Université catholique de Louvain
Louvain School of Statistics

# LSTAT2130 - Bayesian Statistics

Project - Group Q

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# Contents

# Introduction

In this work, the Net Monthly Income (HNI) of household older than 30 years is studied across the two Belgian regions. These regions are denoted by $k = \{1, 2\}$ with respect to Flanders and Wallonia, respectively. The 1228 households were listed with respect to 10 income intervals. The detailed frequency table is given below:

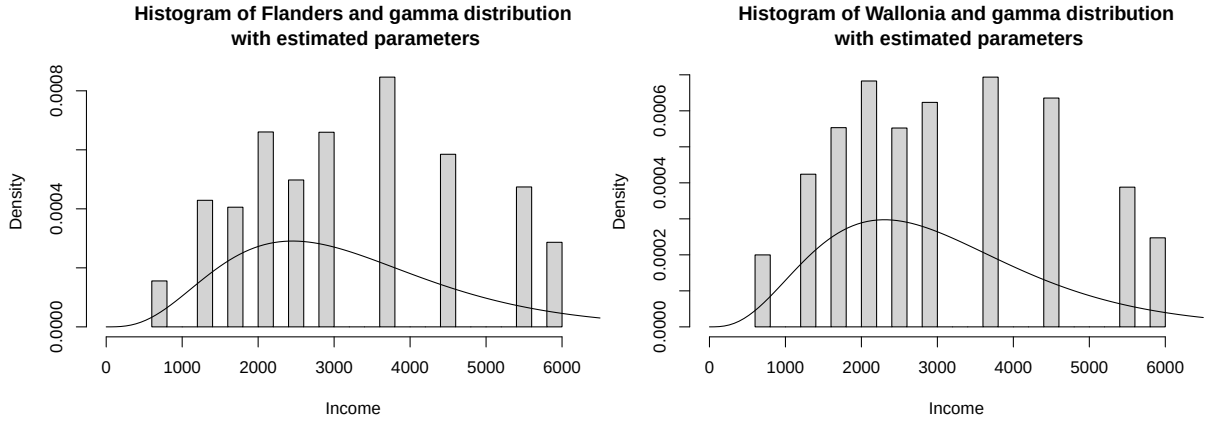
| | Net monthly household income (in euros) | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Region | $\vee$1200 | [1200, 1500) | [1500,1800) | [1800,2300) | [2300,2700) | [2700,3300) | [3300,4000) | [4000,4900) | [4900,6000) | $\wedge$6000 | Total |
| Flanders | 25 | 69 | 65 | 106 | 80 | 106 | 136 | 94 | 76 | 46 | 803 |
| Wallonia | 17 | 36 | 47 | 58 | 47 | 53 | 59 | 54 | 33 | 21 | 425 |

Table 1: Frequency table of the survey

By assuming the income to follow a gamma distribution, one can plot their experimental histogram and plot the theoretical density plot by estimating the shape and rate parameters with Maximum of Likelihood. This allows to get a first sight on the data behavior at hand.

| | Flanders | Wallonia |
|---|---|---|
| $\hat{\mu}$ | 3182.897 | 3042.749 |
| $\hat{\phi}$ | 0.229 | 0.243 |

Table 2: Estimated $\mu$ and $\phi$ for Flanders and Wallonia



# 1 Question 1

## 1.1 (a) Theoretical probability

Let $X$ be the HNI regardless the 2 regions, it is assumed it follows a Gamma distribution with parameters $\theta_k := (\mu_k, \phi_k)$. It can be reparametrised in terms of its mean $\mu$ and dispersion parameter $\phi$ with the following trick:

$$\kappa = \frac{1}{\phi}$$
$$\lambda = \frac{1}{\phi\ \mu}$$

resulting in the following density $f(x)$

$$f(x_k) = \frac{(\phi_k \mu_k)^{-1/\phi_k}}{\Gamma(\phi_k^{-1})} x_k^{1/\phi_k - 1} \exp\left(\frac{-x_k}{\phi_k \mu_k}\right) \tag{1}$$

The associated cumulative distribution function (CDF) is:

$$F(x) = \int_0^x f(u)\ \mathrm{d}u = \frac{\gamma(\phi^{-1}, \frac{x}{\phi\mu})}{\Gamma(\phi^{-1})} \tag{2}$$

where $\Gamma(a)$ and $\gamma(a, b)$ are the complete gamma and lower incomplete gamma functions, defined as:

$$\gamma(a, b) = \int_0^b t^{a-1} \exp(-t) \mathrm{d}t$$
$$\Gamma(a) = \gamma(a, \infty)$$

Then, the probability to fall into a certain HNI interval $I$, for each region, is:

$$P(x \in I_j) = \int_{I_j} \frac{(\phi\mu)^{\frac{-1}{\phi}}}{\Gamma(\phi^{-1})} x^{\frac{1}{\phi}-1} \exp\left(\frac{-x}{\phi\mu}\right)\ \mathrm{d}x \tag{3}$$

Using CDF writing , the probability can be proposed as a difference of CDF :

$$p_j = \begin{cases} F(x_j) & \text{if} \quad j = 1 \\ F(x_{j+1}) - F(x_j) & \text{if} \quad j \in \{2, .., 9\} \\ 1 - F(x_j) & \text{if} \quad j = 10 \end{cases}$$

$$p_j = \begin{cases} \frac{\gamma(\phi^{-1}, \frac{x_j}{\phi\mu})}{\Gamma(\phi^{-1})} & \text{if} \quad j = 1 \\ \frac{1}{\Gamma(\phi^{-1})}\Big(\gamma(\phi^{-1}, \frac{x_{j+1}}{\phi\mu}) - \gamma(\phi^{-1}, \frac{x_j}{\phi\mu})\Big) & \text{if} \quad j \in \{2, .., 9\} \\ 1 - \frac{\gamma(\phi^{-1}, \frac{x_j}{\phi\mu})}{\Gamma(\phi^{-1})} & \text{if} \quad j = 10 \end{cases} \tag{4}$$

## 1.2 (b) Theoretical expression for the likelihood

Assuming the frequency distribution in a given region[1] to be multinomial, one has, writing $P := (p_1, .., p_{10})$ and $Y := (Y_1, ...Y_{10})$:

$$\begin{aligned} Y|P \sim \text{Mul}(Y, P) &= \frac{(\sum y_i)!}{y_1! \dots y_{10}!}\ p_1^{y_1} \times ... \times p_{10}^{y_{10}} \text{ when} \sum_{j=1}^{10} p_j = 1 \\ &= 0 \text{ otherwise} \end{aligned}$$

For such a distribution, the likelihood $L$ is well known. Indeed, up to a multiplicative constant, for a region $k$, it is given by:

$$L(P_k, Y_k) = P(Y_k|P_k) \propto \prod_{j=1}^{10} p_{k,j}^{y_{k,j}}$$

To translate this likelihood in terms of $\mu_k$ and $\phi_k$, one can use the definition of the probability referring to the difference of CDF (see equation 4). By substituting $p_{k,j}$ with it and writing $[0; x_1], [x_1; x_2], ..., [x_9; x_{10}], [x_{10}, +\infty]$ as $I_1, I_2, ..., I_{10}$, the likelihood function becomes, up to a multiplicative constant, as such:

$$L(\mu_k, \phi_k, Y_k) \propto \prod_{j=1}^{10} \left( \frac{1}{\Gamma(\phi^{-1})} \int\limits_{\frac{I_j}{\phi_k \mu_k}} x_j^{(\phi_k^{-1}-1)} e^{-x} \mathrm{d}x \right)^{y_{k,j}} \tag{5}$$

and then taking the logarithm, we obtain the log-likelihood $\ell$ for a certain region:

$$\ell(\mu_k, \phi_k, Y_k) = \sum_{j=1}^{10} y_{k,j} \times \ln(p_{k,j}) \tag{6}$$

where $y_{k,j}$ is the frequency of households in the interval j in the region k, and we recall that $p_{k,j}$ corresponds to the probability, or the area of the $j^{\text{th}}$ interval in the region k. Again, by substituting with the difference of CDF, the log-likelihood becomes:

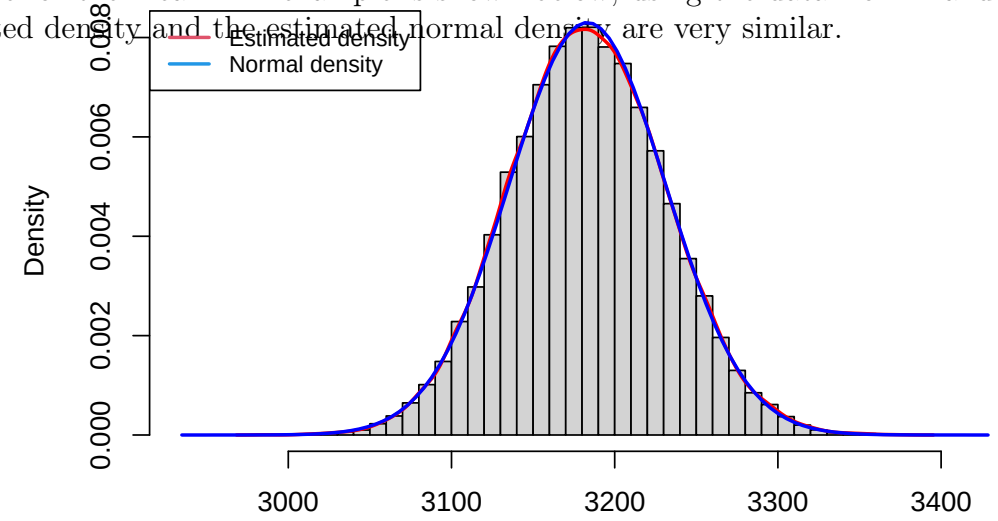
$$\ell(\mu_k, \phi_k, Y_k) = \sum_{j=1}^{10} y_{k,j} \times \ln \left( \frac{1}{\Gamma(\phi_k^{-1})} \int\limits_{\frac{I_j}{\phi_k \mu_k}} x^{(\phi_k^{-1}-1)} e^{-x} \mathrm{d}x \right) \tag{7}$$

[1] As such, the subscript $k$ is dropped for expression of the multinomial

# 2 Question 2

## 2.1 Prior for the mean

The average net monthly household income, regardless the region, is believed to be within the interval (2400, 3600) on a 95% confidence level. A convenient probability function that translates this belief is the Gaussian distribution with a mean at the center and standard deviation such that its 95% confidence interval corresponds to the mentioned bonds. This belief is confirmed by Monte Carlo simulations. Indeed, if one generates a large amount of gamma distributed samples and repeatedly take its mean, one can determine a density estimate for the mean. An example is shown below, using the data from Flanders. The estimated density and the estimated normal density are very similar.




Hence, by assuming such a distribution for the prior, one can easily estimate its parameters. For both regions $\mu_0 = 3000$ (the center of the confidence interval). Then, to get the standard deviation, one can use the decomposition of a classical confidence interval for the mean.

$$3000 - t_{(n_k-1,1-\alpha/2)} \frac{s_k}{\sqrt{n_k}} = 2400$$

$$\rightarrow \hat{\sigma}_0 = \frac{s_k}{\sqrt{n_k}} = \frac{600}{t_{(n_k-1,1-\alpha/2)}}$$

$$\text{where: } t_{n_1-1,1-\alpha/2} \approx t_{n_2-1,1-\alpha/2} \approx 1.96$$

Therefore $\hat{\sigma}_{Fl} \approx \hat{\sigma}_{Wal} \approx 306.12$, then $\mu_k \sim N(\mu_{0,k} = 3000, \sigma_{0,k} = 306.12)$. So we get as a prior for the parameter $\mu$, up to a multiplicative constant:

$$\pi(\mu_k) \propto \exp\Big(-\frac{1}{2\sigma_0^2}(\mu_k - \mu_0)^2\Big) \ \forall k \in \{1, 2\} \tag{8}$$

The issue that one might rise is the fact that the HNI cannot be negative while theoretically, the Gaussian support take negative values. In this case, the probability of having negative values is $5.6249147 \times 10^{-23}$, which can be considered as non-significant.

