Estimation of AR models

- Recall that the **AR(p)** model is defined by the equation

  $$X_t = \sum_{j=1}^{p} \phi_j X_{t-j} + \epsilon_t$$

  where ϵ_t are assumed independent and following a $N(0, \sigma^2)$ distribution.

- Assume p is known and define $\phi = (\phi_1, \phi_2, \phi_3, \ldots, \phi_p)'$, the vector of model coefficients.

- Given the data $x_1, x_2, x_3, \ldots, x_n$, we want to estimate ($\phi$,$\sigma^2$).

Method of moments

- Recall that Yule Walker's equations establish that,

$$\rho_k = \phi_1 \rho_{k-1} + \phi_2 \rho_{k-2} + \ldots + \phi_p \rho_{k-p}$$

- If we write these equations for $k = 1, 2, \ldots, p$, we obtain a system for $\phi_1, \phi_2, \ldots, \phi_p$.
- We can solve this system with an estimator for the autocorrelation ρ_k.
- For example, we could use the sample autocorrelation $\hat{\rho}_k = r_k$ and then solve the p equations for ϕ.
- This method is implemented in R using the function *ar*.

```
# For example try
a=ar(x,method=''yule walker'')
```

```
list(a)
a$ar
# this gives the MOM estimate of ph
# for your data
```

Maximum likelihood estimation

- For MLE, first we need to find the likelihood function for the AR model.
- Since the AR process has a Markovian structure, the joint density of the data is given by the expression

$$\begin{aligned} p(x_1, x_2, \ldots, x_n|\phi, \sigma^2) &= p(x_1, x_2, \ldots, x_p|\phi, \sigma^2) \\ &\quad \prod_{t=p+1}^{n} p(x_t|x_{t-1}, \ldots, x_{t-p}, \phi, \sigma^2) \end{aligned}$$

- Assume the first p observations (initial values) $(x_1, x_2, \ldots, x_p)$ are completely known.

- Then the model likelihood is defined by ignoring $p(x_1, x_2, \ldots, x_p)$ from the above expression, i.e.

$$p(x_1, x_2, \ldots, x_n|\phi, \sigma^2) \propto \prod_{t=p+1}^{n} p(x_t|x_{t-1}, \ldots, x_{t-p}, \phi, \sigma^2)$$

- What is $p(x_t|x_{t-1}, \ldots, x_{t-p}, \phi, \sigma^2)$? From the AR model definition, x_t can be seen as the response of a linear regression with "regressors" $x_{t-1}, x_{t-2}, x_{t-3}, \ldots, x_{t-p}$, then

$$p(x_t|x_{t-1}, \ldots, x_{t-p}, \phi, \sigma^2) = N(x_t|f_i^{'}\phi, \sigma^2)$$

where $f_i^{'} = (x_{t-1}, x_{t-2}, x_{t-3}, \ldots, x_{t-p})$.

- Define F to be a matrix with rows $f_i^{'}$; $i =$ p+1... n and $x = (x_{p+1}, x_{p+2}, \dots, x_n)$.
- The likelihood function of the AR model conditional on the initial values is a multivariate Normal of dimension $n - p$ with mean $F\phi$ and covariance $\sigma^2 I_{(n-p)\times(n-p)}$, i.e. $N(x|F\phi, \sigma^2 I_{(n-p)\times(n-p)})$.
- The Maximum Likelihood Estimator (MLE) for (ϕ, σ^2) is

$$\begin{aligned} \hat{\phi} &= (F^{'}F)^{-1}F^{'}x \\ s^2 &= R/(n-p) \end{aligned}$$

  where $R = (x - F\phi)^{'}(x - F\phi)$.
- For an unbiased estimator of σ^2, we use

$$s_1^2 = R/(n-2p)$$

- The MLE is also given by the “ar” function available in R/Splus.

  ```
  a=ar(x,method=''mle'')
  a$ar # AR coefficients
  a$var # AR variance
  ```

- All these results are valid if we ignore the uncertainty due to the initial values.
- The complete likelihood of the model considers the extra part, $p(x_1, x_2, \ldots, x_p|\phi, \sigma^2)$, which is a complicated function of the parameters.
- For the complete likelihood we require numerical methods (Newton-Raphson) to obtain the MLE of the AR model.

Bayesian analysis of AR(p) model

- In the context of linear regression (initial values known), we can use a non-informative prior for the parameters,

$$p(\phi, \sigma^2) \propto 1/\sigma^2$$

- Using Bayes theorem, the posterior distribution for (ϕ, σ^2) is given by:
  - ϕ conditional on σ^2 follows a multivariate Normal $N(\phi|\hat{\phi}, \sigma^2(F^{'}F)^{-1})$.
  - The marginal distribution for σ^2 follows an Inverse Gamma posterior $IG((n-2p)/2, R/2)$.
  - The marginal distribution for ϕ follows multivariate t distribution with $n - 2p$ degrees of freedom and location parameter $\hat{\phi}$.
- For posterior inference using the complete model

likelihood, we require numerical techniques such as Markov chain Monte Carlo (MCMC) methods.

Inference on characteristic reciprocal roots

- For this, we need to find the solutions to the equation $\Phi(B) = 0$ where $\Phi(B)$ is the characteristic polynomial of the AR process.

- We have close form expressions for this characteristic roots if $p = 1, 2$, but if $p > 2$ it becomes really hard to obtain the solutions.

- We can use the R/Splus function *polyroot* to find the roots.

```
ph = c(2*0.95*cos(0.5),-0.95^2)
 ph
```

```
[1]  1.667407 -0.902500
polyroot(c(1,-ph))
[1] 0.9237711+0.5046585i 0.9237711-0.5046585i
1/polyroot(c(1,-ph))
[1] 0.8337034-0.4554543i 0.8337034+0.4554543i
# For modulus and frequencies
Mod(1/polyroot(c(1,-ph)))
[1] 0.95 0.95
Arg(1/polyroot(c(1,-ph)))
[1] -0.5  0.5
2*pi/Arg(1/polyroot(c(1,-ph))
[1] -12.56637  12.56637
```

- Given some estimate $\hat{\phi}$, we can compute estimates $\hat{\alpha_1}, \hat{\alpha_2}, \ldots, \hat{\alpha_p}$ for the reciprocal roots.

- Bayesian inference for roots. Mapping from ϕ to "roots" is mathematically intractable (unless $p = 1, 2$).
- In general, there is no close form expression to the posterior distribution of the $\alpha' s$, although we know (ϕ, σ^2) follow a Normal/Inverse Gamma posterior.
- We will rely on *Monte Carlo* simulation to study the posterior distribution for the α's.
- *Monte Carlo* simulation scheme:
  - Simulate a value σ^2 from an $IG((n-2p)/2, R/2)$ distribution.
  - Simulate the vector of coefficients ϕ from $N(\phi|\hat{\phi}, \sigma^2(F'F)^{-1})$ distribution.
  - With the simulated value for ϕ solve the equation

$\Phi(B) = 0$. This leads to one generate sample from the posterior distribution of the $\alpha's$.

  - Iterate until we collect M samples and summarize samples.

- This algorithm produces “exact” Monte Carlo samples of a posterior distribution. It does not require convergence monitoring or a burn-in period.

- To simulate a multivariate Normal distribution, we need to use Cholesky’s decomposition (*chol* function in R).

- If z is a k-dimensional vector that follows a multivariate $N(z|m, V)$, where m is the mean and V is the covariance matrix, this function *chol* allows us to find a matrix A such that $V = AA'$.

- To simulate a z vector, we generate $y_1, y_2, \ldots, y_k$ iid N(0,1) random deviates and make

$$z = m + Ay$$

  where $y = (y_1, y_2, \ldots, y_k)$ and A is the Cholesky's decomposition of V.

- If V is numerically close to a singular matrix, we could use the Singular Value Decomposition of V (svd) instead of Cholesky's decomposition.

