

# Dealing with `quasi-` models in R

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Computing “quasi-AIC” (QAIC), in R is a minor pain, because the R Core team (or at least the ones who wrote `glm`, `glmmPQL`, etc.) are purists and don’t believe that quasi- models should report a likelihood. As far as I know, there are three R packages that compute/handle QAIC: `bbmle`, `AICcmodavg` and `MuMIn`.

The basic problem is that quasi- model fits with `glm` return an `NA` for the log-likelihood, while the dispersion parameter ( $\hat{c}$ ,  $\phi$ , whatever you want to call it) is only reported for quasi- models. Various ways to get around this are:

- fit the model twice, once with a regular likelihood model (`family=binomial`, `poisson`, etc.) and once with the `quasi-` variant — extract the log-likelihood from the former and the dispersion parameter from the latter
- only fit the regular model; extract the overdispersion parameter manually with

```
dfun <- function(object) {  
  with(object, sum((weights * residuals^2)[weights > 0])/df.residual)  
}
```

- use the fact that quasi- fits still contain a deviance, even if they set the log-likelihood to `NA`. The deviance is twice the negative log-likelihood (it’s offset by some constant which I haven’t figured out yet, but it should still work fine for model comparisons)

The whole problem is worse for `MASS::glmmPQL`, where (1) the authors have gone to greater efforts to make sure that the (quasi-)deviance is no longer preserved anywhere in the fitted model, and (2) they may have done it for good reason — it is not clear whether the number that would get left in the ‘deviance’ slot at the end of `glmmPQL`’s alternating `lme` and `glm` fits is even meaningful to the extent that regular QAICs are. (For discussion of a similar situation, see the `WARNING` section of `?gamm` in the `mgcv` package.)

Example: use the values from one of the examples in `?glm`:

```
## Dobson (1990) Page 93: Randomized Controlled Trial :
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
```

Fit Poisson and quasi-Poisson models with all combinations of predictors:

```
glmOT.D93 <- glm(counts ~ outcome + treatment, family=poisson)
glmO.D93 <- update(glmOT.D93, . ~ . - treatment)
glmT.D93 <- update(glmOT.D93, . ~ . - outcome)
glmX.D93 <- update(glmT.D93, . ~ . - treatment)
glmQOT.D93 <- update(glmOT.D93, family=quasipoisson)
glmQO.D93 <- update(glmO.D93, family=quasipoisson)
glmQT.D93 <- update(glmT.D93, family=quasipoisson)
glmQX.D93 <- update(glmX.D93, family=quasipoisson)
```

Extract log-likelihoods:

```
(sum(dpois(counts,
           lambda=exp(predict(glmOT.D93)),log=TRUE))) ## by hand
## [1] -23.38066
(logLik(glmOT.D93)) ## from Poisson fit
## 'log Lik.' -23.38066 (df=5)
```

The deviance (`deviance(glmOT.D93)`)=5.129 is not the same as  $-2L$  ( $-2*\log\text{Lik}(\text{glmOT.D93})=46.761$ ), but the calculated differences in deviance are consistent, and are also extractable from the quasi- fit even though the log-likelihood is NA:

```
(-2*(logLik(glmT.D93)-logLik(glmOT.D93))) ## Poisson fit
## 'log Lik.' 5.452305 (df=3)
(deviance(glmT.D93)-deviance(glmOT.D93)) ## Poisson fit
## [1] 5.452305
(deviance(glmQT.D93)-deviance(glmQOT.D93)) ## quasi-fit
## [1] 5.452305
```

Compare hand-computed dispersion (in two ways) with the dispersion computed by `summary.glm()` on a quasi- fit:

```

(dfun(glmOT.D93))
## [1] 1.2933

(sum(residuals(glmOT.D93,"pearson")^2)/glmOT.D93$df.residual)
## [1] 1.2933

(summary(glmOT.D93)$dispersion)
## [1] 1

(summary(glmQOT.D93)$dispersion)
## [1] 1.2933

```

## Examples

bbmle

```

library(bbmle)
(qAIC(glmOT.D93,dispersion=dfun(glmOT.D93)))
## [1] 46.15658

(qAICc(glmOT.D93,dispersion=dfun(glmOT.D93),nobs=length(counts)))
## [1] 90.15658

ICtab(glmOT.D93,glmT.D93,glmO.D93,glmX.D93,
       dispersion=dfun(glmOT.D93),type="qAIC")
##           dqAIC df
## glmO.D93  0.0  3
## glmX.D93  0.2  1
## glmOT.D93 4.0  5
## glmT.D93  4.2  3

ICtab(glmOT.D93,glmT.D93,glmO.D93,glmX.D93,
       dispersion=dfun(glmOT.D93),
       nobs=length(counts),type="qAICc")
##           dqAICc df
## glmX.D93    0.0  1
## glmO.D93    7.8  3
## glmT.D93   12.0  3
## glmOT.D93  43.8  5

detach("package:bbmle")

```

## AICcmodavg

```
if (require("AICcmodavg")) {  
  aictab(list(glmOT.D93,glmT.D93,glmO.D93,glmX.D93),  
         modnames=c("OT","T","O","X"),  
         c.hat=dfun(glmOT.D93))  
  detach("package:AICcmodavg")  
}
```

*## Loading required package: AICcmodavg*

## MuMIn

```
if (require("MuMIn")) {  
  packageVersion("MuMIn")  
  ## from ?QAIC  
  x.quasipoisson <- function(...) {  
    res <- quasipoisson(...)  
    res$aic <- poisson(...)$aic  
    res  
  }  
  glmQOT2.D93 <- update(glmOT.D93,family="x.quasipoisson",  
                       na.action=na.fail)  
  (gg <- dredge(glmQOT2.D93,rank="QAIC", chat=dfun(glmOT.D93)))  
  (ggc <- dredge(glmQOT2.D93,rank="QAICc", chat=dfun(glmOT.D93)))  
  detach("package:MuMIn")  
}
```

*## Loading required package: MuMIn*  
*## Fixed term is "(Intercept)"*  
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Notes: Ictab only gives delta-IC, limited decimal places (on purpose, but how do you change these defaults if you want to?). Need to add 1 to parameters to account for scale parameter. When doing corrected-IC you need to get the absolute number of parameters right, not just the relative number ... Not sure which classes of models each of these will handle (lm, glm, (n)lme, lme4, mle2 ...). Remember need to use overdispersion parameter from most complex model. glmmPQL: needs to be hacked somewhat more severely (does not contain deviance element, logLik has been NA'd out).

package	lm	glm	(n)lme	multinom	polr	lme4	mle2
AICcmodavg	y	y	y	y	y	?	?
MuMIn	?	?	?	?	?	?	?
mle2	?	?	?	?	?	?	?