Quiz 1 - DSCI 562

Review of Regression I

Ordinary Least Squares (OLS) Regression

- Response of continuous nature (hence the "ordinary")
- Response is subject to **regressors** (or explanatory variables/ features/ independent variables)
  - More than 1 regressor => **multiple linear regression**

$$Response = Systematic + Random$$

$$Y_i = \beta_0 + \beta_1 g_1(x_{i1}) + \beta_2 g_2(x_{i2}) + \cdots + \beta_p g_p(x_{ip}) + \epsilon_i$$

- random is the ϵ_i term

Assumptions

1. **Linearity**: the relationship between the response and functions of the regressors is linear
2. Errors are **independent** of each other and are **normally distributed** with mean 0 and variance σ^2

Hence, each Y_i is assumed to be independent and normally distributed.

Estimation

- To fit will need $k+2$ parameters: $\beta_0, \beta_1, \ldots, \beta_k, \sigma^2$
- Minimize the sum of squared errors (SSE) OR maximize the likelihood of the observed data
- **Maximum Likelihood Estimation (MLE)**: find the parameters that maximize the likelihood of the observed data
  - **Likelihood**: the probability of observing the data given the parameters
  - **Log-likelihood**: the log of the likelihood

Inference

- Do a t-test on the parameters to see if they are statistically significant

Limitations of OLS

- OLS allows response to take any real number.
- Examples of non-suitable responses:
  - Non-negative values
  - Binary values (success/failure)
  - Count data

Link Function

- Recall: OLS models a continuous response via its conditional mean

$$\mu_i = E(Y_i|X_i) = \beta_0 + \beta_1 g_1(x_{i1}) + \beta_2 g_2(x_{i2}) + \cdots + \beta_p g_p(x_{ip})$$

- **BUT** this is not suitable for non-continuous responses (e.g. binary, count, non-negative).
- **Solution**: use a **link function** $h(\mu_i)$ to map the conditional mean to the real line

- **Link function**: relate the systematic component, η_i, with the response's mean

$$h(\mu_i) = \eta_i = \beta_0 + \beta_1 g_1(x_{i1}) + \beta_2 g_1(x_{i2}) + \cdots + \beta_p g_p(x_{ip})$$

- **Monotonic**: allows for a one-to-one mapping between the mean of the response variable and the linear predictor

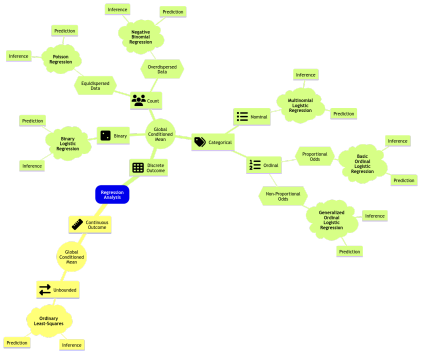
$$\mu_i = h^{-1}(\eta_i)$$

- **Differentiable**: to allow for maximum likelihood estimation (MLE), used to obtain $\hat{\beta}$ $$

Generalized Linear Models (GLM)

- **Generalized Linear Models (GLM)**: a generalization of OLS regression that allows for non-continuous responses

GLM = link function + error distribution



Poisson Regression

- **Poisson regression**: a GLM for count data (Equidispersed)
  - **Equidispersed**: the variance of the response is equal to its mean (i.e. $Var(Y_i) = E(Y_i) = \lambda_i$)
- It assumes a random sample of n count observations Y_is
  - Independent
  - Not Identically Distributed: Each Y_i has its own mean $E(Y_i) = \lambda_i > 0$ and variance $Var(Y_i) = \lambda_i > 0$

$$Y_i \sim Poisson(\lambda_i)$$

- λ_i is the risk of event occurance in a given timeframe or area (definition of Poisson distribution)

Link Function for Poisson Regression

- **Log link function**: the log of the mean of the response variable is linearly related to the regressors

$$h(\mu_i) = log(\mu_i) = \eta_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \cdots + \beta_p X_{ik}$$

Hence,

$$\lambda_i = e^{\eta_i} = e^{\beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \cdots + \beta_p X_{ik}}$$

- This is good since λ_i (mean count) is always positive

Poisson Regression in R

```
glm(Y ~ X, family = poisson, data = dataset)

# view each regression coefficient
tidy(glm_model)
tidy(glm_model, conf.int = TRUE) # for 95% confidence interval

# view model summary
glance(glm_model)
```

Interpretation of Coeffs of Poisson Regression

e.g. $\beta_1 = 0.5$

- β_1 is the expected change in the log of the mean count for a one-unit increase in X_1 holding all other variables constant
- a one-unit increase in X_1 will increase the mean count by $e^{0.5} = 1.65$ times.