Identification of AR roots

- The AR model is invariant for different labeling of the α's, since the characteristic polynomial $\phi(B) = \prod_{i=1}^{p}(1 - \alpha_i B)X_t$.
- The values of the AR coefficients are ϕ are invariant to permutations of the sub-indices for the $\alpha's$
- For identification, complex reciprocal roots are ordered by modulus ($r's$) or by frequencies ($\omega's$)
- If we have C complex pairs of reciprocal roots ordered by modulus then

  $$\alpha_1 = r_1 exp(\pm i\omega_1); \alpha_2 = r_2 exp(\pm i\omega_2); \ldots; \alpha_C = r_C exp(\pm i\omega_C)$$

  with the condition, $r_1 > r_2 > r_3 \ldots > r_C$.

- Ordering the roots by frequencies means that $\omega_1 < \omega_2 < \ldots < \omega_C$.
- For the case of real roots the natural thing to do, is to order them from the smallest to the largest. For R real roots,

$$r_1 < r_2 < r_3 \ldots < r_R$$

- **Example** EEG trace of 400 observations. The ACF/PACF of this series suggests the use of an AR model with $p = 8, 9$, or 10.
- Fitting an AR(10) using R/Splus (it could also been an AR(8) or AR(9) gives the following MOM estimator for the parameters are $\hat{\phi}$ =(0.27,0.03-0.16,-0.18,-0.14,-0.15,-0.23,-0.1,-0.05,-0.11)

and $\hat{\sigma^2} = 3808.58$.

- The reciprocal roots denoted by (r_i, ω_i) and associated to this $\hat{\phi}$ vector are:

$$(.97, .48); (.8, 2.21); (.75, 2.86); (.75, .99); (.74, 1.48)$$

- No real reciprocal were obtained for this AR fit.
- The MLE (rounded to 2 digits) is $\hat{\phi}$ =(0.25,0.04,-0.17,-0.17,-0.13,-0.17,-0.24,-0.11,-0.05,-0.11) , and $\hat{\sigma^2} = 3657.47$.
- The unbiased estimate for σ^2 is 3753.72.
- The MLE for each reciprocal root in terms of modulus

and frequency:

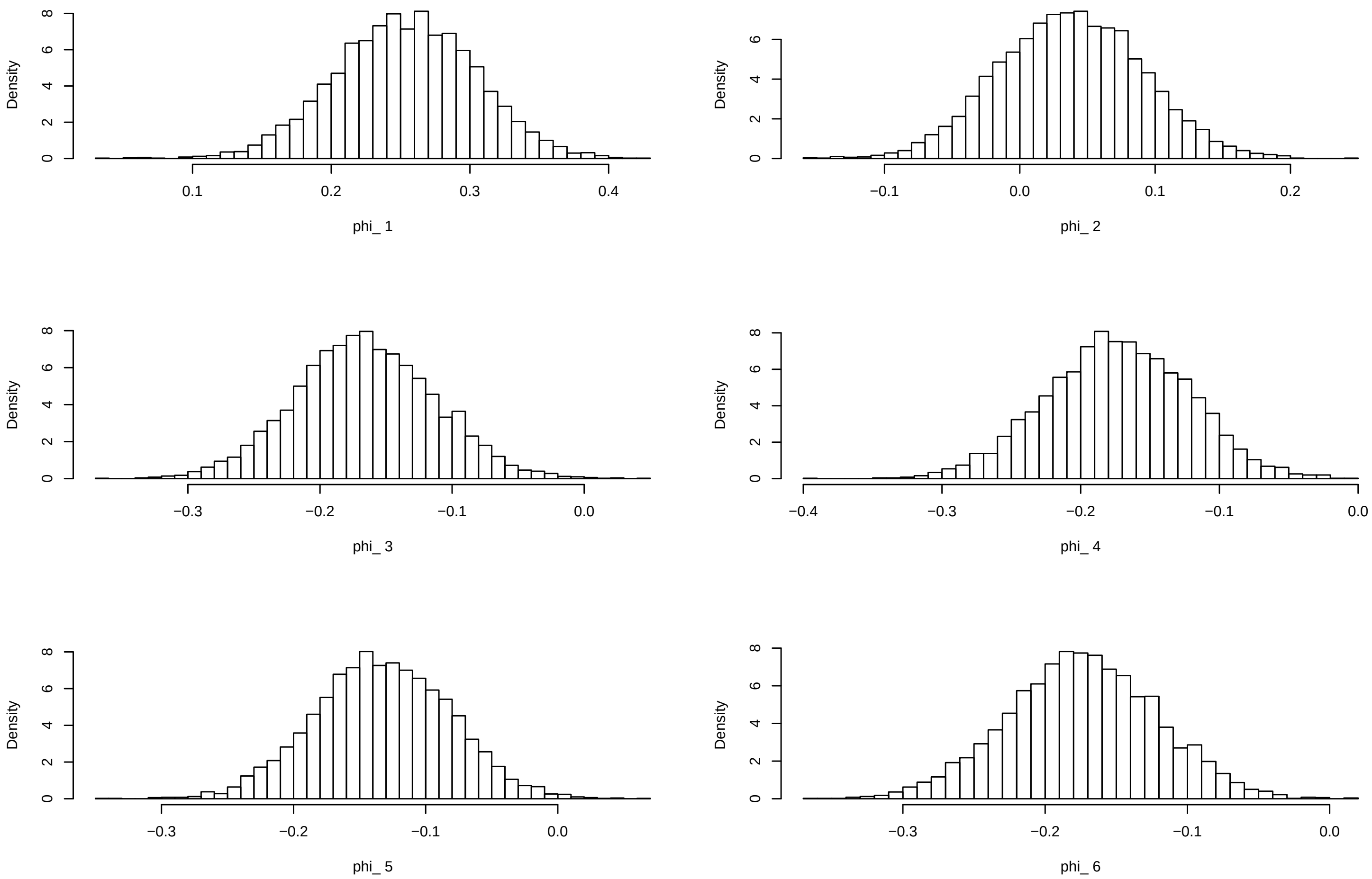
$$(.97, .48); (.8, 2.22); (.77, 2.85); (.75, 1.47); (.74, .99)$$

```
a=ar(eeg,aic=F,order=10,method="mle")
ph=a$ar
v=a$var.pred
round(ph,2)
ar1  ar2   ar3   ar4   ar5   ar6   ar7   ar8
0.25 0.03 -0.16 -0.17 -0.13 -0.17 -0.24 -0.11
ar9   ar10
-0.05 -0.11
round(v,2)
[1] 3609.46
alpha=1/polyroot(c(1,-ph))
round(m<-Mod(alpha),2)
```

