Lecture 2 - Generalized Linear Models: Model Selection and Multinomial Logistic Regression

Contents

Today's Learning Goals

By the end of this lecture, you should be able to:

- Perform likelihood-based model selection through analysis of deviance, Akaike Information Criterion, and Bayesian Information Criterion.
- Extend the link function concept of the generalized linear models (GLMs) to other discrete categorical responses.
- Outline the modelling framework of the Multinomial Logistic regression.
- Fit and interpret the Multinomial Logistic regression.
- Use the Multinomial Logistic regression for prediction.

Loading Libraries

```
options(repr.matrix.max.rows = 7)
library(tidyverse)
library(broom)
library(glmbb)
library(AER)
library(bayesrules)
library(cowplot)
library(janitor)
library(nnet)
```

1. Likelihood-based Model Selection

In **DSCI 561**, you learned about **model selection** in Ordinary Least-squares (OLS) via specific metrics such as the Mallow's C_p, Akaike information criterion (AIC), and Bayesian information criterion (BIC). These metrics are also helpful tools to perform **model selection** in GLMs. Additionally, it is essential to highlight that **many** GLMs are estimated via maximum likelihood.

Having said all this, you will learn today that metrics such as AIC and BIC are likelihood-based. Hence, the concept of maximum likelihood estimation (MLE) will come into play again for model selection **in many GLMs**. Firstly, let us explore model selection for Poisson regression via the dataset from Lecture 1 - Generalized Linear Models: Link Functions and Count Regression.

1.1. The Crabs Dataset

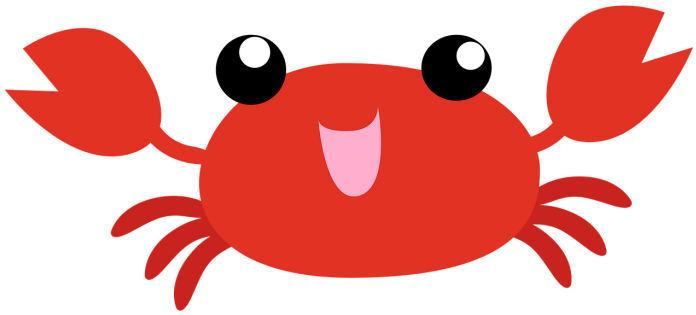


Fig. 6 Hello! I'm the Crab, again!

The data frame `crabs` (Brockmann, 1996) is a dataset detailing the **counts of satellite male crabs** residing around a female crab nest. The code below renames the original response's name, `satell`, to `n_males`.

```
data(crabs)
crabs <- crabs |>
  rename(n_males = satell) |>
  dplyr::select(-y)
crabs
```

A data.frame: 173 × 5

color	spine	width	n_males	weight
<fct>	<fct>	<dbl>	<int>	<int>
medium	bad	28.3	8	3050
dark	bad	22.5	0	1550
light	good	26.0	9	2300
dark	bad	24.8	0	2100
⋮	⋮	⋮	⋮	⋮
light	good	28.0	0	2625
darker	bad	27.0	0	2625
medium	middle	24.5	0	2000

The Crabs Dataset

The data frame `crabs` contains 173 observations on horseshoe crabs (Limulus polyphemus). The response is **the count of male crabs** (`n_males`) around a female breeding nest. It is subject to four explanatory variables **related to the female crab**: `color` of the prosoma with four levels (categorical factor-type), the condition of the posterior `spine` with three levels (categorical factor-type), the continuous variables carapace `width` (cm), and `weight` (g).

1.2. Estimation

To perform model selection, let us estimate two Poisson regression models with `n_males` as a response. **Model 1** will only have the continuous carapace `width` ($X_{\texttt{width}_i}$) as a regressor, whereas **Model 2** will have carapace `width` ($X_{\texttt{width}_i}$) and `color` of the prosoma (with dummy variables $X_{\texttt{color\_darker}_i}$, $X_{\texttt{color\_light}_i}$, and $X_{\texttt{color\_medium}_i}$).

Model 1:

$$h(\lambda_i) = \log(\lambda_i) = \beta_0 + \beta_1 X_{\texttt{width}_i}.$$

Model 2:

$$h(\lambda_i) = \log(\lambda_i) = \beta_0 + \beta_1 X_{\texttt{width}_i} + \beta_2 X_{\texttt{color\_darker}_i} + \beta_3 X_{\texttt{color\_light}_i} + \beta_$$

Then, via `glm()` and `crabs`, we obtain our regression estimates.

```
poisson_model <- glm(n_males ~ width, family = poisson, data = crabs)
poisson_model_2 <- glm(n_males ~ width + color, family = poisson, data = crabs
```

Since we are digging into model selection, let us keep in mind the below **main statistical inquiry**.

Main statistical inquiry

We want to determine which Poisson regression model fits the data better: **Model 1** or **Model 2**.

1.3. Goodness of Fit Test

The **deviance** (D_k) criterion can be used to compare a given model with k regressors with that of a **baseline model**.

Definition of a Saturated or Full Model in Poisson Regression

The usual **baseline model** is the **saturated** or **full model**, which perfectly fits the data because it allows a distinct Poisson mean λ_i for the ith observation in the training dataset ($i = 1, \ldots, n$), **unrelated to the k regressors**.

The **maximized likelihood** of this full model is denoted as $\hat{\ell}_f$. Now, let $\hat{\ell}_k$ be the value of the maximized likelihood computed from our dataset of n observations with k regressors.

We can compare the fits provided by these two models by the deviance D_k given by

(13)

$$D_k = -2\log\left(\frac{\hat{\ell}_k}{\hat{\ell}_f}\right) = -2\left[\log\left(\hat{\ell}_k\right) - \log\left(\hat{\ell}_f\right)\right].$$

Note that D_k expresses **how much our given model deviates from the full model on log-likelihood scale**. This metric is interpreted as follows:

- **Large values** of D_k arise when $\hat{\ell}_k$ is small relative to $\hat{\ell}_f$, indicating that **our given model fits the data poorly compared to the baseline model**.
- **Small values** of D_k arise when $\hat{\ell}_k$ is similar to $\hat{\ell}_f$, indicating that **our given model provides a good fit to the data compared to the baseline model**.

Specifically for Poisson regression with k regressors, it can be shown that D_k (13) is defined as follows:

$$\begin{aligned}\hat{\lambda}_i &= \exp\left(\hat{\beta}_0 + \hat{\beta}_1 x_{i,1} + \cdots + \hat{\beta}_k x_{i,k}\right)\\ D_k &= 2\sum_{i=1}^{n}\left[y_i \log\left(\frac{y_i}{\hat{\lambda}_i}\right) - \left(y_i - \hat{\lambda}_i\right)\right]\end{aligned} \tag{14}$$

where y_i is the ith observed response in the training set of size n. Note that when $y_i = 0$ counts, then $\log\left(\frac{y_i}{\hat{\lambda}_i}\right)$ is assumed as 0.

Definition of Goodness of Fit

Equation (14) depicts the agreement of our model with k regressors to the observed data. Hence, we can use (14) to test the goodness of fit; i.e., **whether our fitted model fits the data better than the saturated model, which makes it correctly specified (with a level of significance α!)**.

