

# Comparison of TAF and icesTAF

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## Preamble

```
library(diff)
tools.prod <- "~/git/ices/tools-prod"
```

## 1 R directory

```
diff_dir(tools.prod)
```

```
## $TAF
## [1] "TAF-internal.R" "TAF-package.R"
##
## $icesTAF
## [1] "draft.data.script.R" "icesTAF-internal.R" "icesTAF-package.R"
## [4] "taf.roxygenise.R"
```

Check out these files:

1. draft.data.script.R
2. taf.roxygenise.R

## 2 Namespace

```
diff_namespace(tools.prod)
```

```
## $TAF
## character(0)
##
## $icesTAF
## [1] "S3method(roxy_tag_parse,roxy_tag_tafAccess)"
## [2] "S3method(roxy_tag_parse,roxy_tag_tafKey)"
## [3] "S3method(roxy_tag_parse,roxy_tag_tafOriginator)"
## [4] "S3method(roxy_tag_parse,roxy_tag_tafPeriod)"
## [5] "S3method(roxy_tag_parse,roxy_tag_tafSource)"
## [6] "S3method(roxy_tag_parse,roxy_tag_tafYear)"
## [7] "export(draft.data.script)"
## [8] "export(taf.roxygenise)"
## [9] "importFrom(glue,glue)"
## [10] "importFrom(jsonlite,parse_json)"
## [11] "importFrom(purrr,flatten)"
## [12] "importFrom(roxygen2,roxy_tag_parse)"
```

Check out these entries:

1. `export(draft.data.script)`
2. `export(taf.roxygenise)`
  - `S3method(roxy_tag_parse,roxy_tag_tafAccess)`
  - `S3method(roxy_tag_parse,roxy_tag_tafKey)`
  - `S3method(roxy_tag_parse,roxy_tag_tafOriginator)`
  - `S3method(roxy_tag_parse,roxy_tag_tafPeriod)`
  - `S3method(roxy_tag_parse,roxy_tag_tafSource)`
  - `S3method(roxy_tag_parse,roxy_tag_tafYear)`

### 3 Environment

```
diff_environment()
```

```
## $TAF
## character(0)
##
## $icesTAF
## [1] "draft.data.script"
## [2] "list2bibtex"
## [3] "loadpkg"
## [4] "roclet_output.roclet_taf"
## [5] "roclet_process.roclet_taf"
## [6] "roxy_tag_parse.roxy_tag_tafAccess"
## [7] "roxy_tag_parse.roxy_tag_tafKey"
## [8] "roxy_tag_parse.roxy_tag_tafOriginator"
## [9] "roxy_tag_parse.roxy_tag_tafPeriod"
## [10] "roxy_tag_parse.roxy_tag_tafSource"
## [11] "roxy_tag_parse.roxy_tag_tafYear"
## [12] "taf_roclet"
## [13] "taf.roxygenise"
```

Check out these objects:

1. draft.data.script
2. taf.roxygenise
  - list2bibtex
  - loadpkg
  - roclet\_output.roclet\_taf
  - roclet\_process.roclet\_taf
  - roxy\_tag\_parse.roxy\_tag\_tafAccess
  - roxy\_tag\_parse.roxy\_tag\_tafKey
  - roxy\_tag\_parse.roxy\_tag\_tafOriginator
  - roxy\_tag\_parse.roxy\_tag\_tafPeriod
  - roxy\_tag\_parse.roxy\_tag\_tafSource
  - roxy\_tag\_parse.roxy\_tag\_tafYear
  - taf\_roclet

## 4 R files

```
files <- intersect(dir(file.path(tools.prod, "TAF/R")),
                  dir(file.path(tools.prod, "icesTAF/R")))
diffs <- sapply(files, diff_file, tools.prod=tools.prod)

## Warning in readLines(file.path(tools.prod, "icesTAF/R", file)): incomplete final
## line found on '~/git/ices/tools-prod/icesTAF/R/process.entry.R'

diffs <- diffs[!sapply(diffs, is.null)]
names(diffs)

## [1] "catage.long.R"      "catage.taf.R"      "catage.xtab.R"
## [4] "detach.packages.R" "download.github.R" "download.R"
## [7] "draft.data.R"      "draft.software.R"  "get.remote.sha.R"
## [10] "line.endings.R"    "makeAll.R"         "makeTAF.R"
## [13] "process.entry.R"   "read.bib.R"        "sourceAll.R"
## [16] "sourceTAF.R"       "summary.taf.R"     "taf.colors.R"
## [19] "taf.library.R"     "taf.skeleton.R"    "taf.sources.R"
```

Based on the `diff_file` output, 21 R files are different.

