qdap-tm Package Compatibility

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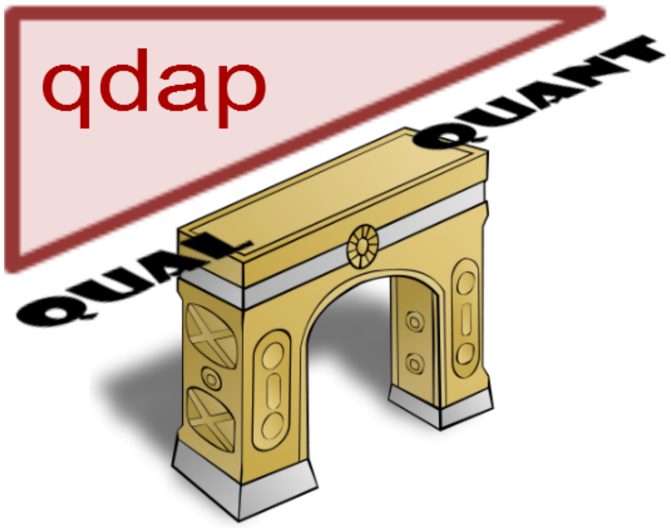


The **qdap** package (Rinker, 2013) is an R package designed to assist in quantitative discourse analysis. The package stands as a bridge between qualitative transcripts of dialogue and statistical analysis and visualization. The **tm** package (Feinerer and Hornik, 2014) is a major R (R Core Team, 2013) 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

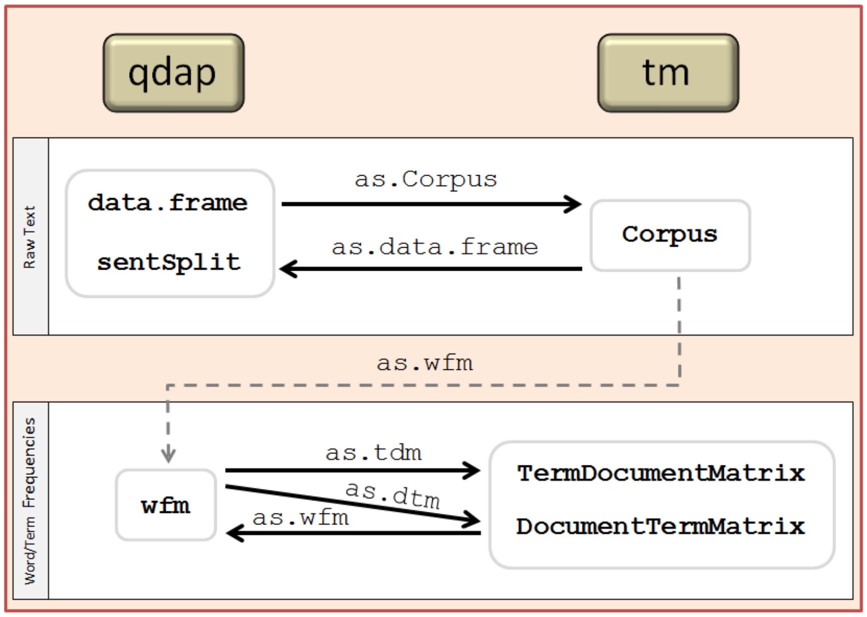
The **qdap** and **tm** packages each have two basic data formats. **qdap** stores raw text data in the form of a `data.frame` augmented with columns of demographic variables whereas **tm** stores raw text as a `Corpus` and annotates demographic information with Meta Data attributes. The structures are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

```r
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

```r
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

```r
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
## greg         1   0       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
## sam          0   1       0
## should       0   0       1
## stinks       0   1       0
## teacher      0   0       1
## too          0   1       0
## we           0   0       1
## what         0   0       1
## you          0   1       0
```

1.2.2 tm's Frequency Counts

```r
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 demographics 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 (19 terms, 3 groups)>>
##
## Non-/sparse entries       : 20/37
## Sparsity                  : 65%
## Maximal term length       : 8
## Less than four characters : 53%
## Hapax legomenon           : 16(84%)
## Dis legomenon             : 3(16%)
## Shannon's diversity index : 2.9
```

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.Corpus` function is used as follows:

```r
with(qdap_dat, as.Corpus(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:

```r
with(qdap_dat, as.Corpus(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:

```r
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:

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

```
## <<TermDocumentMatrix (terms: 19, documents: 3)>>
## Non-/sparse entries: 20/37
## Sparsity           : 65%
## Maximal term length: 8
## Weighting          : term frequency (tf)
```

```
## <<DocumentTermMatrix (documents: 3, terms: 19)>>
## Non-/sparse entries: 20/37
## 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.

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

```
##          doc 1 doc 2 doc 3 doc 4
## computer     1     0     0     0
## do           0     0     1     0
## doc          1     1     1     1
## 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
## greg         1   0       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
## sam          0   1       0
## should       0   0       1
## stinks       0   1       0
## teacher      0   0       1
## 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
## teacher      0   0       1
```

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

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

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

```
##      greg sam teacher
## dumb    1   0       0
## greg    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
## greg    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
## greg    1   0       0
## it's    2   0       0
## liar    0   1       0
## not     1   1       0
## sam     0   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
## greg    1   0       0
## it's    2   0       0
## liar    0   1       0
## sam     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 (43 terms, 4 groups)>>
##
## Non-/sparse entries       : 49/123
## Sparsity                  : 72%
## Maximal term length       : 8
## Less than four characters : 51%
## Hapax legomenon           : 32(74%)
## Dis legomenon             : 9(21%)
## Shannon's diversity index : 3.67
```

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)
```

```r
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

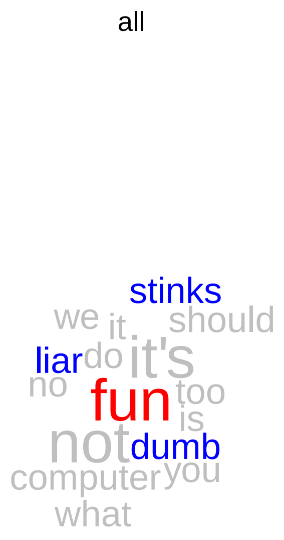
While the **tm** package (and other packages used on **tm** objects) tends to conduct analysis by feeding functions a `TermDocumentMatrix` or `DocumentTermMatrix` **qdap** generally feeds functions raw text directly. There are advantages to both approaches (e.g., the matrix is a mathematical structure 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:

```r
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"))
```



5.2 Further Examples to Try

Here are some further examples to try:

```r
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):

```r
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 Feinerer 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.

References

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Xie Y (2013). *knitr: A general-purpose package for dynamic report generation in R*. R package version 1.1, URL `http://yihui.name/knitr/`.