Collaborative Workflow for SAP

When you think workflow

Workflow includes:

- Editor you use to write code
- Name of your home directory
- Git client you use

Products include:

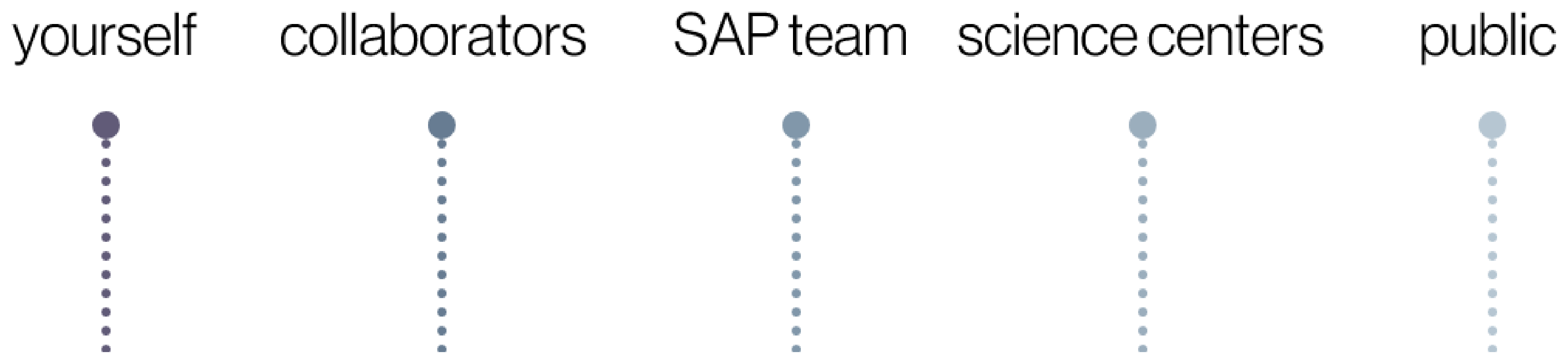
- Raw data
- Packages used for analysis
- Functions you wrote
- Figures and code used to make those figures
- Code someone needs to run to reproduce your results

Don’t hard code anything about workflow into products

Openness as a spectrum

❝ Open Science is the principle and practice of making research products and processes available to all, while respecting diverse cultures, maintaining security and privacy, and fostering collaborations, reproducibility, and equity.

- Varying degrees of openness
- Practice peer-review
- It’s okay to share imperfect code



Tools for Openness

- Use the tools we have to make your work as open as possible
- Google Drive - good for sharing data among collaborators
  - Use R code to pull directly from Google drive into R or onto personal computer
- Github repositories - can keep private until published
- Open science community
  - Openscapes training
  - NMFS R User Group

Benefits of automated workflows

- Save time and energy
  - Can put your energy towards developing models and not the tedious details
- Make things uniform
- Makes onboarding easier
- Help future us
- Helps you avoid mistakes and easier to fix them

Automate as much as possible!