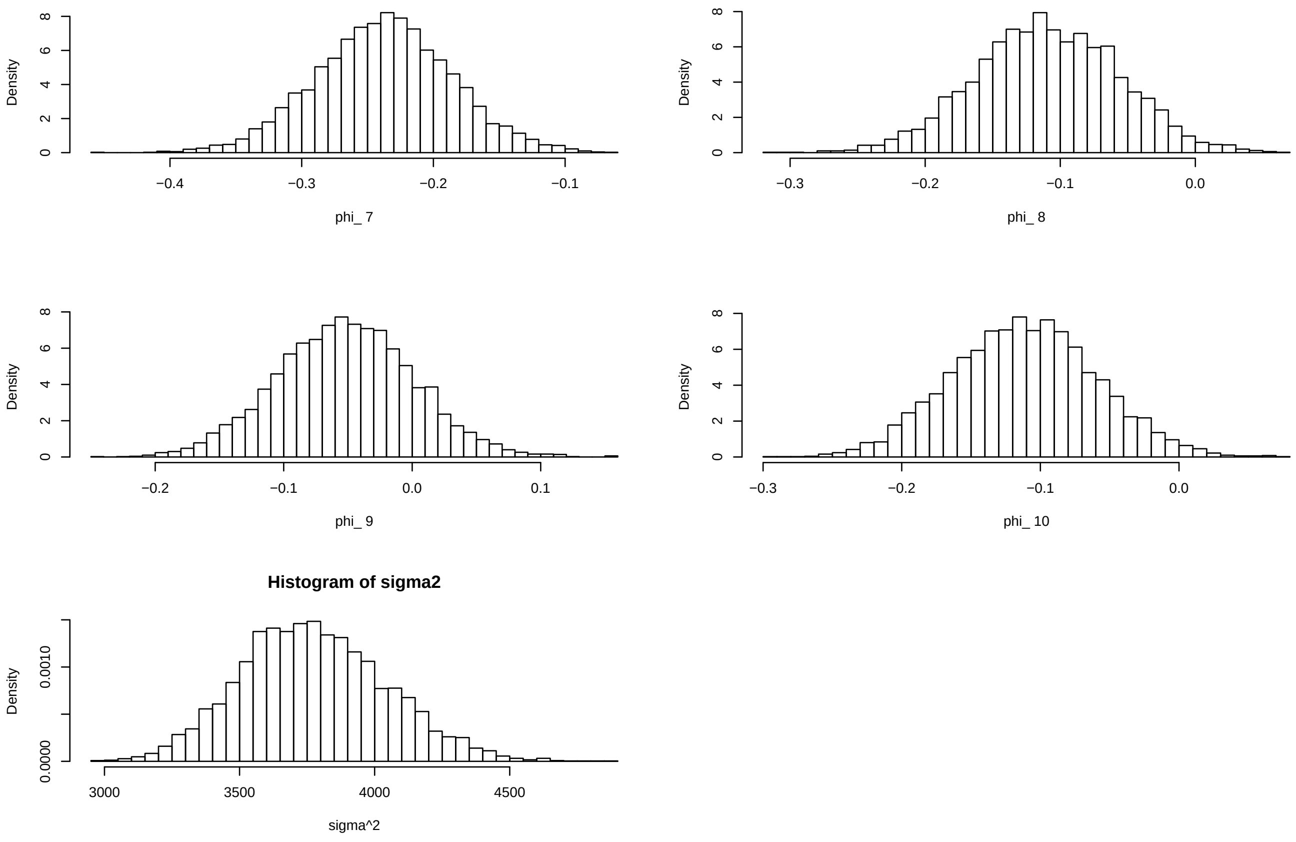
```
[1] 0.97 0.80 0.80 0.97 0.74 0.76
 0.75 0.74 0.75 0.76
round(w<-Arg(alpha),2)
 [1] -0.48 -2.22 2.22 0.48 -1.00
-2.85 1.47 1.00 -1.47 2.85
#order by modulus
m=m[w>0]
w=w[w>0]
rev(m[order(m)])
[1] 0.97 0.79 0.76 0.75 0.74
rev(w[order(m)])
[1] 0.48 2.22 2.85 1.47 0.99
```

- We now show the results for a Bayesian Analysis of an AR(10) model and based on 5000 Monte Carlo samples. The graphs include:
  - Histograms of posterior samples for ϕ coefficients and the variance σ^2
  - Histograms of posterior samples for the α's ordered by modulus.
  - Histograms of posterior samples for the α's ordered by periods (or frequencies).
  - The α's are shown in terms of the pairs (r_i, ω_i) or (r_i, λ_i); $i = 1, 2, \ldots, 5$.

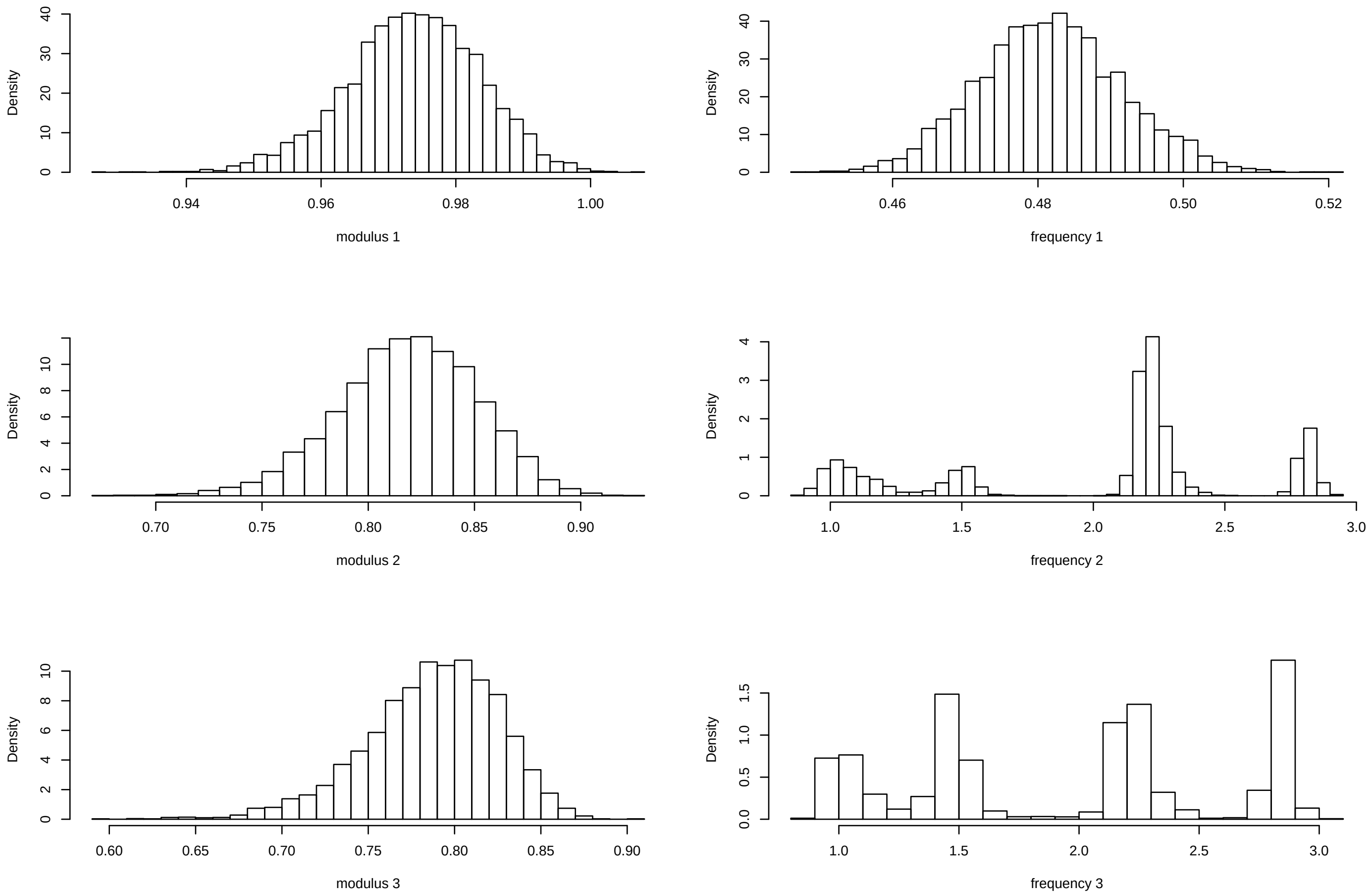
Posterior histograms for $\phi_1 - \phi_6$



