

# Complement: Finite Mixture Model Diagnostics Using Resampling Methods

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## Abstract

This paper illustrates the application of resampling methods for model diagnostics of fitted finite mixture models. Convenience functions to perform these methods are available in package **flexmix**. The results of the application to an artificial example and the **seizure** data set as described in Grün and Leisch (2010) are reproduced.

*Keywords:* R, finite mixture models, resampling, bootstrap.

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## 1. Artificial data set

In the following a finite mixture model is used as the underlying data generating process which is theoretically not identifiable. We are assuming a finite mixture of linear regression models with two components of equal size where the coverage condition is not fulfilled (Hennig 2000). Hence, intra-component label switching (Grün and Leisch 2010) is possible, i.e., there exist two parameterizations implying the same mixture distribution which differ how the components between the covariate points are combined.

We assume that one measurement per object and a single categorical regressor with two levels are given. The usual design matrix for a model with intercept uses the two covariate points  $\mathbf{x}_1 = (1, 0)'$  and  $\mathbf{x}_2 = (1, 1)'$ . The mixture distribution is given by

$$H(y|\mathbf{x}, \Theta) = \frac{1}{2}N(\mu_1, 0.1) + \frac{1}{2}N(\mu_2, 0.1),$$

where  $\mu_k(\mathbf{x}) = \mathbf{x}'\boldsymbol{\alpha}_k$  and  $N(\mu, \sigma^2)$  is the normal distribution.

Now let  $\mu_1(\mathbf{x}_1) = 1$ ,  $\mu_2(\mathbf{x}_1) = 2$ ,  $\mu_1(\mathbf{x}_2) = -1$  and  $\mu_2(\mathbf{x}_2) = 4$ . As Gaussian mixture distributions are generically identifiable the means, variances and component weights are uniquely determined in each covariate point given the mixture distribution. However, as the coverage condition is not fulfilled, the two possible solutions for  $\boldsymbol{\alpha}$  are:

**Solution 1:**  $\boldsymbol{\alpha}_1^{(1)} = (2, -2)'$ ,  $\boldsymbol{\alpha}_2^{(1)} = (1, -2)'$ ,

**Solution 2:**  $\boldsymbol{\alpha}_1^{(2)} = (2, -3)'$ ,  $\boldsymbol{\alpha}_2^{(2)} = (1, -3)'$ .

We specify this artificial mixture distribution using `FLXdlist()`. `FLXdlist()` returns an unfitted finite mixture of class "FLXdlist". The class of fitted finite mixture models "flexmix" extends class "FLXdlist". Each component follows a normal distribution. The parameters specified

in a named list therefore consist of the regression coefficients and the standard deviation. Function `FLXdlist()` has an argument `formula` for specifying the regression in each of the components, an argument `k` for the component weights and `components` for the parameters of each of the components.

```
> library("flexmix")
> Component_1 <- list(Model_1 = list(coef = c(1, -2), sigma = sqrt(0.1)))
> Component_2 <- list(Model_1 = list(coef = c(2, 2), sigma = sqrt(0.1)))
> ArtEx.mix <- FLXdlist(y ~ x, k = rep(0.5, 2),
+                       components = list(Component_1, Component_2))
```

We draw a balanced sample with 50 observations in each covariate point from the mixture model using `rflexmix()` after defining the data points for the covariates. `rflexmix()` can either have an unfitted or a fitted finite mixture as input. For unfitted mixtures data has to be provided using the `newdata` argument. For already fitted mixtures data can be optionally provided, otherwise the data used for fitting the mixture is used.

```
> ArtEx.data <- data.frame(x = rep(0:1, each = 100/2))
> set.seed(123)
> ArtEx.sim <- rflexmix(ArtEx.mix, newdata = ArtEx.data)
> ArtEx.data$y <- ArtEx.sim$y[[1]]
> ArtEx.data$class <- ArtEx.sim$class
```

In Figure~1 the sample is plotted together with the two solutions for combining  $x_1$  and  $x_2$ , i.e., this illustrates intra-component label switching.