The hypothesis are the following:

$$H_0 : \text{Our } \textbf{Model with } k \textbf{ regressors} \text{ fits the data better than the } \textbf{Saturat}$$
$$H_a : \text{otherwise.}$$

Let us test our `poisson_model_2`:

$$h(\lambda_i) = \log(\lambda_i) = \beta_0 + \beta_1 X_{\texttt{width}_i} + \beta_2 X_{\texttt{color\_darker}_i} + \beta_3 X_{\texttt{color\_light}_i} + \beta_4 X_{\texttt{color\_med}}$$

We cannot use `anova()` to perform this hypothesis testing. We will have to do it manually via `glance()`,

```
summary_poisson_model_2 <- glance(poisson_model_2)
summary_poisson_model_2
```

A tibble: 1 × 8

null.deviance	df.null	logLik	AIC	BIC	deviance	df.residual	nob
<dbl>	<int>	<dbl>	<dbl>	<dbl>	<dbl>	<int>	<int
632.7917	172	-457.3212	924.6425	940.4089	559.3448	168	17

Column `deviance` provides D_k and is formally called **residual deviance**, which is the **test statistic**. **Asymptotically**, we have the following **null distribution**:

$$D_k \sim \chi^2_{n-(k+1)}.$$

The degrees of freedom (column `df.residual` in our `glance()` output) are the **difference between the training set size n and the number of regression parameters in our model (including the intercept β_0).**

Let us obtain the corresponding p-value for this test. We can do it using `pchisq()`:

```
pchisq(summary_poisson_model_2$deviance,
  df = summary_poisson_model_2$df.residual,
  lower.tail = FALSE
)
```

1.47103669470051e-43

We obtain a p-value $< .001$, which gives statistical evidence to state that our `poisson_model_2` is **not** correctly specified when compared to the saturated model.

A Note on the Null Deviance

The above `glance()` output contains a metric call `null.deviance`. This metric comes from a Poisson regression model which is only estimated with an intercept, i.e., $\hat{\beta}_0$; let us call it D_0:

$$\hat{\lambda}_i = \exp\left(\hat{\beta}_0\right)$$
$$D_0 = 2\sum_{i=1}^{n}\left[y_i \log\left(\frac{y_i}{\hat{\lambda}_i}\right) - \left(y_i - \hat{\lambda}_i\right)\right]$$

where y_i is the ith observed response in the training set of size n. Note that when $y_i = 0$ counts, then $\log\left(\frac{y_i}{\hat{\lambda}_i}\right)$ is assumed as 0.

Moreover, `df.null` indicates the degrees of freedom of this model, which are $n - 1 = 173 - 1 = 172$ (**the difference between the training set size n and the number of regression parameters in the null model**; which is 1 in this case, i.e., β_0).

Important

A null model is different from a **saturated/baseline/full model**. It is importat to recall that the **saturated/baseline/full model** is a model that perfectly fits the training data, which could be viewed as basically interpolating all the training data points **without caring about any regressor at all**. Mathematically, the saturated model implicates having an exact prediction $\hat{\lambda}_i$ for each y_i:

$$\hat{\lambda}_i = y_i \qquad \text{for } i = 1, \ldots, n.$$

1.4. Analysis of Deviance for Nested Models

We can use analysis of deviance for model selection when two models are nested. Hence, we will test our two Poisson models:

Model 1:

$$h(\lambda_i) = \log(\lambda_i) = \beta_0 + \beta_1 X_{\texttt{width}_i}.$$

Model 2:

$$h(\lambda_i) = \log(\lambda_i) = \beta_0 + \beta_1 X_{\texttt{width}_i} + \beta_2 X_{\texttt{color\_darker}_i} + \beta_3 X_{\texttt{color\_light}_i} + \beta_4$$

This specific model selection will involve a hypothesis testing. The hypotheses are:

$$H_0 : \textbf{Model 1 fits the data better than Model 2}$$
$$H_a : \textbf{Model 2 fits the data better than Model 1.}$$

We have to use the multipurpose function `anova()` in the following way:

```
round(anova(poisson_model,
  poisson_model_2,
  test = "Chi"
), 4)
```

A anova: 2 × 5

	Resid. Df	Resid. Dev	Df	Deviance	Pr(>Chi)
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	171	567.8786	NA	NA	NA
2	168	559.3448	3	8.5338	0.0362

Let D_2 be the deviance (column `Resid. Dev`) for **Model 2** (`poisson_model_2`) in row 2 and D_1 (column `Resid. Dev`) the deviance for **Model 1** (`poisson_model`) in row 1. The **test statistic** Δ_D (column `Deviance`) for the analysis of deviance is given by:

$$\Delta_D = D_1 - D_2 \sim \chi^2_3,$$

which **asymptotically** (i.e., $n \to \infty$) is Chi-squared distributed with 3 degrees of freedom (column `Df`) under H_0 **for this specific case**.

We obtain a $p\text{-value} < .05$, column `Pr(>Chi)`, which gives us evidence to reject H_0 with $\alpha = 0.05$. Hence, we do have evidence to conclude that `poisson_model_2` fits the data better than `poisson_model`. Therefore, **in the context of model selection**, we would choose `poisson_model_2`, that also includes the `color` of the prosoma.

Important

In general, the degrees of freedom are the **regression parameters of difference between both models** (this has an impact on the factor-type explanatory variables with more than one dummy variable). In this example, **Model 2** has three additional parameters: β_2, β_3, and β_4.

Formally, this nested hypothesis testing is called the **likelihood-ratio test**.

1.5. Akaike Information Criterion

One of the drawbacks of the analysis of deviance is that it only allows to test **nested** regression models. Fortunately, we have alternatives for model selection. **The AIC makes possible to compare models that are either nested or not.** For a model with k model terms and a deviance D_k is defined as:

$$\text{AIC}_k = D_k + 2k.$$

Models with **smaller** values of AIC_k are preferred. That said, AIC_k favours models with small values of D_k.

Important

However, AIC_k penalizes for including more regressors in the model. Hence, it discourages overfitting, which is key in model selection.

This is why we select that model with the smallest AIC_k.

The function `glance()` shows us the AIC_k by model.

```
glance(poisson_model) |>
  mutate_if(is.numeric, round, 3)
```

A tibble: 1 × 8

null.deviance	df.null	logLik	AIC	BIC	deviance	df.residual	nobs
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
632.792	172	-461.588	927.176	933.483	567.879	171	173

```
glance(poisson_model_2) |>
  mutate_if(is.numeric, round, 3)
```

A tibble: 1 × 8

null.deviance	df.null	logLik	AIC	BIC	deviance	df.residual	nobs
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
632.792	172	-457.321	924.642	940.409	559.345	168	173

> Following the results of the `AIC` column, we choose `poisson_model_2` over `poisson_model`.

1.6. Bayesian Information Criterion

An alternative to AIC is the Bayesian Information Criterion (BIC). **The BIC also makes possible to compare models that are either nested or not.** For a model with k regressors, n observations used for training, and a deviance D_k; it is defined as:

$$\text{BIC}_k = D_k + k\log(n).$$

Models with **smaller** values of BIC_k are preferred. That said, BIC_k also favours models with small values of D_k.

> Following the results of the `AIC` column, we already chose `poisson_model_2` over `poisson_model`. Nonetheless, the `BIC` is penalizing the `poisson_model_2` for having more model parameters, so `poisson_model` would be chosen under this criterion.

Important

The differences between AIC and BIC will be more pronounced in datasets with large sample sizes n. As the BIC penalty of $k\log(n)$ will always be larger than the AIC penalty of $2k$ when $n > 7$, **BIC tends to select models with fewer regressors than AIC**.

Having said all this, in general, each metric's purpose can be summarized as follows:

- **AIC:** From a given set of models (either nested or non-nested) fitted via a common training dataset, this metric aims to select the model with the best predictive performance even though this model chosen might not be the true one that generates the training data. In essence, this metric is frequentist.
- **BIC:** From a given set of models (either nested or non-nested) fitted via a common training dataset, this metric will tend to select the true model that is generating the training data as the sample size n approaches infinity and **as long as the true model is within this given set of models**. This metric is Bayesian, in essence, since it relies on a prior true model probability distribution in conjunction with our observed evidence (i.e., the likelihoods yielded by each model of this set), which results in a posterior true model probability distribution indicating that true model (i.e., the one with the highest posterior probability).

Note

The math behind the rationale of these two metrics is out of the scope of this course. That said, if you would like to get further insights, you can check *Chapter 7 (Model Assessment and Selection)* in **The Elements of Statistical Learning: Data Mining, Inference, and Prediction**.