Let's look at each R file that is different. In many cases, the difference is trivial, often from development responding to CRAN feedback when we submitted the TAF package, so we can keep the TAF version. In other cases, where discussion and/or action is needed, the  $\Rightarrow$  sign is used and the difference is highlighted and discussed in the next section.

```
diffs[1]
```

```
## $catage.long.R
## $catage.long.R$TAF
## [1] "' ICES (2016)."
```

## [2] "' Report of the working group on the assessment of demersal stocks in the North"

## [3] "' Sea and Skagerrak (WGNSSK)."

## [4] "' \\emph{ICES CM 2016/ACOM:14}, p. 673."

## [5] "' \\doi{10.17895/ices.pub.5329}."

##

```
## $catage.long.R$icesTAF
## [1] "' ICES (2016) Report of the working group on the assessment of demersal stocks"
## [2] "' in the North Sea and Skagerrak (WGNSSK)."
```

## [3] "' \\href{https://doi.org/10.17895/ices.pub.5329}-{\\emph{ICES CM 2016/ACOM:14}},"

## [4] "' p. 673."

(Trivial)

```
diffs[2]
```

```
## $catage.taf.R
## $catage.taf.R$TAF
## [1] "' ICES (2016).'"
## [2] "' Report of the working group on the assessment of demersal stocks in the North"
## [3] "' Sea and Skagerrak (WGNSSK).'"
## [4] "' \\emph{ICES CM 2016/ACOM:14}, p. 673.'"
## [5] "' \\doi{10.17895/ices.pub.5329}.'"
##
## $catage.taf.R$icesTAF
## [1] "' ICES (2016) Report of the working group on the assessment of demersal stocks"
## [2] "' in the North Sea and Skagerrak (WGNSSK).'"
## [3] "' \\href{https://doi.org/10.17895/ices.pub.5329}{\\emph{ICES CM 2016/ACOM:14}},"
## [4] "' p. 673.'"

```

(Trivial)

```
diffs[3]
```

```
## $catage.xtab.R
## $catage.xtab.R$TAF
## [1] "' ICES (2016)."
```

## [2] "' Report of the working group on the assessment of demersal stocks in the North"

## [3] "' Sea and Skagerrak (WGNSSK)."

## [4] "' \\emph{ICES CM 2016/ACOM:14}, p. 673."

## [5] "' \\doi{10.17895/ices.pub.5329}."

##

```
## $catage.xtab.R$icesTAF
## [1] "' ICES (2016) Report of the working group on the assessment of demersal stocks"
```

## [2] "' in the North Sea and Skagerrak (WGNSSK)."

## [3] "' \\href{https://doi.org/10.17895/ices.pub.5329}{\\emph{ICES CM 2016/ACOM:14}},"

## [4] "' p. 673."

(Trivial)



```
diffs[4]
```

```
## $detach.packages.R  
## $detach.packages.R$TAF  
## [1] '#' @return Names of detached packages."
```

```
(Trivial)
```

```
diffs[5]
```

```
## $download.github.R
## $download.github.R$TAF
## [1] "' download.github(\"ices-tools-prod/icesAdvice@1.3-0\")"
## [2] "' download.github(\"ices-tools-prod/icesAdvice@4271797\")"
##
## $download.github.R$icesTAF
## [1] "' download.github(\"ices-tools-prod/icesTAF@2.0-0\")"
## [2] "' download.github(\"ices-tools-prod/icesTAF@d5a8947\")"
```

(Trivial)

```
diffs[6]
```

```
## $download.R
## $download.R$TAF
## [1] '#'          "\"bootstrap/initial/software/catageysa/catageysa.exe\""
##
## $download.R$icesTAF
## [1] '#'          "\"bootstrap/initial/software/catageysa.exe\""
```

(Trivial)

```
diffs[7]
```

```
## $draft.data.R  
## $draft.data.R$TAF  
## [1] " ## TAF:::access.vocab is a string vector of allowed 'access' values"  
##  
## $draft.data.R$icesTAF  
## [1] " ## icesTAF:::access.vocab is a string vector of allowed 'access' values"  
(Trivial)
```

```
diffs[8]
```

```
## $draft.software.R
## $draft.software.R$TAF
## [1] "' draft.software(\"TAF\")"
## [2] "' draft.software(\"TAF\", file=TRUE)"
##
## $draft.software.R$icesTAF
## [1] "' draft.software(\"icesTAF\")"
## [2] "' draft.software(\"icesTAF\", file=TRUE)"
```

