

MARSS and Hwange data

24/09/2020

Read in and visualize data

Prerequisites.

```
library(tidyverse)
theme_set(theme_light())
library(janitor)
library(lubridate)
library(MARSS)
```

Read in the data.

```
wps7293 <- readxl::read_xls("data/Water point surveys 1972 - 1993 - Total Number.xls") %>% clean_names()
wps2001 <- readxl::read_xls("data/Water point surveys 1994 - 2001 - Detailed.xls") %>% clean_names()
wps2005 <- readxl::read_xls("data/Water point surveys 2002 - 2005 - Detailed.xls") %>% clean_names()
```

```
wps7293 %>%
  count(water_point, sort = TRUE)
```

```
## # A tibble: 175 x 2
##   water_point      n
##   <chr>          <int>
## 1 NGWESHLA        173
## 2 KENNEDY 1       172
## 3 KENNEDY 2       167
## 4 NYAMANDHLOVU    167
## 5 SAMAVUNDHLA     159
## 6 MAKOLOLO I      154
## 7 MAKWA           150
## 8 BIG TOMS        148
## 9 LIVINGI         143
## 10 MASUMA DAM     140
## # ... with 165 more rows
```

```
wps7293 %>%
  count(species, sort = TRUE)
```

```
## # A tibble: 32 x 2
##   species      n
##   <chr>        <int>
## 1 Elephant     802
## 2 Zebra        706
```

```
## 3 Kudu 697
## 4 Warthog 678
## 5 Giraffe 588
## 6 Impala 585
## 7 Spotted hyaena 572
## 8 Sable 554
## 9 Buffalo 527
## 10 Black Backed Jackal 448
## # ... with 22 more rows
```

```
wps7293 %>%
  count(year, sort = TRUE)
```

```
## # A tibble: 14 x 2
##   year      n
##   <dbl> <int>
## 1 1990    918
## 2 1992    854
## 3 1988    820
## 4 1982    795
## 5 1989    701
## 6 1991    696
## 7 1987    689
## 8 1993    626
## 9 1985    556
## 10 1984    501
## 11 1973    456
## 12 1975    357
## 13 1986    311
## 14 1972    150
```

```
dat <- wps7293 %>%
  filter(species %in% c("Elephant", "Giraffe", "Lion", "Impala")) %>%
  select(year, species, total) %>%
  mutate(species = as_factor(species))
dat
```