2. Categorical Type Responses

So far, we have dealt with continuous, binary, and count responses using OLS, Binary Logistic, Poisson (or Negative Binomial) regressions, respectively.

Nonetheless, we have not covered those **discrete responses with more than two categories**. Recall that the nature of these responses could be:

- **Nominal.** We have categories that do not follow any specific order—for example, the type of dwelling according to the Canadian census: *single-detached house*, *semi-detached house*, *row house*, *apartment*, and *mobile home*.
- **Ordinal.** The categories, in this case, follow a specific order—for example, a Likert scale of survey items: *strongly disagree*, *disagree*, *neutral*, *agree*, and *strongly agree*.

Moreover, you have seen that **using OLS to fit a model with a binary response variable has important problems**. Frequently, the restricted range is not respected in terms of the fitted values from our training set or if we use the fitted model to make predictions on a different testing set. So then, we use Binary Logistic regression.

> **Important**
>
> Recall that Binary Logistic regression's link function (the **logarithm of the odds** or **logit function**) restricts the corresponding probability of success to a range between 0 and 1 while relating it to the systematic component (i.e., the regressors and its corresponding parameters!).
>
> Nevertheless, this GLM has an important limitation: it is restricted to a Bernoulli trial with only two classes (**success** or **failure**).

Then, we might wonder: **what if we have more than two classes in the categorical response?**

Let us pave the way to two new GLMs to address this matter: **Multinomial and Ordinal Logistic regressions**.

3. Multinomial Logistic Regression

Moving along with GLMs, let us expand the regression mind map as in Fig. 7 to include a new model: **Multinomial Logistic regression**.

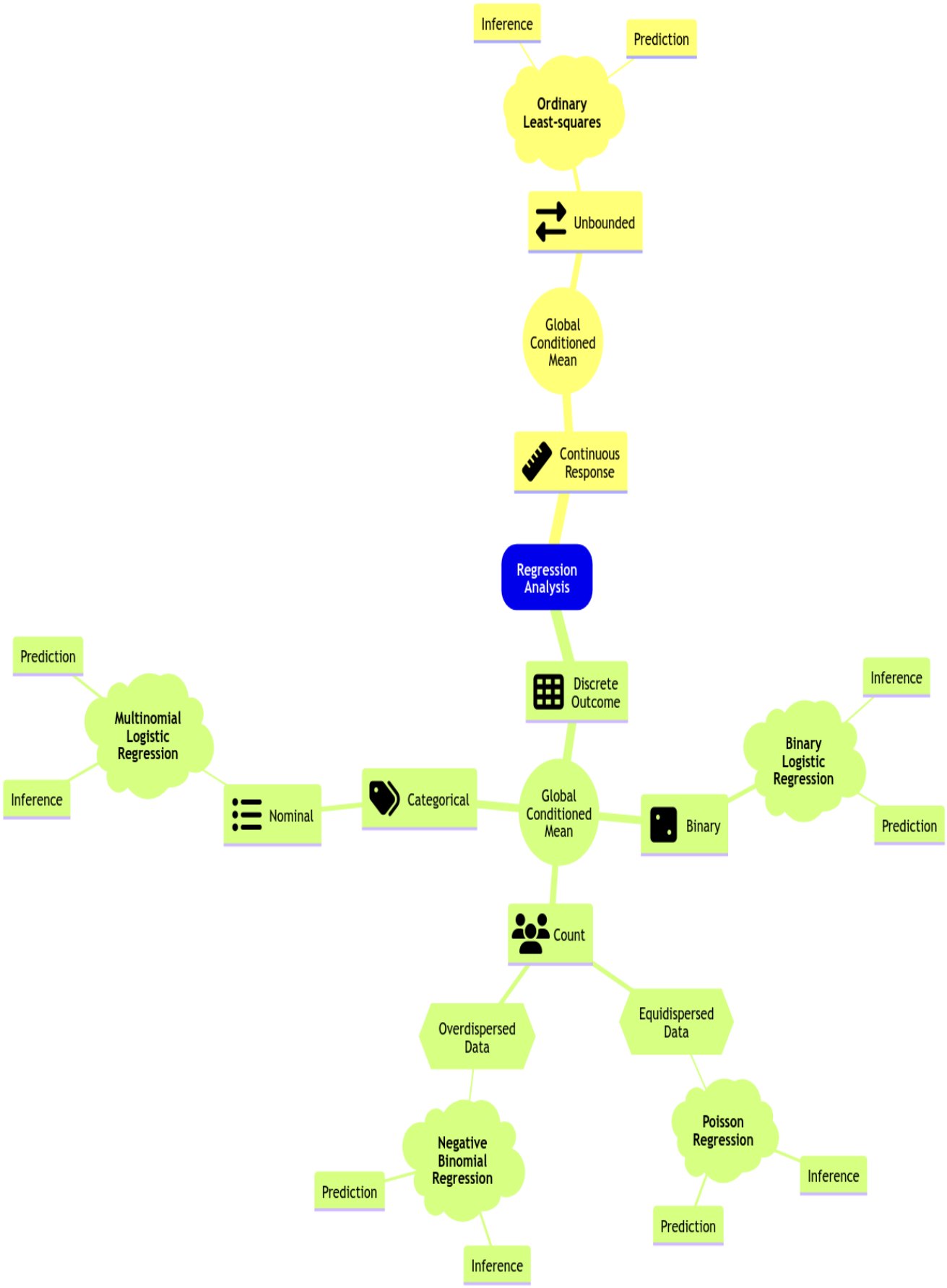


Fig. 7 Expanded regression modelling mind map.

Multinomial Logistic regression is a maximum likelihood-based GLM that addresses inferential (and predictive!) inquiries where the response is **categorical** and **nominal**. To illustrate the use of this GLM, let us introduce an adequate dataset.

3.1. The Spotify Dataset

The `spotify` dataset is a sample of $n = 350$ songs with different variables by column.

The Spotify Dataset

This data comes in the `bayesrules` package. Its description is the following:

> *A sub-sample of the Spotify song data originally collected by Kaylin Pavlik (kaylinquest) and distributed through the `R` for Data Science TidyTuesday project.*

This dataset has 23 variables in total. The $n = 350$ songs belong to 44 different artists.

```
spotify
```

track_id	title	artist	popularity	alb
<chr>	<chr>	<fct>	<dbl>	
7sYAS4CpbV90oSemgaEQat	On & On	Alok	79	2a9AGivapFES2j2E
1YSwQvw1NrEPfA0j1iY8eV	All The Lies	Alok	56	2FdyKqNeEX2H7gUht
39cmB3ZoTOLwOTq7tMNqKa	Hear Me Now	Alok	75	6fpsA5aYbVNLe6y3P
2Dnb6yPGUq0vmGtxzm3bwi	The Wall	Alok	65	0hH9tb1b4Z87g7SHr
⋮	⋮	⋮	⋮	
3SmytDq4CeZ3nKE9777qEx	Save My Grave	Zeds Dead	54	0M5oUKrfgJtfZUKdF
606LnHssjBNoQlrxa9KTYK	Shake	Zeds Dead	49	2S3ydN35socDKdH6R
4kbaxfwAF2FaquuDiWSkDT	Sound Of The Underground	Zeds Dead	48	4xjytv2hkFsqSz2z8

We will start with an in-class question via **iClicker**.

Exercise 4

Having checked the description of the `spotify` dataset, suppose we want to conduct an inferential study. What would be the primary nature of our conclusions?

