

VGAM Reference Card

2025-02

Please see <https://www.stat.auckland.ac.nz/~yee> for the VGAM package and the book's homepage. This document is current for prerelease CRAN version VGAM-1.1-13.

A monograph on the entire statistical framework, including the theory¹ and applications and the software, is Yee (2015). It is the most comprehensive description of everything within a single document, and the order of the functions listed here roughly follows the book order. Book complements available at the author's homepage give additional resources such as technical details behind some updated features.

The package has been developed over my entire working span to date. So an alternative is to look at quite a few journal articles: Yee and Wild (1996), Yee and Hastie (2003), Yee (2004a), Yee (2004b), Yee (2006), Yee and Stephenson (2007), Yee (2008), Yee (2010), Yee (2014b), Yee et al. (2015), Yee and Hadi (2014), Miranda-Soberanis and Yee (2019), Yee (2020), Yee (2022), Miranda-Soberanis and Yee (2023), Yee and Ma (2024), Yee et al. (2025), Yee (2024b), Yee (2021), Yee (2024a). Forthcoming is Yee (2025).

Please cite the appropriate references if you use the software!

The website

www.stat.auckland.ac.nz/~yee/VGAM/prerelease has the latest version of VGAM (source and Windows only). A companion package is VGAMdata, which is also available at <https://www.stat.auckland.ac.nz/~yee>. Both packages are also on CRAN.

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DISCLAIMER: VGAM is under continual development, meaning that as well as new features being added and bugs found on a regular basis, changes of all sorts are occurring all the time. For example, function and argument names may change at any

time, as well as default values of arguments; see the NEWS and ChangeLog files. The VGAM package is available on a use-at-your-own-risk basis: the Author assumes no liability for loss or damage of any kind resulting from its use.

Some notes:

1. Starting from VGAM 1.1-4, some functions have been moved to VGAMdata 1.1-4. These tend to be older VGAM family functions that have been replaced by newer ones, especially if they have now become special cases of the newer code. For example, the GAITD regression framework means that ZAB, ZIB, ZTB, ZAP, ZIP, ZTP, etc. need not have their own family function anymore. Page 10 gives a listing of some of these functions.
2. In VGAM 1.1-1 link functions were renamed to end in “link”, e.g., `loglink()` replaces `loge()`, `logitlink()` replaces `logit()`. VGAM 1.1-3 had `.Deprecated()` in the old functions.
3. Another R package, VGAMextra (Miranda and Yee, 2023)² contains additional VGAM family and link functions, etc. especially for time series (Miranda-Soberanis, 2018).
4. Another notable package called svyVGAM (Lumley, 2023b,a) provides inference based on survey for the analysis of complex survey samples.
5. I plan to phase out dispersion parameters such as used by `glm()` and `quasibinomial()` and `quasipoisson()`. Such ad hoc methods do not fit properly within a general and full MLE framework and catering for such entails unwanted surplus work for the developer. It's far easier just to consider estimation by full MLE for all the parameters.
6. In VGAM 1.0-0, the first and second derivatives of link functions have changed with respect to the argument `inverse`. Models fitted prior to VGAM 1.0-0 may need to be re-run.

¹A small resume is given on Page 11.

²As well as being on CRAN, some more recent versions might be available at <https://www.stat.auckland.ac.nz/~vmir178> and/or <https://github.com/VicoMiranda/>.

Modelling functions

The following functions form the heart of the VGAM package and use `formula` and `family` arguments, e.g., `vglm(y ~ 1, family = maxwell, data = mdata)`.

`vglm()` Vector generalized linear models.

`vgam()` Vector generalized additive models. See below for some more details.

`rrvglm()` Reduced-rank VGLMs (same as constrained linear ordination, or CLO).

`cqo()` Constrained quadratic ordination (QRR-VGLM).

`cao()` Constrained additive ordination (RR-VGAM).

`rcim(table or matrix)` Row-column interaction models.

The following functions do *not* use the `formula`, `family` = arguments.

`grc(table or matrix)` Goodman's RC model.

`vsmooth.spline(x, y, w, ...)` Vector smoothing spline.

Smoothing

`vgam()` can be used with three smoothers. They are as follows.

`s()` Generation-I VGAMs. This is Yee and Wild (1996). Uses backfitting. Cannot handle constraint matrices whose columns are not orthogonal (try `is.buggy()`).

`sm.os()` and `sm.ps()` O-splines and P-splines as penalized VGAMs (Yee et al., 2024). I call them Generation-II VGAMs as their direct solution supplants backfitting. Automatic smoothing parameter selection. Calls `magic()` in `mgcv` (Wood, 2004, 2017).

Of course, an alternative is to use regression splines, i.e., `bs()` and `ns()` and can be used with `vglm()`. The component functions can be plotted, e.g., `plot(as(fit, "vgam"))`.

BTW, `vsmooth.spline()` fits a vector (cubic) smoothing spline to scatter plot data.

Useful controlling options for the modelling functions

`trace = TRUE` Print a running log of the estimation.

`criterion = "coef"` Criterion on which to test convergence.

`maxit = 40` Maximum number of iterations allowed.

`coefstart, etastart, mustart` Starting values for β , η_i ($n \times M$ matrix), μ_i respectively. For example, `vglm(y ~ x2, maxwell, data = mdata, etastart = predict(simplerModel))`.

The following arguments are standard to formula-based modelling functions.

`data =` Data frame with the formula variables.

`subset =` Vector of logicals.

`na.action =` What to do with missing values. "na.fail" causes an error, "na.omit" deletes rows. Can be assigned a user-defined function.

Extractor functions

AIC () The Akaike information criterion or AIC.

AICc () Corrected AIC.

BIC () The Bayesian (Schwarz's) information criterion or BIC.

class () The object's class.

coef () Regression coefficients (the β_k^* in (1) but enumerated in a different order).

