Generalized linear model

Future Crops Statistical Workshop

Patrick Li

RSFAS, ANU

Australian National University

Content summary

- Review of linear model
- Motivation: why beyond linear model?
- Generalized linear model
- Example: GTA analysis

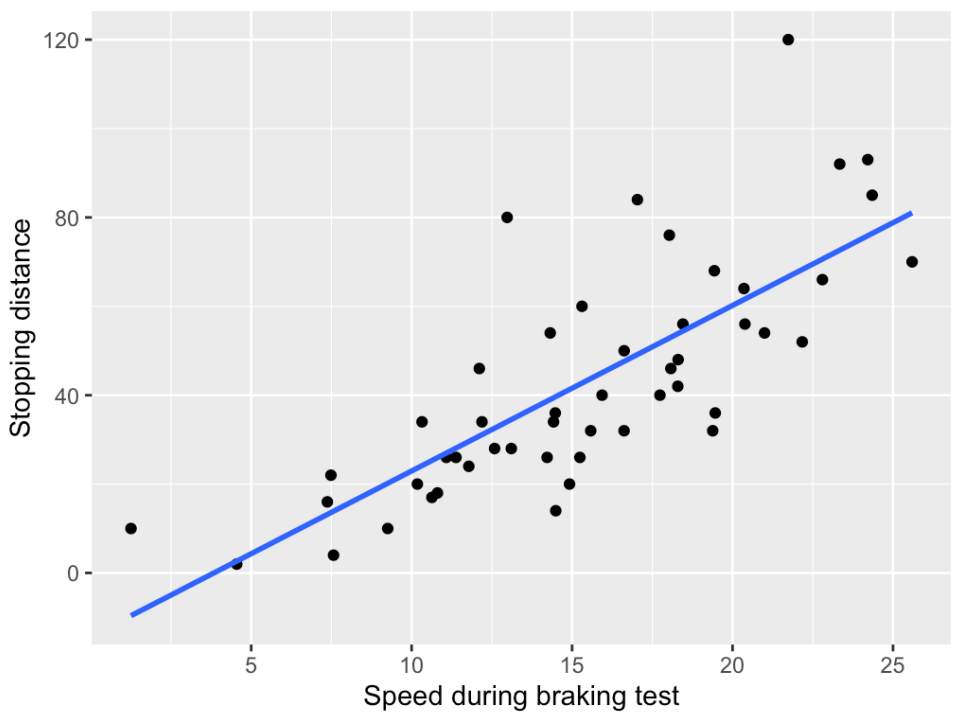
Review of linear model

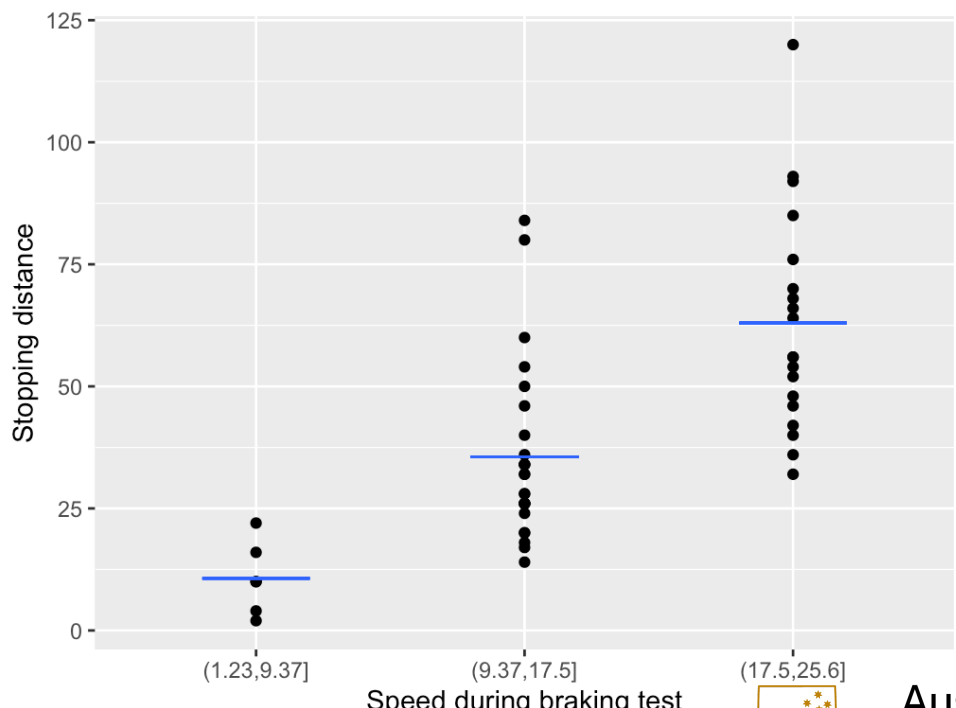
Linear model

We use linear model (LM) to find the **linear relationships** between predictor(s) X and a response variable Y.

