Guide to the ngram Package

Fast n-gram Tokenization

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GUIDE TO THE

ngram PACKAGE

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1 Introduction

An n-gram is an ordered sequence of n “words” taken from a body of text. For example, consider the string formed by the sequence of characters A B A C A B B. This is the “blood code” for the video game Mortal Kombat for the Sega Genesis, but you can pretend it’s a biological sequence or something boring if you prefer. If we examine the 2-grams (or bigrams) of this sequence, they are:

\[
\begin{align*}
A & \quad B, \\
B & \quad A, \\
A & \quad C, \\
C & \quad A, \\
A & \quad B, \\
B & \quad B
\end{align*}
\]

or without repetition:

\[
\begin{align*}
A & \quad B, \\
B & \quad A, \\
A & \quad C, \\
C & \quad A, \\
B & \quad B
\end{align*}
\]

That is, we take the input string and group the “words” 2 at a time (because \(n=2\)). If we form all of the n-grams and record the next “words” for each n-gram (and their frequency), then we can generate new text which has the same statistical properties as the input.

The ngram package (Schmidt, 2016) is an R package for constructing n-grams and generating new text as described above. It also contains a few preprocessing utilities to aid in this process. Additionally, the C code underlying this library can be compiled as a standalone shared library.

2 Installation

2.1 Installing from Source

The sourcecode for this package is available (and actively maintained) on GitHub. To install an R package from source on Windows, you will need to first install the Rtools package. To install an R package from source on a Mac, you will need to install the latest Xcode, which you can get from the App store.

The easiest way to install ngram from GitHub is via the devtools package by Hadley Wickham. To install ngram using devtools, simply issue the command:

```r
library(devtools)
install_github("wrlathematics/ngram")
```

from R.

2.2 Installing from CRAN

The usual

```r
install.packages("ngram")
```
from an R session should do it.

# 3 Background and Utilities

The n-gram processor in the `ngram` package changes its behavior depending on the way the input is formatted. If the input is given as a single string, n-grams crossing “sentence” boundaries will be considered valid. To prevent this from occurring, a vector of sentences may be used as input rather than a single string containing the entire text.

The n-gram tokenizer in the `ngram` package accepts a custom string containing characters to be used as word separators. There may be texts that use a wide variety of word separators, making it impractical to generate a string containing all of them.

The `ngram` package offers several useful utilities to simplify the text and assist with transforming the input to get the appropriate sentence handling behavior.

## 3.1 I/O

Generally speaking, the facilities in base R should be sufficient. Specifically, `readLines()` is a good choice for handling I/O of plain text files. However, for reading in multiple files (say, all `.txt` files in some directory), we offer a simple utility `multiread()`. This function will read all specified files into a named list, where the names are the filenames, and the values are the text contained in the given file as a single string.

So for example, if you want to read in all files ending in `.txt` at some directory/path of interest `path`, you could call:

```r
library(ngram)
multiread(path, extension="txt")
```

In `multiread()`, the extensions `*.txt`, `*txt`, `.txt`, and `txt` are all treated the same.

## 3.2 Concatenating Multiple Strings

Since the n-gram tokenizer expects only single strings, we offer the simple `concatenate()` function:

```r
> str(letters)
## chr [1:26] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j" ...

concatenate(letters)
## [1] "a b c d e f g h i j k l m n o p q r s t u v w x y z"

concatenate(concatenate(letters, collapse=""), letters)
```
So if data is coming from multiple files, the simplest way to merge them together would be to call `multiread()` (described above) if possible. Then you can call `concatenate()` directly on the returned list to produce a single string from all files, or use the tokenizer iteratively, using, say, an `lapply()`. Here is a more explicit example without the use of `multiread()`:

```r
x <- readLines("file1")
y <- readLines("file2")
str <- concatenate(x, y)
```

### 3.3 Splitting Strings

The `ngram` tokenizer always splits words at one or more of the characters provided in the `sep` argument. You can preprocess the input string with R’s regular expression utilities, such as `gsub()`. But for most tasks, the `preprocess()` and `charsplitter` utilities in the `ngram` package should be more than sufficient.