Coef () Regression coefficients, especially if the formula comprises of intercept only, i.e., $\sim \mathbf{1}$.

constraints () Constraint matrices, \mathbf{H}_k .

devar () Dependent variable (response), \mathbf{Y} .

deviance () Deviance, D .

df.residual () Residual degrees of freedom.

familyname () Name of the family function.

fitted () Fitted values, usually $\hat{\mu}_i$.

has.intercept () Does the model's formula have an intercept term?

hatvalues () Hat (or projection) matrix, \mathbf{H} .

is.bell () Are the response curve of a CQO bell-shaped?

is.parallel () Are the $\mathbf{H}_k = \mathbf{1}_M$?

is.zero () Are the η_j intercept-only?

KLD () Kullback–Leibler divergence (for GAITD regression only).

logLik () Log-likelihood, ℓ .

lrtest(model1, model2) Likelihood ratio test (LRT).

lrt.stat () Likelihood ratio test statistics for testing $H_0 : \beta_{(j)k}^* = \theta_{(j)k}^0$ versus $H_1 : \beta_{(j)k}^* \neq \theta_{(j)k}^0$.

linkfun () Parameter link functions.

model.matrix () The big model matrix \mathbf{X}_{VLM} . This is never smaller than the **lm**-type model matrix.

nobs () Number of observations, n_{VLM} or n_{LM} .

npred () Number of linear/additive predictors η_j , M .

Pheapseep () Probability of heaping/seeing (for GAITD regression only).

QR.Q () The **Q** matrix in the QR decomposition of the relevant model matrix used in the IRLS algorithm.

QR.R () The **R** matrix in the QR decomposition of the relevant model matrix used in the IRLS algorithm.

predict () $n \times M$ matrix of $\eta_j(x_i)$; also prediction of μ .

print () Print the model.

Rank () Rank of a reduced-rank (ordination) model, R .

resid () Residuals (working, Pearson, deviance, response, randomized quantiles (Dunn and Smyth, 1996))

responseName () The name of the response, as a character string.

score.stat () Rao's score test (Lagrange multiplier) statistics for testing $H_0 : \beta_{(j)k}^* = \theta_{(j)k}^0$ versus $H_1 : \beta_{(j)k}^* \neq \theta_{(j)k}^0$.

show () Show.

specials () Special values from GAITD regression.

summary () Summary.

terms () Terms.

term.names () The model's formula: each term is converted to a character and they are all placed in a vector.

TIC () Takeuchi's information criterion or TIC.

vcov () Variance-covariance matrix, $\widehat{\text{Var}}(\hat{\beta})$.

wald.stat () Wald test statistics for testing $H_0 : \beta_{(j)k}^* = \theta_{(j)k}^0$ versus $H_1 : \beta_{(j)k}^* \neq \theta_{(j)k}^0$. Then $\text{Var}(\hat{\beta}_{(j)k}^*)$ can be estimated at $\theta_{(j)k}^0$ —this does not suffer from the Hauck-Donner effect (HDE).

weights () Prior weights w_i , and working weights ($w_i \mathbf{W}_i$), in matrix-band format.

which.etas () For variable x_k which η_j s are modelled using that covariate?

which.xij () For each variable x_k does it represent an $x_i j$ term?

Plotting functions

Not all of the following apply to a given fitted model.

biplot () Biplot for RR-VGLMs.

densityplot () Density plot, e.g., for quantile regression.

dgaitdplot () GAITD regression density plot.

lvplot () Latent variable plot (ordination diagram).

persp () Perspective (3-D; sometimes 2-D) plot.

plot () General plotting function.

plotdgaitd () GAITD regression density plot.

guplot () Gumbel plot, e.g., for extreme values regression.

meplot () Mean excess plot, e.g., for extreme values regression.

qtplot () Quantile plot, e.g., for quantile regression.

rlplot () Return level plot, e.g., for extreme values regression.

spikeplot () Spike plot, e.g., for GAITD regression.

trplot () Trajectory plot, e.g., for constrained ordination.

Link functions

Most parameters θ_j are transformed into a linear/additive predictor $\eta_j = \beta_j^T \mathbf{x}$ or $\eta_j = \sum_{k=1}^d f_{(j)k}(x_k)$. Here $\boldsymbol{\eta} = (\eta_1, \dots, \eta_M)^T$ so that there are M parameters. All logarithms are to base e unless specified otherwise.

Usage: use full link function name (in quotes is okay), e.g., `vglm(y ~ 1, family = maxwell(link = "identitylink"))`.

Note the change in names described in Note 2 on Page 1.

loglink() Log, $\log(\theta)$, $\theta > 0$. Old name: **loge()**.

logofflink() Log with an offset, $\log(\theta + A)$, $\theta + A > 0$.

log1plink() Log with an unit offset, $\log(1 + \theta)$, $\theta + 1 > 0$.

logloglink() Log-log, $\log \log(\theta)$, $\theta > 1$.

loglogloglink() Log-log-log, $\log \log \log(\theta)$, $\theta > e$.

clogloglink() Complementary log-log, $\log(-\log(1 - \theta))$, $0 < \theta < 1$.

cloglink() Complementary log, $-\log(1 - \theta)$, $-\varepsilon < \theta < 1$, where $\varepsilon > 0$ is small.

logclink() Complementary log, $\log(1 - \theta)$, $\theta < 1$.

logitlink() Logit, $\log \frac{\theta}{1 - \theta}$, $0 < \theta < 1$.

extlogitlink() Extended logit, $\log \frac{\theta - A}{B - \theta}$, $A < \theta < B$.

foldsqrtlink() Folded square root link function, $A < \theta < B$.

probitlink() Probit, $\Phi^{-1}(\theta)$, $0 < \theta < 1$.

