Fit Bayesian Hierarchical Population Model to Raw Distance-Sampling Data

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Description

`MCBUBayesPower` is a custom package created to fit hierarchical population models to distance-sampling data using Bayesian methods to obtain parameter estimates, to fit models to simulated data sets based on prospective survey designs, and compile simulation results to evaluate statistical power among multiple survey designs. This vignette describes a workflow for using `MCBUBayesPower` to fit models to raw MCBU data collected during previous surveys on St Matthew IKslands.

Raw Data Analysis Workflow

Save a copy of the raw MCBU distance-sampling data set (CSV format) in the data folder and name it `distdata_mcbu.csv`.

Load packages.

```
## Install and load MCBUBayesPower R package
if (!require("devtools")) install.packages("devtools")
devtools::install_github("USFWS/MCBUBayesPower", ref = "master", build_vignettes = TRUE)
library(MCBUBayesPower)

## Install and load jagsUI R package
if (!require("jagsUI")) install.packages("jagsUI")
library(jagsUI)
```

Create folders for saving output

```
## Create folders

create_folders()
```

Fit model treating individual birds as the observation unit (i.e., Model 4), save
output, print traceplots and summaries of MCMC output.

```
## Fit Bayesian hierarchical population model treating individual birds as the observation unit
out4 <- fit_model4(mcbu_data_file = "data/distdata_mcbu.csv",
                   ni = 10500,
                   nb = 500,
                   nt = 3,
                   nc = 3,
                   save_output = TRUE,
                   jags_output_folder = "./output")


traceplot(out4)
options(max.print = 50000)
print(out4, 3)
```

Plot estimated global mean detection function

```
## Plot distance detection functions for individual models (i.e., input provided for 1 model argument)
## or functions from both models (i.e., input provided for both model argument) overlaid on the sample
detfn_plot(mod4_output = out4)

detfn_plot(mod4_output = out4, mod3_output = out3) # Note: must first fit model 3 (i.e., groups as obse
```

**Plot observer-specific detection functions overlaid with recorded observations of
bird groups.**

```
## Plot distance detection functions for individual observers including observed groups
obs_detfn_plot(mcbu_data_file = "data/distdata_mcbu.csv", mod_output = out4)
```

**Plot expected N estimated for each island and total for both islands in 2003 and
2018 and projected for 2028.**

```
## Plot Hall Island
EN_isl_plot(mod_output = out4, estimate = "hall")

## Plot St Matthew Island
EN_isl_plot(mod_output = out4, estimate = "stma")

## Plot total island
EN_isl_plot(mod_output = out4)
```

Plot percent population decline over the study period (15 years), annual exponential population growth rate (r), and annual geometric population growth rate (λ).

```
## Plot all 3
growthN_plot(mod_output = out4, estimate = "hall")
```

Plot estimated difference in density between islands.

```
## Plot estimated difference in island density
density_diff_plot(mod_output = out4)
```

Fit model treating groups of birds as the observation unit (i.e., Model 3), save output, and print traceplots and summaries of MCMC output.

```
## Fit Bayesian hierarchical population model treating groups of birds as the observation unit
out3 <- fit_model4(mcbu_data_file = "data/distdata_mcbu.csv",
                   ni = 10500,
                   nb = 500,
                   nt = 3,
                   nc = 3,
                   save_output = TRUE,
                   jags_output_folder = "./output")


traceplot(out3)
options(max.print = 50000)
print(out3, 3)
```

Simulation and Power Analysis Workflow

Simulate population growth and distance-sampling data sets, fit bayesian population model, estimate model parameters, save output

A subfolder within the `output` folder is created by the `run_mcbu_power` function to store and named based on simulated growth rate and number of surveys over a 10-year period. A subfolder within the simulation folder named `mcmc` also is created to store MCMC output as .Rdata files from individual simulations.

```
## Simulate data, fit model, and save mcmc output
run_mcbu_power(log_lambda0 = log(out4$mean$lambda_pop[,2]),
               r = log(0.75^(1/10)),
               mu_obs = out4$mean$mu_obs,
               sd_obs = out4$mean$sd_obs,
               survey_years = c(2018,2028),
               mcbu_data_file = "data/distdata_mcbu.csv",
               save_output = TRUE,
               batch = 1000,
               M = c(200,100),
               ni = 5500,
               nb = 500,
               nt = 1,
               nc = 1,
               use_parallel = FALSE)
```

Process MCMC output from simulation analysis

Two subfolders are created by the `process_mcbu_power` function alongside the `mcmc` subfolder, one named `figures` when plots need to be saved and one named `summary` for storing summary statistics of MCMC samples.

```
## Process mcmc output
process_mcbu_power(true_pctdecl = 25,
                   output_filepath = "../output/mcbu_power_2surveys_r-0.029/mcmc")
```

Create summary plots of simulation results

```
## Plot histogram of estimator bias for exponential growth rate (r)
bias_plot(bias = bias)


## Plot histogram of estimator coefficient of variation (CV) for exponential growth rate (r)
cv_plot(cv = cv)

## Plot histogram of estimator squared error for exponential growth rate (r)
sq_err_plot(sq_err = sq_err)

## Plot of 95% Bayesian credible intervals for all simulations
ci_cover_plot(pctdecl_ests = pctdecl_ests,
              cover_95 = cover_95,
              true_pctdecl = 25)
```

R Session Info

```
sessionInfo()
```

```
## R version 4.0.3 (2020-10-10)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 19042)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=C
## [2] LC_CTYPE=English_United States.1252
## [3] LC_MONETARY=English_United States.1252
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.1252
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] MCBUBayesPower_0.0.0.9000
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_1.0.5        compiler_4.0.3    prettyunits_1.1.1 remotes_2.2.0
##  [5] tools_4.0.3       testthat_3.0.0    digest_0.6.27     pkgbuild_1.1.0
##  [9] pkgload_1.1.0     evaluate_0.14     memoise_1.1.0     lattice_0.20-41
## [13] rlang_0.4.8       cli_2.2.0         jagsUI_1.5.1      rstudioapi_0.13
## [17] yaml_2.2.1        parallel_4.0.3    xfun_0.19         coda_0.19-4
## [21] withr_2.3.0       stringr_1.4.0     roxygen2_7.1.1    knitr_1.30
## [25] xml2_1.3.2        desc_1.2.0        rjags_4-10        fs_1.5.0
## [29] devtools_2.3.2    rprojroot_2.0.2   grid_4.0.3        glue_1.4.2
## [33] R6_2.5.0          processx_3.4.4    fansi_0.4.1       rmarkdown_2.5
## [37] sessioninfo_1.1.1 callr_3.5.1       purrr_0.3.4       magrittr_2.0.1
## [41] htmltools_0.5.0   ps_1.4.0          ellipsis_0.3.1    usethis_1.6.3
## [45] assertthat_0.2.1  stringi_1.5.3     crayon_1.3.4
```