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## **StatKeyEval**

# <u>A Statistical Framework for Dynamic Keyword Extraction, Evaluation, and Assessment Automation</u>

## Aim:

To implement an API for the available research paper models to give the answers for the short answers

## **Research Paper:**

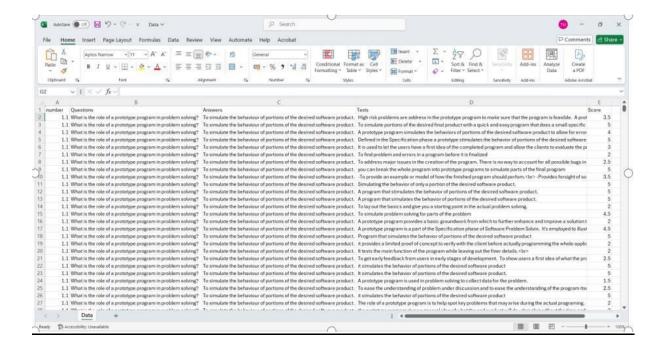
**Title**: Feature Engineering and Ensemble-Based Approach for Improving Automatic Short-Answer Grading Performance

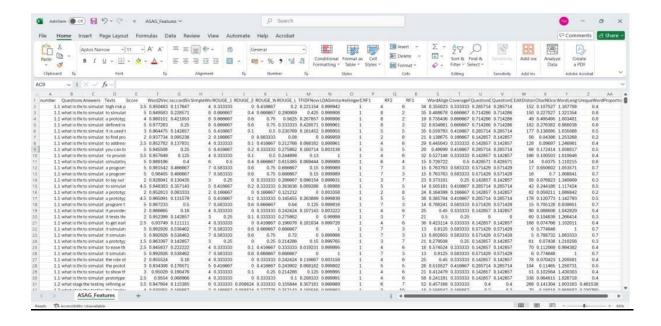
Authors: Archana Sahu and Plaban Kumar Bhowmick.

Conference/Journal: Educational Data Mining Conference (2018)

## **Datasets:**

- 1. UNT Dataset
- 2. SciEntsBank Dataset
- 3. Beetle Dataset





### **Statistical Function for Keyword Extraction**

Relevance(W) =  $\log (1 + \text{FreqRatio}(W))^{\alpha} \times [1 + \text{InverseDistance}(W)]^{\beta} \times \text{Specificity}(W)^{\gamma}$ Where:

- Relevance(W) is the final importance score for word W in the lexical extraction process
- FreqRatio(W) is the ratio of word W's frequency in relevant contexts to its frequency in irrelevant contexts plus a smoothing constant δ: frequency in relevant / (frequency in irrelevant + δ)
- InverseDistance(W) is the reciprocal of the average distance to other key terms plus 1: 1/(average distance to other key terms + 1)
- Specificity(W) is a measure of word uniqueness calculated as log(total corpus words / document frequency of W)
- $\alpha$ ,  $\beta$ , and  $\gamma$  are tunable exponential parameters that control the influence of each component (typical values:  $\alpha$ =0.5,  $\beta$ =0.7,  $\gamma$ =0.4)

#### **Statistical Function for Keyword Mutation**

ExpandMetric $(K_1, K_2) = [\text{SymbioticOverlap}(K_1, K_2) \times \text{LogisticDecay}(|K_1|, |K_2|)] \times [1 + \log(1 + \text{SemanticDensity}(K_1 \cap K_2))]$ 

Where: • ExpandMetric(K<sub>1</sub>, K<sub>2</sub>) is the final expansion benefit score between keyword sets

#### K<sub>1</sub> and K<sub>2</sub>

- SymbioticOverlap(K1, K2) is the quadratic overlap measure calculated as  $|K_1 \cap K_2|^2 / (|K_1| \times |K_2|)$
- LogisticDecay( $|K_1|$ ,  $|K_2|$ ) is a balanced size similarity function calculated as  $2/(1 + \exp(|abs(|K_1| |K_2|))/\lambda))$ , where  $\lambda$  is a scaling parameter

- SemanticDensity( $K_1 \cap K_2$ ) is the sum of co-occurrence frequencies for all word pairs in the intersection
- $|K_1|$  and  $|K_2|$  are the cardinalities (sizes) of the keyword sets
- log is the natural logarithm function
- exp is the exponential function

### **Statistical Functions for Score calculation**

AdjustedMetric(R) = 
$$M \times \left[1 - e^{-R/\tau}\right] \times \left[1 + \beta \times \sin\left(\frac{\pi \times R}{2M}\right)\right]$$

