Appendix B: Code for analysis comparing to historical data

2019-06-05

Section 1: Model estimates from data

Computes model parameter estimates for selected stocks in RAM using NIMBLE.

```
# devtools::install_github("boettiger-lab/sarsop")  ## install package first if necessary.
library(tidyverse)
library(sarsop)
library(nimble)
library(parallel)
library(gridExtra)
library(tictoc)
library(furrr)
tic()
```

```
path <- "../data/appendixB/ramlegacy_v3.0.xlsx"
sheets <- readxl::excel_sheets(path)
ram <- lapply(sheets, readxl::read_excel, path = path)
names(ram) <- sheets

ramlegacy <-
  ram$timeseries_values_views %>%
  select(assessid, stockid, stocklong, year, SSB, TC) %>%
  left_join(ram$stock) %>%
  left_join(ram$area) %>%
  select(assessid, stockid, scientificname,
         commonname, areaname, country, year,
         SSB, TC) %>%
  left_join(ram$timeseries_units_views %>%
              rename(TC_units = TC, SSB_units = SSB)) %>%
  select(scientificname, commonname,
         stockid, areaname, country, year,
         SSB, TC, SSB_units, TC_units)
```

Let's filter out missing data, non-matching units, and obvious reporting errors (catch exceeding total spawning biomass), then we re-scale each series into the 0,1 by appropriate choice of units:

```
df2 <- ramlegacy %>%
  filter(!is.na(SSB), !is.na(TC)) %>%
  filter(SSB_units == "MT", TC_units=="MT") %>%
  filter(SSB > TC) %>%
  select(-SSB_units, -TC_units) %>%
  group_by(stockid) %>%
  mutate(scaled_catch = TC / max(SSB),
         scaled_biomass = SSB / max(SSB))
```

```
stock_ids <- c("PLAICNS", "ARGHAKENARG")
examples <- df2 %>%
  filter(stockid %in% stock_ids) %>%
  ungroup() %>%
  group_by(commonname)
```

```
## Model does not estimate sigma_m; data is insufficient to do so.
gs_code  <- nimble::nimbleCode({
  r ~ dunif(0, 2)
  K ~ dunif(0, 2)
  sigma ~ dunif(0, 1)

  x[1] <- x0
  for(t in 1:(N-1)){
    mu[t] <- x[t] + x[t] * r * (1 - x[t] / K) - min(a[t],x[t])
    x[t+1] ~ dnorm(mu[t], sd = sigma)
  }
})

fit_models <- function(fish, code){
  # fish <- examples %>% filter(stockid == stock_ids[1])

  ## Rescale data
  N <- dim(fish)[1]
  scaled_data <- data.frame(t = 1:N,
                            y = fish$scaled_biomass,
                            a = fish$scaled_catch)
  data = data.frame(x = scaled_data$y)

  ## Compile  model
  constants <- list(N = N, a = scaled_data$a)
  inits <- list(r = 0.5, K = 0.5, sigma = 0.02, x0 = scaled_data$y[1])
  model <- nimbleModel(code, constants, data, inits)
  C_model <- compileNimble(model)

  mcmcspec <- configureMCMC(model, thin = 1e2)
  mcmc <- buildMCMC(mcmcspec)
  Cmcmc <- compileNimble(mcmc, project = model)
  Cmcmc$run(1e6)


  samples <- as.data.frame(as.matrix(Cmcmc$mvSamples))
  burnin <- 1:(0.05 * dim(samples)[1]) # drop first 5%
  samples <- samples[-burnin,1:(length(inits) - 1)] # drop raised vars, burnin
  #gather(samples) %>% ggplot() + geom_density(aes(value)) + facet_wrap(~key, scale='free')

  ## Return fit
  data.frame(stockid = fish$stockid[1],
             commonname = fish$commonname[1],
             r = mean(samples$r),
             K = mean(samples$K),
             sigma_g = mean(samples$sigma),
             r_sd = sd(samples$r),
             K_sd = sd(samples$K),
             sigma_g_sd = sd(samples$sigma),
             stringsAsFactors = FALSE)
}
```

```
set.seed(123)
fits <- examples %>% do(fit_models(., code=gs_code))
```

```
|-------------|-------------|-------------|-------------|
|-------------------------------------------------------|
|-------------|-------------|-------------|-------------|
|-------------------------------------------------------|
```

```
fits
```

```
# A tibble: 2 x 8
# Groups:   commonname [2]
  stockid     commonname          r     K sigma_g   r_sd  K_sd sigma_g_sd
  <chr>       <chr>           <dbl> <dbl>   <dbl>  <dbl> <dbl>      <dbl>
1 ARGHAKENARG Argentine hake  1.04   1.20   0.112 0.179  0.192     0.0267
2 PLAICNS     European Plaice 0.906  1.78   0.127 0.0743 0.156     0.0130
```

```
pars <- fits %>% ungroup() %>% select(commonname, r, K, sigma_g)
pars
```