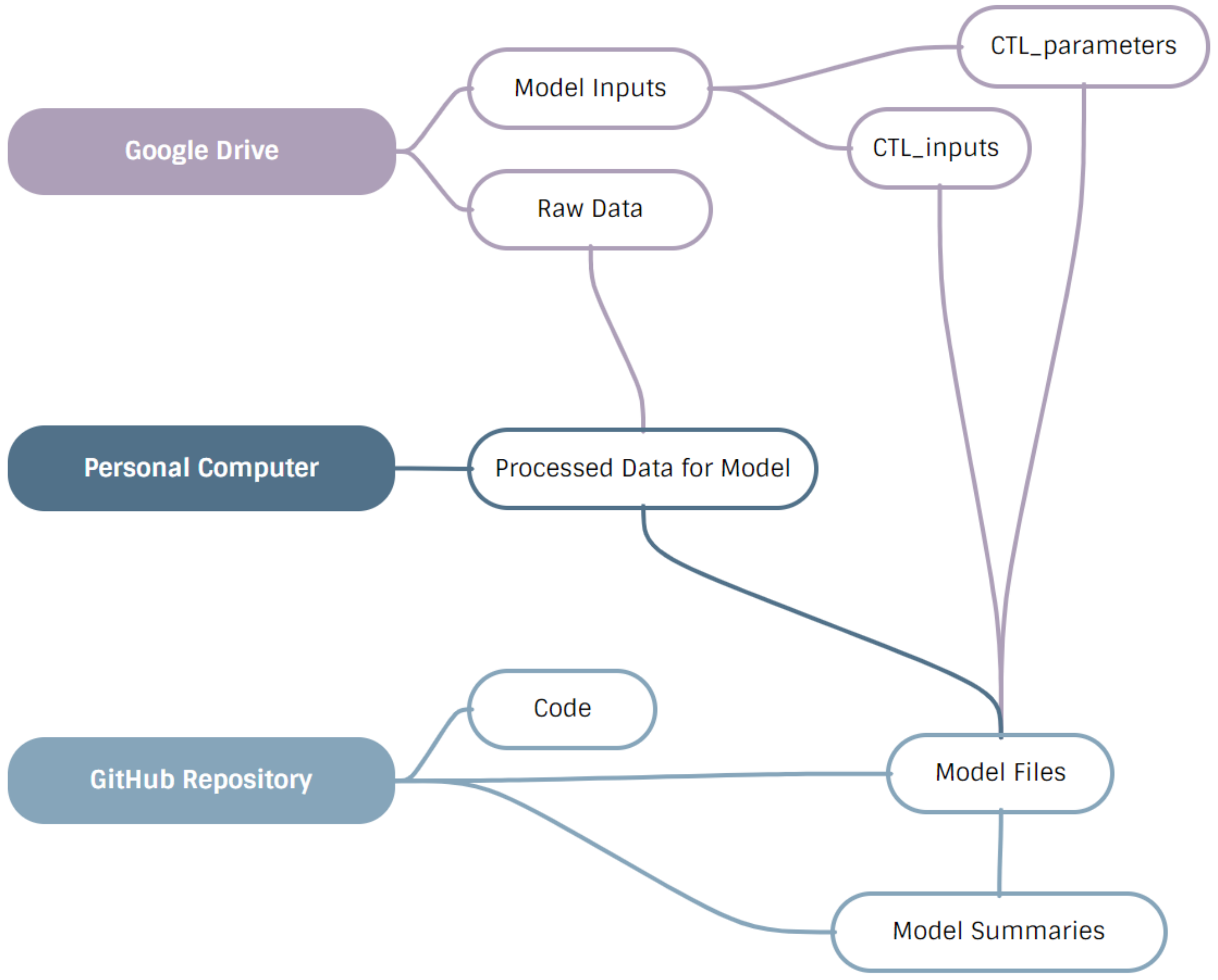
Why SAP should adopt an open and automated workflow

- Anyone can download a repository and reproduce our results
- Makes it easier during WPSAR reviews to run reviewer requests
- Easier onboarding when joining new projects
- Helps share the responsibility among the team
- Share knowledge within the group

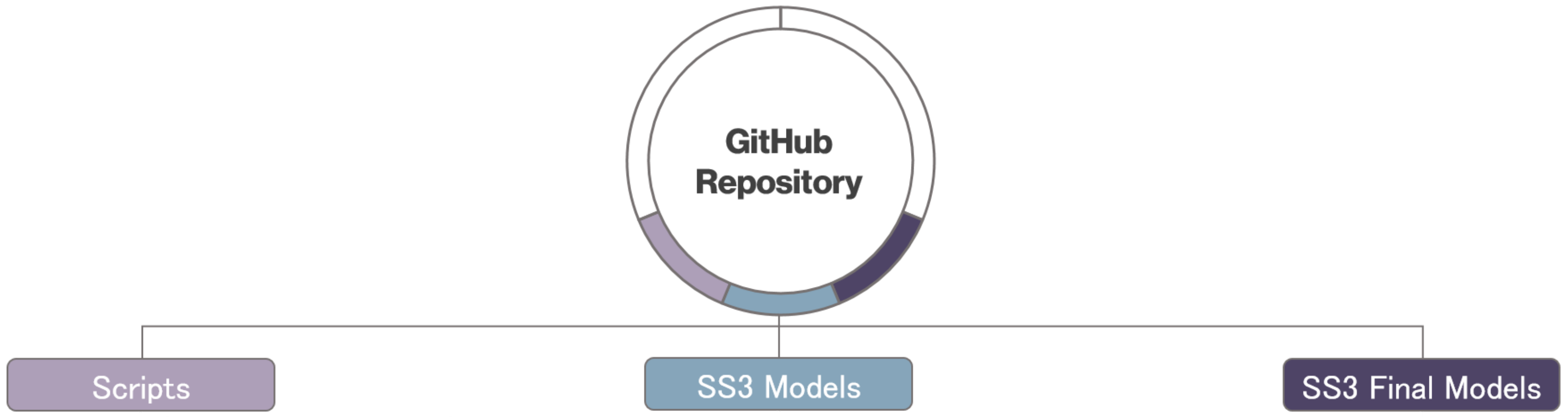
Challenges of American Samoa Bottomfish Assessment

Problems	Solutions
• Develop 9 individual models that have the same structure but different data and parameter values.	• Wrote custom functions to build the model input files and include the correct data and parameter values for each species.
• Develop models simultaneously and update parameter values without having to upload and download new versions of a spreadsheet.	• Set up 2 Google Sheets (inputs and parameters) that we could change and pull the information directly into R with real-time updated information.
• Share quick summaries of each model version easily with people.	• Included pdf reports of summary plots and diagnostics for each model version with 4 input files needed to reproduce those plots.