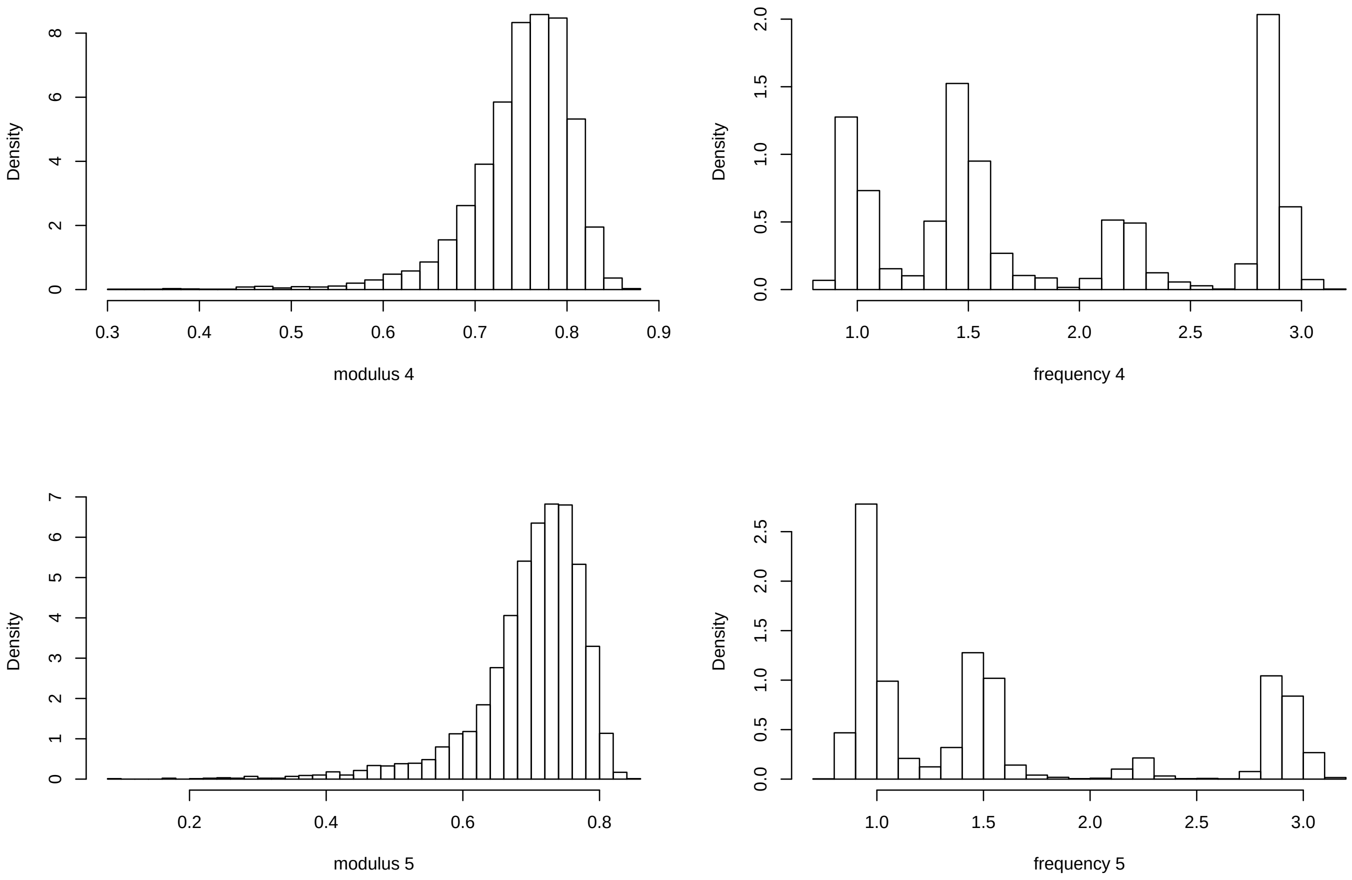
Posterior histograms for $\phi_7 - \phi_{10}$ and σ^2



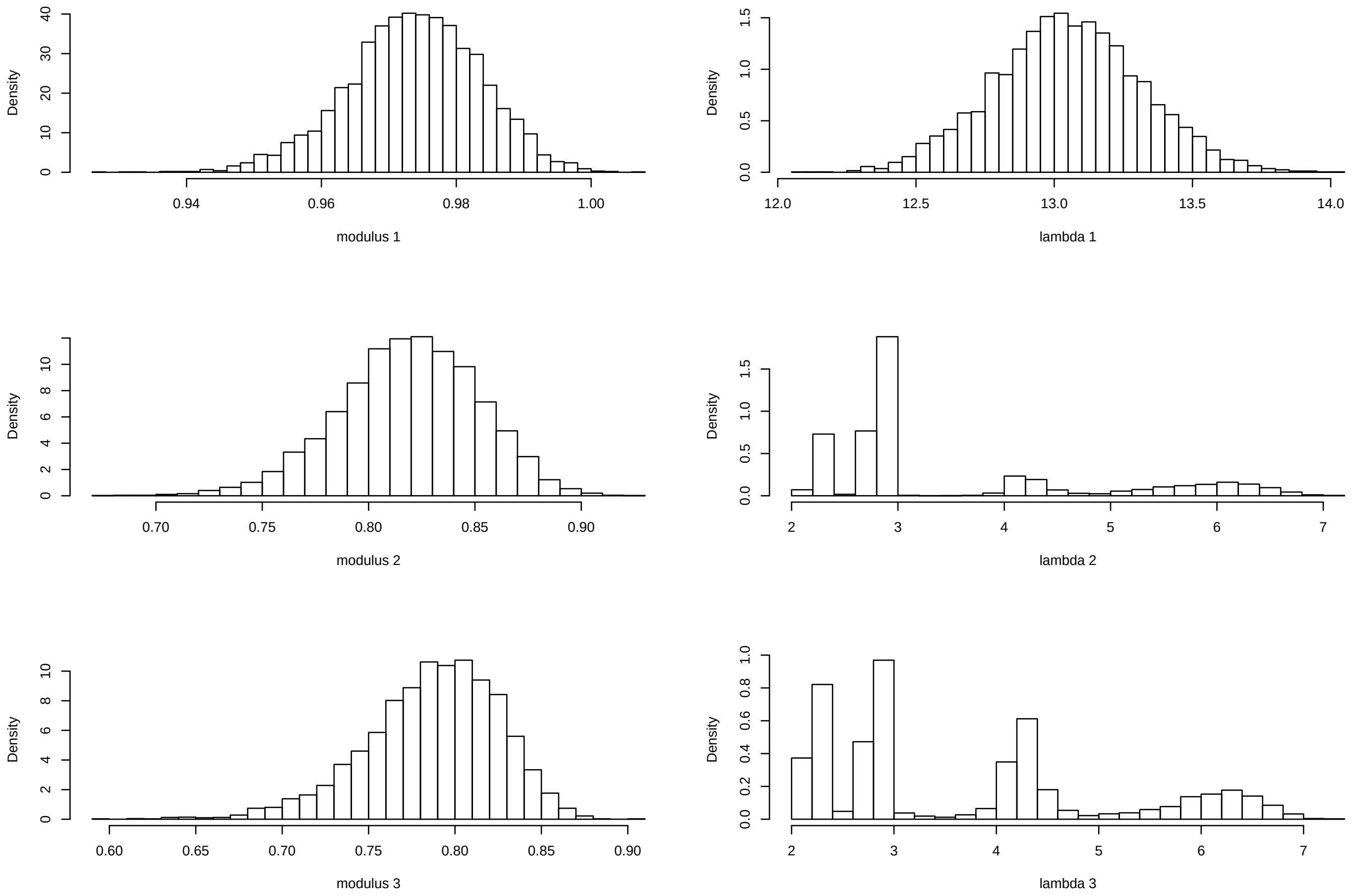
Posterior histograms ordered by modulus of $(r_i, \omega_i), i = 1, 2, 3$



