

## Melakukan analisis univaribel antara PEF dengan Age, height, sex dan asma

### # Mengakses data gabungan PEF dan W5

```
url <- "https://raw.githubusercontent.com/indrawijaya-rshs/UTS-biostatistik-lanjut-  
/refs/heads/main/merged_data_pef_sex_asthma.csv"  
data <- read_csv(url)
```

### # Memilih kolom yang relevan

```
data_new <- data[, c("pidlink", "pef", "age", "height", "sex", "Asthma")]
```

### # Membersihkan missing data

```
data_clean <- data_new[complete.cases(data_new[, c("pef", "age", "height", "sex", "Asthma"))],  
]  
cat("Jumlah baris data awal:", nrow(data_new), "\n")  
cat("Jumlah baris setelah menghapus missing data:", nrow(data_clean), "\n")
```

### # Pemeriksaan awal untuk memastikan data cukup untuk analisis

```
if (nrow(data_clean) < 3) {stop("Error: Jumlah observasi terlalu kecil (< 3) untuk analisis.")}
```

### # Uji normalitas untuk pef

```
shapiro_test <- tryCatch({shapiro.test(data_clean$pef)}, error = function(e) {cat("Error dalam uji  
Shapiro-Wilk:", e$message, "\n")}return(NULL))
```

### # Menentukan metode uji berdasarkan normalitas

```
if (!is.null(shapiro_test)) {  
  cat("\nUji Normalitas untuk PEF (Shapiro-Wilk):\n")  
  cat("p-value:", shapiro_test$p.value, "\n")  
  if (shapiro_test$p.value < 0.05) {  
    cat("PEF tidak terdistribusi normal (p < 0.05), gunakan uji non-parametrik.\n")  
    normality <- "non-parametric"} else {  
    cat("PEF terdistribusi normal (p >= 0.05), gunakan uji parametrik.\n")  
    normality <- "parametric"}} else {  
  cat("Uji normalitas gagal, default ke uji non-parametrik.\n")  
  normality <- "non-parametric"}
```

### # Analisis Univariat

#### # Korelasi antara pef dan age

```
cat("\nKorelasi antara PEF dan Age:\n")  
if (normality == "non-parametric") {  
  corr_age <- cor.test(data_clean$pef, data_clean$age, method = "spearman", exact = FALSE)  
  cat("Uji Spearman: rho =", corr_age$estimate, ", p-value =", corr_age$p.value, "\n")  
} else {  
  corr_age <- cor.test(data_clean$pef, data_clean$age, method = "pearson")
```

```
cat("Uji Pearson: r =", corr_age$estimate, ", p-value =", corr_age$p.value, "\n")
}
```

### # Korelasi antara pef dan height

```
cat("\nKorelasi antara PEF dan Height:\n")
if (normality == "non-parametric") {
  corr_height <- cor.test(data_clean$pef, data_clean$height, method = "spearman", exact = FALSE)
  cat("Uji Spearman: rho =", corr_height$estimate, ", p-value =", corr_height$p.value, "\n")
} else {corr_height <- cor.test(data_clean$pef, data_clean$height, method = "pearson")
  cat("Uji Pearson: r =", corr_height$estimate, ", p-value =", corr_height$p.value, "\n")}
```

### # Hubungan antara pef dan sex

```
cat("\nHubungan antara PEF dan Sex:\n")
if (length(unique(data_clean$sex)) != 2) {
  cat("Error: Kolom 'sex' tidak memiliki tepat dua kategori, uji tidak dilakukan.\n")} else {
  if (normality == "non-parametric") {
    test_sex <- wilcox.test(pef ~ sex, data = data_clean)
    cat("Uji Mann-Whitney U: p-value =", test_sex$p.value, "\n")} else {
    test_sex <- t.test(pef ~ sex, data = data_clean)
    cat("Uji t-test: p-value =", test_sex$p.value, "\n")}
  # Ringkasan statistik PEF berdasarkan sex
  cat("Statistik Deskriptif PEF berdasarkan Sex:\n")
  print(tapply(data_clean$pef, data_clean$sex, summary)))}
```

### # Hubungan antara pef dan Asthma

```
asthma_categories <- length(unique(na.omit(data_clean$Asthma)))
if (asthma_categories != 2) {
  results <- rbind(results, data.frame(
    Variable = "Asthma",
    Test = ifelse(normality == "non-parametric", "Mann-Whitney U", "t-test"),
    Statistic = "N/A",
    P_Value = NA,
    Significance = "Error: Asthma tidak memiliki tepat dua kategori"
  ))
} else {
  if (normality == "non-parametric") {
    test_asthma <- wilcox.test(pef ~ Asthma, data = data_clean)
    results <- rbind(results, data.frame(
      Variable = "Asthma",
      Test = "Mann-Whitney U",
      Statistic = paste("W =", round(test_asthma$statistic, 3)),
      P_Value = test_asthma$p.value,
      Significance = ifelse(test_asthma$p.value < 0.05, "Significant", "Not Significant")
    ))
  }
}
```

```

))
} else {
  test_asthma <- t.test(pef ~ Asthma, data = data_clean)
  results <- rbind(results, data.frame(
    Variable = "Asthma",
    Test = "t-test",
    Statistic = paste("t =", round(test_asthma$statistic, 3)),
    P_Value = test_asthma$p.value,
    Significance = ifelse(test_asthma$p.value < 0.05, "Significant", "Not Significant")
  ))
}
}

```

```

# Format P_Value untuk tampilan
results$P_Value <- round(results$P_Value, 4)

```

```

# Tampilkan tabel hasil
cat("\nTabel Hasil Analisis Univariat PEF dengan Age, Height, Sex, dan Asthma:\n")
print(kable(results, format = "markdown"))

```

```

# Statistik Deskriptif untuk Sex dan Asthma
cat("\nStatistik Deskriptif PEF berdasarkan Sex:\n")
print(tapply(data_clean$pef, data_clean$sex, summary))
cat("\nStatistik Deskriptif PEF berdasarkan Asthma:\n")
print(tapply(data_clean$pef, data_clean$Asthma, summary))

```