Bayesian analysis and antimicrobial resistance

Conor Rosato [1]

[1]University of Liverpool

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Overview

Background

Bayesian Analysis

Background

- PhD titled "Disease Surveillance using Bayesian Methods"
- Six months into post-doc
- Working on antimicrobial resistance related problems

Bayesian methods review

Bayesian Calibration of Anti-microbial Resistance: A Review

CONOR ROSATO[1], ALESSANDRO GERADA[1], ALEX HOWARD[1], JOHN HARRIS[2], SIMON MASKELL[3](Fellow, IEEE), and WILLIAM HOPE[1],

[1]Department of Pharmacology and Therapeutics, University of Liverpool, 6 West Derby St, Liverpool, L7 8TX, United Kingdom
[2]Public Health England, UK
[3]Department of Electrical Engineering and Electronics, University of Liverpool, 9 Brownlow Hill, Liverpool, L69 3GJ, United Kingdom
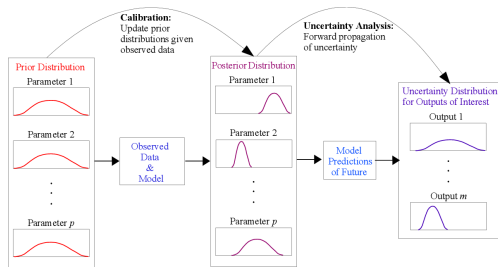Corresponding author: Conor Rosato (e-mail:conrosa@liverpool.ac.uk).

ABSTRACT Antimicrobial resistance (AMR) emerges when disease causing microorganisms develop the ability to withstand the effects of antimicrobial medicines. This phenomenon is often fueled by the human-to-human transmission of pathogens and the overuse of antibiotics. Over the past 50 years, the increased computational power has facilitated the routine application of Bayesian inference algorithms, such as Markov Chain Monte Carlo (MCMC) and Sequential Monte Carlo (SMC) methods. These algorithms are instrumental in calibrating complex statistical models to vast amounts of data. In this comprehensive review, we delineate and exemplify the development and application of Bayesian methods within the context of AMR, offering practical examples. Additionally, we outline recent advancements in the methodology of these inference algorithms and provide insights into their prospective applicability for modeling AMR in the future.

- Population based AMR
  - Spread of MRSA in hospital setting
- En vitro studies
  - The Minimal Inhibitory Concentration (MIC) to establish the susceptibility or resistance of antibiotics when tested against antimicrobials
- Specialised areas of AMR
  - Molecular sequences associated with drug resistance using phylogenetic trees
  - Population pharmacokinetic models - depict relationships between patient characteristics and drug exposure

Bayesian Calibration

- Finding a unique set of model parameters that provide a good description of the system behaviour
- Bayesian methods are naturally suited for calibration because they estimate the input parameter's posterior distributions

Bayesian Calibration

- Advantages
  - Provides a framework for dealing with uncertainty
  - Include prior information when modelling
  - Distribution over any hypotheses rather than point estimates
- Disadvantages
  - Can be hard to select a correct prior
  - Computer time intensive

Bayesian calibration

- Two sampling algorithms include: Markov Chain Monte Carlo and Sequential Monte Carlo methods

Sampling Algorithm	Proposal	Studies
ABC	-	[9], [16], [17], [26], [41]
MCMC	MH	[10]–[14], [23], [28], [29], [34], [39], [40], [48]–[50]
Adaptive MCMC	MH	[14], [15], [49]
MCMC	Gibbs	[22], [24], [32], [44], [46]–[48]
MCMC	Langevin	[32]
MCMC	NUTS	[27], [31], [35], [38], [43]
SMC Sampler	ABC proposal	[37]
Particle-MCMC	MH	[33], [51]
SMC²	MH	[30]

TABLE 2: Inference Algorithms

- PhD focused on being accurate and efficient
- Aiming to work on AMR related problems

An $\mathcal{O}(\log_2 N)$ SMC² Algorithm on Distributed Memory with an Approx. Optimal L-Kernel

Conor Rosato*, Alessandro Varsi†, Joshua Murphy† and Simon Maskell†

* Department of Pharmacology and Therapeutics, University of Liverpool, United Kingdom
† Department of Electrical Engineering and Electronics, University of Liverpool, United Kingdom
Email: {cmrosa, a.varsi, joshua.murphy, smaskell}@liverpool.ac.uk

Abstract—Calibrating statistical models using Bayesian inference often requires both accurate and timely estimates of parameters of interest. Particle Markov Chain Monte Carlo (p-MCMC) and Sequential Monte Carlo Squared (SMC²) are two methods that can an unbiased estimate of the log-likelihood obtained from a particle filter (PF) to evaluate the target distribution. P-MCMC constructs a single Markov chain which is sequential by nature or cannot be readily parallelised using Distributed Memory (DM) architectures. This is in contrast to SMC² which includes processes, such as importance sampling, that are described as embarrassingly parallel. However, difficulties arise when attempting to parallelise resampling. None-the-less, the choice of backward kernel, recycling scheme and comput-

[1]. Theoretically, sampling with a single Markov chain using MCMC is ergodic and ensures convergence to the correct posterior distribution. However, sampling with one MCMC chain cannot readily exploit parallel computing architectures such as Message Passing Interface (MPI). This is due to the next MCMC sample being dependent on the current sample. Running multiple MCMC chains in parallel is a method for overcoming this issue [2]. The challenges of parallelizing a single MCMC chain contrasts with SMC samplers which have inherent steps that can be described as embarrassingly parallel. Sampling N independent samples from a proposal