

# Semiparametric Vector Generalized Linear Models

Estimation and Computation

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Honours Talk

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Motivation

Proposed Model

Fitting the Model

Applications

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Motivation

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Applications

A VGLM (Vector Generalized Linear Model) aims to generalize GLMs to multivariate responses, however, multivariate generalizations of common families of probability distributions (e.g., poisson, gamma, ...) are difficult to construct.

## Motivating Example (Butterfly Dataset)

This dataset contains 66 counts of 14 species of butterflies in Boulder Colorado, USA.

**Table 1:** Snippet of Butterfly Counts for the 3 most common species

site	Pieris.rapae	Colias.philodice	Colias.eurytheme	building	vegetation	habitat
1	0	0	0	2.1	10.8	mixed
2	1	1	2	2.1	10.8	mixed
3	1	1	2	19.8	1.7	mixed
4	0	2	1	5.3	0	mixed
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We would like to fit a joint model, as species could complement or compete with each other within a site.

However, no multivariate generalisation of the poisson distribution allows for both positive and negatively correlated response components.



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For multivariate data, problems arise when specifying a parametric distribution and the response covariance structure. For most cases there is no standard parametric model which could produce a given dataset.

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This model is a vector generalisation of a Semiparametric Generalized Linear Model <sup>1</sup>, which is based on an exponential tilt reformulation of the joint distribution from which the data originates for which the response distribution  $F$  remains unspecified.

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This model is a vector generalisation of a Semiparametric Generalized Linear Model <sup>1</sup>, which is based on an exponential tilt reformulation of the joint distribution from which the data originates for which the response distribution  $F$  remains unspecified.

This allows arbitrary nonparametric response distribution parameter  $F$  and the mean model parameters  $\beta$  to be simultaneously estimated without loss of information.

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Given data

$$(\mathbf{Y}_i, \mathbf{X}_i) \in \mathcal{Y} \times \mathcal{X} \subset \mathbb{R}^K \times \mathbb{R}^q, i = 1, \dots, n$$

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Assume these are independent samples originating from some multivariate exponential family. The joint density can be written in the form

$$dF_i(\mathbf{y}) = \exp\{b_i + \boldsymbol{\theta}_i^T \mathbf{y}\} dF(\mathbf{y}), \quad i = 1, \dots, n$$

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$$dF_i(\mathbf{y}) = \exp\{b_i + \boldsymbol{\theta}_i^T \mathbf{y}\} dF(\mathbf{y}), \quad i = 1, \dots, n$$

where  $dF_i(\mathbf{y})$  is an exponential tilt of the response distribution  $dF(\mathbf{y})$ , with the amount of tilting  $\boldsymbol{\theta}$  determined by the mean  $\boldsymbol{\mu}(\mathbf{X}_i^T \boldsymbol{\beta})$  of the observation  $\mathbf{Y}_i$ .

The normalising constants  $b_i = b(\mathbf{X}_i, \beta, F)$  are defined to be

$$b(\mathbf{X}_i, \beta, F) = -\log \left\{ \int_{\mathcal{Y}} \exp\{\boldsymbol{\theta}_i^T \mathbf{y}\} dF(\mathbf{y}) \right\},$$

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and the vector of tilt parameters  $\boldsymbol{\theta}_i = \boldsymbol{\theta}(\mathbf{X}_i, \beta, F) \in \mathbb{R}^K$  is the implicit solution to

$$\mu_{(k)}(\mathbf{X}_{(k)}^T \beta_{(k)}) = \int_{\mathcal{Y}} y_{(k)} \exp\{b_i + \boldsymbol{\theta}_i^T \mathbf{y}\} dF(\mathbf{y}), \quad k = 1, \dots, K$$

This joint density has the log-likelihood

$$\ell(\beta, F|\mathbf{X}, \mathbf{Y}) = \sum_{i=1}^n \left\{ \log dF(\mathbf{Y}_i) + b_i + \boldsymbol{\theta}_i^T \mathbf{Y}_i \right\}$$

