Autocorrelation 2: Spatial Autocorrelation

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Biol 520C: Statistical modelling for biological data



1. Review

- 2. Spatial Autocorrelation
- 3. Detecting Spatial Autocorrelation
- 4. Correcting Spatial Autocorrelation

Review

и<mark>вс</mark>т О

Last lecture we saw how collecting data over time can result in temporally autocorrelated data, breaking the IID assumption.

We also saw how modifying the off-diagonals of the correlation matrix can correct for temporal autocorrelation.

$$V = \sigma^2 \underbrace{\begin{bmatrix} 1 & \rho & \cdots & \rho \\ \rho & 1 & \cdots & \rho \\ \vdots & \vdots & \ddots & \vdots \\ \rho & \rho & \cdots & 1 \end{bmatrix}}_{\text{correlation matrix}}$$

Finally, we learned a few ways to do this in R using functions from the nlme package.

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We touched on how, with autocorrelated data, each new datapoint does not bring a full independent datapoint worth of information.

When data are autocorrelated $n_{\rm effective} < n$, meaning SEs and CIs shrink faster than they should.

$$SE = \frac{\sigma}{\sqrt{n}} \qquad \qquad 95\% \, CI = \bar{x} \pm 1.96 \frac{\sigma}{\sqrt{n}}$$

This results in over-confidence in our estimates.

Effect is usually strongest on SEs and Cls, but autocorrelation can also impact the accuracy of parameter estimates.

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We also covered the idea that anything that causes some data points to be more similar to each other than others can result in autocorrelation.

This included: x

- **Time**: Data that are close together in time are more related.
- **Space**: Data that are close together in space are more related.

• **Phylogeny**: Species that are closer together on an evolutionary timescale are more related.



(Liang et al., 2019)

Spatial Autocorrelation



Biological data are often collected by measuring quantities over space (e.g., abundances, growth rates, species occurrences, etc.).

When this is the case, spatial autocorrelation can arise when the variation between the values of the datapoints is affected by their spatial distance.

The underlying reason for this is that many of the drivers of biological patterns such as environmental conditions, topography, ecosystem structure/composition act at large spatial scales, making data that are spatially close more similar than data collected further apart.



What if we're studying the effect of rainfall on spp. div. in the Amazon?



Source: Tadashi Fukami and Jes Coyle

Because rainfall is correlated in space, species diversity will also be correlated in space (if the relationship exists).

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Detecting Spatial Autocorrelation

Bubble plots

As with temporal autocorrelation, spatial autocorrelation can be difficult to see in a simple residuals vs. fitted plot (again, not designed for this purpose).

'Bubble plots' are an easy tool to quickly assess the residuals for autocorrelation.

Residuals are plotted in space, and sizes/colours are proportional to their values.

Idea is to look for patterns (absence of a pattern is good).

Bubble plots are quick and easy tools, but can be hard to read and not very formal.





Moran's I



Moran's I is a correlation coefficient that measures the overall spatial autocorrelation of a data set (think of it as \sim weighted covariance):

$$I = \frac{N}{W} \frac{\sum_{i} \sum_{j} w_{ij}(x_i - \bar{x})(x_j - \bar{x})}{\sum_{i} (x_i - \bar{x})^2}$$

N is the number of spatial units indexed by i and j; x is the variable of interest and \bar{x} is the mean of x; w_{ij} is a matrix of spatial weights and W is the sum of all w_{ij} .

Values of I usually range from -1 to +1.



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Many R packages for calculating Moran's I





The *p*-value tells us we have significant spatial autocorrelation

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Moran's I can be a useful tool for identifying the presence of autocorrelation and is quite popular.

The challenge is how to act on this information (i.e., lets you know if you have a problem, but doesn't help in finding a solution)?