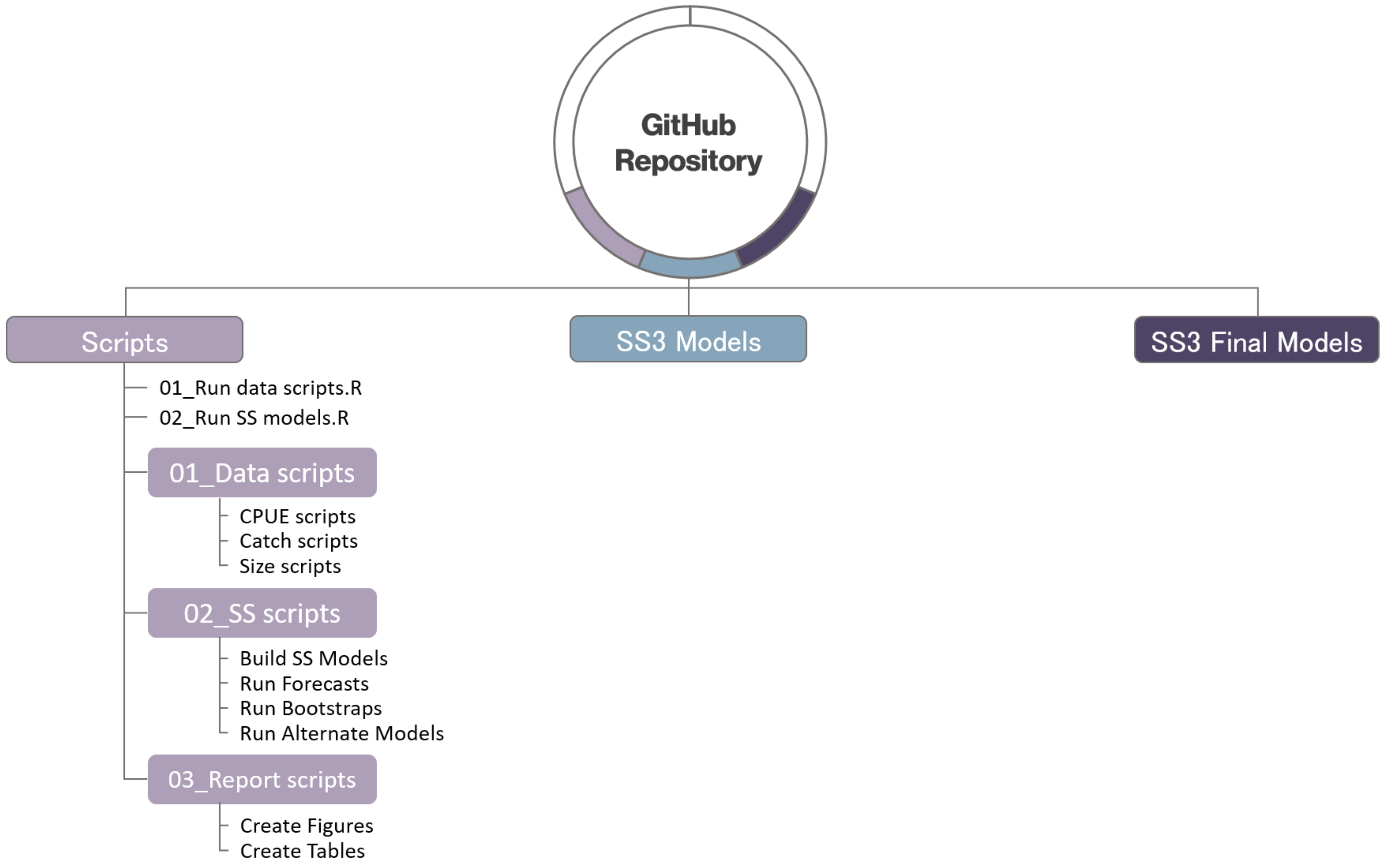
Our Workflow



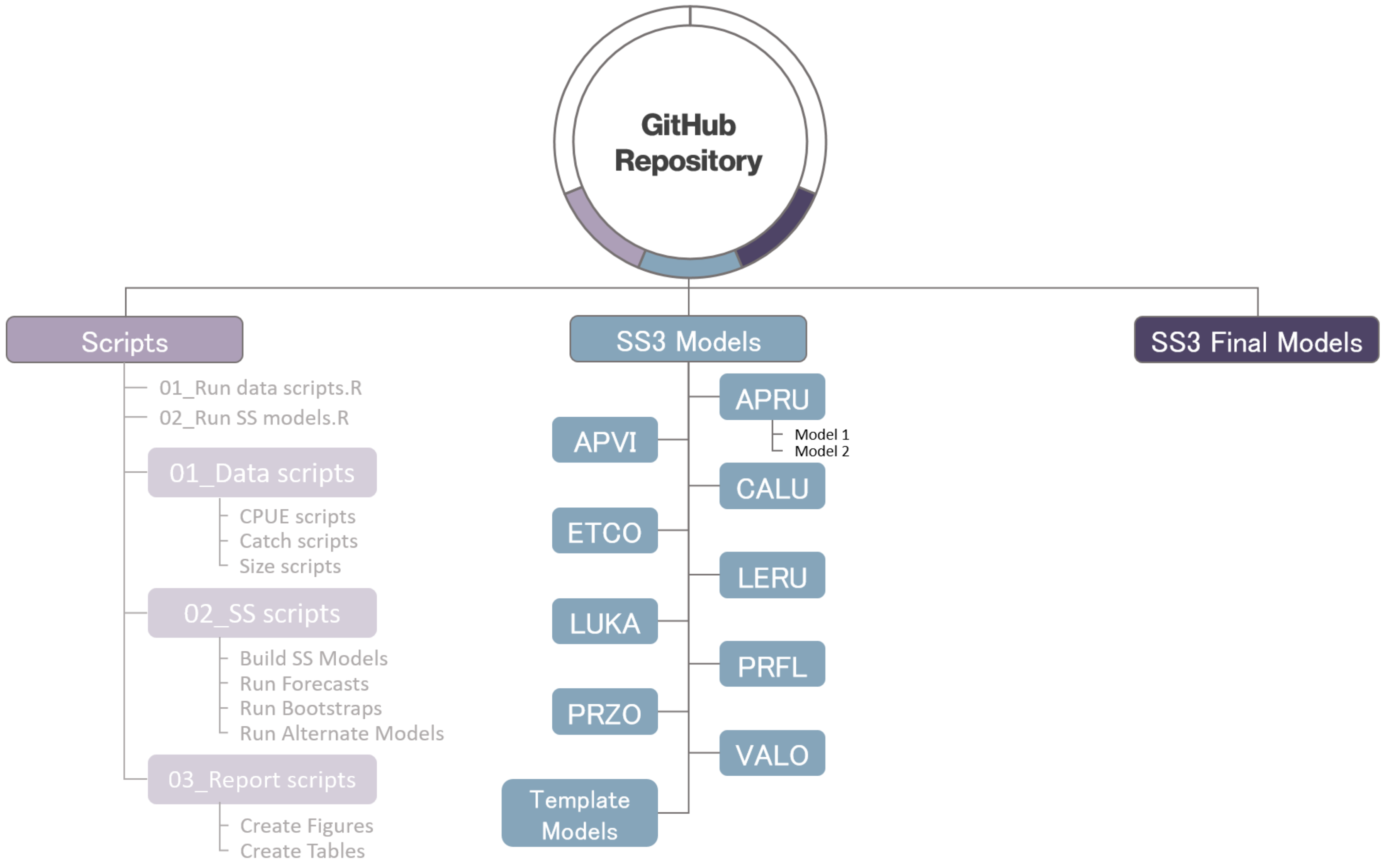
Repository Structure



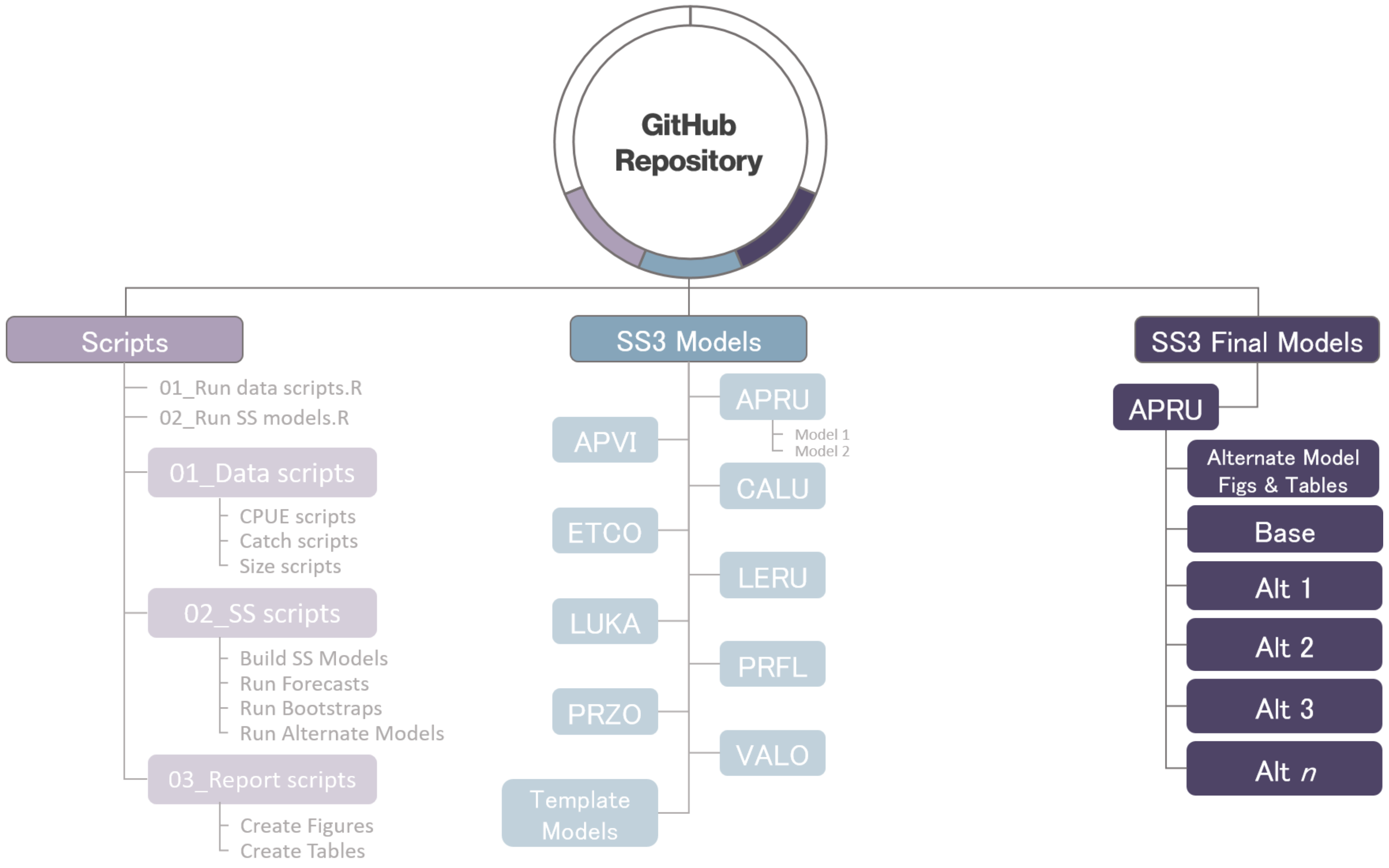
Repository Structure



Repository Structure



Repository Structure



Step 01: Retrieve raw data

```r
library(googledrive)
library(googlesheets4)

########## DOWNLOAD DATA FROM GOOGLE DRIVE ###############
# Check latest data from Google Drive but only download if its more recent than on local repo
a <- drive_reveal(
  drive_ls(
  path="https://drive.google.com/drive/u/1/folders/1pnH38cupmDU4O_KkKDhYWee_p4sTSD6u",
  pattern="Data"),
  what = "modified_time")
a <- arrange(a, by = desc(modified_time))[1,] # Select most recent "Data" zip file

if(dir.exists(file.path(here(..=1),"Data"))){
         Date.CurrentFolder <- as_datetime(
           file.info(paste0(file.path(here(..=1)),"/Data"))$mtime)
} else {
  Date.CurrentFolder <- "1900-01-01 01:01:01 UTC"
  }

Date.GoogleFolder <- as_datetime(map_chr(a$drive_resource, "modifiedTime"))

if(Date.CurrentFolder<Date.GoogleFolder){
    drive_download(file=a$id,
                   overwrite = TRUE,
                   path = file.path(here(..=1),a$name))

