

ADT-Analysis

12-06-2023

```
library(ggplot2)
library(dplyr)
library(broom)
library(ggpubr)
library(tidyverse)
library(readr)
library(effsize)

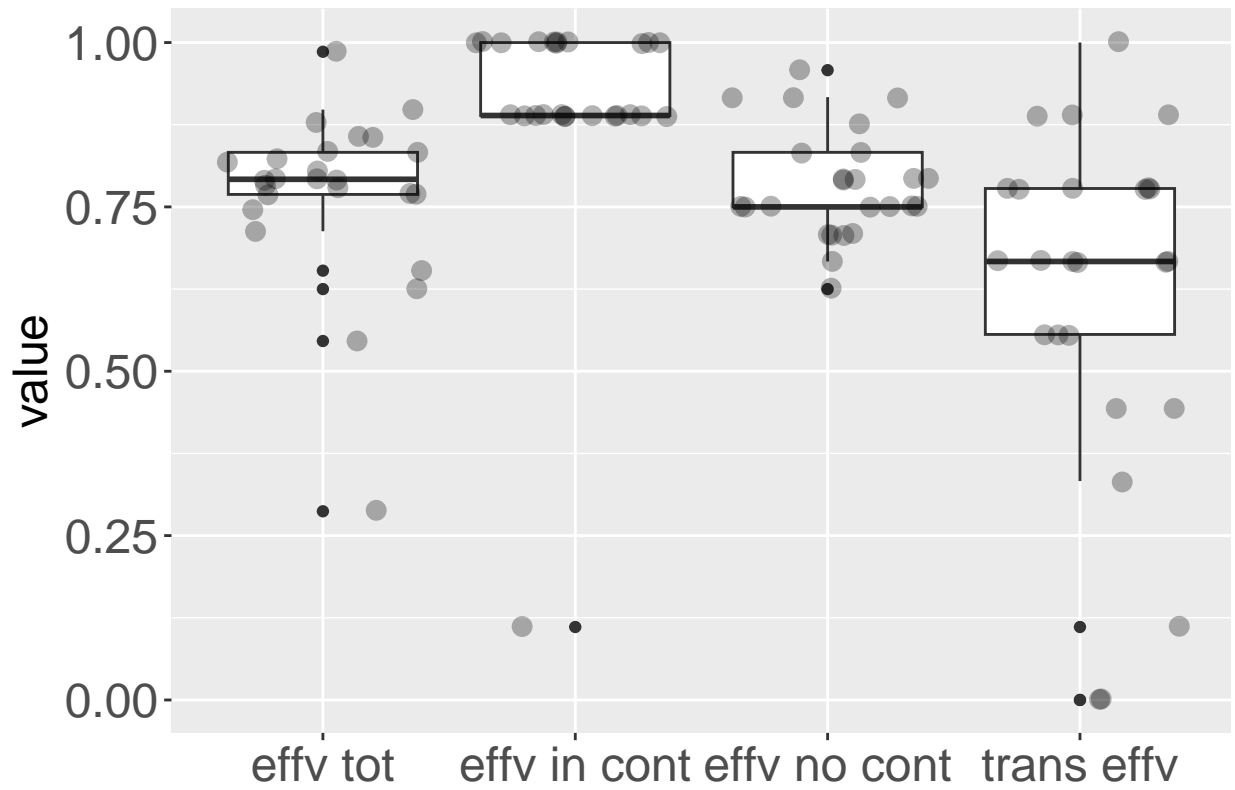
## Warning: package 'effsize' was built under R version 4.3.2
data_adt <- read.csv("./ADT-test-results.csv", na.strings = c("N/A"))
data_adt <- data_adt %>%
  filter(!(is.na(PEOU) | is.na(PU) | is.na(ITU))) %>%
  select(!ID)

SIZE = 18
EQ_SIZE = 6
```

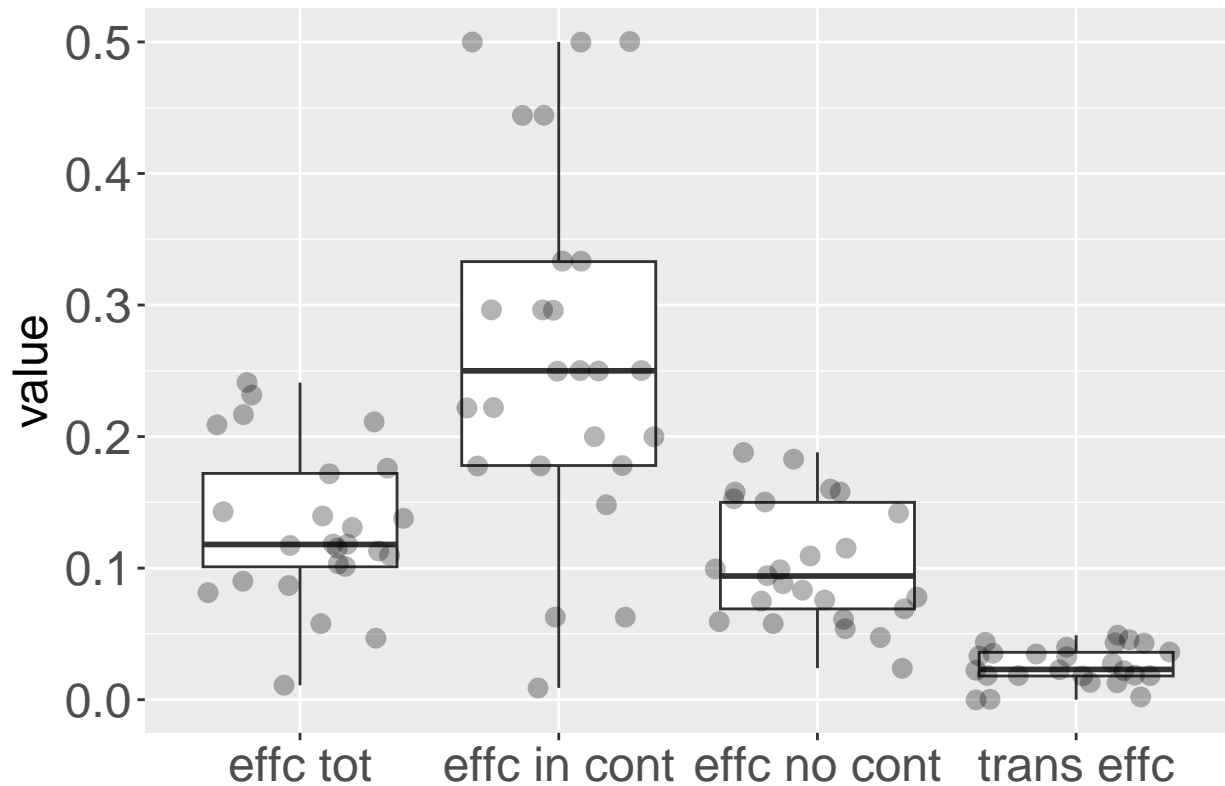
- PEOU: perceived ease of use
- PU: perceived usefulness
- ITU: intention to use
- Effectiveness: how high is the score of the subject
- Efficiency: how fast is the subject

Boxplots of effectiveness and efficiency variables

Average total effectiveness is above 0.75, indicating a generally good level of comprehensibility of ADT principles. Furthermore, the boxplot shows that effectiveness in context is provides the highest contribution, followed by effectiveness not in context and transferability effectiveness. This suggests that while participants understand ADT principles, they find more difficulties in applying them in practice.



For the efficiency variable, we see a similar situation to that observed for effectiveness, thereby confirming that ADT “in action” is perceived as a more difficult task.



Wilcoxon Signed Rank Test for efficiency and effectiveness

We evaluate if the variables of effectiveness and efficiency are significantly higher than target values.

```
ks.test(data_adt$Effectiveness, "pnorm")
```

```
##
## Asymptotic one-sample Kolmogorov-Smirnov test
##
## data: data_adt$Effectiveness
## D = 0.66747, p-value = 4.235e-10
## alternative hypothesis: two-sided
```

```
ks.test(data_adt$Efficiency, "pnorm")
```

```
##
## Asymptotic one-sample Kolmogorov-Smirnov test
##
## data: data_adt$Efficiency
## D = 0.50439, p-value = 5.979e-06
## alternative hypothesis: two-sided
```

Data are not normally distributed, therefore we use a nonparametric test (Wilcoxon signed rank).

```
# Set the desired significance level
alpha <- 0.05
```

```
result <- wilcox.test(data_adt$Effectiveness, mu = 0.6, alternative = "greater")
```

```

result

##
## Wilcoxon signed rank test with continuity correction
##
## data: data_adt$Effectiveness
## V = 298, p-value = 0.000139
## alternative hypothesis: true location is greater than 0.6
# Check if the p-value is lower than the significance level
if (result$p.value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis that Effectiveness is lower than 0.6 is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}

## The null hypothesis that Effectiveness is lower than 0.6 is rejected (p < 0.05 )
# Set the desired significance level
alpha <- 0.05

result <- wilcox.test(data_adt$Efficiency, mu = 0.015, alternative = "greater")
result

##
## Wilcoxon signed rank test with continuity correction
##
## data: data_adt$Efficiency
## V = 324, p-value = 7.381e-06
## alternative hypothesis: true location is greater than 0.015
# Check if the p-value is lower than the significance level
if (result$p.value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis that Efficiency is lower than 0.6 is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}

## The null hypothesis that Efficiency is lower than 0.6 is rejected (p < 0.05 )

```

Both null hypotheses about efficiency and effectiveness are rejected.