## 2.2 Prior for the dispersion parameter

It is certain that $\phi_k$ lies in the interval $(0.0, 10.0)$ in both regions, but there is no knowledge on how the probability mass is broken down. In order to reflect this prior knowledge, one

can assume that the dispersion parameter is uniformly distributed with lower and upper bonds of 0 and 10, respectively, i.e. $\phi_k \sim U(0, 10)$. Hence, up to a multiplicative constant, the prior probability can be represented via the indicator function as below:

$$\pi(\phi_k) \propto \mathbf{1}_{0,10} \; \forall k \in \{1, 2\}$$

### 2.3 The conjugate prior

Since there is no prior information on the dependence structure of the priors, it is recommended to consider them as independent in order to remain as least-informative as possible (this follows the maximal entropy principle). By doing so, the conjugate prior becomes:

$$\begin{aligned} \pi(\mu_k, \phi_k) &= \pi(\mu_k)\ \pi(\phi_k) \\ &\propto \exp\big(-\frac{1}{2\sigma_0^2}(\mu - \mu_0)^2\big)\mathbf{1}_{0;10} \end{aligned} \tag{9}$$

## 3 Question 3

### 3.1 (a) Joint posterior for Flanders

Since the likelihood and prior for $\mu_k$ and $\phi_k$ have been defined, a joint posterior can be expressed as their product (see equation 5 and equation 9). The joint posterior for Flanders, i.e. of $\theta_1 = (\mu_1, \phi_1)$ is defined, up to a multiplicative constant, here below:

$$P(\mu_1, \phi_1|Y_1) \propto \left(\prod_{j=1}^{10}\left(\frac{1}{\Gamma(\phi_1^{-1})}\int\limits_{\frac{I_j}{\phi_1\mu_1}} x^{(\phi_1^{-1}-1)}e^{-x}\mathrm{d}x\right)^{y_{1,j}}\right)\exp\big(-\frac{1}{2\sigma_0^2}(\mu-\mu_0)^2\big)1_{0;10} \tag{10}$$

### 3.2 (b) Write function lpost

Computing the logarithm of this expression, we find the log likelihood posterior, which is, up to an additive constant:

$$h(\mu_1, \phi_1, Y_1) = C^t + \ell(\mu_1, \phi_1, Y_1) + \ln(\pi(\mu_1, \phi_1))$$

Replacing the log-likelihood and log of the prior by their expression (see Equations 7 and 9), the log-posterior can be theoretically written as below:

$$h(\mu_1, \phi_1, Y_1) = C^t + \sum_{j=1}^{10} y_{1,j} \times \ln\left(\frac{1}{\Gamma(\phi^{-1})}\int\limits_{\frac{I_j}{\phi_1\mu_1}} x^{(\phi_1^{-1}-1)}e^{-x}\mathrm{d}x\right) - \frac{1}{2\sigma_0^2}(\mu-\mu_0)^2 + \ln(\mathbf{1}_{0;10}) \tag{11}$$

This expression has been implemented in R by not considering the constant term.

```r
lpost <- function(theta, freq) {
  # Transform mu and phi -> kappa and lambda
  kappa <- kappa(theta[2])
  lambda <- lambda(theta[2], theta[1])

  # Likelihood : sum_j^n[x_j * ln(probability_of_being_in_interval_j)]
  LL <- sum(sapply(1:length(freq), function(j) {
    freq[j] * log(pgammadiff(low = intervals[j], high = intervals[j + 1],
kappa, lambda))
  }))

  # Log posterior
  lpi <- dnorm(theta[1], mu_prior, sigma_prior, log = T) + dunif(theta[2],
0, 10, log = T)
  lpost <- LL + lpi

  names(lpost) <- "lpost"
  return(lpost)
}
```

# 4 Question 4

## 4.1 Approximation of the joint posterior

Laplace approximation is a method that allows to approximate the joint posterior distribution $h(\mu_1, \phi_1, Y_1)$ by a multimodal normal distribution (bimodal in this case).

First, if the Gaussian assumption is sustainable, the modes should correspond to the mean of the functions. Hence, one just need to optimize the function in order to find an estimated mean for the parameters of interest. The standard deviation is found by assuming that the second order Taylor expansion of the distribution function is precise enough. If it's the case, then, at the mode $\tilde{\theta}$, the log-posterior could be written as follow:

$$h(\theta) \approx h(\tilde{\theta}) - \frac{1}{2}(\theta - \tilde{\theta})^t \, \mathcal{I}(\tilde{\theta}) \, (\theta - \tilde{\theta})$$

with $\mathcal{I}(\tilde{\theta})$ the opposite of the hessian matrix (i.e. the matrix composed of the second derivatives). By taking the exponential, one can easily see that it corresponds to the multivariate normal distribution with $\mathcal{I}(\tilde{\theta})$ being the variance-covariance matrix $\Sigma$. This is the reason why the optimization in the Laplace methodology is done by including the Hessian matrix. Accordingly, one has:

$$\begin{cases} \mu_{\theta_1}^t = \big(E(\mu_1), E(\phi_1)\big) \\ \mathbf{\Sigma_1} = \begin{pmatrix} \sigma_{\mu_1} & \sigma_{\mu_1,\phi_1} \\ \sigma_{\phi_1,\mu_1} & \sigma_{\phi_1} \end{pmatrix} \end{cases}$$

In this case, the optimization is done numerically, using starting values close the MLE's. Once done, 50000 bivariate Gaussian observations are generated.

```r
# Starting values
inits <- c(mu = mu_prior, phi = 0.01)
# Laplace approximation
laplace_approx <- function(inits, frequencies) {
  fit <- optim(inits, lpost, control = list(fnscale = -1), hessian = T,
freq = frequencies)
  params <- fit$par
  param_cov_mat <- solve(-fit$hessian)
  samples <- rmvnorm(50000, params, param_cov_mat)

  list(samples = samples, parameters = params, cov = param_cov_mat)
}

laplace_fl <- laplace_approx(inits, flanders)
laplace_fl.mcmc <- mcmc(laplace_fl$samples)
```

A summary of the data generated is available in appendix.

## 4.2 Credible intervals Laplace approximation

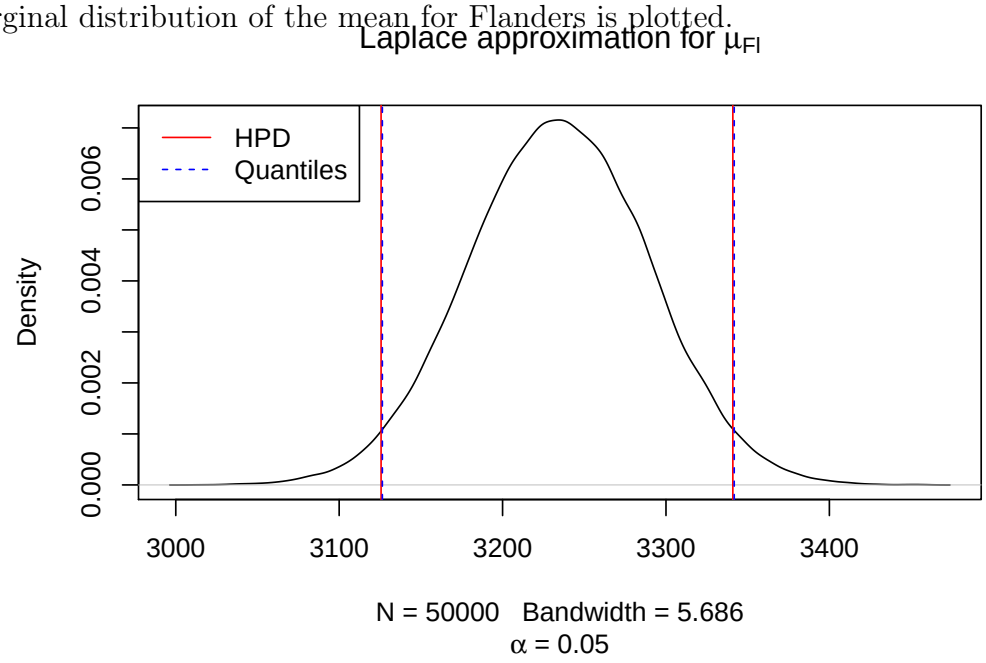
To get the credible interval for $\mu_1$, the marginal posterior distribution of $\mu_1$ is needed. It is given by :

$$P(\mu_1|Y_1) \propto \int p(\mu_1, \phi_1|Y_1)\ \mathrm{d}\phi_1$$

It can be shown that the marginal (univariate) distribution of the bivariate Gaussian distribution $N\big(\mu_{\theta_1}, \mathbf{\Sigma}_1\big)$ also follow a normal distribution:

$$\mu_1|Y_1 \sim N\big(E(\mu_1), \sigma_{\mu_1}\big)$$

Accordingly, a 95% quantile based or HPD based can be easily taken from the generated samples. The interval based on the quantile is [3126, 3342] , while the one based on the highest posterior density is [3126, 3341]. Those are shown in the following graph where the marginal distribution of the mean for Flanders is plotted.



# 5 Question 5

## 5.1 (a) Random walk component-wise Metropololis algorithm

One first needs starting values for $\theta_t := (\mu_t, \phi_t)$. One can take advantage of the MLE estimations of $\kappa$ and $\lambda$ and compute $\mu_0$ and $\phi_0$ using the relations described earlier. At each iteration, a new candidate will be proposed. To build it, it is a good idea to use the variance-covariance matrix computed into the Laplace approximation section since it should, more or less, describe the standard deviations of the parameters of interest $\hat{\sigma}_\mu$ and$\hat{\sigma}_\phi$. A factor, $f_1$ and $f_2$ should multiply their standard deviation in order to optimize the acceptance rate (goal is 40%). Moreover, since the posterior probability is on a log-scale, the comparison of probabilities should be made taking the exponential of the difference of the candidate with the current state. In this work, 10% of the generated data is considered as burn-in.

That being, this gives the following algorithm:

1. $t = 0$: Set starting values of the parameters of interest to their MLE: $\theta_0 := (\hat{\mu}_{MLE}, \hat{\phi}_{MLE})$
2. for $t = 2, \ldots, M$
   - Draw $\mu_{\text{prop}}$ from a normal distribution centered on value derived at $t-1$, i.e. $\mu_{\text{prop}} \sim N(\mu_{t-1}, f_1\hat{\sigma}_\mu)$. The candidate is then $\theta^{\mu}_{prop} := (\mu_{\text{prop}}, \phi_{t-1})$
   - Compute $prob_\mu = \min\left(1, \exp\left(h(\theta^{\mu}_{prop}) - h(\theta_{t-1})\right)\right)$
   - Set $\mu_t = \mu_{\text{prop}}$ with probability $prob_\mu$, $\mu_t = \mu_{t-1}$ otherwise.
   - Draw $\phi_{\text{prop}}$ from a normal distribution centered on value derived at $t-1$, i.e. $\phi_{\text{prop}} \sim N(\phi_{t-1}, f_2\hat{\sigma}_\phi)$. The candidate is then $\theta^{\phi}_{prop} := (\mu_{t-1}, \phi_{\text{prop}})$
   - Compute $prob = \min\left(1, \exp\left(h(\theta^{\phi}_{prop}) - h(\theta_{t-1})\right)\right)$
   - Set $\phi_t = \phi_{\text{prop}}$ with probability $prob_\phi$, $\phi_t = \phi_{t-1}$ otherwise.
   - Set $\theta_t = (\mu_t, \phi_t)$

Which, in R gives the following code:

```
# Metropolis algorithm, mu and phi updated one at the time
metropolis_algorithm <- function(M, theta, sd.propositions, factors,
frequencies) {
  theta <- as.vector(theta)
  sd.propositions <- as.vector(sd.propositions)
  factors <- as.vector(factors)
  frequencies <- as.vector(frequencies)

  thetas <- array(dim = c(M + 1, 2))
  thetas[1, ] <- theta

  accepted <- c(0, 0)

  sigma_mu <- factors[2] * sd.propositions[1]
  sigma_phi <- factors[2] * sd.propositions[2]

  for (i in 2:(M + 1)) {
    theta_mu <- theta_phi <- this_theta <- thetas[i - 1, ]
```

```
    theta_mu[1] <- this_theta[1] + rnorm(1, 0, sigma_mu)
    theta_phi[2] <- this_theta[2] + rnorm(1, 0, sigma_phi)

    thresholds <- c(
      min(exp(lpost(theta_mu, frequencies) - lpost(this_theta,
      frequencies)), 1),
      min(exp(lpost(theta_phi, frequencies) - lpost(this_theta,
      frequencies)), 1)
    )

    accepts <- runif(2) <= thresholds

    thetas[i, ] <- this_theta
    if (accepts[1]) thetas[i, 1] <- theta_mu[1]
    if (accepts[2]) thetas[i, 2] <- theta_phi[2]
    accepted <- accepted + as.integer(accepts)
  }

  colnames(thetas) <- c("mu", "phi")
  names(accepted) <- c("mu", "phi")
  return(list(theta = thetas, accept_rate = accepted / M))
}

burnin <- function(array, percent) {
  tail(array, -percent * nrow(array))
}

sd_hat_mu <- sqrt(laplace_fl$cov[1, 1])
sd_hat_phi <- sqrt(laplace_fl$cov[2, 2])
```

In order to reach an acceptance rate as close as possible to 40%, it was necessary to multiply by factors $f_1 = f_2 = 2.75$. The obtained rates, with $M = 50000$ iterations are such:

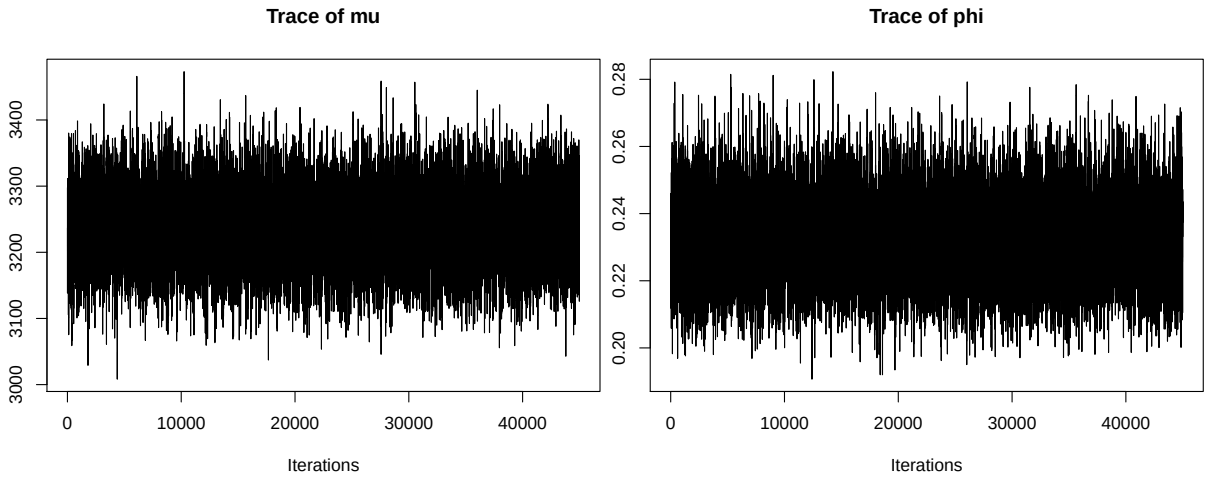
| mu | phi |
|---|---|
| 39.944 | 40.524 |

Table 3: Acceptance rates for the metropolis algorithm

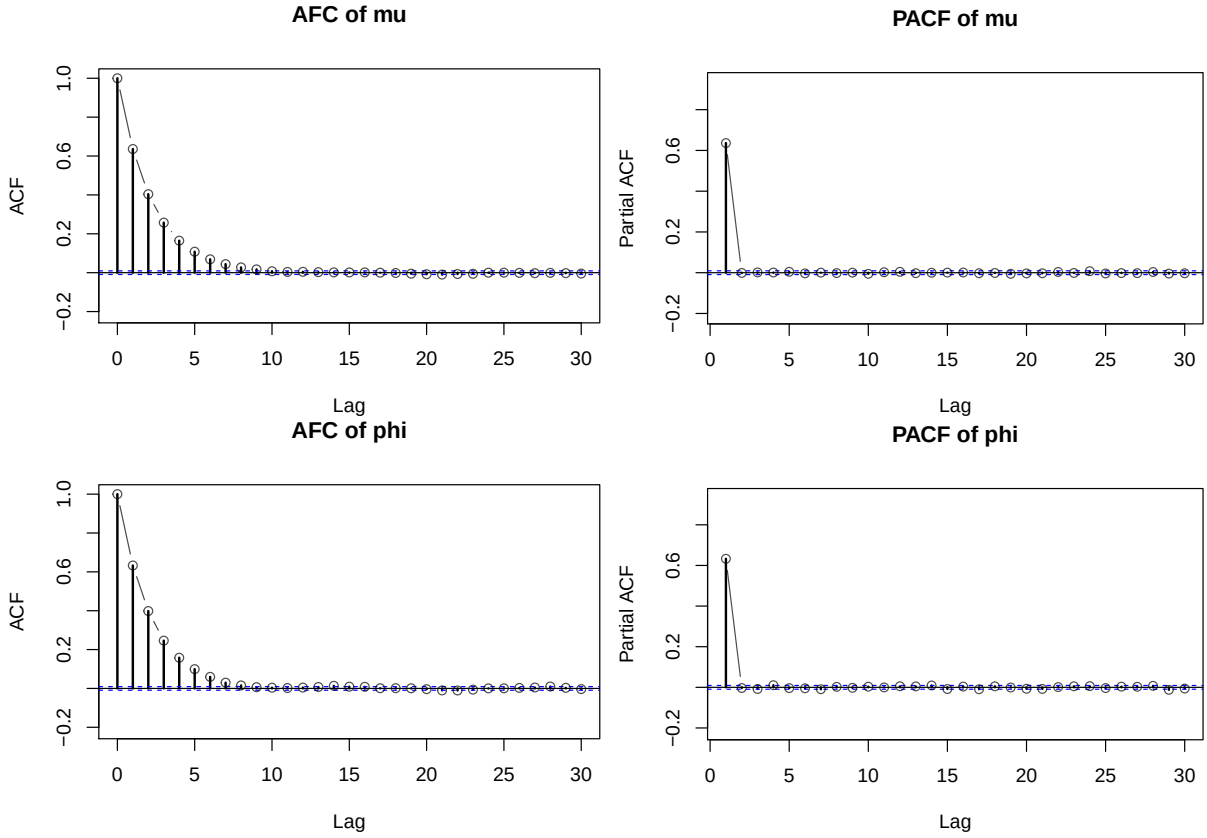
## 5.2 (b) diagnostic for convergence

### Global analysis

The first, trivial, way of checking if the convergence occurred is by a visual analysis of the generated variables. One can look at the traceplot as well as the ACF and PACF.




By doing so, one sees that the mixing seems pretty good. For example, the autocorrelation is significative up to not a too high order. As such, the parameter space of $\theta$ does not seem to be visited too slowly.



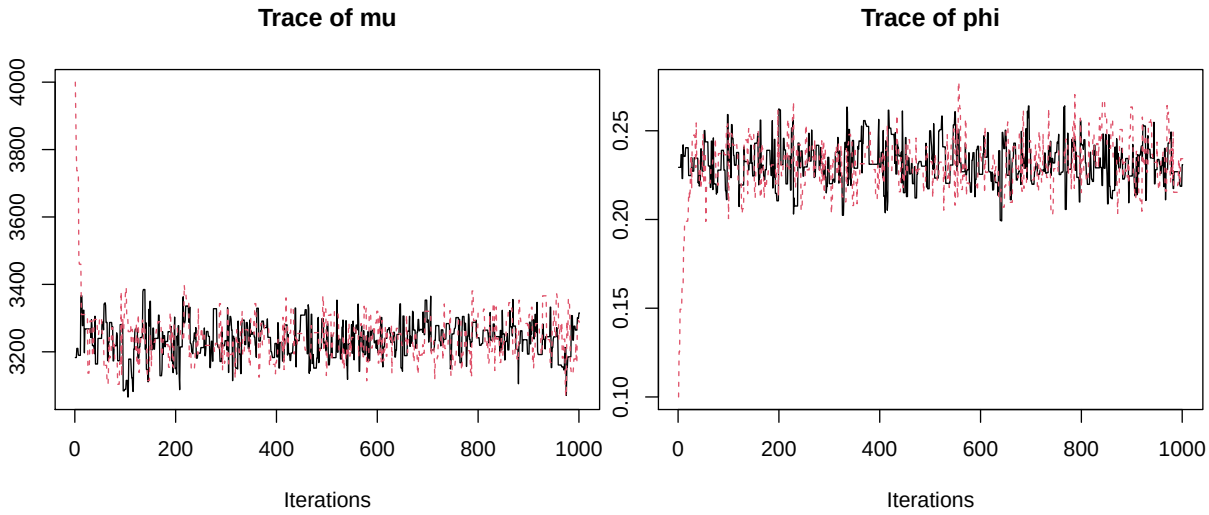

Since the chains clearly seem to be generated with respect to an Autoregressive process, one can compute effectively the effective sample size. It represents how many samples would be generated if there were no autocorrelation.

| mu | phi |
|---|---|
| 10010 | 10140 |

Effective sample size of Metropolis in Flanders

### Gelman-Rubin

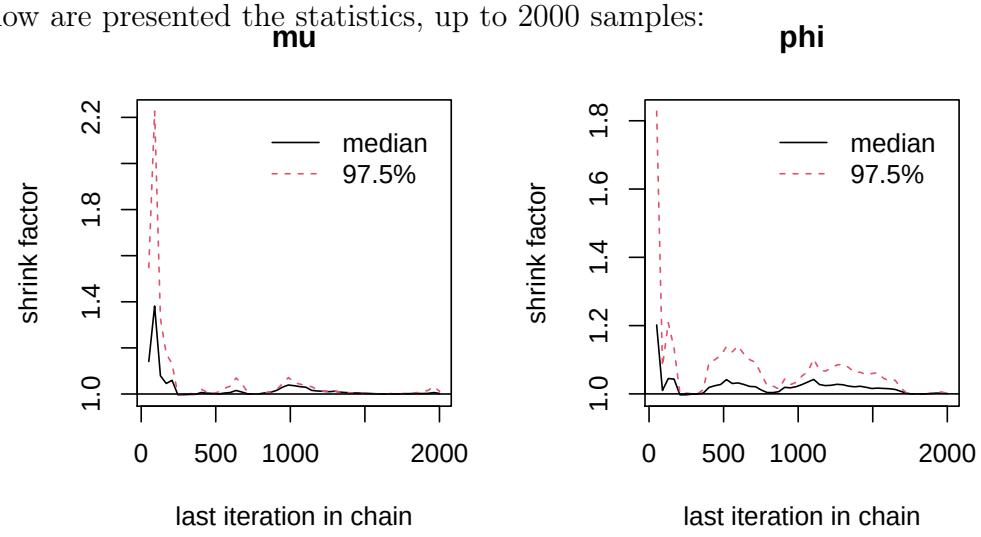
This method requires multiple chains. In this work, the diagnostic will be done with 2 generated chains with two different starting values. As a second chain, more exotic values (but still possible , a priori) are proposed for initialization: 4000 for $\mu_1$ and 0.1 for $\phi_1$. After having run the second chain, the traceplot of both chain is plotted with respect to the first 1000 generations.




It seems that convergence occurs rather quickly. After a early generations, the chains seem to have similar mean variance. This can be more formally assessed with the Gelman-Rubin statistic that one wishes to be smaller that, say, 1.1. Here below is shown the estimated statistic along with its upper bond.

| | Point est. | Upper C.I. |
|---|---|---|
| mu | 1.00 | 1.01 |
| phi | 1.02 | 1.02 |

Those are clearly below, which is a good sign of convergence. To see when convergence may have occurred, one could look at the statistic with respect to the number of generations. Here below are presented the statistics, up to 2000 samples:




Accordingly, the convergence seems to occurs after roughly 1000 observations for both.

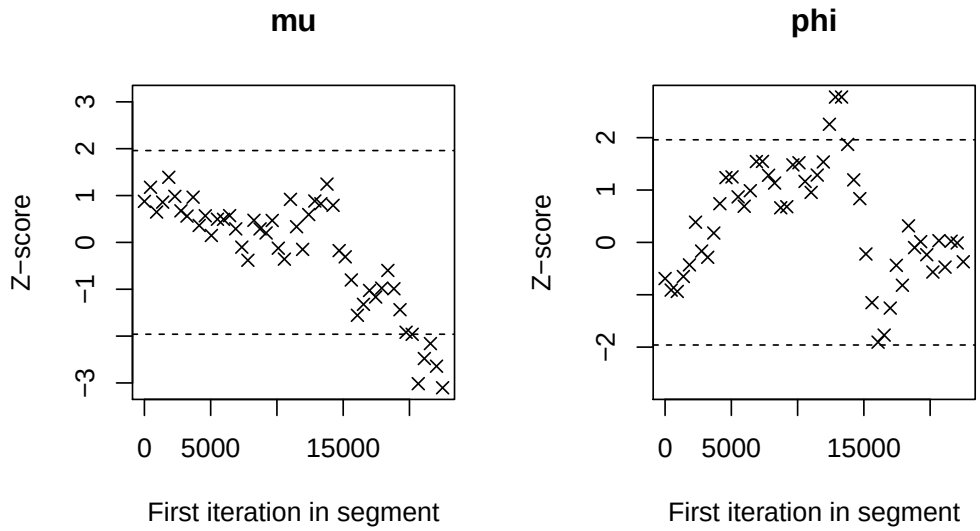
**Geweke diagnostic**

The Geweke diagnostic is useful in the sense that it allows for only one chain to be generated. The chain will be separated into two part: the first accounts for the first 10% of the data while the other accounts for the last 50% of the chain. Under the hypothesis of convergence, the mean of both subsets should be similar. Hence, one can construct a corresponding two means test. The Z-scores are given given here below for $\mu$ and $\phi$, respectively:

```
Fraction in 1st window = 0.1
Fraction in 2nd window = 0.5

    mu    phi
 0.876 -0.691
```

Accordingly, one cannot reject the null hypàothesis of same average parameters value on a 95% confidence level.