```

Step 02: Process data

```r
########## PROCESS CATCH, CPUE, AND SIZE DATA ################
set.seed(123)
source(paste0(here(..=1),"/Scripts/01_Data scripts/01_CPUE_BBS_InitPrep.r"));   rm(list=ls())
source(paste0(here(..=1),"/Scripts/01_Data scripts/02_CPUE_BBS_PropTable.r"));  rm(list=ls())
source(paste0(here(..=1),"/Scripts/01_Data scripts/03a_CPUE_BBS_Wind.r"));      rm(list=ls())
source(paste0(here(..=1),"/Scripts/01_Data scripts/03b_CPUE_BBS_PCA.r"));       rm(list=ls())
source(paste0(here(..=1),"/Scripts/01_Data scripts/04_CPUE_BBS_FinalPrep.r"));  rm(list=ls())
source(paste0(here(..=1),"/Scripts/01_Data scripts/06_CATCH_BBS_FinalPrep.r")); rm(list=ls())
set.seed(123)
source(paste0(here(..=1),"/Scripts/01_Data scripts/07_CATCH_SBS_PropTable.r")); rm(list=ls())
source(paste0(here(..=1),"/Scripts/01_Data scripts/08_CATCH_SBS_FinalPrep.r")); rm(list=ls())
source(paste0(here(..=1),"/Scripts/01_Data scripts/09_CATCH_Final.r"));         rm(list=ls())
source(paste0(here(..=1),"/Scripts/01_Data scripts/10_SIZE.r"));                rm(list=ls())

############### RUN CPUE STANDARDIZATION###########################
# Run CPUE standardization and export indices for input into SS
source(paste0(here(..=1),"/Scripts/01_Data scripts/05_CPUE_BBS_Standardize_Function3.r"))
source(paste0(here(..=1),"/Scripts/01_Data scripts/05_CPUE_BBS_Standardize_Function2.r"))

# Run CPUE standardization for all species, areas combined in a loop
root_dir <- root_dir <- this.path::here(.. = 1)
Species.List <- c("APRU","APVI","CALU","ETCO","LERU","LUKA","PRFL","PRZO","VALO")
for(i in 1:length(Species.List)){
    Standardize_CPUE3(Sp=Species.List[i],Interaction=T,minYr=1988,maxYr=2015)
}
```

Step 03: Set input arguments

Arguments we rarely changed

```r
Lt      <-vector("list",9) # Species options

Lt[[1]]<-list("APRU",               #Name
              "SW_Then",            #M
              "SW_BBS_BIOS",        #Growth
              "Kamikawa",           #Length-Weight
              "SW_BBS_BIOS",        #Maturity
              F,                    #Use InitF?
              c(0.5,1.6),           #Range of R0 prof
              0.29,                 #Btarg. value
              T,                    #Include superyea
              list(c(2019,2020)),#Blocks of supery
              c(2.5,5.5,0.2))       #Proj catch range
```

Arguments we changed frequently

```r
DirName     <- "65_Base" # Name of directory
runmodels   <- T   # Run ss.exe
printreport<- T   # Run ss_diags report
Create_species_report_figs <- F # Produce formatte
                                #figures and table
                                #word document
N_boot      <- 0   # Bootstrap on/off
N_foreyrs   <- 0   # Nyears for forecast
RD          <- F   # Run diagnostics
ProfRes     <- .1 # R0 profile resolution
profile     <- "SR_LN(R0)" # Parameter to profile
Begin       <- c(1967,1986)[1] #Model start year
DeleteForecastFiles <- T #Remove extra files
```