Where:

- AdjustedMetric(R) is the final calibrated value after quantization to the nearest 0.5
- R is the original raw measurement
- M is the maximum threshold value
- $\tau$  is a scaling coefficient governing the saturation rate
- β is a modulation parameter controlling oscillation intensity
- e is the base of the natural logarithm
- sin is the sine function

## **CODE FOR API:** try to build

library(readr)

library(DT)

```
upon with this code:

if (!require("shiny")) install.packages("shiny")

if (!require("tm")) install.packages("tm") if

(!require("dplyr")) install.packages("dplyr") if

(!require("readr")) install.packages("readr") if

(!require("DT")) install.packages("DT")

library(shiny) library(tm)
```

```
# Basic functions extract keywords <- function(text) { text
<- tolower(text) words <- unlist(strsplit(gsub("[[:punct:]]",
" ", text), "\\s+")) words <- words[words != ""]
 stopwords <- c("the", "and", "a", "an", "in", "on", "at", "to", "for", "of", "with",
"is", "are", "was", "were", "be", "been", "being", "have", "has", "had",
          "do", "does", "did", "can", "could", "will", "would", "should", "may",
          "might", "must", "shall", "this", "that", "these", "those", "it", "its",
          "they", "them", "their", "we", "us", "our", "i", "me", "my", "you", "your")
words <- words[!words %in% stopwords] words <- words[nchar(words) > 1]
words <- words[!grepl("^\\d+$", words)] return(unique(words))</pre>
}
calculate score <- function(answer keywords, student keywords) {</pre>
jaccard sim <- length(intersect(answer keywords, student keywords)) /
length(union(answer keywords, student keywords)) raw score <-
jaccard sim * 5 wpcs score <- min(raw score * 1.05, 5) wpcs score
<- round(wpcs score * 2) / 2
 return(list( raw score =
             wpcs score =
raw score,
wpcs score, similarity =
jaccard sim
 ))
}
SCM <- function(corpus, answer keywords, student keywords, threshold = 0.3) { if
(length(corpus) == 0 || length(answer keywords) == 0 || length(student keywords) == 0) 
return(list(mutation candidates = list(), similarity score = 0))
 corpus <- lapply(corpus, function(x) if(length(x) == 0) c("") else x)
candidates <- setdiff(student keywords, answer keywords) if
```

```
(length(candidates) == 0) {
                              return(list(mutation_candidates =
list(), similarity_score = 0))
 }
 candidate freq <- sapply(candidates, function(word) {</pre>
sum(sapply(corpus, function(doc) word %in% doc))
 })
 candidate rel freq <- candidate freq / length(corpus)</pre>
mutation candidates <- list() for (i in
1:length(candidates)) {
                          word <- candidates[i]
freq <- candidate rel freq[i]</pre>
                                if (freq >= threshold)
      mutation candidates[[word]] <- list(
                                                 word
= word,
              score = freq,
                                uniqueness = 1 - freq
   )
 if (length(mutation candidates) > 0) {
sorted candidates <- mutation candidates [order(
sapply(mutation candidates, function(x) x$score),
decreasing = TRUE
  )]
 } else {
sorted candidates <- list()
 jaccard sim <- length(intersect(answer keywords, student keywords)) /
length(union(answer keywords, student keywords))
 return(list(
               mutation candidates =
                      similarity_score =
sorted_candidates,
jaccard sim
 ))
```

```
update keywords <- function(question data) { answer keywords <-
unlist(strsplit(question data$Answer Keywords[1], ", ")) all text keywords
<- lapply(question data$Text Keywords, function(x) { if (is.na(x) || x == "")
return(character(0))
                     unlist(strsplit(x, ", "))
 })
 all student keywords <- unique(unlist(all text keywords)) threshold <- 0.65 scm result
<- SCM(all text keywords, answer keywords, all student keywords, threshold)
mutation candidates <- scm result$mutation candidates new keywords <-
names(mutation candidates)
return(list( new keywords = paste(new keywords,
collapse = ", "), similarity score =
scm result$similarity score
))
}
process batch <- function(data) { if ("Score" %in% colnames(data) &&
!"WPCS Score" %in% colnames(data)) { data <- data %>%
                                                              mutate(
    Score = as.numeric(Score),
    WPCS Score = pmin(Score * 1.05, 5),
    WPCS Score = round(WPCS Score *2) / 2
   )
 if (all(c("Questions", "Answer_Keywords", "Text_Keywords") %in% colnames(data))) {