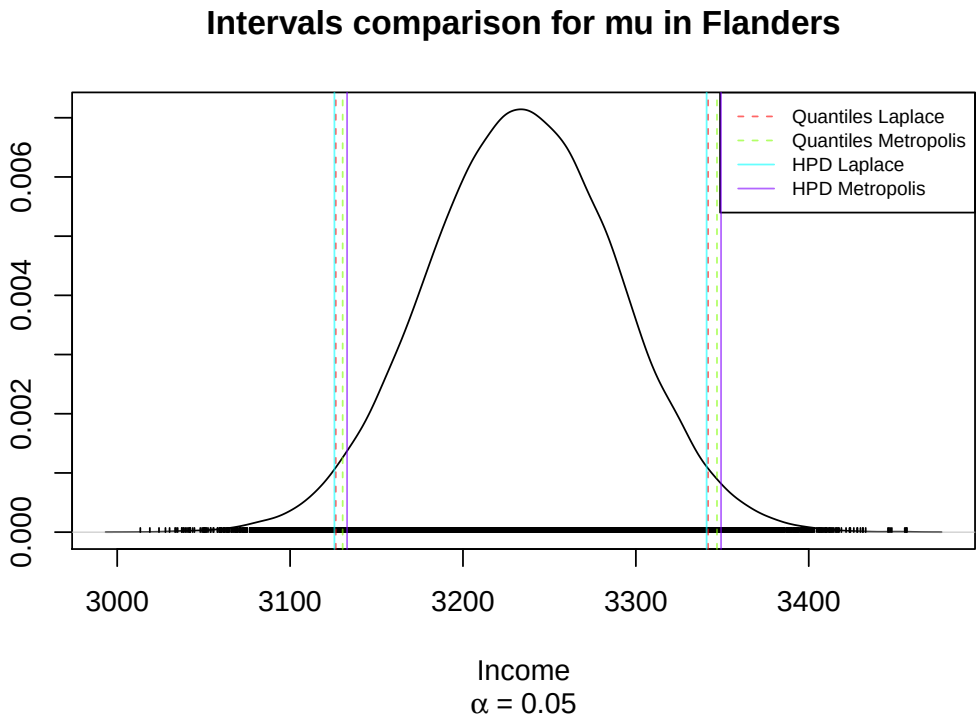
To strengthen the belief of convergence, one can successively discard larger numbers of iterations from the beginning of the chain. From there, the z-score is successively computed and presented here below:




Except for one value, the hypothesis of same mu and phi are never rejected. There is still no proof of non convergence of the generated chains.

## 5.3 (c) Credible intervals for $\mu_1$

It would be interesting to calculate intervals and compare them to those previously found with the Laplace approximation. Using the same method, here are the results obtained.




The intervals being very close to each other, it is difficult to distinguish them visually. Thus, they are shown in the table below.

| | Quantiles | | HPD | |
|---|---|---|---|---|
| **Laplace** | 3126.42 | 3341.76 | 3125.64 | 3340.92 |
| **Metropolis** | 3130.41 | 3346.92 | 3132.97 | 3349.27 |

Table 4: Comparison of credible intervals between Laplace and Metropolis

# 6 Question 6

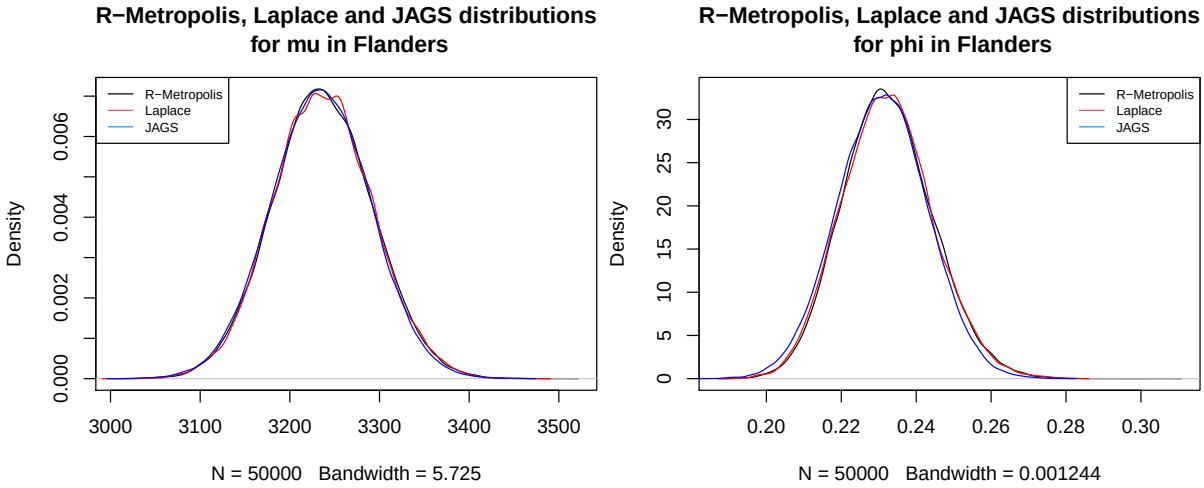
JAGS allows to generate samples from a joint posterior by providing the distributions of the members of this element: first the likelihood and then the conjugate prior. The former is a multinomial distribution where the probability vector is composed of a difference of gamma CDFs. The latter is composed of a normal distribution (mean 3000 and standard deviation 306.12) for the $\mu_k$ and a uniform distribution (with bonds from 0 to 10) for coefficient of dispersion $\phi_k$. Those have been defined earlier and are proposed here below:

```
# JAGS Metropolis Model
metro_model <- function() {
  # Utils
  kappa <- 1 / phi
  lambda <- 1 / (phi * mu)
```

```
  # Probabilities
  for (i in 1:10) {
    pi[i] <- pgamma(intervals[i + 1], kappa, lambda) - pgamma(intervals[i],
kappa, lambda)
  }

  # Likelihood
  y ~ dmulti(pi, n)

  # Priors
  mu ~ dnorm(3000, pow(306.12, -2)) # JAGS syntax: 2nd term is precision,
which is 1/sd^2
  phi ~ dunif(0, 10)
}
```

A summary of the results is available in appendix.

The graphical elements (traceplot, acf, ..) being very similar, only the comparison between the distributions estimated by the different models is presented. It is indeed also noticeable in the figures below that the estimated distributions are very close, either for mu or for phi. With the only small exception of JAGS, for phi which seems to be slightly lower.




Not surprisingly, the intervals obtained via JAGS are very similar to those obtained previously, especially via the Metropolis algorithm in R. (See Table 4)

| | Quantiles | | HPD | |
|---|---|---|---|---|
| **JAGS** | 3129.2 | 3346.4 | 3130.52 | 3347.4 |

Table 5: Credible intervals for the JAGS model

# 7 Question 7

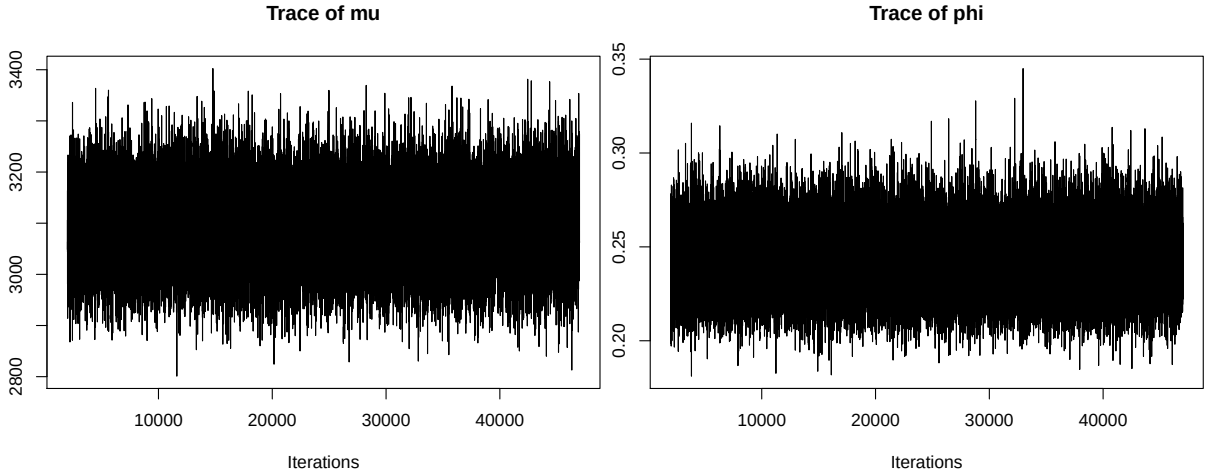
## 7.1 The Metropolis algorithm

The model is exactly the same as in Flanders since the the proposed (log-)posterior distribution is the same and the prior parameters is also proposed to be the same. Then, one needs to fill in the data specific to Wallonia observations from the study and its starting values. Those are proposed to be the MLE's of $\mu_2$ and $\phi_2$ (3043 and 0.243, respectively).

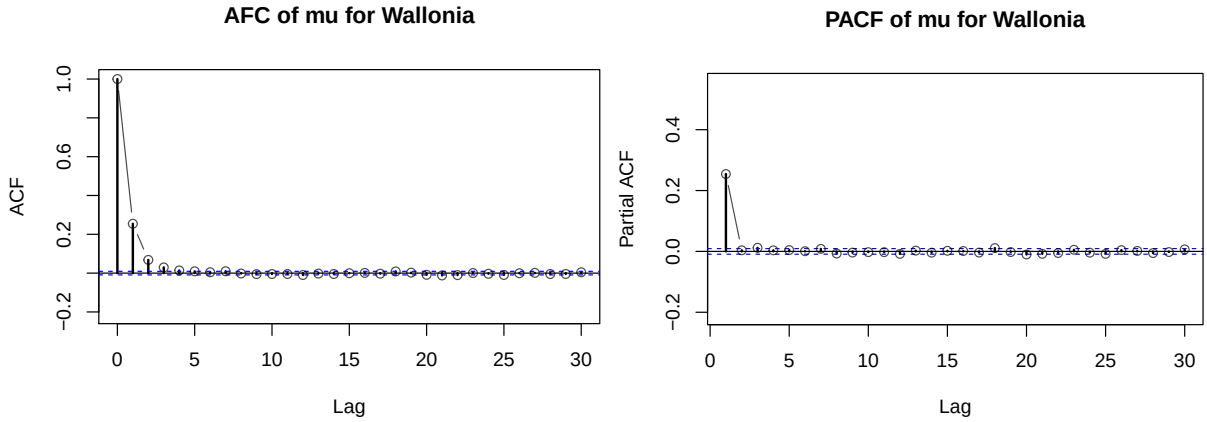
## 7.2 Convergence study

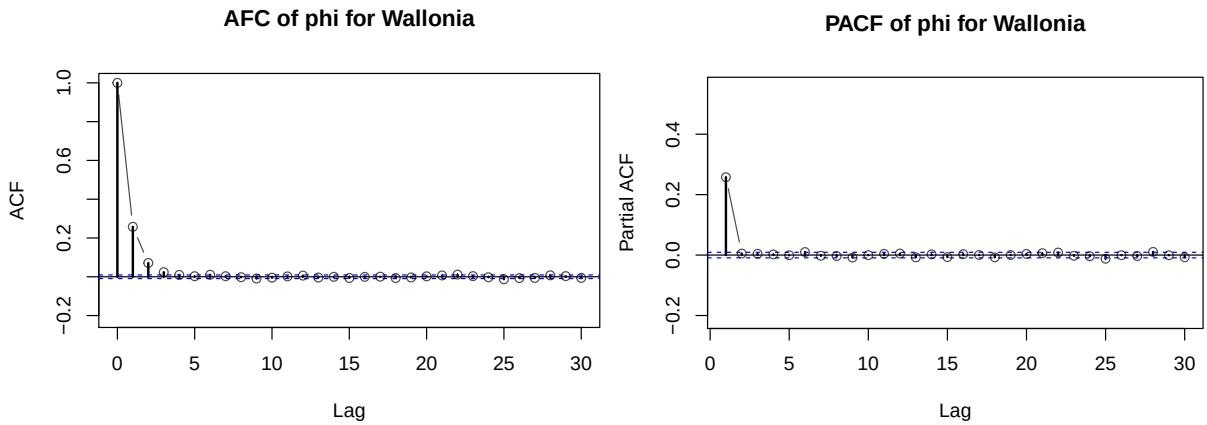
### Global analysis

There is no reason to believe the conclusions regarding the convergence would be different from Flanders. Let's first see the traceplot:




Similarly to Flanders, it does not seem that the mean and variance change over the iterations. Moreover, as it can be shown in the ACFs/PACFs below, the autocorrelation is weaker.





