

# Parameter interpretation and inference

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## Interpreting parameters

- continuous: units: depends whether scaled or not (talk about **scaling parameters**)
- categorical: differences between groups: depends on contrasts
- depends on presence of interactions
- **scale of measurement:** *link scale*

*log* proportional The argument here is that if  $\mu_0 = \exp \beta_0$  and  $\mu_1 = \exp \beta_0 + \beta_1 x$ ,

$$\begin{aligned}\mu_1 &= \exp(\beta_0 + \beta_1 x) \\ &= \mu_0 \exp(\beta_1 x) \\ &\approx \mu_0(1 + \beta_1 x) \quad \text{if } \beta_1 x \ll 1\end{aligned}$$

so for continuous predictors  $\beta_1$  is the proportional change in the mean per unit change in  $x$  (for categorical predictors it's the proportional change between categories).

Predicted values are the expected *geometric* mean of the category.

*logit* log-odds change.

- for  $\beta \Delta x$  small, as for *log* (proportional)
- for intermediate values, linear change in probability with slope  $\approx \beta/4$
- for large values, as for  $\log(1 - x)$

## Inference

### Single vs multi-parameter

*Single-parameter* Wald vs. *likelihood ratio* test (LRT): the former is easier (it's what you get from `summary()`), because Wald standard errors of the estimates ( $\sigma_{\hat{\beta}}$ ) are automatically available from the Hessian of the fitted model, so we can get  $p$ -values via a  $Z$  test on  $\hat{\beta}/\sigma_{\hat{\beta}}$  (this is

what summary gives) and confidence intervals via Normal confidence intervals on  $\hat{\beta}$ .

The *Hauck-Donner effect* occurs in cases of extreme parameter estimates (e.g. in the case of complete or near-complete separation), when the quadratic approximation is extremely poor: the hallmark is large parameter estimates (e.g.  $|\hat{\beta}| > 10$ ) and very large confidence intervals (leading to small Z statistics and large  $p$  values).

You can get LRTs via

- `drop1()`, `test="Chisq"` (only on parameters that can be dropped while respecting marginality, unless you use `scope= .~.`)
- `anova()`, explicitly testing different models:

```
reduced_model <- update(full_model, .~.-foo)
anova(full_model, reduced_model, test="Chisq")
```

where `foo` is the parameter you want to test.

- or by hand (having fitted these models)

```
pchisq(deviance(reduced_model) - deviance(full_model),
       df=df.residual(reduced_model) - df.residual(full_model),
       lower.tail=FALSE)
```

You can get *profile confidence intervals* via `MASS::confint.glm`.

*Multi-parameter* If you want to test a hypothesis that multiple  $\hat{\beta}$  values are simultaneously zero (i.e. you want to see if the overall effect of a factor is significant), you *could* do a Wald test: e.g. to test  $\hat{\beta}_1 = \hat{\beta}_2 = 0$ , you would calculate the sums of squares ( $\hat{\beta}_1^2 + \hat{\beta}_2^2 = 0$ ) and the variance; the scaled result should be  $\chi^2$  distributed.

```
contr <- c(1,1)
t(contr) %*% vcov(model) %*% contr
pchisq(...)
```

This is what `car::Anova()` does. It generally makes more sense to do model comparisons. Do this with `anova()` or `drop1()` (`anova(model)` gives *sequential* (forward/"type I") tests: `anova(model1, model2, model3)` compares a specific sequence of models); these use LRTs (if `test="Chisq"`) or  $F$  tests (if `test="F"`, which you should use when the dispersion parameter is estimated (Gaussian, Gamma, or quasi-likelihood models)).

### Interactions/marginality issues

You have to be very careful when testing main effects in the presence of interactions. `drop1()` generally respects marginality, although you can do `drop1(.~.)` to get `drop1` to test *all* the effects (i.e. not respecting marginality). (<sup>1</sup> is a standard reference from one of the proponents of respecting marginality: see Section 5.)