A. We could draw causation conclusions across all music platforms.

B. We could draw association conclusions on the Spotify platform.

C. We could draw association conclusions across all music platforms.

D. We could draw causation conclusions on the Spotify platform.

Solution to Exercise 4

A sub-sample is defined as a sample taken from a larger sample. That said, we could still use it to draw inferences from a given population of interest. Thus, since we will basically conduct an observational study, the primary nature of our conclusions would be of association. Later on, in **DSCI 554**, we will see that it might be possible to assess causation in observational studies under different modelling assumptions involving further hypothesis tests (which might not be the case in this example!).

Regarding the target population of our conclusions, given that the sample was drawn from the Spotify platform, we would be limited to this specific population. In practice, we should be careful on this matter since you could run into studies whose inferential conclusions go too far regarding the population they want to address (even though their sampling could be narrowly framed!).

Main Statistical Inquiries

I am **big fan** of the electronic dance music (`edm`) catalogue on Spotify. Nevertheless, I do not have access to their whole song database. Still, I want to do the following:

- To statistically measure how danceable this genre is, compared to other genres on the platform, and by how much.
- To statistically measure how euphoric this genre is, compared to other genres on the platform, and by how much.

3.2. Data Wrangling and Summary

In terms of our main statistical inquiries, we will extract these **key variables by song** from the `spotify` dataset:

- `genre`: genre of the playlist where the song belongs (a **categorical** and **nominal** variable).
- `danceability`: a **numerical** score from 0 (not danceable) to 100 (danceable) based on features such as tempo, rhythm, etc.

- `valence`: a **numerical** score from 0 (the song is more negative, sad, angry) to 100 (the song is more positive, happy, **euphoric**).

We will also extract these secondary variables (**not to be used in our analysis**, just for having a more informative training data):

- `title`: song name.
- `artist`: song artist.
- `album_name`: name of the album on which the song appears.

```
spotify_training <- spotify |>
  select(title, artist, album_name, genre, danceability, valence) |>
  mutate(genre = as.factor(genre))
spotify_training
```

A tibble: 350 × 6

title	artist	album_name	genre	danceability	valence
<chr>	<fct>	<chr>	<fct>	<dbl>	<dbl>
On & On	Alok	On & On	pop	74.7	67.0
All The Lies	Alok	All The Lies (Remixes)	pop	70.7	63.4
Hear Me Now	Alok	Hear Me Now	pop	77.8	49.6
The Wall	Alok	The Wall	pop	68.2	53.6
⋮	⋮	⋮	⋮	⋮	⋮
Save My Grave	Zeds Dead	We Are Deadbeats (Vol. 4)	rap	60.4	12.3
Shake	Zeds Dead	Shake	edm	50.1	36.6
Sound Of The Underground	Zeds Dead	Sound Of The Underground	edm	67.5	19.2

Important

Note that factor-type `genre` has six levels (`edm` refers to **electronic dance music** and `r&b` to **rhythm and blues**). Moreover, **from a coding perspective**, `edm` is the **baseline** level (it is located on the **left-hand side** in the `levels()` output).

```
levels(spotify_training$genre)
```

'edm' · 'latin' · 'pop' · 'r&b' · 'rap' · 'rock'

Finally, let us summarize the data by `genre`.

```
spotify_training |>
  tabyl(genre) |>
  adorn_totals("row") |>
  adorn_pct_formatting()
```

A tabyl: 7 × 3

	genre	n	percent
	<fct>	<dbl>	<chr>
1	edm	60	17.1%
2	latin	27	7.7%
3	pop	71	20.3%
4	r&b	104	29.7%
5	rap	62	17.7%
6	rock	26	7.4%
7	Total	350	100.0%

Important

Note that `edm` accounts for 17.1% of the whole training data. On the other hand, `latin` and `rock` account for less than 10% each. Finally, `r&b` has the largest share with 29.7%.

Still, having checked this `genre` composition, we have an acceptable number of songs to draw inference from. Moreover, an imbalanced classification will be dealt with the distributional assumption of the Multinomial Logistic regression.

3.3. Exploratory Data Analysis

As done in our previous lecture, let us take a look at the data first. Note that `genre` is a **discrete nominal response**, so we must be careful about the class of plots we use for exploratory data analysis (EDA). Hence, we could use the following side-by-side plots for both `danceability` and `valence`:

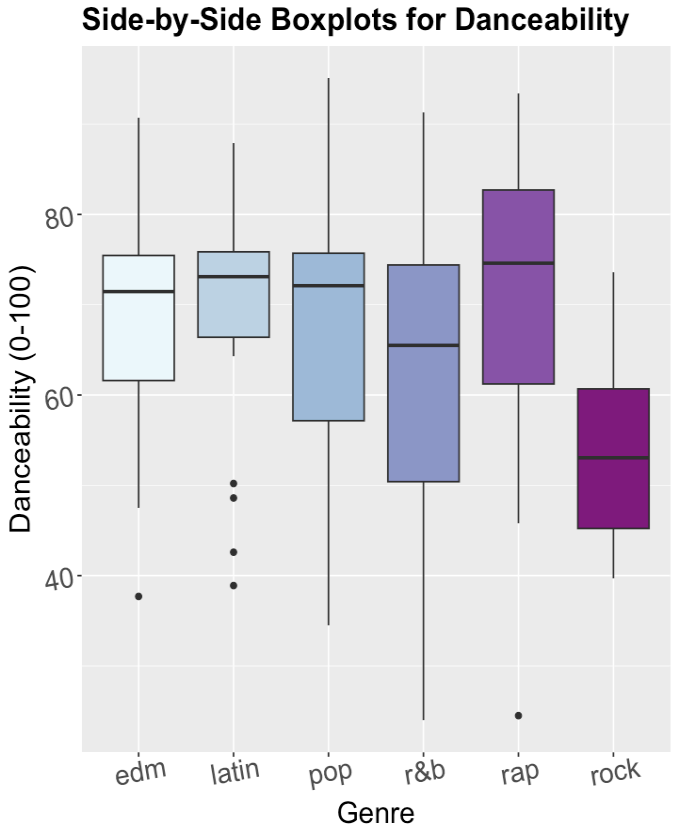
- **Boxplots.**
- **Violin plots.**

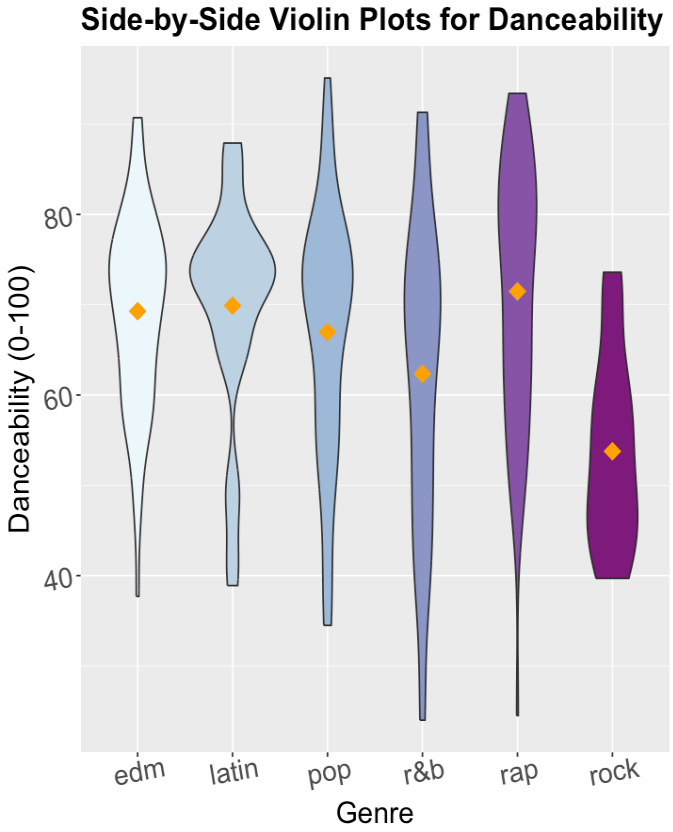
The code below creates side-by-side boxplots and violin plots, where `danceability` or `valence` are on the y-axis, and all categories of `genre` are on the x-axis. Moreover, the side-by-side violin plots show the mean of `danceability` or `valence` by `genre` as orange points.