When the predictor is **numerical**, the LM fits a straight line through the data that best predicts Y from X.

When the predictor is **categorical**, the LM estimates the mean of Y for each group or level.



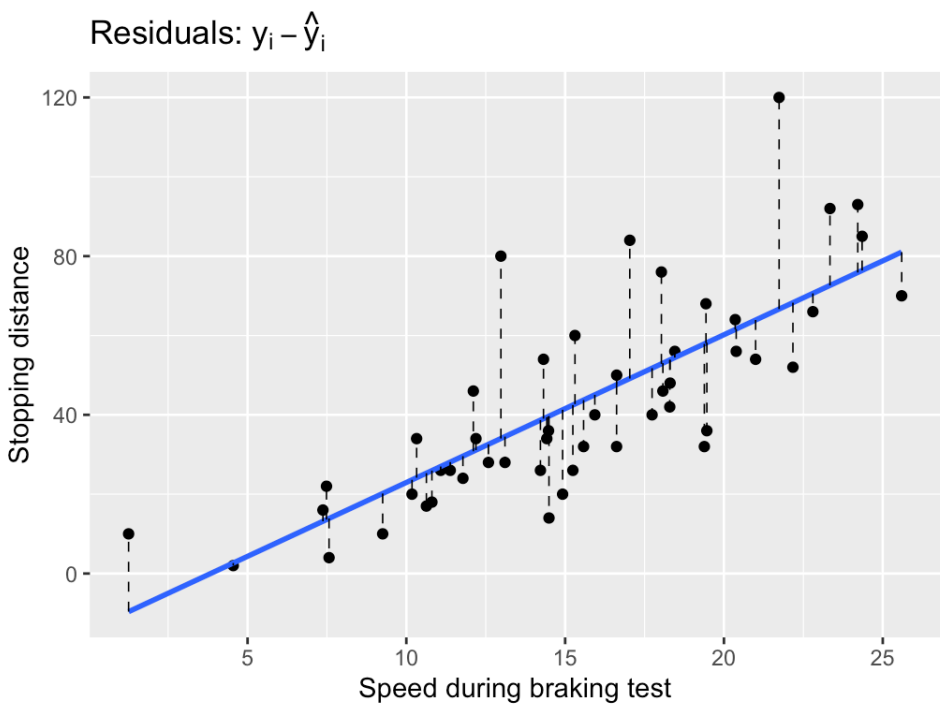


Simple linear model

Mathematically, a simple linear model can be written as

$$y_i = \beta_0 + \beta_1 x_i + \varepsilon_i, \quad \varepsilon_i \sim N(0, \sigma^2), \quad i = 1, \ldots, n,$$

where ε_i represents the random error term, the part of y_i that the model cannot explain from x_i.

