

9 Epidemic Data II

10 Epidemic Data III

**11** Epidemic Data Tools

12 Epidemic Data Tools II



# Mathematics and Statistics

$$\int_{M} d\omega = \int_{\partial M} \omega$$

## Mathematics 4MB3/6MB3 Mathematical Biology

Instructor: David Earn

Lecture 8 Epidemic Data Monday 21 January 2019

- Thanks everyone for doing the contributions survey for Assignment 1.
- Don't stress about the ratings about each other's contributions. The issue is whether some group members did not pull their weight. If somebody didn't try and others had to pick up the slack, that person should be penalized. I will not penalize somebody because they tried but felt they didn't contribute as much to the final document as they could have. Do try to even out the work across the assignments.
- Make sure everyone in your group gets a chance to be in control of the LATEX for one assignment.

#### More Announcements!

#### Assignment 2:

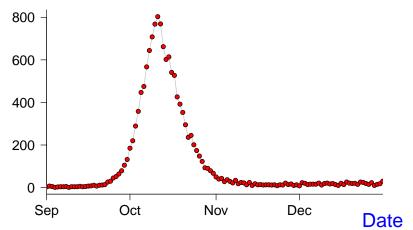
Due Monday 4 February 2019 in class (and by e-mail) at 9:30am.

#### Midterm test:

- Date: Monday 11 March 2019
- Time: 9:30am-11:20am
- Location: Hamilton Hall 410

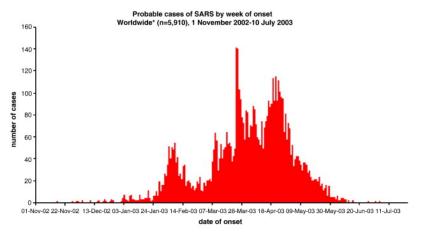
#### P&I Mortality, Philadelphia, 1918

## **P&I** Deaths



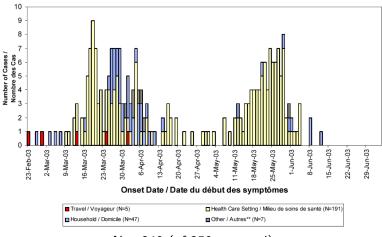
#### Motivating Data – Single epidemic

## 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)

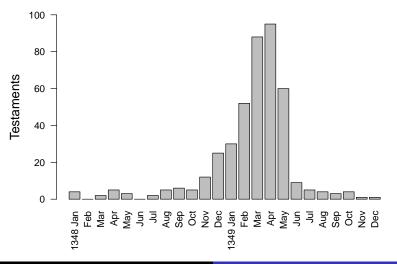
#### Some SARS Facts

High case fatality

- 1918 flu < 3%
- SARS > 10%
- Long hospital stays
  - Mean time from admission to discharge or death:
     ~ 25 days in Hong Kong
- 8098 probable cases, 774 deaths

How bad would it have been if it had not been controlled?

#### The Black Death in London, England, 1348–1349

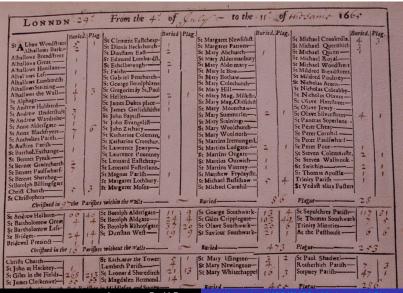


#### London Bill of Mortality, 26 Sept to 3 Oct 1665

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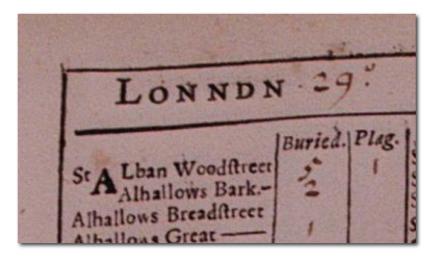
Instructor: David Earn