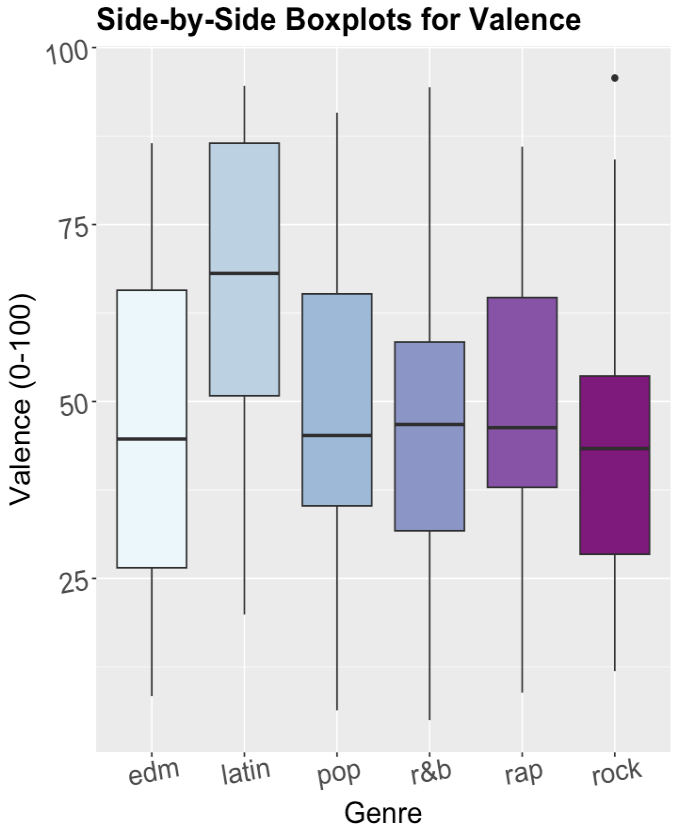
```
options(repr.plot.height = 14, repr.plot.width = 12)

genre_danceability_side_boxplots <- spotify_training |>
  ggplot(aes(genre, danceability)) +
  geom_boxplot(aes(fill = genre)) +
  labs(y = "Danceability (0-100)", x = "Genre") +
  ggtitle("Side-by-Side Boxplots for Danceability") +
  theme(
    plot.title = element_text(size = 19, face = "bold"),
    axis.text = element_text(size = 17, angle = 10),
    axis.title = element_text(size = 18),
    legend.position = "none"
  ) +
  scale_fill_brewer(palette = "BuPu")

genre_danceability_side_violin <- spotify_training |>
  ggplot(aes(genre, danceability)) +
  geom_violin(aes(fill = genre)) +
  labs(y = "Danceability (0-100)", x = "Genre") +
  ggtitle("Side-by-Side Violin Plots for Danceability") +
  stat_summary(
    fun = mean, colour = "orange", geom = "point",
    shape = 18, size = 5
  ) +
  theme(
    plot.title = element_text(size = 19, face = "bold"),
    axis.text = element_text(size = 17, angle = 10),
    axis.title = element_text(size = 18),
    legend.position = "none"
  ) +
  scale_fill_brewer(palette = "BuPu")

genre_valence_side_boxplots <- spotify_training |>
  ggplot(aes(genre, valence)) +
  geom_boxplot(aes(fill = genre)) +
  labs(y = "Valence (0-100)", x = "Genre") +
  ggtitle("Side-by-Side Boxplots for Valence") +
  theme(
    plot.title = element_text(size = 19, face = "bold"),
    axis.text = element_text(size = 17, angle = 10),
    axis.title = element_text(size = 18),
    legend.position = "none"
  ) +
  scale_fill_brewer(palette = "BuPu")

genre_valence_side_violin <- spotify_training |>
  ggplot(aes(genre, valence)) +
  geom_violin(aes(fill = genre)) +
  labs(y = "Valence (0-100)", x = "Genre") +
  ggtitle("Side-by-Side Violin Plots for Valence") +
  stat_summary(
    fun = mean, colour = "orange", geom = "point",
    shape = 18, size = 5
  ) +
  theme(
```

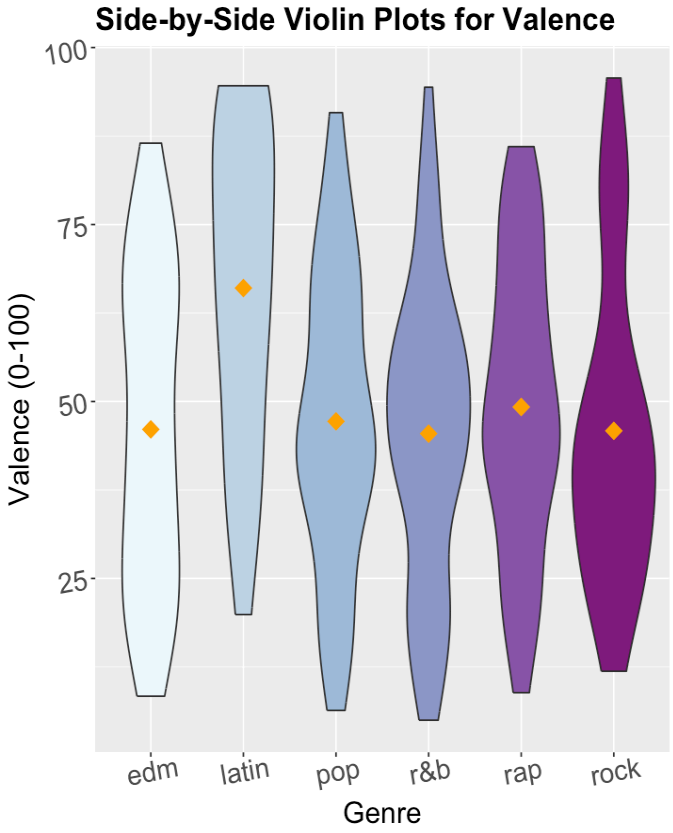
```
    plot.title = element_text(size = 19, face = "bold"),
    axis.text = element_text(size = 17, angle = 10),
    axis.title = element_text(size = 18),
    legend.position = "none"
  ) +
  scale_fill_brewer(palette = "BuPu")
```

```
plot_grid(genre_danceability_side_boxplots, genre_danceability_side_violin,
          genre_valence_side_boxplots, genre_valence_side_violin,
          nrow = 2)
```









Exercise 5

What can we see **descriptively** from the above plots?

Solution to Exercise 5

- In terms of `danceability`, we see similar central tendency measures (i.e, sample medians and means) for `edm`, `latin`, `pop`, and `rap`.
- Surprisingly, `r&b` does not seem as danceable as the above four genres.
- When it comes to `valence`, the `latin` genre seems to be the one with the most positivity (i.e., higher `valence` values). However, we have to be cautious about this conclusion since it is merely descriptive. On the other hand, the rest of the genres show similar central tendency measures.

3.4. Data Modelling Framework

A **Multinomial Logistic Regression model** is a suitable approach to our statistical inquiries given that `genre` is **categorical** and **nominal** (our response of interest) subject to the **numerical** regressors `danceability` and `valence`. Moreover, its corresponding regression estimates will allow us **to measure variable association**.