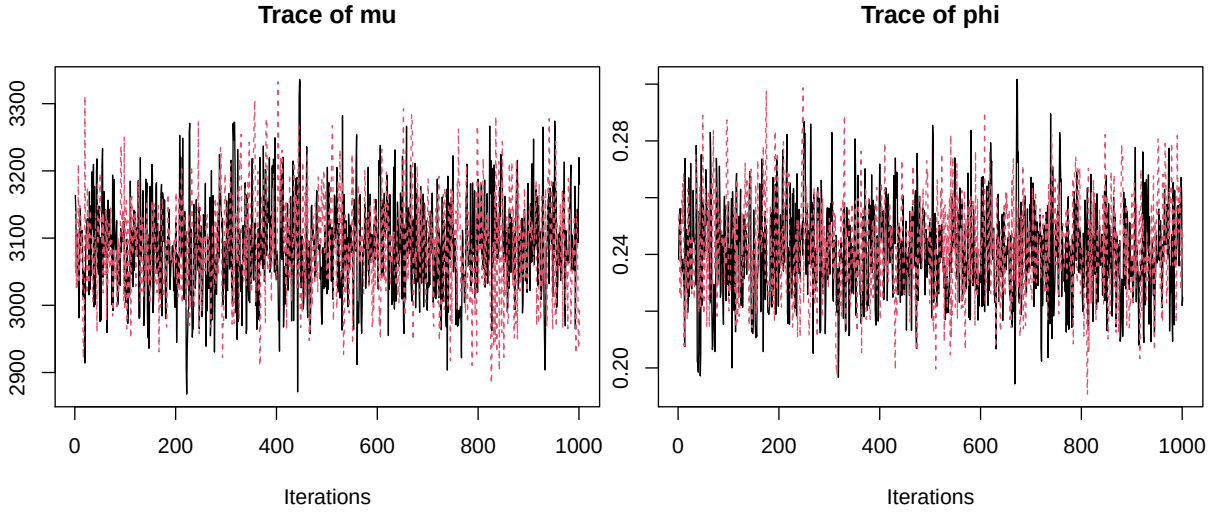

This results in a larger effective sample size, which is good news for convergence assessment. In terms of proportions, it is almost trice bigger. See table below for exact size:

| mu | phi |
|---|---|
| 31206.75 | 28652.20 |

Effective sample size of Metropolis in Wallonia

### Gelman-Rubin

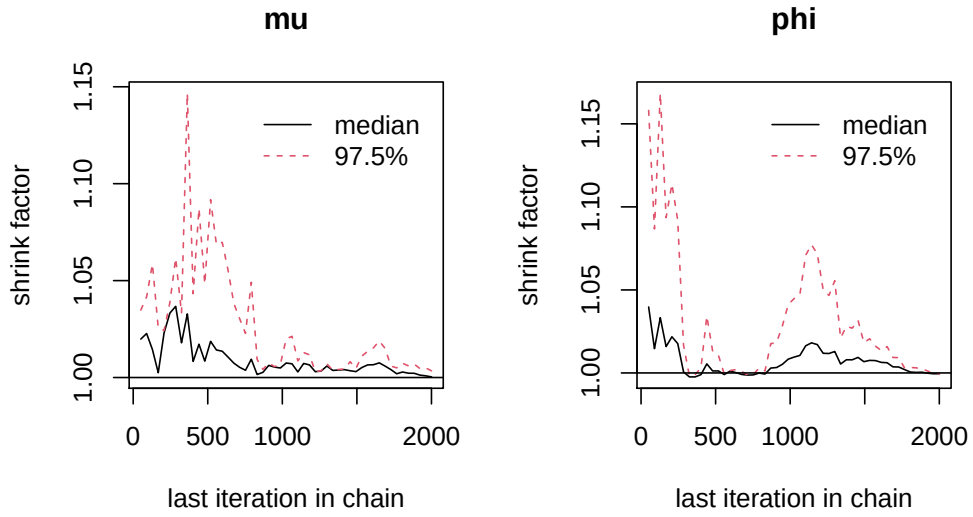
The two proposed starting values for $\mu_2$ and $\phi_2$ are the same as in Flanders section : 4000 for $\mu_1$ and 0.1 for $\phi_1$. After having run the second chain, the traceplot of both chain is plotted with respect to the first 1000 generations after the burn-in.




The shapes of chains remain very similar, indicating convergence. Moreover, the Gelman-rubin statistic upper bond CI is clearly below the 1.1 objective.

| | Point est. | Upper C.I. |
|---|---|---|
| mu | 1.006677 | 1.012692 |
| phi | 1.008471 | 1.041610 |

Applying the statistic with respect to the number of generations, the convergence seems to occur earlier, after less than 1000 chain length



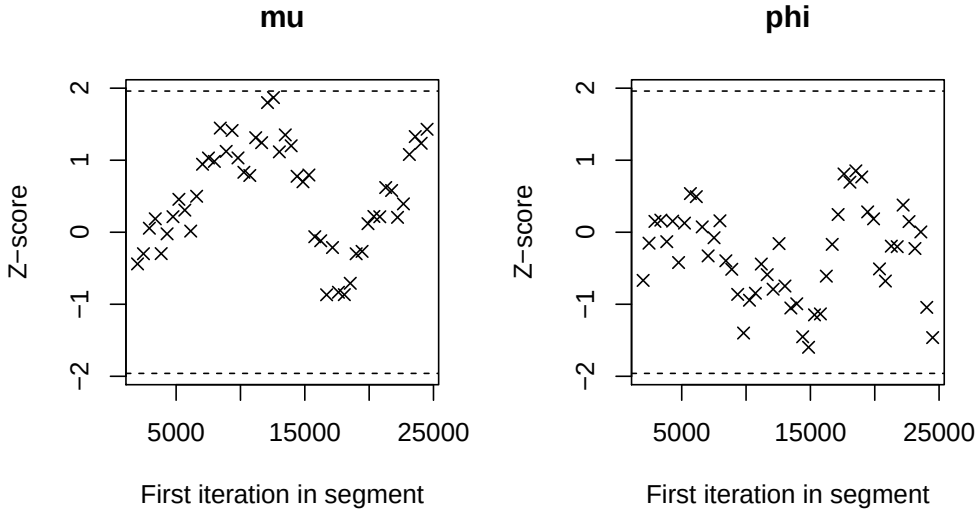

### Geweke diagnostic

The Z-scores are given given here below for $\mu_2$ and $\phi_2$

```
[[1]]

Fraction in 1st window = 0.1
Fraction in 2nd window = 0.5

     mu     phi
-0.4397 -0.6687
```

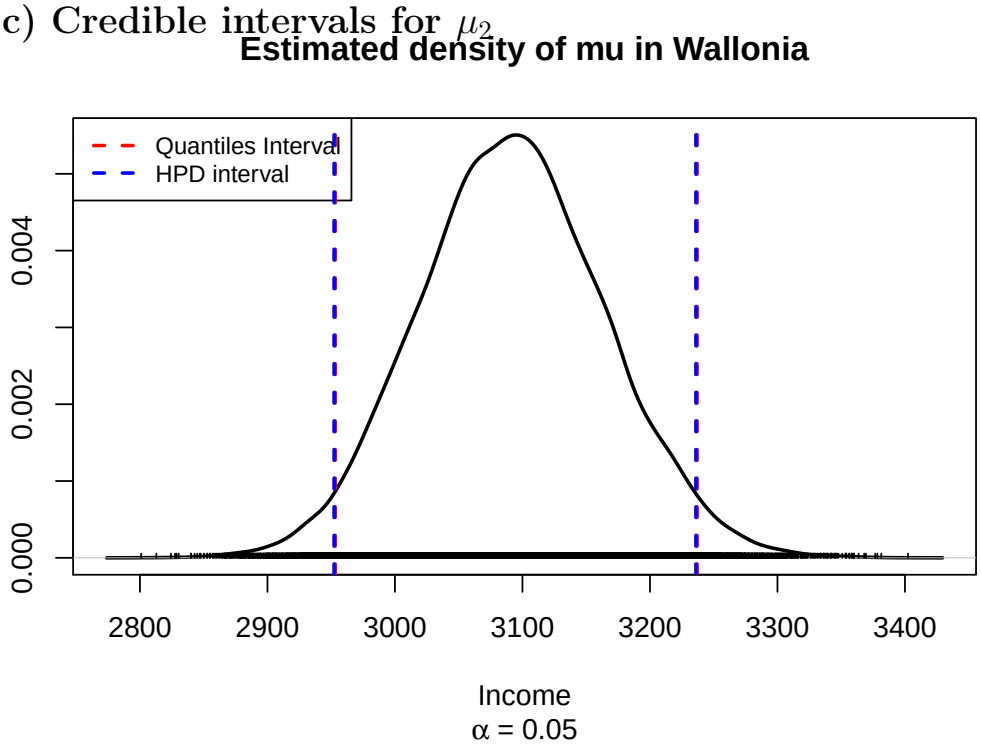
Once again, one cannot reject the hypothesis of same average values although the Z-score are higher this time.

If one plots the Z-score successively with repect to the number of iterations, this gives:




There are a bit more rejected hypotheses but this is not alarming.

## 7.3 (c) Credible intervals for $\mu_2$




The density is again rather symmetric but centered on a smaller value (`3092.4`). The exact values for the intervals in given below:

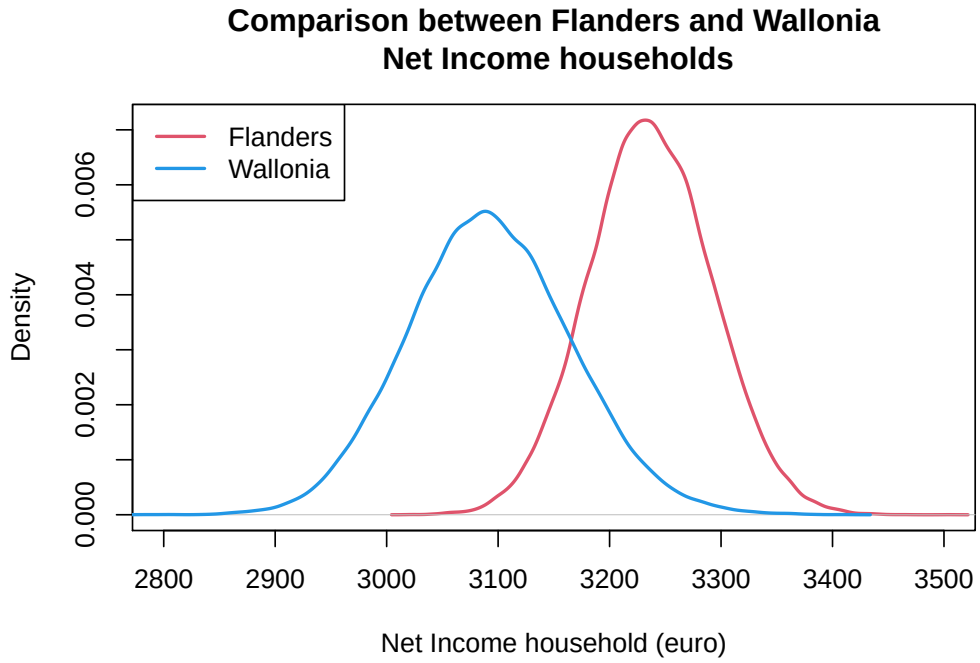
| | Quantiles | | HPD | |
|---|---|---|---|---|
| **Metropolis** | 2953.15 | 3236.97 | 2952.28 | 3236.04 |

Table 6: Comparison of credible intervals in Wallonia

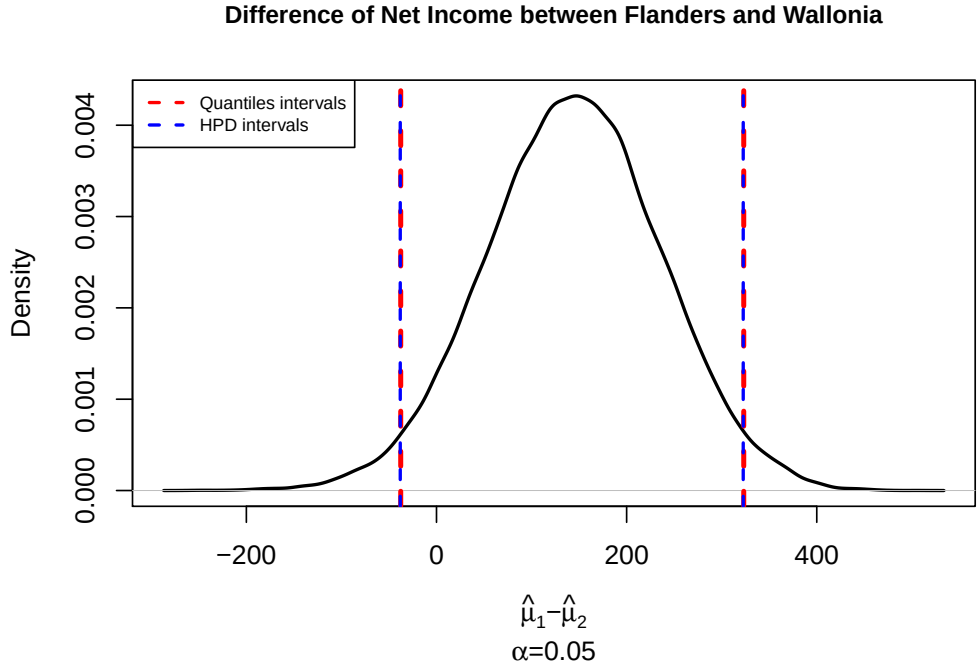
The detailed comparison is terms of values is detailed in te next question.