commonname	r	K	sigma_g
Argentine hake	1.0379274	1.197693	0.1121662
European Plaice	0.9064288	1.777442	0.1273774

Calculations of the Decision Policies for Historical Data

```
options(mc.cores = 6) # Reserve ~ 10 GB per core
log_dir <- "../data/appendixB"
```

```
## Classic Gordon-Schaefer. Note that recruitment occurs *before* harvest
gs <- function(r,K){
  function(x, h){
    x + x * r * (1 - x / K) - pmin(x,h)
  }
}
reward_fn <- function(x,h) pmin(x,h)
discount <- .95
```

Discretize space

Note that the large values of K require we carry the numerical grid out further.

```
states <- seq(0,4, length=150)
actions <- states
observations <- states
```

Consider all parameter values combinations for which we want solutions (both species at each of three possible levels of measurement uncertainty; though we will focus on the `0.1` level for simplicity as overall pattern is the same at `0.15`):

```r
meta <- expand.grid(commonname = pars$commonname,
                    sigma_m = c(0, 0.1, 0.15),
                    stringsAsFactors = FALSE) %>%
  left_join(pars) %>%
  mutate(scenario  = as.character(1:length(sigma_m)))

meta
```

commonname	sigma_m	r	K	sigma_g	scenario
Argentine hake	0.00	1.0379274	1.197693	0.1121662	1
European Plaice	0.00	0.9064288	1.777442	0.1273774	2
Argentine hake	0.10	1.0379274	1.197693	0.1121662	3
European Plaice	0.10	0.9064288	1.777442	0.1273774	4
Argentine hake	0.15	1.0379274	1.197693	0.1121662	5
European Plaice	0.15	0.9064288	1.777442	0.1273774	6

Create the model matrices (transition, observation, and reward matrix):

```r
plan(multiprocess)

models <-
  furrr::future_map(1:dim(meta)[1],
                    function(i){
                      fisheries_matrices(
                        states = states,
                        actions = actions,
                        observed_states = observations,
                        reward_fn = reward_fn,
                        f = gs(meta[i, "r"][[1]], meta[i, "K"][[1]]),
                        sigma_g = meta[i,"sigma_g"][[1]],
                        sigma_m = meta[i,"sigma_m"][[1]],
                        noise = "normal")
                    })
```

Here's the slowest part: computing POMDP alpha vectors.

```r
dir.create(log_dir, FALSE)
plan(multiprocess)
## POMDP solution
system.time(
  alphas <-
    furrr::future_map(1:length(models),
    function(i){
      log_data <- data.frame(model = "gs",
                             r = meta[i, "r"][[1]],
                             K = meta[i, "K"][[1]],
                             sigma_g = meta[i,"sigma_g"][[1]],
                             sigma_m = meta[i,"sigma_m"][[1]],
                             noise = "normal",
                             commonname = meta[i, "commonname"][[1]],
                             scenario = meta[i, "scenario"][[1]])

      sarsop(models[[i]]$transition,
             models[[i]]$observation,
             models[[i]]$reward,
             discount = discount,
             precision = 2e-6,
             timeout = 25000,
             log_dir = log_dir,
             log_data = log_data)
    })
)
```

```
   user  system elapsed 
  3.456   0.585   9.316 
```

Comparison to the static models

```
pars <- examples %>%
  group_by(commonname) %>%
  summarise(N = max(SSB)) %>%
  right_join(
    meta %>%
      select(commonname, r, K) %>%
      distinct())
```

