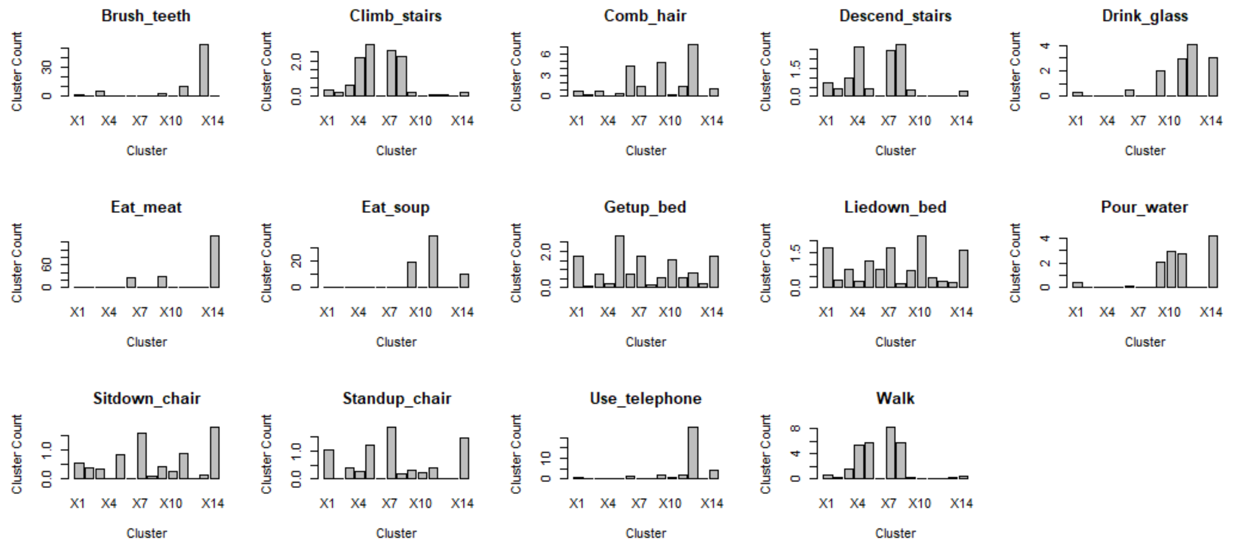
Size of Fixed Length	Sample Overlap (%)	K	Accuracy
32	0	14	0.7684211
32	0	28	0.7298246
32	0	140	0.7473684
64	0	14	0.7649123
64	0	28	0.7228070
64	0	140	0.7017544

I ran regular (not hierarchical) K-means



K-values is 14

	Brush_tee	Climb_sta	Comb_hai	Descend_	Drink_glas	Eat_meat	Eat_soup	Getup_be	Liedown_	Pour_wat	Sitdown_	Standup_	Use_telep	Walk
Brush_tee	4	0	0	0	0	0	0	0	0	0	0	0	0	0
Climb_sta	0	29	0	7	0	0	0	0	0	0	0	0	0	2
Comb_hai	0	0	7	0	0	0	0	0	0	0	0	0	1	0
Descend_	0	1	0	5	0	0	0	0	0	0	0	0	0	1
Drink_glas	0	2	3	0	33	0	0	0	0	0	1	0	2	0
Eat_meat	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Eat_soup	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Getup_be	0	0	0	0	0	0	0	22	2	0	2	5	0	0
Liedown_	0	0	0	0	0	0	0	4	3	0	0	0	0	0
Pour_wat	0	0	1	0	1	0	0	1	0	33	0	1	1	0
Sitdown_	0	1	0	0	0	0	0	1	2	1	26	5	0	1
Standup_	0	1	0	0	0	0	0	6	3	0	5	23	0	0
Use_telep	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Walk	0	0	0	2	0	0	0	0	0	0	0	0	0	30