The `preprocess()` function is a simple utility for making letter case uniform, as well as optionally splitting at punctuation (so that punctuation itself becomes a “word” in the n-gram analysis). Here is a simple example:

```r
x <- "Watch out for snakes!

preprocess(x)
## [1] "watch out for snakes!"

preprocess(x, case=\"upper\", remove.punct=TRUE)
## [1] "WATCH OUT FOR SNAKES"
```

Perhaps more useful is the `charsplitter()` function. Suppose that for the purposes of n-gram tokenization, instead of wanting to call things separated by spaces “words”, you wish to treat every letter as a “word”. This could be accomplished by using `sep=""` when calling `ngram()`, but for the sake of introducing `charsplitter()`, it can also be done simply in this way:

```r
x <- "abacabb"
splitter(x, split.char=TRUE)
## [1] "a b a c a b b"
```

By default, this will preserve spaces as a special token (an underscore by default). You may wish to ignore spaces entirely during tokenization. This too is simple to handle during preprocessing:

```r
y <- "abacabb abacabb"
```


3.4 Dealing with tm

The *tm* package (Feinerer et al., 2008) requires that all data be in the form of its fairly complicated Corpus object. The *ngram* package offers no direct methods for dealing with data in this format. To use *tm*-encapsulated data, you will first need to extract it into a single string or a vector of strings depending on what processing behavior is required.

If you want to extract the text from all documents in a corpus as a single string, you can do something like:

```r
str <- concatenate(lapply(myCorpus, "[", 1))
```

3.5 Summarizing

While not strictly related to n-gram modeling, you may wish to get some basic summary counts of your text. With the assumption that the text is a single string with words separated by one or more spaces, we can very quickly generate these counts via the `string.summary()` function:

```r
x <- "a b a c a b b"
string.summary(x)
```

Now, this “model” is based only on very simple counts, and is easily fooled. For example, the sentence **S.T.A.R. Labs is a research facility in the DC comics universe.** would be
treated as though it were 5 separate sentences. However, the counts are constructed *extremely* quickly, and so they are still useful as a first pass in an analysis.

# 4 Using the Package

The general process for using the `ngram` package goes something like:

1. Prepare the input string; you may find the utilities in Section 3 useful.
2. Tokenize with the `ngram()` function.
3. Generate new text with `babble()`, and/or
4. Extract pieces of the processed ngram data with the `get.*()` functions.

## 4.1 Creating

Let us return to the example sequence of letters from Section 1. If we store this string in `x`:

```r
x <- "A B A C A B B"
```

The next step is to process with `ngram()`:

```r
library(ngram)
ng <- ngram(x, n=2)
```

Simple as that! And the tokenization was designed to be extremely fast; see Section 5 for benchmarks.

## 4.2 Printing

With `ng` as above, we can then inspect the sequence:

```r
ng
## An ngram object with 5 2-grams
```

If you don’t have too many n-grams, you may want to print all of them by calling `print()` directly, with the `print()` argument `output="full"`:

```r
print(ng, output="full")
## C A | 1
## B {1} |
##
## B A | 1
## C {1} |
##
```
Here we see each 3-gram, followed by its next possible “words” and each word’s frequency of occurrence following the given n-gram. So in the above, the first n-gram printed C A has B as a next possible word, because the sequence C A is only ever followed by the “word” B in the input string. On the other hand, A B is followed by A once and B once. The sequence B B is terminal, i.e. followed by nothing; we treat this case specially.

You may just wish to see the first few n-grams; this too is possible, but note that the order here is not particularly informative, in that the first n-gram shown is not necessarily the most/least common, etc. We can achieve this with the print() argument output="truncated". However, in our example, we only have 5 n-grams, and so we will not see any difference between printing with output="full" versus output="truncated". So we will construct a slightly more complicated example:

```r
## B B | 1
## NULL {1} |
## A C | 1
## A {1} |
## A B | 2
## A {1} | B {1} |

Here we see each 3-gram, followed by its next possible “words” and each word’s frequency of occurrence following the given n-gram. So in the above, the first n-gram printed C A has B as a next possible word, because the sequence C A is only ever followed by the “word” B in the input string. On the other hand, A B is followed by A once and B once. The sequence B B is terminal, i.e. followed by nothing; we treat this case specially.

You may just wish to see the first few n-grams; this too is possible, but note that the order here is not particularly informative, in that the first n-gram shown is not necessarily the most/least common, etc. We can achieve this with the `print()` argument output="truncated". However, in our example, we only have 5 n-grams, and so we will not see any difference between printing with output="full" versus output="truncated". So we will construct a slightly more complicated example:

```
Once the ngram representation of the text has been generated, it is very simple to get some interesting summary information. The function `get.phrasetable()` generates a “phrasetable”, or more explicitly, a table of n-grams, and their frequency and proportion in the text:

```r
get.phrasetable(ng)
```

