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*.

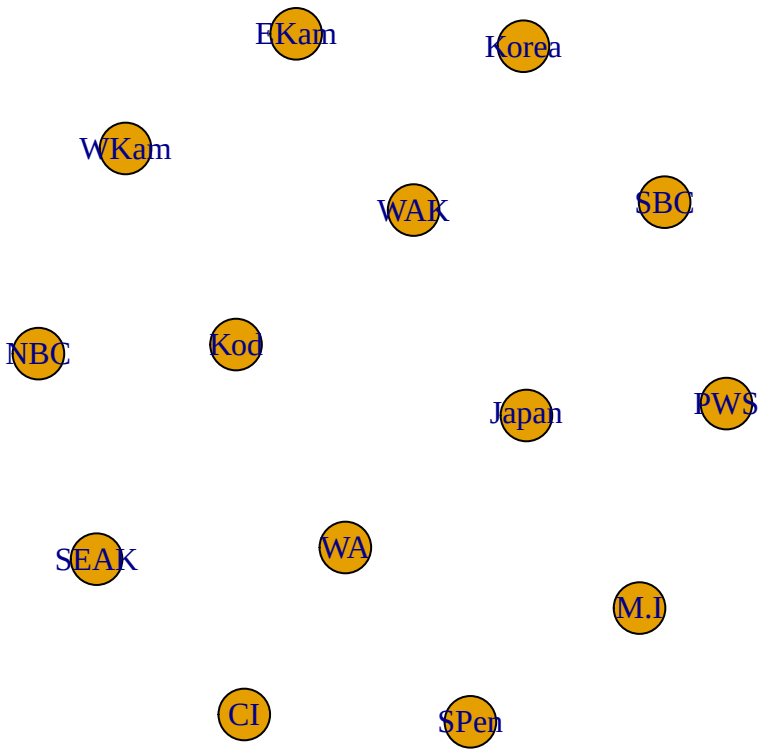
To do so, we first load salmong returns, and remove 0s to allow comparison between Tweedie and lognormal distributions.

```
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 = tinyVAST(
     formula = Biomass_nozeros ~ 0 + Species + Region,
     data = Data,
```