Segmentation of Vector

```
  d <- t(do.call(rbind,lapply(unlist(data), function(x)
return(as.integer(unlist(strsplit(x, " ")))))))
  lst <- lapply(c(1,which(1:ncol(d) %% seg_size == 0) + 1), function(x) {
    if (x + 31 <= ncol(d)) {
      return(c(d[,x:(x+31)]))
    } else {
      return(NA)
    }
  })
```

K-means

```
  segments <- do.call(rbind, lst)
  clusters <- kmeans(segments, k)
```

Generating Histogram

```
output_histogram <- function(cluster) {
  setwd(og_path)
  data <- lapply(dir(og_path, recursive = T), function(x) {
    lines <- readLines(x)
    d <- t(do.call(rbind,lapply(lines, function(y) return(as.integer(unlist(strsplit(y, " ")))))))
    segments <- lapply(c(1,which(1:ncol(d) %% (ncol(cluster$centers)/3) == 0) + 1), function(y) {
      if (y + 31 <= ncol(d)) {
        return(c(d[,y:(y+31)]))
      } else {
        return(NA)
      }
    })
    if (is.na(segments[[length(segments)]])) {
      segments <- segments[-length(segments)]
    }

    predicts <- unlist(lapply(segments, function(y) {
      distances <- apply(clusters$centers, 1, function(z) {
        return(sqrt(sum((y - z)^2)))
      })
      return(which(distances == min(distances)))
    }))

    hist <- sapply(c(1:nrow(cluster$centers)), function(r) {
      return(sum(predicts == r))
    })
    str <- strsplit(x, "/")[[1]][1]
    index <- which(labels == str)
    return(list(str, hist))
  })
  labs <- unlist(lapply(data, function(x) return(x[[1]])))
  hist_data <- do.call(rbind, lapply(data, function(x) return(x[[2]])))
  return(data.frame(labs, hist_data))
}
```