Wilcoxon signed rank for efficiency and effectiveness (detailed variables):

- effectiveness_not_context: rejected

```

# Set the desired significance level
alpha <- 0.05

result <- wilcox.test(data_adt$effectiveness_not_context, mu = 0.6, alternative = "greater")
result

##
## Wilcoxon signed rank test with continuity correction
##

```

```
## data: data_adt$effectiveness_not_context
## V = 325, p-value = 6.017e-06
## alternative hypothesis: true location is greater than 0.6
# Check if the p-value is lower than the significance level
if (result$p.value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis that effectiveness_not_context is lower than 0.6 is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}
```

The null hypothesis that effectiveness_not_context is lower than 0.6 is rejected (p < 0.05)

- efficiency_not_context: rejected

```
# Set the desired significance level
alpha <- 0.05

result <- wilcox.test(data_adt$efficiency_not_context, mu = 0.06, alternative = "greater")
result
```

##

Wilcoxon signed rank test with continuity correction

##

data: data_adt\$efficiency_not_context

V = 297.5, p-value = 0.0001476

alternative hypothesis: true location is greater than 0.06

```
# Check if the p-value is lower than the significance level
if (result$p.value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis that efficiency_not_context is lower than 0.6 is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}
```

The null hypothesis that efficiency_not_context is lower than 0.6 is rejected (p < 0.05)

transferability_effectiveness: not rejected (p-value = 0.1121)

```
# Set the desired significance level
alpha <- 0.05

result <- wilcox.test(data_adt$transferability_effectiveness, mu = 0.6, alternative = "greater")
result
```

##

Wilcoxon signed rank test with continuity correction

##

data: data_adt\$transferability_effectiveness

V = 208, p-value = 0.1121

alternative hypothesis: true location is greater than 0.6

```
# Check if the p-value is lower than the significance level
if (result$p.value < alpha) {
  # Null hypothesis rejected
```

```

    cat("The null hypothesis that transferability_effectiveness is lower than 0.6 is rejected (p <", alpha, ")")
  } else {
    # Null hypothesis not rejected
    cat("The null hypothesis is not rejected (p >=", alpha, ")")
  }
}

```

The null hypothesis is not rejected (p >= 0.05)

- transferability_efficiency: not rejected (p-value= 0.2295)

```

# Set the desired significance level

```

```

alpha <- 0.05

```

```

result <- wilcox.test(data_adt$transferability_efficiency, mu = 0.024, alternative = "greater")
result

```

```

##

```

```

## Wilcoxon signed rank test with continuity correction

```

```

##

```

```

## data: data_adt$transferability_efficiency

```

```

## V = 190.5, p-value = 0.2295

```

```

## alternative hypothesis: true location is greater than 0.024

```

```

# Check if the p-value is lower than the significance level

```

```

if (result$p.value < alpha) {

```

```

  # Null hypothesis rejected

```

```

  cat("The null hypothesis that transferability_efficiency is lower than 0.6 is rejected (p <", alpha, ")")

```

```

} else {

```

```

  # Null hypothesis not rejected

```

```

  cat("The null hypothesis is not rejected (p >=", alpha, ")")

```

```

}

```

The null hypothesis is not rejected (p >= 0.05)

- effectiveness_in_context: rejected

```

# Set the desired significance level

```

```

alpha <- 0.05

```

```

result <- wilcox.test(data_adt$effectiveness_in_context, mu = 0.6, alternative = "greater")
result

```

```

##

```

```

## Wilcoxon signed rank test with continuity correction

```

```

##

```

```

## data: data_adt$effectiveness_in_context

```

```

## V = 300, p-value = 7.603e-05

```

```

## alternative hypothesis: true location is greater than 0.6

```

```

# Check if the p-value is lower than the significance level

```

```

if (result$p.value < alpha) {

```

```

  # Null hypothesis rejected

```

```

  cat("The null hypothesis that effectiveness_in_context is lower than 0.6 is rejected (p <", alpha, ")")

```

```

} else {

```

```

  # Null hypothesis not rejected

```

```

  cat("The null hypothesis is not rejected (p >=", alpha, ")")

```

```

}

```

The null hypothesis that effectiveness_in_context is lower than 0.6 is rejected (p < 0.05)

- efficiency_in_context: rejected

```
# Set the desired significance level
alpha <- 0.05

result <- wilcox.test(data_adt$efficiency_in_context, mu = 0.12, alternative = "greater")
result

##
## Wilcoxon signed rank test with continuity correction
##
## data: data_adt$efficiency_in_context
## V = 309, p-value = 4.191e-05
## alternative hypothesis: true location is greater than 0.12
# Check if the p-value is lower than the significance level
if (result$p.value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis that efficiency_in_context is lower than 0.6 is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}

## The null hypothesis that efficiency_in_context is lower than 0.6 is rejected (p < 0.05 )
```

Effect size for the variables

Reference values for effect size are:

- A value of 0.2 represents a small effect size.
- A value of 0.5 represents a medium effect size.
- A value equal to or larger than 0.8 represents a large effect size.

```
library(lsr)

## Warning: package 'lsr' was built under R version 4.3.2
cohensD(data_adt$Effectiveness, mu = 0.6)

## [1] 1.255714
cohensD(data_adt$Efficiency, mu = 0.015)

## [1] 1.983621
The effect size for effectiveness and efficiency is large
cohensD(data_adt$effectiveness_not_context, mu = 0.6)

## [1] 2.19877
cohensD(data_adt$efficiency_not_context, mu = 0.06)

## [1] 0.9383547
cohensD(data_adt$transferability_effectiveness, mu = 0.6)

## [1] 0.05053103
cohensD(data_adt$transferability_efficiency, mu = 0.024)
```

```
## [1] 0.1412935
```

```
cohensD(data_adt$effectiveness_in_context, mu = 0.6)
```

```
## [1] 1.755117
```

```
cohensD(data_adt$efficiency_in_context, mu = 0.12)
```

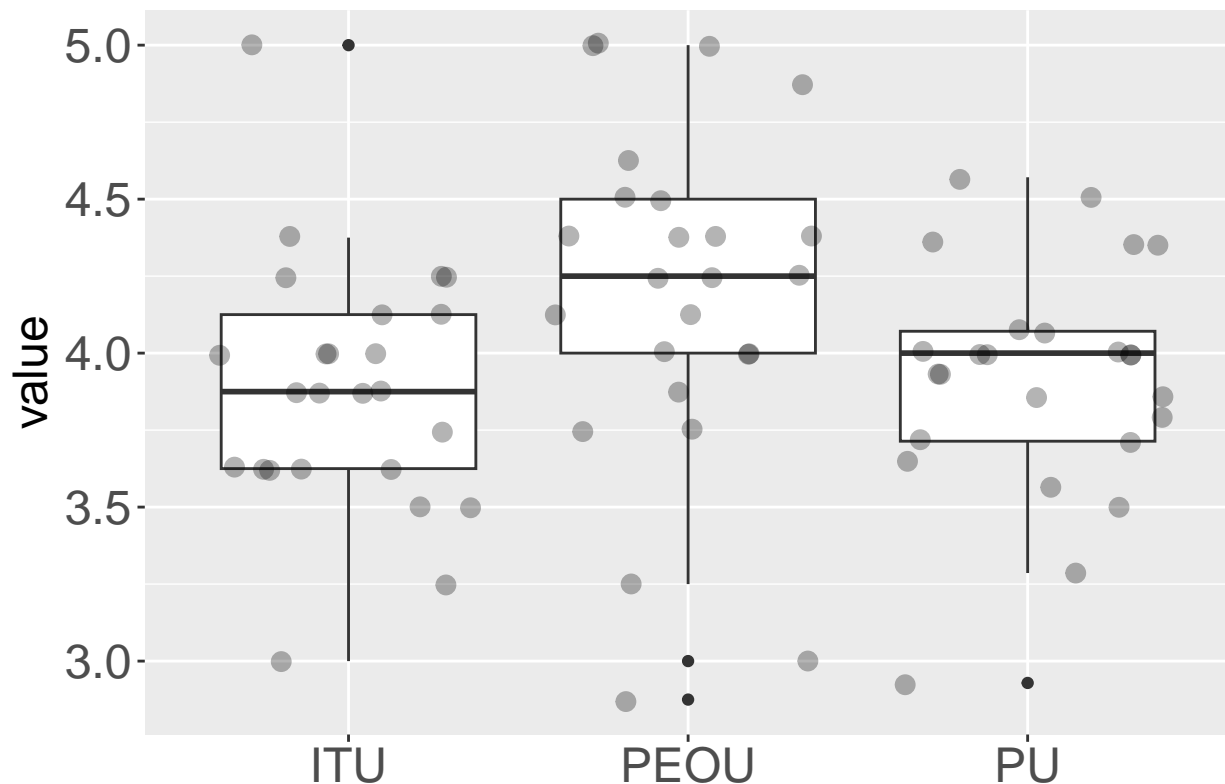
```
## [1] 1.066268
```

The effect size for detailed variables is as follows (note that effect size makes sense only for significant values, i.e., when the hypothesis is rejected).

- Effectiveness not in context: large
- Efficiency not in context: large
- Transferability effectiveness: no effect
- Transferability efficiency: no effect
- Effectiveness in context: large
- Efficiency in context: large

Boxplot of the three variables: PEOU, PU, ITU

The three variables are clearly all above the average value of the Likert scale (i.e., 3), thus suggesting that the general degree of acceptance of the ADT notation is high. We see that, while ITU and PU have comparable values, PEOU receives the highest score. This further confirms that ADTs are considered easy to use by the participants.



Descriptive statistics for all the variables

```
df <- data_adt
col_names <- c("Stat", colnames(df))
# Create a vector with the desired summary statistics
stats <- c("Min", "1st Qu", "Median", "Mean", "3rd Qu", "Max")

# Create an empty matrix to store the summary statistics
summary_mat <- matrix(NA, nrow = length(stats), ncol = ncol(df))

# Iterate over each column of the original dataframe
for (i in 1:ncol(df)) {
  # Compute the summary statistics
  summary_stats <- summary(df[[i]])

  # Store the summary statistics in the matrix
  summary_mat[, i] <- summary_stats
}

# Convert the matrix to a dataframe
summary_df <- as.data.frame(summary_mat)

# Add a row with the mean of each column
#summary_df <- rbind(summary_df, colMeans(df))

# Rename the row names for better readability
row.names(summary_df) <- c(stats)

colnames(summary_df) <- c("PEOU", "PU", "ITU", "Effectiveness", "Efficiency", "Effv. not in Context", "Effc. not in Context", "Transferability Effv.", "Transferability Effc.", "Effv. in Context", "Effc. in Context")

# Transpose the summary dataframe
transposed_df <- t(summary_df)

# Print the transposed dataframe
View(transposed_df)

knitr::kable(transposed_df)
```

	Min	1st Qu	Median	Mean	3rd Qu	Max
PEOU	2.875	4.000	4.250	4.18000	4.500	5.000
PU	2.929	3.714	4.000	3.91996	4.071	4.571
ITU	3.000	3.625	3.875	3.88000	4.125	5.000
Effectiveness	0.287	0.769	0.792	0.76780	0.833	0.986
Efficiency	0.011	0.101	0.118	0.13116	0.172	0.241
Effv. not in Context	0.625	0.750	0.750	0.78336	0.833	0.958
Effc. not in Context	0.024	0.069	0.094	0.10320	0.150	0.188
Transferability Effv.	0.000	0.556	0.667	0.61348	0.778	1.000
Transferability Effc.	0.000	0.018	0.023	0.02604	0.036	0.049
Effv. in Context	0.111	0.889	0.889	0.90672	1.000	1.000
Effc. in Context	0.009	0.178	0.250	0.26412	0.333	0.500

Test of significance against average value 3 of PEOU, PU and ITU

The normality check, performed with the Kolmogorov-Smirnov test, fails for all the variables with p-value well below the 0.05 significance level. We therefore need to apply a nonparametric test (Wilcoxon signed rank) to check whether the three variables are above the average value of the Livert scale (i.e., 3).

```
ks.test(data_adt$PEOU, "pnorm")
```

```
##
## Asymptotic one-sample Kolmogorov-Smirnov test
##
## data: data_adt$PEOU
## D = 0.99798, p-value < 2.2e-16
## alternative hypothesis: two-sided
```

```
ks.test(data_adt$PU, "pnorm")
```

```
##
## Asymptotic one-sample Kolmogorov-Smirnov test
##
## data: data_adt$PU
## D = 0.9983, p-value < 2.2e-16
## alternative hypothesis: two-sided
```

```
ks.test(data_adt$ITU, "pnorm")
```

```
##
## Asymptotic one-sample Kolmogorov-Smirnov test
##
## data: data_adt$ITU
## D = 0.99865, p-value < 2.2e-16
## alternative hypothesis: two-sided
```