Also very sensitive to how you define the weights:

"The idea is to construct a matrix that accurately reflects your assumptions about the particular spatial phenomenon in question. A common approach is to give a weight of 1 if two zones are neighbors, and 0 otherwise, though the definition of 'neighbors' can vary. Another common approach might be to give a weight of 1 to k nearest neighbors, 0 otherwise. An alternative is to use a distance decay function for assigning weights. Sometimes the length of a shared edge is used for assigning different weights to neighbors. The selection of spatial weights matrix should be guided by theory about the phenomenon in question." – Wikipedia

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Semi-variance is a measure of the degree of similarity between pairs of points separated by a specific distance h. Plot of semi-variance vs. separation distance is called a variogram.

$$\hat{\gamma}(s) = rac{1}{2N(h)} \sum_{i=1}^{N(h)} [z(x_i + h) - z(x_i)]^2$$

•	•	•	•	•	•	•	•	•	
•		•	•	•	•	•	•	•	
•	•	•	•	•	•	•	•	•	
•	•	•	•	•	•	•	•	•	
•	•	•	•	•	•	•	•	•	
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Separation Distance



Last lecture we saw how different autocorrelation models could be used to correct for different temporal autocorrelation structures.

The same applies with spatial autocorrelation.

Usefully, the different spatial correlation models all have differently shaped theoretical variograms.

In other words the shape of a dataset's empirical variogram can provide clues on which spatial correlation model is most appropriate.

Correlation models and their variograms



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Correcting Spatial Autocorrelation



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So you find yourself with spatially autocorrelated data. What next?



Here again, 'Dealing with spatial autocorrelation' and 'analysing spatial trends' are not the same thing. Our focus is on the former.

Methods for handling spatial autocorrelation in a regressional framework come primarily from the field of geostatistics.

In practice, they function much like corrections for temporal autocorrelation (i.e., a modification of the model's variance-covariance matrix).

$$V = \begin{bmatrix} \sigma^2 & 0 & \cdots & 0 \\ 0 & \sigma^2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \sigma^2 \end{bmatrix}$$

B

We're going to work with a dataset from Zuur *et al.* (2007) to examine the influence of biogeography on forest composition in Tatarstan, Russia.

The response variable is a measure of boreality (i.e., percent boreal species at a site) and our explanatory variable is a measure of wetness.

Today's starting point is the linear regression model:

Boreality_{*i*} =
$$\beta_0 + \beta_1$$
Wetness_{*i*} + ε_i





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Residuals actually look ok.





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```
library(ape)
library(fields)
library(gstat)
library(sp)
#Spatial data frame of residuals
RES <- data.frame(res = residuals(FIT,
                                   type="normalized"),
                  x = data x.
                  y = data \$ y)
coordinates(RES) <- c("x","v")
#Matrix of distances
w = fields::rdist(cbind(data$x, data$y))
#Calculate Moran's T
ape::Moran.I(RES$res, w = w)
$observed
[1] -0.01024323
$expected
[1] -0.001879699
$sd
[1] 0.001367237
$p.value
[1] 9.52903e-10
```

```
#Calculate variogram
```

vg <- variogram(res ~ 1, data = RES)



Variogram shows initial curvature.

These data are clearly autocorrelated and the results can't be trusted.

Linear spatial correlation in $\ensuremath{\mathbb{R}}$

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```
FIT_lin <- gls(Bor ~ Wet,
                correlation = corLin(c(800, 0.75))
                                       form=~x+v.
                                       nugget = TRUE),
                data = data)
summary(FIT_lin)
Correlation Structure: Linear spatial correlation
 Formula: ~x + v
 Parameter estimate(s):
      range
                  nugget
758 8801793
               0.5601258
AIC(FIT, FIT_lin)
        df
                 ATC
FIT
         3 2844 541
FIT lin
         5 2735.603
Moran.I(RES$res, w = w)
$p.value
[1] 0.6787855
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```



Spherical spatial correlation in R



A spherical spatial correlation structure can be applied via the corSpher() function.

