

fmm: glm — Finite mixtures of generalized linear regression models[Description](#)[Remarks and examples](#)[Quick start](#)[Stored results](#)[Menu](#)[Methods and formulas](#)[Syntax](#)[Also see](#)

Description

`fmm: glm` fits mixtures of generalized linear regression models; see [\[FMM\] fmm](#) and [\[R\] glm](#) for details.

Quick start

Mixture of two normal distributions of `y`

```
fmm 2: glm y, family(gaussian) link(identity)
```

Mixture of two gamma distributions of `y`

```
fmm 2: glm y, family(gamma)
```

Mixture of two gamma regression models of `y` on `x1` and `x2`

```
fmm 2: glm y x1 x2, family(gamma)
```

Same as above, but with class probabilities depending on `z1` and `z2`

```
fmm 2, lcprob(z1 z2): glm y x1 x2, family(gamma)
```

With robust standard errors

```
fmm 2, vce(robust): glm y x1 x2, family(gamma)
```

Constrain coefficients on `x1` and `x2` to be equal across classes

```
fmm 2, lcinvariant(coef): glm y x1 x2
```

Menu

Statistics > FMM (finite mixture models) > Generalized linear model (GLM)

Syntax

Basic syntax

```
fmm # : glm devar [indepvars] [, options]
```

Full syntax

```
fmm # [if] [in] [weight] [, fmmopts]: glm devar [indepvars] [, options]
```

where # specifies the number of class models.

| <i>options</i> | Description |
|----------------|-------------|
|----------------|-------------|

Model

| | |
|--|---|
| <u>family</u> (<i>familyname</i>) | distribution of <i>devar</i> ; default is family(<i>gaussian</i>) |
| <u>link</u> (<i>linkname</i>) | link function; default varies per family |
| <u>noconstant</u> | suppress the constant term |
| <u>exposure</u> (<i>varname_e</i>) | include $\ln(\text{varname}_e)$ in model with coefficient constrained to 1 |
| <u>offset</u> (<i>varname_o</i>) | include <i>varname_o</i> in model with coefficient constrained to 1 |
| <u>asis</u> | retain perfect predictor variables |

indepvars may contain factor variables; see [U] 11.4.3 **Factor variables**.

devar and *indepvars* may contain time-series operators; see [U] 11.4.4 **Time-series varlists**.

For a detailed description of *options*, see *Options* in [R] **glm**.

| <i>familyname</i> | Description |
|--|--|
| <u>gaussian</u> | Gaussian (normal); the default |
| <u>bernoulli</u> | Bernoulli |
| <u>beta</u> | beta |
| <u>binomial</u> [<i>#</i> <i>varname</i>] | binomial; default number of binomial trials is 1 |
| <u>poisson</u> | Poisson |
| <u>nbinomial</u> [<i>mean</i> <u>constant</u>] | negative binomial; default dispersion is mean |
| <u>exponential</u> | exponential |
| <u>gamma</u> | gamma |
| <u>lognormal</u> | lognormal |
| <u>loglogistic</u> | loglogistic |
| <u>weibull</u> | Weibull |

bernoulli, *beta*, *exponential*, *lognormal*, *loglogistic*, and *weibull* are extensions available with **fmm: glm** that are not available with **glm**.

| <i>linkname</i> | Description |
|-----------------|-----------------------|
| <u>identity</u> | identity |
| <u>log</u> | log |
| <u>logit</u> | logit |
| <u>probit</u> | probit |
| <u>cloglog</u> | complementary log–log |

| <i>fmmopts</i> | Description |
|---|--|
| Model | |
| <code>lcinvariant(<i>pclassname</i>)</code> | specify parameters that are equal across classes; default is <code>lcinvariant(none)</code> |
| <code>lcprob(<i>varlist</i>)</code> | specify independent variables for class probabilities |
| <code>lclabel(<i>name</i>)</code> | name of the categorical latent variable; default is <code>lclabel(Class)</code> |
| <code>lcbase(#)</code> | base latent class |
| <code>constraints(<i>constraints</i>)</code> | apply specified linear constraints |
| SE/Robust | |
| <code>vce(<i>vcetype</i>)</code> | <i>vcetype</i> may be <code>oim</code> , <code>opg</code> , <code>robust</code> , or <code>cluster clustvar</code> |
| Reporting | |
| <code>level(#)</code> | set confidence level; default is <code>level(95)</code> |
| <code>nocnsreport</code> | do not display constraints |
| <code>noheader</code> | do not display header above parameter table |
| <code>nodvheader</code> | do not display dependent variables information in the header |
| <code>notable</code> | do not display parameter table |
| <code>display_options</code> | control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling |
| Maximization | |
| <code>maximize_options</code> | control the maximization process |
| <code>startvalues(<i>svmethod</i>)</code> | method for obtaining starting values; default is <code>startvalues(factor)</code> |
| <code>emopts(<i>maxopts</i>)</code> | control EM algorithm for improved starting values |
| <code>noestimate</code> | do not fit the model; show starting values instead |
| <code>collinear</code> | keep collinear variables |
| <code>coeflegend</code> | display legend instead of statistics |
| <p><i>varlist</i> may contain factor variables; see [U] 11.4.3 Factor variables.</p> <p><code>by</code>, <code>collect</code>, <code>statsby</code>, and <code>svy</code> are allowed; see [U] 11.1.10 Prefix commands.</p> <p><code>vce()</code> and weights are not allowed with the <code>svy</code> prefix; see [SVY] svy.</p> <p><code>fweights</code>, <code>iweights</code>, and <code>pweights</code> are allowed; see [U] 11.1.6 weight.</p> <p><code>collinear</code> and <code>coeflegend</code> do not appear in the dialog box.</p> <p>See [U] 20 Estimation and postestimation commands for more capabilities of estimation commands.</p> <p>For a detailed description of <i>fmmopts</i>, see <i>Options</i> in [FMM] fmm.</p> | |
| <i>pclassname</i> | Description |
| <code>cons</code> | intercepts and cutpoints |
| <code>coef</code> | fixed coefficients |
| <code>errvar</code> | covariances of errors |
| <code>scale</code> | scaling parameters |
| <code>all</code> | all the above |
| <code>none</code> | none of the above; the default |

Remarks and examples

For a general introduction to finite mixture models, see [FMM] **fm intro**. For general information about generalized linear regression, see [R] **glm**. For examples using **fm**, see examples in *Contents*.

If you specify both `family()` and `link()`, not all combinations make sense. You may choose from the following combinations:

| | identity | log | logit | probit | cloglog |
|-------------------|----------|-----|-------|--------|---------|
| Gaussian | D | x | | | |
| Bernoulli | | | D | x | x |
| beta | | | D | x | x |
| binomial | | | D | x | x |
| Poisson | | D | | | |
| negative binomial | | D | | | |
| exponential | | D | | | |
| gamma | | D | | | |
| lognormal | | D | | | |
| loglogistic | | D | | | |
| Weibull | | D | | | |

D denotes the default.

Stored results

See *Stored results* in [FMM] **fm**.

Methods and formulas

See *Methods and formulas* in [FMM] **fm**.

Also see

[FMM] **fm** — Finite mixture models using the **fm** prefix

[FMM] **fm intro** — Introduction to finite mixture models

[FMM] **fm postestimation** — Postestimation tools for **fm**

[FMM] **Glossary**

[R] **glm** — Generalized linear models

[SEM] **gsem** — Generalized structural equation model estimation command

[SVY] **svy estimation** — Estimation commands for survey data

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