Introduction to the Bayesian framework in Biometrics

Part II: Bayesian computation

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Introduction

Estimating the *posterior* distribution is often costly

Bayesian computational statistics

Computational aspects of Bayesian inference can get sophisticated but are key to its successful application

Numerical integration – I

Real world applications: $\boldsymbol{\theta} = (\theta_1, \dots, \theta_d)$

 \Rightarrow joint posterior distribution of all d parameters

♠ hard to compute:

- complexe likelihood
- integrating constant $f(y) = \int_{\Theta^d} f(y|\theta) \pi(\theta) d\theta$

Analytical form rarely available

- \Rightarrow numerical computations: integral of d multiplicity
 - difficult when d is big (numerical issues as soon as d > 4)

Numerical integration – II

Even dimension 1 can be tough!

Example:

Let $x_1,...,x_n$ iid according to a Cauchy distribution $\mathscr{C}(\theta,1)$ with prior $\pi(\theta) = \mathscr{N}(\mu,\sigma^2)$ (μ and σ known)

$$p(\theta|x_1,...,x_n) \propto f(x_1,...,x_n|\theta)\pi(\theta)$$
$$\propto e^{-\frac{(\theta-\mu)^2}{2\sigma^2}} \prod_{i=1}^n (1+(x_i-\theta)^2)^{-1}$$

Marginal posterior distributions

Objective: draw conclusion based on the joint *posterior* distribution

⇒ probability of all possible values for each parameter (i.e. their marginal distribution – uni-dimensional)

 $\underline{\wedge}$ Recovering all of the *posterior* density **numerically** requires the calculation of multidimensional integrals for each possible value of the parameter

⇒ a sufficiently precise computation seems unrealistic

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Algorithms based on **sampling simulations** especially **Markov chain Monte Carlo** (MCMC)

Computational Bayesian statistics

Computational solutions

Bayes Theorem ⇒ posterior distribution

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♠ in pratice:

- analytical form rarely available (very particular cases)
- integral to the denominator often very hard to compute

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How can one estimate the *posteriori* distribution ?

- ⇒ sample according to this posterior distribution
 - direct sampling
 - Markov chain Monte Carlo (MCMC)

Monte Carlo method

Monte Carlo : von Neumann & Ulam (Los Alamos Scientific Laboratory – 1955)

⇒ use random numbers to compute quantities whose analytical computation is hard (or impossible)

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- ⇒ use random numbers to compute quantities whose analytical computation is hard (or impossible)
 - Law of Large Numbers (LLN)
 - so-called "Monte Carlo sample"
- compute various functions from that sample distribution

Example: One wants to compute $\mathbb{E}[f(X)] = \int f(x)p_X(x)dx$

If
$$x_i \stackrel{iid}{\sim} p_X$$
, $\mathbb{E}[f(X)] = \frac{1}{N} \sum_{i=1}^{N} f(x_i)$ (LLN)

 \Rightarrow if one knows how to sample from p_X , one can then estimate $\mathbb{E}[f(X)]$

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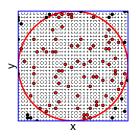
. . .

π estimation:

Intro

π estimation:





A casino roulette (in Monte Carlo ?)

A 36×36 grid

- 1 The probability of being inside the disk while in the square: $p_C = \frac{\pi R^2}{(2R)^2} = \frac{\pi}{4}$
- 2 n points $\{(x_{11}, x_{21}), \dots, (x_{1n}, x_{2n})\} = \{P_1, \dots, P_n\}$ on the 36×36 grid (generated with the roulette)
- 3 Count the number of points inside the disk
- ⇒ Compute the ratio (estimated probability of being inside the disk while in the square): $\hat{p}_C = \frac{\sum P_i \in circle}{P_i}$

π estimation:



A casino roulette (in Monte Carlo ?)



A 36×36 grid

If n = 1000 and 786 points are inside the disk: $\hat{\pi} = 4 \times \frac{786}{1000} = 3.144$

One can improve the estimate by increasing:

- the grid resolution, and also
- the number of points sampled n: $\lim_{n \to +\infty} \widehat{p}_C = p_C = \pi/4$

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Monte Carlo sample \Rightarrow compute various functions e.g. $\pi = 4 \times$ the probability of being inside the disk

Your turn!