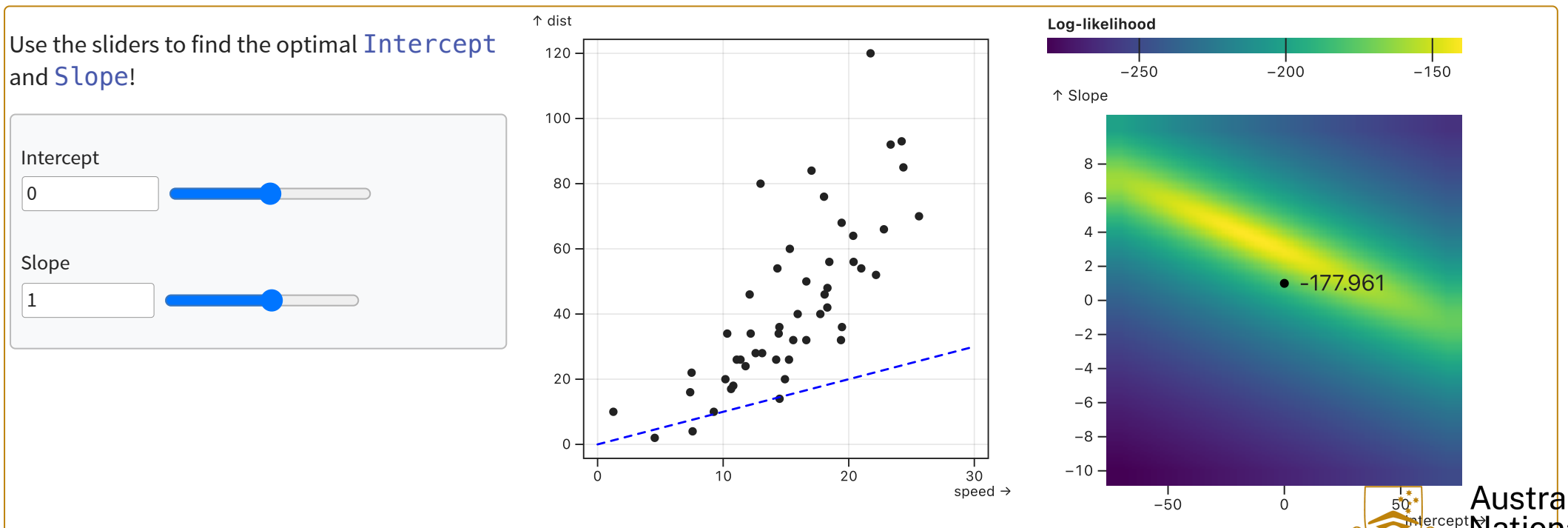


Maximum likelihood estimation

For a given intercept $\hat{\beta}_0$ and slope $\hat{\beta}_1$, the **likelihood** $L(\boldsymbol{\beta})$ quantifies how well the observed data fit the model. We can obtain the optimal $\hat{\beta}_0$ and $\hat{\beta}_1$ by maximizing $L(\boldsymbol{\beta})$:

$$(\hat{\beta}_0, \hat{\beta}_1) = \arg\max_{\beta_0, \beta_1} L(\boldsymbol{\beta}),$$

which is called **maximum likelihood estimation (MLE)**.



Why linear models aren’t enough

Just because a cat can fit into a glass doesn’t mean the cat is glass-shaped!

Figure source

We don’t use linear models because they are truly “correct”. In most cases, they’re not.

We use them mainly because of:

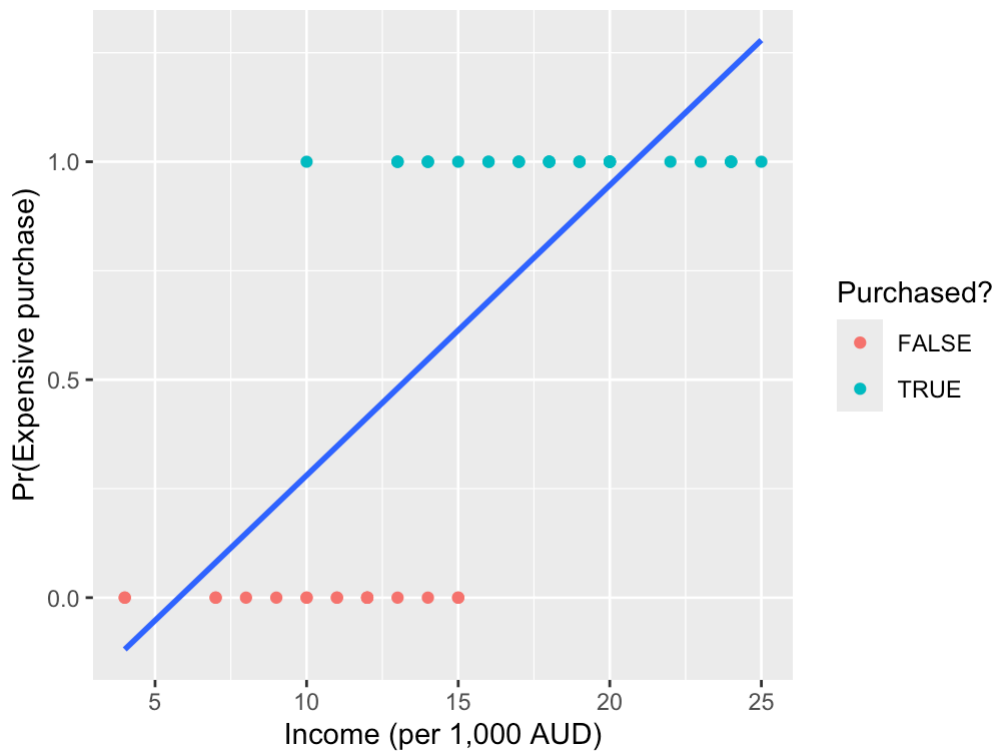
- Convenience
- Good enough as an approximation
- Familiarity
- Computational feasibility
- … and other practical reasons

Motivation: Why go beyond linear models?