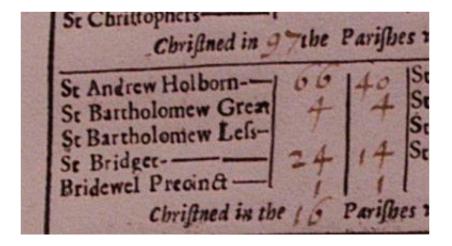
#### Mortality Bills are typically handwritten



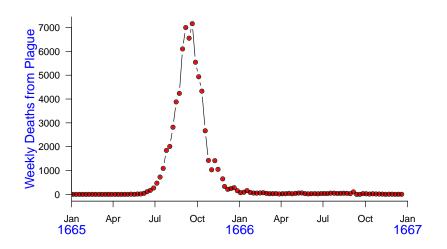
Instructor: David Earn

#### But handwriting is usually very clear

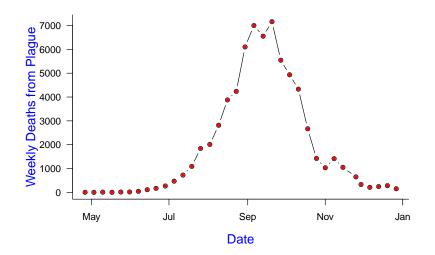




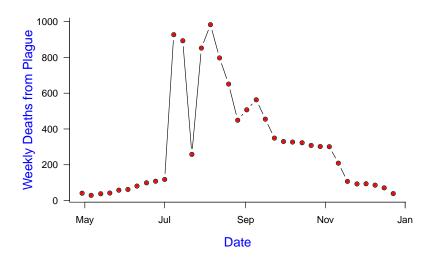
#### The Great Plague of London, 1665



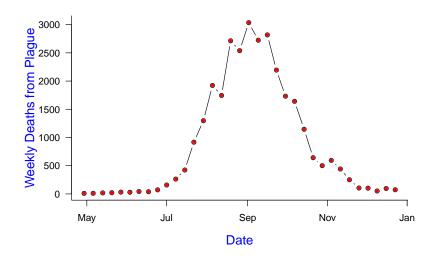
#### The Great Plague of London, 1665



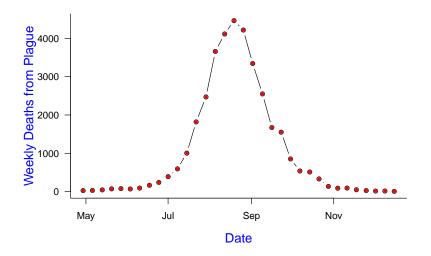
#### London Plague of 1593



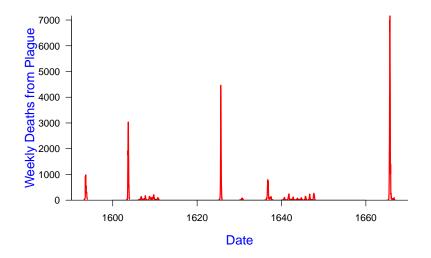
#### London Plague of 1603



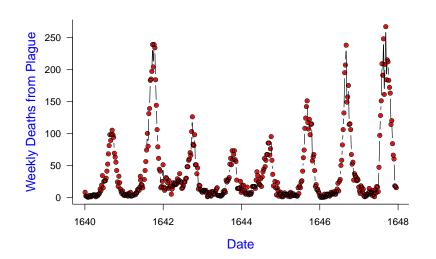
#### London Plague of 1625



#### 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.
- $\label{eq:last} \mathbf{I}/3 \mbox{ Europe's population died in "Black Death" of 1348} \\ \mathbf{I} \sim 300 \mbox{ years for the population to reach the same level.}$
- 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



# Mathematics and Statistics

$$\int_{M} d\omega = \int_{\partial M} \omega$$

## Mathematics 4MB3/6MB3 Mathematical Biology

Instructor: David Earn

Lecture 9 Epidemic Data II Monday 28 Jan 2019

#### Announcements

#### Assignment 2:

Due Monday 4 February 2019 in class (and by e-mail) at 9:30am.

