Methods and Workflow

Juliana Masseloux and Brian Gerber

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Data summary

Species abbreviations

- Black-shanked douc-langur (BSDL)
- Yellow-cheeked gibbon (YCGI)
- Pig-tailed macaque (PTMA)
- Long-tailed macaque (LTMA)
- Common palm civet (CPCI)
- Small-toothed palm civet (STPC)
- Yellow-throated marten (YTMA)
- Black giant squirrel (BGSQ)
- Indian giant flying squirrel (IGFS)

Seasons

- Wet Season: June to October 2019 and May to September 2020
- Dry Season: November 2019 to April 2020 In the occupancy analyses, SE1 is the factor covariate for dry season, with wet season as the intercept.

Covariates

- CC Canopy connections
- FBS Focal branch slope
- FBD Focal branch diameter
- DBH Tree DBH
- CAM Camera height
- CD Canopy level
- CAN Canopy height
- AC Absolute cover
- GRA Distance to grassland
- WA Distance to water
- RO Distance to road

Unstandardized site-level covariates may be loaded into R using > load(unstandardized_covariates)

Covariates were standardized in the model preparation code after removing rows (sites) from the species detection histories with all NAs (see below).

Single-species arboreal occupancy model

MARK data preparation

Import covariate dataset and list of detection histories. Replicate the covariate file into 3 seasons (63 rows).

```r
load("unstandardized_covariates")

load("det_hist_SSOM")

arb_covs = rbind(arb_covs,arb_covs,arb_covs)
```

Create a season-level covariate where the intercept is the wet season (2019 and 2020) and SE1 is the dry season (2020).

```r
SE1 = c(rep(0,21),rep(1,21),rep(0,21))

arb_covs = cbind(arb_covs, SE1)
```

Load the detection history matrix and prepare a MARK input file using package 'RMark' (Laake, 2013).

We provide an example using yellow-throated marten (YTMA), but this code is reproducible by indexing for other species using the abbreviated species names specified in the README.txt file.

```r
YTMA = (det_hist_arb[["YTMA"]])

#identify rows with all NAs

index = which(!!rowSums(!is.na(YTMA)) == FALSE)

#Remove the NA rows from species detection histories and covariate table

YTMA[which(is.na(YTMA), arr.ind = TRUE)]= "."

YTMA = YTMA[-index,]

covs = arb_covs[-index,]

#Standardize new covariates

st.cov = apply(covs[,1:11], 2, FUN=function(x){scale(x)})

st.cov = cbind(st.cov,covs[,12])

rownames(st.cov) = rownames(covs)

#create mark input file
mark_input=as.data.frame(apply(YTMA,1,paste,collapse=""))
mark_input <-data.frame(lapply(mark_input, as.character), stringsAsFactors=FALSE)
colnames(mark_input)= c("ch")

mark_input2=data.frame(mark_input,st.cov)
```

```r
# Process data
ssom.process = process.data(mark_input2, model = "Occupancy")
ssom.ddl = make.design.data(ssom.process)

# Create function to fit all model combinations

fit.models <- function() {

  # Define p models
  p.CAM.CC.FBS = list(formula= ~ CAM + CC + FBS + SE1)
  p.CC.CD = list(formula= ~ CC + CD + SE1)
  p.FBD.CC = list(formula= ~ FBD + CC + SE1)
  p.FBD.FBS.CD = list(formula= ~ FBD + FBS + CD + SE1)
  p.CAM.FBD = list(formula= ~ CAM + FBD + SE1)

  # Define Psi models
  Psi.AC = list(formula = ~ AC)
  Psi.CC = list(formula = ~ CC)
  Psi.DBH = list(formula = ~ DBH)
  Psi.CAN = list(formula = ~ CAN)
  Psi.CD = list(formula = ~ CD)
  Psi.WA = list(formula = ~ WA)
  #Psi.GRA = list(formula = ~ GRA)
  Psi.RO = list(formula = ~ RO)

  # Create model list
  cml = create.model.list("Occupancy")

  # Run and return marklist of models
  return(mark.wrapper(cml, data = ssom.process, ddl = ssom.ddl))
}

YTMA.models <- fit.models()

#save as a MARK input file

export.MARK(ssom.process, "YTMA_SSOM", model = YTMA.models, replace = TRUE, chat = 1,
title = "YTMA SSOM", ind.covariates = "all")
```

This will create an input (.Rinp) file with 35 unique models. This input file can be imported into MARK using File -> RMark Import -> selecting the 'YTMA_SSOM.Rinp' file. Each model can be run using Bayesian analysis by selecting the model and going to the Run tab -> Run current model -> keeping the defaults and checking the 'MCMC estimation' box (Figure 1).