Intro



Practical: exercise 1

Direct sampling methods

Generating random numbers from common probability distributions

Random & pseudo-random numbers

There exist several ways to generate so-called "random" numbers according to known distributions

NB: computer programs do not generate truly random numbers

Rather pseudo-random, which seem random but are actually generated by a deterministic process (depending on a "seed" parameter).

Uniform sample generation

Linear congruential algorithm: sample pseudo-random numbers according to the Uniform distribution on [0,1] (Lehmer, 1948)

- **1** Generate a sequence of integers y_n such as: $y_{n+1} = (ay_n + b) \mod m$
- $2 x_n = \frac{y_n}{m-1}$

choose a, b and m so that y_n has a long period & $(x_1,...,x_n)$ can be considered iid

with y_0 the seed

<u>Remark:</u> $0 \le y_n \le m-1 \Rightarrow$ in practice m very large (e.g. 2^{19937} , default in \mathbb{R} which uses the Mersenne-Twister variation)

In the following, sampling pseudo-random numbers uniformly on [0,1] will be considered reliable and used by the different sampling algorithms

Other usual distributions

Relying on relationships between the different usual distributions starting from $U_i \sim \mathcal{U}_{[0,1]}$

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Binomial Bin(n, p):

$$Y_i = \mathbb{1}_{U_i \le p} \sim \mathsf{Bernoulli}(p)$$

 $X = \sum_{i=1}^{n} Y_i \sim Bin(n, p)$

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Normal $\mathcal{N}(0,1)$ (Box-Müller algorithm):

 U_1 and U_2 are 2 independent uniform variables on [0;1]

$$Y_1 = \sqrt{-2\log U_1} \cos(2\pi U_2)$$
$$Y_2 = \sqrt{-2\log U_1} \sin(2\pi U_2)$$

 \Rightarrow Y₁ & Y₂ are independent random variables each following a $\mathcal{N}(0,1)$

Inverse transform sampling

<u>Definition</u>: For a function F defined on \mathbb{R} , its **generalized inverse** is defined as: $F^{-1}(u) = \inf\{x \text{ tq } F(x) > u\}$

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Property: Let \bullet F be a cumulative probability distribution function

• U be a uniform random variable on [0,1]

Then $F^{-1}(U)$ defines a random variable whith cumulative probability distribution function F

- If $\ \ \,$ one knows F, the cumulative probability distribution function from which to sample
 - 2 one can invert F
- \Rightarrow then one can sample this distribution from a uniform sample on [0,1]

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Sampling according to a distribution defined analytically

Inverse transform sampling: illustration

Example: sample from the Exponential distribution with parameter λ

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- density of the Exponential distribution: $f(x) = \lambda \exp(-\lambda x)$
- its cumulative probability distribution function (its integral): $F(x) = 1 \exp(-\lambda x)$

Let
$$F(x) = u$$

Then $x = \dots$

Inverse transform sampling: illustration

Example: sample from the Exponential distribution with parameter λ

- density of the Exponential distribution: $f(x) = \lambda \exp(-\lambda x)$
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Let
$$F(x) = u$$

Then
$$x = -\frac{1}{\lambda}\log(1-u)$$

$$\Rightarrow$$
 and if $U \sim U_{[0;1]}$, then $X = F^{-1}(U) = -\frac{1}{\lambda}\log(1-U) \sim E(\lambda)$.

Sampling according to a distribution defined analytically

Your turn!



Practical: exercise 2

Acceptance-rejection method

Use an **instrumental distribution** g (which we know how to sample from)

 \Rightarrow to sample from the target distribution f

The general principle is to **choose** g **close to** f and to propose samples from g, to accept some and reject others to get a sample following f.

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The general principle is to **choose** g **close to** f and to propose samples from g, to accept some and reject others to get a sample following f.

