

Autocorrelation 1: Temporal Autocorrelation

Michael Noonan

Biol 520C: Statistical modelling for biological data

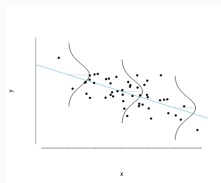
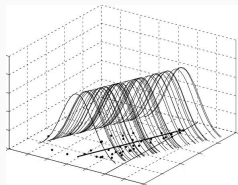
1. Autocorrelation and the IID Assumption
2. Temporal Autocorrelation
3. Correcting Temporal Autocorrelation
4. Correcting Temporal Autocorrelation in R

Autocorrelation and the IID Assumption

Last lecture we saw how differences in variances across groups (i.e., heteroskedasticity) can break the 'identical' part of the IID assumption.

We also saw how adding a variance structure to the model can correct for heteroskedasticity.

Over the next few lectures we'll explore ways in which the 'independent' part of the IID assumption can be broken, what the implications of this mean, and how to correct for it.





© Chris Sorensen

Dr. Sam Wang, Neuroscientist
—Princeton Election Consortium



© ABC News

Nate Silver, Statistician
—FiveThirtyEight.com



© Chris Sorensen

Dr. Sam Wang, Neuroscientist
—Princeton Election Consortium

“It is totally over. If Trump wins more than 240 electoral votes, I will eat a bug.”

Biol 520C: Statistical modelling for biological data



© ABC News

Nate Silver, Statistician
—FiveThirtyEight.com



© Chris Sorensen

Dr. Sam Wang, Neuroscientist
—Princeton Election Consortium

"It is totally over. If Trump wins more than 240 electoral votes, I will eat a bug."

Biol 520C: Statistical modelling for biological data



© ABC News

Nate Silver, Statistician
—FiveThirtyEight.com

"Trump Is Just A Normal Polling Error Behind Clinton."



© Chris Sorensen



© ABC News

Nate Silver, Statistician
—FiveThirtyEight.com

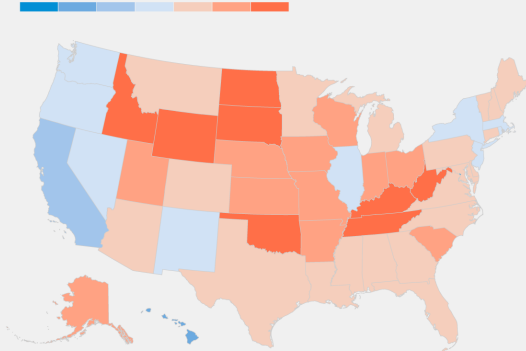
*“Trump Is Just A Normal Polling
Error Behind Clinton”*

Polls underestimated Trump in red states, Clinton in blue states

2016 election results vs. FiveThirtyEight's adjusted polling average by state

REPUBLICAN VOTE MARGIN RELATIVE TO POLLS

-20 -15 -10 -5 0 +5 +10 +15



Are these polling errors
independently distributed?

This same statistical issue that
caused overly confident
predictions of Clinton's 2016
victory can result in
overconfidence in parameter
estimates and predictions in
regression models.

Sample size, n is the denominator when calculating both SEs and CIs.

$$SE = \frac{\sigma}{\sqrt{n}}$$

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

All else equal: $\uparrow n = \downarrow SE \ \& \ \downarrow CI$

But with autocorrelated data each new datapoint is related to a previously collected datapoint and does not bring a full independent datapoint worth of information (e.g., 90% autocorr. \approx 10% new info).

When data are autocorrelated $n_{\text{effective}} < n$, meaning SEs and CIs shrink faster than they should, resulting in a false sense of confidence.