# 8 Question 8

The ultimate goal of this work is comparing the households income divergence between Flanders and Wallonia given some a priori and after a experimental study through 1228 Belgian households. To do so, 50000 samples have been generated through the metropolis algorithm for Flanders and its French-talking counterpart. Their estimated density is jointly represented here below:




There is a 144.34€ difference on average. However, a large part of the density seems to overlap. The density of their difference is shown below along with a 95% quantile based and HPD credible intervals:




On a 95% confidence level, it is impossible to conclude that the average household income level is significantly different between the regions. According to this Bayesian approach,

one can only be up to `88.16` % sure that the Flemish income is higher than in Wallonia. This is computed by looking from which confidence level one can reject the null hypothesis of same average income.

# A Appendix

## A.1 Output

### A.1.1 Summary of the Laplace approximation for Flanders

```
Iterations = 1:50000
Thinning interval = 1
Number of chains = 1
Sample size per chain = 50000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

        Mean     SD  Naive SE Time-series SE
mu  3234.350 55.002 0.2459772      0.2459772
phi    0.231  0.012 0.0000535      0.0000535

2. Quantiles for each variable:

        2.5%      25%      50%      75%    97.5%
mu  3126.946 3197.129 3234.459 3271.786 3341.744
phi    0.208    0.223    0.231    0.239    0.254
```

### A.1.2 Summary of the JAGS model for Flanders

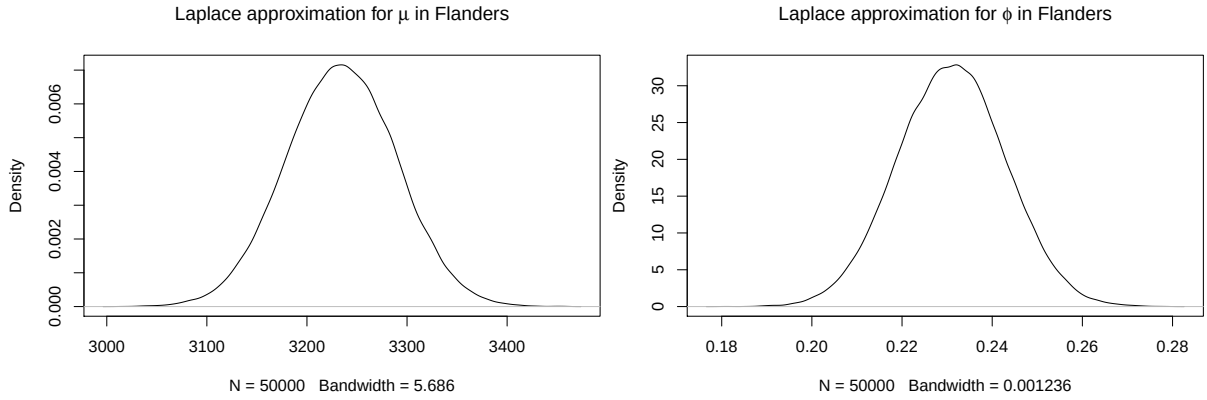
```
Iterations = 2001:52000
Thinning interval = 1
Number of chains = 1
Sample size per chain = 50000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

        Mean     SD  Naive SE Time-series SE
mu  3236.767 55.376 0.2476489      0.3148970
phi    0.232  0.012 0.0000538      0.0000713

2. Quantiles for each variable:

       2.5%      25%      50%     75%    97.5%
mu  3129.20 3199.385 3236.031 3273.85 3346.399
phi    0.21    0.224    0.232    0.24    0.257
```

### A.1.3 Summary of the JAGS model for Wallonia

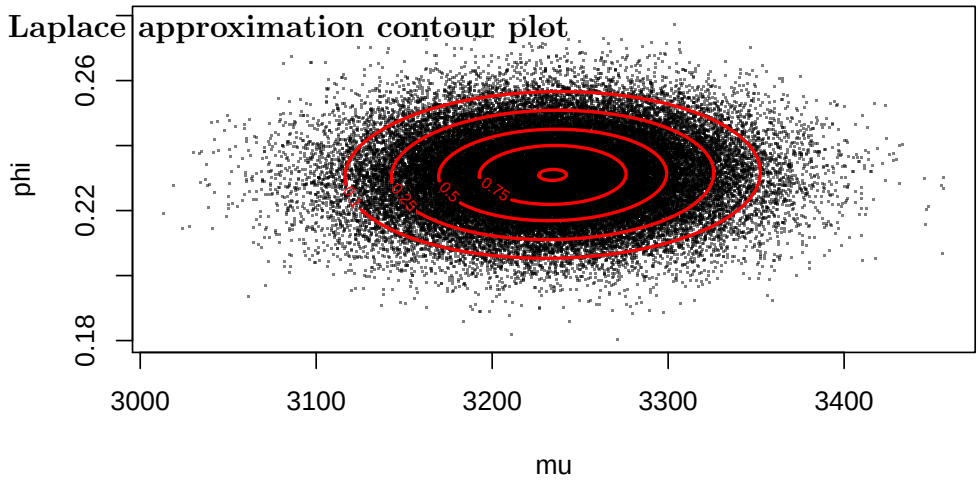
```
Iterations = 2001:52000
Thinning interval = 1
Number of chains = 1
Sample size per chain = 50000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

        Mean      SD  Naive SE Time-series SE
mu  3092.636 73.5955 0.3291292      0.4314644
phi    0.242  0.0172 0.0000771      0.0000981

2. Quantiles for each variable:

       2.5%     25%      50%      75%    97.5%
mu  2952.81 3042.73 3090.922 3140.926 3240.279
phi    0.21    0.23    0.241    0.253    0.278
```

## A.2 Figures

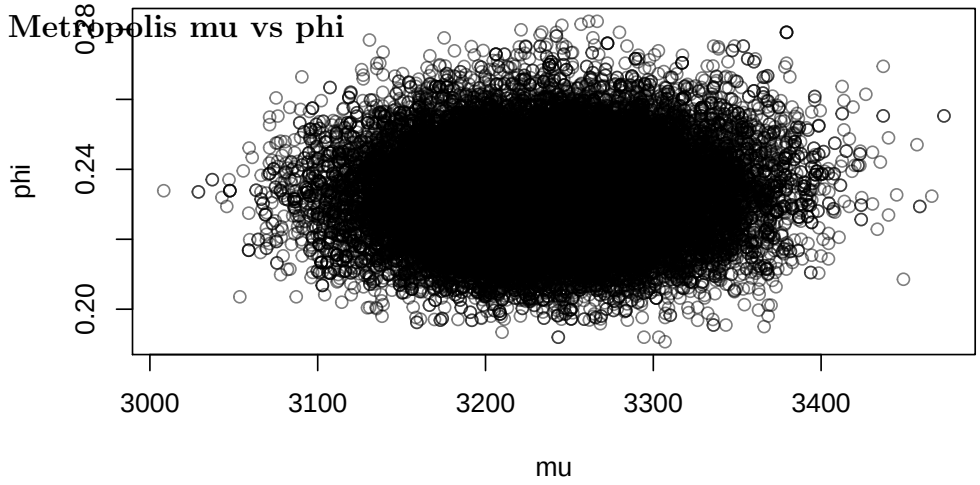
### A.2.1 Laplace approximation density plots