Add corresponding static policy levels on:

```
statics <- function(P){
  f <- gs(P$r, P$K)
  S_star <- optimize(function(x) -f(x,0) + x / discount, c(0, 2* P$K))$minimum
  B_MSY <- S_star
  MSY <- f(B_MSY,0) - B_MSY

  tibble(S_star, F_MSY = MSY / B_MSY, F_TAC = 0.8 * F_MSY,
         commonname = P$commonname, N = P$N)
}

policy_pars <-
  pars %>%
  transpose() %>%
  map_df(statics)
```

Convert example data into discrete index space.

```
index <- function(x, grid) map_int(x, ~ which.min(abs(.x - grid)))
## repeats each series for each static model
ex <- examples %>%
  mutate(biomass = index(scaled_biomass, states),
         catch = index(scaled_catch, actions))  %>%
  left_join(policy_pars) %>%
  left_join(pars) %>%
  ungroup()
```

Static policy calculations:

```
CE_f <- function(S_star, r, K, i)
  index(pmax(gs(r[[1]],K[[1]])(states,0) - S_star[[1]],0), actions)[i]
MSY_f <- function(F_MSY, i) index(states * F_MSY[[1]], actions)[i]
```

```
TAC_f <- function(F_TAC, i) index(states * F_TAC[[1]], actions)[i]
rescale <- function(x, N) states[x]*N

historical <- ex %>%
  group_by(commonname) %>%
  mutate(CE =  CE_f(S_star, r, K, biomass),
         MSY =  MSY_f(F_MSY, biomass),
         TAC =  TAC_f(F_TAC, biomass)) %>%
  select(year, biomass, catch, CE, MSY, TAC, commonname, N) %>%
  gather(model, stock, -year, -commonname, -N) %>%
  mutate(stock = states[stock] * N) %>%
  select(-N)
```

Compute POMDP policy for historical data:

```
set.seed(123456)
pomdp_sims <-
  pmap_dfr(list(models, alphas, 1:dim(meta)[[1]]),
           function(.x, .y, .z){

             ## avoid NSE
             who <- (ex$commonname == meta[.z,"commonname"])
             df <- ex[who,]

             hindcast_pomdp(.x$transition, .x$observation, .x$reward, discount,
                            obs = index(df$scaled_biomass, states),
                            action = index(df$scaled_catch,states),
                            alpha = .y)$df %>%
              mutate(method = "pomdp") %>% # include a column labeling method
              mutate(year = ex[who, "year"][[1]])
           },
           .id = "scenario")
```

Join records:

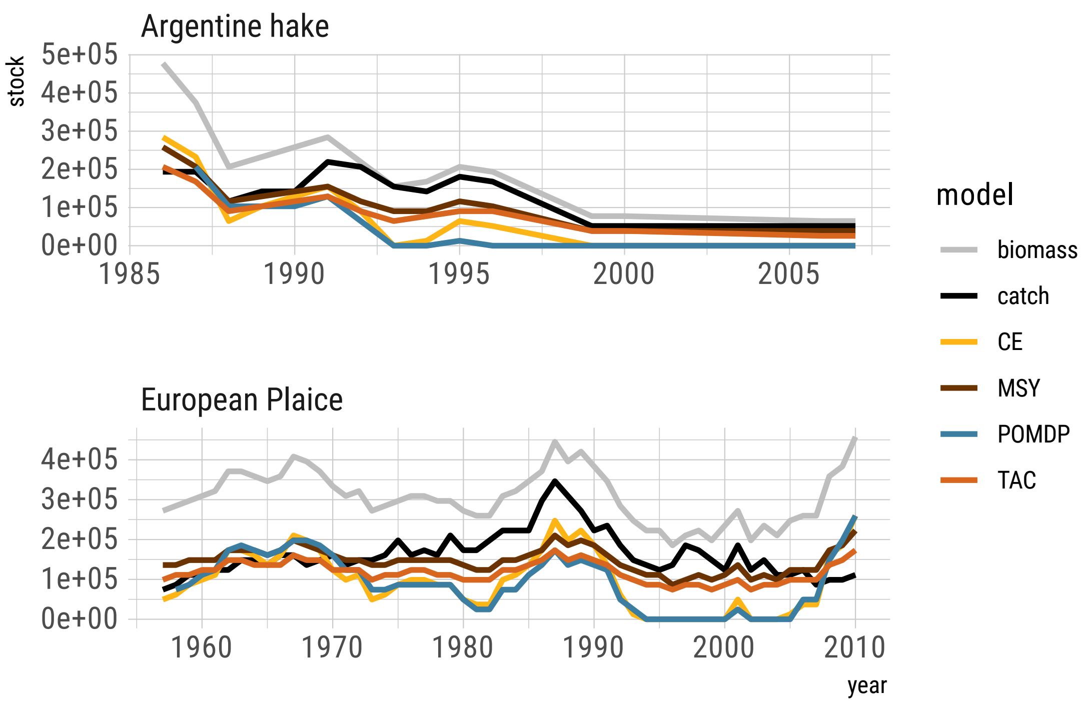
```
pomdp_sims <-
  meta %>%
  select(scenario, commonname,sigma_m) %>%
  left_join(pars) %>%
  right_join(pomdp_sims)
```

```
sims <- pomdp_sims %>%
  mutate(optimal = states[optimal] * N) %>% # original scale
  select(year, optimal, commonname, sigma_m) %>%
  rename(stock = optimal) %>%
  ## treat each sigma_m value as separate 'model'
  mutate(sigma_m = as.factor(sigma_m)) %>%
  mutate(model = recode(sigma_m,
                        "0" = "CE",
                        "0.1" = "POMDP",
                        "0.15" = "POMDP_0.15")) %>%
  select(-sigma_m) %>%
  bind_rows(historical)

write_csv(sims,file.path(log_dir, "appendixB.csv"))
```