Inference of Poisson Regression

- To determine the significance of the parameters $\beta_1, \beta_2, \ldots, \beta_p$, we can do a **Wald statistic**

$$z_j = \frac{\hat{\beta}_j}{SE(\hat{\beta}_j)}$$

- To test the hypothesis:
  - $H_0 : \beta_j = 0$
  - $H_1 : \beta_j \neq 0$

Negative Binomial Regression

- **Negative Binomial Regression**: a GLM for count data (Overdispersed)
  - **Overdispersed**: the variance of the response is greater than its mean (i.e. $Var(Y_i) > E(Y_i) = \lambda_i$)

Check for Overdispersion

```
dispersiontest(glm_model)
```

- if p-value < 0.05, then there is overdispersion (reject null hypothesis)

If use Poisson regression on overdispersed data, then the standard errors will be underestimated => **Type I error** (false positive) increases

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- Recall PMF of **Negative Binomial Distribution**:

$$P(Y_i|m, p_i) = \binom{y+m-1}{y} p_i^y (1-p_i)^m$$

- y_i is the number of failures before experiencing m successes where probability of success is p_i

$$E(Y_i) = \frac{m(1-p_i)}{p_i}$$

$$Var(Y_i) = \frac{m(1-p_i)}{p_i^2}$$

- Rearranging the above equations, we get:

$$E(Y_i) = \lambda_i$$

$$Var(Y_i) = \lambda_i(1 + \frac{\lambda_i}{m})$$

- Interesting information:

$$X \sim Poisson(\lambda) = lim_{m \to \infty} NegativeBinomial(m, p_i)$$

Negative Binomial Regression in R

```
glm.nb(Y ~ X, data = dataset)
```

Since negative binomial has the same link function as Poisson, we can interpret the coefficients the same way.

Likelihood-based Model Selection

Deviance Test

- The deviance (D_k) is used to compare a given model with k regressors (l_k) with the **baseline/ saturated model** (l_0).
  - The baseline model is the "perfect" fit to the data (overfitted), it has a distinct poisson mean (λ_i) for each ith observation.

$$D_k = 2log\frac{\hat{l}_k}{\hat{l}_0}$$

- **Interpretation of** D_k
  - Large value of D_k => poor fit compared to baseline model
  - Small value of D_k => good fit compared to baseline model

D_k in Poisson Regression

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

*note: when $y_i = 0$, log term is defined to be 0.

- Hypothesises are as follows (opposite of normal hypothesis):
  - H_0: Our model with k regressors fits the data better than the saturated model.
  - H_A: Otherwise

```
glance(model) # D_k is "deviance" col

# to get p-value
pchisq(summary_poisson_model_2$deviance,
  df = summary_poisson_model_2$df.residual,
  lower.tail = FALSE
)
```

- Formally `deviance` is **residual deviance**, this is a test statistic.
- Asymptomatically, it has a null distribution of:

$$D_k \sim \chi^2_{n-k-1}$$

- dof: $n-k-1$
  - n is the number of observations
  - k is the number of regressors (including intercept)

Deviance for nested models

```
anova(model_1, model_2, test = "Chisq")
# deviance column is \delta D_k
```

- model_1 is nested in model_2
- H_0: model_1 fits the data better as model_2
- H_A: model_2 fits the data better as model_1

$$\Delta D_k = D_{k_1} - D_{k_2} \sim \chi^2_{k_2 - k_1}$$

Akaike Information Criterion (AIC)

$$AIC_k = D_k + 2k$$

- AIC can be used to compare models that are not nested.
- Smaller AIC is better (means better fit)
- Can get from `glance()` function

Bayesian Information Criterion (BIC)

$$BIC_k = D_k + klog(n)$$

- BIC tends to select models with fewer regressors than AIC.
- smaller BIC is better (means better fit)
- Can get from `glance()` function