Further specifications can be added in the following dialogue box including tuning (4000), burn in (2000), iterations (10,000), and chains (2) (Figure 2).

After the model has finished running, MARK will output an excel sheet with the model WAIC and the real and beta estimates for the model parameters.
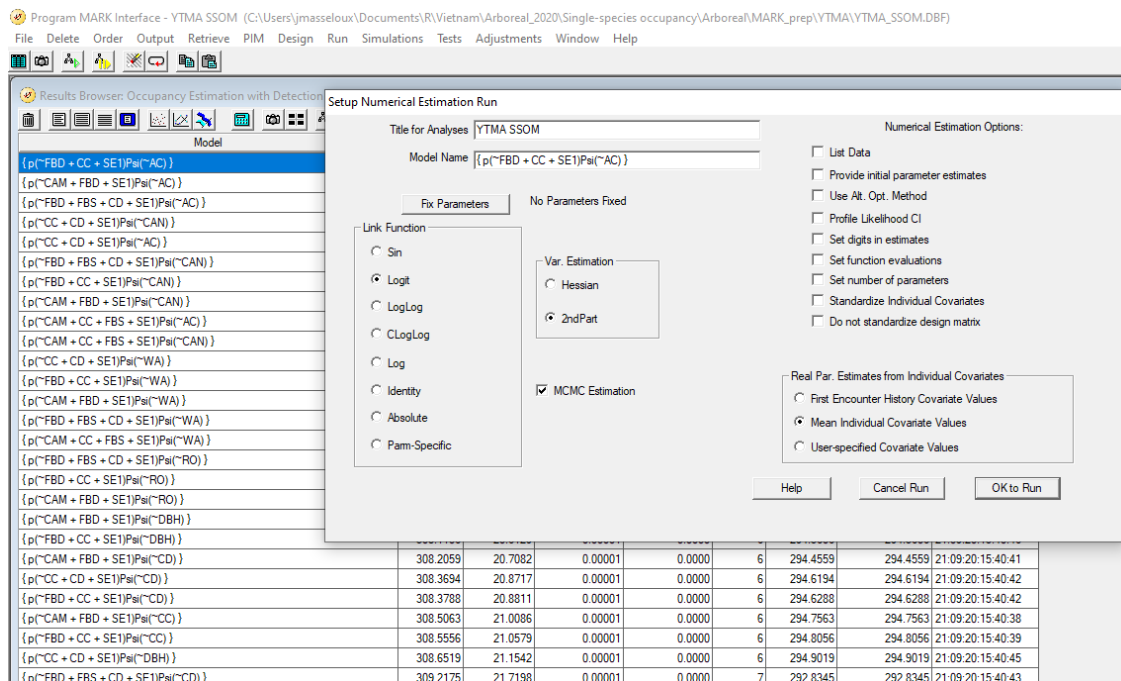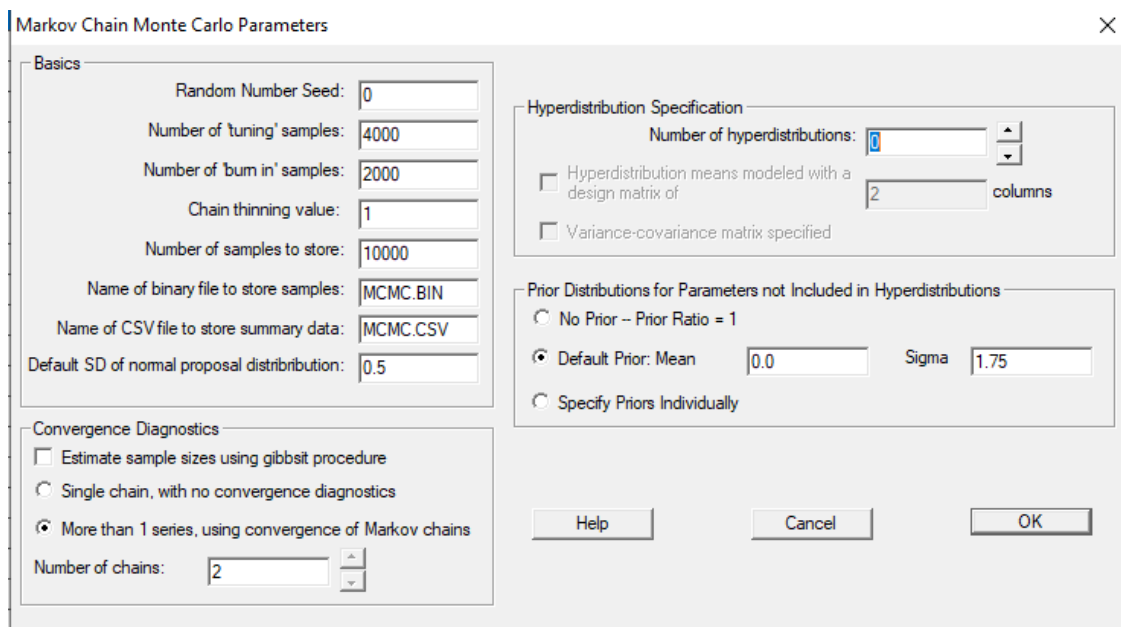
Figure 1: Specifying MCMC estimation

