

```
logLik.bamlss <- function(object, ..., optimizer = FALSE, samples = FALSE)
{
  Call <- match.call()
  Call <- Call[!(names(Call) %in% c("optimizer", "samples"))]
  mn <- as.character(Call)[-1L]
  object <- list(object, ...)
  mstop <- object$mstop
  if(any(names(object) != "")) {
    i <- names(object) == ""
    object <- object[i]
    mn <- mn[i]
  }
  object <- object[mn != "mstop"]
}
```

Advanced Bayesian Methods: Theory and Applications in R

Posterior Summaries

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<https://nikum.org/abm.html>

Posterior Summaries

- While the ultimate outcome of Bayesian inference is the posterior, this is often compressed into posterior summaries, in particular
 - posterior point estimates and
 - posterior measures of uncertainty.
- Typical point estimates:
 - posterior mean (estimated by averages of samples),
 - posterior median (estimated by empirical median),
 - posterior mode (difficult to determine from samples).
- Typical measures of uncertainty:
 - posterior variance / standard deviation (estimated by empirical analogues),
 - posterior quantiles.

Credible Intervals

- A pointwise Bayesian credible interval $[\theta_{s,\text{low}}, \theta_{s,\text{upp}}]$ for a scalar parameter θ_s is characterized by the posterior coverage probability

$$P(\theta_{s,\text{low}} \leq \theta_s \leq \theta_{s,\text{upp}} | \mathbf{y}) \geq 1 - \alpha$$

where $1 - \alpha$ denotes the desired coverage level.

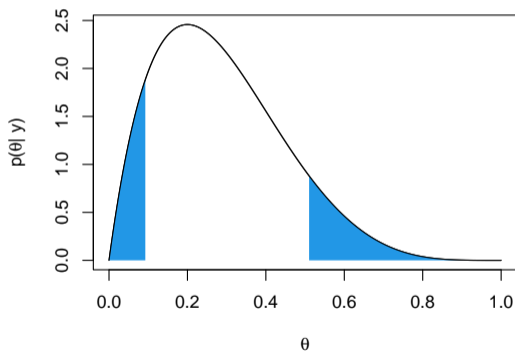
- A simultaneous band for multiple parameters $\{\theta_s, s \in \mathcal{S}\}$ should have

$$P(\theta_{s,\text{low}} \leq \theta_s \leq \theta_{s,\text{upp}}, s \in \mathcal{S} | \mathbf{y}) \geq 1 - \alpha$$

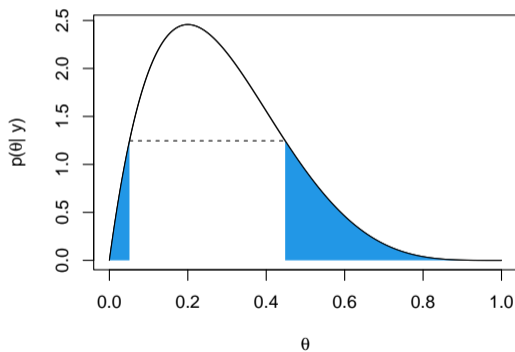
Credible Intervals

- Symmetric and highest posterior density credible intervals:

Symmetric Credible Interval



HPD Credible Interval



Credible Intervals

In R:

```
R> library("HDIInterval")
```

Simulate beta distributed data (as in the density plot before).

```
R> x <- rbeta(1000, shape1 = 2, shape2 = 5)
```

HDI intervals for samples and the beta distribution.

```
R> i <- hdi(x, credMass = 0.8)
```

```
R> j <- hdi(qbeta, credMass = 0.8, shape1 = 2, shape2 = 5)
```

```
R> print(rbind(i, j))
```

	lower	upper
i	0.06738695	0.4619858
j	0.05126051	0.4483045

Bayesian Tests

- To test the hypotheses

$$H_0 : \theta \in \Theta_0 \quad \text{vs.} \quad H_1 : \theta \notin \Theta_0$$

we can compute the posterior probabilities

$$p_0 = P(\theta \in \Theta_0 | \mathbf{y}) \quad \text{and} \quad p_1 = P(\theta \notin \Theta_0 | \mathbf{y}).$$

- The decision can then be based on the ratio

$$\frac{p_1}{p_0}$$

that measures the evidence in favor of H_1 as compared to H_0 .

Bayesian Tests

- H_1 and H_0 are therefore treated symmetrically in the Bayesian context.
- Unfortunately, point hypotheses can not meaningfully be tested in the Bayesian paradigm since then

$$P(\theta = \theta_0 | \mathbf{y}) = 0.$$

- Instead of formally testing hypothesis, the decision between H_0 and H_1 is often made based on model choice procedures in the Bayesian framework.
- As an alternative, one often considers a Bayesian credible interval for θ and evaluates whether θ_0 is contained in the credible interval or not.

