3 Epidemic Data and Time Series Tools

1/90



Mathematics and Statistics $\int_{M} d\omega = \int_{\partial M} \omega$

Mathematics 4MB3/6MB3 Mathematical Biology

Instructor: David Earn

Lecture 3 Epidemic Data and Time Series Tools Tuesday 17 September 2024

- Next week's lecture will be recorded in advance and posted on the Echo 360 page for this course.
 - Live Q&A, either in last hour of scheduled class or at a mutually convenient time.
- Assignments:
 - Assignment 1 due 23 Sep 2024 (next Monday)
 - Assignment 2 due 7 Oct 2024 (good to work on before class on 1 Oct 2024)
- Class on 1 Oct 2024 will be given by Mikael Jagan (install epigrowthfit before that class)
- Lecture on 8 Oct 2024 will pre-recorded and posted

P&I Mortality, Philadelphia, 1918

P&I Deaths



SARS in 2003 (Worldwide)



*This graph does not include 2,527 probable cases of SARS (2,521 from Beijing, China), for whom no dates of onset are currently available.

SARS in 2003 (Toronto)



N = 249 (of 250 reported)

Some SARS Facts

- High case fatality
 - 1918 flu < 3%
 - SARS > 10%
- Long hospital stays
 - Mean time from admission to discharge or death: \sim 25 days in Hong Kong
- 8098 probable cases, 774 deaths
- How bad would it have been if it had not been controlled?

COVID (ancestral) hospitalization and survival in Ontario



Fig. 4 Age-dependent COVID-19 hospitalization probability for known SARS-CoV-2 infection (panel a) and survival probability for hospitalized patients (panel b) in Ontario. We give age-by-age estimates of each probability (points; 95% exact binomial confidence intervals given by vertical lines), where point area is proportional to age-specific sample size. We additionally provide more precise estimates of these probability using a generalized additive model and the survival probability using a generalized additive model and the survival probability using a generalized linear model (curve; 95% confidence bands given by shaded regions). See "Methods" section for details

Papst et al (2021), BMC Public Health, 21:706

The Black Death in London, England, 1348–1349



London Bill of Mortality, 26 Sept to 3 Oct 1665

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London Bill of Mortality, 26 Sept to 3 Oct 1665

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Mortality Bills are typically handwritten



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But handwriting is usually very clear



But handwriting is usually very clear



The Great Plague of London, 1665



The Great Plague of London, 1665



London Plague of 1593



London Plague of 1603



London Plague of 1625



Weekly Deaths from Plague in London, 1592–1666



Weekly Plague in London, 1640–1648



Some Plague Facts

- Plague epidemics recorded from Roman times to early 1900s.
- $\gtrsim 1/3$ Europe's population died in "Black Death" of 1348
 ~ 300 years for the population to reach the same level.
- Recently (2011) established (at McMaster!) that the pathogen that caused The Black Death was Yersinia pestis

[Bos et al. 2011, Nature 478, 506-510]

 More recently (2014) established (again at McMaster!) that the pathogen that caused The Plague of Justinian (541–543 AD) was Yersinia pestis

[Wagner et al. 2014, Lancet Infectious Diseases 14, 319-326]

Y. pestis still a concern?

Yes: Rodent reservoir, antibiotic-resistant strains, bioterrorism

Spatial data for any plagues? Yes, for London in 1665...

Visualization of spatial structure of Great Plague

- GIS encoding of parish boundaries
- Overlay parish boundaries on more modern map for reference
- Colour parishes as they become infected
- Is there evidence for spatial spread or was the spatial pattern random?
- DE low-tech animation...
- CBC high-tech animation...
 - The Nature of Things, 21 August 2014. http://www.cbc.ca/natureofthings/episodes/ secrets-in-the-bones-the-hunt-for-the-black-death-killer

Visualization of entire course of the Great Plague

- What happenned after initial spatial spread?
- Visualize full spatial epidemic structure
- Show magnitude of epidemic in each parish with cylinder.
- Epidemic Visualization (EpiVis) software by Junling Ma.