Final plot, as in paper but including MSY:

```
appendixB <- read_csv(file.path(log_dir, "appendixB.csv"))
appendixB %>%
  filter(model %in% c("biomass", "catch", "POMDP", "CE", "TAC", "MSY")) %>%
  ggplot(aes(year, stock, col=model)) +
  geom_line(lwd=1) +
  scale_color_manual(values = colors) +
  facet_wrap(~commonname, scales = "free", ncol=1)
```



System Information

Total runtime:

```r
toc()
```

```
118.142 sec elapsed
```

Hardware:

```r
system2("grep", c("MemTotal", "/proc/meminfo"), stdout = TRUE)
```

```
[1] "MemTotal:       32938360 kB"
```

```r
system2('grep', '"model name" /proc/cpuinfo', stdout = TRUE)
```

```
 [1] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
 [2] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
 [3] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
 [4] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
 [5] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
 [6] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
 [7] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
 [8] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
 [9] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
[10] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
[11] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
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[13] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
[14] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
[15] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
[16] "model name\t: Intel Xeon E312xx (Sandy Bridge)"
```

Software:

```r
devtools::session_info()
```

```
- Session info ----------------------------------------------------------
 setting  value
 version  R version 3.6.0 (2019-04-26)
 os       Debian GNU/Linux 9 (stretch)
 system   x86_64, linux-gnu
 ui       RStudio
 language (EN)
 collate  en_US.UTF-8
 ctype    en_US.UTF-8
 tz       Etc/UTC
 date     2019-06-05

- Packages --------------------------------------------------------------
 package     * version date       lib
 assertthat    0.2.1   2019-03-21 [1]
 backports     1.1.4   2019-04-10 [1]
 broom         0.5.2   2019-04-07 [1]
 Cairo       * 1.5-10  2019-03-28 [1]
 callr         3.2.0   2019-03-15 [1]
 cellranger    1.1.0   2016-07-27 [1]
 cli           1.1.0   2019-03-19 [1]
 coda          0.19-2  2018-10-08 [1]
 codetools     0.2-16  2018-12-24 [2]
 colorspace    1.4-1   2019-03-18 [1]
 crayon        1.3.4   2017-09-16 [1]
 desc          1.2.0   2018-05-01 [1]
 devtools      2.0.2   2019-04-08 [1]
 digest        0.6.19  2019-05-20 [1]
 dplyr       * 0.8.1   2019-05-14 [1]
 evaluate      0.13    2019-02-12 [1]
 extrafont   * 0.17    2014-12-08 [1]
 extrafontdb   1.0     2012-06-11 [1]
 fansi         0.4.0   2018-10-05 [1]
 forcats     * 0.4.0   2019-02-17 [1]
 fs            1.3.1   2019-05-06 [1]
 furrr       * 0.1.0   2018-05-16 [1]
 future      * 1.13.0  2019-05-08 [1]