#### Midterm test:

- Date: Monday 11 March 2019
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- *Location:* Hamilton Hall 410

5 minute Student Respiratory Illness Survey:

https://surveys.mcmaster.ca/limesurvey2/index.php/893454

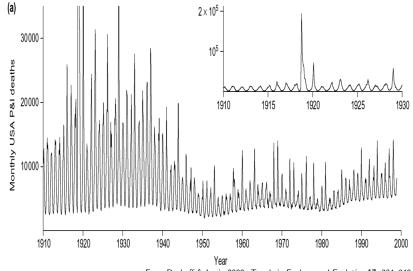
Please complete this anonymous survey to help us monitor the patterns of respiratory illness, over-the-counter drug use, and social contact within the McMaster community. There are no risks to filling out this survey, and your participation is voluntary. You do not need to answer any questions that make you uncomfortable, and all information provided will be kept strictly confidential. Thanks for participating.

-Dr. Marek Smieja (Infectious Diseases)

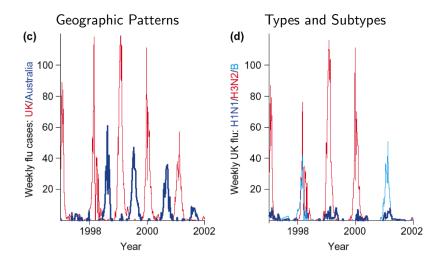
#### Visualization of entire course of the Great Plague

- 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



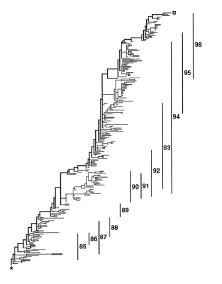
Earn, Dushoff & Levin 2002, Trends in Ecology and Evolution 17, 334-340



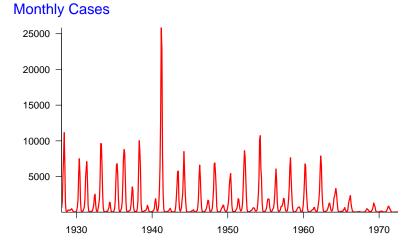
Earn, Dushoff & Levin 2002, Trends in Ecology and Evolution 17, 334-340

#### Influenza Evolution

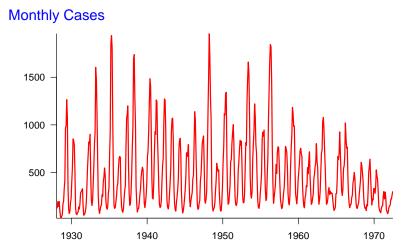
Molecular phylogenetic reconstruction of influenza A/H3N2 evolution, 1985–1996 (Fitch *et al.* 1997)



#### Measles in New York City, 1928–1972

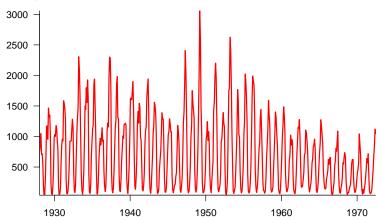


#### Mumps in New York City, 1928–1972



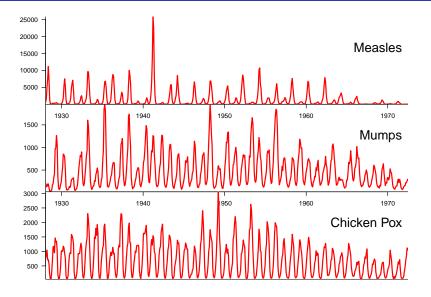
#### Chicken Pox in New York City, 1928–1972

#### **Monthly Cases**

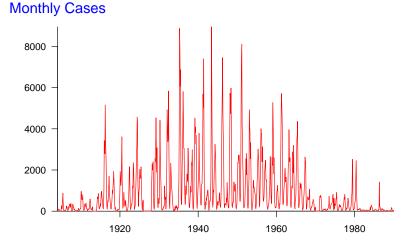


#### emic Data II innuenza; Childhood infectious Diseases

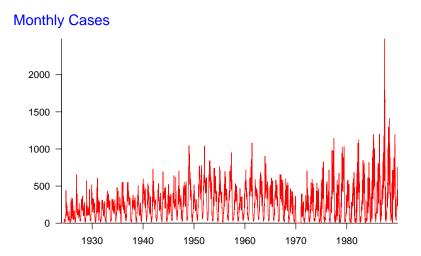
#### Childhood diseases in New York City, 1928–1972