We fit a finite mixture to the sample using `stepFlexmix()`.

```
> set.seed(123)
> ArtEx.fit <- stepFlexmix(y ~ x, data = ArtEx.data, k = 2, nrep = 5,
+                          control = list(iter = 1000, tol = 1e-8, verbose = 0))
```

```
2 : * * * * *
```

The fitted mixture can be inspected using `summary()` and `parameters()`.

```
> summary(ArtEx.fit)
```

Call:

```
stepFlexmix(y ~ x, data = ArtEx.data, control = list(iter = 1000,
  tol = 1e-08, verbose = 0), k = 2, nrep = 5)
```

	prior	size	post>0	ratio
Comp.1	0.56	55	77	0.714
Comp.2	0.44	45	65	0.692

```
'log Lik.' -82.52413 (df=7)
AIC: 179.0483    BIC: 197.2845
```

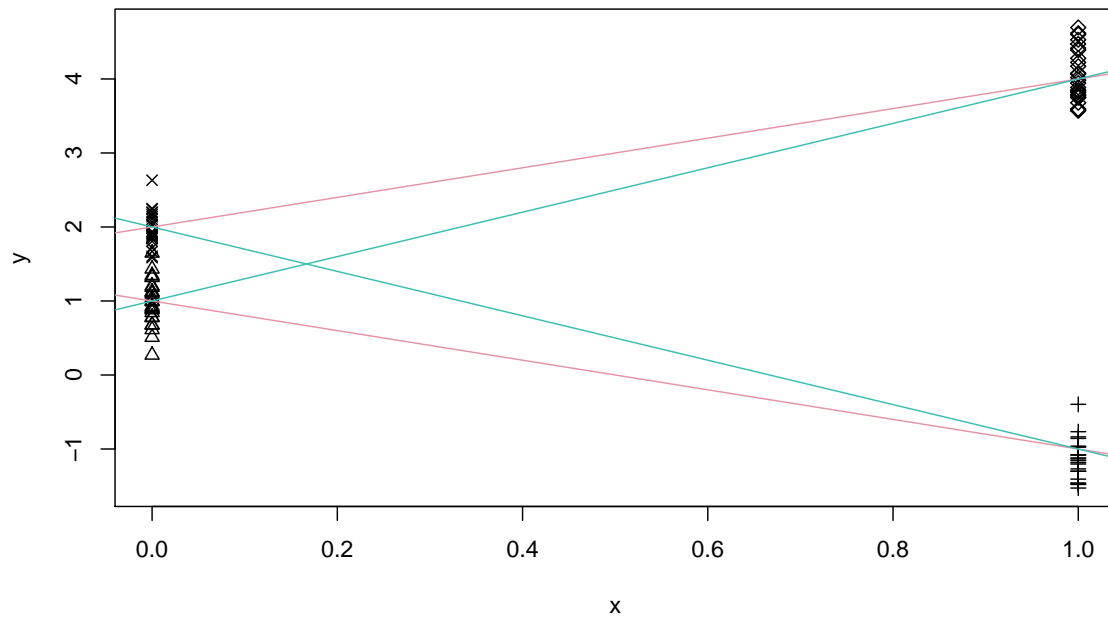


Figure 1: Balanced sample from the artificial example with the two theoretical solutions.

```
> parameters(ArtEx.fit)
```

	Comp.1	Comp.2
coef.(Intercept)	1.9130903	0.9269647
coef.x	2.1270909	-2.0597489
sigma	0.3167696	0.2738558

Obviously the fitted mixture parameters correspond to the parameterization we used to specify the mixture distribution. Using standard asymptotic theory to analyze the fitted mixture model gives the following estimates for the standard deviations.

```
> ArtEx.refit <- refit(ArtEx.fit)
```

```
> summary(ArtEx.refit)
```

```
$Comp.1
```

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	1.914496	0.072060	26.568	< 2.2e-16 ***
x	2.125685	0.093203	22.807	< 2.2e-16 ***

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
$Comp.2
```

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	0.927075	0.068756	13.484	< 2.2e-16 ***

```

x          -2.059859    0.089780 -22.943 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

The fitted mixture can also be analyzed using resampling techniques. For analyzing the stability of the parameter estimates where the possibility of identifiability problems is also taken into account the parametric bootstrap is used with random initialization. Function `boot()` can be used for empirical or parametric bootstrap (specified by the argument `sim`). The logical argument `initialize_solution` specifies if the initialization is in the original solution or random. By default random initialization is made. The number of bootstrap samples is set by the argument `R`. Please note that the arguments are chosen to correspond to those for function `boot` in package **boot** (Davison and Hinkley 1997).

Only a few number of bootstrap samples are drawn to keep the amount of time needed to run the vignette within reasonable limits. However, for a sensible application of the bootstrap methods at least `R` equal to 100 should be used. If the output for this setting has been saved, it is loaded and used in the further analysis. Please see the appendix for the code for generating the saved R output.

```

> set.seed(123)
> ArtEx.bs <- boot(ArtEx.fit, R = 15, sim = "parametric")
> if ("boot-output.rda" %in% list.files()) load("boot-output.rda")
> ArtEx.bs

```

```

Call:
boot(ArtEx.fit, R = 15, sim = "parametric")

```

Function `boot()` returns an object of class "FLXboot". The default plot compares the bootstrap parameter estimates to the confidence intervals derived using standard asymptotic theory in a parallel coordinate plot (see Figure~2). Clearly two groups of parameter estimates can be distinguished which are about of equal size. One subset of the parameter estimates stays within the confidence intervals induced by standard asymptotic theory, while the second group corresponds to the second solution and clusters around these parameter values.