Classification

```
  training <- as.h2o(x = hist_data[unlist(splits),])
  testing <- as.h2o(x = hist_data[-unlist(splits),])

  model <- h2o.randomForest(y = 1, training_frame = training)
  predictions <- predict(model, testing[,-1])
```

```r
library(h2o)

#Gets all the data into a list of vectors, then combines it all into a vector.
#Each element of a vector is a string of three numbers separated by space". e.g.
#[1] "22 49 35" "22 49 35" "22 52 35"
og_path <- getwd()
data <- lapply(dir(getwd()), function(x) {
  # print(paste0(og_path, "/", x))
  setwd(paste0(og_path, "/", x))
  lines <- lapply(dir(getwd(), ".txt"), function(y) {
    return(readLines(y))
  })
  vec <- unlist(lines)
  return(vec)
})

labels <- unique(unlist(lapply(dir(og_path, recursive = T), function(x) return(strsplit(x, "/")[[1]][1]))))

run_kmeans <- function(k, seg_size) {
  d <- t(do.call(rbind,lapply(unlist(data), function(x) return(as.integer(unlist(strsplit(x, " ")))))))
  lst <- lapply(c(1,which(1:ncol(d) %% seg_size == 0) + 1), function(x) {
    if (x + 31 <= ncol(d)) {
      return(c(d[,x:(x+31)]))
    } else {
      return(NA)
    }
  })
  if (is.na(lst[[length(lst)]])) {
    lst <- lst[-length(lst)]
  }
  segments <- do.call(rbind, lst)
  clusters <- kmeans(segments, k)

  return(clusters)
}


output_histogram <- function(cluster) {
  setwd(og_path)
  data <- lapply(dir(og_path, recursive = T), function(x) {
    lines <- readLines(x)
    d <- t(do.call(rbind,lapply(lines, function(y) return(as.integer(unlist(strsplit(y, " ")))))))
    segments <- lapply(c(1,which(1:ncol(d) %% (ncol(cluster$centers)/3) == 0) + 1), function(y) {
      if (y + 31 <= ncol(d)) {
        return(c(d[,y:(y+31)]))
      } else {
        return(NA)
      }
    })
    if (is.na(segments[[length(segments)]])) {
      segments <- segments[-length(segments)]
    }

    predicts <- unlist(lapply(segments, function(y) {
      distances <- apply(clusters$centers, 1, function(z) {
        return(sqrt(sum((y - z)^2)))
      })
      return(which(distances == min(distances)))
    }))

    hist <- sapply(c(1:nrow(cluster$centers)), function(r) {
      return(sum(predicts == r))
    })
    str <- strsplit(x, "/")[[1]][1]
    index <- which(labels == str)
    return(list(str, hist))
  })
  labs <- unlist(lapply(data, function(x) return(x[[1]])))
  hist_data <- do.call(rbind, lapply(data, function(x) return(x[[2]])))
  return(data.frame(labs, hist_data))
}

hist <- output_histogram(clusters1)
# hist_labels <- sapply(hist[,1], function(x) return(labels[[x]]))
# hist <- hist[,-1]

#Takes a matrix of histograms (i.e. obtained from runnuing output_histogram()),
#which returns a matrix with 839 rows (each row corresponds to one of the files)
#and splits the rows into training and test sets. Performs 3-fold cross-validation
#and outputs a confusion table for the classes
validation <- function(hist_data) {
  splits <- lapply(labels, function(x) {
    occur <- grep(x, dir(og_path, recursive = T))
    return(sample(occur, as.integer(2*length(occur)/3)))
  })

  #h2o.init()
  training <- as.h2o(x = hist_data[unlist(splits),])
  testing <- as.h2o(x = hist_data[-unlist(splits),])

  model <- h2o.randomForest(y = 1, training_frame = training)
  predictions <- predict(model, testing[,-1])

  # print(as.vector(predictions[,1]) == "Brush_teeth")
  # print(testing[,1])
  #Creates Confusion Matrix
  rows <- lapply(c(1:14), function(x) {
    x_indices <- which(as.vector(predictions[,1]) == labels[x])
    entries <- unlist(lapply(c(1:14), function(y) {
      y_indices <- which(as.vector(testing[,1]) == labels[y])
      return(length(intersect(x_indices,y_indices)))
    }))
    return(entries)
  })

  confusion_matrix <- do.call(rbind, rows)
  row.names(confusion_matrix) <- labels
  colnames(confusion_matrix) <- labels
  return(list(acc = sum(diag(confusion_matrix))/sum(c(confusion_matrix)),
              conf_mat = confusion_matrix))
}

clusters1 <- run_kmeans(14, 32)
clusters2 <- run_kmeans(28, 32)
clusters3 <- run_kmeans(140, 32)
clusters4 <- run_kmeans(14, 64)
clusters5 <- run_kmeans(28, 64)
clusters6 <- run_kmeans(140, 64)

hist1 <- output_histogram(clusters1)
hist2 <- output_histogram(clusters2)
hist3 <- output_histogram(clusters3)
hist4 <- output_histogram(clusters4)
hist5 <- output_histogram(clusters5)
hist6 <- output_histogram(clusters6)

val1 <- validation(hist1)
val2 <- validation(hist2)
val3 <- validation(hist3)
val4 <- validation(hist4)
val5 <- validation(hist5)
val6 <- validation(hist6)

# > sapply(c(1:6), function(x) return(eval(parse(text=paste0("val",x,"$acc")))))
# [1] 0.7684211 0.7298246 0.7473684 0.7649123 0.7228070 0.7017544
#So val1 has the best accuracy.

#Calculating mean quantized vectors, for each action
quantized_action <- lapply(labels, function(x) {
  occur <- grep(x, hist1[,1])
  df <- hist1[occur,-1]
  return(colMeans(df))
})

par(mfrow=c(3,5))
mean_quantized_barplots <- lapply(c(1:14), function(x) {
  barplot(quantized_action[[x]], main = labels[x],
          xlab = "Cluster", ylab = "Cluster Count")
})
```