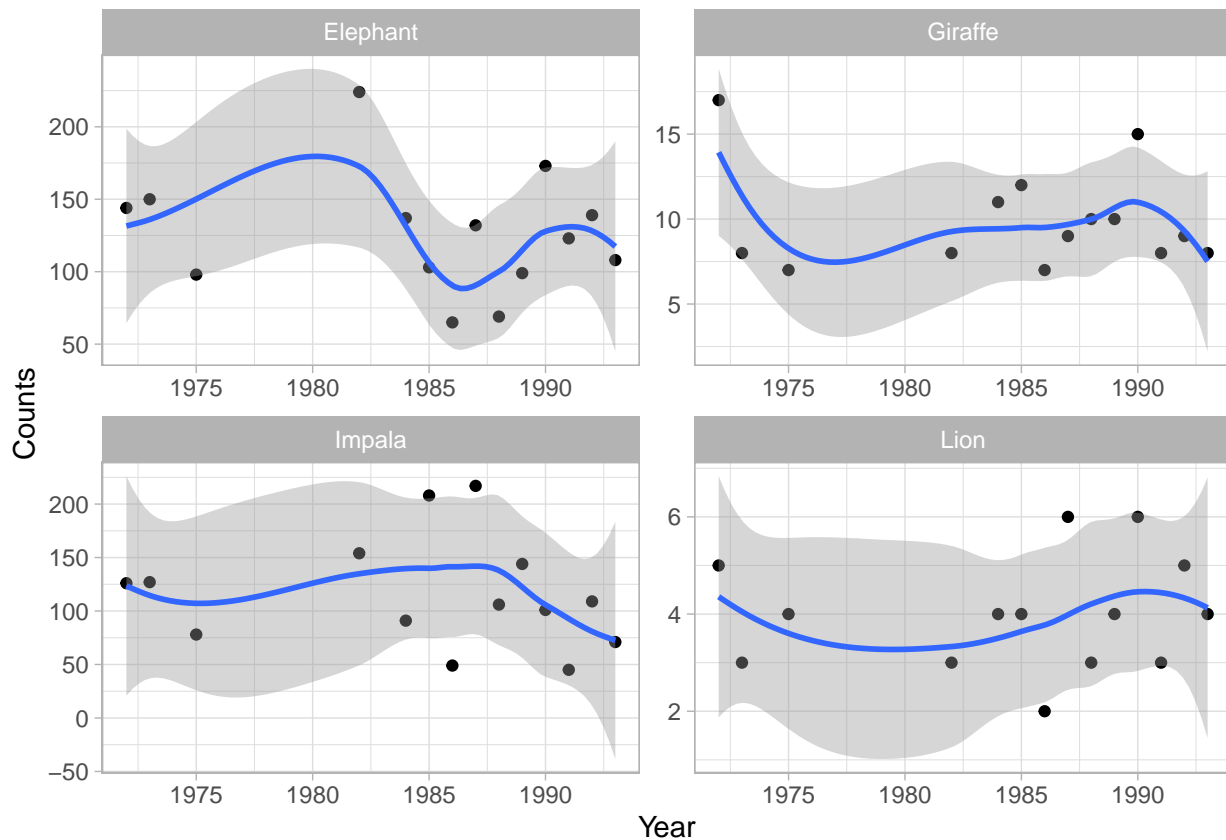
```
## # A tibble: 2,252 x 3
##   year species total
##   <dbl> <fct>   <dbl>
## 1 1972 Elephant    24
## 2 1972 Giraffe     7
## 3 1972 Impala      6
## 4 1972 Elephant   303
## 5 1972 Giraffe    25
## 6 1972 Lion        1
## 7 1972 Elephant  129
## 8 1972 Giraffe    10
## 9 1972 Impala   511
## 10 1972 Lion        1
## # ... with 2,242 more rows
```

Plot all data.

```

dat %>%
  group_by(year, species) %>%
  summarise(mean_biomass = round(mean(total))) %>%
  ggplot() +
  aes(x = year, y = mean_biomass) +
  geom_point() +
  geom_smooth() +
  labs(x = "Year",
       y = "Counts",
       color = "Species") +
  facet_wrap(~species, scales = "free")

```



MARSS model in the frequentist framework

We consider a model with the following assumptions: * All prey species share the same process variance. * All predator species share the same process variance. * Prey and predator species have different measurement variances. * Measurement errors are independent. * Process errors are independent.

We fit this model with the MARSS package. We need to specify the ingredients first.

```

Q <- matrix(list(0), 4, 4)
diag(Q) <- c("Prey", "Prey", "Prey", "Predator")
R <- matrix(list(0), 4, 4)
diag(R) <- c("Prey", "Prey", "Prey", "Predator")
model.0 <- list(
  B = "unconstrained", U = "zero", Q = Q,

```

```

Z = "identity", A = "zero", R = R,
x0 = "unequal", tinitx = 1
)
model.0

```

```

## $B
## [1] "unconstrained"
##
## $U
## [1] "zero"
##
## $Q
##      [,1] [,2] [,3] [,4]
## [1,] "Prey" 0    0    0
## [2,] 0      "Prey" 0    0
## [3,] 0      0      "Prey" 0
## [4,] 0      0      0      "Predator"
##
## $Z
## [1] "identity"
##
## $A
## [1] "zero"
##
## $R
##      [,1] [,2] [,3] [,4]
## [1,] "Prey" 0    0    0
## [2,] 0      "Prey" 0    0
## [3,] 0      0      "Prey" 0
## [4,] 0      0      0      "Predator"
##
## $x0
## [1] "unequal"
##
## $tinitx
## [1] 1

```

Then we fit the model.

```

mod.0 <- dat %>%
  group_by(year, species) %>%
  summarise(mean_biomass = round(mean(total))) %>%
  ungroup() %>%
  pivot_wider(names_from = species, values_from = mean_biomass) %>%
  select(-year) %>%
  t() %>%
  MARSS(model = model.0)

```

```

## Stopped at iter=227 in MARSSkem at x0 update.
## There are 0s on R diagonal. x0 assoc with these must be fixed (not estimated)
## when using the EM algorithm. Try method="BFGS". Type MARSSinfo("x0R0") for help.
## par, kf, states, iter, loglike are the last values before the error.
## Try control$safe=TRUE which uses a slower but slightly more robust algorithm.
## Use control$trace=1 to generate a more detailed error report. See user guide for insight.