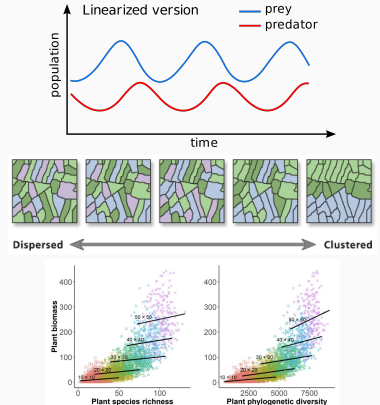
Effect is usually strongest on SEs and CIs, but autocorrelation can also

impact the mean: $\bar{x} = \frac{1}{n} \left(\sum_{i=1}^n x_i \right) = \frac{x_1 + \dots + x_n}{n}$

Anything that causes some data points to be more similar to each other than others can result in autocorrelation.

Over the next three lectures we will be covering the three most common sources of autocorrelation in biological data:

- **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.



Temporal Autocorrelation

As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

When this is the case, autocorrelation can arise in two ways:

1. The autocorrelation timescale of the process we're measuring.

As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

When this is the case, autocorrelation can arise in two ways:

1. The autocorrelation timescale of the process we're measuring.

As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

When this is the case, autocorrelation can arise in two ways:

1. The autocorrelation timescale of the process we're measuring.

As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

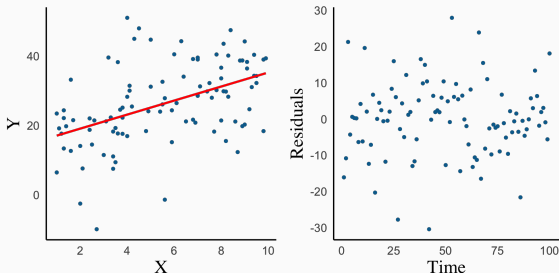
When this is the case, autocorrelation can arise in two ways:

1. The autocorrelation timescale of the process we're measuring.

As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

When this is the case, autocorrelation can arise in two ways:

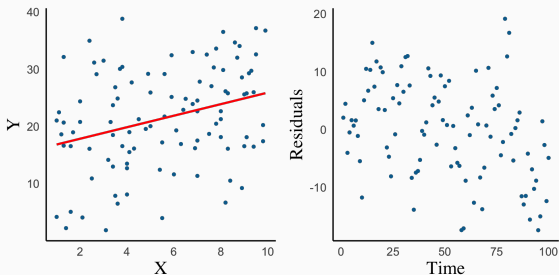
1. The autocorrelation timescale of the process we're measuring.



As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

When this is the case, autocorrelation can arise in two ways:

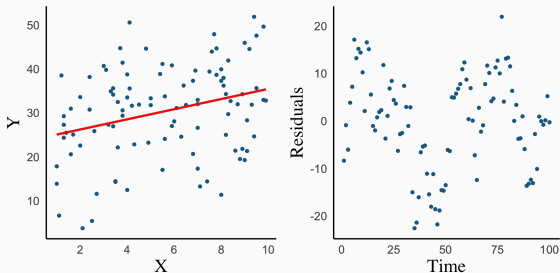
1. The autocorrelation timescale of the process we're measuring.



As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

When this is the case, autocorrelation can arise in two ways:

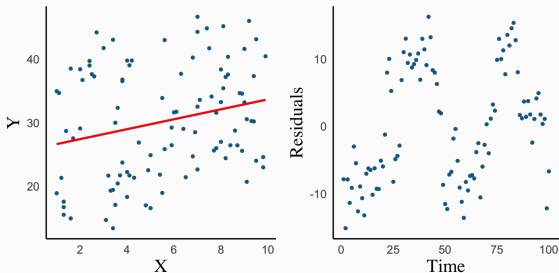
1. The autocorrelation timescale of the process we're measuring.



As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

When this is the case, autocorrelation can arise in two ways:

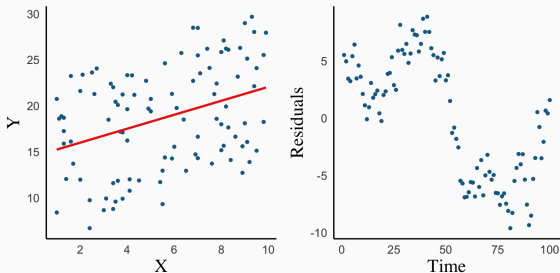
1. The autocorrelation timescale of the process we're measuring.