(Trivial)

```
diffs[9]
```

```
## $get.remote.sha.R
## $get.remote.sha.R$TAF
## [1] "' get.remote.sha(\"ices-tools-prod\", \"icesAdvice\", \"master\")"
## [2] "' get.remote.sha(\"ices-tools-prod\", \"icesAdvice\", \"1.3-0\")"
## [3] "' get.remote.sha(\"ices-tools-prod\", \"icesAdvice\", \"1.3-0\", seven=FALSE)"
##
## $get.remote.sha.R$icesTAF
## [1] "' get.remote.sha(\"ices-tools-prod\", \"icesTAF\", \"master\")"
## [2] "' get.remote.sha(\"ices-tools-prod\", \"icesTAF\", \"3.0-0\")"
## [3] "' get.remote.sha(\"ices-tools-prod\", \"icesTAF\", \"3.0-0\", seven=FALSE)"
```

(Trivial)

```
diffs[10]
```

```
## $line endings.R  
## $line endings.R$TAF  
## [1] "' file <- system.file(package=\"TAF\", \"DESCRIPTION\")"  
##  
## $line endings.R$icesTAF  
## [1] "' file <- system.file(package=\"icesTAF\", \"DESCRIPTION\")"
```

(Trivial)

```
diffs[11]
```

```
## $makeAll.R
## $makeAll.R$TAF
## [1] "' TAF scripts that will be run as needed: \\verb{utilities.R}, \\verb{data.R},"
## [2] "' \\verb{model.R}, \\verb{output.R}, and \\verb{report.R}."
## [3] "  scripts <- c(\"utilities.R\", \"data.R\", \"model.R\", \"output.R\", \"report.R\")"
##
## $makeAll.R$icesTAF
## [1] "' TAF scripts that will be run as needed: \\verb{data.R}, \\verb{model.R},"
## [2] "' \\verb{output.R}, and \\verb{report.R}."
## [3] "  scripts <- c(\"data.R\", \"model.R\", \"output.R\", \"report.R\")"
```

(Trivial)



```
diffs[12]
```

```
## $makeTAF.R
```

```
## $makeTAF.R$TAF
```

```
## [1] "          utilities.R=sourceTAF(\"utilities.R\"),"
```

```
(Trivial)
```

```
diffs[13]
```

```
## $process.entry.R
## $process.entry.R$TAF
## [1] "    ## TAF:::access.vocab is a string vector of allowed 'access' values"
## [2] "    script <- file_path_as_absolute(paste0(key, \".R\"))"
##
## $process.entry.R$icesTAF
## [1] "    ## icesTAF:::access.vocab is a string vector of allowed 'access' values"
## [2] "    script <- tools::file_path_as_absolute(paste0(key, \".R\"))"
```

(Trivial)

diffs[14]

```
## $read.bib.R
## $read.bib.R$TAF
## [1] " # remove comments (# or %)"
## [2] " x <- x[!grepl(\"^\\\\s*[%#].*$\", x)]"
## [3] " # remove empty lines"
## [4] " x <- trimws(x)"
## [5] " x <- x[nzchar(x)]"
## [6] " x <- paste(c(\"}\", x), collapse = \"\")"
## [7] " x <- paste0(\"@\", strsplit(x, \"\\\\}\\s*\")[1][-1], \"}\")"
## [8] "       y <- gsub(\"\\\\s*=\\\\s*\\\\{\\\\s*\", \"\\\\\" = \"\\\\\"\", y)"
## [9] "       paste0(\"list(\" , paste(paste0(\"\\\\\"\", y, \"\\\\\"\"), collapse = \",\"), \"\")")
## [10] " x <- paste0(\"list(\" , paste(x, collapse = \",\"), \"\")")
## [11] " bib <- eval(parse(text = x))"
##
## $read.bib.R$icesTAF
## [1] \"#' @importFrom jsonlite parse_json"
## [2] " # remove comments"
## [3] " x <- paste(x[!grepl(\"^\\\\s*[%#].*$\", x)], collapse = \"\")"
## [4] " x <- paste0(\"@\", strsplit(x, \"\\\\}\\s*\")[1], \"}\")"
## [5] "       y <- gsub(\"\\\\s*=\\\\s*\\\\{\\\\s*\", \"\\\\\":\\\\\"\", y)"
## [6] "       paste0(\"{\", paste(paste0(\"\\\\\"\", y, \"\\\\\"\"), collapse = \",\"), \"}\")"
## [7] " x <- paste0(\"[\", paste(x, collapse = \",\"), \"]\")"
## [8] " bib <- jsonlite::parse_json(x)"
```

⇒ This rewrite of `read.bib` (22 Mar 2021, Colin) removed the dependency on the **jsonlite** package.