```
FIT_Sph <- gls(Bor ~ Wet,
               correlation = corSpher(c(800, 0.75),
                                     form=~x+y,
                                     nugget = TRUE),
               data = data)
summary(FIT_Sph)
Correlation Structure: Spherical spatial correlation
Formula: ~x + v
Parameter estimate(s):
      range
                 nugget
939.3200338
              0.5211218
AIC(FIT, FIT_Sph)
        df
                ATC
FIT
         3 2844 541
FIT Sph
         5 2732,666
Moran.I(RES$res, w = w)
$p.value
[1] 0.6511908
```

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Gaussian spatial correlation in $\ensuremath{\mathbb{R}}$



A Gaussian spatial correlation structure can be applied via the corGaus() function.

```
FIT_Gau <- gls(Bor ~ Wet,
               correlation = corGaus(c(800, 0.75),
                                        form=~x+v.
                                        nugget = TRUE),
                data = data)
summary (FIT_Gau)
Correlation Structure: Gaussian spatial correlation
 Formula: ~x + y
 Parameter estimate(s):
      range
                  nugget
460.3947751
              0.6112509
AIC(FIT, FIT_Gau)
        df
                 ATC
FIT
         3 2844 541
FIT Gau
         5 2736.292
Moran.I(RES$res, w = w)
$p.value
[1] 0.6275071
```





Exponential spatial correlation in R



Semi-variance

1.00

0.50

0.25

0.00

500 1000

Semi-variance 0.75 THE UNIVERSITY OF BRITISH COLUMBIA Okanagan Campus

Exponential $\Phi = 1$

Separation Distance

An exponential spatial correlation structure can be applied via the corExp() function.

```
FIT_Exp <- gls(Bor ~ Wet,
               correlation = corExp(c(800, 0.75)),
                                       form = x + y,
                                       nugget = TRUE),
                data = data)
summary(FIT_Exp)
Correlation Structure: Exponential spatial correlation
 Formula: ~x + y
 Parameter estimate(s):
      range
                  nugget
481.1743349
              0.4849357
AIC(FIT, FIT_Exp)
        df
                 AIC
FIT
         3 2844 541
FIT_Exp
         5 2732.224
Moran.I(RES$res, w = w)
$p.value
[1] 0.6519741
```

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Rational quad. spatial correlation



A rational quadratic spatial correlation structure can be applied via the corRatio() function.

```
FIT_Rat <- gls(Bor ~ Wet,
               correlation = corRatio(c(800, 0.75),
                                        form=~x+y,
                                        nugget = TRUE).
                data = data)
summary(FIT_Rat)
Correlation Structure: Rational quadratic spatial
      correlation
 Formula: ~x + v
 Parameter estimate(s):
      range
                  nugget
373.0351282
              0.5627731
AIC(FIT, FIT Rat)
        df
                 A T C
FIT
         3 2844.541
FIT_Rat 5 2732.930
Moran.I(RES$res, w = w)
$p.value
[1] 0.6508174
```



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BC

We just fit 6 different models, but how do we know which correlation structure to go with?

#Ordered by lowest to highest AIC
TABLE <- TABLE[order(TABLE\$AIC),]</pre>

#Calculate Delta AICs TABLE\$DeltaAIC <- TABLE\$AIC - TABLE\$AIC[1]

#Evidence compared to AIC best model TABLE\$Evidence <- 1/exp(-TABLE\$DeltaAIC/2)</pre>

TABLE

	df	AIC	DeltaAIC	Evidence
FIT_Exp	5	2732.224	0.000000	1.000000e+00
$\texttt{FIT}_\texttt{Sph}$	5	2732.666	0.4423134	1.247519e+00
FIT_Rat	5	2732.930	0.7063538	1.423583e+00
FIT_lin	5	2735.603	3.3797773	5.418877e+00
FIT_Gau	5	2736.292	4.0685720	7.646790e+00
FIT	3	2844.541	112.3174833	2.451498e+24