In the following the DIP-test is applied to check if the parameter estimates follow a unimodal distribution. This is done for the aggregated parameter estimates where unimodality implies that this parameter is not suitable for imposing an ordering constraint which induces a unique labelling. For the separate component analysis which is made after imposing an ordering constraint on the coefficient of  $x$  rejection the null hypothesis of unimodality implies that identifiability problems are present, e.g.~due to intra-component label switching.

```

> require("diptest")
> parameters <- parameters(ArtEx.bs)
> Ordering <- factor(as.vector(apply(matrix(parameters[, "coef.x"],
+                                     nrow = 2), 2, order)))
> Comp1 <- parameters[Ordering == 1,]
> Comp2 <- parameters[Ordering == 2,]
> dip.values.art <- matrix(nrow = ncol(parameters), ncol = 3,

```

```
> print(plot(ArtEx.bs, ordering = "coef.x", col = Colors))
```

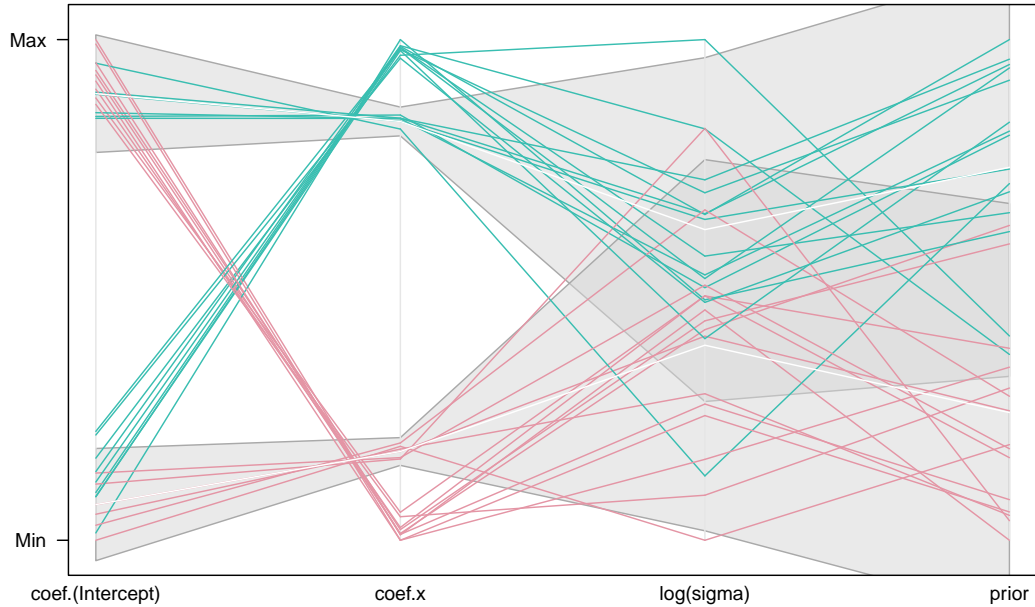


Figure 2: Diagnostic plot of the bootstrap results for the artificial example.

```
+               dimnames=list(colnames(parameters),
+                               c("Aggregated", "Comp 1", "Comp 2")))
> dip.values.art[, "Aggregated"] <- apply(parameters, 2, dip)
> dip.values.art[, "Comp 1"] <- apply(Comp1, 2, dip)
> dip.values.art[, "Comp 2"] <- apply(Comp2, 2, dip)
> dip.values.art
```

	Aggregated	Comp 1	Comp 2
coef.(Intercept)	0.18549534	0.1691587	0.1700720
coef.x	0.19083739	0.1536419	0.1604434
log(sigma)	0.05440133	0.0724579	0.0876057
prior	0.07764922	0.0762874	0.0762874

The critical value for column **Aggregated** is 0.088 and for the columns of the separate components 0.119. The component sizes as well as the standard deviations follow a unimodal distribution for the aggregated data as well as for each of the components. The regression coefficients are multimodal for the aggregate data as well as for each of the components. While from the aggregated case it might be concluded that imposing an ordering constraint on the intercept or the coefficient of  $x$  is suitable, the component-specific analyses reveal that a unique labelling was not achieved.