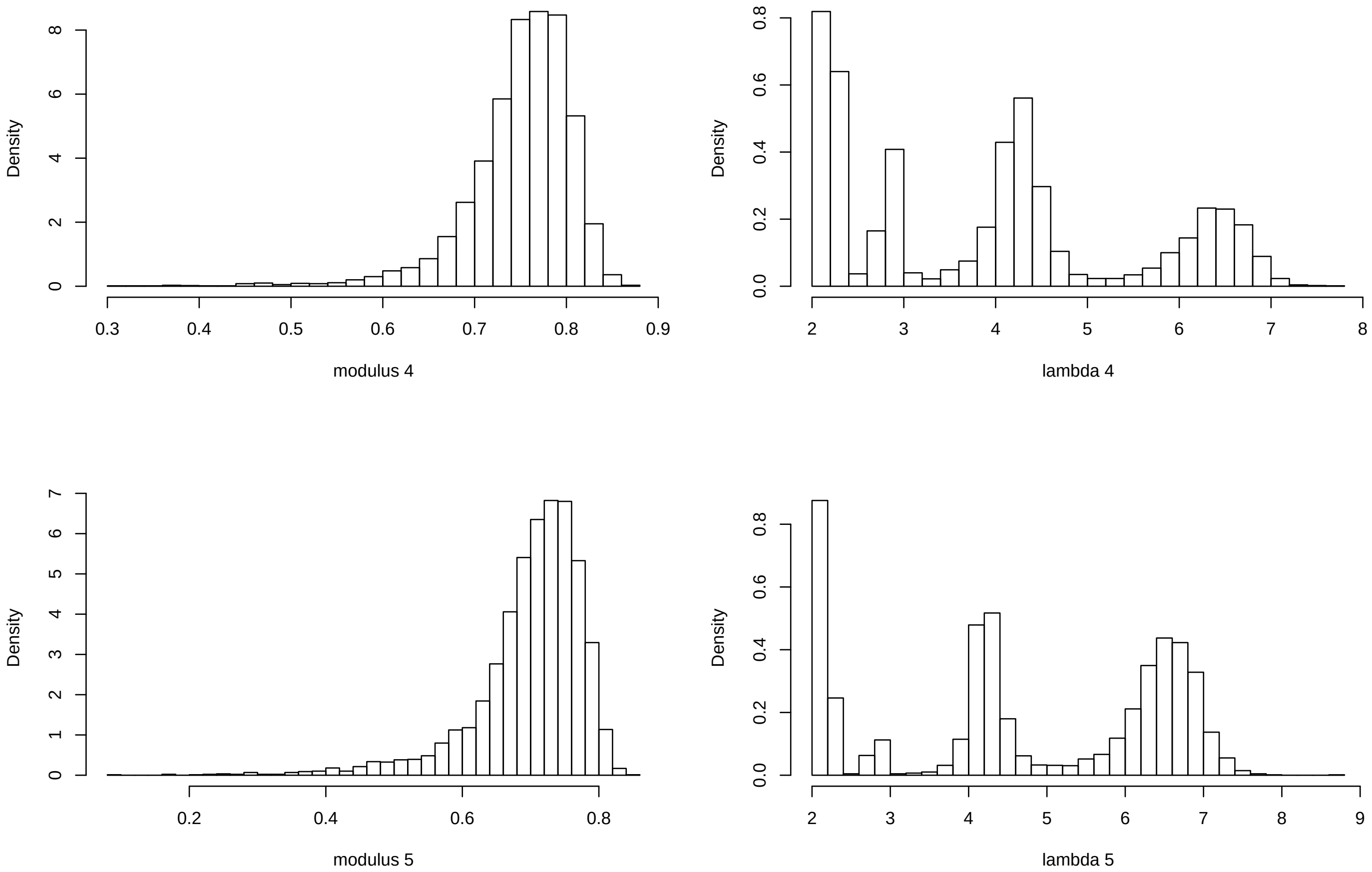
Posterior histograms ordered by modulus of $(r_i, \omega_i), i = 4, 5$



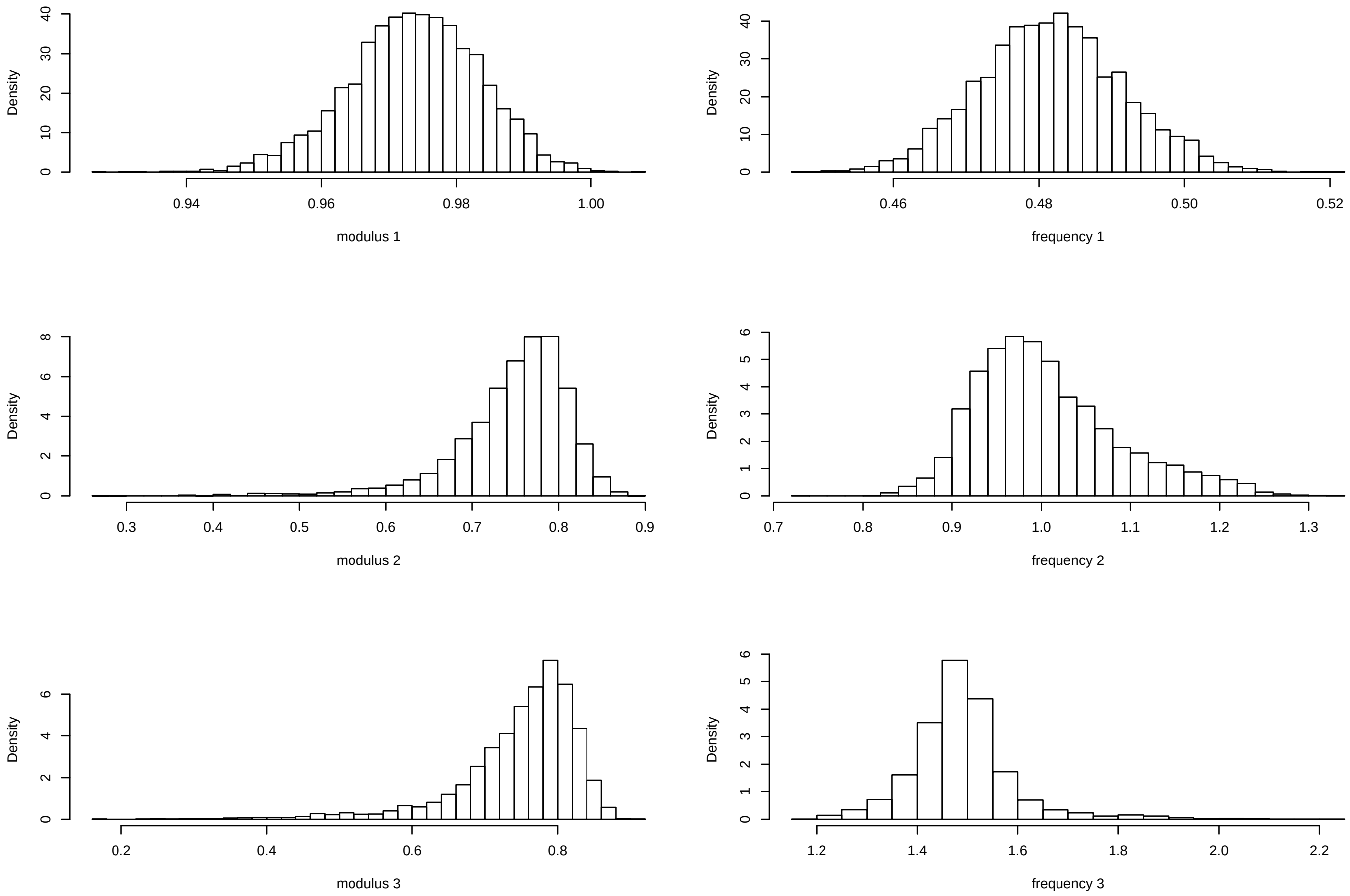
Posterior histograms ordered by modulus of $(r_i, \lambda_i), i = 1, 2, 3$