Your options with respect to marginality are:

- don't test main effects at all in the presence of interactions
- test main effects, but be very careful/aware that the meaning of the main effects depends on the parameterization/contrasts used
- split the data set and run separate analyses for each category involved in the interaction

<sup>1</sup> Venables, W. N. (1998). Exegeses on linear models. 1998 International S-PLUS User Conference, Washington, DC

### Finite-size issues

In general LRTs are better than Wald tests, but even they make a (weaker) asymptotic assumption (not that the log-likelihood surface is quadratic, but that the deviance is  $\chi^2$  distributed). People generally ignore this problem since the number of observations is usually sufficiently large that this is a reasonable approximation, but [rarely used!] *Bartlett corrections* <sup>2</sup> are one approach to correcting for this issue.

If the dispersion parameter is estimated (rather than fixed, as it is for Poisson and binomial models), then we should use *F* tests ("quasi-LRT" for want of a better term) rather than  $\chi^2$ , because the deviance differences are now scaled by the ( $\chi^2$ -distributed)  $\hat{\phi}$  (note that this does *not* address the issue of whether the deviance itself is really  $\chi^2$  distributed).

<sup>2</sup> McCullagh, P. and J. A. Nelder (1989). *Generalized Linear Models*. London: Chapman and Hall; and Cordeiro, G. M. and S. L. P. Ferrari (1998, August). A note on bartlett-type correction for the first few moments of test statistics. *Journal of Statistical Planning and Inference* 71(1-2), 261–269

### Bootstrapping

You can use bootstrap or parametric bootstrap samples to get more *p*-values/confidence intervals that account for : for example, non-parametric bootstrapping resamples the data with replacement (using `sample(., replace=TRUE)`).

Set up data and model:

```
data(lizards, package="brglm")
lizards <- transform(lizards,
                     gprop = grahami/(grahami+opalinus),
                     N = grahami+opalinus)
modell <- glm(gprop~height+diameter+light+time,
```

```
family=binomial, weights=N, data=lizards)
```

A function to take a bootstrap sample of the data, refit the model, and extract the coefficients:

```
bootFun <- function() {
  bootdat <- lizards[sample(nrow(lizards), replace=TRUE), ]
  newmodel <- update(model1, data=bootdat)
  return(coef(newmodel))
}
```

Use a for loop to compute the samples:

```
nsamp <- 1000
set.seed(101)
bootParms <- matrix(NA, nrow=nsamp, ncol=length(coef(model1)))
for (i in 1:nsamp) {
  bootParms[i,] <- bootFun()
}
```

There are a variety of different approaches for computing bootstrap confidence intervals, but a simple one is to find the quantiles of the bootstrapped coefficients. Get 2.5% and 97.5% quantiles of each column (MARGIN=2 specifies columns rather than rows), and transpose the results (because apply always returns its results column-wise):

```
ptab <- t(apply(bootParms, MARGIN=2, quantile, c(0.025, 0.975)))
rownames(ptab) <- names(coef(model1))
print(ptab)
```

##		2.5%	97.5%
##	(Intercept)	1.4634553	2.6372131
##	height>=5ft	0.7257110	1.7953832
##	diameter>2in	-1.2393941	-0.4427184
##	lightshady	-1.4986304	-0.2987468
##	timemidday	-0.5150444	0.5834759
##	timelate	-1.6807495	-0.3471012

Compute two-sided  $p$ -values:

```
bootp <- apply(bootParms,
  MARGIN=2,
  function(x) 2*min(mean(x<0), mean(x>0)))
cbind(coef(summary(model1)), bootp)
```

##		Estimate	Std. Error	z value	Pr(> z )	bootp
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## (Intercept)	1.9446882	0.3414768	5.6949348	1.234191e-08	0.000
## height>=5ft	1.1299913	0.2570898	4.3953169	1.106113e-05	0.000
## diameter>2in	-0.7626343	0.2112694	-3.6097720	3.064662e-04	0.000
## lightshady	-0.8472755	0.3223825	-2.6281682	8.584606e-03	0.004
## timemidday	0.2271105	0.2501770	0.9077995	3.639842e-01	0.332
## timelate	-0.7368117	0.2990005	-2.4642486	1.373008e-02	0.006

## References

- Cordeiro, G. M. and S. L. P. Ferrari (1998, August). A note on bartlett-type correction for the first few moments of test statistics. *Journal of Statistical Planning and Inference* 71(1-2), 261–269.
- McCullagh, P. and J. A. Nelder (1989). *Generalized Linear Models*. London: Chapman and Hall.
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