## 2. Seizure

In Wang, Puterman, Cockburn, and Le (1996) a Poisson mixture regression is fitted to data from a clinical trial where the effect of intravenous gammaglobulin on suppression of epileptic seizures is investigated. The data used were 140 observations from one treated patient, where treatment started on the 28<sup>th</sup> day. In the regression model three independent variables were included: treatment, trend and interaction treatment-trend. Treatment is a dummy variable indicating if the treatment period has already started. Furthermore, the number of parental observation hours per day were available and it is assumed that the number of epileptic seizures per observation hour follows a Poisson mixture distribution. The number of epileptic seizures per parental observation hour for each day are plotted in Figure~3. The fitted mixture distribution consists of two components which can be interpreted as representing 'good' and 'bad' days of the patients.

The mixture model can be formulated by

$$H(y|\mathbf{x}, \Theta) = \pi_1 P(\lambda_1) + \pi_2 P(\lambda_2),$$

where  $\lambda_k = e^{\mathbf{x}'\alpha_k}$  for  $k = 1, 2$  and  $P(\lambda)$  is the Poisson distribution.

The data is loaded and the mixture fitted with two components.

```
> data("seizure", package = "flexmix")
> model <- FLXMRglm(family = "poisson", offset = log(seizure$Hours))
> control <- list(iter = 1000, tol = 1e-10, verbose = 0)
> set.seed(123)
> seizMix <- stepFlexmix(Seizures ~ Treatment*log(Day),
+                        data = seizure, k = 2, nrep = 5,
+                        model = model, control = control)
```

```
2 : * * * * *
```

The fitted regression lines for each of the two components are shown in Figure~3.

The parametric bootstrap with random initialization is used to investigate identifiability problems and parameter stability. The diagnostic plot is given in Figure~2. The coloring is according to an ordering constraint on the intercept. Clearly the parameter estimates corresponding to the solution where the bad days from the base period are combined with the good days from the treatment period and vice versa for the good days of the base period can be distinguished and indicate the slight identifiability problems of the fitted mixture.

```
> parameters <- parameters(seizMix.bs)
> Ordering <- factor(as.vector(apply(matrix(parameters[, "coef.(Intercept)"],
+                                         nrow = 2), 2, order)))
> Comp1 <- parameters[Ordering == 1,]
> Comp2 <- parameters[Ordering == 2,]
```

For applying the DIP test also an ordering constraint on the intercept is used. The critical value for column **Aggregated** is 0.088 and for the columns of the separate components 0.119.

```

> par(mar = c(5, 4, 2, 0) + 0.1)
> plot(Seizures/Hours~Day, data=seizure, pch = as.integer(seizure$Treatment))
> abline(v=27.5, lty=2, col="grey")
> matplot(seizure$Day, fitted(seizMix)/seizure$Hours, type="l",
+         add=TRUE, col=1, lty = 1, lwd = 2)