Binary data

Fitting a linear model is often **inappropriate** for many types of response variables. For example, with binary data:

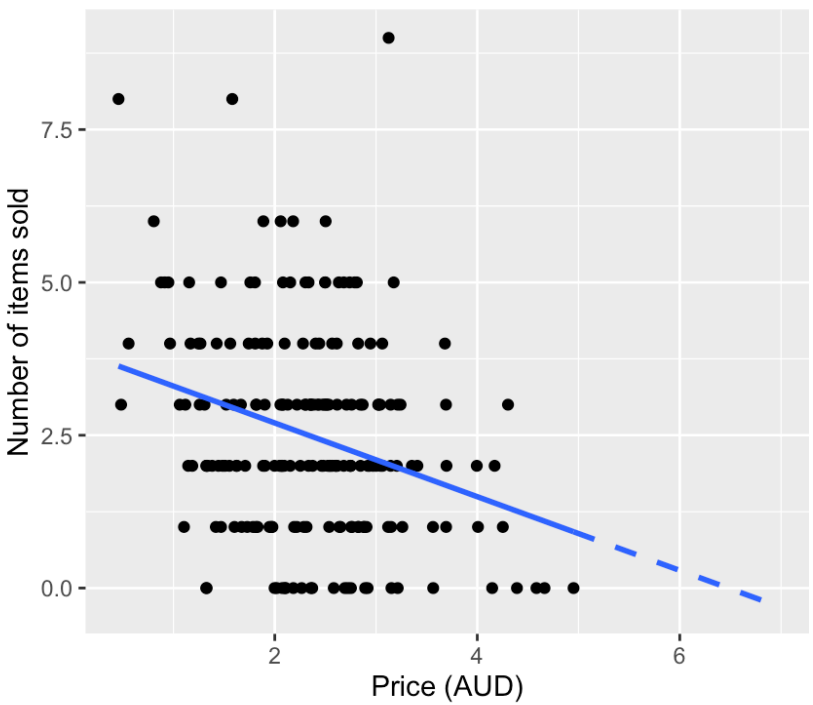
> Linear models can predict probabilities **outside the [0, 1] range**.