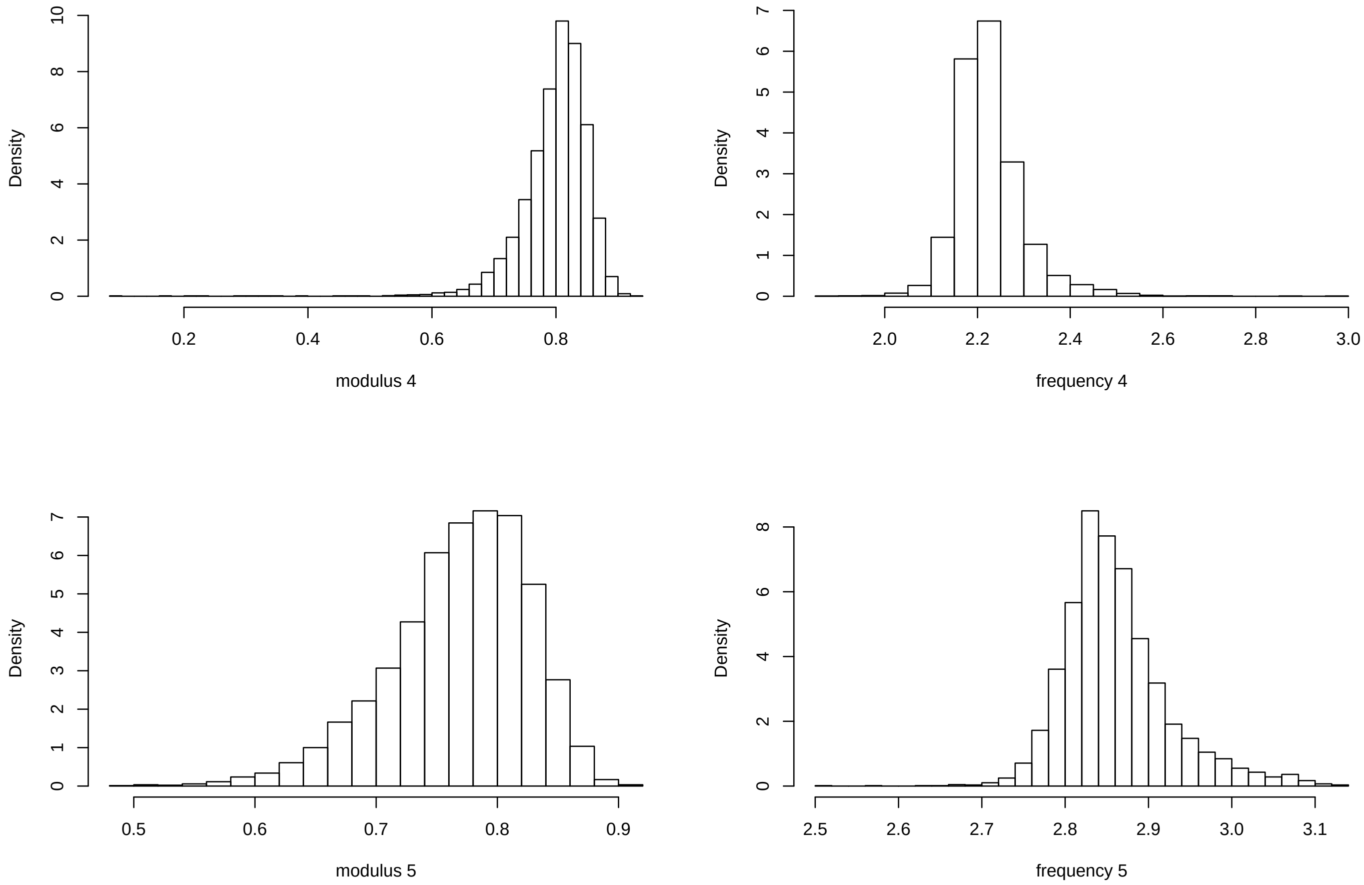
Posterior histograms ordered by modulus of $(r_i, \lambda_i), i = 4, 5$



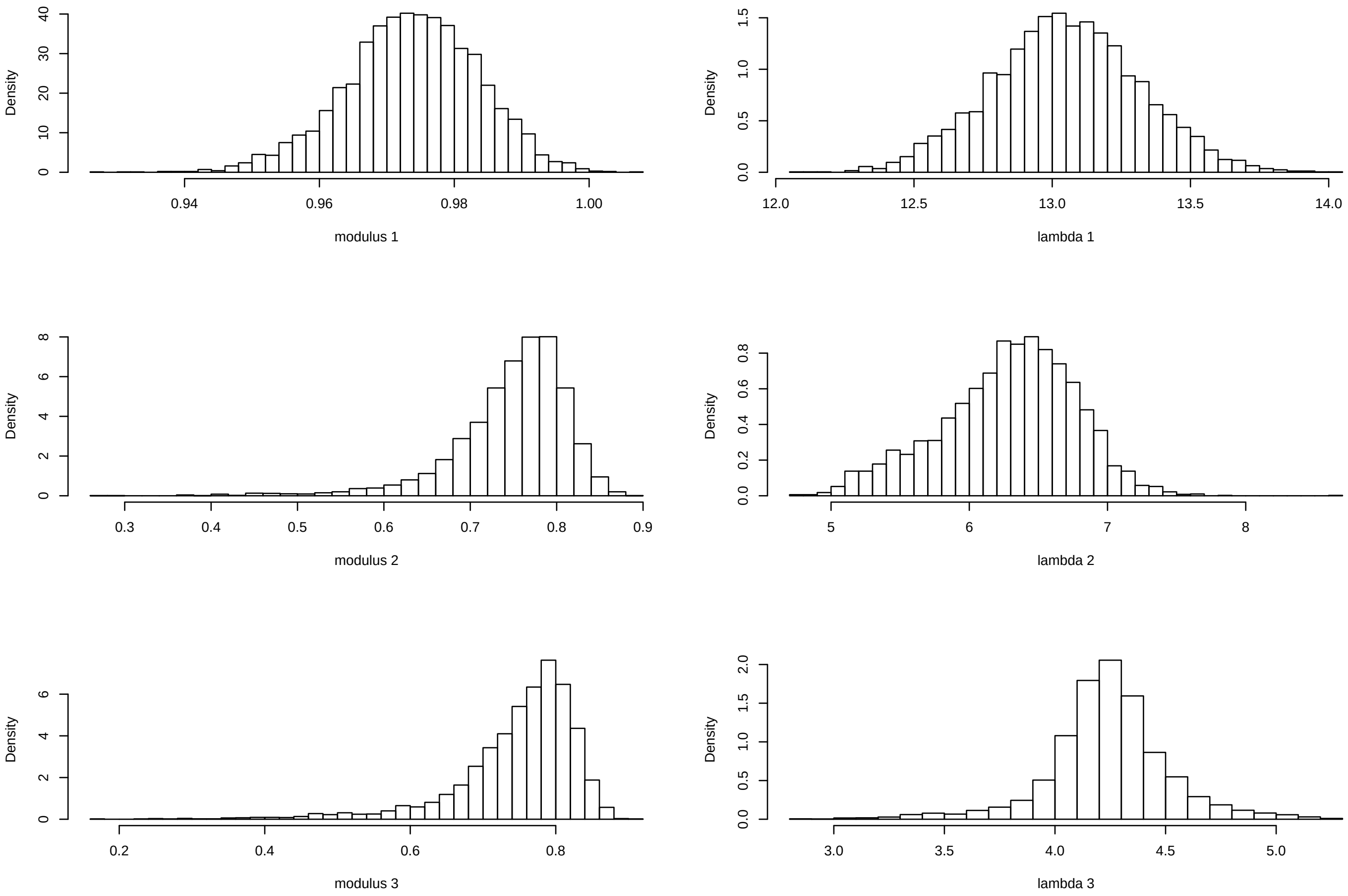
Posterior histograms ordered by wavelength of $(r_i, \omega_i), i = 1, 2, 3$