#### Measles in Ontario, 1904–1989

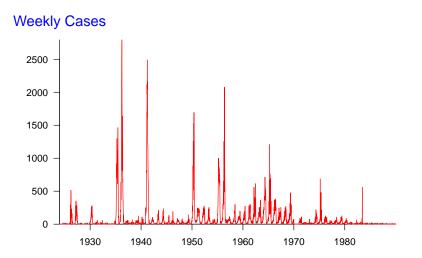


#### Chicken Pox in Ontario, 1924–1989



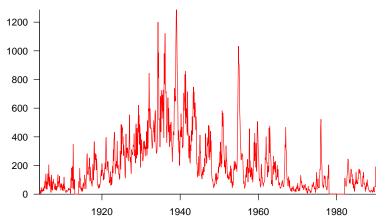
Instructor: David Earn Mathematics 4MB3/6MB3 Mathematical Biology

#### Rubella in Ontario, 1924–1989

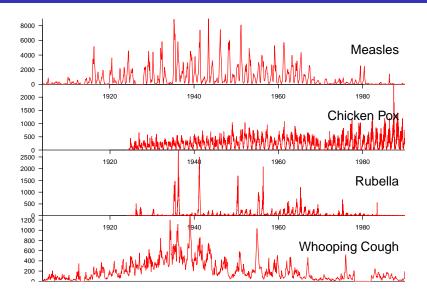


## Whooping Cough in Ontario, 1904–1989





#### 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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Instructor: David Earn

athematics 4MB3/6MB3 Mathematical I



Mathematics and Statistics

$$\int_{M} d\omega = \int_{\partial M} \omega$$

# Mathematics 4MB3/6MB3 Mathematical Biology

Instructor: David Earn

Lecture 10 Epidemic Data III Monday 28 Jan 2019

#### Announcements

#### Assignment 2:

Due Monday 4 February 2019 in class (and by e-mail) at 9:30am.

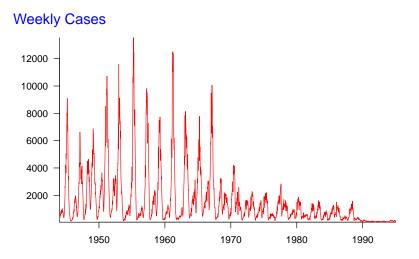
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#### Recurrent epidemics of childhood infections

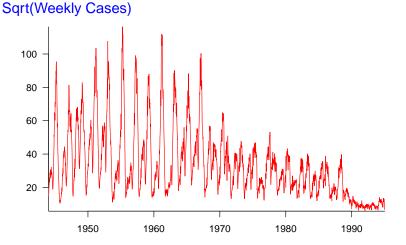
- Childhood diseases in New York City, 1928–1972
- Childhood diseases in Ontario, 1904–1989

# Measles incidence in England and Wales, 1944–1995



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

## Measles incidence in England and Wales, 1944–1995



## Why study measles epidemics?

- In 2017, ~ 110,000 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!

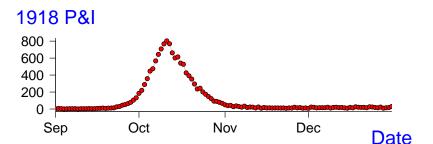
## Modelling population dynamics of childhood infections

- 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.