3.4.1. Primary Intuition of the Multinomial Logistic Regression Model

Digging into the Multinomial Logistic regression model will require checking **Binary Logistic regression** first. Hence, let us do it quickly. Thus, suppose we are initially interested in two genres: `edm` and `latin`.

```
bin_spotify_training <- spotify_training |>
  filter(genre %in% c("edm", "latin")) |>
  mutate(genre = droplevels(genre))
bin_spotify_training
```

A tibble: 87 × 6

title	artist	album_name	genre	danceability	valence
<chr>	<fct>	<chr>	<fct>	<dbl>	<dbl>
Toda La Noche	Alok	Toda La Noche	latin	73.5	61.6
On & On	Alok	On & On	edm	74.7	67.0
The Wall	Alok	The Wall	edm	68.2	53.6
Tell Me Why	Alok	Tell Me Why	edm	56.1	19.5
⋮	⋮	⋮	⋮	⋮	⋮
Renegades - Stash Konig Remix	X Ambassadors	Renegades (Stash Konig Remix)	edm	66.3	78.9
Shake	Zeds Dead	Shake	edm	50.1	36.6
Sound Of The Underground	Zeds Dead	Sound Of The Underground	edm	67.5	19.2

Note `edm` is the baseline level (i.e., it appears on the left-hand side in the `levels()` output).

```
levels(bin_spotify_training$genre)
```

'edm' · 'latin'

Assuming we have a **training set** of n elements, recall that the ith response (for $i = 1, \ldots, n$) in a **Binary Logistic regression** is

$$Y_i = \begin{cases} 1 & \text{if the genre is } \texttt{latin}, \\ 0 & \text{if the baseline genre is } \texttt{edm}. \end{cases}$$

Therefore

$$Y_i \sim \text{Bernoulli}(p_i),$$

whose probability of success is p_i.

In this model, we will use the following **link function** (where $X_{i,\texttt{dance}}$ anf $X_{i,\texttt{val}}$ are the `danceability` and `valence` scores for the ith song, respectively):

$$\begin{aligned}\text{logit}(p_i) &= \log\left(\frac{p_i}{1-p_i}\right)\\ &= \log\left[\frac{P(Y_i = \texttt{latin} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}})}{P(Y_i = \texttt{edm} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}})})\right]\\ &= \beta_0 + \beta_1 X_{i,\texttt{dance}} + \beta_2 X_{i,\texttt{val}}.\end{aligned}$$

In plain words, the **natural logarithm** of the **odds** is equal to a **systematic component** containing the regressors $X_{i,\texttt{dance}}$ and $X_{i,\texttt{val}}$.

Recall that this model can be fitted as follows:

```
spotify_bin_log_model <- glm(
  formula = genre ~ danceability + valence,
  data = bin_spotify_training,
  family = binomial
)
```

Note that only `valence` is statistically significant for the response `genre` (p-value $< .001$).

```
tidy(spotify_bin_log_model, conf.int = TRUE, exponentiate = TRUE) |>
  mutate_if(is.numeric, round, 2)
```

A tibble: 3 × 7

term	estimate	std.error	statistic	p.value	conf.low	conf.high
<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
(Intercept)	0.36	1.70	-0.60	0.55	0.01	8.91
danceability	0.97	0.03	-1.23	0.22	0.92	1.02
valence	1.05	0.01	3.47	0.00	1.02	1.08

Then, we make the corresponding coefficient interpretations (the previous output already provides the estimate on the odds scale via `exponentiate = TRUE`):

> For each unit increase in the `valence` score in the Spotify catalogue, the song is 1.05 times more likely to be `latin` than `edm`.

3.4.2. More than One Logit Function

What if our response is nominal and has more than two categories? In that case, let us suppose that a given **discrete nominal response Y_i has categories $1, 2, \ldots, m$.**

> **Important**
>
> Categories $1, 2, \ldots, m$ **are merely labels here**. Thus, they **do not** implicate an ordinal scale.

This regression approach assumes a **Multinomial distribution** where $p_{i,1}, p_{i,2}, \ldots, p_{i,m}$ are the probabilities that Y_i will belong to categories $1, 2, \ldots, m$ respectively; i.e.,

$$P(Y_i = 1) = p_{i,1} \quad P(Y_i = 2) = p_{i,2} \quad \ldots \quad P(Y_i = m) = p_{i,m},$$

where

$$\sum_{j=1}^{m} p_{i,j} = p_{i,1} + p_{i,2} + \cdots + p_{i,m} = 1.$$

> **Important**
>
> A particular highlight is that the Binomial distribution is the special Multinomial case when $m = 2$.

The Multinomial Logistic regression **also models the logarithm of the odds**. However, only one logarithm of the odds (or **logit**) will not be enough anymore. Recall we can capture the odds between two categories with a single logit function. **What about adding some other ones?**

Here is what we can do:

1. Pick one of the categories to be the **baseline**. For example, the category "1".
2. For each of the **other** categories, we model the logarithm of the odds to the baseline category.

Now, **what is the math for the general case with m response categories and k regressors?** For the ith observation, we end up with a system of $m-1$ link functions in the Multinomial Logistic regression model as follows:

$$\begin{aligned}
\eta_i^{(2,1)} &= \log\left[\frac{P(Y_i = 2 \mid X_{i,1}, \ldots, X_{i,k})}{P(Y_i = 1 \mid X_{i,1}, \ldots, X_{i,k})}\right] = \beta_0^{(2,1)} + \beta_1^{(2,1)} X_{i,1} + \beta_2^{(2,1)} X_{i,2} + \ldots \\
\eta_i^{(3,1)} &= \log\left[\frac{P(Y_i = 3 \mid X_{i,1}, \ldots, X_{i,k})}{P(Y_i = 1 \mid X_{i,1}, \ldots, X_{i,k})}\right] = \beta_0^{(3,1)} + \beta_1^{(3,1)} X_{i,1} + \beta_2^{(3,1)} X_{i,2} + \ldots \\
&\vdots \\
\eta_i^{(m,1)} &= \log\left[\frac{P(Y_i = m \mid X_{i,1}, \ldots, X_{i,k})}{P(Y_i = 1 \mid X_{i,1}, \ldots, X_{i,k})}\right] = \beta_0^{(m,1)} + \beta_1^{(m,1)} X_{i,1} + \beta_2^{(m,1)} X_{i,2} + .
\end{aligned} \tag{15}$$

Important

Note that the superscript $(j,1)$ in (15) indicates that the equation is on level j (for $j = 2, \ldots, m$) with respect to level 1. Furthermore, **the regression intercept and coefficients are different for each link function**.

With some algebraic manipulation, we can show that the probabilities $p_{i,1}, p_{i,2}, \ldots, p_{i,m}$ of Y_i belonging to categories $1, 2, \ldots, m$ are:

$$\begin{aligned}
p_{i,1} &= P(Y_i = 1 \mid X_{i,1}, \ldots, X_{i,k}) = \frac{1}{1 + \sum_{j=2}^{m} \exp\left(\eta_i^{(j,1)}\right)} \\
p_{i,2} &= P(Y_i = 2 \mid X_{i,1}, \ldots, X_{i,k}) = \frac{\exp\left(\eta_i^{(2,1)}\right)}{1 + \sum_{j=2}^{m} \exp\left(\eta_i^{(j,1)}\right)} \\
&\vdots \\
p_{i,m} &= P(Y_i = m \mid X_{i,1}, \ldots, X_{i,k}) = \frac{\exp\left(\eta_i^{(m,1)}\right)}{1 + \sum_{j=2}^{m} \exp\left(\eta_i^{(j,1)}\right)}.
\end{aligned} \tag{16}$$

Important

If we sum all m probabilities in (16), the sum will be equal to 1 for the ith observation. **This is particularly important when we want to use this model for making predictions in classification matters**.