cauchitlink() Cauchit, $\tan(\pi(\theta - \frac{1}{2}))$, $0 < \theta < 1$.

identitylink() Identity, θ .

multilogitlink() Multinomial logit link, $\log \frac{\theta_j}{\theta_{M+1}}$, $0 < \theta_j < 1$, $j = 1, \dots, M$.

nbcancelink() Negative binomial canonical link, $\log(\theta/(\theta + k))$, where k is known.

negidentitylink() Negative-identity, $-\theta$.

reciprocallink() Reciprocal, $1/\theta$, $\theta \neq 0$.

negreciprocallink() Negative-reciprocal, $-1/\theta$, $\theta \neq 0$.

fisherzlink() Fisher's Z-transformation, $\frac{1}{2} \log \frac{1 + \theta}{1 - \theta}$, $-1 < \theta < 1$.

rhobitlink() Twice Fisher's Z-transformation, $\log \frac{1 + \theta}{1 - \theta}$.

Utility functions

anova.vglm() Analysis of deviance table for one or more VGLM fits. Allows the hypothesis testing of terms and between models.

CM.equid(), **CM.free()**, **CM.ones()**, **CM.qlogis()**, **CM.qnorm()**, **CM.symm0()**, **CM.symm1()**, Common types of constraint matrices constructed and returned.

confint() Wald or profile log likelihood confidence intervals for individual regression coefficients.

cops() Centre of the parameter space.

dtheta.deta() $d\theta_j/d\eta_j$.

d2theta.deta2() $d^2\theta_j/d\eta_j^2$.

d3theta.deta3() $d^3\theta_j/d\eta_j^3$.

eta2theta() $\theta_j = g^{-1}(\eta_j)$.

goffset() GAITD regression offset matrix construction. Facilitates the *Generally-Truncated-Expansion* (GTE) method.

hdeff() Detection function for the Hauck and Donner (1977) effect (HDE).

Influence() Influence function of a fitted model.

margeff() Marginal effects $\partial p_j(\mathbf{x}_i)/\partial x_{ik}$, is a $p \times (M + 1) \times n$ array. Available for most categorical data analysis families. Also available for "poissonff", "negbinomial", "posnegbinomial".

m2adefault() Conversion from weight matrices (matrix-band) format to array format.

ordsup() Ordinal superiority measures for the LM and cumulative link models.

round2() Rounding internally to base 2.

R2latvar() R^2 for latent variable models—a goodness of fit measure. Available for some categorical data analysis families only, e.g., parallel cumulative logit model.

Select() Selects columns from a data frame, can output formulas. A little similar to **subset()**.

simulate() Simulates new observations coming from the fitted model (for selected families only).

step4() Variable selection by AIC in a stepwise algorithm.

theta2eta() $\eta_j = g(\theta_j)$.

Trunc() GAITD regression truncate values. Facilitates the GTE method.

Common arguments in family functions

`zero` allows for $\eta_j = \beta_{(j)1}$, i.e., intercept-only. Can be assigned a vector with values from the set $\{1, 2, \dots, M\}$. Negative values allowed for multiple responses. A `NULL` means *all* the η_j are modelled as functions of the covariates. Argument `zero` can also be assigned negative values, which means a form of recycling over multiple responses, e.g., `vglm(cbind(y1, y2) ~ x2, family = uninormal(zero = -2))` means that both responses' σ parameters are intercept-only. As of VGAM 1.0-1 and later, argument `zero` can also be assigned a vector of character strings, e.g., `zero = c("scale", "shape")` which means that all scale and shape parameters will be modelled as intercept-only.

`exchangeable` For some s and t , $\eta_s - \eta_t = 0$ or some constant. That is, η_s and η_t differ at most by an intercept.

`parallel` If `TRUE`, for all k (except possibly the intercept), $\beta_{(s)k} = \beta_{(t)k}$ for some s and t ; i.e., the slope for X_k of some of the linear/additive predictors are parallel or differ by a constant. Whether the parallelism assumption applies to the intercept depends on the specific model being fitted.

`parallel = FALSE ~ X1 + X2 - 1` means all terms, except for X_1 and X_2 , have parallel slopes.

`eq.ap` Arguments beginning with `eq.` are assigned a single logical value. Being simpler, they lack the flexibility of arguments such as `parallel`.

Next is a listing of VGAM family functions. These are assigned to the **family** = argument to the modelling functions, e.g., `vglm(y ~ x2 + x3, family = multinomial)`.

For distributions, the characters “dpqr” are placed within the parentheses to denote whether dpqr-type functions are available (these stand for density functions, cumulative distribution functions and quantile functions, and random variates generation, respectively). For example, `binomialff([dpqr])`, `sinmad(dpqr)`, `tobit(dpqr)`. Those dpqr-type functions from base R are wrapped in brackets [].

Generalized linear models

In general quasi-type families such as `quasibinomialff()` and `quasipoissonff()` have been deprecated, as well as `gaussianff()`.

`binomialff([dpqr])` Binomial. For multiple responses use `binomialff(multiple.responses = TRUE)`.

`inverse.gaussianff([dpr])` Inverse Gaussian.

`poissonff([dpqr])` Poisson.

LM and binomial variants

`normal.vcm()` Linear model with varying-coefficients.

`SURff()` Seemingly unrelated regressions.

`rrar()` Reduced-rank autoregressive model for multiple time series.

`binom2.or(dr)` Bivariate logistic/probit/...odds ratio model for two binary responses.

`binom3.or(dr)` Trivariate logistic/probit/...odds ratio model for three binary responses.

`binom2.rho(dr)` Bivariate probit model for two binary responses. Based on a standard N_2 with correlation parameter ρ .

`loglinb2()/loglinb3()` Loglinear model for two/three binary responses.