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One way to estimate the densities  $dF(\mathbf{Y}_i)$  is by replacing them with the histogram estimators  $p_i$ , which are assigned to values in the observed support  $\{\mathbf{Y}_i \in \mathbb{R}^k | i = 1, 2, \dots, n\}$

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This produces empirical log-likelihood.

$$\ell(\beta, \mathbf{p}) = \sum_{i=1}^n \log p_i + b_i + \boldsymbol{\theta}_i^T \mathbf{Y}_i$$



$(\hat{\beta}, \hat{p})$  are then the joint maximisers of the empirical log likelihood.

$$(\hat{\beta}, \hat{p}) = \arg \max \ell(\beta, p)$$

Subject to empirical analogous of the normalising constraints

$$1 = \sum_{i=1}^n p_i \exp\{b_j + \boldsymbol{\theta}_j^T \mathbf{Y}_i\}, \quad j = 1, 2, 3, \dots, n$$

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$$1 = \sum_{i=1}^n p_i \exp\{b_j + \theta_j^T \mathbf{Y}_i\}, \quad j = 1, 2, 3, \dots, n$$

and the mean constraints

$$\mu_{(k)}(\mathbf{X}_{(k)j}^T \beta_{(k)}) = \sum_{i=1}^n p_i Y_{(k)i} \exp\{b_j + \theta_j^T \mathbf{Y}_i\} \quad j = 1, \dots, n, k = 1, \dots, K$$

There have been some results shown for the conducting parameter inference in the univariate case of this model (Huang [2014](#); Huang and P. Rathouz [2017](#)), which generalise to this model.

For testing the null hypothesis

$$H_0 : \beta_{(k)j} = 0, \\ k = 1, \dots, K, j = 1, \dots, q_k$$

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$$\frac{\hat{\beta}_{(k)j}}{\sqrt{\hat{\Sigma}_{(k)j,(k)j}}} \sim t_{n-q_k}$$

where the standard errors are derived from the empirical log-likelihood

$$\hat{\Sigma} = \left\{ \text{Var} \left[ \nabla \ell(\boldsymbol{\beta}, \boldsymbol{\rho}) \right] \right\}^{-1}$$

For Point Hypothesis  $H_0 : \beta = \beta^*$

$$2\{\ell(\hat{\beta}) - \ell(\beta^*)\} \sim \chi_Q^2, \quad Q = \sum_{k=1}^K q_k$$



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$$2\{\ell(\hat{\beta}) - \ell(\hat{\beta}_0)\} \sim \chi_r^2$$

For finite samples the following adjustment can be made

$$2\{\ell(\hat{\beta}) - \ell(\hat{\beta}_0)\} \sim rF_{r, n-Q}$$

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Currently the model is fit computationally in MATLAB using non-linear constrained optimization to maximise the empirical log-likelihood.<sup>2</sup>

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<sup>2</sup>The code is available at GitHub <https://github.com/gden173/vspglm>

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which are subject to  $nK + n$  mean and normalising constraints.

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Contains 66 counts of 14 species of butterfly in Boulder Colorado, USA.

**Table 2:** Snippet of Butterfly Counts for the 3 most common species

site	Pieris.rapae	Colias.philodice	Colias.eurytheme	building	vegetation	habitat
1	0	0	0	2.1	10.8	mixed
2	1	1	2	2.1	10.8	mixed
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We can fit this model directly to the counts of the each butterfly species using separate mean models, without the need to specify any association between species.