Let f be the targeted density function

Let g be a proposal density function (from which one knows how to sample) such that, for all x: $f(x) \le Mg(x)$

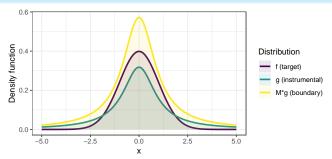
While $i \le n$:

- 1 Sample $x_i \sim g$ and $u_i \sim \mathcal{U}_{[0,1]}$
- 2 If $u_i \le \frac{f(x_i)}{Mg(x_i)}$, accept the draw: $y_i := x_i$ else **reject** it and return to 1.

$$\Rightarrow (v_1, \dots, v_n) \stackrel{iid}{\sim} f$$

Sampling according to a distribution defined analytically

Acceptance-rejection: importance of the proposal



Example of a proposal and a target ditribution for the accept-reject algorithm

Remarque: The smaller M, the greater acceptance rate

 \Rightarrow the more the algorithm is efficient at sampling from f (less iterations for a sample size n)

So one wishes g the as close as possible to f!

 $\underline{\wedge}$ g will necessarily have heavier tail than the target

⇒ when the number of parameters increases, acceptance rate decrease svery rapidly (curse of dimension)

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MCMC Algorithms

Markov chain definition

Markov chain: discrete time stochastic process

Definition: a series of random variables X_0, X_1, X_2, \ldots (all valued over the same state space) with the "memoryless" Markov property:

MCMC Algorithms •oooooooooo

$$p(X_i = x | X_0 = x_0, X_1 = x_1, \dots, X_{i-1} = x_{i-1}) = p(X_i = x | X_{i-1} = x_{i-1})$$

The set E of all possible values of X_i is called the **state space**

2 parameters:

- 1 initial distribution $p(X_0)$
- tansition probabilities $T(x,A) = p(X_i \in A | X_{i-1} = x)$

NB: only homogeneous Markov chains considered here:

$$p(X_{i+1} = x | X_i = y) = p(X_i = x | X_{i-1} = y)$$

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Markov chains properties

<u>Property</u>: a Markov chain is **irreducible** if all sets of non-zero probability can be reached from any starting point (i.e. any state is accessible from any other)

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Property: a Markov chain is **aperiodic** if nothing induces periodic behavior of the trajectories

Stationary law & ergodic theorem

<u>Definition</u>: A probability distribution \tilde{p} is called **invariant law** (or **stationary law**) for a Markov chain if it verifies the following property: if $X_i \sim \tilde{p}$, then $X_{i+j} \sim \tilde{p} \ \forall j \geq 1$

Remark: a Markov chain can admit several stationary laws

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Ergodic theorem (infinite space): A positive irreducible and recurrent Markov chain admits a single invariant probability distribution \tilde{p} and converges towards it

Doudou (a hamster) follows a Markov chain every minute with 3 states:

- S sleep
- E eat
- W work out
- ⇒ its activity in 1min only depends on its current activity

Matrix of transition probabilities:

$$P = \begin{pmatrix} X_i / X_{i+1} & S & E & W \\ S & 0.9 & 0.05 & 0.05 \\ E & 0.7 & 0 & 0.3 \\ W & 0.8 & 0 & 0.2 \end{pmatrix}$$

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- 1) Is the Markov chain irreducible? recurrent? aperiodic?
- 2) Suppose Doudou is now asleep. What about in 2 min? in 10 min?
- 3) Suppose now that Doudou is working out. What about in 10 min?

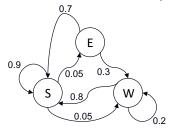
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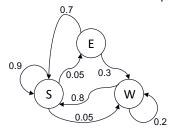
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- 2) Suppose Doudou is now asleep. What about in 2 min ? in 10 min ? ...
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1) Is the Markov chain irreducible? recurrent? aperiodic?



2) Suppose Doudou is now asleep. What about in 2 min? in 10 min?

$$x_0 = \begin{pmatrix} 1 \\ 0 \\ 0 \end{pmatrix}^T$$
 $x_2 = x_0 P^2 = \begin{pmatrix} 0.885 \\ 0.045 \\ 0.070 \end{pmatrix}^T$ $x_{10} = x_2 P^8 = x_0 P^{10} = \begin{pmatrix} 0.884 \\ 0.044 \\ 0.072 \end{pmatrix}^T$

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 $x_{10} = x_0 P^{10} = \begin{pmatrix} 0.884 \\ 0.044 \\ 0.072 \end{pmatrix}^T$

Here, the Markov chain being aperiodic, recurrent and irreducible, there is a stationary law: $\tilde{p} = \tilde{p}P$.