Multinomial Logistic Regression

- Is a MLE-based GLM for when the response is **categorical** and **nominal**.
  - **Nominal**: unordered categories
    - e.g. red, green, blue
  - **Ordinal**: ordered categories
    - e.g. low, medium, high
- Similar to binomial logistic regression, but with more than 2 categories.
- Link function is the **logit** function.
  - need more than 1 logit function to model the probabilities of each category.
  - One category is the **baseline category**, the other categories are **compared to the baseline category**.

$$\eta_i^{[model2, model1]} = \log\left[\frac{P(Y_i = \texttt{model 2} \mid X_{i,1}, X_{i,2}, X_{i,3})}{P(Y_i = \texttt{model 1} \mid X_{i,1}, X_{i,2}, X_{i,3})}\right] = \beta_0^{[\texttt{model 2,model 1}]} + \beta_1^{[\texttt{model 2,model 1}]} X_{i,1} + \beta_2^{[\texttt{model 2,model 1}]} X_{i,2} -$$

$$\eta_i^{[model3, model1]} = \log\left[\frac{P(Y_i = \texttt{model 3} \mid X_{i,1}, X_{i,2}, X_{i,3})}{P(Y_i = \texttt{model 1} \mid X_{i,1}, X_{i,2}, X_{i,3})}\right] = \beta_0^{[\texttt{model 3,model 1}]} + \beta_1^{[\texttt{model 3,model 1}]} X_{i,1} + \beta_2^{[\texttt{model 3,model 1}]} X_{i,2} -$$

With some algebra, we can get the following (For m categories):

$$p_{i,\texttt{model 1}} = \frac{1}{1 + \sum_{j=2}^{m} e^{\eta_i^{[\texttt{model j,model 1}]}}}$$

$$p_{i,\texttt{model 2}} = \frac{e^{\eta_i^{[\texttt{model 2,model 1}]}}}{1 + \sum_{j=2}^{m} e^{\eta_i^{[\texttt{model j,model 1}]}}}$$

- All probabilities sum to 1.

Nuances: Baseline Category

- The baseline level is the level that is not included in the model.
  - can find using `levels()` function, the first level is the baseline level.

```
levels(data$response) # to check levels

# to change levels
data$response <- recode_factor(data$response,
  "0" = "new_level_0",
  "1" = "new_level_1",
)
```

Estimation of MLR

```
model <- multinom(response ~ regressor_1 + regressor_2 + regressor_3,
  data = data)

# to get test statistics
mlr_output <- tidy(model,
  conf.int = TRUE, # to get confidence intervals (default is 95%)
  exponentiate = TRUE) # to get odds ratios
# default result is log odds ratios

# can filter p-values
mlr_output |> filter(p.value < 0.05)

# predict
predict(model, newdata = data, type = "probs")
# sum of all probabilities is 1
```

Inference of MLR

- Check if regressor is significant using **Wald test**.

$$z_j^{(a,c)} = \frac{\hat{\beta}_j^{(a,c)}}{SE(\hat{\beta}_j^{(a,c)})}$$

- For large sample sizes, $z_j^{(a,c)} \sim N(0,1)$
- To test the hypothesis:
  - H_0: $\beta_j^{(a,c)} = 0$
  - H_A: $\beta_j^{(a,c)} \neq 0$

Coefficient Interpretation for MLR

e.g. $\beta_1^{(b,a)} = 0.5$

- For a 1 unit increase in X_1, the odds of being in category b is $e^{0.5} = 1.65$ times the odds of being in category a.

e.g. $\beta_2^{(c,a)} = -0.5$

- For a 1 unit increase in X_2, the odds of being in category c decrease by 39% [$ 1 - (e^(-0.5)) = 1 - 0.61 = 0.39$] less than being in category a.

Ordinal Logistic Regression

- **Ordinal**: has a natural ordering
- There might be loss of information when using MLR for ordinal data
- We are going to use the **proportional odds model** for ordinal data
  - It is a **cumulative logit model**

Preprocessing for Ordinal Data

- Reorder the levels of the response variable

```
data$response <- as.ordered(data$response)
data$response <- fct_relevel(
  data$response,
  c("unlikely", "somewhat likely", "very likely")
)
levels(data$response)
```

Data Model for OLR

- For a response with m responses and k regressors, the model is:
- We will have:
  - $m-1$ equations (link functions: logit)