Bayesian Tests

In R:

```
R> library("bamlss")
```

Simulate some data.

```
R> set.seed(123)
```

```
R> n <- 1000
```

```
R> x1 <- rnorm(n)
```

```
R> x2 <- rnorm(n)
```

```
R> y <- 1.2 + 0.5 * x1 + rnorm(n, sd = 0.2)
```

Estimate linear model using MCMC.

```
R> b <- bamlss(y ~ x1 + x2)
```


Bayesian Tests

95% Credible intervals.

```
R> confint(b, model = "mu", level = 0.95)
```

	2.5%	97.5%
(Intercept)	1.183167435	1.20773499
x1	0.483302348	0.50753724
x2	-0.006737225	0.01728374

Inference for Derived Quantities

- Goal: Conduct Bayesian inference for a derived quantity

$$\eta = g(\theta).$$

- Convenient feature of MCMC: If $\theta^{[1]}, \dots, \theta^{[T]}$ is a sample from the posterior of θ , $g(\theta^{[1]}), \dots, g(\theta^{[T]})$ will be a sample from the posterior of the transformed parameter.
- No restrictions on the transformation $g(\cdot)$ and no need to deal with asymptotic considerations

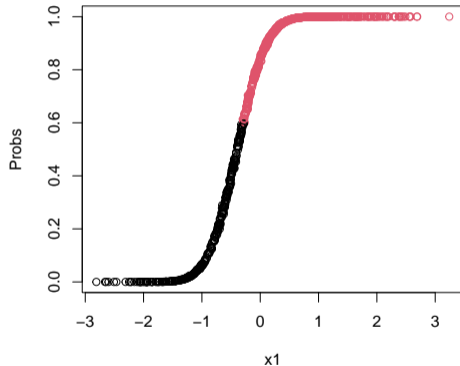
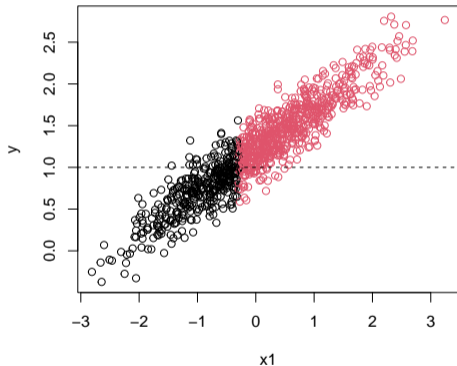
Inference for Derived Quantities

Example in R:

```
R> nd <- data.frame("x1" = x1, "x2" = x2)
R> par <- predict(b, newdata = nd, type = "parameter", FUN = identity)
R> print(names(par))
R> print(dim(par$mu))
R> Probs <- NULL
R> for(i in 1:ncol(par$mu)) {
+   tpar <- list("mu" = par$mu[, i], "sigma" = par$sigma[, i])
+   p <- 1 - family(b)$p(1, tpar) ## Same as 1 - pnorm(1, ...).
+   Probs <- cbind(Probs, p)
+ }
R> Probs <- apply(Probs, 1, mean)
R> col <- rep(1, n)
R> col[Probs > 0.6] <- 2
R> par(mfrow = c(1, 2), mar = c(4, 4, 1, 1))
R> plot(x1, y, col = col)
```

Inference for Derived Quantities

```
R> abline(h = 1, lty = 2)
R> plot(x1, Probs, col = col)
```



Bayesian Information Criteria

- Bayesian information criterion (BIC)

$$\text{BIC}(M_l) = -2\ell(\hat{\theta}_l) + \log(n)\text{df}_l$$

where df_l is the number of parameters in model l .

Bayesian Information Criteria

- Deviance information criterion (DIC)

$$\text{DIC} = \overline{D(\boldsymbol{\theta})} + \text{pd}_{\text{DIC}}$$

where

$$\overline{D(\boldsymbol{\theta})} = -2 \log(p(\mathbf{y}|\boldsymbol{\theta})) = \frac{1}{T} \sum_{t=1}^T D(\boldsymbol{\theta}^{[t]})$$

denotes the model deviance and

$$\text{pd}_{\text{DIC}} = \overline{D(\boldsymbol{\theta})} - D(\bar{\boldsymbol{\theta}}) = \frac{1}{T} \sum_{t=1}^T D(\boldsymbol{\theta}^{[t]}) - D\left(\frac{1}{T} \sum_{t=1}^T \boldsymbol{\theta}^{[t]}\right)$$

provides an estimate for the effective parameter count.

Bayesian Information Criteria

- Widely applicable information criterion (WAIC)

$$\text{WAIC} = 2 (D_{\text{WAIC}} + p_{\text{WAIC}}) \quad \text{with} \quad D_{\text{WAIC}} = - \sum_{i=1}^n \log \left(\frac{1}{T} \sum_{t=1}^T p(y_i | \theta^{[t]}) \right)$$

as the measure of model fit,

$$p_{\text{WAIC}} = \sum_{i=1}^n \widehat{\text{Var}}(\log(p(y_i | \theta)))$$

as the measure of model complexity, and the empirical variance

$$\widehat{\text{Var}}(a) = \frac{1}{T-1} \sum_{t=1}^T (a_t - \bar{a})^2.$$

Bayesian Information Criteria

Example in R:

```
R> library("bamlss")
```

```
R> data("cars")
```

Two models, simple linear and a polynomial model

```
R> m1 <- bamlss(dist ~ speed, data = cars)
```

```
R> m2 <- bamlss(dist ~ poly(speed, 3), data = cars)
```


Bayesian Information Criteria

Compute information criteria.

```
R> BIC(m1, m2)
```

	df	BIC
m1	3.077717	428.3615
m2	5.014228	434.6961

```
R> DIC(m1, m2)
```

	DIC	pd
m1	419.3991	3.077717
m2	420.0945	5.014228

```
R> WAIC(m1, m2)
```

	WAIC1	WAIC2	p1	p2
m1	419.4495	420.1763	3.128132	3.491537
m2	419.5214	420.6983	4.441135	5.029594