P&I mortality in U.S.A., 1910–1998



Influenza Incidence Patterns (lab confirmed)



Earn, Dushoff & Levin 2002, Trends in Ecology and Evolution 17, 334-340

Influenza Evolution

Molecular phylogenetic reconstruction of influenza A/H3N2 evolution, 1985–1996 (Fitch *et al.* 1997)



Measles in New York City, 1928–1972





Mumps in New York City, 1928–1972



Chicken Pox in New York City, 1928–1972

Monthly Cases



Childhood diseases in New York City, 1928–1972



Measles in Ontario, 1904–1989



Chicken Pox in Ontario, 1924–1989



Rubella in Ontario, 1924–1989



Whooping Cough in Ontario, 1904–1989





Childhood diseases in Ontario, 1904–1989


Ontario Disease Notification Data

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Dominion Bureau of Statistics Disease Notification Data

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Mathematical Biology

All Historical Canadian Infectious Disease Data

https://canmod.net/digitization/

Recurrent epidemics of childhood infections

- Childhood diseases in New York City, 1928–1972
- Childhood diseases in Ontario, 1904–1989

Measles incidence in England and Wales, 1944–1995



Measles incidence in England and Wales, 1944–1995



Why study measles epidemics?

- ~ 140,000 annual deaths from measles
- A major cause of vaccine-preventable deaths.
- Potential impact in developed countries during vaccine scares (e.g., MMR scare in UK in 1990s).
- Understand past patterns
- Predict future patterns
- Manipulate future patterns
- Develop vaccination strategy that can...



Other reasons to model infectious disease epidemics

Mathematical models make hypotheses and inferences precise

- Give better advice to policymakers
- Make better predictions
- Host-pathogen dynamics are important aspects of ecosystem dynamics
 - Infectious disease models more likely to be successful than predator-prey models
- Excellent data for human infectious diseases
 - Models can be tested!

Modelling population dynamics of childhood infections

- The basic SIR model cannot explain recurrent epidemics.
- What should we do?... The usual options:
 - **1** Get depressed, drop the course.
 - 2 Keep developing models until we can explain recurrent epidemics.

 First, let's talk about tools that allow us to make our questions about time series data more precise.

Epidemic Data Analysis

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Time Plots of Temporal Epidemic Patterns



Weekly Measles in England and Wales



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Time Plots of Transformed Data



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Times Plots of Smoothed Data

- Reveal trends clouded by noise or seasonality
- Moving Average:

$$x_t \to \frac{1}{2a+1} \sum_{i=-a}^{a} x_{t+i}$$

• Replace original data points x_t with averages of nearby points.

Linear filter:

$$x_t o \sum_{i=-\infty}^{\infty} \lambda_i x_{t+i}$$

- Generalization of moving average.
- Weights λ_i can be nonlinear functions of *i*.

Times Plots of Smoothed Data



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Times Plots of Smoothed Data



Time Plot

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Times Plots of Smoothed Data



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Correlation

- Recurrent epidemics with number of cases in the past and the future.
- Given N pairs of observations of different quantities, {(x_i, y_i) : i = 1,..., N}, the *correlation coefficient* is defined to be

$$r = \frac{\sum_{i=1}^{N} (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^{N} (x_i - \bar{x})^2 \sum_{i=1}^{N} (y_i - \bar{y})^2}}$$

where \bar{x} and \bar{y} are the means of $\{x_i\}$ and $\{y_i\}$, respectively.

Correlation

Properties of the correlation coefficient:

- $-1 \le r \le 1$ (Proof? Cauchy-Schwarz inequality)
- r = 1 \iff all points lie on a line with positive slope ("complete positive correlation")
- $r = -1 \iff$ all points lie on a line with negative slope ("complete negative correlation")
- $r \simeq 0 \implies$ "uncorrelated"
- Interpretation: r² is the proportion of the variance in y explained by a linear function of x.