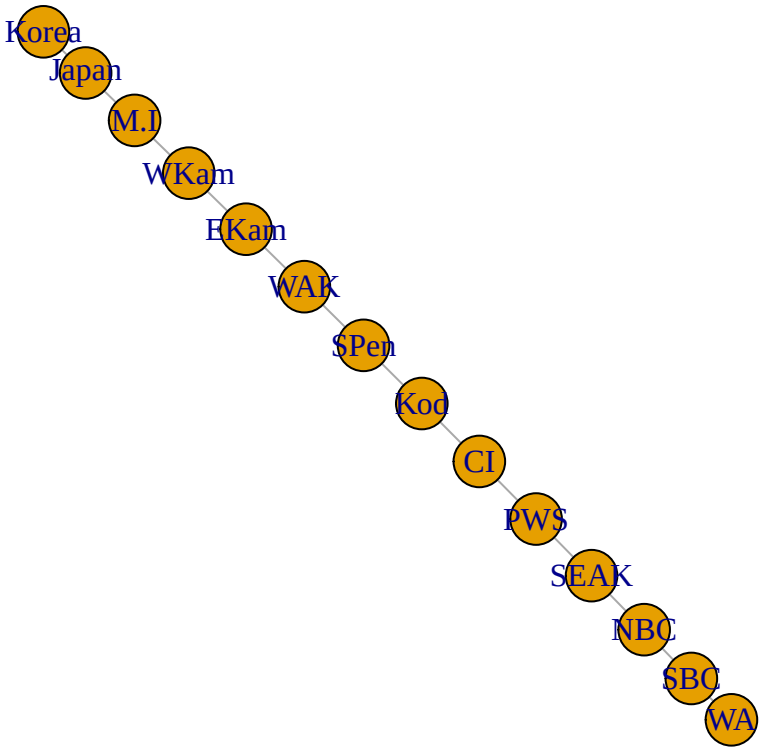
```
    dsem = dsem,
    data_colnames = list(variable="Species", time="Year", space="Region", distribution="Species"),
    family = list( "chum" = lognormal(),
                   "pink" = lognormal(),
                   "sockeye" = lognormal() ),
    spatial_graph = unconnected_graph,
    control = tinyVASTcontrol( trace=0, profile="alpha_j" ) )
#> Warning in nlminb(start = opt$par, objective = obj$fn, gradient = obj$gr, : NA/NaN function evaluati

# 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	0.059	13.710	0.000
1	sockeye	sockeye	2	NA	-2	0.195	0.059	3.308	0.001
1	pink	pink	3	NA	-1	0.050	0.019	2.640	0.008
1	pink	pink	4	NA	-2	0.882	0.022	39.933	0.000
1	chum	chum	5	NA	-1	0.675	0.103	6.584	0.000
1	chum	chum	6	NA	-2	0.293	0.100	2.940	0.003
2	pink	pink	7	NA	0	0.648	0.039	16.766	0.000
2	chum	chum	8	NA	0	0.294	0.035	8.352	0.000
2	sockeye	sockeye	9	NA	0	0.421	0.036	11.620	0.000

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 = tinyVAST(
     formula = Biomass_nozeros ~ 0 + Species + Region,
     data = Data,
     dsem = dsem,
     data_colnames = list(variable="Species", time="Year", space="Region", distribution="Species"),
     family = list( "chum" = lognormal(),
                          "pink" = lognormal(),
                          "sockeye" = lognormal() ),
     spatial_graph = adjacency_graph,
     control = tinyVASTcontrol( trace=0, profile="alpha_j" ) )
#> Warning in nlminb(start = opt$par, objective = obj$fn, gradient = obj$gr, : NA/NaN function evaluati

# 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	0.081	18.529	0.000
1	sockeye	sockeye	2	NA	-2	-0.502	0.082	-6.113	0.000
1	pink	pink	3	NA	-1	0.010	0.009	1.094	0.274
1	pink	pink	4	NA	-2	0.978	0.010	100.556	0.000
1	chum	chum	5	NA	-1	1.685	0.113	14.979	0.000
1	chum	chum	6	NA	-2	-0.688	0.113	-6.108	0.000
2	pink	pink	7	NA	0	0.575	0.041	14.158	0.000
2	chum	chum	8	NA	0	0.077	0.023	3.421	0.001
2	sockeye	sockeye	9	NA	0	0.232	0.029	7.977	0.000

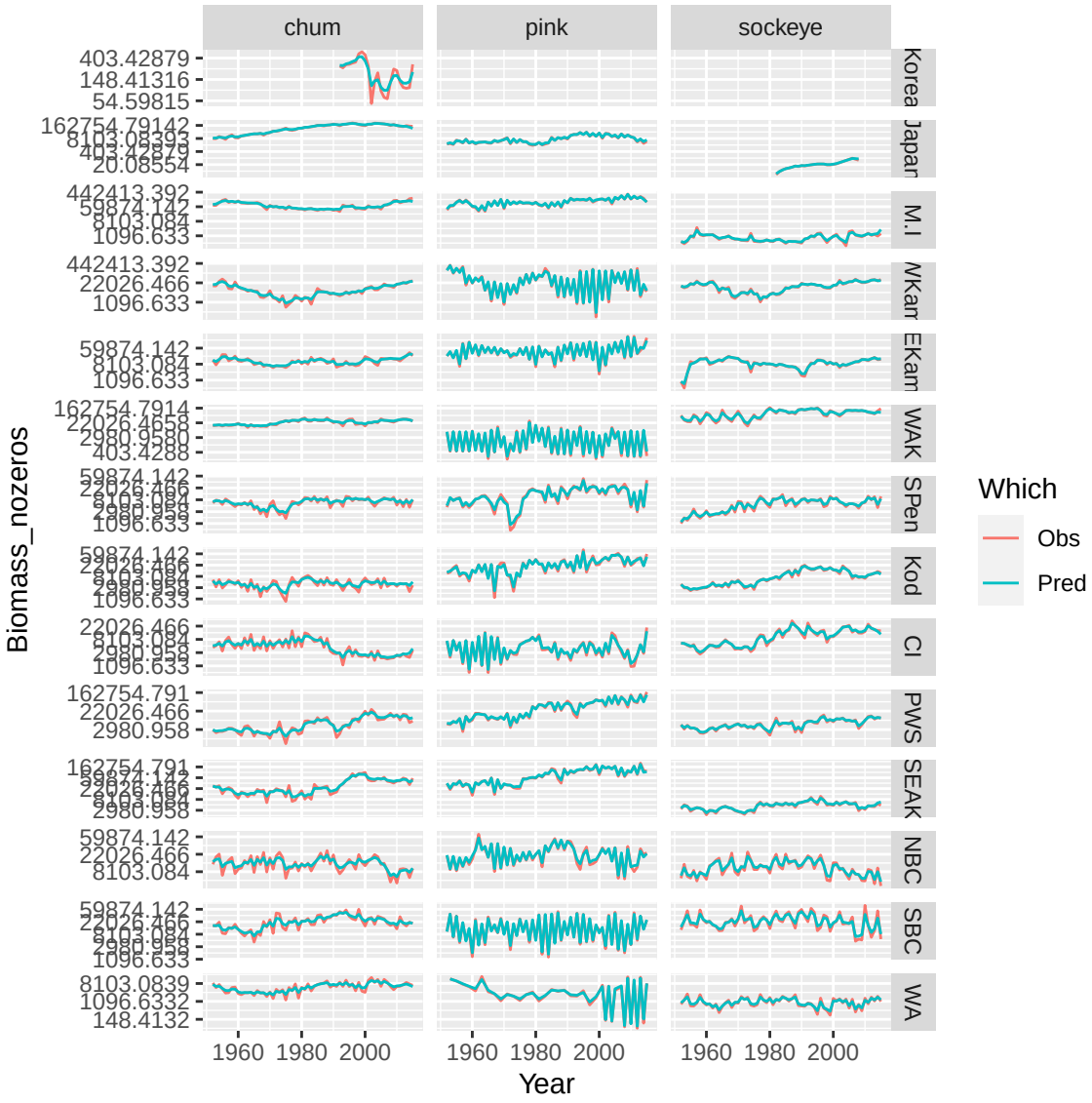
We can use AIC to compare these two models. This comparison suggests that spatial adjancency is not a parsimonious way to describe correlations among time-series.

```
# AIC for unconnected time-series
AIC(mytiny0)
#> [1] 49086.47
# 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), "Whi

# 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')  #
```


chum
pink
sockeye
Korea
Japan
M.I
WKam
EKam
WAK
SPen
Kod
CI
PWS
SEAK
NBC
SBC
WA
Biomass_nozeros
Year
1960
1980
2000
Which
Obs
Pred