As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

When this is the case, autocorrelation can arise in two ways:

1. The autocorrelation timescale of the process we're measuring.



As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

When this is the case, autocorrelation can arise in two ways:

2. The rate/duration at which we're collecting data.

As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

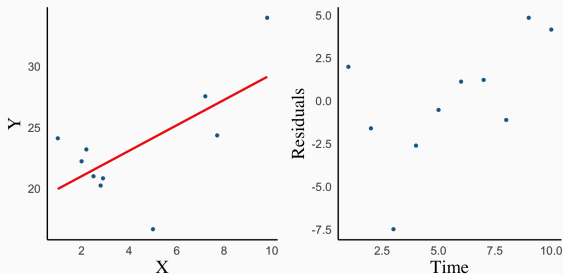
When this is the case, autocorrelation can arise in two ways:

2. The rate/duration at which we're collecting data.

As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

When this is the case, autocorrelation can arise in two ways:

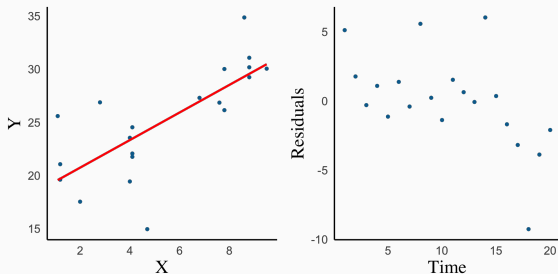
2. The rate/duration at which we're collecting data.



As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

When this is the case, autocorrelation can arise in two ways:

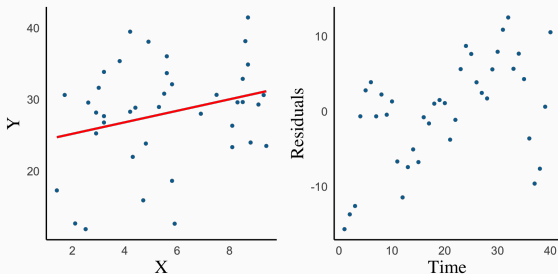
2. The rate/duration at which we're collecting data.



As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

When this is the case, autocorrelation can arise in two ways:

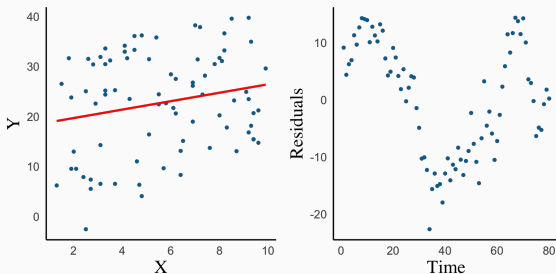
2. The rate/duration at which we're collecting data.



As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

When this is the case, autocorrelation can arise in two ways:

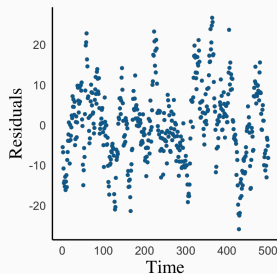
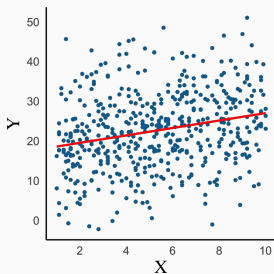
2. The rate/duration at which we're collecting data.



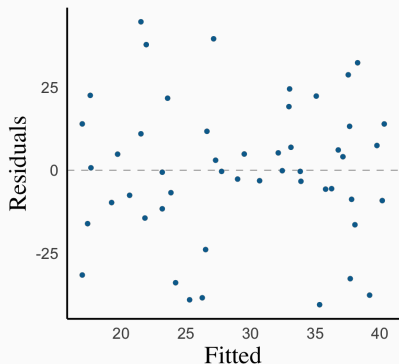
As biologists, we often find ourselves measuring things over time (e.g., population sizes, animal locations, CO₂ levels, reaction times, etc.).