Going back to our example, let us set the Multinomial Logistic regression model with `genre` as a response subject to `danceability` and `valence` as a continuous regressor. Level `edm` will be the baseline:

```
levels(spotify_training$genre)
```

'edm' · 'latin' · 'pop' · 'r&b' · 'rap' · 'rock'

Specifically, this case will implicate a **system of $m-1=6-1=5$ regression equations** (where $X_{i,\texttt{dance}}$ anf $X_{i,\texttt{val}}$ are the `danceability` and `valence` scores for the ith song, respectively):

$$
\begin{aligned}
\eta_i^{(\texttt{latin,edm})} &= \log\left[\frac{P(Y_i=\texttt{latin}\mid X_{i,\texttt{dance}},X_{i,\texttt{val}})}{P(Y_i=\texttt{edm}\mid X_{i,\texttt{dance}},X_{i,\texttt{val}})}\right]=\beta_0^{(\texttt{latin,edm})}+\beta_1^{(\texttt{latin,edm})}X\\
\eta_i^{(\texttt{pop,edm})} &= \log\left[\frac{P(Y_i=\texttt{pop}\mid X_{i,\texttt{dance}},X_{i,\texttt{val}})}{P(Y_i=\texttt{edm}\mid X_{i,\texttt{dance}},X_{i,\texttt{val}})}\right]=\beta_0^{(\texttt{pop,edm})}+\beta_1^{(\texttt{pop,edm})}\\
\eta_i^{(\texttt{r\&b,edm})} &= \log\left[\frac{P(Y_i=\texttt{r\&b}\mid X_{i,\texttt{dance}},X_{i,\texttt{val}})}{P(Y_i=\texttt{edm}\mid X_{i,\texttt{dance}},X_{i,\texttt{val}})}\right]=\beta_0^{(\texttt{r\&b,edm})}+\beta_1^{(\texttt{r\&b,edm})}\\
\eta_i^{(\texttt{rap,edm})} &= \log\left[\frac{P(Y_i=\texttt{rap}\mid X_{i,\texttt{dance}},X_{i,\texttt{val}})}{P(Y_i=\texttt{edm}\mid X_{i,\texttt{dance}},X_{i,\texttt{val}})}\right]=\beta_0^{(\texttt{rap,edm})}+\beta_1^{(\texttt{rap,edm})}\\
\eta_i^{(\texttt{rock,edm})} &= \log\left[\frac{P(Y_i=\texttt{rock}\mid X_{i,\texttt{dance}},X_{i,\texttt{val}})}{P(Y_i=\texttt{edm}\mid X_{i,\texttt{dance}},X_{i,\texttt{val}})}\right]=\beta_0^{(\texttt{rock,edm})}+\beta_1^{(\texttt{rock,edm})}X
\end{aligned}
\tag{17}
$$

Important

In a Multinomial Logistic regression model, each link function has its own intercept and regression coefficients.

The modelling system of 5 logit functions (17) can also be mathematically represented as follows (which might be helpful for our subsequent coefficient interpretation:

$$\begin{aligned}
\frac{P(Y_i = \texttt{latin} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}})}{P(Y_i = \texttt{edm} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}})} &= \exp\left[\beta_0^{(\texttt{latin,edm})}\right] \exp\left[\beta_1^{(\texttt{latin,edm})} X_{i,\texttt{dance}}\right] \text{ex} \\
\frac{P(Y_i = \texttt{pop} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}})}{P(Y_i = \texttt{edm} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}})} &= \exp\left[\beta_0^{(\texttt{pop,edm})}\right] \exp\left[\beta_1^{(\texttt{pop,edm})} X_{i,\texttt{dance}}\right] \exp \\
\frac{P(Y_i = \texttt{r\&b} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}})}{P(Y_i = \texttt{edm} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}})} &= \exp\left[\beta_0^{(\texttt{r\&b,edm})}\right] \exp\left[\beta_1^{(\texttt{r\&b,edm})} X_{i,\texttt{dance}}\right] \exp \\
\frac{P(Y_i = \texttt{rap} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}})}{P(Y_i = \texttt{edm} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}})} &= \exp\left[\beta_0^{(\texttt{rap,edm})}\right] \exp\left[\beta_1^{(\texttt{rap,edm})} X_{i,\texttt{dance}}\right] \exp \\
\frac{P(Y_i = \texttt{rock} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}})}{P(Y_i = \texttt{edm} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}})} &= \exp\left[\beta_0^{(\texttt{rock,edm})}\right] \exp\left[\beta_1^{(\texttt{rock,edm})} X_{i,\texttt{dance}}\right] \exp
\end{aligned} \tag{18}$$

Finally, the probabilities of Y_i belonging to categories `edm`, `latin`, `pop`, `r&b`, `rap`, and `rock` are:

$$p_{i,\texttt{edm}} = P(Y_i = \texttt{edm} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}}) = \frac{}{1 + \exp\left(\eta_i^{(\texttt{latin,edm})}\right) + \exp\left(\eta_i^{(\texttt{pop,edm})}\right) + }$$

$$p_{i,\texttt{latin}} = P(Y_i = \texttt{latin} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}}) = \frac{\text{e}}{1 + \exp\left(\eta_i^{(\texttt{latin,edm})}\right) + \exp\left(\eta_i^{(\texttt{pop,edm})}\right) -}$$

$$p_{i,\texttt{pop}} = P(Y_i = \texttt{pop} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}}) = \frac{\text{exp}}{1 + \exp\left(\eta_i^{(\texttt{latin,edm})}\right) + \exp\left(\eta_i^{(\texttt{pop,edm})}\right) + }$$

$$p_{i,\texttt{r\&b}} = P(Y_i = \texttt{r\&b} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}}) = \frac{\text{exp}}{1 + \exp\left(\eta_i^{(\texttt{latin,edm})}\right) + \exp\left(\eta_i^{(\texttt{pop,edm})}\right) + }$$

$$p_{i,\texttt{rap}} = P(Y_i = \texttt{rap} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}}) = \frac{\text{exp}}{1 + \exp\left(\eta_i^{(\texttt{latin,edm})}\right) + \exp\left(\eta_i^{(\texttt{pop,edm})}\right) + }$$

$$p_{i,\texttt{rock}} = P(Y_i = \texttt{rock} \mid X_{i,\texttt{dance}}, X_{i,\texttt{val}}) = \frac{\text{ex}}{1 + \exp\left(\eta_i^{(\texttt{latin,edm})}\right) + \exp\left(\eta_i^{(\texttt{pop,edm})}\right) +}$$

Now, let us discuss some in-class questions:

Exercise 6

Answer **TRUE** or **FALSE**:

Now that we removed the restriction of only one link function, we also removed the distributional assumption for Y_i. Hence, our model has no distributional assumption.

A. TRUE

B. FALSE

Solution to Exercise 6

It is **FALSE**.

We have not removed any distributional assumption. We just replaced the distributional assumption to Multinomial.

Exercise 7

Answer **TRUE** or **FALSE**:

From the statistical point of view, the model is now non-parametric.

A. TRUE

B. FALSE

Solution to Exercise 7

It is **FALSE**.

We are specifying the model function for each one of the logit functions while assuming a Multinomial distribution. Recall each one of these logit functions has its set of regression parameters (i.e., regression coefficients and intercepts). Moreover, we relate these regression parameters to the corresponding means via the $m-1$ link functions.

Exercise 8

Suppose that, given our inquiries, a peer suggests we fit two separate OLS with `genre` as a regressor and `danceability` **OR** `valence` as the responses. Can you think of some drawbacks of this suggested approach?

Solution to Exercise 8

There are some key drawbacks we can mention here:

- First, OLS modelling allows the response to be unbounded, which is against the nature of `danceability` and `valence` (both range from 0 to 100).
- Secondly, OLS modelling assumes an overall response variance of σ^2, which is not flexible enough for this case (each row in the training set is a different song, and genders can vary!).
- Finally, using such a basic approach more than once is impractical when we can use a more clever model (**such as Multinomial Logistic regression**) that addresses all inquiries simultaneously.

3.5. Estimation

All parameters in the Multinomial Logistic regression model are also unknown. To fit the model with the package `nnet`, we use the function `multinom()`, which obtains the corresponding estimates. The estimates are obtained through **maximum likelihood**, where we assume a **Multinomial joint probability mass function** of the n responses Y_i.