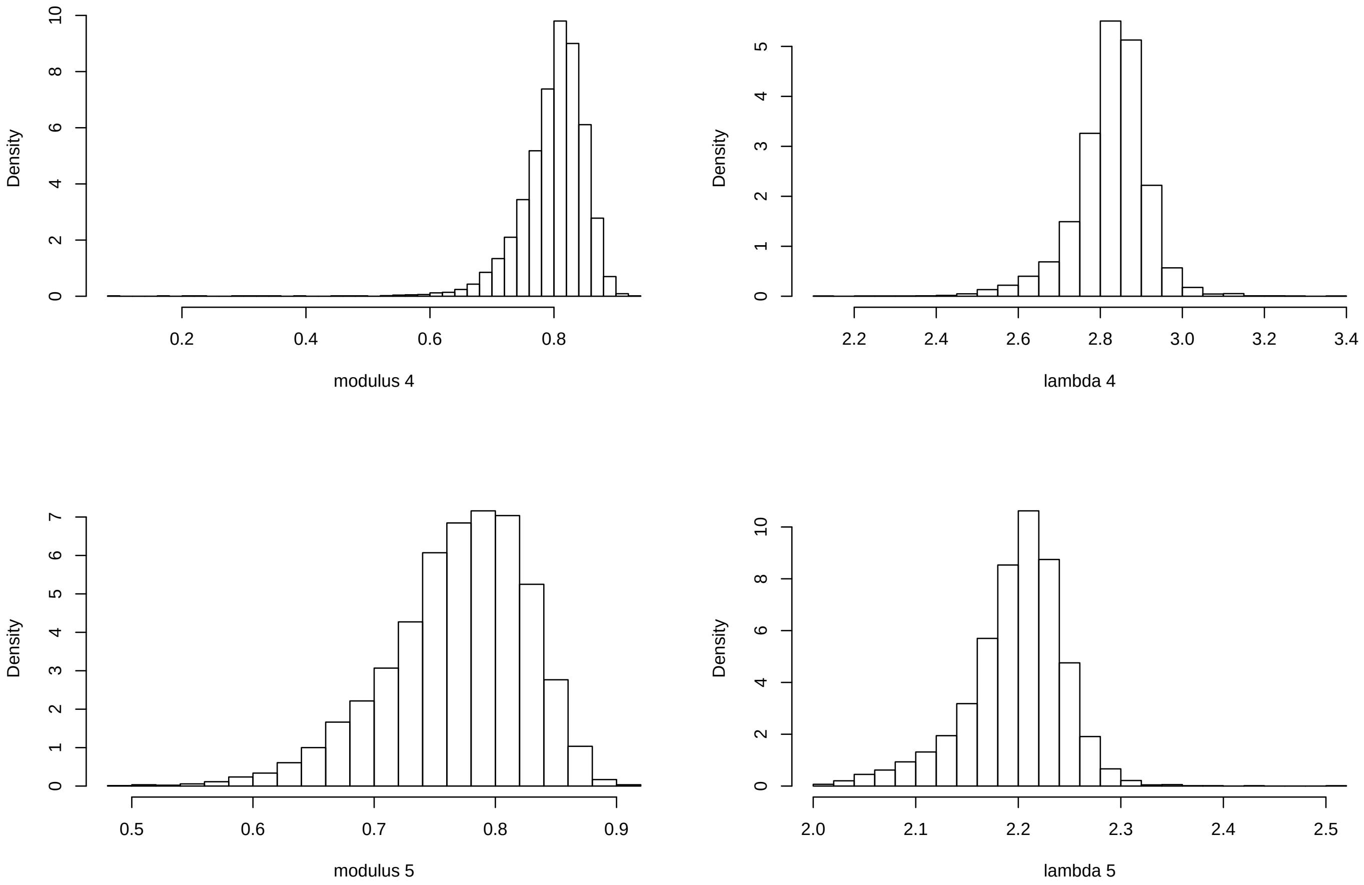
Posterior histograms ordered by wavelength of $(r_i, \omega_i), i = 4, 5$



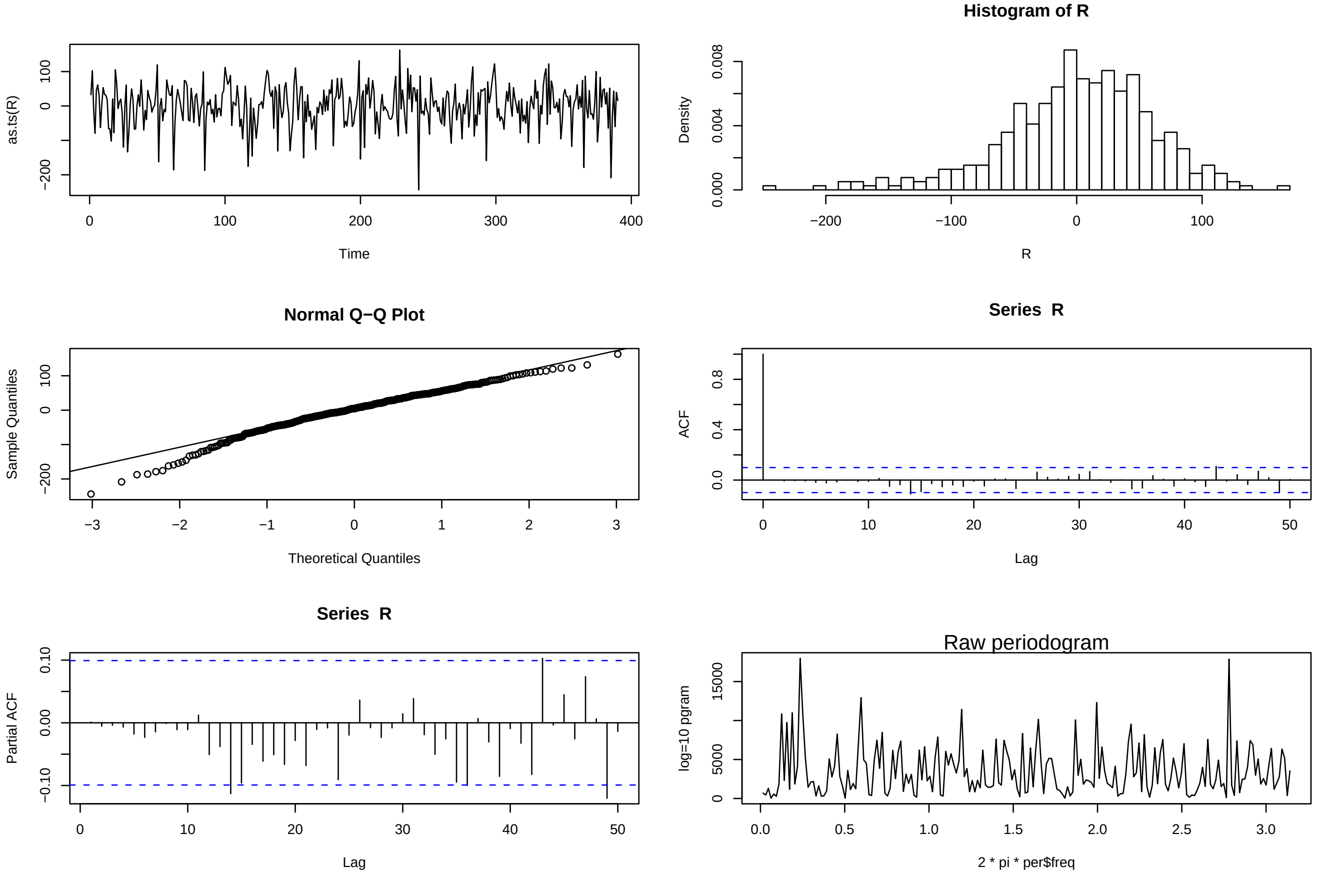
Posterior histograms ordered by wavelength of $(r_i, \lambda_i), i = 1, 2, 3$