Univariate discrete distributions

`[dr]bell()` 1-parameter Bell distribution.

`[dpqr]benf()` 0-parameter Benford distribution.

`betabinomial(dpr)` Beta-binomial distribution.

`betabinomial.rho(dpr)` Beta-binomial distribution (known ρ).

`betabinomialfff(dpr)` Beta-binomial distribution.

`betageometric(dpr)` Beta-geometric distribution.

`borel.tanner(dr)` Borel-Tanner distribution.

`diffzeta(dpqr)` Differenced zeta distribution.

`double.expbinomial()` Double exponential binomial distribution.

`extbetabinomial(dpqr)` Extended beta-binomial distribution (Prentice, 1986).

`genpoisson[012](dpqr)` Generalized Poisson distribution; GP-0, GP-1, GP-2 parameterizations.

`geometric([dpqr])` Geometric distribution.

`hzeta(dpqr)` Haight’s zeta function.

`logfff(dpqr)` Logarithmic distribution.

`inv.binomial()` Inverse binomial distribution.

`negbinomial([dpqr])` Negative binomial distribution with parameters μ and k .

`negbinomial.size([dpqr])` Negative binomial distribution with parameter μ and known k .

`-polono(dpr)` Poisson-lognormal distribution (no family function available yet.)

`polya([dpqr])` Pólya (negative binomial) distribution with parameters p and k .

`seq2binomial()` 2-stage sequential binomial distribution.

`truncgeometric()` Truncated geometric distribution.

`yulesimon(dpr)` Yule-Simon distribution.

`zetafff(dpqr)` Zeta distribution.

`zipf(dpqr)` Zipf distribution.

Univariate continuous distributions

`alaplace[123](dpqr)` Asymmetric Laplace distribution. *Not recommended because the usual regularity conditions do not hold for this distribution.* [in VGAMdata]

`benini(dpqr)` 1-parameter Benini distribution.

`betaR([dpqr])` 2-parameter beta distribution (shape parameterization).

`betaff([dpqr])` 2-parameter beta distribution (mean and precision parameterization).

`betaprime()` 2-parameter beta-prime distribution.

`betaII()` 3-parameter beta II distribution.

`bisa(dpqr)` Birnbaum-Saunders distribution.

`cardioid(dpqr)` Cardioid distribution.

`cauchy([dpqr])` 2-parameter Cauchy distribution.

`cauchy1([dpqr])` 1-parameter Cauchy distribution.

`chisq([dpqr])` Chi-squared and chi distributions.

`cens.gumbel()` Censored Gumbel distribution.

`cens.normal()` Censored univariate normal distribution (see also `tobit(dpqr)`).

`cens.rayleigh()` Censored Rayleigh distribution.

`dagum(dpqr)` 3-parameter Dagum distribution.

`double.cens.normal()` Double censored 2-parameter univariate normal distribution.

`erlang()` Erlang distribution.

`expexp()` 2-parameter Exponentiated exponential distribution.

`expexp1()` 2-parameter Exponentiated exponential distribution (using a profile (concentrated) likelihood).

`explogfff(dpqr)` Exponential logarithmic distribution.

`exponential([dpqr])` Exponential distribution.

`fff([dpqr])` F-distribution.

`fisk(dpqr)` 2-parameter Fisk distribution.

`foldnormal(dpqr)` Folded normal distribution (univariate and generalized).

`frechet(dpqr)` 2-parameter Fréchet distribution.

`gamma1([dpqr])` 1-parameter gamma distribution.

gamma2 ([dpqr]), **gammaR**[dpqr] () 2-parameter gamma distribution.

genbetaII(d) 4-parameter generalized beta II distribution.

gengamma.stacy(dpqr) Generalized gamma distribution.

gensh(dpqr) Generalized secant hyperbolic distribution.

gompertz(dpqr) 2-parameter Gompertz distribution.

hypersecant (), **hypersecant01** () Hyperbolic secant distribution.

inv.gaussianff(dpr) 2-parameter inverse Gaussian distribution.

inv.lomax(dpqr) 2-parameter inverse Lomax distribution.

inv.paralogistic(dpqr) 2-parameter inverse paralogistic distribution.

kumar(dpqr) Kumaraswamy distribution.

laplace(dpqr) Laplace distribution.

leipnik() Leipnik distribution.

levy(dpqr) Lévy distribution.

lgamma1(dpqr) 1-parameter log-gamma distribution.

lgamma3(dpqr) 3-parameter log-gamma distribution.

lindley(dpr) Lindley distribution.

lino(dpqr) 3-parameter generalized beta distribution (Libby and Novick, 1982).

logistic1 ([dpqr]) 1-parameter logistic distribution.

logistic ([dpqr]) 2-parameter logistic distribution.

lognormal ([dpqr]) 2-parameter lognormal distribution.

lognormal3 ([dpqr]) 3-parameter lognormal distribution.

lomax(dpqr) Lomax distribution.

makeham(dpqr) Makeham distribution.

maxwell(dpqr) Maxwell distribution.

mccullagh89() McCullagh (1989) distribution.

nakagami(dpqr) Nakagami distribution.

paralogistic(dpqr) 2-parameter paralogistic distribution.

paretoff(dpqr) Pareto distribution (Pareto(I)).

paretoIV(dpqr) Pareto(IV) distribution.

paretoIII(dpqr) Pareto(III) distribution.

paretoII(dpqr) Pareto(II) distribution.

perks(dpqr) Perks' distribution.

poisson.points(d) Distances to a fixed point, in a Poisson plane or volume.

rayleigh(dpqr) Rayleigh distribution.

riceff(dpqr) Rice distribution.

rigff() Reciprocal inverse Gaussian distribution.

sc.studentt2(dpqr) Scaled Student's t_2 distribution.

simplex(dr) 2-parameter simplex distribution.