When this is the case, autocorrelation can arise in two ways:

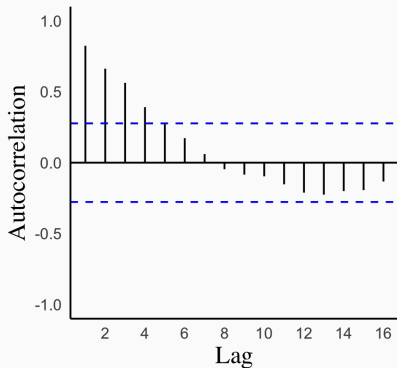
2. The rate/duration at which we're collecting data.

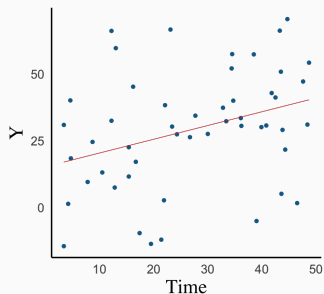


Autocorrelation can be difficult to see in a simple residuals vs. fitted plot (not designed for this purpose).



Instead we typically plot autocorrelation functions (ACFs)



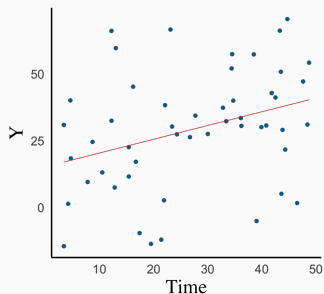


Resid _t	Resid _{t+0}
1	1
2	2
3	3
4	4
5	5
...	...
i	i

$$\text{var}_t = \frac{1}{n} \sum (\text{resid}_t \times \text{resid}_t)$$

$$\text{var}_{t+0} = \frac{1}{n} \sum (\text{resid}_t \times \text{resid}_{t+0})$$

$$\text{ACF}_0 = \text{var}_{t+0} / \text{var}_t$$

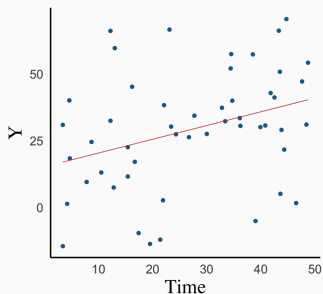


Resid _t	Resid _{t+1}
1	2
2	3
3	4
4	5
5	6
...	...
i - 1	i

$$\text{var}_t = \frac{1}{n} \sum (\text{resid}_t \times \text{resid}_t)$$

$$\text{var}_{t+1} = \frac{1}{n} \sum (\text{resid}_t \times \text{resid}_{t+1})$$

$$\text{ACF}_1 = \text{var}_{t+1} / \text{var}_t$$

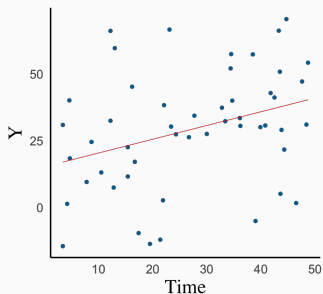


Resid _t	Resid _{t+2}
1	3
2	4
3	5
4	6
5	7
...	...
i - 2	i

$$\text{var}_t = \frac{1}{n} \sum (\text{resid}_t \times \text{resid}_t)$$

$$\text{var}_{t+2} = \frac{1}{n} \sum (\text{resid}_t \times \text{resid}_{t+2})$$

