On the use of a local \hat{R} to improve MCMC convergence diagnostic

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Context

Limits of extrapolation associated with Bayesian extreme value models.

Aim: Understand the risks of hazardous meteorological events.



Inondations : le Lot-et-Garonne touché par la "crue la plus importante depuis quarante ans" (Source: lemonde.fr, Février 2021)

MCMC

Bayesian inference on $\theta \sim \pi \implies$ computation of $\mathbb{E}_{\pi}[f(\theta)] = \int f(\theta)\pi(\theta)d\theta$.

MCMC (Markov Chain Monte Carlo):

Monte Carlo

 $\mathbb{E}[f(\theta)] \approx \frac{1}{n} \sum_{i=1}^{n} f(\theta_i)$ $\theta_{i+1} \mid \theta_i \sim P(\theta_i, \cdot)$

Markov Chain

$$\theta_{i+1} \mid \theta_i \sim P(\theta_i, \cdot)$$

MCMC

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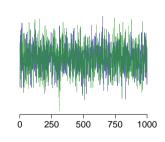
MCMC (Markov Chain Monte Carlo):

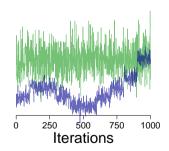
$$\begin{array}{c|c} \mathsf{Monte} \; \mathsf{Carlo} & \mathsf{Markov} \; \mathsf{Chain} \\ \mathbb{E}[f(\theta)] \approx \frac{1}{n} \sum_{i=1}^n f(\theta_i) & \theta_{i+1} \mid \theta_i \sim P(\theta_i, \cdot) \end{array}$$

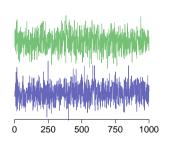
- Algorithms: Metropolis–Hastings, Gibbs sampling, Hamiltonian Monte Carlo (HMC) (Neal, 2011), No U-Turn Sampler (NUTS) (Hoffman and Gelman, 2014), etc.
- Librairies: JAGS (Plummer et al., 2003), Stan (Carpenter et al., 2017), PyMC3 (Salvatier et al., 2016)...

Has the chain(s) converged? Need for multiple chains

Simulations







Introduced by Gelman and Rubin (1992). Consider m chains of size n, with $\theta^{(i,j)}$ denoting the ith draw from chain j. Comparison of the **between-variance** B and the **within-variance** W of the chains:

$$\hat{R} = \sqrt{rac{\hat{W} + \hat{B}}{\hat{W}}}$$

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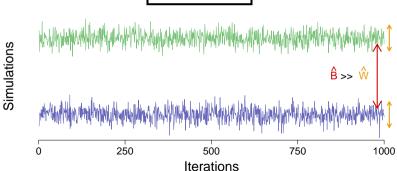
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Between var :
$$\hat{B} = \frac{1}{m-1} \sum_{j=1}^{m} (\overline{\theta}^{(.,j)} - \overline{\theta}^{(.,)})^2$$
, where $\overline{\theta}^{(.,j)} = \frac{1}{n} \sum_{i=1}^{n} \theta^{(i,j)}$, $\overline{\theta}^{(.,i)} = \frac{1}{m} \sum_{j=1}^{m} \overline{\theta}^{(.,j)}$, Within var : $\hat{W} = \frac{1}{m} \sum_{j=1}^{m} s_j^2$, where $s_j^2 = \frac{1}{n-1} \sum_{i=1}^{n} (\theta^{(i,j)} - \overline{\theta}^{(i,j)})^2$.

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Inference from iterative simulation using multiple sequences

A Gelman, DB Rubin - Statistical science, 1992 - projecteuclid.org

The Gibbs sampler, the algorithm of Metropolis and similar iterative simulation methods are potentially very helpful for summarizing multivariate distributions. Used naively, however, iterative simulation can give misleading answers. Our methods are simple and generally ...

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Recent improvement: rank- \hat{R} Vehtari et al. (2021)

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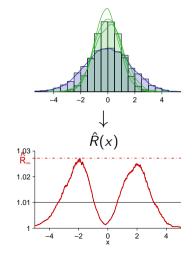
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Local version of \hat{R} , or $\hat{R}(x)$

Idea: compute \hat{R} on indicator variables $\mathbb{I}(\theta^{(i,j)} \leq x) \in \{0,1\}$ for a given quantile x

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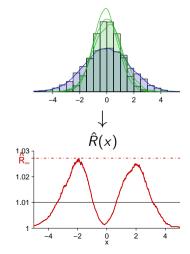
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Benefits:

- It is local
 detects (non-)convergence locally
- Bernoulli variables
 all moments exist (no need for ranks)
- Detects many false negatives
- Scalar summary:

$$\hat{R}_{\infty} = \sup_{x} \hat{R}(x)$$



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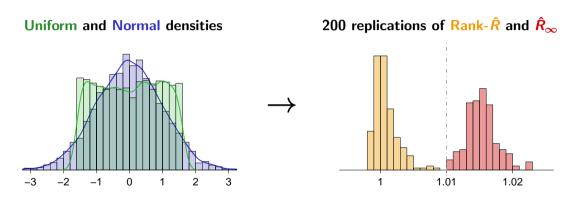
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\hat{R}_{∞} where Rank- \hat{R} is fooled



https://theomoins.github.io/localrhat/Simulations.html

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Theoretical properties

Assume chain Z = j has distribution F_j (stationarity assumption, to focus on mixing). Then,

$$\mathbb{E}[I(\theta \le x) \mid Z = j] = F_j(x), \quad \text{and} \quad \text{Var}[I(\theta \le x) \mid Z = j] = F_j(x) - F_j^2(x)$$

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Theoretical B(x) and W(x):

$$B(x) = \frac{1}{m} \sum_{j=1}^{m} F_j^2(x) - \left(\frac{1}{m} \sum_{j=1}^{m} F_j(x)\right)^2, \qquad W(x) = \frac{1}{m} \sum_{j=1}^{m} \left(F_j(x) - F_j^2(x)\right).$$

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Proposition (Moins et al., 2022)

R(x), the population version of $\hat{R}(x)$, can be written

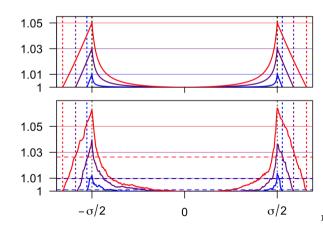
$$R(x) := \sqrt{\frac{W(x) + B(x)}{W(x)}} = \sqrt{1 + \frac{\sum_{j=1}^{m} \sum_{k=j+1}^{m} (F_k(x) - F_j(x))^2}{m \sum_{j=1}^{m} F_j(x) (1 - F_j(x))}}.$$

Population R(x)

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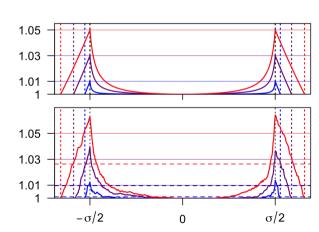


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Properties:

- $R \equiv 1 \iff \text{all } F_i \text{ are equal}$
- R > 1
- $\lim_{\infty} R = 1$
- R_{∞} invariant to monotone transformation



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Convergence properties of $\hat{R}(x)$

Assumption of a Markov chain central limit theorem:

$$\sqrt{nm}(\hat{F}(x) - F(x)) \xrightarrow{d} \mathcal{N}\left(0, \sigma^{2}(x)\right), \quad \text{with} \quad \hat{F}(x) = \frac{1}{nm} \sum_{i=1}^{m} \sum_{i=1}^{n} \mathbb{I}\left\{\theta^{(i,j)} \leq x\right\}$$

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 \hookrightarrow Number of samples to obtain the same variance in the i.i.d case.

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Proposition (Moins et al., 2022)

Assume that all m chains are mutually independent and have converged to a common distribution F. Then for any $x \in \mathbb{R}$,

$$\mathrm{ESS}(x)(\hat{R}^2(x)-1) \stackrel{d}{\longrightarrow} \chi^2_{m-1}$$
 as $n \to \infty$.

Threshold elicitation: $\hat{R}(x)$

Let $z_{m-1,1-\alpha}$ be the quantile of level $1-\alpha$ of the χ^2_{m-1} distribution, and introduce the associated threshold (type I error)

$$R_{\lim,\alpha}(x) := \sqrt{1 + rac{z_{m-1,1-lpha}}{\mathsf{ESS}(x)}} \quad \Longrightarrow \quad \mathbb{P}(\hat{R}(x) \geq R_{\lim,lpha}(x)) \simeq lpha.$$

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ESS(x)	α	m	$R_{\lim,\alpha}(x)$
400	0.05	2	1.005
		4	1.010
		8	1.017
		15	1.029
		50	1.080
		100	1.144

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 \hookrightarrow 1.01 seems reasonable in the most common configurations.

Threshold elicitation: \hat{R}_{∞} ?