Derivations and discussions:

- MathWorld on r^2 , Wikipedia on r^2
- Wikipedia on general coefficient of determination

Autocorrelation

- Given a single sequence of observations $\{x_t : t = 1, ..., N\}$, we can compute the correlation of each observation with the observation k time steps in the future.
- Thus, we consider the pairs of observations $\{(x_t, x_{k+t}) : t = 1, \dots, N - k\}$ and define the *autocorrelation coefficient at lag k* to be

$$r_{k} = \frac{\sum_{t=1}^{N-k} (x_{t} - \bar{x}_{1,N-k}) (x_{k+t} - \bar{x}_{k+1,N})}{\sqrt{\sum_{t=1}^{N-k} (x_{t} - \bar{x}_{1,N-k})^{2} \sum_{t=1}^{N-k} (x_{k+t} - \bar{x}_{k+1,N})^{2}}}$$

where $\bar{x}_{1,N-k}$ and $\bar{x}_{k+1,N}$ are the means of first and last N-kobservations, respectively.

Autocorrelation

• If number of observations N is large and lag $k \ll N$ then

$$r_k \simeq rac{\sum_{t=1}^{N-k} (x_t - ar{x})(x_{k+t} - ar{x})}{\sum_{t=1}^{N} (x_t - ar{x})^2}$$

- Approximation of r_k is worse for larger lags k
- Plot of autocorrelation r_k as a function of lag k is called the correlogram.

Correlogram



Peaks in correlogram ⇒ periodicities in original time series.
 Correlograms of temporal segments are often informative.

Correlogram: exact vs. approximate r_k



- Can we compute the dominant periods in the time series? (Rather than estimating them by eye from the correlogram.)
- Express the time series as a Fourier series:

$$x_t = a_0 + \left(\sum_{p=1}^{(N/2)-1} \left(a_p \cos \omega_p t + b_p \sin \omega_p t\right)\right) + a_{N/2} \cos \pi t \,,$$

where $\omega_p = 2\pi p/N$.

Compute the *Fourier coefficients* {a_p}, {b_p} by taking inner products with cos ω_pt and sin ω_pt.

■ Fourier coefficients of *x*_t are:

$$a_0 = \bar{x} = \frac{1}{N} \sum_t x_t ,$$

$$a_p = \frac{2}{N} \sum_t x_t \cos \omega_p t , \qquad b_p = \frac{2}{N} \sum_t x_t \sin \omega_p t ,$$

$$a_{N/2} = \frac{1}{N} \sum_t (-1)^t x_t ,$$

where sum is over observation times.

• Estimated power spectral density (PSD) at frequency ω_p is*:

$$I(\omega_p) = \frac{N}{4\pi} (a_p^2 + b_p^2)$$

*The normalization by $N/4\pi$ is the convention chosen by Chatfield (2004, "Analysis of Time Series: An Introduction"). Other normalization conventions are also in common use.

- There are many different ways to express the power spectral density (aka power spectrum).
- Most common/useful equivalence is that the power spectrum is the discrete Fourier transform of the correlogram:

$$I(\omega_p) = \frac{1}{\pi} \left(r_0 + 2 \sum_{k=1}^{N-1} r_k \cos \omega_p k \right)$$

Plot of estimated power spectrum as a function of frequency ω_p is called the *frequency periodogram* or just the *periodogram*.



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Spectral Density Properties

- Periodogram is discrete Fourier transform of correlogram
- Same information in correlogram and periodogram
- Periodogram usually easier to interpret
- In (R, calculate power spectrum with spectrum()
- The power spectrum *l*(ω_p) partitions the variance in the time series with respect to frequency ω_p.
 - Parseval's theorem implies $\frac{1}{N} \sum_{t} (x_t \bar{x})^2 = \frac{1}{2\pi N} \sum_{p>0} I(\omega_p)$. But $\frac{1}{N} \sum_{t} (x_t - \bar{x})^2 = \text{Var}\{x_t\}$, hence $I(\omega_p)/(2\pi N)$ is the proportion of the variance in the time series associated with period $2\pi/\omega_p$. [For details, see Chatfield (2004).]