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$$\frac{1}{N} \sum_{i=1}^{N} f(X_{n+i}) \xrightarrow[N \to +\infty]{} \mathbb{E}[f(X)]$$

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$$\overbrace{X_0 \to X_1 \to X_2 \to \cdots \to X_n}^{\text{Markov chain convergence}} \xrightarrow{X_{n+1} \to X_{n+2} \to \cdots \to X_{n+N}} X_{n+1} \xrightarrow{X_{n+2} \to \cdots \to X_{n+N}} X_{n+1}$$

General framework of MCMC algorithms

MCMC algorithms uses an acceptance-rejection framework

- 1 Initialise $x^{(0)}$
- **2** For t = 1 ... n + N:
 - a Propose a new candidate $y^{(t)} \sim q(y^{(t)}|x^{(t-1)})$
 - **b** Accept $y^{(t)}$ with probability $\alpha(x^{(t-1)}, y^{(t)})$: $x^{(t)} := y^{(t)}$

if t > n, "save" $x^{(t)}$ (as part of the final Monte Carlo sample)

where q is the instrumental distribution for proposing new samples and α is the acceptance probability.

Choosing the instrumental distribution

Not absolutely optimal choice for the instrumental distribution q proposing new samples

⇒ infinite possibilities: some better than others

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To guaranty convergence towards the target \tilde{p} :

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- q must not generate periodic values

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To guaranty convergence towards the target \tilde{p} :

- the support of q has to cover the support of \tilde{p}
- q must not generate periodic values

NB: ideally q is easy and fast to compute

Metropolis-Hastings algorithm

- 1 Initialise $x^{(0)}$
- 2 For t = 1, ..., n + N:
 - a Sample $y^{(t)} \sim q(y^{(t)}|x^{(t-1)})$
 - **b** Compute the acceptance probability $\tilde{p}(y^{(t)}) = min \left\{ 1 \tilde{p}(y^{(t)}) / \tilde{p}(x^{(t-1)}) \right\}$

$$\alpha^{(t)} = \min \left\{ 1, \frac{\tilde{p}(y^{(t)})}{q(y^{(t)}|x^{(t-1)})} \middle/ \frac{\tilde{p}(x^{(t-1)})}{q(x^{(t-1)}|y^{(t)})} \right\}$$

c Acceptance-rejection step: sample $u^{(t)} \sim \mathcal{U}_{[0;1]}$ $x^{(t)} = \begin{cases} y^{(t)} \text{ if } u^{(t)} \leq \alpha^{(t)} \\ x^{(t-1)} \text{ else} \end{cases}$

$$\alpha^{(t)} = \min \left\{ 1, \frac{\tilde{p}(y^{(t)})}{\tilde{p}(x^{(t-1)})} \frac{q(x^{(t-1)}|y^{(t)})}{q(y^{(t)}|x^{(t-1)})} \right\}$$

 \Rightarrow computable even if \tilde{p} is known only up to a constant ! (like the posterior)

Metropolis-Hastings: particular cases

Sometimes $\alpha^{(t)}$ computation simplifies:

- independent Metropolis-Hastings: $q(y^{(t)}|x^{(t-1)}) = q(y^{(t)})$
- random walk Metropolis-Hastings: $q(y^{(t)}|x^{(t-1)}) = g(y^{(t)} x^{(t-1)})$ If g is symetric (g(-x) = g(x)), then:

$$\frac{\tilde{p}(y^{(t)})}{\tilde{p}(x^{(t-1)})}\frac{q(y^{(t)}|x^{(t-1)})}{q(x^{(t-1)}|y^{(t)})} = \frac{\tilde{p}(y^{(t)})}{\tilde{p}(x^{(t-1)})}\frac{g(y^{(t)}-x^{(t-1)})}{g(x^{(t-1)}-\tilde{y}^{(t)})} = \frac{\tilde{p}(y^{(t)})}{\tilde{p}(x^{(t-1)})}$$

Pro and cons of Metropolis-Hastings

- e very simple & very general
- eallow sampling from uni- or multi-dimensional distributions
- 8 choice of the proposal is crucial, but hard
 - ⇒ huge impact on algorithm performances
- e quickly becomes inefficient dimension is too high

NB: a high rejection rate often implies important computation timings

Simulated annealing

Change $\alpha^{(t)}$ computation during the algorithm:

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$$\alpha^{(t)} = \min \left\{ 1, \left(\frac{\tilde{p}(y^{(t)})}{\tilde{p}(x^{(t-1)})} \frac{q(x^{(t-1)}|y^{(t)})}{q(y^{(t)}|x^{(t-1)})} \right)^{\frac{1}{T(t)}} \right\}$$

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Ex: $T(t) = T_0 \left(\frac{T_f}{T_0}\right)^{\frac{1}{n}} \Rightarrow$ particularly useful for avoiding local optima

Gibbs sampler

When the dimension $\nearrow \Rightarrow$ very hard to propose probable values

Gibbs samplers: re-actualisation coordinate by coordinate, while conditioning on the most recent values (no acceptance-rejection)

1 Initialise
$$x^{(0)} = (x_1^{(0)}, \dots, x_d^{(0)})$$

2 For
$$t = 1, ..., n + N$$
:

a Sample
$$x_1^{(t)} \sim p(x_1|x_2^{(t-1)},...,x_d^{(t-1)})$$

b Sample
$$x_2^{(t)} \sim p(x_2|x_1^{(t)}, x_3^{(t-1)}, \dots, x_d^{(t-1)})$$

d Sample
$$x_i^{(t)} \sim p(x_i|x_1^{(t)},...,x_{i-1}^{(t)},x_{i+1}^{(t-1)},...,x_d^{(t-1)})$$

f Sample
$$x_d^{(t)} \sim p(x_d | x_2^{(t)}, \dots, x_{d-1}^{(t)})$$

NB: if the conditional distribution is unknown for some coordinates, an acceptance-rejection step can be included for this coordinate only (*Metropolis within gibbs*)

Your turn!



Practical: exercise 3

MCMC in practice

MCMC softwares

- BUGS: Bayesian inference Using Gibbs Sampling 1989 MRC BSU University of Cambridge (UK)
 - ⇒ flexible software for Bayesian analysis in complex statistical models through MCMC algorithms
 - <u>WinBUGS</u>: A clic + Windows only + stopped development https://www.mrc-bsu.cam.ac.uk/software/bugs/the-bugs-project-winbugs/
 - OpenBUGS: A clic + Windows only + Linux partially
 https://www.mrc-bsu.cam.ac.uk/software/bugs/openbugs/
 - <u>JAGS</u>:
 [©] command line +
 [®] interface
 http://mcmc-jags.sourceforge.net/
- STAN: specialized for high-dimensional problems http://mc-stan.org/

rjags

JAGS software is modern and efficient:

- relies on the BUGS language to specify a Bayesian model
- R interface thanks to rjags package
- results analysis with 😱 packages
 - o coda
 - HDInterval

Markov chain convergence

In Bayesian analysis, MCMC algorithms are used to obtain a **Monte Carlo sample** from the *posterior* distribution

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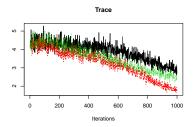
- Initialisation of several Markov chains from different initial values
- ⇒ If convergence is reached, then these chains must be overlapping

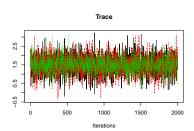
Graphical diagnostics

- Trace
- Posterior density
- Running Quantiles
- Gelman-Rubin diagram
- Auto-correlogram

Trace

coda::traceplot()

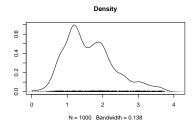


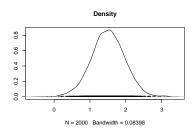


- e chain traces must overlap and mix
- / n.iter and/or / burn-in

Posterior density

coda::densplot()