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$$\begin{aligned}\mu_{(k)i} &= \mathbb{E}[Y_{(k)i} | \mathbf{X}_i] = \exp\{\mathbf{X}_i^T \boldsymbol{\beta}_{(k)}\}, \\ i &= 1, 2, \dots, 66, \quad k = 1, 2, \dots, 14\end{aligned}$$

```
butterfly = fit_vspglm(...  
  ["colias.philodice ~ (building,urban,habitat)",...  
  "pieris.rapae ~ (building, urban, habitat)", ...  
  "colias.eurytheme ~ (building, urban, habitat)"], ...  
  tbl, {'log', 'log', 'log'})
```

**Figure 1:** Formula Syntax to fit 3 separate unconstrained models using the same covariates and log link functions

# Butterfly Dataset

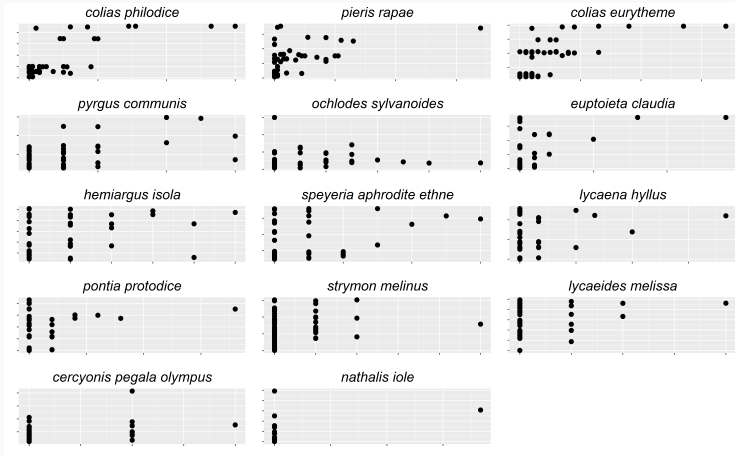
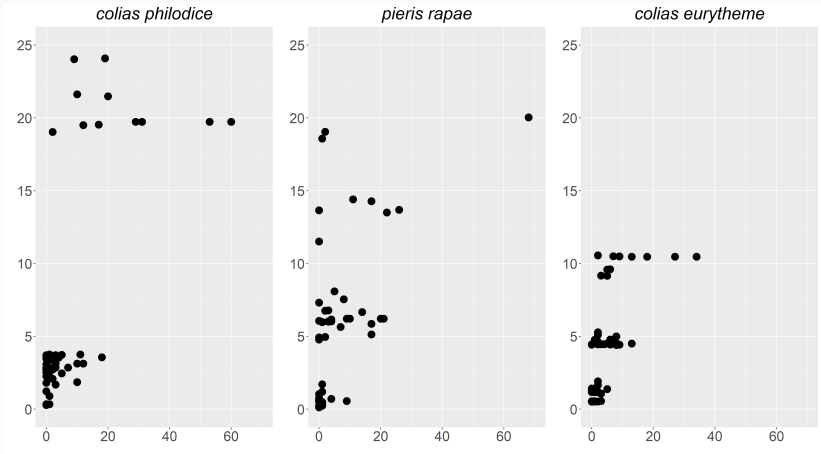


Figure 2: Predictions (y-axis) vs Observed counts (x-axis)



# Butterfly Dataset



**Figure 3:** Predictions (y-axis) vs Observed counts (x-axis) for the 3 butterfly species with the greatest number of observed counts

Contains 981 observations of patients admitted to hospital with 3rd degree burns.

**Table 3:** Snippet of Burns Dataset

	<b>age</b>	<b>burns</b>	<b>death</b>
1	3	6.9	1
2	39	7.4	1
3	42	3.9	1
4	21	6.1	1
⋮	⋮	⋮	⋮

Response vector has two components  $\mathbf{Y} = (Y_{\text{death}}, Y_{\text{burn}})$  , which are binary and continuous, and a single covariate  $\mathbf{X} = (X_{\text{age}})$ .

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This suggests the two marginal mean models

$$\mu_{(1)} = \mathbb{E}[\text{death}|\text{age}] = \frac{\exp\{\beta_{(1)1} + \beta_{(1)2}\text{age}\}}{1 + \exp\{\beta_{(1)1} + \beta_{(1)2}\text{age}\}}$$

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$$\mu_{(2)} = \mathbb{E}[\text{burns}|\text{age}] = \beta_{(2)1} + \beta_{(2)2}\text{age}$$

The code for fitting this model is

```
model = fit_vspglm(["death~age", "burns~age"], tbl, {'logit', 'id'})
```

## Burn Injury Data Set

This data set has been analysed several times using a variety of VGLMS, with Huang ([2017](#)) using GEEs to fit these mean models.