```

We may get the estimates in a more readable format. For example, let's have a look to the interactions. These estimates describe the effect of the density of species j on the per capita growth rate of species i .

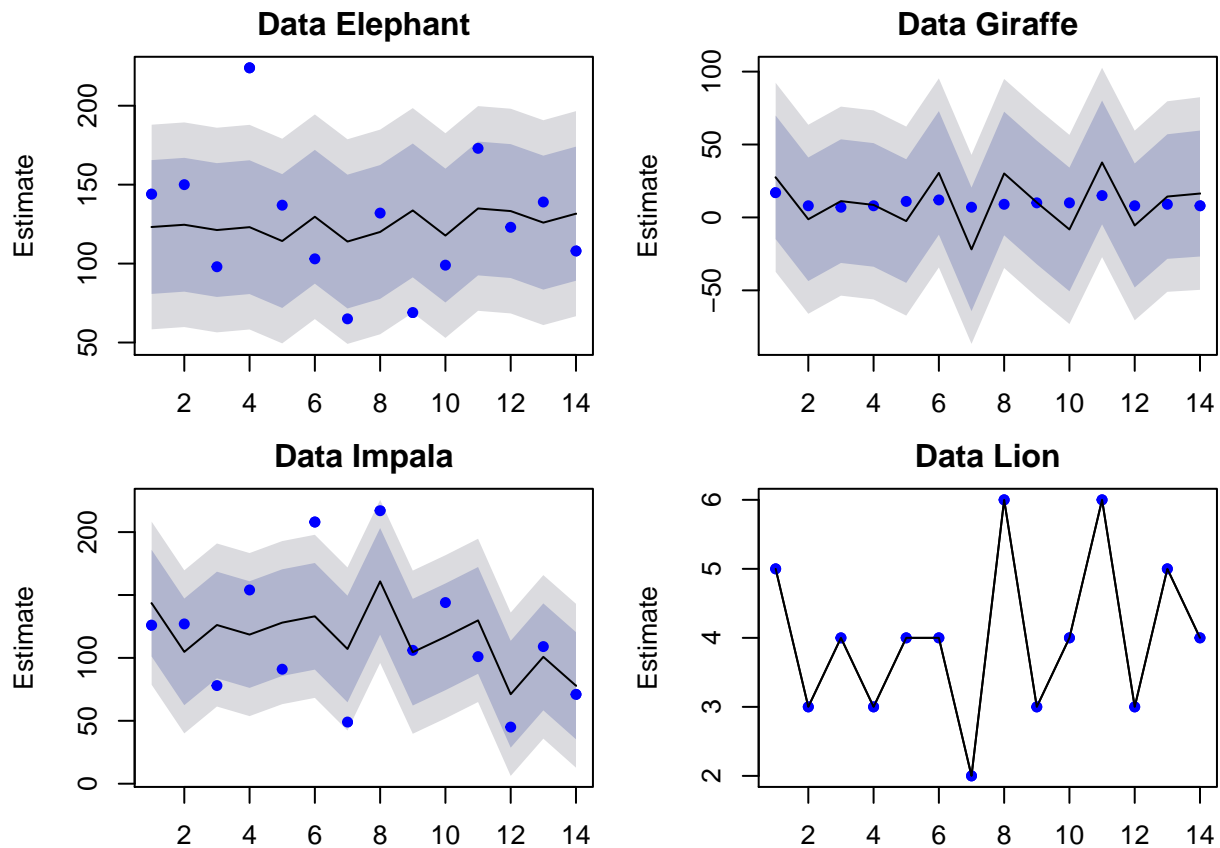
```
B.0 <- coef(mod.0, type = "matrix")$B[1:4, 1:4]
rownames(B.0) <- colnames(B.0) <- c("Elephant", "Giraffe", "Impala", "Lion")
print(B.0, digits = 2)
```

```
##           Elephant Giraffe  Impala   Lion
## Elephant    0.604  -0.775  0.1141  11.03
## Giraffe    -0.282  -1.459  0.0186  14.19
## Impala     0.466  -1.159  1.0190 -13.40
## Lion       0.026  -0.086 -0.0017  0.43
```