Data are not normally distributed, therefore we use a nonparametric test (Wilcoxon signed rank).

```
# Set the desired significance level
```

```
alpha <- 0.05
```

```
result <- wilcox.test(data_adt$PEOU, mu = 3, alternative = "greater")
result
```

```
##
## Wilcoxon signed rank test with continuity correction
##
## data: data_adt$PEOU
## V = 299, p-value = 1.077e-05
## alternative hypothesis: true location is greater than 3
# Check if the p-value is lower than the significance level
if (result$p.value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis that PEOU is lower than the average score is rejected (p < ", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >= ", alpha, ")")
}
```

```
## The null hypothesis that PEOU is lower than the average score is rejected (p < 0.05 )
```

```

result <- wilcox.test(data_adt$PU, mu = 3, alternative = "greater")
result

##
## Wilcoxon signed rank test with continuity correction
##
## data: data_adt$PU
## V = 324, p-value = 7.109e-06
## alternative hypothesis: true location is greater than 3
# Check if the p-value is lower than the significance level
if (result$p.value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis that PU is lower than the average score is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}

## The null hypothesis that PU is lower than the average score is rejected (p < 0.05 )
result <- wilcox.test(data_adt$ITU, mu = 3, alternative = "greater")
result

##
## Wilcoxon signed rank test with continuity correction
##
## data: data_adt$ITU
## V = 300, p-value = 9.282e-06
## alternative hypothesis: true location is greater than 3
# Check if the p-value is lower than the significance level
if (result$p.value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis that ITU is lower than the average score is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}

## The null hypothesis that ITU is lower than the average score is rejected (p < 0.05 )

```

For all the tests we can reject the NULL hypothesis. More specifically, we reject the following hypotheses.

1. ADT is perceived as difficult to use
2. ADT is perceived as not useful
3. There is no intention to use ADT

Effect size for the three variables

Effect size for the variables

```

library(lsr)

cohensD(data_adt$PEOU, mu = 3)

```

```
## [1] 2.097433
```

```
cohensD(data_adt$PU, mu = 3)
```

```
## [1] 2.485847
```

```
cohensD(data_adt$ITU, mu = 3)
```

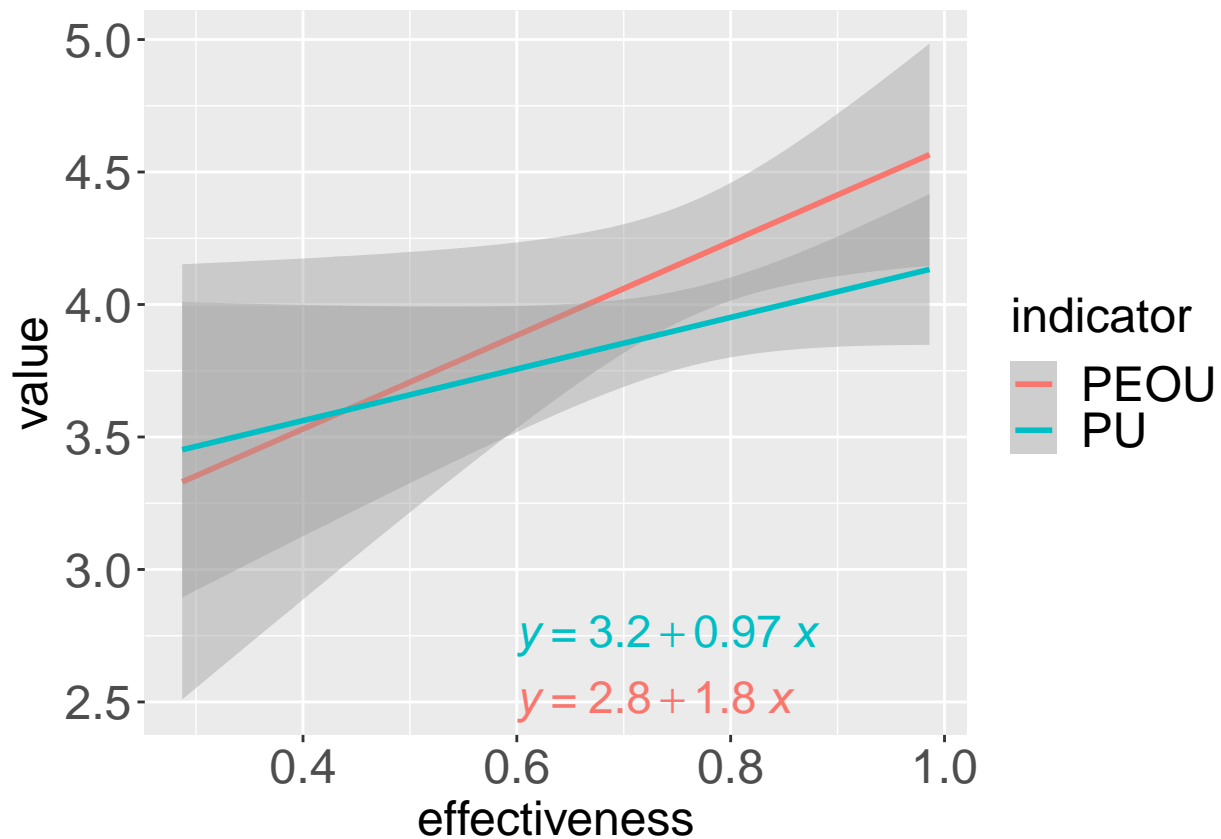
```
## [1] 2.185815
```

The effect size is medium for PEOU and large for PU and ITU.

PEOU and PU against efficiency and effectiveness, using a linear model as a fitting/interpolation function

We now explore the relation with total effectiveness.

```
data_adt %>%  
  pivot_longer(  
    cols = c("PEOU", "PU"),  
    names_to = "indicator",  
    values_to = "value"  
  ) %>%  
  ggplot(aes(x = Effectiveness, y = value, color = indicator)) +  
  geom_smooth(method = lm) +  
  labs(  
    x = "effectiveness"  
  ) +  
  theme(axis.text = element_text(size = SIZE),  
        axis.title = element_text(size = SIZE),  
        legend.text = element_text(size = SIZE),  
        legend.title = element_text(size = SIZE)) +  
  stat_regline_equation(size=EQ_SIZE, show.legend = FALSE, label.y = c(2.5, 2.75), label.x = c(0.6))  
  
## `geom_smooth()` using formula = 'y ~ x'
```



Statistical analysis of effectiveness against PEOU

```
mdl <- lm(PEOU ~ Effectiveness, data = data_adt)
summary(mdl)
```

```
##
## Call:
## lm(formula = PEOU ~ Effectiveness, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.08582 -0.30712  0.02282  0.23528  1.21186
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.8235     0.6206   4.549 0.000143 ***
## Effectiveness  1.7667     0.7968   2.217 0.036772 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5216 on 23 degrees of freedom
## Multiple R-squared:  0.1761, Adjusted R-squared:  0.1403
## F-statistic: 4.916 on 1 and 23 DF, p-value: 0.03677
# Get the summary of the model
mdl_summary <- summary(mdl)
```

```

# Extract the p-value
p_value <- mdl_summary$coefficients["Effectiveness", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}

```

The null hypothesis is rejected (p < 0.05)

Statistical analysis of effectiveness against PU

```

mdl <- lm(PU ~ Effectiveness, data = data_adt)
summary(mdl)

```

```

##
## Call:
## lm(formula = PU ~ Effectiveness, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.77501 -0.14883  0.03019  0.13340  0.55648
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    3.1724     0.4211   7.534 1.18e-07 ***
## Effectiveness  0.9736     0.5406   1.801  0.0848 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3539 on 23 degrees of freedom
## Multiple R-squared:  0.1236, Adjusted R-squared:  0.08549
## F-statistic: 3.244 on 1 and 23 DF,  p-value: 0.08483

# Get the summary of the model
mdl_summary <- summary(mdl)

# Extract the p-value
p_value <- mdl_summary$coefficients["Effectiveness", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected

```

```
cat("The null hypothesis is not rejected (p >=", alpha, ")")
}
```

```
## The null hypothesis is not rejected (p >= 0.05 )
```

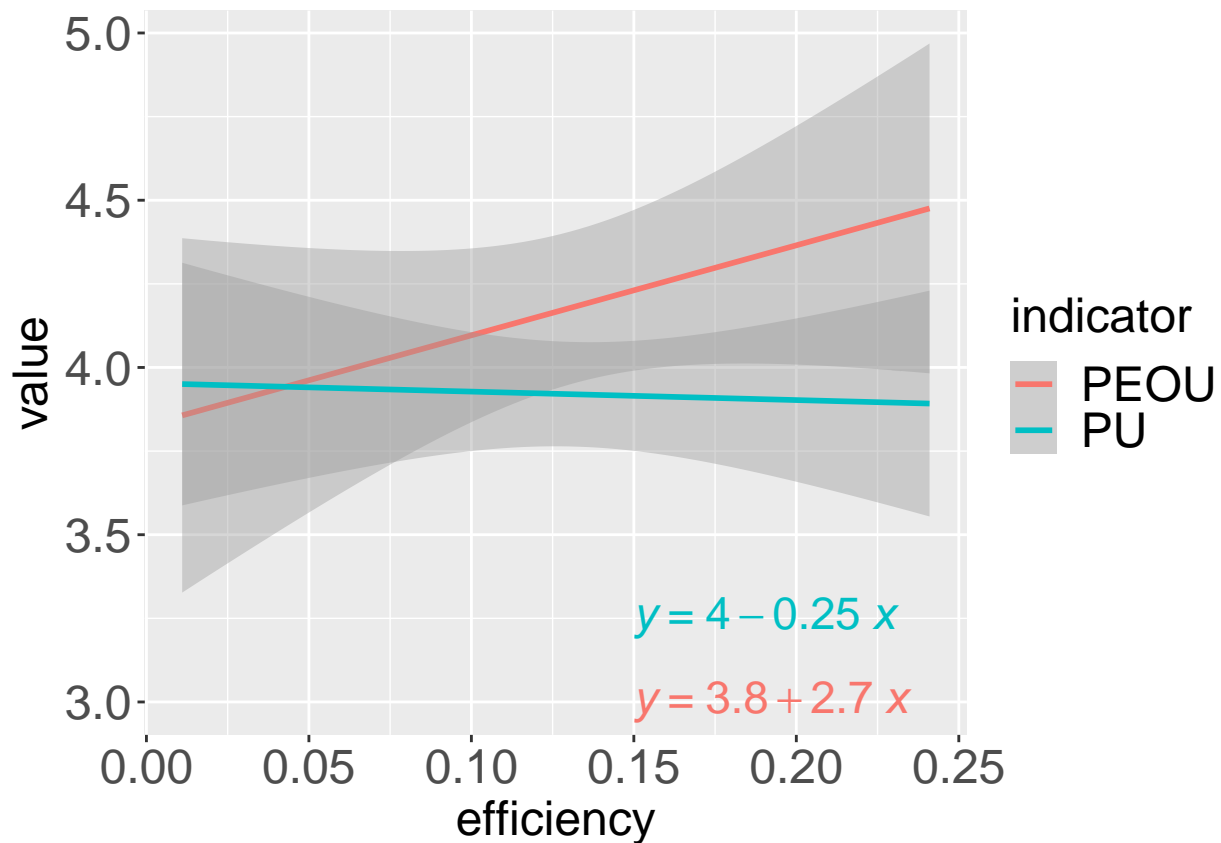
From the plot, we see that when effectiveness grows also PEOU and PU grows. From the statistical analysis, however, we see that while the relationship between effectiveness and PEOU is significant, the one with PU is not. Therefore the first NULL hypothesis is rejected, while the second NULL hypothesis cannot be rejected.