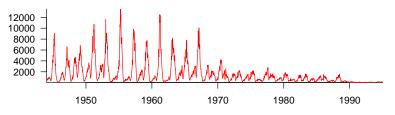
# Epidemic Data Analysis

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

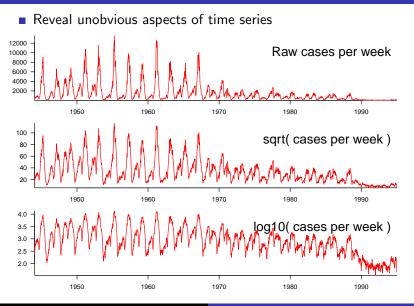
# Time Plots of Temporal Epidemic Patterns



#### Weekly Measles in England and Wales



## Time Plots of Transformed Data



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

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

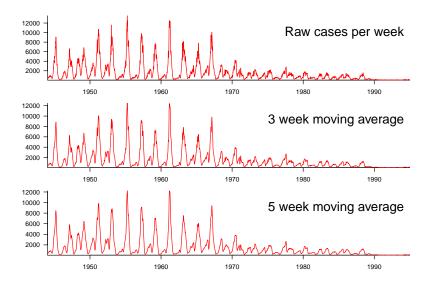
$$x_t \to \frac{1}{2a+1} \sum_{i=-a}^{a} x_{t+i}$$

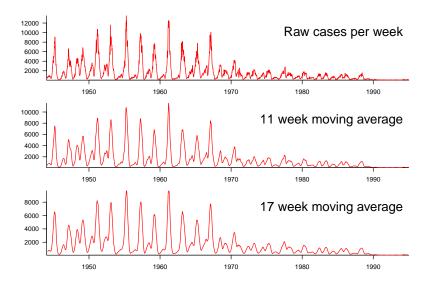
Replace original data points  $x_t$  with averages of nearby points.

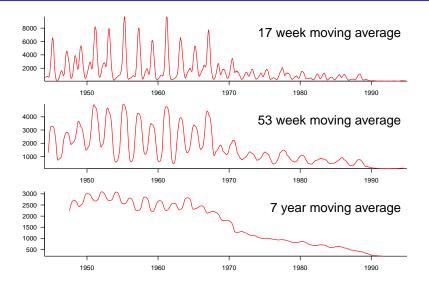
Linear filter:

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

- Generalization of moving average.
- Weights  $\lambda_i$  can be nonlinear functions of *i*.







- Recurrent epidemics with number of cases in the past and the future.
- Given *N* pairs of observations of different quantities, {(*x<sub>i</sub>*, *y<sub>i</sub>*) : *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 ⇐⇒ 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: r<sup>2</sup> 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

- Given a single sequence of observations {*x<sub>t</sub>* : *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<sub>t</sub>, x<sub>k+t</sub>) : t = 1,..., N k} and define the *autocorrelation coefficient at lag k* to be

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

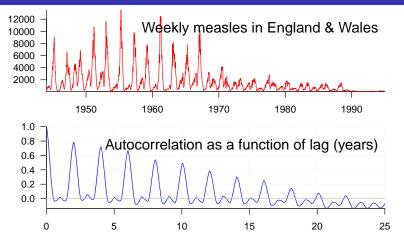
where  $\bar{x}_{1,N-k}$  and  $\bar{x}_{k+1,N}$  are the means of first and last N-k observations, respectively.

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

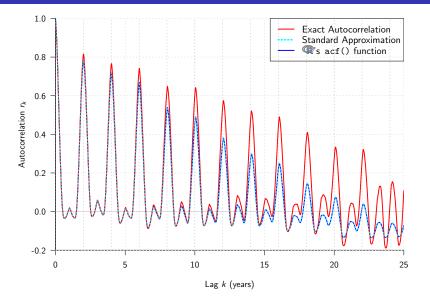
$$r_k \simeq rac{\sum_{t=1}^{N-k} (x_t - ar{x})(x_{k+t} - ar{x})}{\sum_{t=1}^{N} (x_t - ar{x})^2}$$

- Approximation of  $r_k$  is worse for larger lags k
- Plot of autocorrelation r<sub>k</sub> 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.



- 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<sub>p</sub>}, {b<sub>p</sub>} by taking inner products with cos ω<sub>p</sub>t and sin ω<sub>p</sub>t.

Fourier coefficients of x<sub>t</sub> 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  $\omega_p$  is\*:

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

\*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.