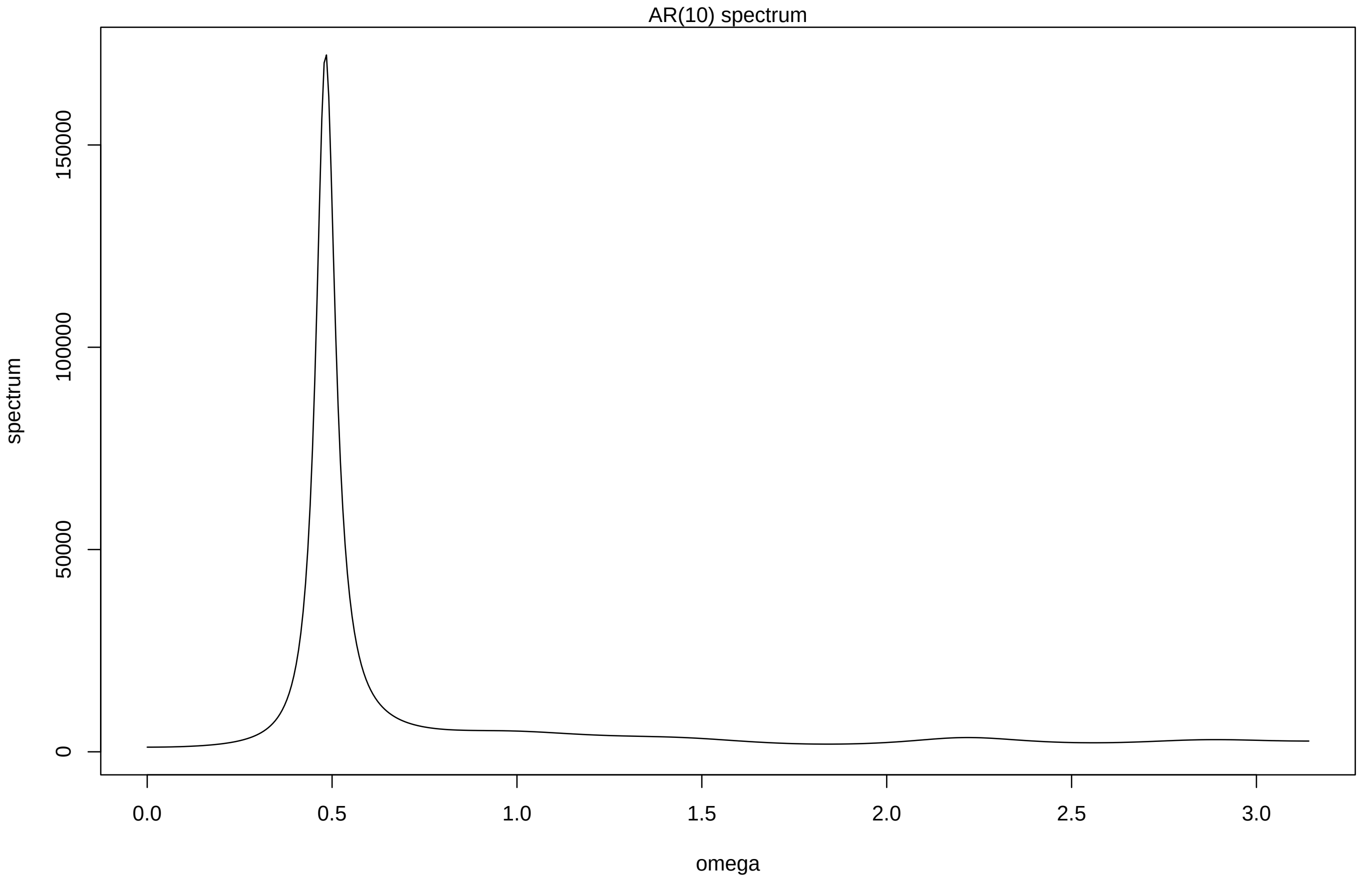
Posterior histograms ordered by wavelength of $(r_i, \omega_i), i = 4, 5$



Graphs based on residuals obtained at the MLE $\hat{\phi}$



AR(10) spectrum computed at the MLE



- Computing the “approximate” test for white noise for the model residuals gives $T = 17138.13$ and a p-value of .839543.
- The p-value is “large” so we don’t have any evidence against the null hypothesis of the residuals following a white noise process.
- Using this Bayesian approach, we make statements about this process following a stationary series or not.
- For our 5000 samples, we can count have many of this samples produce a characteristic reciprocal root with a modulus greater than one.
- The relative frequency of the event “modulus greater than one” gives us an estimate of the posterior

probability of this EEG series comes from "a non-stationary process".

- For these 5000 samples, the posterior probability is 0.026.
- In a similar way, we can compute the posterior probability of having at least one real root under the AR(10) process (0.0032).

Code for Bayesian AR estimation

```
eeg=scan("eeg")

# Building F matrix for AR(10)
n <- length(eeg)
x <- eeg[11:n]
f1 <- eeg[10:(n-1)]; f2 <- eeg[9:(n-2)]
f3 <- eeg[8:(n-3)]; f4 <-  eeg[7:(n-4)]
f5 <- eeg[6:(n-5)]; f6 <-  eeg[5:(n-6)]
f7 <- eeg[4:(n-7)]; f8 <-  eeg[3:(n-8)]
f9 <- eeg[2:(n-9)]; f10 <-eeg[1:(n-10)]
#
Fdes <- cbind(f1,f2,f3,f4,f5,f6,f7,f8,f9,f10)
```

```
#  F^tF mle and R
FF.t<- t(Fdes)%*%Fdes
FF.inv <-solve(t(Fdes)%*%Fdes)
phhat <- FF.inv%*%t(Fdes)%*%x
R <- (x - (Fdes)%*%phhat)
s <- (ssq=sum (R*R))/(n-10)

# Compute Cholesky decomposition
FF.inv <- 0.5*(FF.inv + t(FF.inv))
FF.inv.cd <- t(chol(FF.inv))

# ar 10 function that draws from the
# posterior for (phi,sigma^2)
```

```
ar10 <- function (m)
{
phhatmat <- matrix(phhat,10,m)
v <- rchisq(m,(n-20))
v <-ssq/v
# generation of ph
norbi <- matrix(rnorm(10*m),ncol=m)
normv <- t(sqrt(v)*t(norbi))
ph <- (FF.inv.cd%*%normv) + phhatmat
#result
ph <- t(ph)
return(ph,v)
}
phlist=ar10(5000)
```

```
phsim=phlist$ph
sigma2=phlist$v

# Compute roots for draws of coefficients
coef=cbind(rep(1,5000),-phsim)
roots=1/t(apply(coef,1,polyroot))
mod=Mod(roots)
om=Arg(roots)
#
# Ordering by modulus
lam=2*pi/om
lam[om<=1e-9|om>=pi-1e-9]=0
om[om<=1e-9|om >=pi-1e-9]=0
mod[om<=1e-9|om >=pi-1e-9]=0
```

```
#
lm=matrix(NA,nrow=dim(lam)[1],ncol=dim(lam)[2])
md=matrix(NA,nrow=dim(mod)[1],ncol=dim(mod)[2])
w=matrix(NA,nrow=dim(om)[1],ncol=dim(mod)[2])
#
for(i in 1:5000){ind=order(mod[i,]);
              w[i,]=om[i,ind];
              lm[i,]=lam[i,ind];
              md[i,]=mod[i,ind]}
# Some residual analysis
ts.plot(as.ts(R))
hist(R,nclass=30,prob=T,density=-1)
qqnorm(R)
qqline(R)
```