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StatKeyEval

A Statistical Framework for Dynamic Keyword Extraction, Evaluation, and Assessment Automation

Aim:

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

Research Paper:

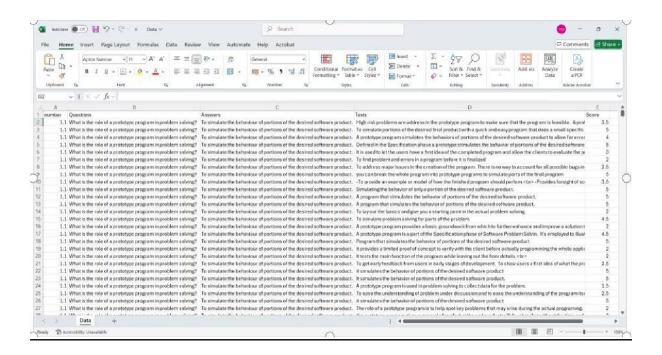
Title: Feature Engineering and Ensemble-Based Approach for Improving Automatic Short-Answer Grading Performance

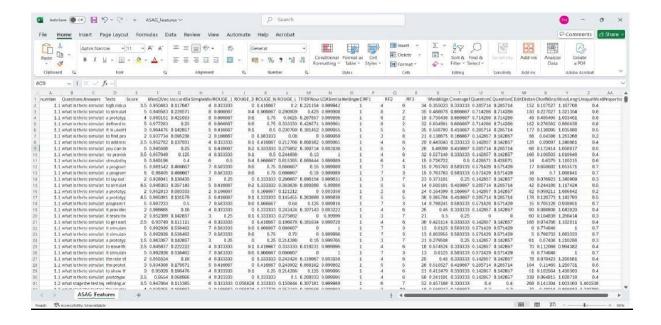
Authors: Archana Sahu and Plaban Kumar Bhowmick.

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)
- 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

 $\begin{aligned} & \operatorname{ExpandMetric}(K_1,K_2) = \left[\operatorname{SymbioticOverlap}(K_1,K_2) \times \operatorname{LogisticDecay}(|K_1|,|K_2|)\right] \times \\ & \left[1 + \log\left(1 + \operatorname{SemanticDensity}(K_1 \cap K_2)\right)\right] \end{aligned}$

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

K₁ and K₂

- 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 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)

library(readr) library(DT)

```
# 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))
}
calculate score <- function(answer keywords, student keywords)
{ 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 =
               similarity =
wpcs score,
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)
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,
                                uniqueness = 1 - freq
= word,
   )
 if (length(mutation_candidates) > 0)
{ sorted candidates <--
mutation candidates[order( sapply(mutation candidat
es, 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 == "")
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)
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 (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)
  }
  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$score
<- score result
                                          cat("WPCS Score: ", results$score$wpcs score,
  output$score output <- renderPrint({</pre>
"/5.0\n", sep = "")
                     cat("Similarity: ", round(results\$score\$similarity * 100, 2), "\n",
            cat("Matching: ", length(intersect(results$model keywords,
sep = "")
results$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)
  tryCatch({
                batch data <- read csv(input$file upload$datapath, col names =
input$header)
                 results$batch data <- batch data
   output$results table <-
renderDT({ datatable(results$batch data, options =
list(pageLength = 5))
   })
  }, error = function(e) {
                            showNotification("Error
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$batch stats <- renderPrint({
("WPCS Score" %in% colnames(processed data))
{ cat("Records: ", nrow(processed data), "\n")
                                                        cat("Average Score: ",
    if ("Score" %in% colnames(processed data)) {
round(mean(processed_data$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)RESULT:

