The data set "betablockers" is loaded from the package "flexmix".

```r
> library(flexmix)
> data(betablocker)
> betablocker$Treatment <- as.factor(betablocker$Treatment)
```

First a simple logit model is fitted with the only covariate "Treatment".

```r
> GlmT <- glm(cbind(Deaths, Total - Deaths) ~ Treatment, family = "binomial",
+           data = betablocker)
> summary(GlmT)
```

Call:
`glm(formula = cbind(Deaths, Total - Deaths) ~ Treatment, family = "binomial",
       data = betablocker)`

Deviance Residuals:
```
  Min 1Q Median 3Q Max
-5.316 -1.492 -0.134 1.707 5.856
```

Coefficients:

| Estimate | Std. Error | z value | Pr(>|z|) |
|----------|------------|---------|----------|
| (Intercept) | -2.1971 | 0.0336 | -65.42 | < 2e-16 *** |
| TreatmentTreated | -0.2574 | 0.0494 | -5.21 | 1.9e-07 *** |

---

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 332.99 on 43 degrees of freedom
Residual deviance: 305.76 on 42 degrees of freedom
AIC: 527.2

Number of Fisher Scoring iterations: 4

Now the logit model is extended by the factor "Center" which has 22 different values. The deviance reduces from 305.76 with 42 degrees of freedom to 23.62 with 21 degrees of freedom.
> GlmTC <- glm(cbind(Deaths, Total - Deaths) ~ Treatment + as.factor(Center),
+     family = "binomial", data = betablocker)
> summary(GlmTC)

Call:
  glm(formula = cbind(Deaths, Total - Deaths) ~ Treatment + as.factor(Center),
     family = "binomial", data = betablocker)

Deviance Residuals:
     Min       1Q   Median       3Q      Max
-1.828   -0.618    0.004   0.535   1.921

Coefficients:
                                    Estimate Std. Error   z value Pr(>|z|)
(Intercept)                         -2.3493    0.4260   -5.52  3.5e-08 ***
TreatmentTreated                    -0.2610    0.0499   -5.23  1.7e-07 ***
as.factor(Center)2                  0.1739    0.4832    0.36   0.719
as.factor(Center)3                  0.2428    0.5004    0.49   0.628
as.factor(Center)4                 -0.0391    0.4309   -0.09   0.928
as.factor(Center)5                 -0.0217    0.4480   -0.05   0.961
as.factor(Center)6                  0.1685    0.5395    0.31   0.755
as.factor(Center)7                  0.5966    0.4308   1.38   0.166
as.factor(Center)8                  0.2715    0.4373    0.62   0.535
as.factor(Center)9                  0.3888    0.4462    0.87   0.384
as.factor(Center)10                 0.0958    0.4293    0.22   0.823
as.factor(Center)11                 0.0520    0.4363    0.12   0.905
as.factor(Center)12                 0.9153    0.4406    2.08   0.038 *
as.factor(Center)13                 0.6357    0.4720   -1.35   0.178
as.factor(Center)14                -0.3065    0.4375   -0.70   0.484
as.factor(Center)15                 1.0016    0.4505    2.22   0.026 *
as.factor(Center)16                 0.8799    0.4449    1.98   0.048 *
as.factor(Center)17                 0.3997    0.4573    0.87   0.382
as.factor(Center)18                -0.5635    0.5059   -1.11   0.265
as.factor(Center)19                -1.0144    0.5436   -1.87   0.062 .
as.factor(Center)20                 0.8759    0.4447    1.97   0.049 *
as.factor(Center)21                 0.1966    0.4436    0.44   0.658
as.factor(Center)22                -0.5812    0.4451   -1.31   0.192
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 332.993  on 43 degrees of freedom
    Residual deviance: 23.621  on 21 degrees of freedom
    AIC: 287.1

Number of Fisher Scoring iterations: 4

In the following two mixed models are fitted with Gauss–Hermite–Quadrature, so "glmmML" is needed.
> library(glmmML)

First the random intercept model with 4 quadrature points is fitted.

> MixedGH4 <- glmmML(cbind(Deaths, Total - Deaths) ~ Treatment, cluster=Center,
+                   method = c("ghq"), n.points = 4, boot = 0, data=betablocker)
> summary(MixedGH4)

Call: glmmML(formula = cbind(Deaths, Total - Deaths) ~ Treatment, data = betablocker,

coef se(coef)    z  Pr(>|z|)
(Intercept)     -2.196 0.1131 -19.42 0.0e+00
TreatmentTreated -0.261 0.0499 -5.23 1.7e-07

Scale parameter in mixing distribution: 0.487 gaussian
Std. Error: 0.084

LR p-value for H_0: sigma = 0: 9.28e-47

Residual deviance: 101 on 41 degrees of freedom AIC: 107

Now we use 20 quadrature points but there is no big difference in coefficients.