- $m-1$ intercepts
- k regression coefficients

Link Functions for m responses OLR

$$\begin{gathered}\text{Level } m-1 \text{ or any lesser degree versus level } m \\ \text{Level } m-2 \text{ or any lesser degree versus level } m-1 \text{ or any higher degree} \\ \vdots \\ \text{Level 1 versus level 2 or any higher degree}\end{gathered}$$

$$\eta_i^{(m-1)} = \log\left[\frac{P(Y_i \le m-1 \mid X_{i,1},\ldots,X_{i,k})}{P(Y_i = m \mid X_{i,1},\ldots,X_{i,k})}\right] = \beta_0^{(m-1)} - \beta_1 X_{i,1} - \beta_2 X_{i,2} - \ldots - \beta_k X_{i,k}$$

$$\eta_i^{(m-2)} = \log\left[\frac{P(Y_i \le m-2 \mid X_{i,1},\ldots,X_{i,k})}{P(Y_i > m-2 \mid X_{i,1},\ldots,X_{i,k})}\right] = \beta_0^{(m-2)} - \beta_1 X_{i,1} - \beta_2 X_{i,2} - \ldots - \beta_k X_{i,k}$$

$$\vdots$$

$$\eta_i^{(1)} = \log\left[\frac{P(Y_i = 1 \mid X_{i,1},\ldots,X_{i,k})}{P(Y_i > 1 \mid X_{i,1},\ldots,X_{i,k})}\right] = \beta_0^{(1)} - \beta_1 X_{i,1} - \beta_2 X_{i,2} - \ldots - \beta_k X_{i,k}.$$

Probability that Y_i is in level j

$$p_{i,j} = P(Y_i = j \mid X_{i,1},\ldots,X_{i,k}) = P(Y_i \le j \mid \ldots) - P(Y_i \le j-1 \mid \ldots)$$

- i is the index of the observation
- j is the level of the response variable

$$\sum_{j=1}^{m} p_{i,j} = 1$$

Estimation of OLR

- use `MASS::polr` function

```
ordinal_model <- polr(
  formula = response ~ regressor_1 + regressor_2,
  data = data,
  Hess = TRUE # Hessian matrix of log-likelihood
)
```

Inference of OLR

- Similar to MLR using **Wald test**

```
cbind(
  tidy(ordinal_model),
  p.value = pnorm(abs(tidy(ordinal_model)$statistic),
    lower.tail = FALSE
  ) * 2
)
# confidence intervals

confint(ordinal_model) # default is 95%
```

Coefficient Interpretation of OLR

- e.g. $\beta_1 = 0.6$
  - For a one unit increase in X_1, the odds of being in a higher category is $e^{0.6} = 1.82$ times the odds of being in a lower category, holding all other variables constant.

Predictions

```
predict(ordinal_model, newdata = data, type = "probs")
# returns probabilities for each level
```

- To get the **corresponding predicted** cumulative odds for a new observation, use `VGAM::vglm` function

```
olr <- vglm(
  response ~ regressor_1 + regressor_2,
  propodds, # for proportional odds model
  data,
)

# can also predict using this model, same as code block above
predict(olr, newdata = data, type = "response")

# get predicted cumulative odds
predict(olr, newdata = data, type = "link") |>
  exp() # to get odds instead of log odds
```

- Interpret the predicted cumulative odds as:
  - e.g. $logitlink(P[Y_i \ge j]) = 2.68$
    - A student with [data for X_i] is 2.68 times more likely to be in j or higher category than in category $j-1$ or lower, holding all other variables constant.
  - e.g. $logitlink(P[Y_i \ge 2]) = 0.33$
    - A student with [data for X_i] is 3.03 (1/0.33) times more likely to be in j category or lower than in category j or higher, holding all other variables constant.

Non-proportional Odds

- If the proportional odds assumption is not met, we can use the **partial proportional odds model**.
- Test for proportional odds assumption using the **Brant-Wald test**.
  - H_0: Our OLR model globally fulfills the proportional odds assumption.
  - H_A: Our OLR model does not globally fulfill the proportional odds assumption.

```
brant(ordinal_model)
```

- If the proportional odds assumption is not met, we can use the **generalized ordinal logistic regression model**.
  - Basically all βs are allowed to vary across the different levels of the response variable.

