Chapter 30: Pattern Matching and Replacement

This topic covers matching string patterns, as well as extracting or replacing them. For details on defining complicated patterns see Regular Expressions.

Section 30.1: Finding Matches

```
# example data
test_sentences <- c("The quick brown fox", "jumps over the lazy dog")</pre>
```

Is there a match?

grep1() is used to check whether a word or regular expression exists in a string or character vector. The function returns a TRUE/FALSE (or "Boolean") vector.

Notice that we can check each string for the word "fox" and receive a Boolean vector in return.

```
grepl("fox", test_sentences)
#[1] TRUE FALSE
```

Match locations

grep takes in a character string and a regular expression. It returns a numeric vector of indexes. This will return which sentence contains the word "fox" in it.

```
grep("fox", test_sentences)
#[1] 1
```

Matched values

To select sentences that match a pattern:

```
# each of the following lines does the job:
test_sentences[grep("fox", test_sentences)]
test_sentences[grep1("fox", test_sentences)]
grep("fox", test_sentences, value = TRUE)
# [1] "The quick brown fox"
```

Details

Since the "fox" pattern is just a word, rather than a regular expression, we could improve performance (with either grep or grep1) by specifying fixed = TRUE.

```
grep("fox", test_sentences, fixed = TRUE)
#[1] 1
```

To select sentences that don't match a pattern, one can use **grep** with invert = TRUE; or follow subsetting rules with -grep(...) or !grep1(...).

In both grepl(pattern, x) and grep(pattern, x), the x parameter is vectorized, the pattern parameter is not. As a result, you cannot use these directly to match pattern[1] against x[1], pattern[2] against x[2], and so on.

Summary of matches

After performing the e.g. the **grep1** command, maybe you want to get an overview about how many matches where TRUE or FALSE. This is useful e.g. in case of big data sets. In order to do so run the **summary** command:

```
# example data
test_sentences <- c("The quick brown fox", "jumps over the lazy dog")

# find matches
matches <- grep1("fox", test_sentences)

# overview
summary(matches)</pre>
```

Section 30.2: Single and Global match

When working with regular expressions one modifier for PCRE is g for global match.

In R matching and replacement functions have two version: first match and global match:

- sub(pattern, replacement, text) will replace the first occurrence of pattern by replacement in text
- gsub(pattern, replacement, text) will do the same as sub but for each occurrence of pattern
- regexpr(pattern, text) will return the position of match for the first instance of pattern
- gregexpr(pattern, text) will return all matches.

Some random data:

```
set.seed(123)
teststring <- paste0(sample(letters,20),collapse="")
# teststring
#[1] "htjuwakqxzpgrsbncvyo"</pre>
```

Let's see how this works if we want to replace vowels by something else:

```
sub("[aeiouy]"," ** HERE WAS A VOWEL** ",teststring)
#[1] "htj ** HERE WAS A VOWEL** wakqxzpgrsbncvyo"

gsub("[aeiouy]"," ** HERE WAS A VOWEL** ",teststring)
#[1] "htj ** HERE WAS A VOWEL** w ** HERE WAS A VOWEL** kqxzpgrsbncv ** HERE WAS A VOWEL** ** HERE
WAS A VOWEL** "
```

Now let's see how we can find a consonant immediately followed by one or more vowel:

```
regexpr("[^aeiou][aeiou]+",teststring)
#[1] 3
#attr(,"match.length")
#[1] 2
#attr(,"useBytes")
#[1] TRUE
```

We have a match on position 3 of the string of length 2, i.e. ju

Now if we want to get all matches:

```
gregexpr("[^aeiou][aeiou]+",teststring)
#[[1]]
#[1] 3 5 19
#attr(,"match.length")
#[1] 2 2 2
```

```
#attr(,"useBytes")
#[1] TRUE
```

All this is really great, but this only give use positions of match and that's not so easy to get what is matched, and here comes regmatches it's sole purpose is to extract the string matched from regexpr, but it has a different syntax.

Let's save our matches in a variable and then extract them from original string:

```
matches <- gregexpr("[^aeiou][aeiou]+",teststring)
regmatches(teststring,matches)
#[[1]]
#[1] "ju" "wa" "yo"</pre>
```

This may sound strange to not have a shortcut, but this allow extraction from another string by the matches of our first one (think comparing two long vector where you know there's is a common pattern for the first but not for the second, this allow an easy comparison):

```
teststring2 <- "this is another string to match against"
regmatches(teststring2, matches)
#[[1]]
#[1] "is" " i" "ri"</pre>
```

Attention note: by default the pattern is not Perl Compatible Regular Expression, some things like lookarounds are not supported, but each function presented here allow for perl=TRUE argument to enable them.

Section 30.3: Making substitutions

```
# example data
test_sentences <- c("The quick brown fox quickly", "jumps over the lazy dog")</pre>
```

Let's make the brown fox red:

Now, let's make the "fast" fox act "fastly". This won't do it:

sub only makes the first available replacement, we need gsub for global replacement:

See Modifying strings by substitution for more examples.

Section 30.4: Find matches in big data sets

In case of big data sets, the call of grep1("fox", test_sentences) does not perform well. Big data sets are e.g. crawled websites or million of Tweets, etc.

The first acceleration is the usage of the perl = TRUE option. Even faster is the option fixed = TRUE. A complete example would be:

```
# example data
test_sentences <- c("The quick brown fox", "jumps over the lazy dog")

grepl("fox", test_sentences, perl = TRUE)
#[1] TRUE FALSE</pre>
```

In case of text mining, often a corpus gets used. A corpus cannot be used directly with **grep1**. Therefore, consider this function:

```
searchCorpus <- function(corpus, pattern) {
  return(tm_index(corpus, FUN = function(x) {
    grepl(pattern, x, ignore.case = TRUE, perl = TRUE)
  }))
}</pre>
```