Figure 2: Specifications for Bayesian SSOM MARK analysis

Multi-scale arboreal occupancy model

MARK data preparation

Detection history for semi-arboreal multi-scale occupancy models can be loaded into R using `load(det_hist_MSOM)`

Because 'RMark' cannot yet import multi-scale occupancy models into MARK, the multi-scale models have to be individually input into program MARK.

The detection history and covariates can still be formatted in RMark and imported into MARK following the same code as above using the 'det_hist_MSOM' dataset. The covariate data should be duplicated to apply to both arboreal and terrestrial sites using `new.cov = cbind(st.cov,st.cov)` and have the dimensions 116 x 12 to match the detection history matrix.

The MARK input file will be specified as follows:

```r
mark_input=as.data.frame(apply(YTMA,1,paste,collapse=""))
mark_input <- data.frame(lapply(mark_input, as.character), stringsAsFactors=FALSE)
colnames(mark_input)= c("ch")

mark_input2=data.frame(mark_input,new.cov)

mscale.proc=process.data(mark_input2,model="MultScalOcc",begin.time=1,mixtures=27)

export.MARK(mscale.proc, "YTMA_MSOM", replace = TRUE, title = "YTMA mscale", ind.covariates = "all")
```

This will create an input (.Rinp) file which can be imported into MARK using File -> RMark Import -> selecting the 'YTMA_MSOM.Rinp' file.