```

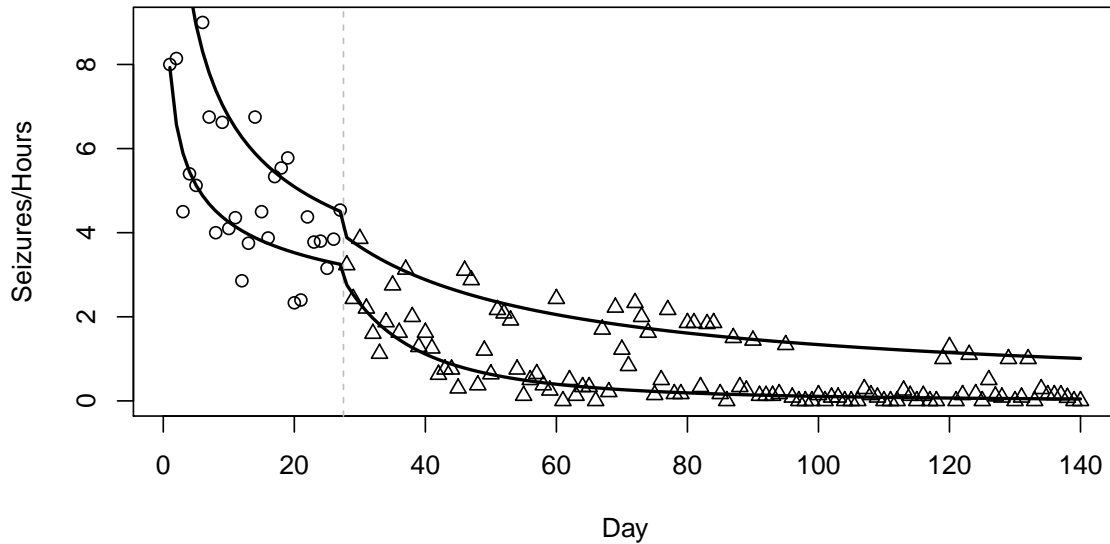


Figure 3: Seizure data with the fitted values for the Wang *et al.* model. The plotting character for the observed values in the base period is a circle and for those in the treatment period a triangle.

```

> dip.values.art <- matrix(nrow = ncol(parameters), ncol = 3,
+                          dimnames=list(colnames(parameters),
+                          c("Aggregated", "Comp 1", "Comp 2")))
> dip.values.art[, "Aggregated"] <- apply(parameters, 2, dip)
> dip.values.art[, "Comp 1"] <- apply(Comp1, 2, dip)
> dip.values.art[, "Comp 2"] <- apply(Comp2, 2, dip)
> dip.values.art

```

	Aggregated	Comp 1	Comp 2
coef.(Intercept)	0.11424627	0.08251065	0.06239055
coef.TreatmentYes	0.14724776	0.11290550	0.08763688
coef.log(Day)	0.08771107	0.07954399	0.04785066
coef.TreatmentYes:log(Day)	0.16430740	0.08548046	0.08940126
prior	0.15660112	0.08275558	0.08275558

For the aggregate results the hypothesis of unimodality cannot be rejected for the trend. For the component-specific analyses unimodality cannot be rejected only for the intercept

```

> set.seed(123)
> seizMix.bs <- boot(seizMix, R = 15, sim = "parametric")
> if ("boot-output.rda" %in% list.files()) load("boot-output.rda")
> print(plot(seizMix.bs, ordering = "coef.(Intercept)", col = Colors))

```

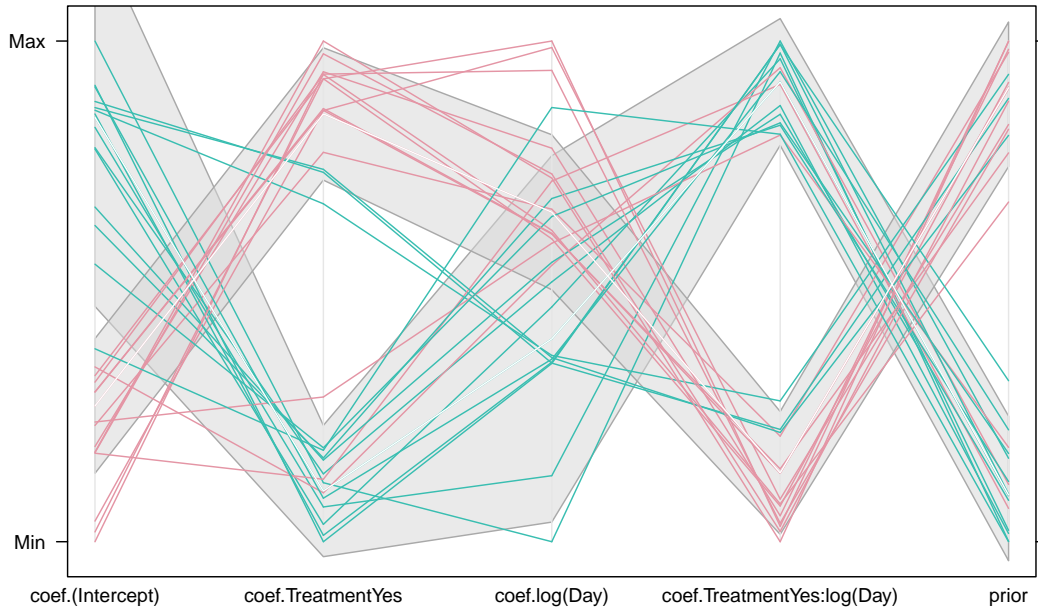


Figure 4: Diagnostic plot of the bootstrap results for the `seizure` data.

(where the ordering condition was imposed on) and again the trend. For all other parameter estimates unimodality is rejected which indicates that the ordering constraint was able to impose a unique labelling only for the own parameter and not for the other parameters. This suggests identifiability problems.

## A. Generation of saved R output

```

> set.seed(123)
> ArtEx.bs <- boot(ArtEx.fit, R = 200, sim = "parametric")
> set.seed(123)
> seizMix.bs <- boot(seizMix, R = 200, sim = "parametric")
> save(ArtEx.bs, seizMix.bs, file = "boot-output.rda")

```

## References

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