

Simultaneous autoregressive process

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```
library(tinyVAST)
library(igraph)
```

`tinyVAST` is an R package for fitting vector autoregressive spatio-temporal (VAST) models using a minimal and user-friendly interface. We here show how it can fit a multivariate second-order autoregressive (AR2) model including spatial correlations using a simultaneous autoregressive (SAR) process specified using *igraph*.

To do so, we first load salmon returns, and remove 0s to allow comparison between Tweedie and lognormal distributions.

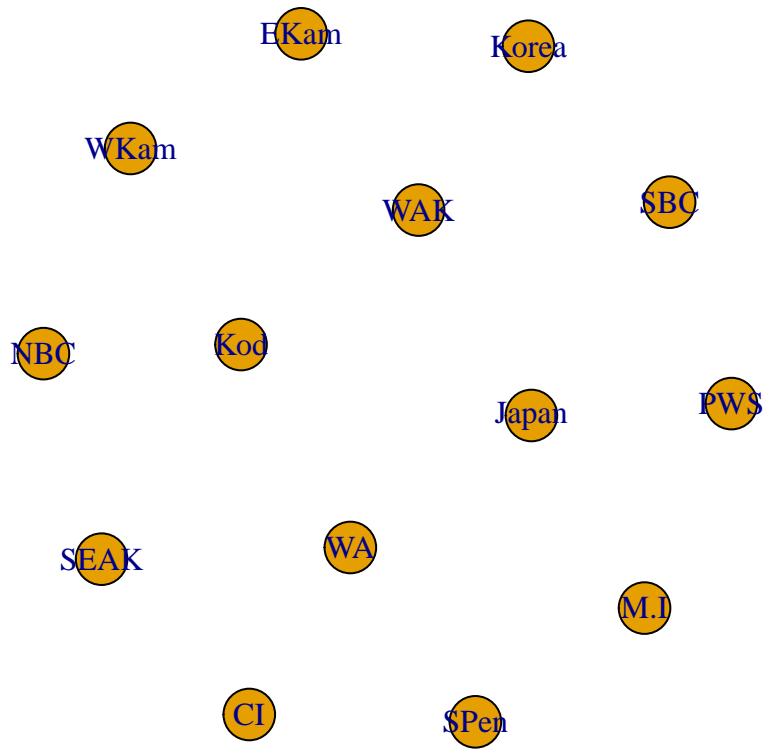
```
data( salmon_returns )

# Transform data
salmon_returns$Biomass_nozeros = ifelse( salmon_returns$Biomass==0,
                                         NA, salmon_returns$Biomass )

Data = na.omit(salmon_returns)
```

We first explore an AR2 process, with independent variation among regions. This model shows a substantial first-order autocorrelation for sockeye and chum, and substantial second-order autocorrelation for pink salmon. An AR(2) process is stationary if $\phi_1 + \phi_2 < 1$ and $\phi_2 - \phi_1 < 1$, and this stationarity criterion suggests that each time-series is close to (but not quite) nonstationary.

```
# Define graph for SAR process
unconnected_graph = make_empty_graph( nlevels(Data$Region) )
V(unconnected_graph)$name = levels(Data$Region)
plot(unconnected_graph)
```



```
# Define SEM for AR2 process
dsem = "
  sockeye -> sockeye, -1, lag1_sockeye
  sockeye -> sockeye, -2, lag2_sockeye

  pink -> pink, -1, lag1_pink
  pink -> pink, -2, lag2_pink

  chum -> chum, -1, lag1_chum
  chum -> chum, -2, lag2_chum
"

# Fit tinyVAST model
mytiny0 = fit(
  formula = Biomass_nozeros ~ 0 + Species + Region,
  data = Data,
```

```

dsem = dsem,
data_colnames = list(variable="Species", time="Year", spatial="Region", distribution="Species"),
family = list( "chum" = lognormal(),
               "pink" = lognormal(),
               "sockeye" = lognormal() ),
spatial_graph = unconnected_graph,
control = tinyVASTcontrol( trace=0, profile="alpha_j", getsd=FALSE ) )
#> Warning in nlminb(start = opt$par, obj = obj$fn, gr = obj$gr, control = list(eval.max = control$eval