4. PEOU will not be determined by effectiveness: reject
5. PU will not be determined by effectiveness: fail to reject

Relation with efficiency

```
data_adt %>%
  pivot_longer(
    cols = c("PEOU", "PU"),
    names_to = "indicator",
    values_to = "value"
  ) %>%
  ggplot(aes(x = Efficiency, y = value, color = indicator)) +
  geom_smooth(method = lm) +
  labs(
    x = "efficiency"
  ) +
  theme(axis.text = element_text(size = SIZE),
        axis.title = element_text(size = SIZE),
        legend.text = element_text(size = SIZE),
        legend.title = element_text(size = SIZE)) +
  stat_regline_equation(size=EQ_SIZE, show.legend = FALSE, label.y = c(3, 3.25), label.x = c(0.15))

## `geom_smooth()` using formula = 'y ~ x'
```



Statistical analysis of efficiency against PEOU

```
mdl <- lm(PEOU ~ Efficiency, data = data_adt)
summary(mdl)
```

```
##
## Call:
## lm(formula = PEOU ~ Efficiency, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.1082  -0.3505   0.1054   0.2439   1.0464
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.8272     0.2753  13.901 1.11e-12 ***
## Efficiency    2.6902     1.9231   1.399  0.175
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5517 on 23 degrees of freedom
## Multiple R-squared:  0.07841,    Adjusted R-squared:  0.03834
## F-statistic: 1.957 on 1 and 23 DF,  p-value: 0.1752

# Get the summary of the model
mdl_summary <- summary(mdl)
```

```

# Extract the p-value
p_value <- mdl_summary$coefficients["Efficiency", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}

```

The null hypothesis is not rejected (p >= 0.05)

Statistical analysis of efficiency against PU

```

mdl <- lm(PU ~ Efficiency, data = data_adt)
summary(mdl)

```

```

##
## Call:
## lm(formula = PU ~ Efficiency, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.00366 -0.18575  0.07646  0.13986  0.64391
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.9532     0.1885  20.972  <2e-16 ***
## Efficiency   -0.2532     1.3167  -0.192   0.849
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3777 on 23 degrees of freedom
## Multiple R-squared:  0.001605, Adjusted R-squared:  -0.0418
## F-statistic: 0.03697 on 1 and 23 DF, p-value: 0.8492

# Get the summary of the model
mdl_summary <- summary(mdl)

# Extract the p-value
p_value <- mdl_summary$coefficients["Efficiency", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected

```

```
cat("The null hypothesis is not rejected (p >=", alpha, ")")
}
```

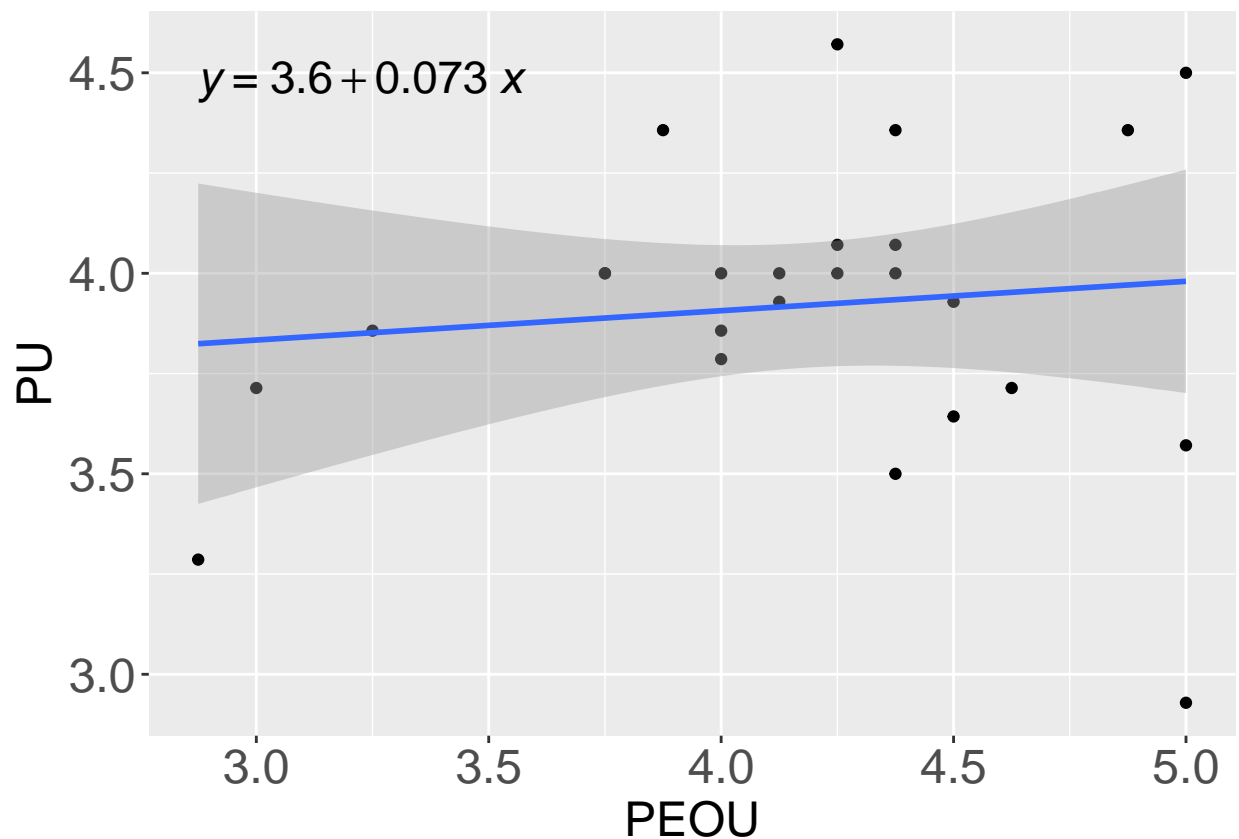
```
## The null hypothesis is not rejected (p >= 0.05 )
```

From the plot, we see that while PEOU grows with efficiency, PU appears to slightly decrease. From the statistical analysis, however, we see that none of the relationships are significant. Therefore none of the NULL hypothesis can be rejected.

6. PEOU will not be determined by efficiency: fail reject
7. PU will not be determined by efficiency: fail to reject

Relation between PU and PEOU

```
## `geom_smooth()` using formula = 'y ~ x'
```



Statistical analysis of PU against PEOU

```
mdl <- lm(PU ~ PEOU, data = data_adt)
summary(mdl)
```

```
##
## Call:
## lm(formula = PU ~ PEOU, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.05101 -0.12078  0.06576  0.13676  0.64591
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3.61384    0.57471   6.288 2.04e-06 ***
## PEOU         0.07323    0.13631   0.537   0.596
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3757 on 23 degrees of freedom
## Multiple R-squared:  0.01239,    Adjusted R-squared:  -0.03054
## F-statistic: 0.2886 on 1 and 23 DF,  p-value: 0.5962
```

```
# Get the summary of the model
mdl_summary <- summary(mdl)

# Extract the p-value
p_value <- mdl_summary$coefficients["PEOU", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}
```

The null hypothesis is not rejected (p >= 0.05)

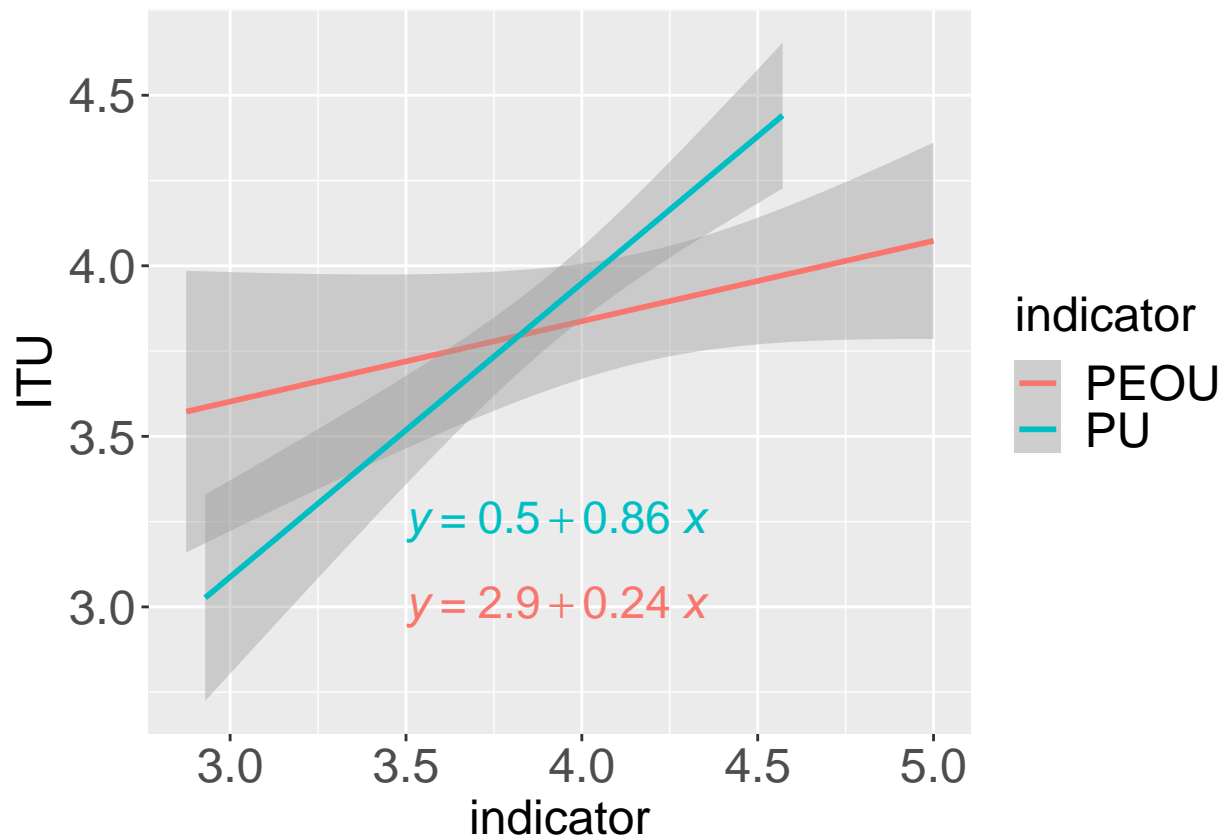
We see that although there is a slight increase of PU when PEOU grows, the relationship has no statistical significance. Therefore:

8. PU will not be determined by PEOU: fail to reject

Relation between ITU and PEOU; ITU and PU

```
data_adt %>%
  pivot_longer(
    cols = c("PEOU", "PU"),
    names_to = "indicator",
    values_to = "value"
  ) %>%
  ggplot(aes(x = value, y = ITU, color = indicator)) +
  geom_smooth(method = lm) +
  labs(
    x = "indicator"
  ) +
  theme(axis.text = element_text(size = SIZE),
        axis.title = element_text(size = SIZE),
        legend.text = element_text(size = SIZE),
        legend.title = element_text(size = SIZE)) +
  stat_regline_equation(size=EQ_SIZE, show.legend = FALSE, label.y = c(3, 3.25), label.x = c(3.5))
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



Statistical analysis of PU against ITU

```
mdl <- lm(ITU ~ PU, data = data_adt)
summary(mdl)
```

```
##
## Call:
## lm(formula = ITU ~ PU, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.33404 -0.19893 -0.07393  0.17422  0.55933
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.5041     0.5456   0.924   0.365
## PU            0.8612     0.1386   6.214 2.44e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2513 on 23 degrees of freedom
## Multiple R-squared:  0.6267, Adjusted R-squared:  0.6105
## F-statistic: 38.61 on 1 and 23 DF,  p-value: 2.436e-06
##
# Get the summary of the model
mdl_summary <- summary(mdl)
```

```

# Extract the p-value
p_value <- mdl_summary$coefficients["PU", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}

```

The null hypothesis is rejected (p < 0.05)

Statistical analysis of PEOU against ITU

```

mdl <- lm(ITU ~ PEOU, data = data_adt)
summary(mdl)

```

```

##
## Call:
## lm(formula = ITU ~ PEOU, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.82323 -0.17595  0.03742  0.19187  1.10351
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2.8950     0.5940   4.874 6.38e-05 ***
## PEOU           0.2356     0.1409   1.672   0.108
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3883 on 23 degrees of freedom
## Multiple R-squared:  0.1084, Adjusted R-squared:  0.06967
## F-statistic: 2.797 on 1 and 23 DF,  p-value: 0.108

# Get the summary of the model
mdl_summary <- summary(mdl)

# Extract the p-value
p_value <- mdl_summary$coefficients["PEOU", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {

```

```
# Null hypothesis not rejected
cat("The null hypothesis is not rejected (p >=", alpha, ")")
}
```

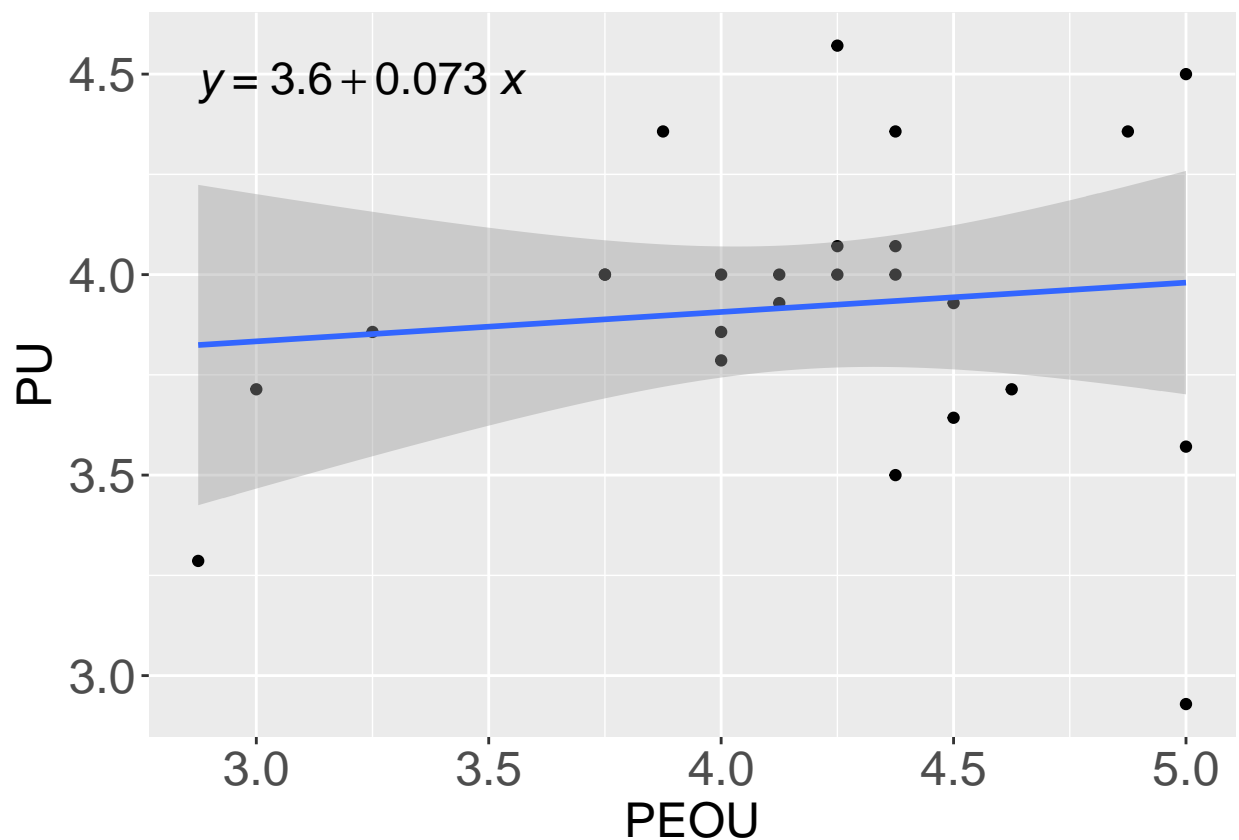
```
## The null hypothesis is not rejected (p >= 0.05 )
```

We clearly see from the plot above that both PEOU and PU tend to grow with ITU. However, from the analysis below, we see that PEOU and PU do not have any relationship. Therefore:

8. PU will not be determined by PEOU: fail to reject
9. ITU will not be determined by PEOU: fail to reject
10. ITU will not be determined by PU: reject

Relation between PU and PEOU

```
## `geom_smooth()` using formula = 'y ~ x'
```



Statistical analysis of PU against PEOU

```
mdl <- lm(PU ~ PEOU, data = data_adt)
summary(mdl)
```

```
##
## Call:
## lm(formula = PU ~ PEOU, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.05101 -0.12078  0.06576  0.13676  0.64591
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3.61384    0.57471   6.288 2.04e-06 ***
## PEOU         0.07323    0.13631   0.537   0.596
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3757 on 23 degrees of freedom
## Multiple R-squared:  0.01239,    Adjusted R-squared:  -0.03054
## F-statistic: 0.2886 on 1 and 23 DF,  p-value: 0.5962

# Get the summary of the model
mdl_summary <- summary(mdl)

# Extract the p-value
p_value <- mdl_summary$coefficients["PEOU", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}

## The null hypothesis is not rejected (p >= 0.05 )
```

Evaluation by single measures of effectiveness/efficiency

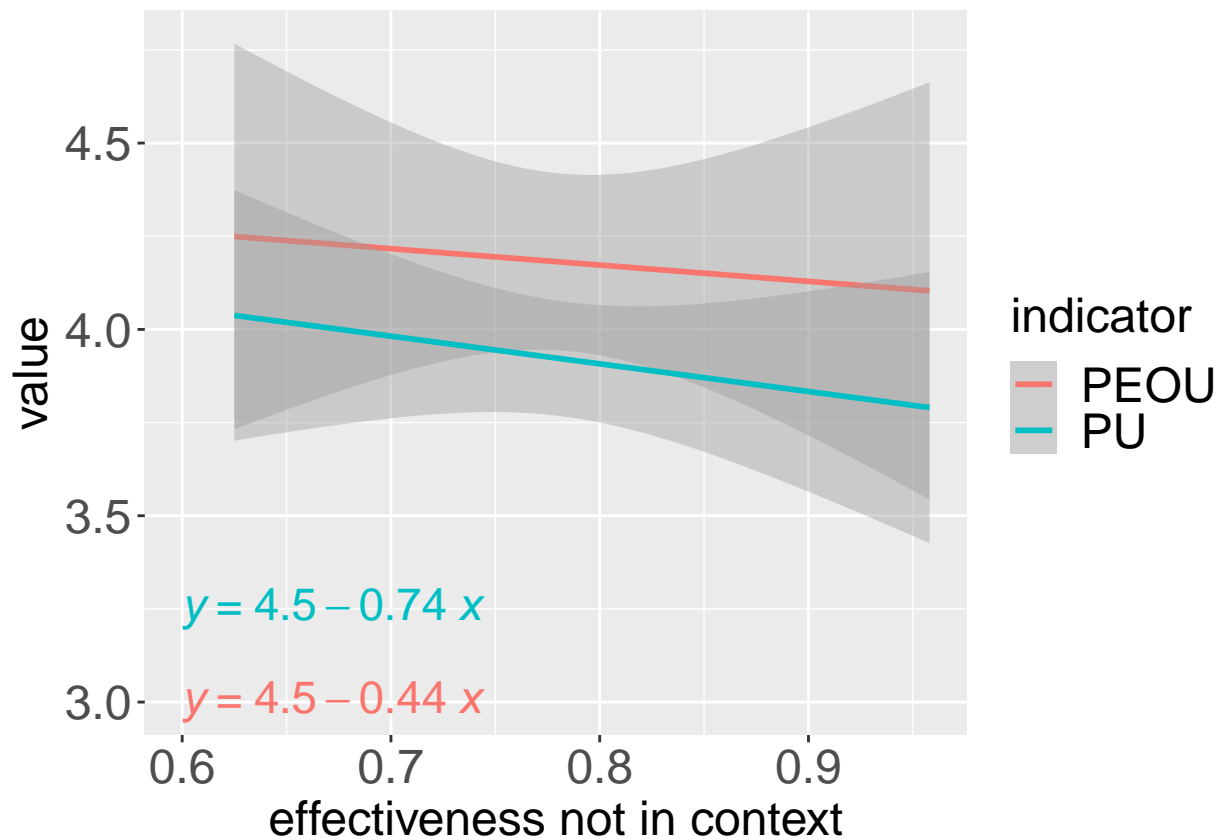
11. PEOU will not be determined by effectiveness not in context: fail to reject
12. PU will not be determined by effectiveness not in context: fail to reject
13. PEOU will not be determined by efficiency not in context: fail to reject
14. PU will not be determined by efficiency not in context: fail to reject
15. PEOU will not be determined by effectiveness in context: reject
16. PU will not be determined by effectiveness in context: fail to reject
17. PEOU will not be determined by efficiency in context: fail to reject
18. PU will not be determined by efficiency in context: fail to reject
19. PEOU will not be determined by transferability effectiveness: fail to reject
20. PU will not be determined by transferability effectiveness: reject
21. PEOU will not be determined by transferability efficiency: fail to reject
22. PU will not be determined by transferability efficiency: fail to reject