$$\text{ACF}_2 = \text{var}_{t+2} / \text{var}_t$$

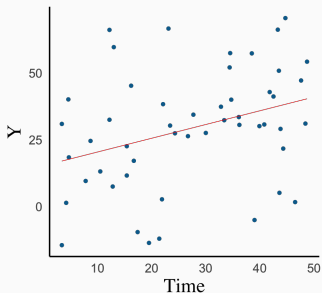


Resid _t	Resid _{t+3}
1	4
2	5
3	6
4	7
5	8
...	...
i - 3	i

$$\text{var}_t = \frac{1}{n} \sum (\text{resid}_t \times \text{resid}_t)$$

$$\text{var}_{t+3} = \frac{1}{n} \sum (\text{resid}_t \times \text{resid}_{t+3})$$

$$\text{ACF}_3 = \text{var}_{t+3} / \text{var}_t$$



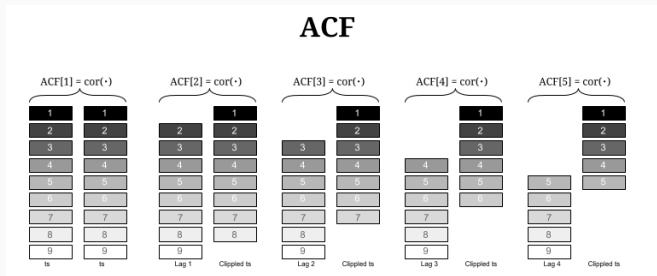
Resid_t	Resid_{t+i-1}
1	i

$$\text{var}_t = \frac{1}{n} \sum (\text{resid}_t \times \text{resid}_t)$$

$$\text{var}_{t+i-1} = \frac{1}{n} \sum (\text{resid}_t \times \text{resid}_{t+i-1})$$

$\text{ACF}_{i-1} = \text{var}_{t+i-1} / \text{var}_t$ Continue until you've run through the whole dataset.

Schematically, calculating the ACF looks like this:



Source: Notes on statistics and probability

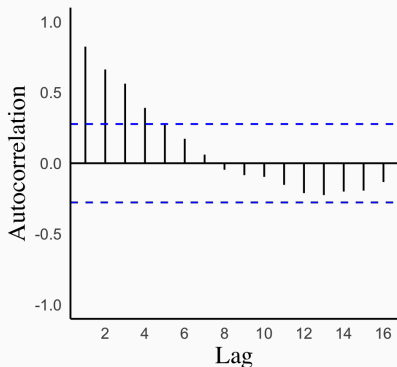
What happens to the sample size as the lag increases?

ACF is typically used as a visual diagnostic tool.

Ranges from 1 to -1 and autocorrelation at lag 0 = 1.

Usually accompanied by dashed lines telling you where significance lies (95% CIs).

You can do this in R via the `acf()` function.



Correcting Temporal Autocorrelation



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

'Dealing with temporal autocorrelation' and 'analysing temporal trends' are **not** the same thing.

This lecture focuses only on tools for dealing with the lack of independence associated with temporal data.

If you're interested in analysing temporal trends you need to apply time series analysis, which we will not cover this in this course.

The models we've been working with so far:

$$y_i = \beta_0 + \beta_1 \times x_i + \varepsilon_i \quad \varepsilon_i \sim \mathcal{N}(0, V) \quad V = \sigma^2 \begin{bmatrix} 1 & 0 & \dots & 0 \\ 0 & 1 & \dots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \dots & 1 \end{bmatrix}$$

The diagonal defines the variances. All 1s indicates homogeneity of variances.

The off-diagonals define the co-variances. The 0s indicate independence.

Multiplying this out would give you an $n \times 1$ matrix equal to σ^2 .

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

Correcting for autocorrelation 'simply' involves identifying the autocorrelation structure of the residuals and modifying the variance-covariance matrix.

When the residuals are autocorrelated, the off-diagonals $\neq 0$.

$$V = \sigma^2 \begin{bmatrix} 1 & 0 & \cdots & 0 \\ 0 & 1 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & 1 \end{bmatrix}$$

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

The simplest case is when all the covariances are constant, non-zero value. This is referred to as 'compound symmetry'.

The degree of correlation between residuals (ρ) is equal to

$$\rho = \frac{\theta}{\theta + \sigma^2}.$$

$$V = \underbrace{\begin{bmatrix} \theta + \sigma^2 & \theta & \dots & \theta \\ \theta & \theta + \sigma^2 & \dots & \theta \\ \vdots & \vdots & \ddots & \vdots \\ \theta & \theta & \dots & \theta + \sigma^2 \end{bmatrix}}_{\text{variance-covariance matrix}}$$

Often too simplistic for real autocorrelation structures, but can sometimes be useful.

The first order auto-regressive (AR1) structure defines a correlation structure in which the degree of correlation between two observations is proportional to the relative amount of elapsed time.

The degree of correlation between a pair of residuals is defined as $\rho^{|t-s|}$

$|t - s|$ is the absolute difference between the current time (t) and the previous time (s).

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

E.g., If $\rho = 0.5$ and two residuals are separated by two units of time, the correlation is $0.5^2 = 0.25$.

AR-1 correlation is a useful correlation structure for ecological data.

The auto-regressive moving-average (ARMA) model is a general model with two parameters:

1. p : The number of autoregressive parameters.
2. q : The number of moving average parameters.

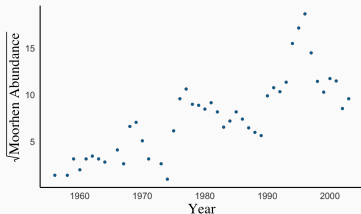
ARMA models are very flexible, but can be challenging to work with.

They can also be very slow to fit on large datasets.

Correcting Temporal Autocorrelation in \mathbb{R}

We're going to work with a dataset from Reed *et al.* (2007) to examine the abundance of moorhen (*Gallinula galeata*) on the Hawaiian Island Kauai.

The data are comprised of bird counts over years as well as annual rainfall.



Today's starting point is the linear regression model:

$$\sqrt{\text{Birds}_i} = \beta_0 + \beta_1 \text{Rainfall}_i + \beta_2 \text{Year}_i + \varepsilon_i$$

Note: The $\sqrt{\quad}$ transformation was to clean up heteroskedasticity. We could have used the methods we learned last lecture, but we'll keep it simple today.

```
library(nlme)

data <- read.csv("Hawaii.csv")

data$Birds <- sqrt(data$Moorhen.Kauai)

FIT <- gls(Birds ~ Rainfall + Year, na.action = na.omit,
          data = data)
```

Generalized least squares fit by REML

Model: Birds ~ Rainfall + Year

Data: data

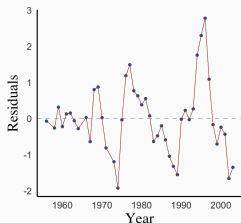
	AIC	BIC	logLik
	228.4798	235.4305	-110.2399

Coefficients:

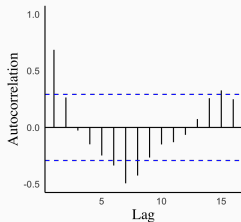
	Value	Std. Error	t-value	p-value
(Intercept)	-477.6634	56.41907	-8.466346	0.0000
Rainfall	0.0009	0.04989	0.017245	0.9863
Year	0.2450	0.02847	8.604858	0.0000

Residual standard error: 2.608391

Degrees of freedom: 45 total; 42 residual



```
acf(residuals(FIT, type = "
      normalized"))
```



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

Our model is:

$$\sqrt{Birds_i} = \beta_{\text{Intercept}} + \beta_1 \times \text{Rainfall}_i + \beta_2 \times \text{Year}_i + \varepsilon_i \quad \varepsilon_i \sim \mathcal{N}(0, V)$$

To account for the year over year autocorrelation in moorhen counts we can modify the covariances of variance-covariance matrix

$$V = \begin{bmatrix} var_{1958} & COV_{1958,1959} & \cdots & \cdots & COV_{1958,2003} \\ COV_{1959,1958} & var_{1959} & \cdots & \ddots & \vdots \\ COV_{1960,1958} & COV_{1960,1959} & var_{1960} & \ddots & \vdots \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ COV_{2003,1958} & \cdots & \cdots & COV_{2003,2002} & var_{2003} \end{bmatrix}$$

Applying autocorrelated structures to the residuals can be done using the `correlation` option in the `glms()` function.