The effect of species j on species i is given by the cell at i -th row and j -th column. The B matrix suggests that Lion has a negative effect on impala and positive on Elephant and Giraffe. In the diagonal, we have the strength of density-dependence: if species i is density-independent, then $B_{i,i}$ equals 1, like Impala; smaller $B_{i,i}$ means more density dependence, like Giraffe.

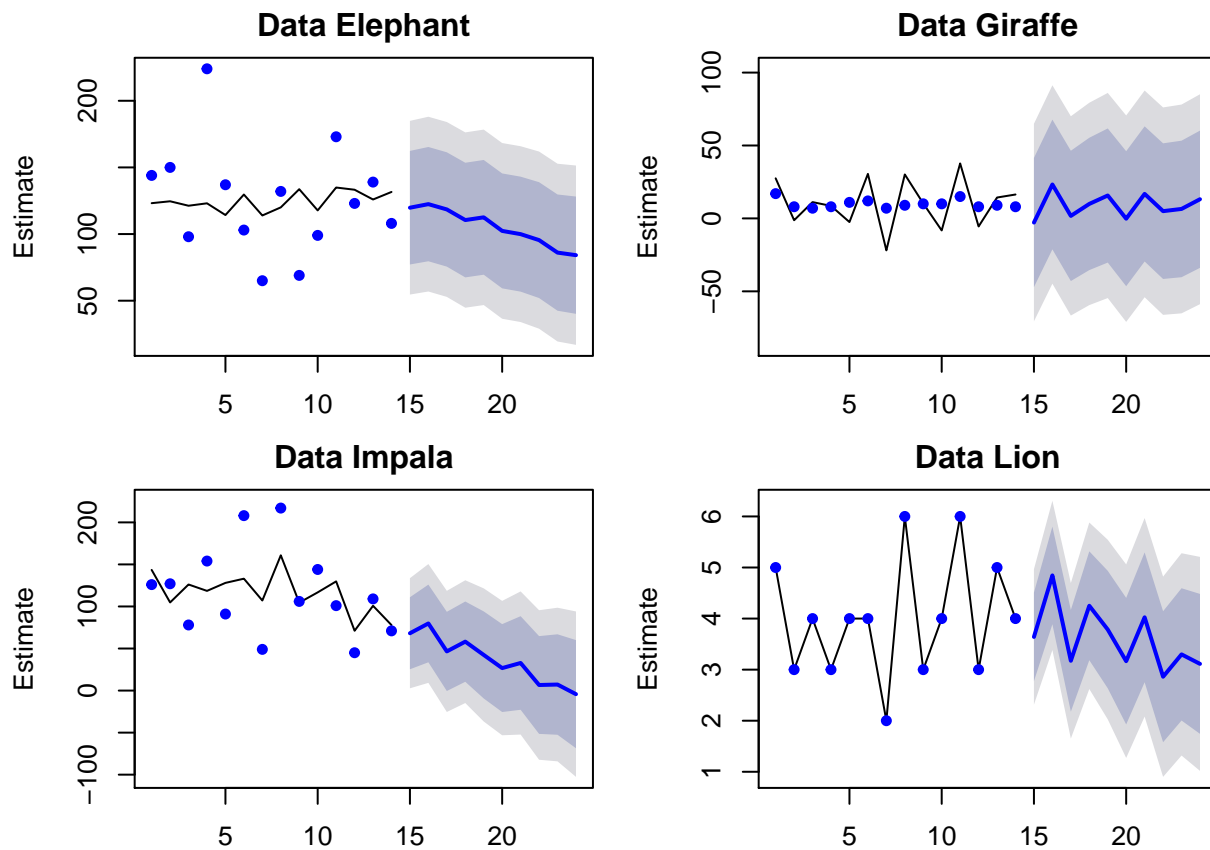
Compare observations to fitted values.

```
fr <- forecast.marssMLE(mod.0, h=0)
plot(fr)
```