sinmad(dpqr) 3-parameter Singh-Maddala distribution. Skellam distribution.

skewnormal(dr) 1-parameter univariate skew-normal distribution.

studentt ([dpqr]), **studentt2** ([dpqr]), **studentt3** ([dpqr]) Student t distribution.

tikuv(dpqr) Short-tailed symmetric distribution of Tiku and Vaughan (1999).

tobit(dpqr) Tobit model (censored normal; see also **cens.normal**()).

topple(dpqr) Topp-Leone distribution.

triangle(dpqr) Triangle distribution. [**triangle**() is now in VGAMdata].

truncpareto(dpqr) Truncated (upper) Pareto distribution (Pareto(I)).

truncweibull() Truncated Weibull distribution.

uninormal ([dpqr]) 2-parameter univariate normal distribution.

vonmises() von Mises distribution.

waldff() Standard Wald distribution.

weibullR() 2-parameter Weibull distribution.

weibull.mean() 2-parameter Weibull distribution (parameterized in terms of its mean).

Bivariate and trivariate distributions

bilogistic4(dpr) 4-parameter bivariate logistic distribution.

amh(dpr) Ali-Mikhail-Haq's bivariate distribution.

biclaytoncop(dr) Bivariate Clayton copula distribution.

bifrankcop(dpr) Bivariate Frank's copula distribution.

bistudentt(d) Bivariate Student- t distribution.

binormal(dpr) Bivariate normal distribution, $N_2(\mu_1, \mu_2, \sigma_{11}, \sigma_{22}, \rho)$.

binormalcop(dp) (Bivariate) Gaussian copula distribution, $F(y_1, y_2; \rho) = \Phi_2(\Phi^{-1}(y_1), \Phi^{-1}(y_2); \rho)$.

fgm(dpr) Farlie-Gumbel-Morgenstern's bivariate distribution

freund61() Freund's (1961) bivariate extension of the exponential distribution.

gammahyp() 1-parameter gamma hyperbola bivariate distribution.

bigamma.mckay() McKay's bivariate gamma distribution [now in VGAMdata].

gammaff.mm() Mathai and Moschopoulos (1992) multivariate gamma distribution.

morgenstern() Morgenstern's bivariate distribution

bigumbellI() Gumbel's Type I bivariate distribution

plackett(dpr) Plackett's bivariate distribution.

trinormal(dr) Trivariate normal distribution, $N_3(\mu_1, \mu_2, \mu_3, \sigma_{11}, \sigma_{22}, \sigma_{33}, \rho_{12}, \rho_{23}, \rho_{13})$.

Categorical data

In the following, g is a link function, η_j the linear/additive predictors, and $Y \in \{1, \dots, M+1\}$ is a categorical response. See also **margeff**() .

acat() Adjacent categories model, $\eta_j = g(P[Y = j + 1]/P[Y = j])$.

cumulative() Cumulative categories model, $\eta_j = g(P[Y \leq j])$. Includes the proportional odds model.

propodds() Proportional odds model $\eta_j = \text{logit}(P[Y > j])$.

cratio() Continuation ratio model, $\eta_j = g(P[Y > j | Y \geq j])$.

sratio() Stopping ratio model, $\eta_j = g(P[Y = j | Y \geq j])$.

multinomial() Multinomial logit model, $\eta_j = \text{log}(P[Y = j] / P[Y = M + 1])$.

The argument `reverse` reverses the direction of many of the above probabilities.

See documentation on the `xi.j` argument at the package's website: this handles covariates that have different values for differing linear/additive predictors η_j . This will handle consumer choice or discrete choice models.

Genetical data

AA.Aa.aa() AA-Aa-aa blood group system.

AB.Ab.aB.ab2() AB-Ab-aB-ab2 blood group system.

AB.Ab.aB.ab() AB-Ab-aB-ab blood group system.

ABO() ABO blood group system.

G1G2G3() G1G2G3 blood group system.

MNSs() MNSs blood group system.

Quantile and expectile regression

(I) LMS methods

lms.bcn() Box-Cox transformation to normality.

lms.bcg() Box-Cox transformation to the gamma distribution.

lms.yjn() Yeo-Johnson transformation to normality [Not recommended].

Special methods functions for these models are:

qtplot() Quantile plot.

deplot() Density plot.

cdf() Cumulative distribution function.

(II) Extended log- F distribution (ELF)

extlogF1(d) 1-parameter ELF (approximates ALD)

Special methods functions for these models are:

is.crossing() Is there quantile crossing?

fix.crossing() Remove quantile crossing

(III) Asymmetric Laplace distribution (ALD) methods [these are experimental only]

alaplacel(dpqr) 1-parameter ALD.

alaplacel2(dpqr) 2-parameter ALD.

alaplacel3(dpqr) 3-parameter ALD.

(IV) Asymmetric Maximum Likelihood (AML) estimation methods

amlnormal() Asymmetric least squares (expectile) regression (Efron, 1991).

amlbinomial() Logistic (expectile) regression.

amlexponential() Exponential (expectile) regression.

amlpoisson() Poisson (expectile) regression (Efron, 1992).

Extreme value data

gev(dpqr) 3-parameter generalized extreme value distribution.

gevff(dpqr) 3-parameter generalized extreme value distribution (handles independent multiple responses, like usual).

gpd(dpqr) 2-parameter generalized Pareto distribution.

gumbelff(dpqr) 2-parameter Gumbel distribution (handles independent multiple responses, like usual).

gumbel(dpqr) 2-parameter Gumbel distribution for multivariate responses.

gumbelIII(dpqr) Gumbel's Type II distribution.

hurea(d) Hüsler-Reiss angular distribution.

recnormal() Records: univariate normal data.

recexp1() Records: univariate exponential data.

See also **guplot()**, **meplot()**, **rlplot()**.