The **icesTAF** package has the old `read.bib` (28 Oct 2020, Colin) version that depends on **jsonlite**. Implementing **icesTAF** as a layer on top of **TAF**, this version will disappear.

```
diffs[15]
```

```
## $sourceAll.R
## $sourceAll.R$TAF
## [1] "' TAF scripts that will be run if they exist: \\verb{utilities.R},"
##
## $sourceAll.R$icesTAF
## [1] "' TAF scripts that will be run if they exist: \\verb{utilities.R}"
(Trivial)
```

```
diffs[16]
```

```
## $sourceTAF.R
## $sourceTAF.R$TAF
## [1] '#' sure that only files, not objects in memory, are carried over between"
## [2] '#' scripts."
##
## $sourceTAF.R$icesTAF
## [1] '#' sure that only files, not objects, are carried over between scripts."
(Trivial)
```

```
diffs[17]
```

```
## $summary.taf.R
## $summary.taf.R$TAF
## [1] "' ICES (2016).'"
## [2] "' Report of the working group on the assessment of demersal stocks in the North"
## [3] "' Sea and Skagerrak (WGNSSK).'"
## [4] "' \\emph{ICES CM 2016/ACOM:14}, p. 673.'"
## [5] "' \\doi{10.17895/ices.pub.5329}.'"
##
## $summary.taf.R$icesTAF
## [1] "' ICES (2016) Report of the working group on the assessment of demersal stocks"
## [2] "' in the North Sea and Skagerrak (WGNSSK).'"
## [3] "' \\href{https://doi.org/10.17895/ices.pub.5329}{\\emph{ICES CM 2016/ACOM:14}},"
## [4] "' p. 673.'"

```

(Trivial)

```
diffs[18]

## $taf.colors.R
## $taf.colors.R$TAF
## [1] "' opar <- par(mfrow=c(3,1))" "' par(opar)"
##
## $taf.colors.R$icesTAF
## [1] "' par(mfrow=c(3,1))"

(Trivial)
```

```
diffs[19]
```

```
## $taf.library.R  
## $taf.library.R$icesTAF  
## [1] '#' @importFrom utils installed.packages"
```

```
(Trivial)
```



```
diffs[20]
```

```
## $taf.skeleton.R
## $taf.skeleton.R$TAF
## [1] "          \"library(TAF)\\n\\nmkdir(\\\\"%s\\")\\n\\n\""
##
## $taf.skeleton.R$icesTAF
## [1] "          \"library(icesTAF)\\n\\nmkdir(\\\\"%s\\")\\n\\n\""
(Trivial)
```

```
diffs[21]
```

```
## $taf.sources.R  
## $taf.sources.R$TAF  
## [1] '#' @return List of metadata entries."
```

(Trivial)

## 5 Discussion and actions

diffs[14]

```
## $read.bib.R
## $read.bib.R$TAF
## [1] " # remove comments (# or %)"
## [2] " x <- x[!grepl(\"^\\\\s*[%#].*$\", x)]"
## [3] " # remove empty lines"
## [4] " x <- trimws(x)"
## [5] " x <- x[nzchar(x)]"
## [6] " x <- paste(c(\"}\", x), collapse = \"\")"
## [7] " x <- paste0(\"@\", strsplit(x, \"\\\\}\\s*@\" )[[1]][-1], \"}\")"
## [8] "       y <- gsub(\"\\\\s*=\\\\s*\\\\{\\\\s*\", \"\\\\\" = \"\\", y)"
## [9] "       paste0(\"list(\" , paste(paste0(\"\\\\\"\", y, \"\\\\\"\"), collapse = \",\"), \")\")"
## [10] " x <- paste0(\"list(\" , paste(x, collapse = \",\"), \")\")"
## [11] " bib <- eval(parse(text = x))"
##
## $read.bib.R$icesTAF
## [1] \"' @importFrom jsonlite parse_json"
## [2] " # remove comments"
## [3] " x <- paste(x[!grepl(\"^\\\\s*[%#].*$\", x)], collapse = \"\")"
## [4] " x <- paste0(\"@\", strsplit(x, \"\\\\}\\s*@\" )[[1]], \"}\")"
## [5] "       y <- gsub(\"\\\\s*=\\\\s*\\\\{\\\\s*\", \"\\\\\":\\\\\"\", y)"
## [6] "       paste0(\"{\", paste(paste0(\"\\\\\"\", y, \"\\\\\"\"), collapse = \",\"), \"}\")"
## [7] " x <- paste0(\"[\", paste(x, collapse = \",\"), \"]\")"
## [8] " bib <- jsonlite::parse_json(x)"
```

⇒ This rewrite of `read.bib` (22 Mar 2021, Colin) removed the dependency on the **jsonlite** package.

The **icesTAF** package has the old `read.bib` (28 Oct 2020, Colin) version that depends on **jsonlite**. Implementing **icesTAF** as a layer on top of **TAF**, this version will disappear.

## 6 Conclusions

Implemented as a layer on top of **TAF**, the **icesTAF** package only includes two user-level functions:

- `draft.data.script()`
- `taf.roxygenise()`

These are conveniently provided in two files: `draft.data.script.R` and `taf.roxygenise.R`.