Mathematics and Statistics

$$\int_{M} d\omega = \int_{\partial M} \omega$$

# Mathematics 4MB3/6MB3 Mathematical Biology

Instructor: David Earn

Lecture 11 Epidemic Data Tools Wednesday 30 Jan 2019

## Announcements

#### Assignment 2:

Due Monday 4 February 2019 in class (and by e-mail) at 9:30am.

#### Midterm test:

- Date: Monday 11 March 2019
- Time: 9:30am-11:20am
- *Location:* Hamilton Hall 410

5 minute Student Respiratory Illness Survey:

https://surveys.mcmaster.ca/limesurvey2/index.php/893454

Please complete this anonymous survey to help us monitor the patterns of respiratory illness, over-the-counter drug use, and social contact within the McMaster community. There are no risks to filling out this survey, and your participation is voluntary. You do not need to answer any questions that make you uncomfortable, and all information provided will be kept strictly confidential. Thanks for participating.

-Dr. Marek Smieja (Infectious Diseases)

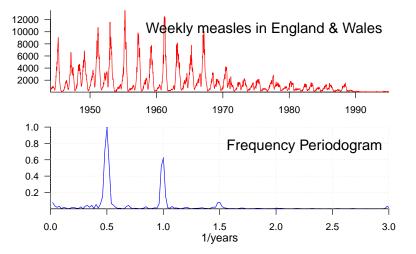
## Last time...

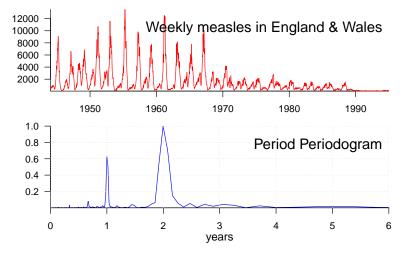
- Statistical description of time series: time plot, moving average
- Correlation coefficient: properties
- Autocorrelation
- Correlogram
- Exact vs. approximate autocorrelation
- Power spectral density (PSD)

- 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:

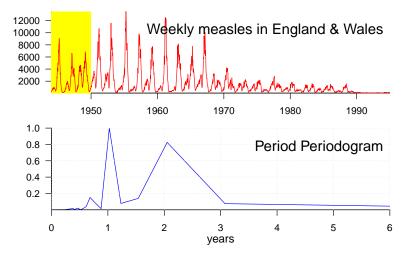
$$I(\omega_p) = \frac{1}{\pi} \left( r_0 + 2 \sum_{k=1}^{N-1} r_k \cos \omega_p k \right)$$

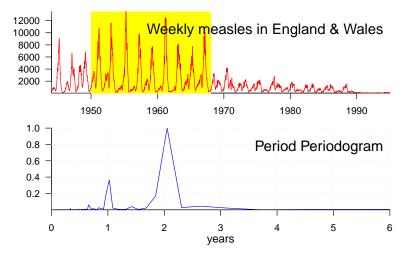
Plot of estimated power spectrum as a function of frequency ω<sub>p</sub> is called the *frequency periodogram* or just the *periodogram*.





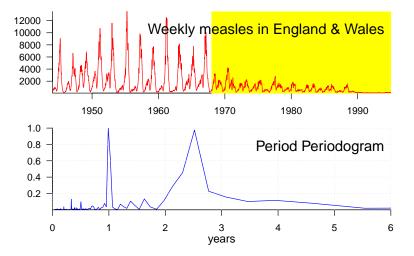
# Spectral Density of Temporal Segments



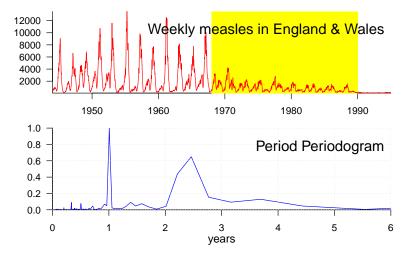


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#### Spectral Density of Temporal Segments