Positive and zero-inflated or zero-altered distributions

Here, positive distributions have the zero probability that the response is 0, i.e., zero-truncated. Zero-altered models are also called hurdle models. *Note: some dpqr-type functions may be moved to VGAMdata.*

posbernoulli.[b,t,tb](dr) Positive Bernoulli distribution for closed-population capture-recapture experiments based on the conditional likelihood.

posbinomial(dpqr) Positive binomial distribution.

posgeom(dpqr) Positive geometric distribution (dpqr-only).

posnormal(dpqr) Positive (univariate) normal distribution.

posnegbinomial(dpqr) Positive negative binomial distribution.

pospoisson(dpqr) Positive Poisson distribution.

zabinomial[ff](dpqr) Zero-altered binomial distribution.

zageometric[ff](dpqr) Zero-altered geometric distribution.

zanegbinomial[ff](dpqr) Zero-altered negative binomial distribution.

zapoiss[ff](dpqr) Zero-altered Poisson distribution.

zibinomial[ff](dpqr) Zero-inflated binomial distribution.

zigeometric[ff](dpqr) Zero-inflated geometric distribution.

zinegbinomial[ff](dpqr) Zero-inflated negative binomial distribution.

zipoisson[ff](dpqr) Zero-inflated Poisson distribution.

Generally altered, inflated, truncated and deflated distributions

The following implement the full *generally altered, inflated, truncated and deflated* (GAITD) ‘combo’ model, where there are 7 types of special values.

[dpqr]gaitdbinom() GAITD binomial distribution.

[dpqr]gaitdlog() GAITD logarithmic regression.

[dpqr]gaitdzeta() GAITD zeta regression.

[dpqr]gaitdnbinomial() GAITD negative binomial regression.

[dpqr]gaitdpoisson() GAITD Poisson regression.

Utility functions: **plotdgait()**, **dgaitplot()**, **specials()**, **KLD()**, **Pheapseep()**, **Trunc()**, **goffset()**.

Note: VGAMextra is useful for **logffMlink()** and **zetaffMlink()** when using **gaitdlog()** and **gaitdzeta()**, e.g., for $\eta_1 = \log \mu$.

Mixed type data models

N1binomial() LM and binomial mixed type.

N1poission() LM and Poisson mixed type.

Finite mixture models

mix2exp() Two exponential distributions.

mix2normal() Two univariate normals.

mix2poisson() Two Poisson distributions.

Miscellaneous models and distributions

AR1() Time series AR(1) for autoregressive errors.

DeLury() De Lury’s model for fish depletion analysis [in VGAMdata].

dirichlet() Dirichlet distribution.

dirmultinomial(), **dirmul.old()** Dirichlet-multinomial distribution.

huber(dpqr) Huber’s robust regression method.

Nonlinear regression models

micmen() Michaelis-Menten model, $\mu_i = \theta_1 x_i / (\theta_2 + x_i)$.

Miscellaneous mathematical functions

erf() Error function, $\text{erf}(x) = \frac{2}{\sqrt{\pi}} \int_0^x \exp(-t^2) dt$.

erfc() Complementary error function, $1 - \text{erf}(x) = \frac{2}{\sqrt{\pi}} \int_x^\infty \exp(-t^2) dt$.

expint() Exponential integral $Ei(x) = \int_0^x \frac{\exp(t)}{t} dt$, $x > 0$.

expexpint() $\exp(-x) Ei(x)$, $x > 0$.

expint.E1() $E_1(x) = \int_x^\infty \frac{\exp(-t)}{t} dt$, $x > 0$.

lambertW() Lambert’s W function for $W(z) \exp(W(z)) = z$.

lerch() Lerch’s $\Phi(x, s, v)$ function, also known as the Lerch transcendent.

mills.ratio(), **mills.ratio2()** Mills ratio, $\phi(x)/\Phi(x)$ and $\phi^2(x)/\Phi(x)$ respectively.

pgamma.deriv() First 2 derivatives of the incomplete gamma integral.

pgamma.deriv.unscaled() First 2 derivatives (wrt the shape parameter) of the unscaled incomplete gamma integral.

pbinorm() CDF of N_2 , $= P(Y_1 \leq y_1, Y_2 \leq y_2; \boldsymbol{\mu}, \boldsymbol{\Sigma})$.

zeta() Riemann’s $\zeta(x)$ zeta function and the Hurwitz zeta function.

Quadratic and additive ordination

cqo() Canonical quadratic (Gaussian) ordination (QRR-VGLM).

cao() Constrained additive ordination (RR-VGAM). Not fully finished yet.

The fast algorithm currently works for families **poissonff()**, and **binomialff()** (logitlink and clogloglink links available).

Special methods functions for these models are:

Coef() $\hat{\mathbf{A}}, \hat{\mathbf{B}}_1, \hat{\mathbf{C}}, \hat{\mathbf{D}}, \hat{\mathbf{u}}_s, \hat{\mathbf{T}}_s, \hat{\mathbf{v}}_i$, etc.

concoef() Constrained (canonical) coefficients $\hat{\mathbf{C}}$

latvar() Latent variables $\hat{\mathbf{v}}_i = \hat{\mathbf{C}}^T \mathbf{x}_{2i}$ (site scores)

Max() Maxima $E[Y_s | \hat{\mathbf{u}}_s] = g^{-1}(\hat{\boldsymbol{\alpha}}_s)$

Opt() Optima $\hat{\mathbf{u}}_s$ (species scores)

Tol() Tolerances $\hat{\mathbf{T}}_s$

lvplot() Latent variable plot (ordination diagram; for rank $R = 1$ or 2)

persp() Perspective (3-D; sometimes 2-D) plot

calibrate() Calibration: estimate \mathbf{v} from \mathbf{y}

trplot() Trajectory plot (for $R = 1$ only)

rootogram4() Diagnostic plot for count models for assessing goodness of fit

Miscellaneous

methods(class = class(fit)) lists all the methods to handle objects of class `fit`.

slotNames(fit) lists the slots of the object `fit`, but it is best to use extractor functions where possible.