Open the Parameter Index chart (PIM tab) -> Right click each detection (p) row and select 'constant' then renumber without overlap. The PIM should resemble Figure 3:
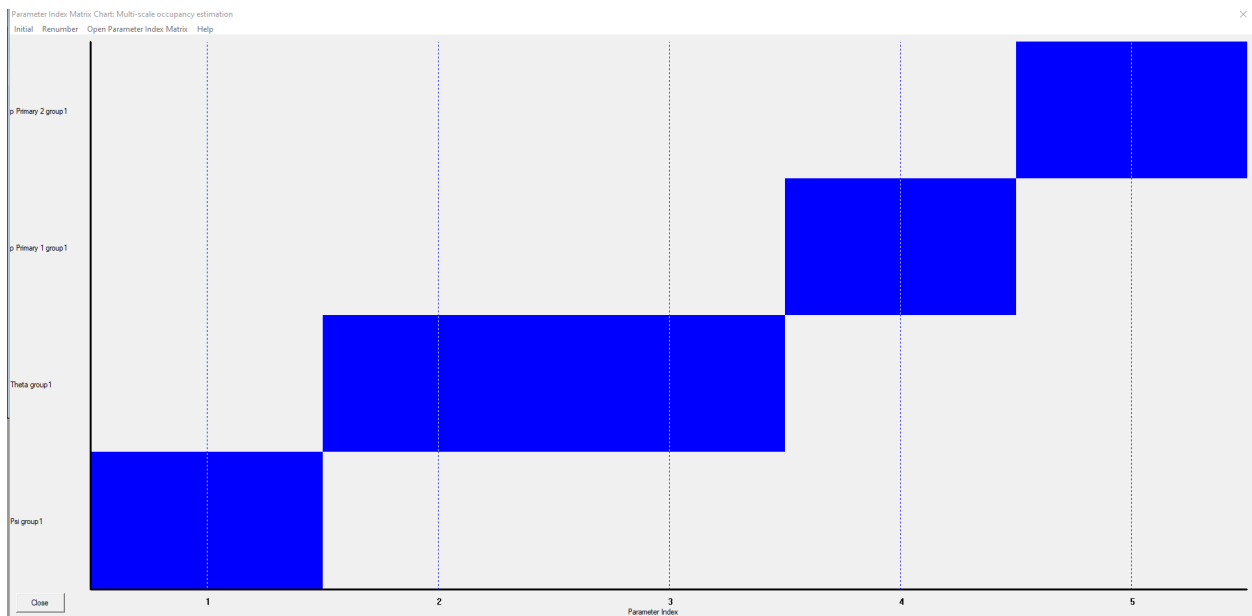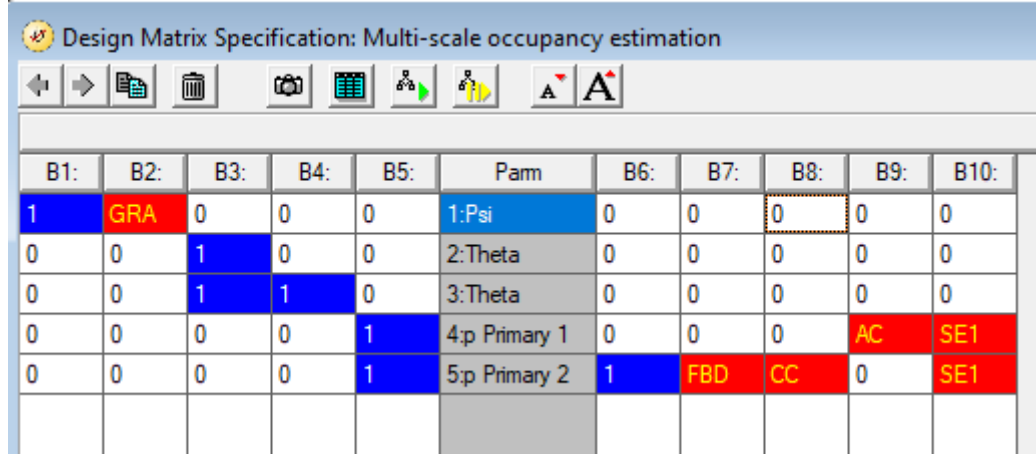

Figure 3: Specifications for MSOM PIM

Design a new model by going to Design -> Reduced and fill the Design Matrix with the PIM specifications and the covariates on occupancy and detection per the list of model hypotheses detailed in Appendix D. Make sure the detection covariates are applied to the correct method. Row 4 (p 1) refers to the terrestrial scale, and Row 5 (p 2) to the arboreal scale. Thus model psi(GRA) theta(.) p(arb:FBD + arb:CC + terr:AC + SE1) will look like Figure 4.

Figure 4: Specifications for MSOM design matrix

Once a model has been prepared, run using Bayesian analysis following the same method for SSOM above.

Generalized linear mixed models

Data for arboreal species general linear mixed models (GLMMs) can be loaded into R using `load(GLMM_arb)`

Count: number of independent detections (> 30 minutes between detections of same species)

Effort: total number of site-level active camera trap days (all GLMM models offset by effort)

Negative-binomial GLMMs were fit using a Bayesian framework R using the package 'rstanarm' (Goodrich, Gabry, and Brilleman 2020). See Appendix G for further details on methods and model hypotheses.