

# Multinomial Regression

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sparklyr requires a dplyr compatible back-end to Spark.

```
library(dplyr, warn.conflicts = FALSE)
library(sparklyr)
# start the sparklyr session
master <- "local"
# master <- "spark://master:7077"
sc <- spark_connect(master)
```

## 6.6 Multinomial Regression

We now look at the classification problem in which there are  $k > 2$  groups.

### 6.6.1 Basics

Multinomial regression is a relatively simple extension of logistic regression. We now have  $k - 1$  logit transformations expressed linearly in terms of the  $X$ 's. The last group is used as the denominator in these logits.

We can then compute  $P(G = l | X = x)$ , for  $l = 1, 2, \dots, k - 1$ .  $P(G = k | X = x)$  is obtained by subtraction.

### 6.6.2 Multinomial Models

The diabetes data from the Reaven and Miller study has diabetic-related measurements on 145 patients:

- \* RelWeight - relative weight
- \* GluFast - blood sugar level prior to the glucose tolerance test
- \* GluTest - average blood sugar level during the test
- \* InsTest - average insulin level during the test
- \* SSPG - a measure of how glucose and insulin interact
- \* CClass - clinical diagnosis (3=Normal, 2=Chemical Diabetic, 1=Overt Diabetic)

The dataset is small, but it illustrates binomial models using two levels (by combining Overt and Chemical Diabetics) or multinomial models using three levels.

The `diabetes.csv` file is read into an R data frame and the `CClass` variable is converted from an `int` to a factor with `chr` values.

```
diabetes_df <- read.csv("diabetes.csv", header = TRUE) %>%
  mutate(GluDiff = GluTest - GluFast) %>%
  mutate(CClass = factor(CClass, labels = c("o", "c", "n")))
diabetes_sdf <- copy_to(sc, diabetes_df, "diabetes_sdf")
head(diabetes_sdf)
```

```
## # Source: spark<??> [?? x 7]
##   RelWeight GluFast GluTest InsTest  SSPG CClass GluDiff
##   <dbl>    <int>    <int>    <int> <int> <chr>    <int>
## 1     0.81      80     356     124   55 n        276
## 2     0.95      97     289     117   76 n        192
```

```
## 3      0.94      105      319      143      105 n      214
## 4      1.04       90      356      199      108 n      266
## 5       1       90      323      240      143 n      233
## 6      0.76       86      381      157      165 n      295
```

It would be possible to binarize CClass by combining o and c to d using:

```
mutate(CClass = recode(CClass, "o" = "d", "c" = "d", "n" = "n"))
```

but we will keep 3 groups.

The `ml_logistic_regression` function accommodates  $k > 2$ .

```
diabetes_logistic_fit <- diabetes_sdf %>%
  ml_logistic_regression(CClass ~ GluDiff)
diabetes_logistic_fit
```

```
## Formula: CClass ~ GluDiff
##
## Coefficients:
## (Intercept)      GluDiff
## n      57.71914 -0.17196850
## c     -21.56761  0.07146432
## o     -36.15153  0.10050418
```

The output gives the coefficient estimates for each of the three groups. The normal group appears to be quite different than the chemical and overt disbetics.

```
diabetes_logistic_predict <- ml_predict(diabetes_logistic_fit)
diabetes_logistic_predict
```

```
## # Source: spark<?> [?? x 16]
##   RelWeight GluFast GluTest InsTest  SSPG CClass GluDiff features label
##   <dbl>    <int>    <int>    <int> <int> <chr>    <int> <list>    <dbl>
## 1      0.81      80      356      124    55 n      276 <dbl> [1...    0
## 2      0.95      97      289      117    76 n      192 <dbl> [1...    0
## 3      0.94     105      319      143   105 n      214 <dbl> [1...    0
## 4      1.04      90      356      199   108 n      266 <dbl> [1...    0
## 5       1       90      323      240   143 n      233 <dbl> [1...    0
## 6      0.76      86      381      157   165 n      295 <dbl> [1...    0
## 7      0.91     100      350      221   119 n      250 <dbl> [1...    0
## 8      1.1       85      301      186   105 n      216 <dbl> [1...    0
## 9      0.99      97      379      142    98 n      282 <dbl> [1...    0
## 10     0.78      97      296      131    94 n      199 <dbl> [1...    0
## # ... with more rows, and 7 more variables: rawPrediction <list>,
## #   probability <list>, prediction <dbl>, predicted_label <chr>,
## #   probability_n <dbl>, probability_c <dbl>, probability_o <dbl>
```

The f1 performance measure, which combines precision and recall is:

```
ml_multiclass_classification_evaluator(diabetes_logistic_predict, label_col = "CClass",
  prediction_col = "prediction", metric_name = "f1")
```

whereas the accuracy is:

```
ml_multiclass_classification_evaluator(diabetes_logistic_predict, label_col = "CClass",
  prediction_col = "prediction", metric_name = "accuracy")
```

```
spark_disconnect(sc)
```