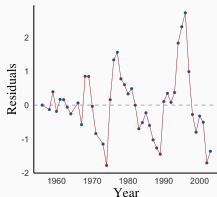
Compound symmetric errors can be applied via the `corCompSymm()` function.

```
FIT_CompSymm <- gls(Birds ~ Rainfall + Year,  
  na.action = na.omit,  
  correlation = corCompSymm(form = ~ Year),  
  data = data)
```

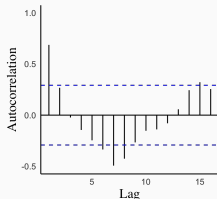
```
summary(FIT_CompSymm)  
...  
Correlation Structure: Compound symmetry  
Formula: ~Year  
Parameter estimate(s):  
  Rho  
3.392348e-18  
...
```

```
AIC(FIT, FIT_CompSymm)
```

	df	AIC
FIT	4	228.4798
FIT_CompSymm	5	230.4798



```
acf(residuals(FIT_CompSymm,  
  type = "normalized"))
```



AIC shows we made the fit worse, and the residuals are still autocorr. :(

AR-1 errors can be applied via the `corAR1()` function.

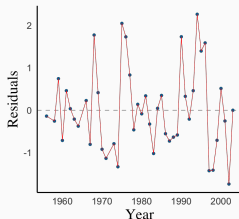
```
FIT_AR1 <- gls(Birds ~ Rainfall + Year,
              na.action = na.omit,
              correlation = corAR1(form = ~ Year),
              data = data)
```

```
summary(FIT_AR1)
```

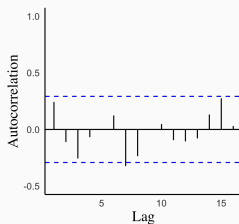
```
...
Correlation Structure: ARMA(1,0)
Formula: ~Year
Parameter estimate(s):
  Phi1
0.7734303
...
```

```
AIC(FIT, FIT_CompSymm, FIT_AR1)
```

	df	AIC
FIT	4	228.4798
FIT_CompSymm	5	230.4798
FIT_AR1	5	199.1394



```
acf(residuals(FIT_AR1, type
              = "normalized"))
```



AIC shows an improvement and the residuals are no longer autocorr.

ARMA errors can be applied via the `corARMA()` function.

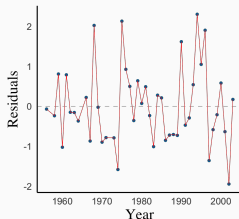
```
FIT_ARMA1 <- gls(Birds ~ Rainfall + Year,
  na.action = na.omit,
  correlation = corARMA(form = ~ Year,
    p = 2),
  data = data)
```

```
summary(FIT_ARMA1)
```

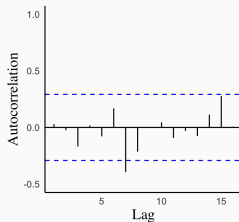
```
...
Correlation Structure: ARMA(2,0)
Formula: ~Year
Parameter estimate(s):
  Phi1      Phi2
0.9668205 -0.3220174
...
```

```
AIC(FIT, FIT_CompSymm, FIT_AR1, FIT_ARMA1)
```

	df	AIC
FIT	4	228.4798
FIT_CompSymm	5	230.4798
FIT_AR1	5	199.1394
FIT_ARMA1	6	196.8777



```
acf(residuals(FIT_ARMA1,
  type = "normalized"))
```



AIC shows a marginal improvement and the residuals are ok.