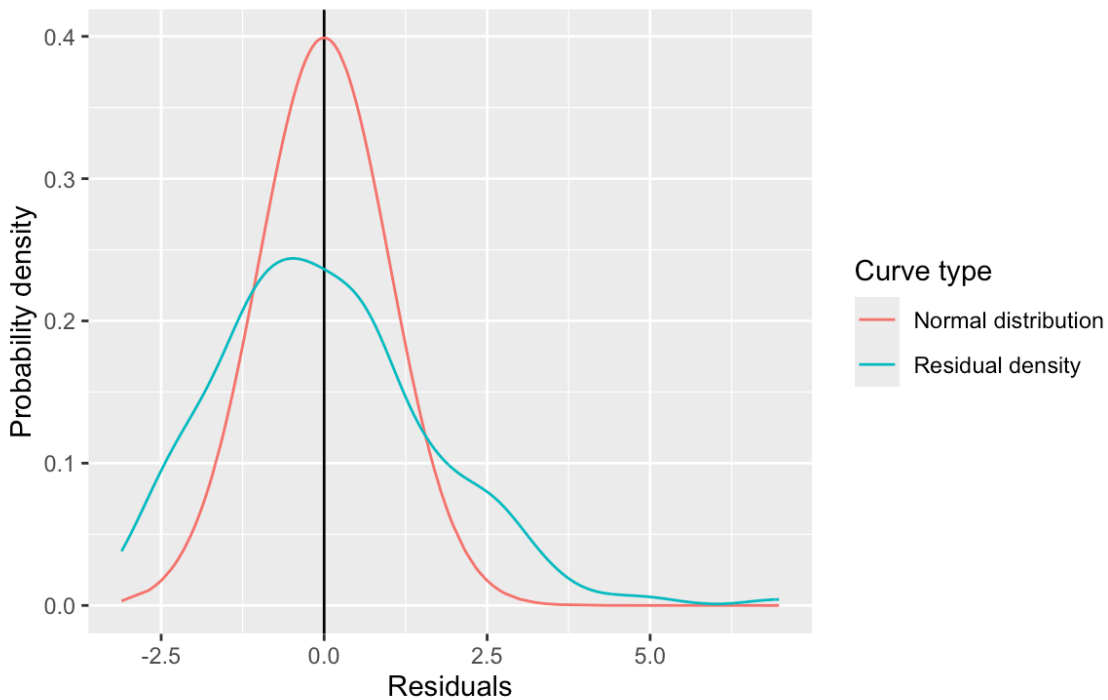


Count data

With count data:

> Linear models don't work well for low-count data because they can't capture its skewed shape and may produce negative predicted values.