Linear Fixed Effects Model

- **Linear Fixed Effects Model (LFE)** is a generalization of the linear regression model
- **Fixed Effects**: the parameters of the model
  - constant for all observations

Limitations

- **Data Hierarchy**: the data is organized in a hierarchy
  - Can be due to **sampling levels**
  - e.g. investmests in different firms, students in different schools (sampling schemes may be different in different schools)
- Might have some correlation between datapoints in firms/ schools
  - violates the independence assumption (i.i.d. observations)

Example: Investments in different firms

- Goal: assessing the association of gross investment with market_value and capital in the population of American firms.
- Data: 11 firms, 20 observations per firm
  - 2 heirachical levels: firm and observation

1. Trial 1: ignore firm

```
ordinary_model <- lm(
  formula = investment ~ market_value + capital,
  data = Grunfeld)
```

2. Trial 2: Different intercepts for different firms

```
model_varying_intercept <- lm(
  # -1: so that baseline is not included as first intercept
    formula = investment ~ market_value + capital + firm - 1,
    data = Grunfeld)
```

3. Trial 3: OLS regeression for each firm

- This does NOT solve our goal.
- We want to find out among all firms, not one specific firm.

```
model_by_firm <- lm(
  investment ~ market_value + firm + capital + firm,
  data = Grunfeld)
```

Linear Mixed Effects Model

- Fundamental idea:
  - data subsets of elements share a correlation structure
  - i.e. all n rows of training data are not independent

$$\text{mixed effect} = \text{fixed effect} + \text{random effect}$$

$$\beta_{0j} = \beta_0 + b_{0j}$$

- β_{0j}/ mixed effect: the intercept for the jth school/ firm
- β_0/ fixed effect: the average intercept
- b_{0j}/ random effect: the deviation of the jth school/ firm from the average intercept
  - $b_{0j} \sim N(0, \sigma_0^2)$
  - independent of the error term ϵ
- **Variance of the ith observation**:
  - $\sigma_0^2 + \sigma_\epsilon^2$

Full Equation for LME

$$y_{ij} = \beta_{1j} + \beta_{1,2} x_{1ij} + \beta_{2j} x_{2ij} + \epsilon_{ij} = (\beta_0 + b_{1j}) + (\beta_1 + b_{1j}) x_{1ij} + (\beta_2 + b_{2j}) x_{2ij} + \epsilon_{ij}$$

For i in $1, 2, \ldots, n_j$ and j in $1, 2, \ldots, J$

Note: $(b_{0j}, b_{1j}, b_{2j}) \sim N(\mathbf{0}, \mathbf{D})$

- $\mathbf{0}$: vector of zero, e.g. $(0, 0, 0)^T$
- $\mathbf{D}$: generic covariance matrix

$$\mathbf{D} = \begin{bmatrix} \sigma_0^2 & \sigma_{01} & \sigma_{02} \\ \sigma_{10} & \sigma_1^2 & \sigma_{12} \\ \sigma_{20} & \sigma_{21} & \sigma_2^2 \end{bmatrix} = \begin{bmatrix} \sigma_0^2 & \rho_{01}\sigma_0\sigma_1 & \rho_{02}\sigma_0\sigma_2 \\ \rho_{10}\sigma_0\sigma_1 & \sigma_1^2 & \rho_{12}\sigma_1\sigma_2 \\ \rho_{20}\sigma_0\sigma_2 & \rho_{21}\sigma_1\sigma_3 & \sigma_2^2 \end{bmatrix}$$

- ρ_{uv}: pearson correlation between uth and vth random effects

Model Fitting of LME

- use the `lmer` function from the `lme4` package

```
mixed_intercept_model <- lmer(
  response ~ regressor_1 + regressor_2 +
    (1 | school), # random intercept by firm
  data
)

full_model <- lmer(
  response ~ regressor_1 + regressor_2 +
    (regressor_1 + regressor_2| school),
    # random intercept and slope by firm
  data
)
```

- Equation for mixed intercept model:

$$y_{ij} = (\beta_0 + b_{0j}) + \beta_1 x_{1ij} + \beta_2 x_{2ij} + \epsilon_{ij}$$

- Equation for full model:

$$y_{ij} = (\beta_0 + b_{0j}) + (\beta_1 + b_{1j}) x_{1ij} + (\beta_2 + b_{2j}) x_{2ij} + \epsilon_{ij}$$

Inference of LME

- Cannot do inference using normal t-test

```
summary(mixed_intercept_model)
summary(full_model)

# obtain coefficients
coef(mixed_intercept_model)$firm
coef(full_mixed_model)$firm
```

Prediction with LME

1. Predict on *existing* group

2. Predict on *new* group

```
predict(full_model,
  newdata = tibble(school = "new_school", regressor_1 = 1, regressor_2 = 2))
```