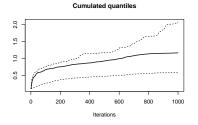


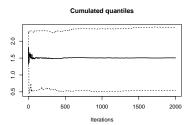
- e density must be smooth and uni-modal
- / n.iter and/or / burn-in

34/42

Running quantiles

coda::cumuplot()





- erunning quantiles must be stable across iterations
- / n.iter and/or / burn-in

Gelman-Rubin statistic

- variation between the different chains
- · variation within a given chain

If the algorithm has properly converged, the between-chain variation must be close to zero

$$\theta_{[c]} = (\theta_{[c]}^{(1)}, \dots, \theta_{[c]}^{(N)})$$
 the N-sample from chain number $c = 1, \dots, C$

Gelman-Rubin statistic:
$$R = \frac{\frac{N-1}{N}W\frac{1}{N}B}{W}$$

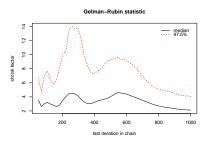
- between-chain variance: $B = \frac{N}{C-1} \sum_{c=1}^{C} (\bar{\theta}_{[C]} \bar{\theta}_{.})^2$
- chain average: $\bar{\theta}_{[c]} = \frac{1}{N} \sum_{t=1}^{N} \theta_{[c]}^{(t)}$
- global average: $\bar{\theta} = \frac{1}{C} \sum_{c=1}^{C} \bar{\theta}_{[C]}$
- within-chain variance: $s_{[c]}^2 = \frac{1}{N-1} \sum_{t=1}^N (\theta_{[c]}^{(t)} \bar{\theta}_{[C]})^2$

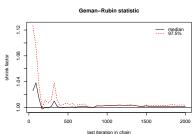
$$N \to +\infty \& B \to 0 \Rightarrow R \to 1$$

Other statistics exist...

Gelman-Rubin diagram

coda::gelman.plot()





- Gelman-Rubin statistic median must remain under the 1,01 threshold (or 1,05)
- / n.iter and/or / burn-in

Effective Sample Size (ESS)

Markov property ⇒ **auto-correlation** between values sampled after one another (dependent sampling) :

- reduce the amount of information available within a sample size n
- slows down LLN convergence

Effective sample size quantifies this:

$$ESS = \frac{N}{1 + 2\sum_{k=1}^{+\infty} \rho(k)}$$

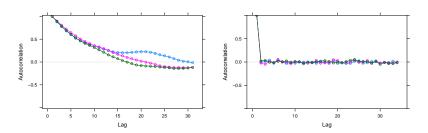
where $\rho(k)$ is the auto-correlation with lag k.

Space out saved samples (e.g. every 2, 5, or 10 iterations)

⇒ reduces dependency within the Monte Carlo sample generated

Auto-correlation

coda::acfplot()



- e auto-correlations must decrease rapidly to oscillate around zero
- / thin and/or / n.iter and/or / burn-in

Monte Carlo error

For a given parameter, quantifies the error introduced through the Monte Carlo method

(standard deviation of the Monte Carlo estimator across the chains)

- That error must be consistent from one chain to another
- The larger N (number of iterations), the smaller the Monte Carlo error will be

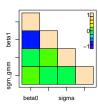
⚠ This Monte Carlo error must be small with respect to the estimated variance of the *posterior* distribution

Estimation

Thanks to MCMC algorithms, one can obtain a Monte Carlo sample from the posterior distribution for a Bayesian model

Monte Carlo method can then be used to get posterior estimates :

- Point estimates (posterior mean, posterior median, ...)
- Credibility interval (shortest: Highest Density Interval HDI with R package HDInterval)
- Correlations between parameters



Deviance Information Criterion (DIC)

Deviance is: $D(\theta) = -2\log(p(\theta|\mathbf{y})) + C$ with C a constant

Deviance Information Criterion is then:

$$DIC = \overline{D(\theta)} + p_D$$

where $p_D = \left(D(\overline{\theta}) - \overline{D(\theta)}\right)$ represents a penalty for the effective number of parameters

⇒ DIC allows to compare different models estimated on the same data the smaller the DIC, the better the model!

[M Plummer, Penalized loss functions for Bayesian model comparison, Biostatistics, 2008]

Your turn!



Practical: exercise 4