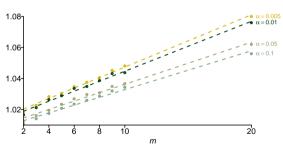
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Estimation using replications:

m	0.005	0.01	0.05	0.1
2	1.018	1.016	1.012	1.010
3	1.023	1.022	1.016	1.014
4	1.027	1.025	1.020	1.018
8	1.038	1.037	1.031	1.028
10	1.043	1.041	1.036	1.033
20	1.080	1.076	1.062	1.056



Limitations of the different \hat{R}

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Abstract

Diagnosing convergence of Markov chain Monte Carlo is crucial and remains an essentially unsolved problem. Among the most popular methods, the potential scale reduction factor, commonly named \hat{R} , is an indicator that monitors the convergence of output chains to a target distribution, based on a comparison of the between- and within-variances. Several improvements have been suggested since its introduction in the 90s. Here, we aim at better understanding the \hat{R} behavior by proposing a localized version that focuses on quantiles of the target distribution. This new version relies on key theoretical properties of the associated population value. It naturally leads to proposing a new indicator \hat{R}_{∞} , which is shown to allow both for localizing the Markov chain Monte Carlo convergence in different quantiles of the target distribution, and at the same time for handling some convergence issues not detected by other \hat{R} versions.

T. Moins, J. Arbel, A. Dutfoy & S. Girard. (2022+) "On the use of a local R-hat to improve MCMC convergence diagnostic" https://hal.inria.fr/hal-03600407/document

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Multivariate case

If parameter θ is d-dimensional: simple multivariate extension by computing \hat{R} on indicator variables $I(\theta_1^{(i,j)} \leq x_1, \dots, \theta_d^{(i,j)} \leq x_d)$

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As before, population version $R(\mathbf{x})$, with $\mathbf{x} = (x_1, \dots, x_d)$:

$$R(\mathbf{x}) = \sqrt{1 + \frac{\sum_{j=1}^{m} \sum_{k=j+1}^{m} (F_j(\mathbf{x}) - F_k(\mathbf{x}))^2}{m \sum_{j=1}^{m} F_j(\mathbf{x}) (1 - F_j(\mathbf{x}))}}.$$

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- $R \equiv 1 \iff \text{all } F_i \text{ are equal}$
- *R* ≥ 1
- R_{∞} invariant to monotone transformation \implies if convergence of margins, we can compute R on M copulas (instead of M CDFs)

Multivariate case: upper bound

Assume m=2 chains, with copulas C_1 and C_2 (in dim d), index denoted by $R_{\infty}(C_1, C_2)$.

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Lemma

Let (C_-, C_+) two bounding copulas in the sense that

$$\begin{cases} C_{-}(\boldsymbol{u}) \leq C_{1}(\boldsymbol{u}) \leq C_{+}(\boldsymbol{u}) \\ C_{-}(\boldsymbol{u}) \leq C_{2}(\boldsymbol{u}) \leq C_{+}(\boldsymbol{u}) \end{cases} \forall \boldsymbol{u} \in [0,1]^{d}.$$

Then $R_{\infty}(C_1, C_2) \leq R_{\infty}(C_-, C_+)$.

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Then

$$R_{\infty}(C_1,C_2) \leq R_{\infty}(C_-,C_+).$$

Proposition (Moins et al., 2022)

Let W_d and M_d the lower and upper Fréchet-Hoeffding copulas in dimension d. Then

$$R_{\infty}(C_1,C_2) \leq R_{\infty}(W_d,M_d) = \sqrt{\frac{d+1}{2}}.$$

Fréchet-Hoeffding copula bounds (comonotone random variables):

$$W_d(u) := \max \left\{ 1 - d + \sum_{i=1}^d u_i, 0 \right\} \quad \text{and} \quad M_d(u) := \min \left\{ u_1, \dots, u_d \right\}.$$

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Let us refine the upper bound by comparing with the independent copula $\Pi_d(\mathbf{u}) := \prod_{i=1}^d u_i$:

• Positive Lower Orthant Dependence (PLOD) copula:

$$\Pi_d(\boldsymbol{u}) \leq C(\boldsymbol{u}) \leq M_d(\boldsymbol{u}) \text{ for all } \boldsymbol{u} \in [0,1]^d$$

• Negative Lower Orthant Dependence (NLOD) copula:

$$W_d(\boldsymbol{u}) \leq C(\boldsymbol{u}) \leq \Pi_d(\boldsymbol{u})$$
 for all $\boldsymbol{u} \in [0,1]^d$

Fréchet-Hoeffding copula bounds (comonotone random variables):

$$W_d(oldsymbol{u}) := \max \left\{ 1 - d + \sum_{i=1}^d u_i, 0
ight\} \quad ext{and} \quad M_d(oldsymbol{u}) := \min \left\{ u_1, \ldots, u_d
ight\}.$$

Let us refine the upper bound by comparing with the independent copula $\Pi_d(\mathbf{u}) := \prod_{i=1}^d u_i$:

- Positive Lower Orthant Dependence (PLOD) copula:
 - $\Pi_d(\boldsymbol{u}) \leq C(\boldsymbol{u}) \leq M_d(\boldsymbol{u}) \text{ for all } \boldsymbol{u} \in [0,1]^d$
- Negative Lower Orthant Dependence (NLOD) copula: $W_d(\boldsymbol{u}) \leq C(\boldsymbol{u}) \leq \Pi_d(\boldsymbol{u})$ for all $\boldsymbol{u} \in [0,1]^d$

 \triangle This does not define a total order on copulas!