Forecast 10 years ahead.

```
fr <- forecast.marssMLE(mod.0, h = 10)
plot(fr)
```



Try again, with a simpler model.

```
Q <- matrix(list(0), 4, 4)
diag(Q) <- c("all", "all", "all", "all")
R <- matrix(list(0), 4, 4)
diag(R) <- c("all", "all", "all", "all")
model.0 <- list(
  B = "unconstrained", U = "zero", Q = Q,
  Z = "identity", A = "zero", R = R,
  x0 = "unequal", tinitx = 1
)
model.0
```

```
## $B
## [1] "unconstrained"
##
## $U
## [1] "zero"
##
## $Q
##      [,1] [,2] [,3] [,4]
## [1,] "all" 0    0    0
## [2,] 0    "all" 0    0
```

```
## [3,] 0      0      "all" 0
## [4,] 0      0      0      "all"
##
## $Z
## [1] "identity"
##
## $A
## [1] "zero"
##
## $R
##      [,1] [,2] [,3] [,4]
## [1,] "all" 0    0    0
## [2,] 0     "all" 0    0
## [3,] 0     0     "all" 0
## [4,] 0     0     0     "all"
##
## $x0
## [1] "unequal"
##
## $tinitx
## [1] 1
```

Then we fit the model.

```
mod.0 <- dat %>%
  group_by(year, species) %>%
  summarise(mean_biomass = round(mean(total))) %>%
  ungroup() %>%
  pivot_wider(names_from = species, values_from = mean_biomass) %>%
  select(-year) %>%
  t() %>%
  MARSS(model = model.0)
```

```
## Warning! Reached maxit before parameters converged. Maxit was 500.
## neither abstol nor log-log convergence tests were passed.
##
## MARSS fit is
## Estimation method: kem
## Convergence test: conv.test.slope.tol = 0.5, abstol = 0.001
## WARNING: maxit reached at 500 iter before convergence.
## Neither abstol nor log-log convergence test were passed.
## The likelihood and params are not at the ML values.
## Try setting control$maxit higher.
## Log-likelihood: -213.3287
## AIC: 470.6574 AICc: 501.3241
##
##      Estimate
## R.all      15.33054
## B.(1,1)    -0.00245
## B.(2,1)     0.02059
## B.(3,1)     0.04521
## B.(4,1)    -0.01532
## B.(1,2)    13.11363
```

```
## B.(2,2)          0.20074
## B.(3,2)          9.89028
## B.(4,2)          0.72821
## B.(1,3)         -0.30259
## B.(2,3)          0.03413
## B.(3,3)          0.47642
## B.(4,3)         -0.00785
## B.(1,4)          8.13902
## B.(2,4)          0.18946
## B.(3,4)         -11.47843
## B.(4,4)         -0.16077
## Q.all            7.35896
## x0.X.Elephant 143.82620
## x0.X.Giraffe   11.54587
## x0.X.Impala   125.70464
## x0.X.Lion       4.60775
## Initial states (x0) defined at t=1
##
## Standard errors have not been calculated.
## Use MARSSparamCIs to compute CIs and bias estimates.
##
## Convergence warnings
## Warning: the R.all parameter value has not converged.
## Warning: the Q.all parameter value has not converged.
## Warning: the logLik parameter value has not converged.
## Type MARSSinfo("convergence") for more info on this warning.
```

We may get the estimates in a more readable format. For example, let's have a look to the interactions. These estimates describe the effect of the density of species j on the per capita growth rate of species i .

