Using the koRpus Package for Corpus Analysis

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The R package `tm.plugin.koRpus` is an extension to the `koRpus` package, enhancing its usability for actual corpus analysis. It adds new classes and methods to `koRpus`, which are designed to work with complete text corpora in both `koRpus` and `tm` formats. This vignette gives you a quick overview.

1 What is tm.plugin.koRpus?

While the `koRpus` package focusses mostly on analysis steps of individual texts, `tm.plugin.koRpus` adds several new object classes and respective methods, which can be used to analyse complete text corpora in a single step. These classes are also a first step to combine object classes of both, the `koRpus` and `tm` packages.

There are three basic classes, which are hierarchically nested:

- class `kRp.topicCorpus` holds a list (named by topics) of objects of
  - class `kRp.sourcesCorpus`, which in its `sources` slot holds a list of objects of
    * class `kRp.corpus`, which in turn contains objects of both `koRpus` and `tm` classes.

The idea behind this is to be able to categorize corpora on at least two levels. The default assumes that these levels are different *sources* and different *topics*, but apart from this naming (which is coded into the classes) you can actually use this for whatever levels you like.

If you don't need these levels, you can just use the function `simpleCorpus()` to create objects of class `kRp.corpus`. It represents a flat corpus of texts. To distinguish texts which came from different sources, use the function `sourcesCorpus()`, which will generate sub-corpora for each source given. And one level higher up, use the function `topicCorpus()`, to sort `kRp.sourcesCorpus` objects by different topics. Objects of this class will only be valid if there are texts of each topic from each source.

2 Tokenizing corpora

As with koRpus, the first step for text analysis is tokenizing and possibly POS tagging. This step is performed by the functions mentioned above, simpleCorpus(), sourcesCorpus(), or topicCorpus(), respectively. The package includes four sample texts taken from Wikipedia[1] in its tests directory we can use for an elaborate demonstration:

```
> library(tm.plugin.koRpus)
> # set tha root path to the sample files
> sampleRoot <- file.path(path.package("tm.plugin.koRpus"), "tests",
+   "testthat", "samples")
> # now we can define the topics (names of the vector elements)
> # and their main path
> samplePaths <- c(
>   C3S=file.path(sampleRoot, "C3S"),
>   GEMA=file.path(sampleRoot, "GEMA")
> )
> # we also define the sources
> sampleSources <- c(
>   wpa="Wikipedia_alt",
>   wpn="Wikipedia_neu"
> )
> # and finally, we can tokenize all texts
> sampleTexts <- topicCorpus(paths=samplePaths, sources=sampleSources,
+   tagger="tokenize", lang="de")

processing topic "C3S", source "Wikipedia_alt", 1 texts...
processing topic "C3S", source "Wikipedia_neu", 1 texts...
processing topic "GEMA", source "Wikipedia_alt", 1 texts...
processing topic "GEMA", source "Wikipedia_neu", 1 texts...
```

Should you need to get hold of the nested objects inside kRp.sourcesCorpus or kRp.topicCorpus class objects, or replace them with updated ones, you can do so by using the methods corpusTagged(), corpusSources(), or corpusTopics():

```
> allC3SSources <- corpusSources(corpusTopics(sampleTexts, "C3S"))
> names(allC3SSources)

[1] "wpa" "wpn"
```

3 Analysing corpora

After the initial tokenizing, we can analyse the corpus by calling the provided methods, for instance lexical diversity:

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[1]see the file tests/testthat/samples/License_of_sample_texts.txt for details

```
> sampleTexts <- lex.div(sampleTexts, char=FALSE, quiet=TRUE)
> corpusSummary(sampleTexts)

               text   topic source CTTR HD-D (vocd-D) Herdan's C Maas a Maas lgV0
wpaC3S01    wpaC3S01   C3S    wpa 6.13       38.14        0.95   0.16       6.21
wpnC3S01    wpnC3S01   C3S    wpn 6.82       38.05        0.94   0.17       6.10
wpaGEMA01 wpaGEMA01   GEMA    wpa 7.07       37.61        0.94   0.17       6.11
wpnGEMA01 wpnGEMA01   GEMA    wpn 7.13       37.87        0.94   0.16       6.24
          MATTR MSTTR    MTLD MTLD-MA Root TTR Summer  TTR Uber index Yule's K
wpaC3S01   0.81  0.79 100.16      NA     8.68   0.93 0.78      39.92    49.92
wpnC3S01   0.82  0.76 123.01      NA     9.65   0.92 0.73      36.46    54.88
wpaGEMA01  0.80  0.78 106.94     192    10.00   0.92 0.71      35.96    65.08
wpnGEMA01  0.81  0.79 111.64      NA    10.08   0.92 0.73      37.47    60.14
```

As you can see, `corpusSummary()` fetches a data frame from the object which contains
the summarised results of all texts below the given object level. That is, if wou are
only interested in the results for texts of the first topic, simply apply `corpusSummary()`
on the result of `corpusTopics()`:

```
> corpusSummary(corpusTopics(sampleTexts, "C3S"))

             text   topic source CTTR HD-D (vocd-D) Herdan's C Maas a Maas lgV0
wpaC3S01 wpaC3S01   C3S    wpa 6.13       38.14        0.95   0.16       6.21
wpnC3S01 wpnC3S01   C3S    wpn 6.82       38.05        0.94   0.17       6.10
          MATTR MSTTR    MTLD MTLD-MA Root TTR Summer  TTR Uber index Yule's K
wpaC3S01   0.81  0.79 100.16      NA     8.68   0.93 0.78      39.92    49.92
wpnC3S01   0.82  0.76 123.01      NA     9.65   0.92 0.73      36.46    54.88
```

There are quite a number of `corpus*()` getter/setter methods for slots of these objects,
e.g., `corpusReadability()` to get the `readability()` results from objects of class
`kRp.corpus`.

Using the summary data.frame, you could now perform ANOVAs or plot interactions:

```
> library(sciplot)
> lineplot.CI(
+   x.factor=corpusSummary(sampleTexts)[["source"]],
+   response=corpusSummary(sampleTexts)[["MTLD"]],
+   group=corpusSummary(sampleTexts)[["topic"]],
+   type="l",
+   main="MTLD",
+   xlab="Media source",
+   ylab="Lexical diversity score",
+   col=c("grey", "black"),
+   lwd=2
+ )
```
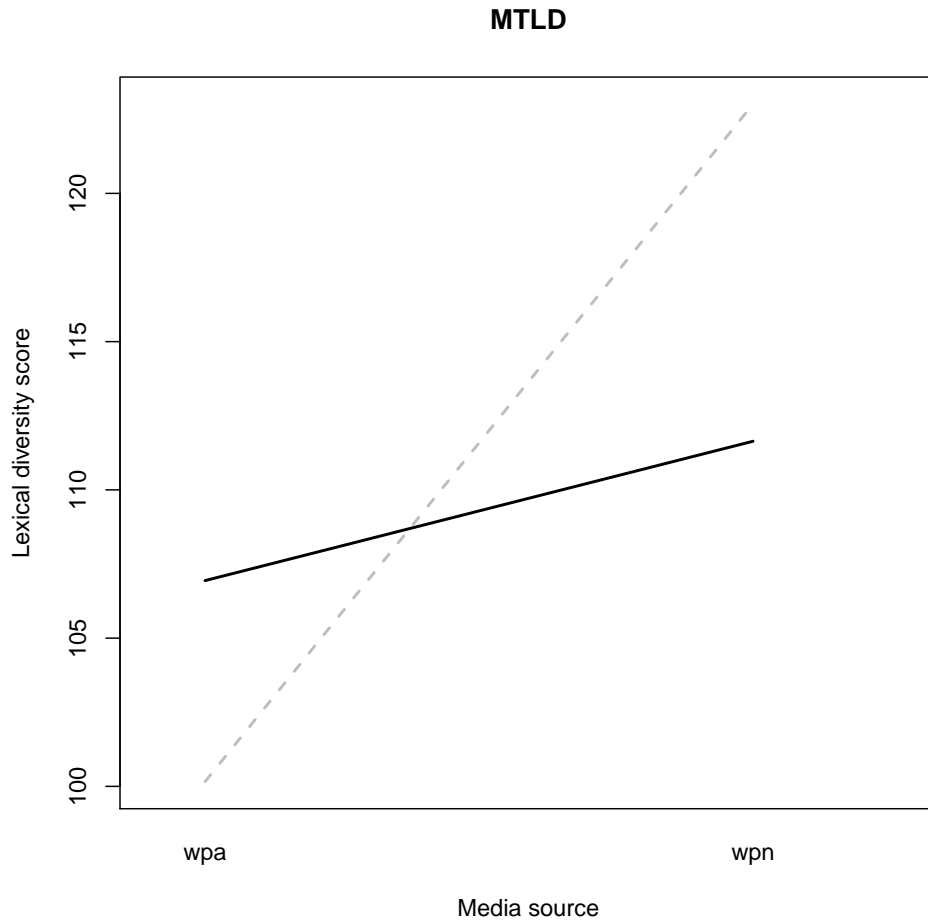
MTLD