We can perhaps better see the value of this in a more interesting string:

```r
set.seed(12345)
text <- rcorpus(100, alphabet = letters[1:3], maxwordlen = 1)
text
```

```{r}
# head(get.phrasetable(ngram(text, n = 3)))
```

Presently, there are two other “getters”, namely `get.ngrams()` and `get.string()`. Each of these basically does what it sounds like. The first produces the unique n-grams as a vector of strings (in no particular order), while the second produces the input string that was used during tokenization:

```r
> get.ngrams(ng)
[1] "C A" "B A" "B B" "A C" "A B"
```
4.4 Babbling

We might want to use n-grams as god intended: amusement. We can easily generate new strings with the same statistical properties as the input strings via a very simple markov chain/sampling scheme. We for this, we use `babble()`:

```r
babble(ng, 10)
babble(ng, 10)
babble(ng, 10)
```

This generation includes a random process. For this, we developed our own implementation of MT19937, and so R’s seed management does not apply. To specify your own seed, use the `seed=` argument:

```r
babble(ng, 10, seed=10)
babble(ng, 10, seed=10)
babble(ng, 10, seed=10)
```

4.5 Important Notes About the Internal Representation

The entirety of the interesting bits of the `ngram` package take place outside of R (completely in C). Observe:

```r
str(ng)
## Formal class 'ngram' [package "ngram"] with 6 slots
## ..@ str_ptr:<externalptr>
## ..@ strlen : int 1
## ..@ n : int 2
## ..@ ngl_ptr:<externalptr>
## ..@ ngsize : int 5
## ..@ sl_ptr :<externalptr>
```

So everything is wrangled up top as an S4 class, and underneath the data is stored as 2 linked lists, outside the purview of R. This means that, for example, that you cannot save the n-gram object with a call to `save()`. If you do and you shut down and restart R, the pointers will no longer be valid.
Extracting a the data into a native R data structure is not currently possible. Full support is planned for a later release. Some pieces can be extracted. At this time, `get.ngrams()` and `get.string()` are implemented, but `get.nextwords()` is not.

```r
get.nextwords(ng)
# Error in .local(ng, ...) : Not yet implemented
```

## 5 Benchmarks

### 5.1 tau

The `tau` (Buchta et al., 2015) package offers, among other things, a framework for constructing n-grams from a text, via its `textcnt()` function.

In `ngram`, the use of `get.phrasetable(ngram(x, n=3))` roughly corresponds to `textcnt(x, n=3, split=" ", method="string")` in `tau`. Although `get.phrasetable()` returns proportions in addition to counts, and in the form of a more costly dataframe compared to `tau`'s vector of counts, we are still able to achieve very good performance.

```r
library(rbenchmark)
library(tau)
library(ngram)

x <- ngram::rcorpus(50000)
reps <- 15
cols <- c("test", "replications", "elapsed", "relative")
benchmark(tau=textcnt(x, n=3, split=" ", method="string"),
          ngram=get.phrasetable(ngram(x, n=3)), replications=reps,
          columns=cols)
```

Evaluating this script gives:

```
## test replications elapsed relative
## 2 ngram 15 0.958 1.000
## 1 tau 15 137.994 144.044
```

In fact, a good portion of the time in the `ngram` runs here is in converting the internal C data structure over to an R one. The original purpose of the `ngram` package was merely amusement, babbling n-grams. If we just compare the run times for this, the difference is striking:

```r
library(tau)
library(ngram)
x <- ngram::rcorpus(100000)
```
tautime <- system.time(pt1 <- textcnt(x, n=3, split=" ", method="string"))[3]
ngtime <- system.time(pt2 <- ngram(x, n=3))[3]
cat("tau: ", tautime, "\n")
cat("ngram: ", ngtime, "\n")
cat("tau/ngram: ", tautime/ngtime, "\n")

If we evaluate this, we see:
```
## tau: 36.576
## ngram: 0.048
## tau/ngram: 762
```

Here, ngram is primed for babbling, in that it has already stored all “next words”, while tau only contains what we call the phrasetable of 3-grams.

### 5.2 RWeka

The ngram package has a separate tokenizer to produce returns similar to those in the RWeka package. However, ngram is significantly faster:
```
library(memuse)
library(ngram)
library(RWeka)
x = ngram::rcorpus(nwords=1e6, alphabet="a")
memuse(x)
## 4.292 MiB

system.time(ngram_asweka(x, min=2, max=2))
## user  system elapsed
##   0.216 0.044  0.261

system.time(NGramTokenizer(x, Weka_control(min=2, max=2)))
## user  system elapsed
##  500.228  0.528  500.056
```
References