> MixedGH20 <- glmmML(cbind(Deaths, Total - Deaths) ~ Treatment, cluster=Center,
+                      method = c("ghq"), n.points = 20, boot = 0, data=betablocker)
> summary(MixedGH20)

Call: glmmML(formula = cbind(Deaths, Total - Deaths) ~ Treatment, data = betablocker,

coef se(coef)    z  Pr(>|z|)
(Intercept)     -2.196 0.1131 -19.42 0.0e+00
TreatmentTreated -0.261 0.0499 -5.23 1.7e-07

Scale parameter in mixing distribution: 0.487 gaussian
Std. Error: 0.0841

LR p-value for H_0: sigma = 0: 9.28e-47

Residual deviance: 101 on 41 degrees of freedom AIC: 107

> set.seed(5)

Finally we fit the discrete mixture models for which the function "stepFlexmix" is used. Here we use three components defined by option "k=3".

> detach(package:glmmML)

> MixFix3 <- stepFlexmix(cbind(Deaths, Total - Deaths) ~ 1 | Center, 
+                        model = FLXMRglmfix(family = "binomial", fixed = ~ Treatment), k = 3, nrep = 5, 
+                        data = betablocker)
Typing the name of the fitted model yields the sizes of the three clusters.

```r
> MixFix3
```

Call:
`stepFlexmix(cbind(Deaths, Total - Deaths) ~ 1 | Center, model = FLXMRglmfix(family = "binomial", fixed = ~Treatment), data = betablocker, k = 3, nrep = 5)`

Cluster sizes:
1  2  3
24 10 10
convergence after 12 iterations

The coefficients are printed by the command "parameters()".

```r
> parameters(MixFix3)
```

```
Comp.1 Comp.2 Comp.3
coef.TreatmentTreated -0.258 -0.258 -0.258
coef.(Intercept)      -2.250 -2.834 -1.610
```

The command "summary()" returns for example the estimated component weights and the BIC. The coefficients with standard errors and p-values can be found by "summary(refit())".

```r
> library(flexmix)
> summary(MixFix3)
```

Call:
`stepFlexmix(cbind(Deaths, Total - Deaths) ~ 1 | Center, model = FLXMRglmfix(family = "binomial", fixed = ~Treatment), data = betablocker, k = 3, nrep = 5)`

```
prior size post>0 ratio
Comp.1 0.512 24 32 0.750
Comp.2 0.239 10 20 0.500
Comp.3 0.249 10 22 0.455

'log Lik.' -159 (df=6)
AIC: 331   BIC: 341
```

```r
> summary(refit(MixFix3))
```

```
$Comp.1

             Estimate Std. Error    z value  Pr(>|z|) 
TreatmentTreated  -0.2582 0.0499097 -5.17 2.33e-07 ***
(Intercept)        -2.2502 0.0404917 -55.52 < 2e-16 ***

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

4
|               | Estimate | Std. Error | z value | Pr(>|z|) |
|---------------|----------|------------|---------|----------|
| TreatmentTreated | -0.2582  | 0.0499     | -5.17   | 2.3e-07  *** |
| (Intercept)    | -2.8337  | 0.0751     | -37.74  | < 2e-16  *** |

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

---

```
set.seed(5)

Finally the discrete mixture model with 4 components is fitted.
```

```r
MixFix4 <- stepFlexmix(cbind(Deaths, Total - Deaths) ~ 1 | Center, model = FLXMRglmfix(family = "binomial", fixed = ~ Treatment), k = 4, nrep = 5, data = betablocker)
```

```
4 : * * * * *
```

```r
MixFix4

Call:
stepFlexmix(cbind(Deaths, Total - Deaths) ~ 1 | Center, model = FLXMRglmfix(family = "binomial", fixed = ~ Treatment), data = betablocker, k = 4, nrep = 5)
```

Cluster sizes:
1 2 3 4
24 2 8 10

convergence after 13 iterations

```r
parameters(MixFix4)

Comp.1  Comp.2  Comp.3  Comp.4
coef.TreatmentTreated -0.258 -0.258 -0.258 -0.258
coef.(Intercept) -2.258 -1.786 -1.440 -2.833
```

```r
summary(MixFix4)

Call:
stepFlexmix(cbind(Deaths, Total - Deaths) ~ 1 | Center, model = FLXMRglmfix(family = "binomial", fixed = ~ Treatment), data = betablocker, k = 4, nrep = 5)

prior size post>0 ratio
Comp.1  0.4820  24   32  0.7500
Comp.2  0.0988  2   26  0.0769
```
### Summary

| Component | Estimate | Std. Error | z value | Pr(>|z|) |
|-----------|----------|------------|---------|----------|
| **Comp.1** | Treatment Treated | -0.2584 | 0.0499 | -5.18 | 2.2e-07 *** |
|           | (Intercept) | -2.2578 | 0.0430 | -52.50 | < 2e-16 *** |
| **Comp.2** | Treatment Treated | -0.2584 | 0.0499 | -5.18 | 2.2e-07 *** |
|           | (Intercept) | -1.7872 | 0.0834 | -21.42 | < 2e-16 *** |
| **Comp.3** | Treatment Treated | -0.2584 | 0.0499 | -5.18 | 2.2e-07 *** |
|           | (Intercept) | -1.4395 | 0.0700 | -20.57 | < 2e-16 *** |
| **Comp.4** | Treatment Treated | -0.2584 | 0.0499 | -5.18 | 2.2e-07 *** |
|           | (Intercept) | -2.8333 | 0.0751 | -37.71 | < 2e-16 *** |

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

AIC: 328  BIC: 342

$log \text{ Lik.}$: -156 (df=8)