Let's stay in the case m = 2 chains.

Corollary (Moins et al., 2022)

For any two PLOD d-variate copulas C_1 and C_2 , $R_{\infty}(C_1, C_2) \leq R_{\infty}(\Pi_d, M_d)$ with

$$\begin{cases} R_{\infty}(\Pi_2, \textcolor{red}{\textit{M}_2}) = \sqrt{\frac{1}{2} + \frac{1}{\sqrt{3}}} \approx 1.038 & \text{if } d = 2, \\ \sqrt{\frac{d}{2\log d}}(1 + o(1)) \leq R_{\infty}(\Pi_d, \textcolor{red}{\textit{M}_d}) \leq \sqrt{\frac{d+1}{2}} & \text{as } d \to \infty. \end{cases}$$

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Corollary (Moins et al., 2022)

For any two NLOD d-variate copulas C_1 and C_2 , $R_{\infty}(C_1, C_2) \leq R_{\infty}(\Pi_d, W_d)$ with

$$R_{\infty}(\Pi_d, W_d) = \sqrt{1 + \frac{1}{2} \frac{1}{\left(1 - \frac{1}{d}\right)^{-d} - 1}}.$$

Asymmetric behaviour:

- $R_{\infty}(\Pi_d, M_d)$ diverges with d at the (almost) same rate as $R_{\infty}(M_d, W_d)$,
- $R_{\infty}(\Pi_d, W_d) \xrightarrow[d \to \infty]{} 1.136.$

Illustration with m = 2 chains with bivariate normal distributions:

$$oldsymbol{ heta}^{(i,1)} \sim \mathcal{N}\left(egin{pmatrix} 0 \ 0 \end{pmatrix}, egin{pmatrix} 1 & 0 \ 0 & 1 \end{pmatrix}
ight), \quad oldsymbol{ heta}^{(i,2)} \sim \mathcal{N}\left(egin{pmatrix} 0 \ 0 \end{pmatrix}, egin{pmatrix} 1 & oldsymbol{
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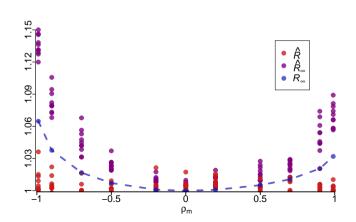
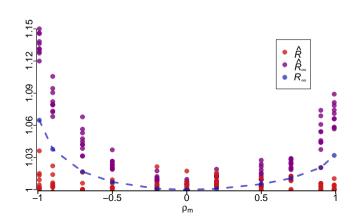


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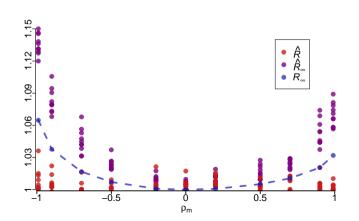
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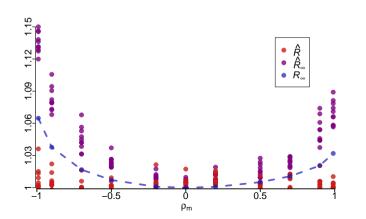
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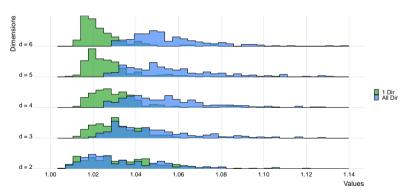


- PLOD and NLOD bounds when |
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- Asymmetry which favour NLOD when d = 2,
- It can be inverted by computing \hat{R}_{∞}^- on $\mathbb{I}\{\theta_1^{(\cdot)} \leq x_1, \theta_2^{(\cdot)} \geq x_2\}.$

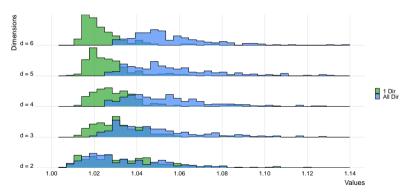
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Alternative: computation of \hat{R}_{∞} for a univariate function of the parameters