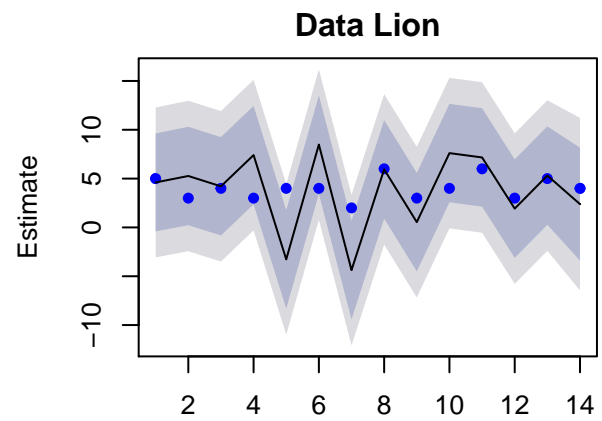
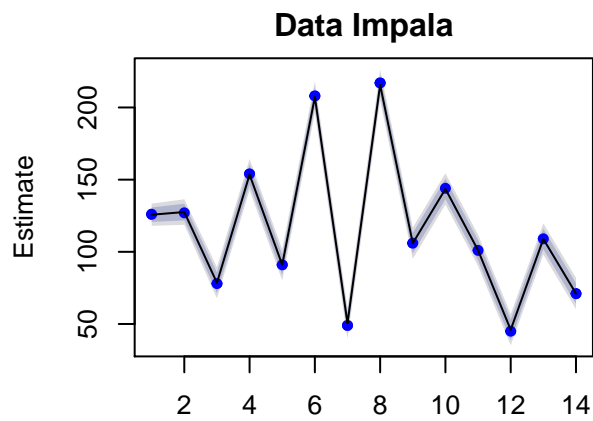
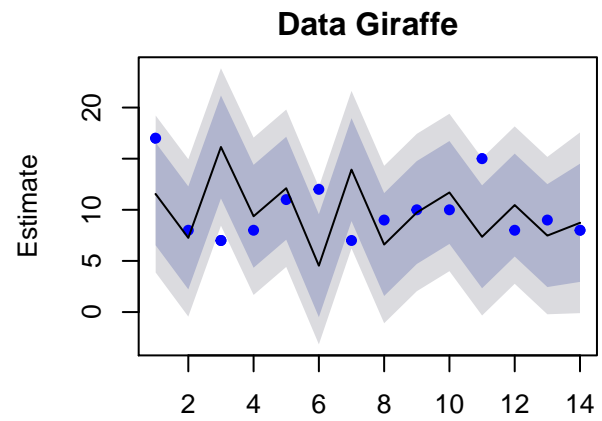
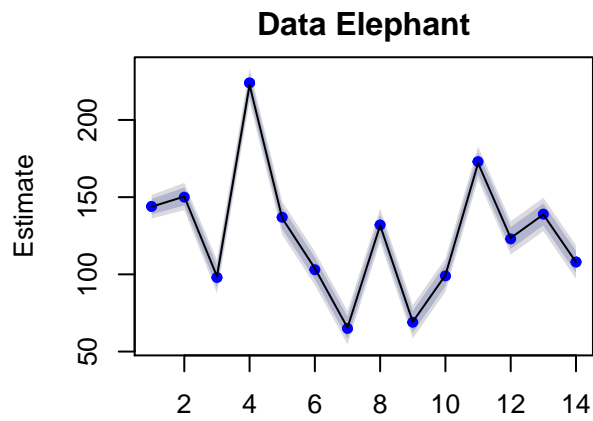
```
B.0 <- coef(mod.0, type = "matrix")$B[1:4, 1:4]
rownames(B.0) <- colnames(B.0) <- c("Elephant", "Giraffe", "Impala", "Lion")
print(B.0, digits = 2)
```

```
##           Elephant Giraffe Impala  Lion
## Elephant -0.0024   13.11 -0.3026   8.14
## Giraffe   0.0206    0.20  0.0341   0.19
## Impala    0.0452    9.89  0.4764 -11.48
## Lion      -0.0153    0.73 -0.0079  -0.16
```

The effect of species j on species i is given by the cell at i -th row and j -th column. The B matrix suggests that Lion has a negative effect on impala and positive on Elephant and Giraffe. In the diagonal, we have the strength of density-dependence: if species i is density-independent, then $B_{i,i}$ equals 1, like Impala; smaller $B_{i,i}$ means more density dependence, like Giraffe.

Compare observations to fitted values.

```
fr <- forecast.marssMLE(mod.0, h=0)
plot(fr)
```

Forecast 10 years ahead.

```
fr <- forecast.marssMLE(mod.0, h = 10)
plot(fr)
```