Figure 1: Well, the example texts aren't so impressive here, as there's not much variance in one text per source and topic.

3.1 Frequency analysis

The object classes make it quite comfortable to analyse type frequencies of corpora. There is a method `read.corp.custom()` for these classes, that will do this analysis recursively on all levels:

```
> sampleTexts <- read.corp.custom(sampleTexts, caseSens=FALSE)
> sampleTextsWordFreq <- query(corpusFreq(sampleTexts), var="wclass",
+   query=kRp.POS.tags(lang="de", list.classes=TRUE, tags="words"))
```

```
> head(sampleTextsWordFreq, 10)

    num      word lemma        tag wclass lttr freq          pct  pmio    log10
3     3       die      word.kRp   word    3   30 0.037220844 37220 4.570776
4     4       der      word.kRp   word    3   21 0.026054591 26054 4.415874
5     5      gema      word.kRp   word    4   17 0.021091811 21091 4.324097
6     6       und      word.kRp   word    3   17 0.021091811 21091 4.324097
7     7     einer      word.kRp   word    5   12 0.014888337 14888 4.172836
8     8       von      word.kRp   word    3   12 0.014888337 14888 4.172836
11   11       ist      word.kRp   word    3   10 0.012406948 12406 4.093632
12   12       bei      word.kRp   word    3    9 0.011166253 11166 4.047898
13   13       das      word.kRp   word    3    8 0.009925558  9925 3.996731
14   14   urheber      word.kRp   word    7    8 0.009925558  9925 3.996731
   rank.avg rank.min rank.rel.avg rank.rel.min inDocs                idf
3     263.0      263     99.24528     99.24528      4                  0
4     262.0      262     98.86792     98.86792      4                  0
5     260.5      260     98.30189     98.11321      4                  0
6     260.5      260     98.30189     98.11321      4                  0
7     258.5      258     97.54717     97.35849      4                  0
8     258.5      258     97.54717     97.35849      4                  0
11    256.0      255     96.60377     96.22642      4                  0
12    254.0      254     95.84906     95.84906      4                  0
13    252.5      252     95.28302     95.09434      4                  0
14    252.5      252     95.28302     95.09434      2 0.301029995663981
```

In combination with the wordcloud package, this can directly be used to plot word clouds:

```
> require(wordcloud)
> colors <- brewer.pal(8, "RdGy")
> wordcloud(
+    head(sampleTextsWordFreq[["word"]], 200),
+    head(sampleTextsWordFreq[["freq"]], 200),
+    random.color=TRUE,
+    colors=colors
+  )
```

Figure 2: The 200 most frequent words in the example corpus