```
R version 3.3.1 (2016-06-21) -- "Bug in Your Hair"
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Platform: x86_64-w64-mingw32/x64 (64-bit)

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  Natural language support but running in an English locale

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Type 'contributors()' for more information and
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Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> library(memisc)
Loading required package: lattice
Loading required package: MASS

Attaching package: 'memisc'

The following objects are masked from 'package:stats':

    contr.sum, contr.treatment, contrasts

The following object is masked from 'package:base':

    as.array

> library(stringi)
> #options(error=recover)
> project_folder<-"D:\\OPS\\cchs_analysis"
> new_dir<-setwd(project_folder)
> load(file="CCHS_2014.sav")
> vbl1<-description(cchs2014.ds)
> vbl2<-stri_replace_fixed(vbl1,"**","\'")
Error: could not find function "stri_replace_fixed"
> vbl2<-stri_replace_all_fixed(vbl1,"**","\'")
> # the problem is that vbl2 has lost the attributes of your variables, it is just a character ve
ctor
> # with one entry per variable.
> # if there any way other than a for loop (there must be) that would let me replace the descript
ions in order in my ds with the elements  of vbl2
> description(cchs2014.ds)<-vbl2
Error in (function (classes, fdef, mtable)  :
  unable to find an inherited method for function 'annotation<-' for signature '"data.set", "anno
tation.list"'
In addition: Warning message:
In annotation(x)["description"] <- value :
  number of items to replace is not a multiple of replacement length
> length(vbl2)
[1] 1129
> length(vbl1)
[1] 1129
> length(description(cchs2014.ds))
[1] 1129
>
```