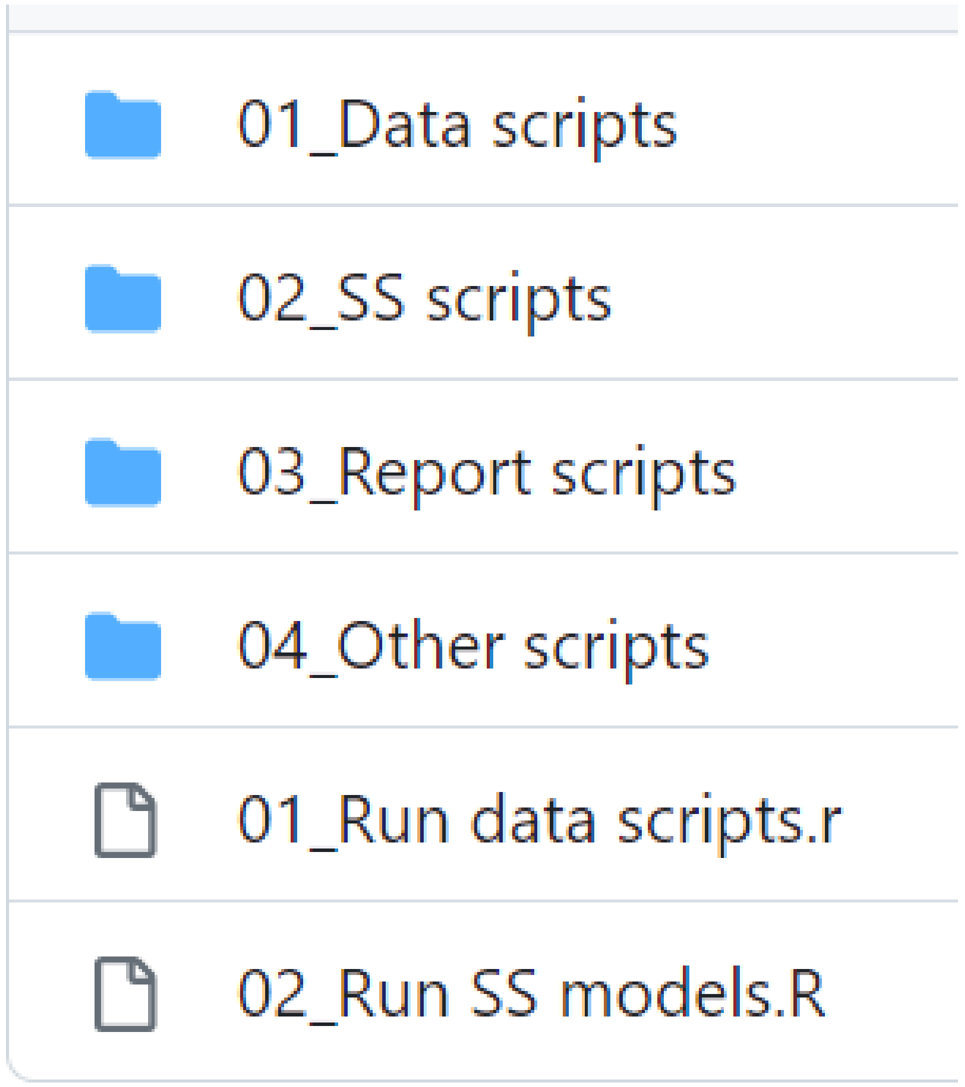
Step 04: Build models and run

- The core function is `Build_All_SS()`
- Wrapper function for modular functions:
  - `Build_Data()` , `Build_Control()` , `Build_Starter()` , `Build_Forecast()`
- Incorporate parameter information stored in Google Sheets

```r
if(readGoogle == T){
     ctl.params <- read_sheet("1XvzGtPls8hnHHGk7nmVwhggom4Y1Zp-gOHNw4ncUs8E",
                          sheet=species)
     ctl.inputs <- read_sheet("11lPJV7Ub9eoGbYjoPNRpcpeWUM5RYl4W65rHHFcQ9fQ",
                              sheet=scenario)

 }else{
   ctl.inputs <- readxl::read_excel(file.path(root_dir, "Data", "CTL_inputs.xlsx"),
                                    sheet=scenario)
   ctl.params <- readxl::read_excel(file.path(root_dir, "Data", "CTL_parameters.xlsx"),
                      sheet=species)
 }
```

Modular code

- Created “smaller” functions for each step
- Used the main function as a wrapper so could run everything from 1 script and easy to turn functions on and off
  - bootstraps
  - diagnostics
  - forecasting
  - alternate models
  - summary reports
  - creating specific plots and tables



01_Data scripts
02_SS scripts
03_Report scripts
04_Other scripts
01_Run data scripts.r
02_Run SS models.R

Step 05: Produce model diagnostics reports

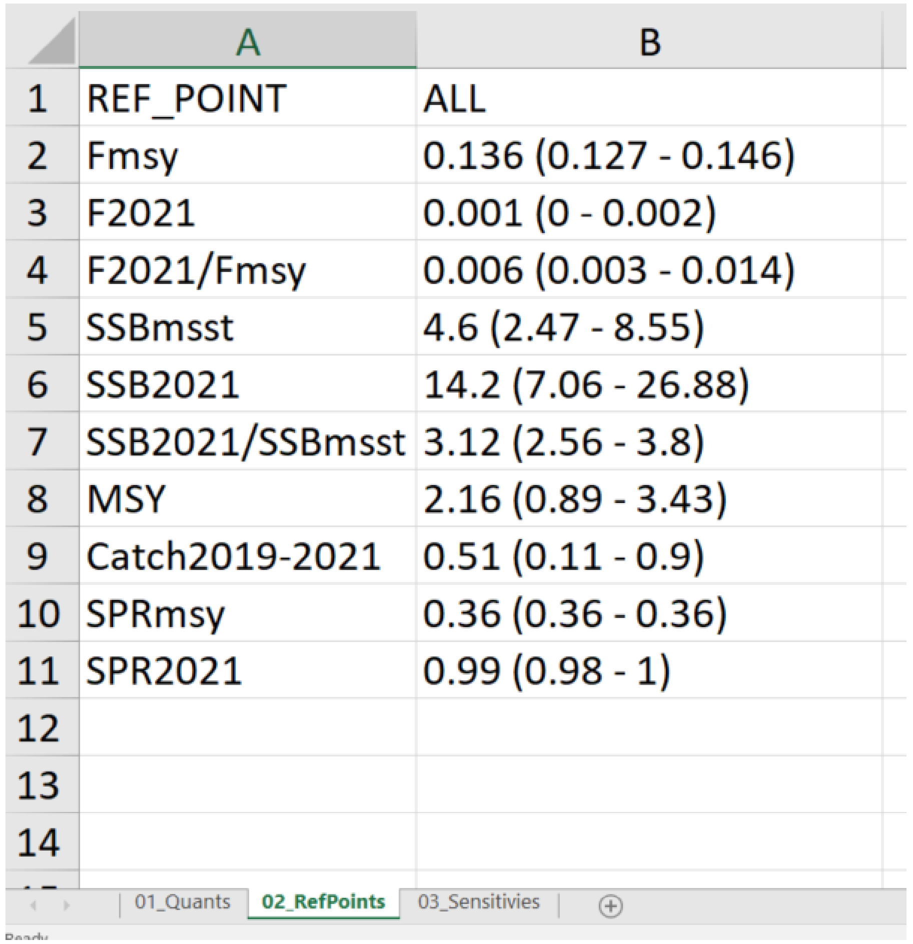
- `r4ss::SS_plots()`
- Created a custom qmd with model diagnostic plots and tables
  - runs test, likelihood profiles, retrospectives, jitters, etc.
- Created html and pdf versions
  - PDFs were synced with the repository so anyone could look at the diagnostics for a certain model without cloning the repository onto their computer