 gdtools       0.1.8   2019-04-02 [1]
 generics      0.0.2   2018-11-29 [1]
 ggplot2     * 3.1.1   2019-04-07 [1]
 ggthemes    * 4.2.0   2019-05-13 [1]
 globals       0.12.4  2018-10-11 [1]
 glue          1.3.1   2019-03-12 [1]
 gridExtra   * 2.3     2017-09-09 [1]
 gtable        0.3.0   2019-03-25 [1]
 haven         2.1.0   2019-02-19 [1]
 highr         0.8     2019-03-20 [1]
 hms           0.4.2   2018-03-10 [1]
 hrbrthemes  * 0.6.0   2019-01-21 [1]
 htmltools     0.3.6   2017-04-28 [1]
 httr          1.4.0   2018-12-11 [1]
 igraph        1.2.4.1 2019-04-22 [1]
 jsonlite      1.6     2018-12-07 [1]
 knitr         1.23    2019-05-18 [1]
 labeling      0.3     2014-08-23 [1]
 lattice       0.20-38 2018-11-04 [2]
 lazyeval      0.2.2   2019-03-15 [1]
 linprog       0.9-2   2012-10-17 [1]
 listenv       0.7.0   2018-01-21 [1]
 lubridate     1.7.4   2018-04-11 [1]
```

```
magrittr      1.5     2014-11-22 [1]
Matrix        1.2-17  2019-03-22 [2]
MDPtoolbox    4.0.3   2017-03-03 [1]
memoise       1.1.0   2017-04-21 [1]
modelr        0.1.4   2019-02-18 [1]
munsell       0.5.0   2018-06-12 [1]
nimble      * 0.7.1   2019-03-12 [1]
nlme          3.1-139 2019-04-09 [2]
packrat       0.5.0   2018-11-14 [1]
pillar        1.4.0   2019-05-11 [1]
pkgbuild      1.0.3   2019-03-20 [1]
pkgconfig     2.0.2   2018-08-16 [1]
pkgload       1.0.2   2018-10-29 [1]
plyr          1.8.4   2016-06-08 [1]
prettyunits   1.0.2   2015-07-13 [1]
printr      * 0.1     2017-05-19 [1]
processx      3.3.1   2019-05-08 [1]
ps            1.3.0   2018-12-21 [1]
purrr       * 0.3.2   2019-03-15 [1]
R6            2.4.0   2019-02-14 [1]
Rcpp          1.0.1   2019-03-17 [1]
readr       * 1.3.1   2018-12-21 [1]
readxl        1.3.1   2019-03-13 [1]
remotes       2.0.4   2019-04-10 [1]
reshape2      1.4.3   2017-12-11 [1]
rlang         0.3.4   2019-04-07 [1]
rmarkdown     1.12    2019-03-14 [1]
rprojroot     1.3-2   2018-01-03 [1]
rstudioapi    0.10    2019-03-19 [1]
Rttf2pt1      1.3.7   2018-06-29 [1]
rvest         0.3.4   2019-05-15 [1]
sarsop      * 0.6.0   2019-06-04 [1]
scales        1.0.0   2018-08-09 [1]
sessioninfo   1.1.1   2018-11-05 [1]
stringi       1.4.3   2019-03-12 [1]
stringr     * 1.4.0   2019-02-10 [1]
testthat      2.1.1   2019-04-23 [1]
tibble      * 2.1.1   2019-03-16 [1]
tictoc      * 1.0     2014-06-17 [1]
tidyr       * 0.8.3   2019-03-01 [1]
tidyselect    0.2.5   2018-10-11 [1]
tidyverse   * 1.2.1   2017-11-14 [1]
tinytex       0.13    2019-05-14 [1]
usethis       1.5.0   2019-04-07 [1]
utf8          1.1.4   2018-05-24 [1]
vctrs         0.1.0   2018-11-29 [1]
withr         2.1.2   2018-03-15 [1]
xfun          0.7     2019-05-14 [1]
xml2          1.2.0   2018-01-24 [1]
yaml          2.2.0   2018-07-25 [1]
zeallot       0.1.0   2018-01-28 [1]
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[1] /usr/local/lib/R/site-library
[2] /usr/local/lib/R/library
```