Basic Time Series Analysis of Epidemic Data



More on **Time Series** Tools

- Pre-war measles
- Post-war pre-vaccination measles
- Vaccination era measles
- Vaccination era measles until 1990

Time series analysis functions

R has built-in tools for time series analysis:

- Time plot: plot() etc.
- Linear filter (e.g., moving average): filter()
- Correlogram (auto-correlation function): acf()
- Periodogram (power spectrum): spectrum()

You will use all of these functions in **Assignment 4.**
More sophisticated spectral method

- Traditional power spectrum measures frequency content of entire time series.
- Wavelet decomposition is local in time.
 - Reveals changes in the spectrum over time without having to identify distinct temporal segments yourself.
 - Nice intro to wavelet analysis of time series: Torrence and Compo (1998) "A Practical Guide to Wavelet Analysis" *Bulletin of the American Meteorological Society* 79, 61–78
 - ∃ Q packages for wavelet analysis of time series (*e.g.*, WaveletComp, wavelets), and at least one book on wavelet methods in Q

Wavelet Spectrum of Monthly Measles in New York City



Krylova & Earn 2013, J. R. Soc. Interface 10, 20130098

Wavelet Spectrum of Weekly Measles in New York City



Figure 5. Observed measles dynamics in NVC from 1891 to 1984. (a) Square root of measles case reports, normalized by total concurrent population. (b) Colour depth plot of a continuous wavelet transform of the square root of normalized observed NYC measles cases (colour warmth scales with spectral power and 95% significance contours are shown in black). Shaded regions in the upper left and right indicate the cone of influence.

Hempel & Earn 2015, J. R. Soc. Interface 12, 20150024

Epidemic Data and Time Series Tools

Wavelets

Wavelet Spectrum of Weekly Smallpox in London



Krylova & Earn 2020, PLoS Biology 18(12):e3000506

Statistical Modelling of Time Series

Instructor: David Earn Mathematics 4MB3/6MB3 Mathematical Biology

Statistical Modelling of Time Series

- Imagine time series $\{X_t\}$ is generated by random processes.
- Simplest case: X_t (number of cases at time t) is simply a random variable with a known distribution,

$$X_t = \mu + Z_t \tag{(*)}$$

where $\mu = \text{time}$ average number of cases and $\{Z_t\} = \text{sequence of random variables with zero mean.}$

- Might be a reasonable model for importation of new, infectious individuals into a focal community.
- Bad model for epidemics: ignores transmission from one individual to another.
 - There must be a correlation between the number of individuals in the focal community who are infected now and the number who will be infected in the near future.

Statistical Modelling of Time Series: AR and MA

- So, imagine that that successive data points in $\{X_t\}$ are correlated.
- For example, perhaps the data are generated by an autoregressive (AR) process:

 $X_{t}-\mu = \alpha_{1}(X_{t-1}-\mu) + \alpha_{2}(X_{t-2}-\mu) + \dots + \alpha_{p}(X_{t-p}-\mu) + Z_{t},$

where the α_i are constants that determine the degree of correlation along the time series.

Alternatively, the data might be generated by a moving average (MA) process.

$$X_t - \mu = \beta_0 Z_t + \beta_1 Z_{t-1} + \dots + \beta_q Z_{t-q},$$

where the β_i are constants that define a weighted average.

Statistical Modelling of Time Series: ARMA

More generally, the data might be generated by an autoregressive moving average "ARMA(p,q)" process:

$$X_{t} - \mu = \alpha_{1}(X_{t-1} - \mu) + \alpha_{2}(X_{t-2} - \mu) + \dots + \alpha_{p}(X_{t-p} - \mu) + \beta_{0}Z_{t} + \beta_{1}Z_{t-1} + \dots + \beta_{q}Z_{t-q}.$$

Statistical Modelling of Time Series: ARIMA

Finally, an autoregressive integrated moving average "ARIMA(p, d, q)" model includes weighted differences of the time series:

$$X_{t} - \mu = \alpha_{1}(X_{t-1} - \mu) + \alpha_{2}(X_{t-2} - \mu) + \dots + \alpha_{p}(X_{t-p} - \mu) + \gamma_{1}(X_{t-1} - X_{t-2}) + \gamma_{2}(X_{t-2} - X_{t-3}) + \dots + \beta_{0}Z_{t} + \beta_{1}Z_{t-1} + \dots + \beta_{q}Z_{t-q}.$$

- The "I" in ARIMA refers to the original time series X_t , which is an "integrated" version of the differenced time series.
- Technically, an ARIMA model is just an ARMA model with differently labelled coefficients, but explicit differences are often helpful conceptually (e.g., they can "stationarize" a time series).