Step 06: Generate formatted tables and figures

Quarto document produced a .docx with figures and tables formatted for the report

```r
library(openxlsx)
library(flextable)

set_flextable_defaults(
  font.size = 11, font.family = "Arial",
  border.color = "black", font.color = "black")
border <- officer::fp_border()

refpoints <- read.xlsx(file.path("./", "scr", "01_tables.xlsx"),
                       sheet = "02_RefPoints")
refpoints.ft <- flextable(refpoints)

refpoints.ft <- set_header_labels(refpoints.ft, REF_POINT = "Reference point", ALL = "Value")
refpoints.ft <- hline_bottom(refpoints.ft, border = border)
refpoints.ft <- hline_top(refpoints.ft, border = border, part = "header")
refpoints.ft <- hline_bottom(refpoints.ft, border = border, part = "header")

refpoints.ft <- compose(refpoints.ft, i = 1, j = 1, part = "body",
                        value = as_paragraph(as_i("F"), as_sub("MSY"),
                                             " (yr", as_sup("-1"), ")"))

refpoints.ft <- compose(refpoints.ft, i = 4, j = 1, part = "body",
                        value = as_paragraph(as_i("SSB"), as_sub("MSST")))
```

Formatted tables for report



	A	B
1	REF_POINT	ALL
2	Fmsy	0.136 (0.127 - 0.146)
3	F2021	0.001 (0 - 0.002)
4	F2021/Fmsy	0.006 (0.003 - 0.014)
5	SSBmsst	4.6 (2.47 - 8.55)
6	SSB2021	14.2 (7.06 - 26.88)
7	SSB2021/SSBmsst	3.12 (2.56 - 3.8)
8	MSY	2.16 (0.89 - 3.43)
9	Catch2019-2021	0.51 (0.11 - 0.9)
10	SPRmsy	0.36 (0.36 - 0.36)
11	SPR2021	0.99 (0.98 - 1)
12		
13		
14		

Reference point	Value
F_{MSY} (yr^{-1})	0.136 (0.127 - 0.146)
F_{2021} (yr^{-1})	0.001 (0 - 0.002)
F_{2021}/F_{MSY}	0.006 (0.003 - 0.014)
SSB_{MSST}	4.6 (2.47 - 8.55)
SSB_{2021} (mt)	14.2 (7.06 - 26.88)
SSB_{2021}/SSB_{MSST}	3.12 (2.56 - 3.8)
MSY (mt)	2.16 (0.89 - 3.43)
Catch$_{2019\text{-}2021}$ (mt)	0.51 (0.11 - 0.9)
SPR_{MSY}	0.36 (0.36 - 0.36)
SPR_{2021}	0.99 (0.98 - 1)

Lessons learned in our process

- Use packages that work with all platforms of R
- Make functions flexible enough to give you options but don’t worry about coding every single possibility
- Develop as you go, streamline as you go
- Make code modular

Small changes you can implement now

- More comments, or use software such as Quarto or RMarkdown for literate programming
- Read other people’s code
- Make sure you are using relative paths and including all the packages you used in that script
- When naming scripts, give them informative names and try sequencing them
- Get in the habit of syncing code with repository regularly

Discussion points

- Is this system useful for single-species assessments?
    - I think its useful for any assessment with more than 1 person working on it
- How can we help each other with setting these systems up?
    - coworking time in small groups
    - set up GitHub repository templates for a common set-up
- How can this be useful for international assessments?
- What about reference manager software?
- What are some good tools people use for project management?
    - GitHub Projects