We could also try adding a moving average term via q .

```
FIT_ARMA2 <- gls(Birds ~ Rainfall + Year,
  na.action = na.omit,
  correlation = corARMA(c(0.3, -0.3, 0.3),
    form = ~ Year,
    p = 2,
    q = 1),
  data = data)
```

```
summary(FIT_ARMA2)
```

```
...
```

```
Correlation Structure: ARMA(2,1)
```

```
Formula: ~Year
```

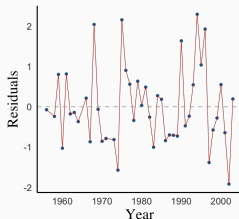
```
Parameter estimate(s):
```

```
      Phi1      Phi2      Theta1
0.89422729 -0.26715887 0.08293474
```

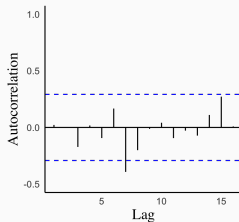
```
...
```

```
AIC(FIT, FIT_CompSymm, FIT_AR1,
  FIT_ARMA1, FIT_ARMA2)
```

	df	AIC
FIT	4	228.4798
FIT_CompSymm	5	230.4798
FIT_AR1	5	199.1394
FIT_ARMA1	6	196.8777
FIT_ARMA2	7	198.8578



```
acf(residuals(FIT_ARMA2,
  type = "normalized"))
```



AIC is slightly worse, but the residuals are ok.

Original Model

Generalized least squares fit by REML

Model: Birds ~ Rainfall + Year

Data: data

	AIC	BIC	logLik
	228.4798	235.4305	-110.2399

Coefficients:

	Value	Std.Error	t-value	p-value
(Intercept)	-477.6634	56.41907	-8.466346	0.0000
Rainfall	0.0009	0.04989	0.017245	0.9863
Year	0.2450	0.02847	8.604858	0.0000

Correlation:

	(Intr)	Ranfl1
Rainfall	-0.036	
Year	-1.000	0.020

Residual standard error: 2.608391

Degrees of freedom: 45 total; 42 residual

ARMA(2,0) Model

Generalized least squares fit by REML

Model: Birds ~ Rainfall + Year

Data: data

	AIC	BIC	logLik
	196.8777	207.3037	-92.43886

Coefficients:

	Value	Std.Error	t-value	p-value
(Intercept)	-471.8304	94.30829	-5.003064	0.0000
Rainfall	-0.0170	0.02771	-0.614301	0.5423
Year	0.2422	0.04764	5.083189	0.0000

Correlation:

	(Intr)	Ranfl1
Rainfall	0.001	
Year	-1.000	-0.006

Residual standard error: 2.657647

Degrees of freedom: 45 total; 42 residual

Correlation Structure: ARMA(2,0)

Formula: ~Year

Parameter estimate(s):

Phi1	Phi2
0.9668205	-0.3220174

We covered several ways to model temporally autocorrelated data:

Type	Covariance ρ	DF	R Function
IID	0	0	<code>corSymm()</code>
Compound Symetric	$\rho = \frac{\theta}{\theta + \sigma^2}$	1	<code>corCompSymm()</code>
AR-1	$\rho^{ t-s }$	1	<code>corAR1()</code>
ARMA	variable	variable	<code>corARMA()</code>

For the bird data, going from IID to AR-1 offered a big improvement, and then fine-tuning via more complicated ARMA structures resulted in only marginal improvements over AR-1. This is common in practice.

Unless there are serious issues remaining in your residuals, the pragmatic solution is to stop when you have a reasonably appropriate model.

References

- 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.
- Reed, J., Elphick, C., Zuur, A., Ieno, E. & Smith, G. (2007). Time series analysis of hawaiian waterbirds. In: *Analysing ecological data*. Springer, pp. 615–631.
- Zuur et al. (2009) — Chapter 6