R Notebook

Setting global options for chunks and knitr

Load packages needed

```r
library(devtools)
library(sinew)
```

Initialize a new package

```r
devtools::create('test')
knitr::opts_knit$set(root.dir = 'test')
```

Add some basics: Package License and `data_raw` subdirectory

```r
devtools::use_mit_license('test')
devtools::use_data_raw('test')
```

Write the toy functions to `data_raw/test.R`

```r
cat('#some comment
yy <- function(a=4){
  head(runif(10),a)
  # a comment
}

zz <- function(v=10,a=8){
  head(runif(v),a)
}

yy(6)

zz(30,3)',sep='\n',file='test/data-raw/test.R')
```

What does the RStudio skeleton look like?

`Shift+Alt+Cmd+R` (macOS)

```r
#' Title
#'
#' @param a
#'
#' @return
#' @export
#'
#' @examples
yy <- function(a=4){
  head(runif(10),a)
  # a comment
}
```

Split the `tests/data-raw/test.R` into single R files in the `test/R` subdirectory

```r
sinew::untangle(file = 'test/data-raw/test.R',dir.out = 'test/R',keep.body = FALSE)
```

Append the appropriate namespaces to the functions

```
sinew::pretty_namespace('test/R')

sinew::pretty_namespace('test/R',overwrite = TRUE)
```

Create sinew roxygen2 skeletons populated with information from within the functions.

And replace the placeholders with information.

```
sinew::makeOxyFile(input = 'test/R/yy.R',overwrite = FALSE)

file.remove('test/R/oxy-yy.R')

sinew::makeOxyFile(input = 'test/R',overwrite = TRUE)
```

Append to the `DESCRIPTION` file the the `imports` field

```
sinew::makeImport('test/R',format = 'description',desc_loc = 'test')

rstudioapi::navigateToFile('test/DESCRIPTION')
```

Looking back yy should have a summary function

```
yy <- function(a=4,b=2){

  x <- utils::head(stats::runif(10*b),a)

  stats::quantile(x,probs=.95)

  # a comment
}
```

Now the roxygen2 header is not in synch with the function. Use `sinew::moga` to update the roxygen2 header with new formals and import fields. Make Oxygen Great Again (moga)

```
sinew::moga(path = 'test/R/yy.r',overwrite = FALSE)

sinew::moga(path = 'test/R/yy.r',overwrite = FALSE,force.fields = 'seealso')

sinew::moga(path = 'test/R/yy.r',overwrite = TRUE,force.fields = 'seealso')
```

Compile the roxygen2 headers into Rd files in `man` and update the `NAMESPACE` file

```
devtools::document(pkg = 'test')
```

Run R CMD check --as-cran

```
devtools::check(pkg = 'test',cran = TRUE)
```

Install the package, look at the documentation and run the functions.

```
devtools::install('test')

library(test)

?test::yy

?test::zz

test::yy()
```

```
test::zz()
```

Interactive sinew

```
rstudioapi::navigateToFile('test/R/yy.R')
```