Note

We will not dig into mathematical derivations regarding maximum likelihood estimation (MLE) for this model since it would require digging into matrix notation, which is out of this course's scope. That said, you can find more information on this matter **here**.

```
spotify_mult_log_model <- multinom(
  formula = genre ~ danceability + valence,
  data = spotify_training
)
```

```
# weights:  24 (15 variable)
```

```
initial  value 627.115814
iter  10 value 582.728217
iter  20 value 559.441415
final  value 559.441352
converged
```

3.6. Inference

We can determine whether a regressor is statistically associated with the logarithm of the odds through hypothesis testing for the parameters $\beta_j^{(u,v)}$ **by link function**. We also use the **Wald statistic** $z_j^{(u,v)}$:

$$z_j^{(u,v)} = \frac{\hat{\beta}_j^{(u,v)}}{\text{se}\left(\hat{\beta}_j^{(u,v)}\right)}$$

to test the hypotheses

$$H_0 : \beta_j^{(u,v)} = 0$$
$$H_a : \beta_j^{(u,v)} \neq 0.$$

Provided the sample size n is large enough, z_j has an **approximately Standard Normal distribution** under H_0.

R provides the corresponding p**-values** for each $\beta_j^{(u,v)}$. The smaller the p-value, the stronger the evidence against the null hypothesis H_0. As in the previous regression models, we would set a predetermined significance level α (usually taken to be 0.05) to infer if the p-value is small enough. If the p-value is smaller than the predetermined level α, then you could claim that there is evidence to reject the null hypothesis. Hence, p-values that are small

enough indicate that the data provides evidence in favour of **association** (**or causation in the case of an experimental study!**) between the response variable and the jth regressor.

Furthermore, given a specified level of confidence where α is the significance level, we can construct approximate $(1-\alpha)\times 100\%$ **confidence intervals** for the corresponding true value of $\beta_j^{(u,v)}$:

$$\hat{\beta}_j^{(u,v)} \pm z_{\alpha/2}\text{se}\left(\hat{\beta}_j^{(u,v)}\right),$$

where $z_{\alpha/2}$ is the upper $\alpha/2$ quantile of the **Standard Normal distribution**.

We can also use the function `tidy()` from the `broom` package along with argument `conf.int = TRUE` to get the 95% confidence intervals **by default**.

```
options(repr.matrix.max.rows = 15)

mult_output <- tidy(spotify_mult_log_model,
  conf.int = TRUE, exponentiate = TRUE
) |>
  mutate_if(is.numeric, round, 3)
mult_output
```

A tibble: 15 × 8

y.level	term	estimate	std.error	statistic	p.value	conf.low	conf.high
<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
latin	(Intercept)	0.101	1.419	-1.617	0.106	0.006	1.628
latin	danceability	0.981	0.020	-0.976	0.329	0.943	1.020
latin	valence	1.052	0.013	4.007	0.000	1.026	1.079
pop	(Intercept)	2.492	0.893	1.023	0.306	0.433	14.337
pop	danceability	0.985	0.013	-1.112	0.266	0.959	1.011
pop	valence	1.006	0.009	0.661	0.508	0.988	1.024
r&b	(Intercept)	14.547	0.811	3.302	0.001	2.969	71.274
r&b	danceability	0.963	0.013	-3.016	0.003	0.939	0.987
r&b	valence	1.008	0.008	0.973	0.331	0.992	1.025
rap	(Intercept)	0.388	0.997	-0.949	0.342	0.055	2.740
rap	danceability	1.010	0.014	0.704	0.482	0.982	1.039
rap	valence	1.006	0.009	0.611	0.541	0.988	1.024
rock	(Intercept)	27.651	1.037	3.202	0.001	3.624	210.986
rock	danceability	0.918	0.019	-4.508	0.000	0.885	0.953
rock	valence	1.024	0.013	1.930	0.054	1.000	1.050

The 15 exponentiated estimated regression parameters (via `exponentiate = TRUE` in `tidy()`) from the right-hand side of (18) appear in the column `estimate`. Note that column `y.level` is related to the **non-baseline** level per function. Finally, to draw our inferential conclusions, let us filter those p-values less than 0.05 from `mult_output`:

```
mult_output |>
  dplyr::filter(p.value < 0.05)
```

A tibble: 5 × 8

y.level	term	estimate	std.error	statistic	p.value	conf.low	conf.high
<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
latin	valence	1.052	0.013	4.007	0.000	1.026	1.079
r&b	(Intercept)	14.547	0.811	3.302	0.001	2.969	71.274
r&b	danceability	0.963	0.013	-3.016	0.003	0.939	0.987
rock	(Intercept)	27.651	1.037	3.202	0.001	3.624	210.986
rock	danceability	0.918	0.019	-4.508	0.000	0.885	0.953

Since our baseline response is `edm`, we can conclude the following with $\alpha = 0.05$ **on the Spotify platform**:

- There is a statistical difference in `danceability` in `edm` versus `r&b` and `rock`.
- There is a statistical difference in `valence` in `edm` versus `latin`.

3.7. Coefficient Interpretation

Interpretation of the Multinomial Logistic regression coefficients is **quite similar** to the Binary Logistic regression. Let us interpret those significant regression coefficientes from column `estimate`:

> $\beta_2^{(\texttt{latin,edm})}$: for each unit increase in the `valence` score in the Spotify catalogue, the song is 1.052 times more likely to be `latin` than `edm`.

> $\beta_1^{(\texttt{r\&b,edm})}$: for each unit increase in the `danceability` score in the Spotify catalogue, the odds for a song for being `r&b` decrease by $(1 - 0.963) \times 100\% = 3.7\%$ compared to `edm`.

> $\beta_1^{(\texttt{ock,edm})}$: for each unit increase in the `danceability` score in the Spotify catalogue, the odds for a song for being `rock` decrease by $(1 - 0.918) \times 100\% = 8.2\%$ compared to `edm`.

Important

If we want to use another `genre` as a baseline under this modelling approach, we would need to relevel our factor-type response and rerun the whole process.

Also, this example does not include categorical regressors. Nevertheless, interpreting their corresponding estimated regression coefficients is analogous to **Binary Logistic regression** using the baseline response level.

3.8. Predictions

Suppose we want to predict the genre probabilities for a given song with a `danceability` score of `27.5` and `valence` of `30`. We could use the model `spotify_mult_log_model` for making such prediction as follows:

```
pred_probs <- round(predict(spotify_mult_log_model, tibble(danceability = 27.5
  type = "probs"), 2)
pred_probs
```

edm: 0.06 **latin:** 0.02 **pop:** 0.12 **r&b:** 0.41 **rap:** 0.04 **rock:** 0.34

```
sum(pred_probs) # Due to rounding, sum is 0.99 and not 1.
```

0.99

Note we have to use `type = "probs"` in the function `predict()` to obtain these predictions. Therefore, this given song has more chances of being `r&b`.

3.9. Model Selection

To perform model selection, we can use the same techniques from the Binary Logistic regression model (check 8. Model Selection). That said, some `R` coding functions might not be entirely available for the `multinom()` models. Still, these statistical techniques and metrics can be manually coded.

4. Wrapping Up on Model Selection and Multinomial Logistic Regression

- MLE can be used as a tool in model selection to assess the goodness of fit of our estimated models (via some training data).
- Deviance is a suitable model selection method for nested models.
- Conversely, AIC and BIC are adequate metrics for model selection when comparing non-nested models.
- An important advantage of deviance, AIC, and BIC is that they can be used across different regression models (as long as they are estimated via MLE).
- Multinomial Logistic regression is a key approach for categorical and nominal responses when we have more than two categories.
- The above regression is an extension of Binary Logistic regression. Hence, we establish a modelling system of logit functions before performing the corresponding parameter estimation. Note that inference and coefficient interpretation are conducted in a similar fashion compared to Binary Logistic regression.