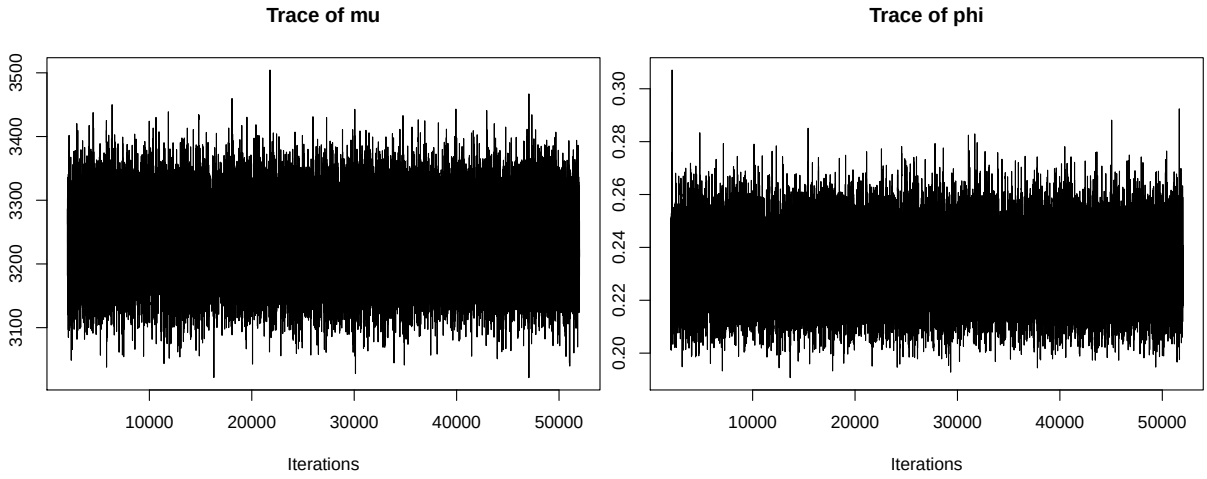

### A.2.2 Laplace approximation contour plot



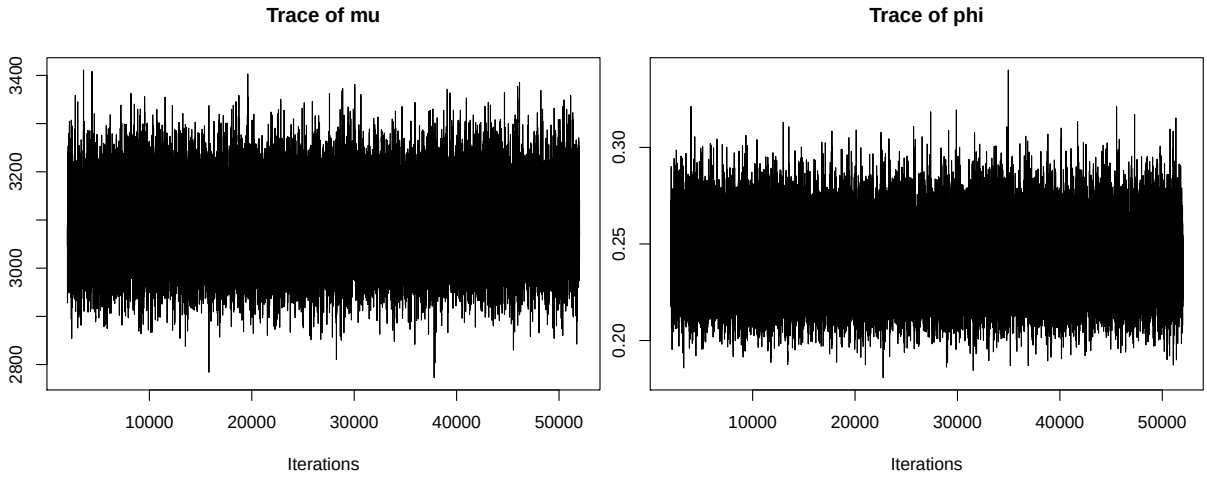
### A.2.3 Metropolis mu vs phi



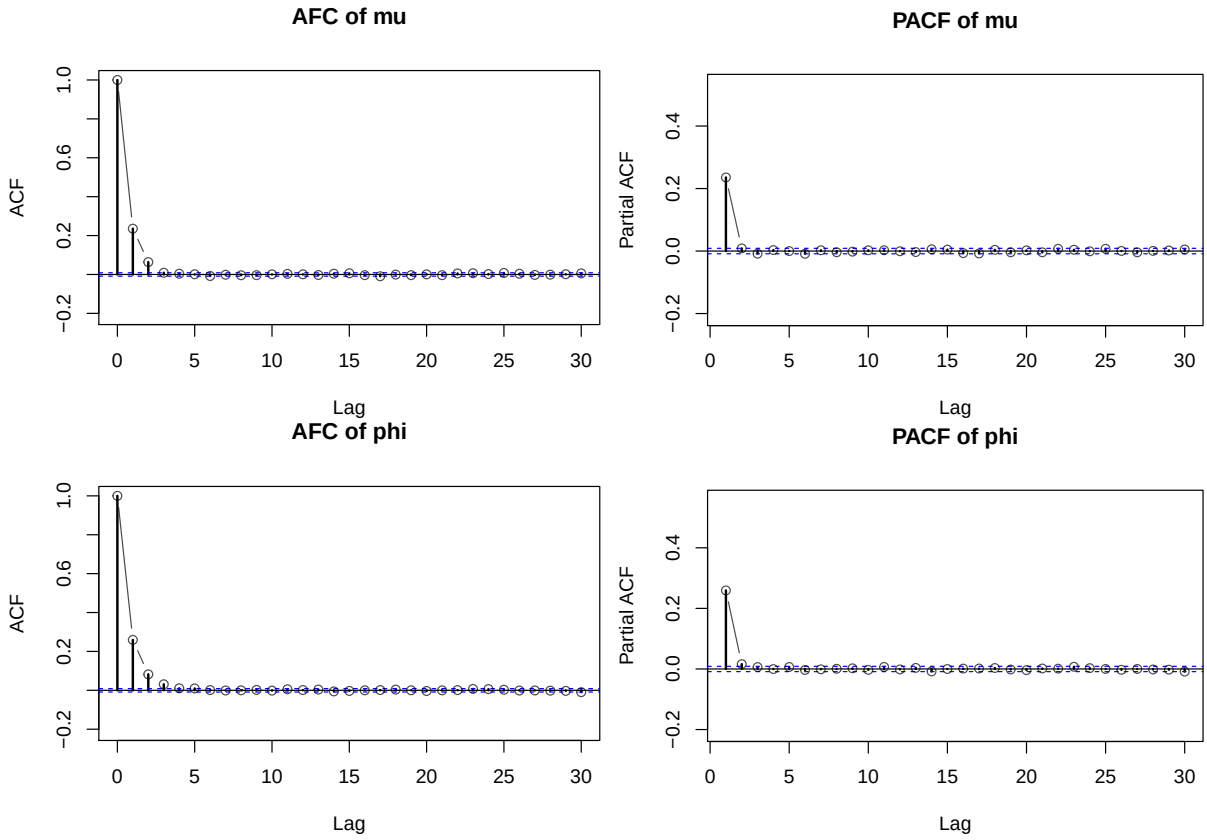

### A.2.4 JAGS traceplot for Flanders



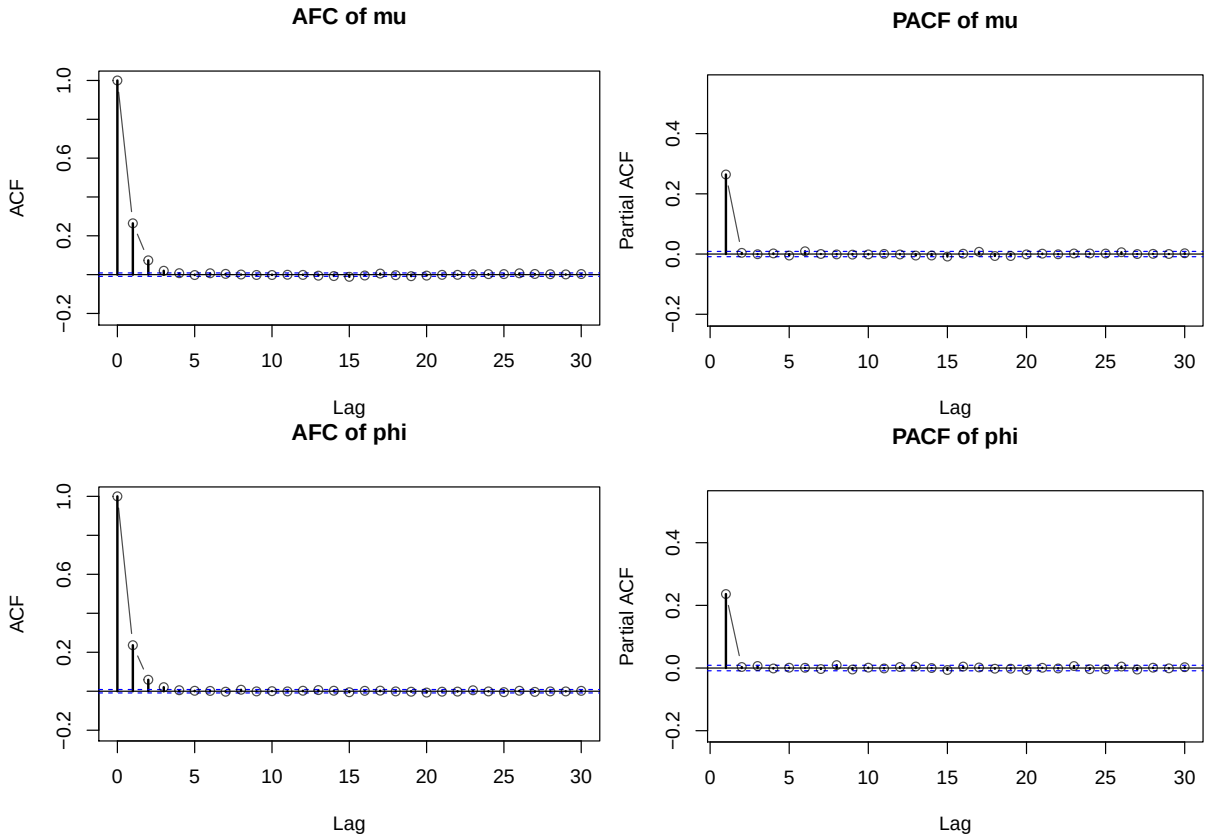

### A.2.5 JAGS traceplot for Wallonia



### A.2.6 JAGS ACF/PACF for Flanders




### A.2.7 JAGS ACF/PACF for Wallonia



## A.3 Code

```r
# Require the necessary packages

if (!require(mvtnorm)) {install.packages("mvtnorm");require(mvtnorm)}
if (!require(EnvStats)) {install.packages("EnvStats");require(EnvStats)}
if (!require(R2WinBUGS)) {install.packages("R2WinBUGS");require(R2WinBUGS)}
if (!require(coda)) {install.packages("coda");require(coda)}
if (!require(rjags)) {install.packages("rjags");require(rjags)}
if (!require(latex2exp)) {install.packages("latex2exp");require(latex2exp)}

# Setup of the table
data <- matrix(
  data = c(
    25, 69, 65, 106, 80, 106, 136, 94, 76, 46,
    17, 36, 47, 58, 47, 53, 59, 54, 33, 21
  ),
  nrow = 2, byrow = T
)

rownames(data) <- c("Flanders", "Wallonia")
colnames(data) <- c(
  "<1200", "[1200-1500)", "[1500-1800)", "[1800-2300)", "[2300-2700)",
  "[2700-3300)", "[3300-4000)", "[4000-4900)", "[4900-6000)", ">=6000"
)

flanders <- data[1, ]
wallonia <- data[2, ]
flanders.n <- sum(flanders)
wallonia.n <- sum(wallonia)
flanders.prop <- prop.table(flanders)
wallonia.prop <- prop.table(wallonia)

# Intervals of the frequency table
intervals <- c(0, 1200, 1500, 1800, 2300, 2700, 3300, 4000, 4900, 6000,
Inf)
intervals.mean <- c(600, 1350, 1650, 2050, 2500, 3000, 3650, 4450, 5450,
6000)

# Utility function to compute the prob of being between high and low
pgammadiff <- function(low, high, kappa, lambda) {
  pgamma(high, kappa, lambda) - pgamma(low, kappa, lambda)
}

# Utility fonctions
kappa <- function(phi) {
  1 / phi
}
lambda <- function(phi, mu) {
  1 / (phi * mu)
}
```

```r
alpha <- .05

# Estimate the parameters by simulation

obtain_the_estimated_parameters <- function(row, boot = F, simulations =
10000) {
  if (boot) {
    sim_prop <- rowSums(rmultinom(simulations, sum(data),
prop.table(data)[row, ]))
  } else {
    sim_prop <- data[row, ]
  }

  sim_data <- unlist(sapply(1:ncol(data), function(i) {
    rep(intervals.mean[i], sim_prop[i])
  }))
  est_gam <- egamma(sim_data)

  est_kappa <- est_gam$parameters["shape"]
  est_lambda <- 1 / est_gam$parameters["scale"]

  est_mu <- est_kappa / est_lambda
  est_phi <- 1 / est_kappa

  return(list(mu = est_mu, phi = est_phi, kappa = est_kappa, lambda =
  est_lambda, sim = sim_data))
}

estim_params_fl <- obtain_the_estimated_parameters(1, T)
estim_params_wal <- obtain_the_estimated_parameters(2, T)

estim_mu_fl <- estim_params_fl$mu
estim_phi_fl <- estim_params_fl$phi
estim_fl <- estim_params_fl$sim
estim_mu_wal <- estim_params_wal$mu
estim_phi_wal <- estim_params_wal$phi
estim_wal <- estim_params_wal$sim


hist(estim_fl, freq = F, xlim = c(0, 6500), main = "Histogram of Flanders
and gamma distribution\n with estimated parameters", xlab = "Income")
curve(dgamma(x, estim_params_fl$kappa, estim_params_fl$lambda), xlim = c(0,
6500), add = T)

hist(estim_wal, freq = F, xlim = c(0, 6500), main = "Histogram of Wallonia
and gamma distribution\n with estimated parameters", xlab = "Income")
curve(dgamma(x, estim_params_wal$kappa, estim_params_wal$lambda), xlim =
c(0, 6500), add = T)

# Set the priors
```

```r
mu_prior <- 3000
sigma_prior <- 306.12

(function(N) {
  moyenne <- sapply(1:N, function(i) {
    mean(rgamma(1000, estim_params_fl$kappa, estim_params_fl$lambda))
  })

  hist(moyenne, probability = T, breaks = 30, main = "", xlab = "Mean",
  xlim = c(min(moyenne) - 50, 50 + max(moyenne)))
  lines(density(moyenne), col = "red", lwd = 2)
  curve(dnorm(x, mean = mean(moyenne), sd = sd(moyenne)), add = T, col =
  "blue", lwd = 2)
  legend("topleft", legend = c("Estimated density", "Normal density"), col
  = c(2, 4), lty = 1, cex = 0.8, lwd = 2)
})(30000)

lpost <- function(theta, freq) {
  # Transform mu and phi -> kappa and lambda
  kappa <- kappa(theta[2])
  lambda <- lambda(theta[2], theta[1])

  # Likelihood : sum_j^n[x_j * ln(probability_of_being_in_interval_j)]
  LL <- sum(sapply(1:length(freq), function(j) {
    freq[j] * log(pgammadiff(low = intervals[j], high = intervals[j + 1],
kappa, lambda))
  }))

  # Log posterior
  lpi <- dnorm(theta[1], mu_prior, sigma_prior, log = T) + dunif(theta[2],
0, 10, log = T)
  lpost <- LL + lpi

  names(lpost) <- "lpost"
  return(lpost)
}

# Starting values
inits <- c(mu = mu_prior, phi = 0.01)
# Laplace approximation
laplace_approx <- function(inits, frequencies) {
  fit <- optim(inits, lpost, control = list(fnscale = -1), hessian = T,
freq = frequencies)
  params <- fit$par
  param_cov_mat <- solve(-fit$hessian)
  samples <- rmvnorm(50000, params, param_cov_mat)

  list(samples = samples, parameters = params, cov = param_cov_mat)
}

laplace_fl <- laplace_approx(inits, flanders)
```

```r
laplace_fl.mcmc <- mcmc(laplace_fl$samples)

# Credible intervals of Laplace (HPD vs QB)
marginal_post_Fl <- rnorm(1e6, laplace_fl$parameters["mu"],
sqrt(laplace_fl$cov[1, 1]))

QB_LP <- quantile(marginal_post_Fl, probs = c(alpha / 2, 1 - alpha / 2))
HPD_LP <- HPDinterval(as.mcmc(marginal_post_Fl), prob = 1 - alpha)

plot(density(laplace_fl$samples[, 1]), main = expression(paste("Laplace
approximation for ", mu[Fl])), sub = expression(paste(alpha, " = ", 0.05)))
legend("topleft",
  legend = c("HPD", "Quantiles"),
  col = c("red", "blue"), lty = 1:2
)

abline(v = c(HPD_LP[1], HPD_LP[2]), col = "red", lty = 1)
abline(v = c(QB_LP[1], QB_LP[2]), col = "blue", lty = 2)

# Metropolis algorithm, mu and phi updated one at the time
metropolis_algorithm <- function(M, theta, sd.propositions, factors,
frequencies) {
  theta <- as.vector(theta)
  sd.propositions <- as.vector(sd.propositions)
  factors <- as.vector(factors)
  frequencies <- as.vector(frequencies)

  thetas <- array(dim = c(M + 1, 2))
  thetas[1, ] <- theta

  accepted <- c(0, 0)

  sigma_mu <- factors[2] * sd.propositions[1]
  sigma_phi <- factors[2] * sd.propositions[2]

  for (i in 2:(M + 1)) {
    theta_mu <- theta_phi <- this_theta <- thetas[i - 1, ]

    theta_mu[1] <- this_theta[1] + rnorm(1, 0, sigma_mu)
    theta_phi[2] <- this_theta[2] + rnorm(1, 0, sigma_phi)

    thresholds <- c(
      min(exp(lpost(theta_mu, frequencies) - lpost(this_theta,
      frequencies)), 1),
      min(exp(lpost(theta_phi, frequencies) - lpost(this_theta,
      frequencies)), 1)
    )

    accepts <- runif(2) <= thresholds

    thetas[i, ] <- this_theta
```

```
    if (accepts[1]) thetas[i, 1] <- theta_mu[1]
    if (accepts[2]) thetas[i, 2] <- theta_phi[2]
    accepted <- accepted + as.integer(accepts)
  }

  colnames(thetas) <- c("mu", "phi")
  names(accepted) <- c("mu", "phi")
  return(list(theta = thetas, accept_rate = accepted / M))
}

burnin <- function(array, percent) {
  tail(array, -percent * nrow(array))
}

sd_hat_mu <- sqrt(laplace_fl$cov[1, 1])
sd_hat_phi <- sqrt(laplace_fl$cov[2, 2])

# Run the algorithm
metro_fl1 <- metropolis_algorithm(5e4,
  theta = c(mu = estim_mu_fl, phi = estim_phi_fl),
  sd.propositions = c(
    mu = sd_hat_mu,
    phi = sd_hat_phi
  ),
  factors = c(mu = 2.75, phi = 2.75),
  frequencies = flanders
)

# Remove burnin samples
metro_fl1.theta <- burnin(metro_fl1$theta, 0.1)
metro_fl1.theta.mcmc <- as.mcmc(metro_fl1.theta)

traceplot(metro_fl1.theta.mcmc)

# Plot slightly modified acf and pacf
plot.acf.pacf <- function(data, lag.max = 30, linked_by_line = T, titles =
c("ACF", "PACF"), ...) {

  ts.acf <- acf(x = data, lag = lag.max, plot = F)
  ts.pacf <- pacf(x = data, lag = lag.max, plot = F)

  # Add lines to improve the visualization
  plot(ts.acf, ylim = c(min(ts.acf$acf) - 0.2, min(max(ts.acf$acf + 0.3),
  1)), main = titles[1], lwd = 2, ...)
  if (linked_by_line) {
    lines(ts.acf$lag, ts.acf$acf, type = "b", col = rgb(0, 0, 0, .7))
  }

  plot(ts.pacf, ylim = c(min(ts.pacf$acf) - 0.2, min(max(ts.pacf$acf +
  0.3), 1)), main = titles[2], lwd = 2, ...)