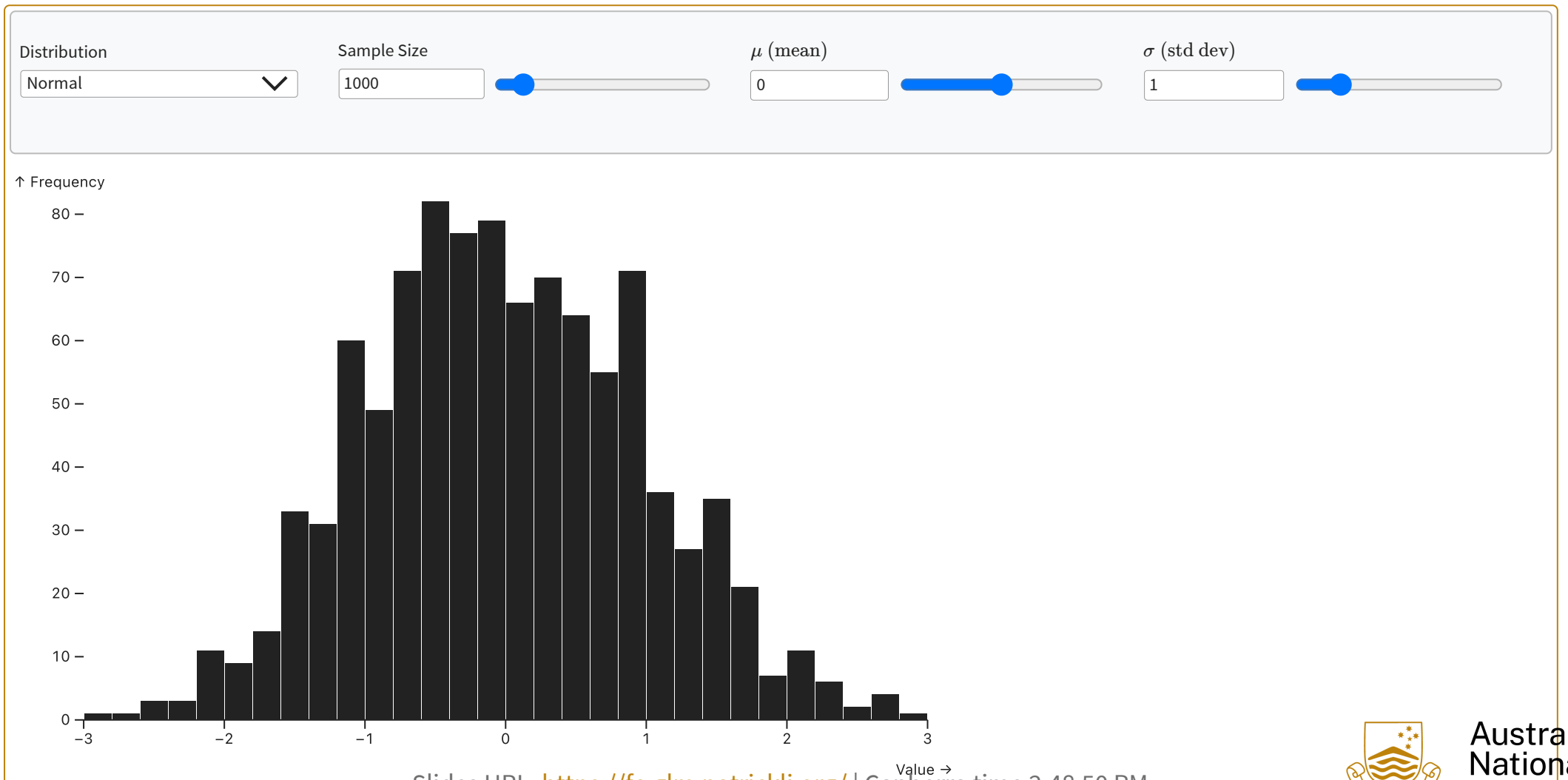




Generalized linear model

Exponential family

Generalized linear models provide a flexible framework for modeling data whose distribution belongs to the exponential family.



Model components

A **generalized linear model (GLM)** has three key components:

- The response Y follows a distribution from the **exponential family**.
- A **linear predictor**, for example, $\eta = \beta_0 + \beta_1 X$.
- A **link function** $g\big(E(Y \mid X)\big) = \eta$.

Canonical link function

A GLM can use different link functions for the same distribution, but there is always **one preferred link** that gives particularly nice mathematical properties. This is called the **canonical link function**.

Common generalized linear models

Distribution	Support	Typical uses	Link name	Link function $g(\mu)$
Normal	$(-\infty, +\infty)$	Linear-response data	Identity	$g(\mu) = \mu$
Exponential	$(0, +\infty)$	Exponential-response data, scale parameters	Negative inverse	$g(\mu) = -\mu^{-1}$
Gamma	$(0, +\infty)$	Positive continuous outcomes	Inverse	$g(\mu) = \mu^{-1}$
Inverse Gaussian	$(0, +\infty)$	Skewed positive continuous outcomes	Inverse squared	$g(\mu) = \mu^{-2}$
Poisson	$0, 1, 2, \ldots$	Count of occurrences in fixed time/space	Log	$g(\mu) = \ln(\mu)$
Bernoulli	$0, 1$	Outcome of single yes/no occurrence	Logit	$g(\mu) = \ln \frac{\mu}{1-\mu}$
Binomial	$0, 1, \ldots, N$	Count of "yes" out of N trials	Logit	$g(\mu) = \ln \frac{\mu}{N-\mu}$
Categorical	$[0, K)$	Outcome of single K-way occurrence	Generalized logit	$g(\mu) = \ln \frac{\mu_1}{1-\mu_1}$

Simple poisson regression

A simple Poisson regression can be expressed as

$$Y_i \sim \text{Poisson}(\lambda_i), \quad \log(\lambda_i) = \beta_0 + \beta_1 X_i, \quad i = 1, \ldots, n.$$

We then estimate $\hat{\beta}_0$ and $\hat{\beta}_1$ by maximizing the **likelihood**.

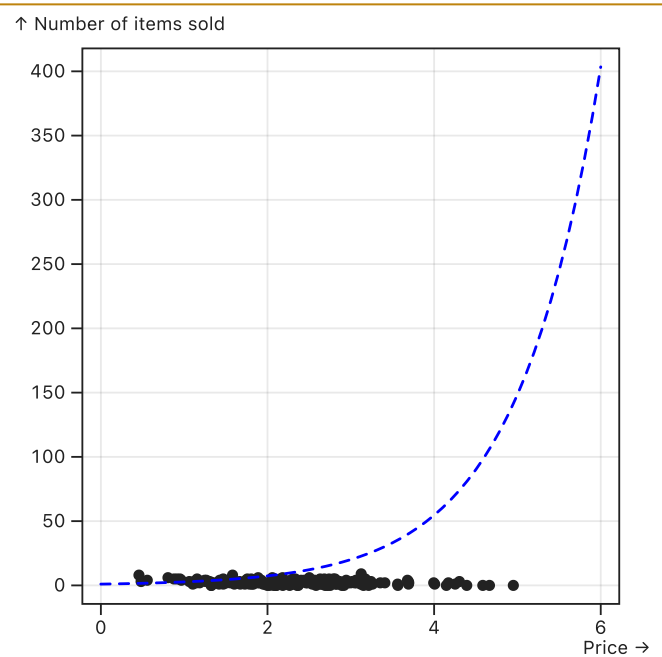
Use the sliders to find the optimal β_0 and β_1!