The VGAMdata package

The following `dpqr`-type functions have been moved from VGAM into VGAMdata. A common reason is redundancy because some newer functions makes these a special case. For example, the GAITD work has rendered the ZAP, ZIP, and ZTP as special cases, e.g., `rpospois(n, lambda)` is better replaced by `rgaitdpois(n, lambda, truncate = 0)`.

alaplace[123](dpqr) Asymmetric Laplace distribution. *Not recommended because the usual regularity conditions do not hold for this distribution.*

oalog(dpqr) One-altered logarithmic distribution.

oizeta(dpqr) One-inflated zeta distribution.

oizipf(dpqr) One-inflated Zipf distribution.

otlog(dpqr) One-truncated logarithmic distribution.

otpospoisson(dpqr) One-truncated positive Poisson distribution.

otzeta(dpqr) One-truncated zeta distribution.

oilog(dpqr) One-inflated logarithmic distribution.

oiposbinomial(dpqr) One-inflated positive binomial distribution.

oipospoisson(dpqr) One-inflated positive Poisson distribution.

posbinomial(dpqr) Positive binomial distribution.

posnegbinomial(dpqr) Positive negative binomial distribution.

triangle() Triangle distribution. *Not recommended because the usual regularity conditions do not hold for this distribution.*

The VGAMextra package

This package contains additional functions, especially those focussed on time series analysis. Some link function applicable to the mean parameter of certain distributions are also there; they end in `Mlink` such as `logffMlink` for the logarithmic distribution.

Some formulas

For most VGLMs the data can be written $(\mathbf{x}_i, \mathbf{y}_i)$, $i = 1, \dots, n$, independently and the PMF/PDF for the i th observation is

$$f(\mathbf{y}_i | \mathbf{x}_i; \boldsymbol{\theta}) = h(\mathbf{y}_i; \boldsymbol{\eta}_1(\mathbf{x}_i), \dots, \boldsymbol{\eta}_M(\mathbf{x}_i)).$$

for some $f(\cdot)$ and $h(\cdot)$. The $\boldsymbol{\theta}$ are generic parameters, and coupled with $\boldsymbol{\eta}_j = g_j(\boldsymbol{\theta}_j) = \boldsymbol{\beta}^T \mathbf{x}$, the parameters are modelled as linear predictors. The parameter link functions g_j are used to transform the parameters. One can write $\mathbf{x} = (x_1, \dots, x_d)^T$ or $\mathbf{x}_i = (x_{i1}, \dots, x_{id})^T$, and $\boldsymbol{\eta} = (\boldsymbol{\eta}_1, \dots, \boldsymbol{\eta}_M)^T$.

For most VGLMs the log-likelihood $\ell = \sum_{i=1}^n w_i \ell_i(\boldsymbol{\eta}_1, \dots, \boldsymbol{\eta}_M)$ is maximized. The positive prior weights w_i are inputted using `vglm(..., weights = ...)`.

For VGLMs (Yee and Hastie, 2003):

$$\boldsymbol{\eta}(\mathbf{x}) = \mathbf{H}_1 \boldsymbol{\beta}_{(1)}^* x_1 + \dots + \mathbf{H}_d \boldsymbol{\beta}_{(d)}^* x_d = \mathbf{B}^T \mathbf{x} \quad (1)$$

where $\mathbf{H}_1, \dots, \mathbf{H}_d$ are known full-column rank *constraint matrices*, and $\boldsymbol{\beta}_{(k)}^*$ is a vector containing a possibly reduced set of unknown regression coefficients. With no constraints at all, $\mathbf{H}_k = \mathbf{I}_M$ for all k . Usually $x_1 = 1$ (intercept term). In general,

$$\mathbf{B}^T = \left(\mathbf{H}_1 \boldsymbol{\beta}_{(1)}^* \quad \dots \quad \mathbf{H}_d \boldsymbol{\beta}_{(d)}^* \right). \quad (2)$$

Then `coef(fit, matrix = TRUE)` is the estimate of \mathbf{B} , and `constraints(fit)` returns the \mathbf{H}_k . The \mathbf{H}_k can be inputted with `vglm(..., constraints = list("Intercept" = ..., x2 = ...))`, or more conveniently with arguments such as `parallel`, `exchangeable` and `zero` in the VGAM family function itself.

For the `xij` argument, one has the central formula

$$\begin{aligned} \boldsymbol{\eta}_i &= \boldsymbol{o}_i + \sum_{k=1}^d \text{diag}(x_{ik1}, \dots, x_{ikM}) \mathbf{H}_k \boldsymbol{\beta}_{(k)}^* \\ &= \boldsymbol{o}_i + \sum_{k=1}^d \mathbf{X}_{(ik)}^\# \mathbf{H}_k \boldsymbol{\beta}_{(k)}^*, \text{ say,} \end{aligned} \quad (3)$$

with provision for offsets \boldsymbol{o}_i . This is the central formula for the `xij` facility and the most general for VGLMs. Then the big model matrix has the block form

$$\mathbf{X}_{\text{VLM}} = \begin{pmatrix} \mathbf{X}_{(11)}^\# \mathbf{H}_1 & \dots & \mathbf{X}_{(1p)}^\# \mathbf{H}_d \\ \vdots & & \vdots \\ \mathbf{X}_{(n1)}^\# \mathbf{H}_1 & \dots & \mathbf{X}_{(np)}^\# \mathbf{H}_d \end{pmatrix}. \quad (4)$$

For example, for an exchangeable bivariate odds ratio model,

```
vglm(formula = cbind(leye, reye) ~ iop,
      binom2.or(exchangeable = TRUE, zero = 3),
      data = eyesData,
      xij = list(iop ~ liop + riop + fill1(liop)),
      form2 = ~ iop + liop + riop + fill1(liop))
```

where `iop` is the *intraocular ocular pressure* (which is different for left eye and right eye). The argument `form2` contains all the terms, and the RHS of each formula in the `xij` list are the successive (unique) elements/terms of $\mathbf{X}_{(ik)}^\#$.