  if (linked_by_line) {
```

```
    lines(ts.pacf$lag, ts.pacf$acf, type = "b", col = rgb(0, 0, 0, .7))
  }
}

plot.acf.pacf(metro_fl1.theta[, 1], titles = c("AFC of mu", "PACF of mu"))
plot.acf.pacf(metro_fl1.theta[, 2], titles = c("AFC of phi", "PACF of
phi"))

# out of 48 000 observations
effectiveSize(metro_fl1.theta.mcmc)

# Run the algorithm with another initial theta
metro_fl2 <- metropolis_algorithm(50000,
  theta = c(mu = 4000, phi = 0.1),
  sd.propositions = c(
    mu = sd_hat_mu,
    phi = sd_hat_phi
  ),
  factors = c(mu = 2.75, phi = 2.75),
  frequencies = flanders
)

metro_fl2.theta <- metro_fl2$theta
metro_fl2.theta.mcmc <- as.mcmc(metro_fl2.theta)

# Traceplot of the two metropolis, comparison
traceplot(list(
  head(as.mcmc(metro_fl1$theta), 1000),
  head(as.mcmc(metro_fl2$theta), 1000)
))

gelman.diag(list(head(metro_fl1.theta.mcmc, 1000),
head(metro_fl2.theta.mcmc, 1000)))$psrf

gelman.plot(list(
  head(as.mcmc(metro_fl1$theta), 2000),
  head(as.mcmc(metro_fl2$theta), 2000)
))

# Z-Score plot
geweke.plot(metro_fl1.theta.mcmc, nbins = 50)

# Credible intervals of the Metropolis
QB_ME <- quantile(metro_fl1.theta[, 1], probs = c(alpha / 2, 1 - alpha /
2))
HPD_ME <- HPDinterval(as.mcmc(metro_fl1.theta[, 1]), prob = 1 - alpha)

# Comparison of Laplace vs Metropolis
credible_intervals_comparison <- function(alpha) {
  colors <- rainbow(n = 4, alpha = .6)
```

```
  densplot(laplace_fl.mcmc[, 1], main = "Intervals comparison for mu in
  Flanders", xlab="Income", sub = expression(paste(alpha, " = ", 0.05)))
  legend("topright",
    legend = c("Quantiles Laplace", "Quantiles Metropolis", "HPD Laplace",
    "HPD Metropolis"), col = colors, lty = c(2, 2, 1, 1), cex = .7
  )

  abline(v = c(QB_LP[1], QB_LP[2]), col = colors[1], lty = 2)
  abline(v = c(QB_ME[1], QB_ME[2]), col = colors[2], lty = 2)
  abline(v = c(HPD_LP[1], HPD_LP[2]), col = colors[3], lty = 1)
  abline(v = c(HPD_ME[1], HPD_ME[2]), col = colors[4], lty = 1)

  # return(list(QB=QB,HPD=HPD))
}

credible_intervals_comparison(.05)

# JAGS Metropolis Model
metro_model <- function() {
  # Utils
  kappa <- 1 / phi
  lambda <- 1 / (phi * mu)

  # Probabilities
  for (i in 1:10) {
    pi[i] <- pgamma(intervals[i + 1], kappa, lambda) - pgamma(intervals[i],
kappa, lambda)
  }

  # Likelihood
  y ~ dmulti(pi, n)

  # Priors
  mu ~ dnorm(3000, pow(306.12, -2)) # JAGS syntax: 2nd term is precision,
which is 1/sd^2
  phi ~ dunif(0, 10)
}
model.file <- "resources/metropolis.bug"
write.model(metro_model, model.file)
# Test with Flanders
jags_fl <- jags.model(
  file = model.file,
  inits = list(list(mu = estim_mu_fl, phi = estim_phi_fl)),
  data = list(n = 803, intervals = intervals, y = flanders),
  n.chains = 1,
  quiet = T
)

update(jags_fl, 1000)

out_fl <- coda.samples(model = jags_fl, c("mu", "phi"), n.iter = 50000)
```

```r
out_fl.matrix <- as.matrix(out_fl)

plot(density(out_fl.matrix[, "mu"]), main = "R-Metropolis, Laplace and JAGS
distributions\n for mu in Flanders")
lines(density(metro_fl1.theta[, 1]), col = "red")
lines(density(laplace_fl$samples[, 1]), col = "blue")
legend("topleft", legend=c("R-Metropolis", "Laplace", "JAGS"),
col=c(1,2,4), lty=1, cex=.7)

plot(density(out_fl.matrix[, "phi"]), main = "R-Metropolis, Laplace and
JAGS distributions\n for phi in Flanders")
lines(density(metro_fl1.theta[, 2]), col = "red")
lines(density(laplace_fl$samples[, 2]), col = "blue")
legend("topright", legend=c("R-Metropolis", "Laplace", "JAGS"),
col=c(1,2,4), lty=1, cex=.7)

# Credible intervals of JAGS model
QB_JA <- quantile(out_fl.matrix[, 1], probs = c(alpha / 2, 1 - alpha / 2))
HPD_JA <- HPDinterval(mcmc(out_fl.matrix[, 1]), prob = 1 - alpha)

jags_wal <- jags.model(
  file = model.file,
  inits = list(list(mu = estim_mu_wal, phi = estim_phi_wal)),
  data = list(n = 425, intervals = intervals, y = wallonia),
  n.chains = 1,
  quiet = T
)

update(jags_wal, 1000)

out_wal <- coda.samples(model = jags_wal, c("mu", "phi"), n.iter = 50000) #
want same chain length as in metropolis Flanders
out_wal.matrix <- as.matrix(out_wal)

traceplot(out_wal)
plot.acf.pacf(out_wal.matrix[, 1], titles = c("AFC of mu for Wallonia",
"PACF of mu for Wallonia"))
plot.acf.pacf(out_wal.matrix[, 2], titles = c("AFC of phi for Wallonia",
"PACF of phi for Wallonia"))
# out of 50 000 observations
effectiveSize(out_wal)

jags_wal2 <- jags.model(
  file = model.file,
  inits = list(list(mu = 4000, phi = 0.1)),
  data = list(n = 425, intervals = intervals, y = wallonia),
  n.chains = 1,
  quiet = T
)

update(jags_wal2, 1000)
```

```r
out_wal2 <- coda.samples(model = jags_wal2, c("mu", "phi"), n.iter = 45000)
# want same chain length as in metropolis Flanders
out_wal2.matrix <- as.matrix(out_wal2)

# Traceplot of the two metropolis, comparison
traceplot(list(
  head(as.mcmc(out_wal.matrix), 1000),
  head(as.mcmc(out_wal2.matrix), 1000)
))

gelman.diag(list(head(as.mcmc(out_wal.matrix), 1000),
head(as.mcmc(out_wal2.matrix), 1000)))$psrf

gelman.plot(list(
  head(as.mcmc(out_wal.matrix), 2000),
  head(as.mcmc(out_wal2.matrix), 2000)
))

# Z-Score plot
geweke.plot(out_wal, nbins = 50)
# Credible intervals of the Metropolis
QB_ME_WAL <- quantile(out_wal.matrix[, 1], probs = c(alpha / 2, 1 - alpha
/ 2))
HPD_ME_WAL <- HPDinterval(out_wal[,1], prob = 1 - alpha)

densplot(out_wal[,1], main = "Estimated density of mu in Wallonia",
xlab="Income",
         lwd=2, sub = expression(paste(alpha, " = ", 0.05)))
legend("topleft", legend= c("Quantiles Interval", "HPD interval"), cex =
0.8,
       col = c('red', 'blue'), lwd=2, lty = 2)

abline(v=QB_ME_WAL, col='red', lty=2, lwd=2)
abline(v=unlist(HPD_ME_WAL), col='blue', lty=2, lwd=2)
# Compare the income between region
plot(density(out_fl.matrix[, "mu"]),
  main = "Comparison between Flanders and Wallonia\n Net Income
  households",
  lty = 1, xlim = c(2800, 3500), xlab = "Net Income household (euro)", col
  = 2, lwd = 2
)
legend("topleft", legend = c("Flanders", "Wallonia"), col = c(2, 4), lwd =
2, lty = 1)
lines(density(out_wal.matrix[, "mu"]), col = 4, lwd = 2)

# Credible intervals of the difference
diff_of_mu <- out_fl.matrix[, 1] - out_wal.matrix[, 1]
plot(density(diff_of_mu),
  main = "Difference of Net Income between Flanders and Wallonia",
  xlab = expression(paste(hat(mu)[1], "-", hat(mu)[2])), cex.main = 0.9,
  lwd = 2,
```

```
  sub = expression(paste(alpha, "=", 0.05))
)
legend("topleft", legend = c("Quantiles intervals", "HPD intervals"), col
= c("red", "blue"), lty = 2, cex = 0.7, lwd = 2)
abline(v = quantile(diff_of_mu, probs = c(0.025, 0.975)), col = "red", lty
= 2, lwd = 3)
abline(v = HPDinterval(as.mcmc(diff_of_mu)), col = "blue", lty = 2, lwd =
2)

# ============ APPENDIX =========== #
summary(laplace_fl.mcmc)

summary(out_fl)

summary(out_wal)

plot(density(laplace_fl$samples[, 1]),
  main = expression(paste("Laplace approximation for ", mu, " in
  Flanders"))
)
plot(density(laplace_fl$samples[, 2]),
  main = expression(paste("Laplace approximation for ", phi, " in
  Flanders"))
)

# Contour plot of the Laplace approximation
(function() {
  lvls <- c(0.01, 0.25, 0.5, 0.75, 0.9)

  x1 <- seq(2400, 3600, length = 3000)
  y1 <- seq(0.1, 0.4, length = 3000)

  z1 <- outer(x1, y1, function(x, y) {
    dmvnorm(cbind(x, y), colMeans(laplace_fl$samples),
    cov(laplace_fl$samples), log = T)
  })

  R <- exp(z1 - max(z1))

  plot(
    x = laplace_fl$samples[, 1], y = laplace_fl$samples[, 2],
    xlab = "mu", ylab = "phi", pch = ".", col = rgb(0, 0, 0, .5)
  )

  contour(x1, y1, R,
    lwd = 2, add = T,
    levels = exp(-0.5 * qchisq(lvls, 2)),
    labels = (1 - lvls), col = "red", method = "edge"
  )
})()
plot(metro_fl1.theta[, 1], metro_fl1.theta[, 2], xlab = "mu", ylab = "phi",
col = rgb(0, 0, 0, .5))
```

```r
traceplot(out_fl)

traceplot(out_wal)

plot.acf.pacf(out_fl.matrix[, 1], titles = c("AFC of mu", "PACF of mu"))
plot.acf.pacf(out_fl.matrix[, 2], titles = c("AFC of phi", "PACF of phi"))

plot.acf.pacf(out_wal.matrix[, 1], titles = c("AFC of mu", "PACF of mu"))
plot.acf.pacf(out_wal.matrix[, 2], titles = c("AFC of phi", "PACF of phi"))
```