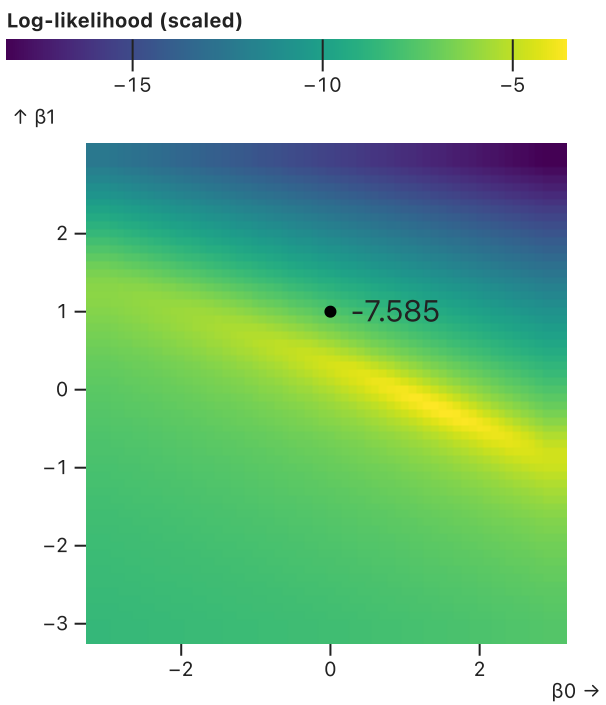
β_0

0

β_1

1





Deviance

In generalized linear models, the **deviance** D measures **how far** our model is from a perfect fit. It is defined as a transformation of the likelihood L:

$$D = 2\big(\log L(\hat{\theta}_s) - \log L(\hat{\theta})\big),$$

where $L(\hat{\theta}_s)$ is the likelihood of the **saturated model**, a model that fits each observation y_i perfectly for $i = 1, \ldots, n$.

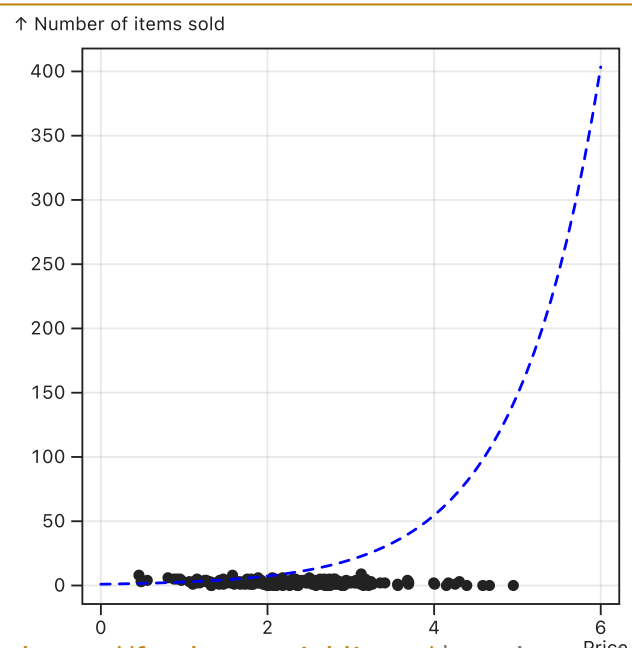
Use the sliders to find the optimal β_0 and β_1!

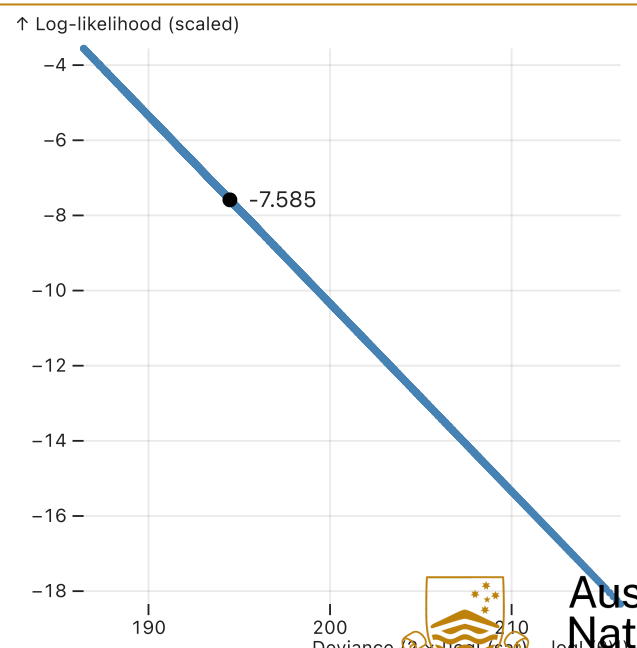
β_0

0

β_1

1





Deviance test

In a GLM, we can test the null hypothesis $H_0 : \beta_1 = 0$ against the alternative $H_1 : \beta_1 \neq 0$. Under H_0,

$$D_R - D_M \sim \chi^2_1,$$

where D_R is the deviance of the **restricted model** (excluding β_1) and D_M is the deviance of the **full model**. The degree of freedom of the χ^2 correspond to the number of parameter restrictions imposed.

