

sa4ss

Chantel Wetzel

2020-12-07

Getting Started

Want to create an assessment document using **sa4ss**?

Load up the package available on github:

```
remotes::install_github("nwfs-assess/sa4ss")
library(sa4ss)
```

Now that the package is installed in R, let's create a document.

Step 1

Set the working directory. The document template will be created in the defined location.

```
setwd("C:/Assessments/2021/copper_rockfish_2021/write_up/wa")
```

Step 2

Call the draft function to create a general document with species, authors, and title created:

```
sa4ss::draft(authors = c("Chantel R. Wetzel",
                        "Brian J. Langseth",
                        "Jason M. Cope",
                        "Theresa Tsou",
                        "Kristen E. Hinton"),
             species = "Copper Rockfish",
             latin = "Sebastes caurinus",
             coast = "Washington US West",
             type = c("sa"),
             create_dir = FALSE,
             edit = FALSE)
```

The above example will automatically populate a document for copper rockfish with the above authors and their associated affiliation. **sa4ss** has a list of common authors and their affiliations already set-up. In order for authors to be found in the available list and their affiliation the names need to be entered exactly as expected here: <https://github.com/nwfs-assess/sa4ss/blob/master/data-raw/authors.csv>.

Step 3

Create an Rdata object based upon the base model. The base model can be located anywhere on your machine.

```
sa4ss::read_model(mod_loc = "C:/Assessments/2021/copper_rockfish_2021/models/base")
```

This will create an Rdata object called 00mod.Rdata in your working directory.

Step 4

Render the pdf document based on the draft template created:

```
bookdown::render_book("00a.Rmd", clean = FALSE, output_dir = getwd())
```

This will create build the pdf document which will be save directly in the working directory. However, one may prefer to have the pdf saved in a specific folder. One default approach is the call the render_book function without specifying the output_dir which will put the pdf document in a separate folder in the working directory.

```
bookdown::render_book("00a.Rmd", clean = FALSE)
```

Editing the Document

A number of documents in the specified directory should not be available. These documents correspond to different sections required by the Groundfish Terms of Reference.

When editing make sure to render the document on a regular basis by using either of the above calls to:

```
bookdown::render_book("00a.Rmd", clean = FALSE, output_dir = getwd())
```

This will allow users to identify errors quickly. If the document rendered correctly the user should see that "Output created: __main.pdf" followed by miscellaneous other warnings in the R terminal.

Error in Rendering

If you see an error and the document fails to render you will want to:

1. Open the __main.tex file, read the error message in the R terminal, and navigate to that line in the __main.tex file.
2. Correct the error in the Rmd files.
3. Delete the __main.Rmd file in the folder.
4. Rerun the render line of code:

```
bookdown::render_book("00a.Rmd", clean = FALSE, output_dir = getwd())
```

Updating the Base Model

If the base model changes, the user will need to rerun the **read_model** function to load in the output from the new model run and locate and/or create figures and tables

```
sa4ss::read_model(mod_loc = "C:/Assessments/2021/copper_rockfish_2021/models/new_base")
```

This will create a new model output file which will replace the old file and be used to update the document to the new model the next time the document is rendered.

Tips & Tricks

If you are creating an area-specific assessment document for species you may want to use the same text across multiple documents. This can be easily done by creating separate folder for sections of text that will be shared across documents. Text should be included in a file with an Rmd extension and can be called using a code chunk with the **knit_child** command in the **knitr** package:

```
other_loc = file.path('folder', 'child_example.Rmd')
res <- knitr::knit_child(other_loc, quiet = TRUE)
cat(res, sep = '\n')
#>
#>
#> Here is the text in the child document.
```