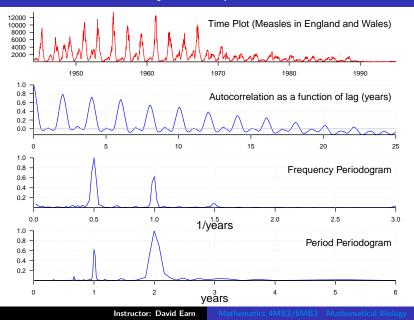
## Spectral Density of Temporal Segments



## 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  $I(\omega_p)$  partitions the variance in the time series with respect to frequency  $\omega_p$ .
  - 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



#### Spectral Density of Temporal Segments

- 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:

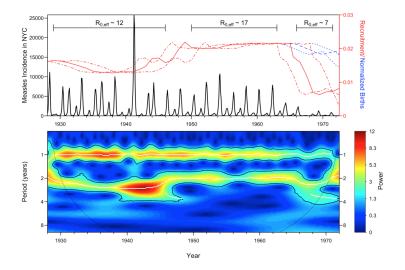
- Time plot: plot() etc.
- Linear filter (e.g., moving average): filter()
- Correlogram (auto-correlation function): acf()
- Periodogram (power spectrum): spectrum()

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
  - $\blacksquare \exists \mathbf{Q} \mathsf{P} \mathsf{packages}$  for wavelet analysis of time series (*e.g.*, WaveletComp, wavelets), and at least one book on wavelet methods in @

#### 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

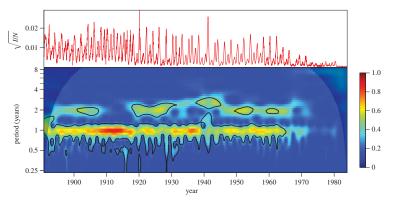


Figure 5. Observed measles dynamics in NYC from 1891 to 1984. (a) Square root of measles case reports, normalized by total concurrent population. (b) Colour depth plot of a continuous wavelet transform of the square root of normalized observed NYC measles cases (colour warmth scales with spectral power 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

# 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<sub>t</sub> (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<sub>t</sub>} are correlated.
- For example, perhaps the data are generated by an autoregressive (AR) process:

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

where the  $\alpha_i$  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  $\beta_i$  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<sub>t</sub>, 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).

#### 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.



Mathematics and Statistics

$$\int_{M} d\omega = \int_{\partial M} \omega$$

# Mathematics 4MB3/6MB3 Mathematical Biology

Instructor: David Earn

Lecture 12 Epidemic Data Tools II Monday 4 Feb 2019 Assignment 1: returned today

Read my solutions and ask if you don't understand them.

#### Assignment 2:

Due TODAY in class (and by e-mail) at 9:30am. Do the Group contribution survey for Assignment 2 TODAY.

Assignment 3 is posted.
 Due Monday 25 February 2019 at 9:30am

#### Midterm test:

- Date: Monday 11 March 2019
- Time: 9:30am–11:20am
- Location: Hamilton Hall 410

#### 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

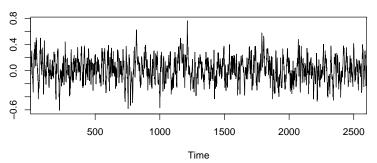
## Statistical Modelling of Time Series



- 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.

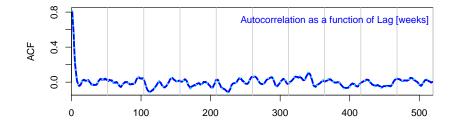
#### ARMA Example (50 years of weekly data)

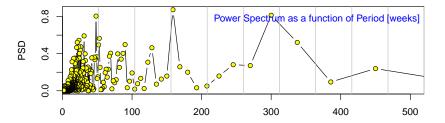
my.model <- list(ar=c(1,-0.5,0.5,-0.25),ma=c(-0.25,0.5))</pre> my.sim <- arima.sim(n=52\*50,model=my.model,sd=0.1)</pre> plot(my.sim,main="ARMA Example",ylab="",xaxs="i")



**ARMA Example** 

## 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.
  - Not for measles... at least not for the main patterns...

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## Statistical Modelling of Time Series: Limitations

- 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?
  - 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.