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What kind of process generated our data?

- How can we tell if our data were generated by such a process? Can we identify an AR(p), MA(q) or ARMA(p,q) process?
- Compare time plots of these processes with time plot of our data? (Comparison by eye often challenging/unreliable.)
- Compare autocorrelation functions (correlograms) of these processes with correlogram of our data? (Better.)
- Compare power spectra (periodograms) of these processes with periodogram of our data? (Even better.)
- Compare wavelet spectra of these processes with wavelet spectrum of our data? (Better yet.)

Statistical Modelling of Time Series: ARMA fitting

- Looking at the power spectra of ARMA models would be instructive.
- But is there a better approach to discovering if an ARMA model could explain our data?
- Find the best fit ARMA parameters by minimizing the residual sum of squares. *e.g.*, for an AR model, minimize:

$$S = \sum_{t=p+1}^{N} \left[(x_t - \mu) - \alpha_1 (x_{t-1} - \mu) - \cdots - \alpha_p (x_{t-p} - \mu) \right]^2.$$

- More generally, we can find the best fit parameters of an ARIMA(p, d, q) model
 - Non-trivial, but there are standard methods
- Compare models with Akaike Information Criterion (AIC), which penalizes models that have more parameters
 - See Earn (2009) review article for more discussion of this.

Time series tools discussed so far...

- Statistical description of time series: time plot, moving average, correlation coefficient, autocorrelation, correlogram, power spectral density (PSD), periodogram, wavelet spectrum
- Time series models: AR, MA, ARMA, ARIMA

Statistical Modelling of Time Series



- Simulate any ARIMA(p, d, q) model with arima.sim()
- Fit an AR model to a time series with ar()
- Fit an ARIMA model to a time series with arima()
- Alternatively, there are specialized time series modelling packages.

ARMA Example (50 years of weekly data)

my.model <- list(ar=c(1,-0.5,0.5,-0.25),ma=c(-0.25,0.5))
my.sim <- arima.sim(n=52*50,model=my.model,sd=0.1)
plot(my.sim,main="ARMA Example",ylab="",xaxs="i")</pre>



ARMA Example

Time

ARMA Example (ACF and PSD up to 10 year lag)





Statistical Modelling of Time Series: Forecasting

- Once we have a fitted model, we can then use it to *forecast* future observations
- Validate this procedure by using part of the data to fit the model and then forecast the remainder of the data (cf. cross-validation)
- How successful is this likely to be for an infectious disease time series?
 - Conceivably good for chicken pox in NYC.
 - Less likely to be good for measles... at least for the main patterns...
 - One of the project options is to look at this more carefully.

Statistical Modelling of Time Series: Limitations

- It might be best to remove mean, trend and seasonality before fitting an ARMA model
 - But this means we will remove the aspects of the data about which we care most!
- The fitted parameters of an ARMA model have no obvious biological meaning
 - The model completely ignores any understanding we have of infectious disease transmission
- Statistical models use the time series itself to parameterize an ARMA (or more general) process
 - It would be better to have a model that we can parameterize from independently collected data and then see if that model can explain the observed time series

Mechanistic Mathematical Modelling

- SIR and all that...
- Takes into account transmission process...
- So why did we just spend time talking about statistical modelling of time series?
 - Important to be familiar with time series models that are in common use.
 - Helps us appreciate the value of mechanistic modelling.
 - Some processes that affect disease dynamics might be better modelled as ARMA or similar processes.
 - Weather (*e.g.*, perhaps model $\beta = \beta(t)$ as an ARMA process)
 - Immigration
 - Ruling out an ARMA model (or at least one with a modest number of parameters) is a step towards finding a good model.
 - A combination of mechanistic and time series models could be useful.