# Summarize output
Summary = summary(mytiny0, what="dsem")
knitr::kable( Summary, digits=3)

```

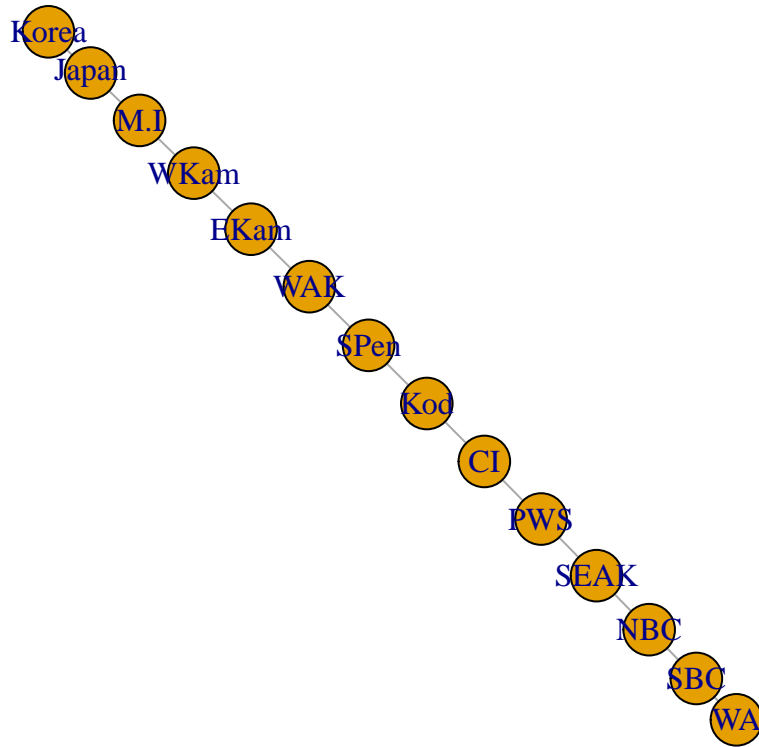
heads	to	from	parameter	start	lag	Estimate	Std_Error	z_value	p_value
1	sockeye	sockeye	1	NA	-1	0.807	NA	NA	NA
1	sockeye	sockeye	2	NA	-2	0.195	NA	NA	NA
1	pink	pink	3	NA	-1	0.050	NA	NA	NA
1	pink	pink	4	NA	-2	0.882	NA	NA	NA
1	chum	chum	5	NA	-1	0.675	NA	NA	NA
1	chum	chum	6	NA	-2	0.293	NA	NA	NA
2	pink	pink	7	NA	0	0.648	NA	NA	NA
2	chum	chum	8	NA	0	0.294	NA	NA	NA
2	sockeye	sockeye	9	NA	0	0.421	NA	NA	NA

We also explore an SAR process for adjacency among regions

```

# Define graph for SAR process
adjacency_graph = make_graph( ~ Korea - Japan - M.I - WKam - EKam -
                              WAK - SPen - Kod - CI - PWS -
                              SEAK - NBC - SBC - WA )
plot(adjacency_graph)

```



```

# Fit tinyVAST model
mytiny = fit(
  formula = Biomass_nozeros ~ 0 + Species + Region,
  data = Data,
  dsem = dsem,
  data_colnames = list(variable="Species", time="Year", spatial="Region", distribution="Species"),
  family = list( "chum" = lognormal(),
                 "pink" = lognormal(),
                 "sockeye" = lognormal() ),
  spatial_graph = adjacency_graph,
  control = tinyVASTcontrol( trace=0, profile="alpha_j", getsd=FALSE ) )
#> Warning in nlminb(start = opt$par, obj = obj$fn, gr = obj$gr, control = list(eval.max = control$eval

# Summarize output
Summary = summary(mytiny, what="dsem")
knitr::kable( Summary, digits=3)

```

heads	to	from	parameter	start	lag	Estimate	Std_Error	z_value	p_value
1	sockeye	sockeye	1	NA	-1	1.505	NA	NA	NA
1	sockeye	sockeye	2	NA	-2	-0.502	NA	NA	NA
1	pink	pink	3	NA	-1	0.010	NA	NA	NA
1	pink	pink	4	NA	-2	0.978	NA	NA	NA
1	chum	chum	5	NA	-1	1.685	NA	NA	NA
1	chum	chum	6	NA	-2	-0.688	NA	NA	NA
2	pink	pink	7	NA	0	0.575	NA	NA	NA
2	chum	chum	8	NA	0	0.077	NA	NA	NA
2	sockeye	sockeye	9	NA	0	0.232	NA	NA	NA

We can use AIC to compare these two models. This comparison suggests that spatial adjacency is not a parsimonious way to describe correlations among time-series.

```
# AIC for unconnected time-series
AIC(mytiny0)
#> [1] 49088.47
# AIC for SAR spatial variation
AIC(mytiny)
#> [1] 49755.91
```

Finally, we can plot observations and predictions for the selected model

```
# Compile long-form dataframe of observations and predictions
Resid = rbind( cbind(Data[,c('Species','Year','Region','Biomass_nozeros')], "Which"="Obs"),
               cbind(Data[,c('Species','Year','Region')], "Biomass_nozeros"=predict(mytiny0,Data), "Which"="Predict")

# plot using ggplot
library(ggplot2)
ggplot( data=Resid, aes(x=Year, y=Biomass_nozeros, col=Which) ) + # , group=yhat.id
  geom_line() +
  facet_grid( rows=vars(Region), cols=vars(Species), scales="free" ) +
  scale_y_continuous(trans='log') #
```

