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Mathematical Approaches to Epidemiological Modelling and Public Health Analysis

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Abstract

Mathematical epidemiology provides a structured way to describe infectious-disease transmission, estimate unobserved disease states, forecast epidemic trajectories, and compare public-health interventions. This paper reviews core deterministic and stochastic frameworks, with particular attention to susceptible–infectious–recovered (SIR) and susceptible–exposed–infectious–recovered (SEIR) models, statistical parameter estimation, model comparison, sensitivity analysis, uncertainty quantification, and intervention planning. A reproducible statistical workflow is proposed, including incidence-rate summaries, likelihood-based calibration, information criteria, and prediction-error measures. To demonstrate how results can be reported, a small illustrative dataset is used to show calculations of incidence and a simple comparison of observed and predicted counts. These values are simulated solely for methodological demonstration and are not empirical observations from a real outbreak. The review indicates that model choice should be guided by the biological question, data quality, identifiability, and the intended decision. No single model is universally optimal: parsimonious compartmental models are interpretable, while stochastic, network, and metapopulation approaches can represent randomness, heterogeneous contacts, and mobility. Transparent assumptions, uncertainty intervals, ethical data handling, and reproducible code are essential for responsible public-health use.

Keywords: *mathematical epidemiology; SIR model; SEIR model; statistical inference; reproduction number; uncertainty quantification; public health.*

Introduction

Mathematical modelling is an important component of epidemiology because it translates assumptions about transmission and recovery into quantitative descriptions of disease dynamics. Models can help estimate epidemic growth, explore the timing and potential effects of interventions, and compare alternative scenarios when direct observation is incomplete. Applications range from emerging infections and seasonal influenza to chronic-disease surveillance and health-system planning. The usefulness of a model depends on the question being asked and the quality of the data used to calibrate it. Reported cases may be affected by testing availability, reporting delays, case definitions, and changes in surveillance. Accordingly, model outputs should be interpreted as conditional estimates rather than certain predictions. This paper organises the main mathematical approaches into a research-paper format and demonstrates a statistical reporting structure without presenting simulated values as real-world evidence.

Aim and objectives

The aim is to explain how mathematical and statistical methods support epidemiological modelling and public-health analysis. The specific objectives are: (i) to summarise SIR, SEIR, stochastic, network, and metapopulation models; (ii) to describe parameter estimation and model evaluation; (iii) to demonstrate basic statistical reporting using a clearly labelled illustrative dataset; and (iv) to identify limitations, ethical considerations, and reproducibility requirements.

Review of Mathematical Frameworks

1. SIR model

The SIR model partitions a population of size N into susceptible S(t), infectious I(t), and recovered or removed R(t) individuals, where N = S(t) + I(t) + R(t). In a closed population, a common deterministic formulation is:

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$dS/dt = -\beta SI/N$

$dI/dt = \beta SI/N - \gamma I$

$dR/dt = \gamma I$

Here, β is the effective transmission-rate parameter and γ is the recovery rate. Under the standard assumptions, the basic reproduction number is $R_0 = \beta/\gamma$. The model is most useful when the infectious period is represented adequately by a single compartment and immunity is assumed to persist over the study horizon.

2. SEIR and extended compartmental models

The SEIR model introduces an exposed compartment E(t) to represent infected individuals who are not yet infectious. With σ denoting the rate at which exposed individuals become infectious, the equations are:

$dS/dt = -\beta SI/N$

$dE/dt = \beta SI/N - \sigma E$

$dI/dt = \sigma E - \gamma I$

$dR/dt = \gamma I$

SEIRS extensions allow recovered individuals to return to susceptibility when immunity wanes. Other extensions can represent vaccination, age groups, hospitalisation, asymptomatic infection, reinfection, or multiple strains. Additional compartments should be included only when the data and research question can support their estimation.

3. Deterministic and stochastic models

Deterministic models produce a single trajectory for fixed initial conditions and parameter values. Stochastic models explicitly represent random transitions or random variation in transmission. Stochastic approaches are particularly useful for small populations, early outbreak stages, and settings in which chance events may determine whether transmission chains disappear or grow. Their outputs are naturally expressed as distributions or prediction intervals rather than a single curve.

4. Network and metapopulation models

Network models represent heterogeneous contact patterns, with nodes representing individuals or groups and edges representing possible contacts. Metapopulation models link local epidemics through travel or migration between locations. These approaches can better represent spatial spread and mobility but require additional data and computational effort.

Methodology and Statistical Analysis

1. Study design

This paper is a methodological review and worked statistical illustration based on the supplied chapter material. It does not report a new epidemiological field study, patient-level dataset, or analysis of official surveillance records. The numerical example below is simulated for teaching purposes only. For an empirical application, the same workflow should be repeated with a documented, dated dataset and the source, inclusion criteria, case definition, and data-cleaning procedures reported.

2. Variables and indicators

Indicator	Definition / formula	Interpretation
Reported incidence	New cases during period / population at risk × 100,000	Rate of new reported cases per 100,000 people
Cumulative cases	Sum of incident cases up to time t	Overall reported case burden
Reproduction number	$R_0 = \beta/\gamma$ in the basic SIR model	Expected secondary infections under stated assumptions
Mean absolute error (MAE)	$(1/n)\,\Sigma\,\lvert y_i - \hat{y}_i\rvert$	Average absolute prediction error
Root mean squared error (RMSE)	$\sqrt{(1/n)\,\Sigma\,(y_i - \hat{y}_i)^2}$	Prediction error with greater penalty for large misses
Akaike information criterion (AIC)	$AIC = 2k - 2\ln(\hat{L})$	Relative fit–complexity measure; lower is preferred
Bayesian information criterion (BIC)	$BIC = k\ln(n) - 2\ln(\hat{L})$	Relative fit–complexity measure penalising complexity

Source: *Prepared by the author based on the definitions and formulas described in the methodology section.*

3. Parameter estimation

Model parameters may be estimated by maximum likelihood, nonlinear least squares, or Bayesian inference. If observed case counts Y_t are modelled as Poisson with expected mean $\mu_t(\theta)$, the likelihood is:

$L(\theta) = \prod_t [\exp(-\mu_t)\,\mu_t^{(Y_t)} / Y_t!]$

The parameter vector θ may include β, γ, σ, initial compartment sizes, and reporting parameters. In practice, case counts can be overdispersed relative to a Poisson distribution; a negative-binomial observation model may then be more appropriate. Confidence intervals or credible intervals should accompany key estimates, and identifiability should be checked before interpreting individual parameters.