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GEE model parameters

$$\hat{\mu}_{(1)} = \frac{\exp\{-3.6891 + 0.0508\text{age}\}}{1 + \exp\{-3.6891 + 0.0508\text{age}\}}$$

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VSPGLM model parameters

$$\hat{\mu}_{(1)} = \frac{\exp\{-3.657 + 0.0509\text{age}\}}{1 + \exp\{-3.657 + 0.0509\text{age}\}}$$

$$\hat{\mu}_{(2)} = 6.7318 + 0.0027\text{age}$$



	$se(\hat{\beta})$
$\beta_{\text{death,age}}$	0.0051
$\beta_{\text{burns,age}}$	0.0017

**Table 4:** GEE corrected standard errors

	$se(\hat{\beta})$
$\beta_{\text{death,age}}$	0.0045
$\beta_{\text{burns,age}}$	0.0019

**Table 5:** VSPGLM standard errors

Contains  $n = 41$  observations of itching scores ( $Y_L, Y_R$ ) for the left and right eye after the application of sorbinil or a placebo, measured on a Likert scale between 0 and 4.

**Table 6:** Snippet of Sorbinil dataset

$n = 6$		$n = 14$		$n = 14$		$n = 7$	
sorbinil	sorbinil	sorbinil	placebo	placebo	sorbinil	placebo	placebo
Left	Right	Left	Right	Left	Right	Left	Right
2	2	1	1.5	2.5	2	3	3
1	1	2	2.5	2.5	2.5	2	3
0.5	2	3	1	3	3	2.5	2.5
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$

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The following symmetric model was found to be adequate

$$\mu_L = \beta_0 + \beta_1 \mathcal{I}_L, \quad \mu_R = \beta_0 + \beta_1 \mathcal{I}_R$$

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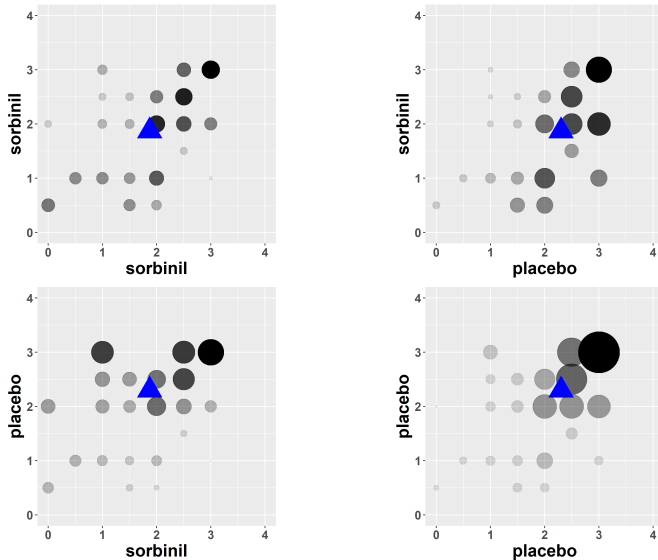
$$\mu_L = \beta_0 + \beta_1 \mathcal{I}_L, \quad \mu_R = \beta_0 + \beta_1 \mathcal{I}_R$$

This model finds a significant effect that sorbinil reduces itching scores by 0.43.

The code to fit this symmetric model is






```
sorbinil = fit_vspglm(["(Y_L, Y_R) ~ (I_L & I_R)"], tbl, {'id'})
```

