## liar   0  1     0
```

4 Apply Functions Intended for TermDocumentMatrix to wfm Object

At times it is convenient to apply a function intended for a **tm** TermDocumentMatrix or DocumentTermMatrix directly to a **qdap** wfm object. **qdap**'s `apply_as_tm` function enables these functions to be used directly on a wfm.

4.1 A Minimal wfm Object

Let us begin with a slightly larger wfm minimal example:

```
a <- with(DATA, wfm(state, list(sex, adult)))

## <<A word-frequency matrix (41 terms, 4 groups)>>
##
## Non-/sparse entries      : 45/119
## Sparsity                 : 73%
## Maximal term length     : 8
## Less than four characters : 49%
## Hapax legomenon         : 32(78%)
## Dis legomenon           : 7(17%)
## Shannon's diversity index : 3.62
```

4.2 A Small Demonstration

Here we will use the **tm** package's `removeSparseTerms` to remove sparse terms from a wfm object and return a Word Frequency Matrix object (wfm class).

```
out <- apply_as_tm(a, tm::removeSparseTerms, sparse=0.6)
```

```
summary(out)
```

```
## <<A word-frequency matrix (3 terms, 4 groups)>>
##
## Non-/sparse entries      : 7/5
```

```
## Sparsity : 42%
## Maximal term length : 4
## Less than four characters : 67%
## Hapax legomenon : 0(0%)
## Dis legomenon : 1(33%)
## Shannon's diversity index : 1.06
```

```
class(out)
```

```
## [1] "wfm" "true.matrix" "matrix"
```

4.3 Further Examples to Try

Here are some further examples to try:

```
apply_as_tm(a, tm::findAssocs, "computer", .8)
apply_as_tm(a, tm::findFreqTerms, 2, 3)
apply_as_tm(a, tm::Zipf_plot)
apply_as_tm(a, tm::Heaps_plot)
apply_as_tm(a, tm::plot.TermDocumentMatrix, corThreshold = 0.4)

library(proxy)
apply_as_tm(a, tm::weightBin)
apply_as_tm(a, tm::weightBin, to.qdap = FALSE)
apply_as_tm(a, tm::weightSMART)
apply_as_tm(a, tm::weightTfIdf)
```

5 Apply Functions Intended for qdap Dataframes to tm Corpus

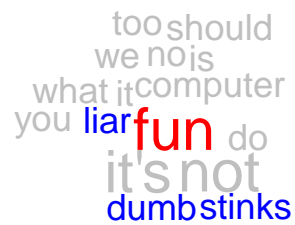
While the **tm** package (and other packages used on **tm** objects) tends to conduct analysis by feeding functions a **TermDocumentMatrix** or **DocumentTermMatrix** **qdap** generally feeds functions raw text directly. There are advantages to both approaches (e.g., the matrix is a mathematical structure while raw text maintains word order). Many **qdap** functions can be used on the **Corpus** structure via the `apply_as_df` function.

5.1 A Small Demonstration

Here we will use the `qdap` package's `trans_cloud` function, on our minimal `tm` Corpus, to produce a word cloud with particular words highlighted:

```
matches <- list(  
  good = "fun",  
  bad = c("dumb", "stinks", "liar")  
)  
  
apply_as_df(tm_dat, trans_cloud, grouping.var=NULL,  
  target.words=matches, cloud.colors = c("red", "blue", "grey75"))
```

all



5.2 Further Examples to Try

Here are some further examples to try:

```

library(tm)
reut21578 <- system.file("texts", "crude", package = "tm")
reuters <- Corpus(DirSource(reut21578),
  readerControl = list(reader = readReut21578XML))

apply_as_df(reuters, word_stats)
apply_as_df(reuters, formality)
apply_as_df(reuters, word_list)
apply_as_df(reuters, polarity)
apply_as_df(reuters, Dissimilarity)
apply_as_df(reuters, diversity)
apply_as_df(tm_dat, pos_by)
apply_as_df(reuters, flesch_kincaid)
apply_as_df(tm_dat, trans_venn)
apply_as_df(reuters, gantt_plot)
apply_as_df(reuters, rank_freq_mplot)
apply_as_df(reuters, character_table)
apply_as_df(reuters, trans_cloud)

matches2 <- list(
  oil = qcv(oil, crude),
  money = c("economic", "money")
)

(termco_out <- apply_as_df(reuters, termco, match.list = matches2))
plot(termco_out, values = TRUE, high="red")

(wordcor_out <- apply_as_df(reuters, word_cor, word = unlist(matches2)))
plot(wordcor_out)

(f_terms <- apply_as_df(reuters, freq_terms, at.least = 3))
plot(f_terms)

finds <- apply_as_df(reuters, freq_terms, at.least = 5,
  top = 5, stopwords = Top100Words)
apply_as_df(reuters, dispersion_plot, match.terms = finds[, 1],

```

```
total.color = NULL)
```

6 Conclusion

This vignette described the various data formats for the **qdap** and **tm** packages. It also demonstrated some of the basic functionality of the **qdap** functions designed to navigate between the two packages. For more information on the **tm** package (Feinerer *et al.*, 2008) use:

```
browseVignettes(package = "tm")
```

Likewise, the user may view additional information about the **qdap** package (Rinker, 2013):

```
browseVignettes(package = "qdap")
```

Acknowledgments

qdap relies heavily on the **tm** package. The **tm** package has extended text analysis to the R platform. Thank you to Ingo Feuerer and Kurt Hornik for their work on this and many other R packages.

This document was produced with **knitr** (Xie, 2013). Thank you to Yihui Xie for the **knitr** package and his many other contributions to the R community.

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