```
EXP_FIT <- corExp(c(481.1743349,
0.4849357),
form = ~D,
nugget = TRUE)
```

EXP_FIT2 <- Initialize(EXP_FIT,data=D)

selected_mod <- Variogram(EXP_FIT2)





Original Model

Generalized least squares fit by REML Model: Bor ⁻ Wet Data: data AIC BIC logLik 2844.541 2857.365 -1419.271

Coefficients:

 Value Std.Error
 t-value p-value

 (Intercept)
 13.05622
 0.151194
 86.35430
 0

 Wet
 165.80355
 10.599111
 15.64316
 0

Correlation:

(Intr)

Wet O

Residual standard error: 3.490577 Degrees of freedom: 533 total; 531 residual

Exponential spatial correlation model

```
Generalized least squares fit by REML
Model: Bor <sup>-</sup> Wet
Data: data
AIC BIC logLik
2732.224 2753.597 -1361.112
```

```
Coefficients:
```

	Value	Std.Error	t-value	p-value
(Intercept)	12.55226	0.678111	18.510619	0
Wet	75.43166	13.541700	5.570325	0

```
Correlation:
(Intr)
Wet 0.041
```

Residual standard error: 3.707339 Degrees of freedom: 533 total; 531 residual

```
Correlation Structure: Exponential spatial
correlation
Formula: "x + y
Parameter estimate(s):
range nugget
481.1743349 0.4849357
```



We covered several ways to model spatially autocorrelated data:

Туре	Description	R Function
IID	0	—
Linear	$\Phi = 1 - (1rac{D}{ ho}) I(d < ho)$	corLin()
Spherical	$\Phi = 1(1-1.5(rac{d}{ ho})+0.5(rac{d}{ ho})3)I(d< ho)$	corSpher()
Gaussian	$\Phi = 1 - e^{-(\frac{D}{\rho})^{2^{\prime}}}$	corGaus()
Exponential	$\Phi = 1 - e^{-rac{D}{ ho}}$	corExp()
Rational quadratic	$\Phi = rac{1}{1+(rac{ ho}{ ho})^2}$	corRatio()

The model structures can be difficult to interpret, but their variograms have very recognizable features. Familiarising yourself with them will help you quickly narrow down what structure to use.



Fitting models with complex correlation structures can be quite slow at times.

```
system.time(gls(Bor ~ Wet, data = data))
user system elapsed
0.001 0.000 0.001
```

```
CORR <- corSpher(c(800, 0.75),
form=~x+y,
nugget = TRUE)
```

```
user system elapsed
9.781 0.109 9.893
```

Took nearly 10,000 times longer!

Can also run into numerical issues without good starting values.

uata = uata)

```
Error in gls(Bor ~ Wet, correlation = corLin(
    form = ~x + y, nugget=TRUE), :
    false convergence (8)
```

If that happens you need to provide better starting guesstimates or modify the optimiser. Neither of which are particularly enjoyable.

B

Experimental designs that do not consider spatial autocorrelation risk being subsampled.

A spatial autocorrelated data point will add little independent information, but inflate n (Dormann *et al.*, 2007).





Corrections exist to deal with issues of statistical bias, but they can't inject more information into a dataset when none exists.

Good study design should consider spatial autocorrelation a priori.

If you had to collect more data for the boreality study how far apart would you sample? > 500 m

References

- Dormann, C.F., McPherson, J.M., Araújo, M.B., Bivand, R., Bolliger, J., Carl, G., Davies, R.G., Hirzel, A., Jetz, W., Kissling, W.D. *et al.* (2007). Methods to account for spatial autocorrelation in the analysis of species distributional data: a review. *Ecography*, 30, 609–628.
- Liang, M., Liu, X., Parker, I.M., Johnson, D., Zheng, Y., Luo, S., Gilbert, G.S. & Yu, S. (2019). Soil microbes drive phylogenetic diversity-productivity relationships in a subtropical forest. *Science advances*, 5, eaax5088.
- Zuur, A., Ieno, E.N. & Smith, G.M. (2007). *Analyzing ecological data*. Springer.