StatKeyEval

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

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

Research Paper:

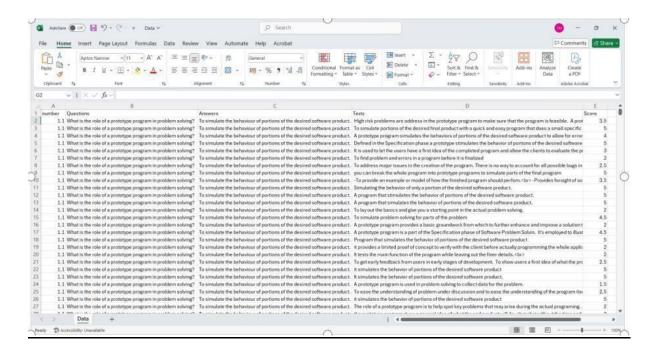
Title: Feature Engineering and Ensemble-Based Approach for Improving Automatic Short-Answer Grading Performance

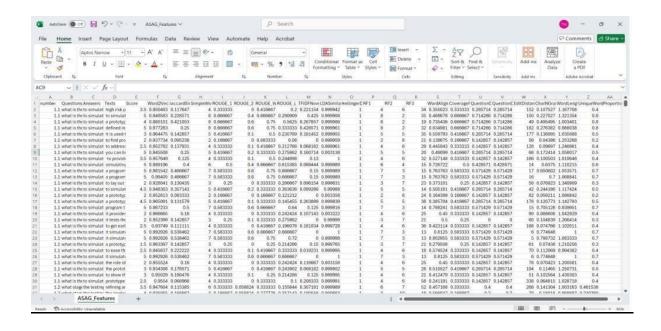
Authors: Archana Sahu and Plaban Kumar Bhowmick.

Conference/Journal: Educational Data Mining Conference (2018)

Datasets:

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





Statistical Function for Keyword Extraction

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

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)
- α , β , and γ are tunable exponential parameters that control the influence of each component (typical values: α =0.5, β =0.7, γ =0.4)

Statistical Function for Keyword Mutation

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

Where: • ExpandMetric (K_1, K_2) is the final expansion benefit score between keyword sets

K_1 and K_2

• SymbioticOverlap(K_1 , K_2) 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 λ 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
- τ 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 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)

library(dplyr)
```

```
# 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 = raw score,
wpcs score = wpcs score,
similarity = jaccard sim
 ))
}
SCM <- function(corpus, answer keywords, student keywords, threshold = 0.3) { if
(length(corpus) == 0 \parallel length(answer keywords) == 0 \parallel length(student keywords) == 0) 
return(list(mutation candidates = list(), similarity score = 0))
 }
```

```
corpus \leq- 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) mutation candidates
<- list() for (i in
1:length(candidates)) { word <- candidates[i]
                                                  freq
<- candidate_rel_freq[i] if (freq >= threshold)
      mutation candidates[[word]] <- list(
                                                word
             score = freq,
= word,
                                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 =
sorted candidates, similarity score = 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 == "")
                     unlist(strsplit(x, ", "))
return(character(0))
 })
 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)
return(.x)
            }) %>% ungroup()
                                    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 (commaseparated)"),
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 <- reactive Values(
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$student_answer) score_result
<- calculate score(model kw, student kw) results$model keywords <-
model kw results$student keywords <- student kw results$score
```

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

```
})
 })
 observeEvent(input$process btn, {
req(results$batch data)
  processed_data <- process_batch(results$batch_data) results$processed_data</pre>
<- processed data
  output$results table <- renderDT({
datatable(results$processed data, options = list(pageLength = 5))
  })
  output$batch stats <- renderPrint({
                                       if
("WPCS_Score" %in% colnames(processed_data)) { cat("Records:
", nrow(processed data), "\n")
    if ("Score" %in% colnames(processed_data)) { cat("Average Score: ",
round(mean(processed data$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")
}
```

shinyApp(ui = ui, server = server)**RESULT:**