result <- data %>%
                     group by(Questions) %>% group modify(~{
mutation result <- update keywords(.x)
    .x$New Keywords <- mutation result$new keywords
    .x$Similarity Score <- mutation result$similarity score
    .x$Combined Keywords <- ifelse(.x$New Keywords != "",
paste(.x$Answer Keywords, .x$New Keywords, sep = ", "),
```

```
.x$Answer_Keywords)
                        ungroup()
return(.x)
             }) %>%
return(result)
}
return(data)
}
# Ultra simple UI ui <- fluidPage(
titlePanel("Keyword Analysis"),
# Single Analysis Tab
h3("Single Analysis"),
textInput("question", "Question"), textAreaInput("model answer", "Model
Answer"), textInput("manual keywords", "Model Answer Keywords (comma-
separated)"), textAreaInput("student_answer", "Student Answer"),
actionButton("analyze btn", "Analyze"),
hr(),
h4("Results:"),
verbatimTextOutput("score_output"),
verbatimTextOutput("keywords_output"), hr(),
# Batch Processing Tab
h3("Batch Processing"),
fileInput("file_upload", "Upload CSV File"),
checkboxInput("header", "File has header", TRUE),
```

```
actionButton("process_btn", "Process"),
downloadButton("download_results", "Download"),
hr(),
 DTOutput("results table"),
verbatimTextOutput("batch_stats")
)
# Server logic server <- function(input,
output, session) { results <--
reactiveValues( model keywords =
NULL, student keywords = NULL,
score = NULL, batch data = NULL,
processed data = NULL
 )
 observeEvent(input$analyze btn, {
req(input$model answer, input$student answer)
  if (input$manual keywords != "") {
                                        model kw <-
unlist(strsplit(input$manual_keywords, ", "))
                                              model kw <-
trimws(model_kw)
  } else {
   model kw <- extract keywords(input$model answer)</pre>
  student_kw <- extract_keywords(input$student_answer)</pre>
score_result <- calculate_score(model_kw, student_kw)</pre>
```

```
results$model keywords <- model kw
results\student keywords <- student kw results\score
<- score result
  output$score output <- renderPrint({</pre>
                                          cat("WPCS Score: ", results\$score\$wpcs score,
"/5.0\n", sep = "")
                     cat("Similarity: ", round(results$score$similarity * 100, 2), "%\n",
sep = "")
            cat("Matching: ", length(intersect(results$model keywords,
results\student_keywords)),
      " out of ", length(union(results$model keywords, results$student keywords)), "\n", sep="")
  })
  output$keywords output <- renderPrint({
                                               cat("Model
Answer Keywords:\n")
cat(paste(results$model keywords, collapse = ", "), "\n\n")
cat("Student Answer Keywords:\n")
cat(paste(results$student keywords, collapse = ", "))
  })
 })
 observeEvent(input$file upload, {
req(input$file upload)
                batch data <- read csv(input$file upload$datapath, col names =
  tryCatch({
input$header)
                 results$batch data <- batch data
   output$results table <- renderDT({
datatable(results$batch data, options = list(pageLength = 5))
   })
                            showNotification("Error
  }, error = function(e) {
reading file", type = "error")
```

```
})
 })
 observeEvent(input$process btn, {
req(results$batch data)
  processed data <- process batch(results$batch data)</pre>
results$processed_data <- processed_data
  output$results table <- renderDT({
datatable(results$processed data, options = list(pageLength = 5))
  })
  output$batch stats <- renderPrint({
                                        if
("WPCS_Score" %in% colnames(processed_data)) {
cat("Records: ", nrow(processed data), "\n")
                                                   cat("Average Score: ",
    if ("Score" %in% colnames(processed data)) {
round(mean(processed_data$Score, na.rm = TRUE), 2), "\n")
                                                                 cat("Average WPCS: ",
round(mean(processed data$WPCS Score, na.rm = TRUE), 2), "\n")
    if ("Similarity Score" %in% colnames(processed data)) {
     cat("Average Similarity: ", round(mean(processed_data$Similarity_Score, na.rm = TRUE) *
100, 2), "%\n")
    }
   } else {
cat("Data loaded")
}
  })
 })
```

```
output$download_results <- downloadHandler(
filename = function() {
    "results.csv"
    },
    content = function(file) {
    write_csv(results$processed_data, file)
    }
    )
}</pre>
```

shinyApp(ui = ui, server = server)<u>RESULT:</u>