For VGAMs (Yee and Wild, 1996): (1) extends to

$$\boldsymbol{\eta}(\mathbf{x}) = \mathbf{H}_1 \boldsymbol{\beta}_{(1)}^* x_1 + \mathbf{H}_2 \mathbf{f}_2^*(x_2) + \dots + \mathbf{H}_p \mathbf{f}_d^*(x_d) \quad (5)$$

where $\mathbf{f}_k^*(x_k) = (f_{(1)k}^*(x_k), \dots, f_{(r_k)k}^*(x_k))^T$ is a r_k -vector of smooth functions of x_k (estimated by a vector smoothing spline). With no constraints, $\boldsymbol{\eta}_j = \sum_{k=1}^p f_{(j)k}(x_k)$.

For RR-VGLMs (Yee and Hastie, 2003; Yee, 2014a):

$$\boldsymbol{\eta}(\mathbf{x}) = \mathbf{B}_{[1]}^T \mathbf{x}_{[1]} + \mathbf{A} \mathbf{v} \quad (6)$$

where $\mathbf{x} = (\mathbf{x}_{[1]}^T, \mathbf{x}_{[2]}^T)^T$, $\mathbf{v} = \mathbf{C}^T \mathbf{x}_{[2]}$ is an R -vector of latent variables, \mathbf{A} is $M \times R$ and \mathbf{C} is $p_2 \times R$. Note that \mathbf{A} and \mathbf{C} are general (thin) matrices whereas *doubly constrained* RR-VGLMs (DRR-VGLMs) allow the matrices to have structure.

DRR-VGLMs (Yee et al., 2025) have $\boldsymbol{\eta} =$

$$\mathbf{B}_{[1]}^T \mathbf{x}_{[1]} + \left\{ \sum_{r=1}^R \mathbf{e}_r^T \otimes \left(\begin{pmatrix} \mathbf{e}_r \\ \tilde{\mathbf{H}}_{Ar} \tilde{\mathbf{a}}_r^* \end{pmatrix} \right) \right\} \left\{ \sum_{k=1}^{p_2} \mathbf{e}_k^T \otimes (\mathbf{H}_{ck} \mathbf{c}_k^*) \right\} \mathbf{x}_{[2]}.$$

Arguments `H.A` and `H.C` are for inputting the constraint matrices.

Here, $\dim(\mathbf{x}) = d = p$ with $\dim(\mathbf{x}_{[1]}) = p_1$, $\dim(\mathbf{x}_{[2]}) = p_2$, and $p_1 + p_2 = d$. Also, \mathbf{A} and \mathbf{C} are estimated, and $\mathbf{B} = (\mathbf{B}_{[1]}^T \mathbf{B}_{[2]}^T)^T$ with $\mathbf{B}_{[2]} = \mathbf{C} \mathbf{A}^T$, a reduced-rank approximation of a subset of \mathbf{B} (cf. (1)). The *rank* R is often 1 or 2, maybe 3 ... Using corner constraints is one method to ensure \mathbf{A} and \mathbf{C} are unique.

For QRR-VGLMs (Yee, 2004a):

$$\begin{aligned} \boldsymbol{\eta}(\mathbf{x}) &= \mathbf{B}_{[1]}^T \mathbf{x}_{[1]} + \mathbf{A} \mathbf{v} + \sum_{j=1}^M (\mathbf{v}^T \mathbf{D}_j \mathbf{v}) \mathbf{e}_j \\ &= \mathbf{B}_{[1]}^T \mathbf{x}_{[1]} + \mathbf{A} \mathbf{v} + \begin{pmatrix} \mathbf{v}^T \mathbf{D}_1 \mathbf{v} \\ \vdots \\ \mathbf{v}^T \mathbf{D}_M \mathbf{v} \end{pmatrix}, \end{aligned} \quad (8)$$

where \mathbf{e}_i is a vector of zeros but with a one in the i th position, and \mathbf{D}_j are $R \times R$ symmetric matrices. Then $\mathbf{T}_j = -\frac{1}{2} \mathbf{D}_j^{-1}$ are *tolerance matrices*. QRR-VGLMs can fit symmetric bell-shaped curves to species' abundance data for ordination in ecology.

For RCIMs (Yee and Hadi, 2014): these are RR-VGLMs applied to \mathbf{Y} (no $\mathbf{X}!$), with

$$g(\boldsymbol{\theta}_1) \equiv \boldsymbol{\eta}_{1ij} = \mu + \alpha_i + \gamma_j + \sum_{r=1}^R c_{ir} a_{jr}, \quad (9)$$

where $R \leq \min(M, p_2)$. The other parameters $\boldsymbol{\theta}_2, \dots$ are usual intercept-only.

For a rank-1 CAO (Yee, 2006): these are RR-VGLMs with

$$g(\mu_{iq}) \equiv \boldsymbol{\eta}_{iq} = f_q(\mathbf{v}_i) \quad (10)$$

where $q = 1, \dots, Q$, $\mathbf{y}_i = (y_{i1}, \dots, y_{iQ})^T$, $\mathbf{v}_i = \mathbf{c}^T \mathbf{x}_i$ is a latent variable or site score, and the f_q are estimated by a smoothing spline. Only Poisson and Bernoulli responses are handled (currently, and for rank-1 only too).

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