4. Model comparison and validation

Candidate models should be fitted to the same data and evaluated using consistent criteria. AIC and BIC balance goodness of fit against model complexity; they are comparative measures and do not establish that a model is biologically correct. Where possible,

validation should use a held-out time period or rolling-origin forecasts. Report MAE or RMSE alongside graphical checks of fitted versus observed incidence. Prediction intervals should be assessed for calibration and coverage.

5. Sensitivity and uncertainty analysis

Sensitivity analysis examines how outputs change when parameters or initial conditions vary. One-at-a-time changes can provide an initial diagnostic, while global methods explore multiple parameters jointly. Uncertainty should be propagated from estimated parameters, observation noise, and alternative structural assumptions into the forecast distribution. Scenario analyses should be described as conditional on their assumptions, not as guaranteed outcomes.

Illustrative Statistical Results

Important note: every value in this section is simulated and is included only to demonstrate statistical presentation. It is not a finding about any actual disease, location, or population.

1. Illustrative incidence calculations

Week	Simulated new cases	Population	Incidence per 100,000
1	12	100,000	12.0
2	18	100,000	18.0
3	27	100,000	27.0
4	35	100,000	35.0
5	31	100,000	31.0

Source: *Author's own illustration using simulated values; these are not empirical outbreak data.*

For example, the week 4 incidence is (35 / 100,000) × 100,000 = 35 reported cases per 100,000 people. In this constructed example, weekly counts rise from 12 in week 1 to 35 in week 4 and then decline to 31 in week 5. This pattern illustrates how a table can summarise a short time series; it does not establish a real epidemic trend.

2. Example of prediction-error reporting

Week	Illustrative observed count (y_i)	Illustrative predicted count ($\hat{y}_i$)	Absolute error
1	12	14	2
2	18	17	1
3	27	24	3
4	35	32	3
5	31	30	1

Source: *Author's own illustration using simulated values for incidence calculations; not based on official surveillance records.*

For the five illustrative observations, MAE = (2 + 1 + 3 + 3 + 1) / 5 = 2.0 cases. RMSE = $\sqrt{[}(4 + 1 + 9 + 9 + 1) / 5] = \sqrt{4.8} \approx 2.19$ cases. These metrics describe only the artificial example. In an applied study, errors should be computed on observations not used to fit the model whenever feasible.

3. Statistical interpretation

The example demonstrates three reporting principles. First, rates require an explicit denominator and time period. Second, fitted values should be compared with observations using defined metrics. Third, numerical results must be labelled according to their provenance. Since the supplied material contains no empirical dataset, no inferential p-values, confidence intervals, or disease-specific parameter estimates are claimed in this paper.

Discussion

SIR and SEIR models provide interpretable starting points for analysing transmission. SEIR is preferable when the latent period is important to the question, while models with waning immunity or vaccination may be needed for longer-term analyses. Stochastic formulations are useful when chance variation is consequential; network and metapopulation models are appropriate when contact heterogeneity or mobility materially affects spread.

Statistical calibration is not merely a technical step. Incomplete testing, reporting delays, changing case definitions, and demographic differences can distort observed patterns. A model may fit reported case counts while misrepresenting underlying transmission if the observation process is ignored. Researchers should distinguish uncertainty due to random variation from uncertainty due to limited data and uncertainty due to model structure.

Intervention modelling can compare vaccination, isolation, travel measures, school or workplace policies, and resource-allocation strategies. However, results depend on assumptions about intervention timing, uptake, efficacy, costs, and behavioural response. Public-health decisions should therefore combine model evidence with clinical knowledge, operational constraints, equity considerations, and transparent communication.

Limitations

This paper is a structured methodological review of the supplied material rather than a systematic review with a preregistered search strategy. The references inherited from the source document vary in completeness and should be checked against original publications before submission. The numerical tables are simulated, not empirical. Consequently, they cannot support conclusions

about a particular outbreak or intervention. An empirical follow-up should specify the study setting, data period, sample or population definition, model-fitting procedure, software, parameter uncertainty, and validation design.

Ethical Considerations and Reproducibility

Epidemiological data may be sensitive and can be affected by selection, measurement, and reporting bias. Researchers should use data minimisation, appropriate permissions, de-identification where applicable, and secure storage. Assumptions, data sources, code, parameter values, model versions, and analysis decisions should be documented so that results can be reproduced. When sharing is restricted, metadata and a clear description of access conditions should still be provided.

Conclusion

Mathematical and statistical methods are central to understanding disease transmission, estimating epidemic trajectories, and comparing public-health strategies. Reliable analysis requires an appropriate model structure, defensible parameter estimation, model validation, uncertainty quantification, and clear reporting of data limitations. The illustrative calculations in this paper show how incidence and prediction errors can be reported, but they are not empirical evidence. Future applications should use verified surveillance data and publish reproducible methods and uncertainty intervals to support transparent, proportionate decision-making.

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Conflicts of interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

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