# Sorbinil Dataset



**Figure 4:** Reweighted Sorbinil pmf at group medians (left = y axis, right = x axis)



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## Trivariate Poisson Model

$$\alpha \sim \mathcal{N}(0, \sigma_0^2), \quad \sigma \in \mathbb{R}_+$$

$$\mathbf{X} \sim \text{U}[-1, 1]^3$$

$$Y_1 | \alpha, \mathbf{X}_{(1)} \sim \text{Pois}(\exp(\mathbf{X}_{(1)}^T \boldsymbol{\beta}_{(1)} + \alpha))$$

$$Y_2 | \alpha, \mathbf{X}_{(2)} \sim \text{Pois}(\exp(\mathbf{X}_{(2)}^T \boldsymbol{\beta}_{(2)} + 0.5\alpha))$$

$$Y_3 | \alpha, \mathbf{X}_{(3)} \sim \text{Pois}(\exp(\mathbf{X}_{(3)}^T \boldsymbol{\beta}_{(3)} - 0.3\alpha))$$

# Trivariate Poisson Simulation Results

**Table 7:** Simulation results for trivariate Poisson model using a sample size of  $n = 200$  and  $N = 1000$  simulations

$\beta$	$\hat{\beta}$	$ \beta - \hat{\beta} $	Errors		$p \leq 0.05$	CI		
			$\hat{\sigma}$	$\text{se}(\hat{\beta})$		90%	95%	99%
0.4	0.40	0.004	0.13	0.12	0.88	0.89	0.94	0.99
-0.8	-0.79	0.002	0.13	0.14	0.99	0.93	0.96	0.99
0	0.001	0.001	0.13	0.12	0.05	0.89	0.95	0.99

## Trivariate Mixed Effects Simulation

$$\alpha \sim \mathcal{N}(0, \sigma_0^2)$$

$$\mathbf{X} \sim \text{U}[-1, 1]^3$$

$$\mathbf{Y}_1 | \mathbf{X}_{(1)}, \alpha \sim \mathcal{N}(\mathbf{X}_{(1)}^T \boldsymbol{\beta}_{(1)} + \alpha, \sigma_1^2)$$

$$\mathbf{Y}_2 | \mathbf{X}_{(2)}, \alpha \sim \text{Pois}(\exp(\mathbf{X}_{(2)}^T \boldsymbol{\beta}_{(2)} + 0.5\alpha))$$

$$\mathbf{Y}_3 | \mathbf{X}_{(3)}, \alpha \sim \text{Gamma}(\lambda, \exp(\mathbf{X}_{(3)}^T \boldsymbol{\beta}_{(3)} - 0.3\alpha))$$

# Trivariate Mixed Effects Simulation Results

**Table 8:** Simulation results for trivariate mixed effects model using a sample size of  $n = 200$  and  $N = 1000$  simulations

Margin	$\beta$	$\hat{\beta}$	$ \beta - \hat{\beta} $	Errors		$p \leq 0.05$	CI			
				$\hat{\sigma}$	$\text{s\!e}(\hat{\beta})$			90%	95%	99%
Normal	1	1.005	0.0058	0.17	0.18	1	0.90	0.95	0.99	
Poisson	-0.5	-0.49	0.0005	0.13	0.13	0.96	0.83	0.88	0.93	
Gamma	0.4	0.39	0.004	0.12	0.13	0.85	0.89	0.93	0.97	

## Multivariate Normal Simulation Results

**Table 9:** Simulation results for bivariate normal model using sample size of  $n = 200$  and  $N = 1000$  simulations

$\beta$	$\hat{\beta}$	$ \beta - \hat{\beta} $	Errors		$p \leq 0.05$	CI		
			$\hat{\sigma}$	$\text{s}\hat{\text{e}}(\hat{\beta})$		90%	95%	99%
-1	-0.99	0.0004	0.11	0.11	1	0.91	0.95	0.99
0	-0.0004	0.0004	0.11	0.11	0.05	0.90	0.95	0.99
0.5	0.49	0.009	0.14	0.13	0.95	0.88	0.94	0.98
2.2	2.19	0.003	0.14	0.14	1	0.90	0.94	0.98

**Table 10:** Type 1 errors at significance levels of 0.10, 0.05 and 0.01 using sample sizes of  $n = 75, 150$ , and  $N = 3000$  simulations

$n$	Type 1 Errors		
	0.10	0.05	0.01
75	0.119	0.060	0.012
150	0.097	0.050	0.013