To perform the test, we compute the **test statistic** $X^2 = D_R - D_M$, and compare it to the **critical value** of the χ^2_1 distribution, $\chi^2_{1,1-\alpha}$.

- $\chi^2_{1,1-0.1} \approx 2.706$
- $\chi^2_{1,1-0.05} \approx 3.841$
- $\chi^2_{1,1-0.01} \approx 6.635$

Simple possion model (deviance test)

Model	Description	Deviance	DOF
$\log(\lambda_i) = \beta_0$	A constant model where the mean response is the same for all observations.	268.502	199
$\log(\lambda_i) = \beta_0 + \beta_1 x_i$	A model where the log of the mean response is a linear function of the predictor.	248.672	198

Since

$$D_R - D_M = 268.502 - 248.672 = 19.83 > \chi^2_{1,0.95},$$

we reject the null hypothesis $H_0 : \beta_1 = 0$.

Recap of the GTA data

1. In the GTA analysis, each **sample** (s), either pure or a fixed admixture, such as GTAMix1 (85% BASS, 15% Maximus CL), is evaluated.
2. For each sample, multiple **devices** (d) are tested, and each evaluation produces predictions for one or more **varieties** (v), for example, (80% BASS, 20% Maximus CL).
3. Note that for the same evaluations, we sometimes have **replicates** (r).
4. These predicted percentages can be converted into predicted counts using the **number of seeds actually classified** (n_{sdr}) by the device in that evaluation.

Device consistency

We assess the **consistency of device predictions** by fitting a Poisson model:

$$n_{svdr} \sim \text{Poisson}(\lambda_{svdr}), \quad \log(\lambda_{svdr}) = \log(n_{sdr}) + \alpha_{vsdr},$$

where n_{svdr} is the number of **predicted seeds of a variety** evaluated by a specific device in a given sample and replicate, and n_{sdr} is the **total number of seeds** classified by that device in the same sample and replicate.

Unrestricted model

Rewriting the model gives:

$$\log\left(\lambda_{svdr}\right) - \log(n_{sdr}) = \alpha_{vsdr},$$

$$\log\left(\frac{\lambda_{svdr}}{n_{sdr}}\right) = \alpha_{vsdr},$$

which represents the log of the **expected percentage of a variety in a sample estimated by the model**, for example, 82.2% BASS in GTAMix1.

> By including α_{vsdr} in the model, we allow this estimated percentage to **vary across variety, sample, device and replicate**.

Restricted model

Next, we consider a **restricted version** of this model

$$n_{svdr} \sim \text{Poisson}(\lambda_{svdr}), \quad \log(\lambda_{svdr}) = \log(n_{sdr}) + \alpha_{vsr}.$$

In this version, α is **not allowed to vary across devices**, effectively imposing constraints on the model parameters. Hence, we refer to it as the **restricted model**.

Tesing device consistency

Model	Description	Deviance	DOF
$\log(\lambda_{svdr}) = \log(n_{sdr}) + \alpha_{vsr}$	α varies by variety × sample × replicate but **not across devices**.	70.062	324
$\log(\lambda_{svdr}) = \log(n_{sdr}) + \alpha_{vsdr}$	α varies by variety × sample × device × replicate.	0.000	0

Since

$$D_R - D_M = 70.062 - 0 = 70.062 > \chi^2_{324,0.95},$$

we reject the null hypothesis that **device predictions are consistent**.

Takeaways

- Linear models work well for continuous, normally distributed data but can fail with binary or count outcomes.
- GLMs extend linear models to handle diverse data from the exponential family using link functions.
- Model evaluation uses deviance to measure fit, with deviance tests comparing nested models.

Thanks! Any questions?

tengmcing

patrick.li@anu.edu.au

patrickli.org

Australian National University