```
data_adt %>%
  pivot_longer(
    cols = c("PEOU", "PU"),
    names_to = "indicator",
    values_to = "value"
  ) %>%
  ggplot(aes(x = effectiveness_not_context, y = value, color = indicator)) +
```

```
geom_smooth(method = lm) +
labs(
  x = "effectiveness not in context"
) +
theme(axis.text = element_text(size = SIZE),
      axis.title = element_text(size = SIZE),
      legend.text = element_text(size = SIZE),
      legend.title = element_text(size = SIZE)) +
stat_regline_equation(size=EQ_SIZE, show.legend = FALSE, label.y = c(3, 3.25), label.x = c(0.6))
```

Relation with effectiveness not in context

`geom_smooth()` using formula = 'y ~ x'



Statistical analysis of effectiveness not in context against PEOU

```
mdl <- lm(PEOU ~ effectiveness_not_context, data = data_adt)
summary(mdl)
```

```
##
## Call:
## lm(formula = PEOU ~ effectiveness_not_context, data = data_adt)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
##	-1.26485	-0.24938	0.05538	0.26902	0.89651

```
##
```

```
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.5232     1.1056   4.091 0.000448 ***
## effectiveness_not_context -0.4381     1.4037  -0.312 0.757780
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5735 on 23 degrees of freedom
## Multiple R-squared:  0.004217,    Adjusted R-squared:  -0.03908
## F-statistic: 0.0974 on 1 and 23 DF,  p-value: 0.7578

# Get the summary of the model
mdl_summary <- summary(mdl)

# Extract the p-value
p_value <- mdl_summary$coefficients["effectiveness_not_context", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}
```

The null hypothesis is not rejected (p >= 0.05)

Statistical analysis of effectiveness not in context against PU

```
mdl <- lm(PU ~ effectiveness_not_context, data = data_adt)
summary(mdl)
```

```
##
## Call:
## lm(formula = PU ~ effectiveness_not_context, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.01573 -0.21930  0.08645  0.12627  0.62627
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.5015     0.7185   6.265 2.16e-06 ***
## effectiveness_not_context -0.7424     0.9123  -0.814   0.424
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3727 on 23 degrees of freedom
## Multiple R-squared:  0.02799,    Adjusted R-squared:  -0.01427
## F-statistic: 0.6623 on 1 and 23 DF,  p-value: 0.4241
```

```

# Get the summary of the model
mdl_summary <- summary(mdl)

# Extract the p-value
p_value <- mdl_summary$coefficients["effectiveness_not_context", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}

```

```
## The null hypothesis is not rejected (p >= 0.05 )
```

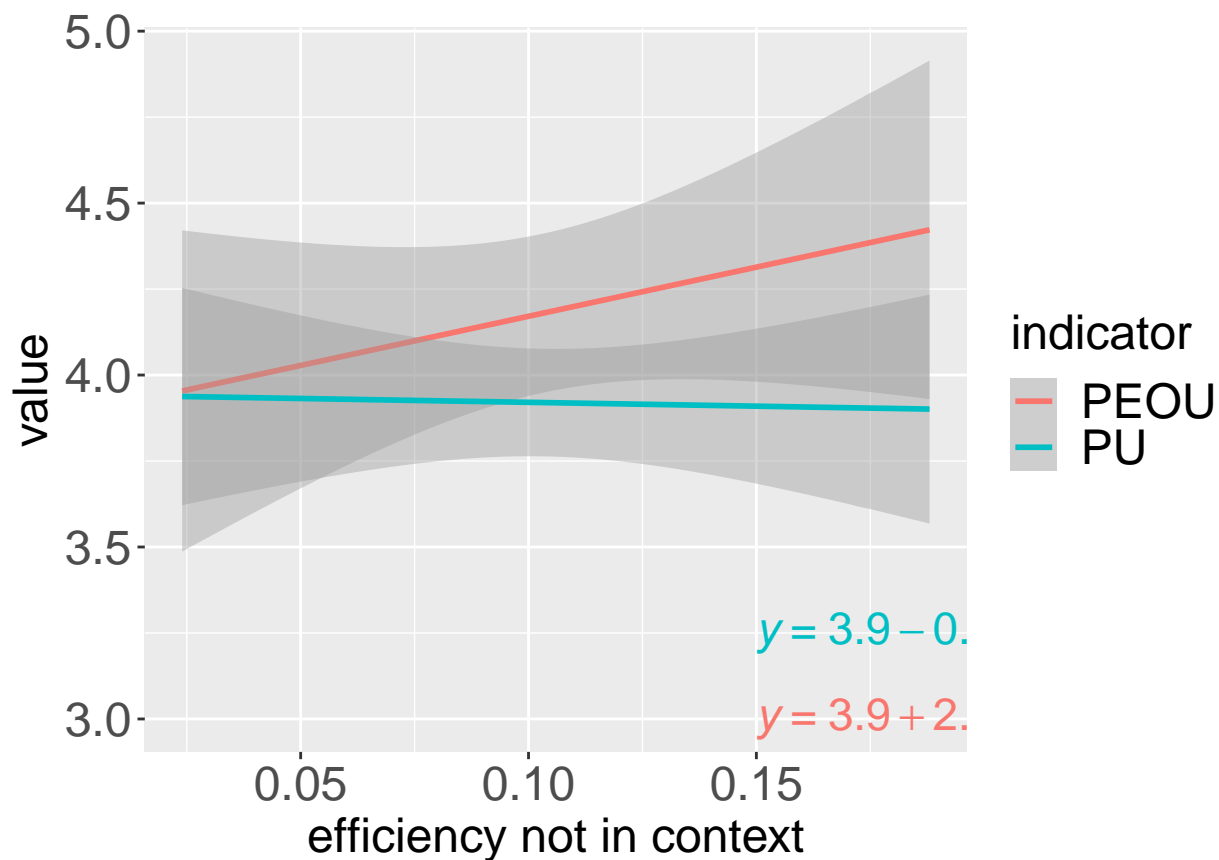
```

data_adt %>%
  pivot_longer(
    cols = c("PEOU", "PU"),
    names_to = "indicator",
    values_to = "value"
  ) %>%
  ggplot(aes(x = efficiency_not_context, y = value, color = indicator)) +
  geom_smooth(method = lm) +
  labs(
    x = "efficiency not in context"
  ) +
  theme(axis.text = element_text(size = SIZE),
        axis.title = element_text(size = SIZE),
        legend.text = element_text(size = SIZE),
        legend.title = element_text(size = SIZE)) +
  stat_regline_equation(size=EQ_SIZE, show.legend = FALSE, label.y = c(3, 3.25), label.x = c(0.15))

```

Relation with efficiency not in context

```
## `geom_smooth()` using formula = 'y ~ x'
```



Statistical analysis of efficiency against PEOU

```
mdl <- lm(PEOU ~ efficiency_not_context, data = data_adt)
summary(mdl)

##
## Call:
## lm(formula = PEOU ~ efficiency_not_context, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.3216 -0.3366  0.1506  0.3356  0.9463
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.885      0.279  13.924 1.08e-12 ***
## efficiency_not_context  2.857      2.477   1.153   0.261
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5588 on 23 degrees of freedom
## Multiple R-squared:  0.05467,    Adjusted R-squared:  0.01357
## F-statistic:  1.33 on 1 and 23 DF,  p-value: 0.2606
##
## Get the summary of the model
mdl_summary <- summary(mdl)
```

```

# Extract the p-value
p_value <- mdl_summary$coefficients["efficiency_not_context", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}

```

The null hypothesis is not rejected (p >= 0.05)

Statistical analysis of efficiency against PU

```

mdl <- lm(PU ~ efficiency_not_context, data = data_adt)
summary(mdl)

```

```

##
## Call:
## lm(formula = PU ~ efficiency_not_context, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.99301 -0.19730  0.07241  0.13850  0.64475
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.9430     0.1887  20.895  <2e-16 ***
## efficiency_not_context -0.2231     1.6755  -0.133    0.895
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3779 on 23 degrees of freedom
## Multiple R-squared:  0.0007704, Adjusted R-squared:  -0.04267
## F-statistic: 0.01773 on 1 and 23 DF,  p-value: 0.8952
# Get the summary of the model
mdl_summary <- summary(mdl)

# Extract the p-value
p_value <- mdl_summary$coefficients["efficiency_not_context", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected

```

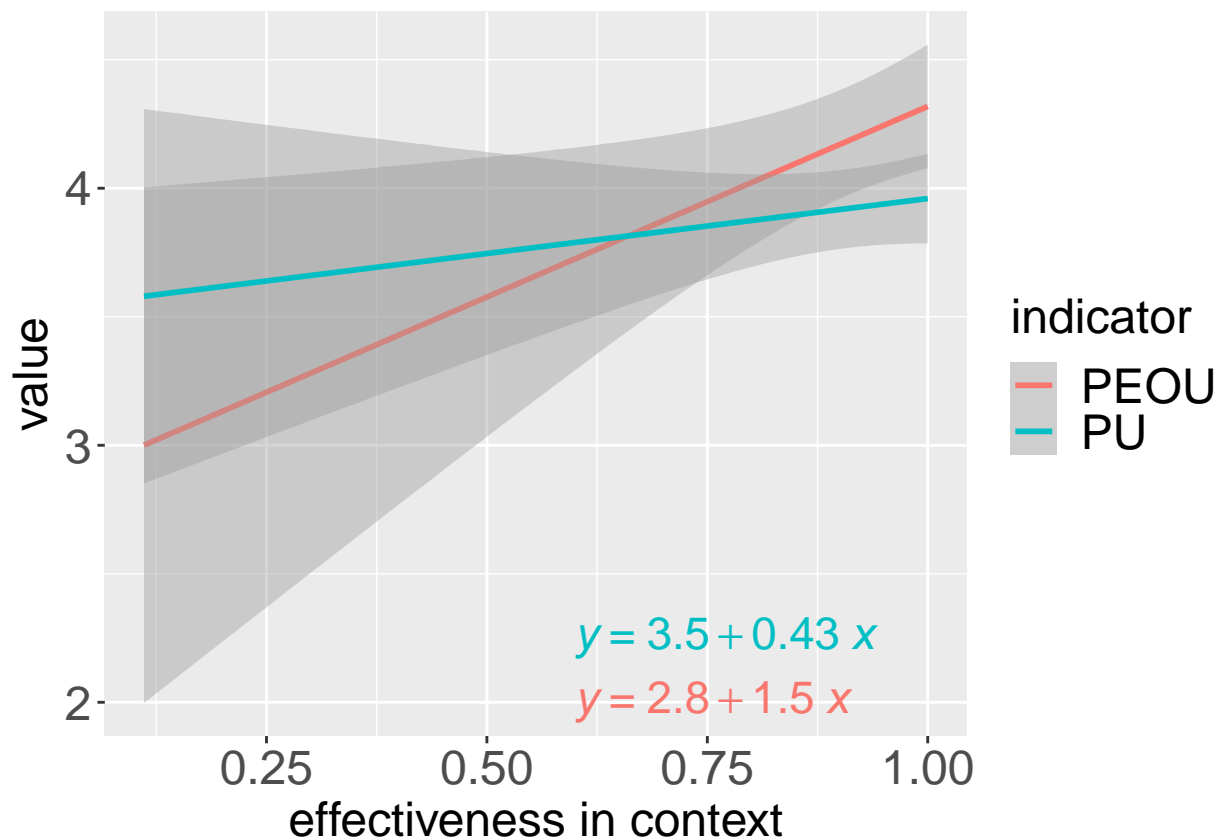
```
cat("The null hypothesis is not rejected (p >=", alpha, ")")
}
```

```
## The null hypothesis is not rejected (p >= 0.05 )
```

```
data_adt %>%
  pivot_longer(
    cols = c("PEOU", "PU"),
    names_to = "indicator",
    values_to = "value"
  ) %>%
  ggplot(aes(x = effectiveness_in_context, y = value, color = indicator)) +
  geom_smooth(method = lm) +
  labs(
    x = "effectiveness in context"
  ) +
  theme(axis.text = element_text(size = SIZE),
        axis.title = element_text(size = SIZE),
        legend.text = element_text(size = SIZE),
        legend.title = element_text(size = SIZE)) +
  stat_regline_equation(size=EQ_SIZE, show.legend = FALSE, label.y = c(2, 2.25), label.x = c(0.6))
```

Relation with effectiveness in context

```
## `geom_smooth()` using formula = 'y ~ x'
```



Statistical analysis of effectiveness in context against PEOU

```
mdl <- lm(PEOU ~ effectiveness_in_context, data = data_adt)
summary(mdl)
```

```
##
## Call:
## lm(formula = PEOU ~ effectiveness_in_context, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.27873 -0.15373 -0.02873  0.22127  0.84627
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.8356     0.5498   5.158 3.16e-05 ***
## effectiveness_in_context  1.4827     0.5958   2.488  0.0205 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5101 on 23 degrees of freedom
## Multiple R-squared:  0.2121, Adjusted R-squared:  0.1779
## F-statistic: 6.192 on 1 and 23 DF,  p-value: 0.02051
# Get the summary of the model
mdl_summary <- summary(mdl)

# Extract the p-value
p_value <- mdl_summary$coefficients["effectiveness_in_context", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p < ", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >= ", alpha, ")")
}
```

The null hypothesis is rejected (p < 0.05)

Statistical analysis of effectiveness not in context against PU

```
mdl <- lm(PU ~ effectiveness_in_context, data = data_adt)
summary(mdl)
```

```
##
## Call:
## lm(formula = PU ~ effectiveness_in_context, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.98338 -0.12638  0.04016  0.13422  0.61116
##
```

```
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.5323     0.3991   8.852 7.25e-09 ***
## effectiveness_in_context 0.4275     0.4325   0.989   0.333
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3703 on 23 degrees of freedom
## Multiple R-squared:  0.04076,    Adjusted R-squared:  -0.0009505
## F-statistic: 0.9772 on 1 and 23 DF,  p-value: 0.3332

# Get the summary of the model
mdl_summary <- summary(mdl)

# Extract the p-value
p_value <- mdl_summary$coefficients["effectiveness_in_context", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

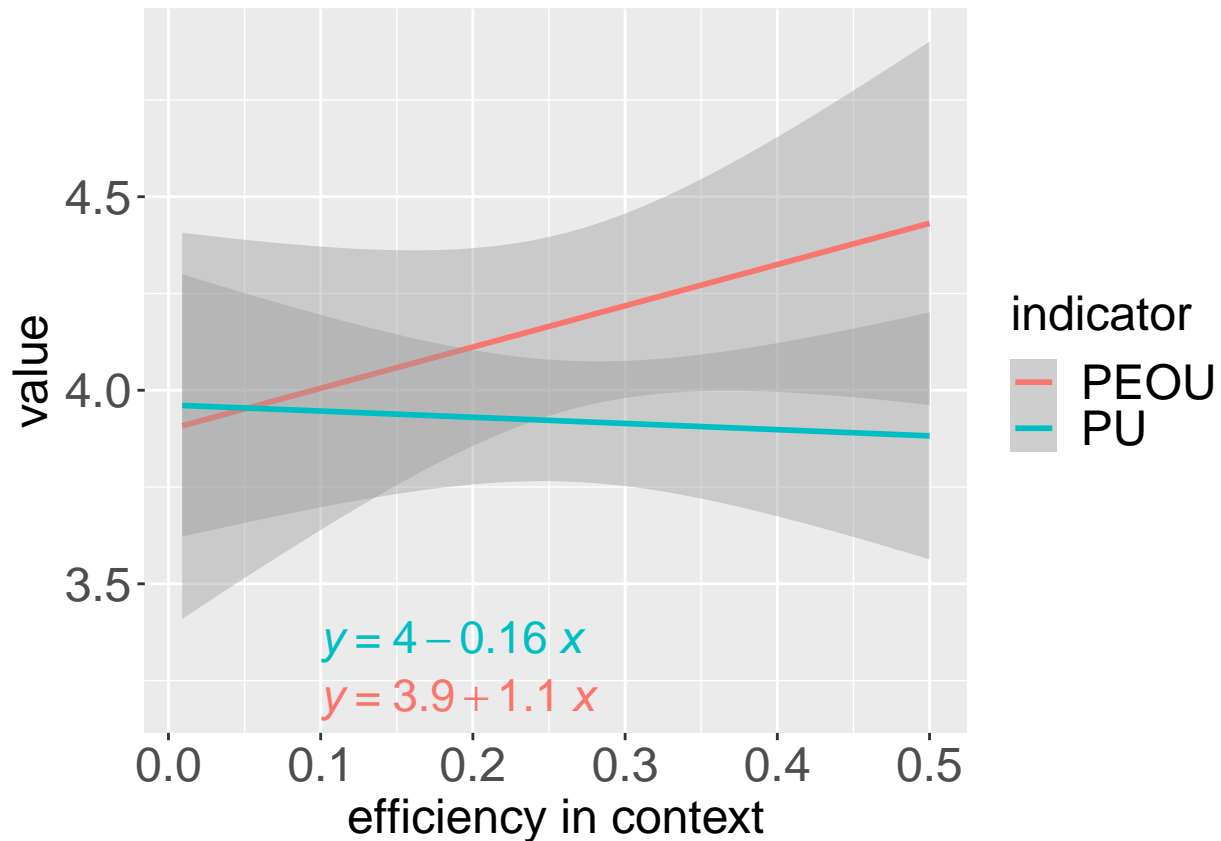
# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}
```

```
## The null hypothesis is not rejected (p >= 0.05 )
```

```
data_adt %>%
  pivot_longer(
    cols = c("PEOU", "PU"),
    names_to = "indicator",
    values_to = "value"
  ) %>%
  ggplot(aes(x = efficiency_in_context, y = value, color = indicator)) +
  geom_smooth(method = lm) +
  labs(
    x = "efficiency in context"
  ) +
  theme(axis.text = element_text(size = SIZE),
        axis.title = element_text(size = SIZE),
        legend.text = element_text(size = SIZE),
        legend.title = element_text(size = SIZE)) +
  stat_regline_equation(size=EQ_SIZE, show.legend = FALSE, label.y = c(3.2, 3.35), label.x = c(0.1))
```

Relation with efficiency not in context

```
## `geom_smooth()` using formula = 'y ~ x'
```



Statistical analysis of efficiency against PEOU

```
mdl <- lm(PEOU ~ efficiency_in_context, data = data_adt)
summary(mdl)
```

```
##
## Call:
## lm(formula = PEOU ~ efficiency_in_context, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.09069 -0.30635  0.08505  0.25332  1.03431
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.8986     0.2479   15.73 8.45e-14 ***
## efficiency_in_context  1.0656     0.8390    1.27  0.217
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5555 on 23 degrees of freedom
## Multiple R-squared:  0.06554,    Adjusted R-squared:  0.02491
## F-statistic: 1.613 on 1 and 23 DF,  p-value: 0.2168
```

Get the summary of the model

```
mdl_summary <- summary(mdl)
```

```

# Extract the p-value
p_value <- mdl_summary$coefficients["efficiency_in_context", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}

```

The null hypothesis is not rejected (p >= 0.05)

Statistical analysis of efficiency against PU

```

mdl <- lm(PU ~ efficiency_in_context, data = data_adt)
summary(mdl)

```

```

##
## Call:
## lm(formula = PU ~ efficiency_in_context, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.00956 -0.17715  0.07778  0.13725  0.64077
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.9623     0.1684  23.530  <2e-16 ***
## efficiency_in_context -0.1602     0.5699  -0.281    0.781
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3774 on 23 degrees of freedom
## Multiple R-squared:  0.003423, Adjusted R-squared:  -0.03991
## F-statistic: 0.07899 on 1 and 23 DF, p-value: 0.7812

```

```

# Get the summary of the model
mdl_summary <- summary(mdl)

# Extract the p-value
p_value <- mdl_summary$coefficients["efficiency_in_context", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected

```

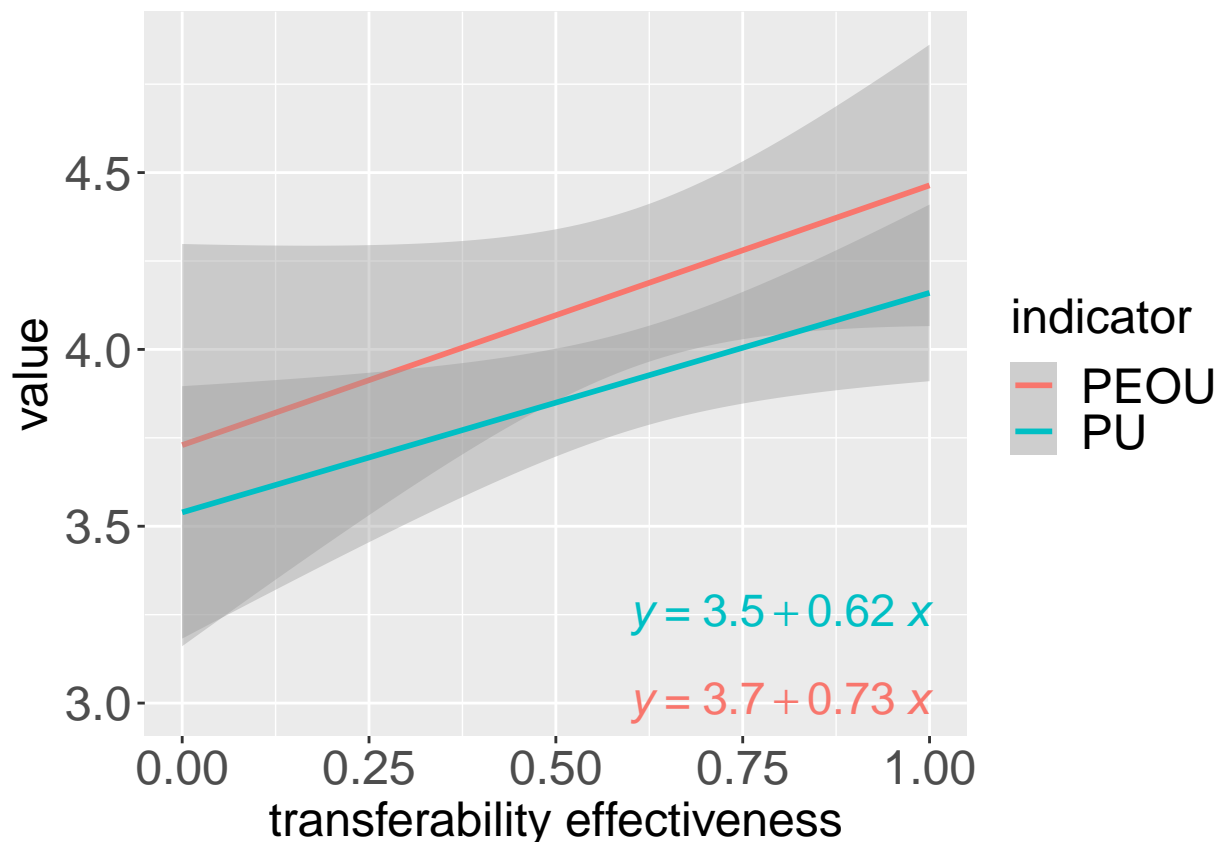
```
cat("The null hypothesis is not rejected (p >=", alpha, ")")
}
```

```
## The null hypothesis is not rejected (p >= 0.05 )
```

```
data_adt %>%
  pivot_longer(
    cols = c("PEOU", "PU"),
    names_to = "indicator",
    values_to = "value"
  ) %>%
  ggplot(aes(x = transferability_effectiveness, y = value, color = indicator)) +
  geom_smooth(method = lm) +
  labs(
    x = "transferability effectiveness"
  ) +
  theme(axis.text = element_text(size = SIZE),
        axis.title = element_text(size = SIZE),
        legend.text = element_text(size = SIZE),
        legend.title = element_text(size = SIZE)) +
  stat_regline_equation(size=EQ_SIZE, show.legend = FALSE, label.y = c(3, 3.25), label.x = c(0.6))
```

Relation with transferability effectiveness

```
## `geom_smooth()` using formula = 'y ~ x'
```



Statistical analysis of effectiveness in context against PEOU

```
mdl <- lm(PEOU ~ transferability_effectiveness, data = data_adt)
summary(mdl)
```

```
##
## Call:
## lm(formula = PEOU ~ transferability_effectiveness, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.13235 -0.34431  0.03069  0.19917  1.27055
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.7295     0.2749  13.567 1.84e-12 ***
## transferability_effectiveness  0.7344     0.4122   1.782   0.088 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5387 on 23 degrees of freedom
## Multiple R-squared:  0.1213, Adjusted R-squared:  0.08307
## F-statistic: 3.174 on 1 and 23 DF,  p-value: 0.08802
```

```
# Get the summary of the model
```

```
mdl_summary <- summary(mdl)
```

```
# Extract the p-value
```

```
p_value <- mdl_summary$coefficients["transferability_effectiveness", "Pr(>|t|)"]
```

```
# Set the desired significance level
```

```
alpha <- 0.05
```

```
# Check if the p-value is lower than the significance level
```

```
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p < ", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >= ", alpha, ")")
}
```

```
## The null hypothesis is not rejected (p >= 0.05 )
```

Statistical analysis of transferability effectiveness not in context against PU

```
mdl <- lm(PU ~ transferability_effectiveness, data = data_adt)
summary(mdl)
```

```
##
## Call:
## lm(formula = PU ~ transferability_effectiveness, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.61021 -0.23396  0.04682  0.18523  0.48004
##
```

```
## Coefficients:
##
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.5392     0.1725  20.515 2.77e-16 ***
## transferability_effectiveness  0.6206     0.2587   2.399  0.0249 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3381 on 23 degrees of freedom
## Multiple R-squared:  0.2002, Adjusted R-squared:  0.1654
## F-statistic: 5.755 on 1 and 23 DF,  p-value: 0.02494
```

```
# Get the summary of the model
mdl_summary <- summary(mdl)

# Extract the p-value
p_value <- mdl_summary$coefficients["transferability_effectiveness", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

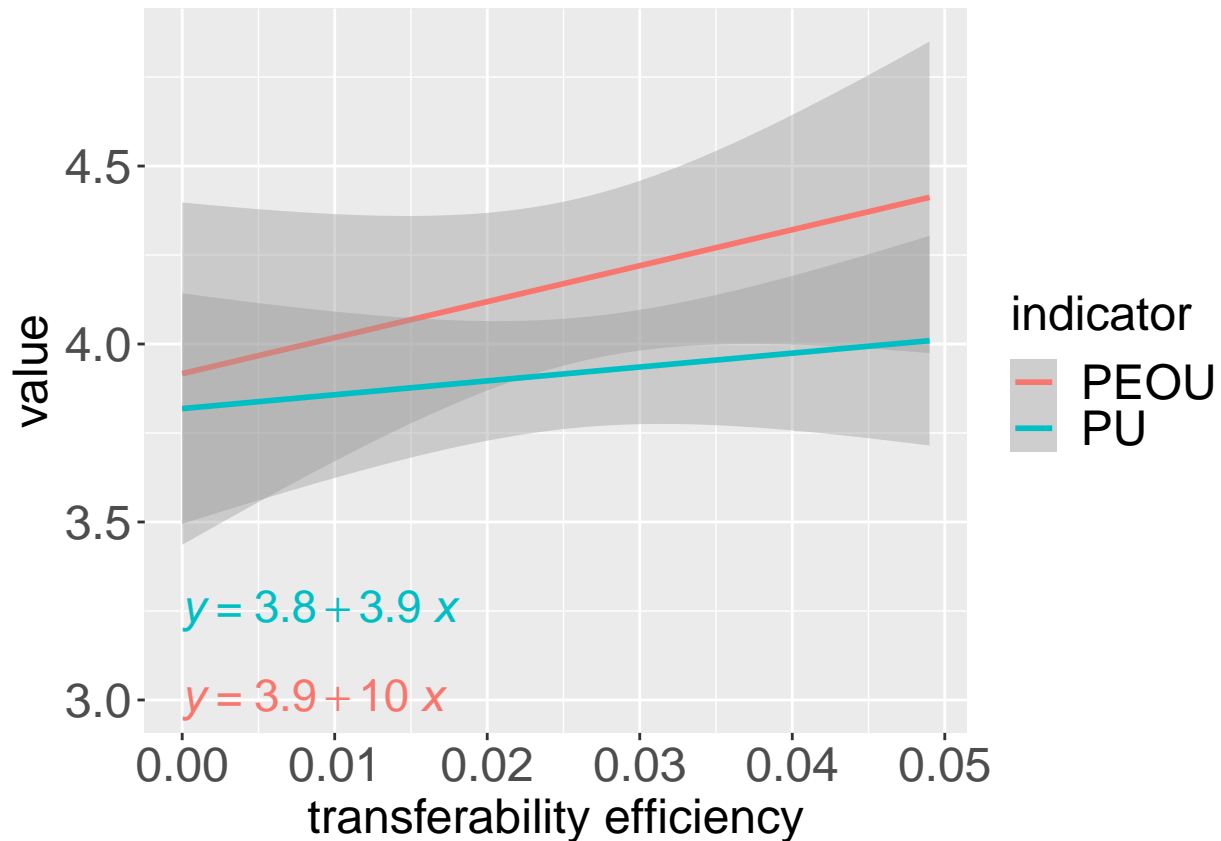
# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}
```

```
## The null hypothesis is rejected (p < 0.05 )
```

```
data_adt %>%
  pivot_longer(
    cols = c("PEOU", "PU"),
    names_to = "indicator",
    values_to = "value"
  ) %>%
  ggplot(aes(x = transferability_efficiency, y = value, color = indicator)) +
  geom_smooth(method = lm) +
  labs(
    x = "transferability efficiency"
  ) +
  theme(axis.text = element_text(size = SIZE),
        axis.title = element_text(size = SIZE),
        legend.text = element_text(size = SIZE),
        legend.title = element_text(size = SIZE)) +
  stat_regline_equation(size=EQ_SIZE, show.legend = FALSE, label.y = c(3, 3.25), label.x = c(0))
```

Relation with transferability efficiency

```
## `geom_smooth()` using formula = 'y ~ x'
```



Statistical analysis of transferability efficiency against PEOU

```
mdl <- lm(PEOU ~ transferability_efficiency, data = data_adt)
summary(mdl)
```

```
##
## Call:
## lm(formula = PEOU ~ transferability_efficiency, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.11154 -0.22373  0.01616  0.24324  1.08321
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.9168    0.2325  16.844 1.97e-14 ***
## transferability_efficiency 10.1080    7.8468   1.288   0.21
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.555 on 23 degrees of freedom
## Multiple R-squared:  0.06729,    Adjusted R-squared:  0.02674
## F-statistic: 1.659 on 1 and 23 DF,  p-value: 0.2105
##
## Get the summary of the model
mdl_summary <- summary(mdl)
```

```

# Extract the p-value
p_value <- mdl_summary$coefficients["transferability_efficiency", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected
  cat("The null hypothesis is not rejected (p >=", alpha, ")")
}

```

The null hypothesis is not rejected (p >= 0.05)

Statistical analysis of transferability efficiency against PU

```

mdl <- lm(PU ~ transferability_efficiency, data = data_adt)
summary(mdl)

```

```

##
## Call:
## lm(formula = PU ~ transferability_efficiency, data = data_adt)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.88956 -0.15237  0.04515  0.11615  0.62394
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.8186     0.1565  24.392  <2e-16 ***
## transferability_efficiency  3.8941     5.2827   0.737    0.468
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3737 on 23 degrees of freedom
## Multiple R-squared:  0.02308,    Adjusted R-squared:  -0.01939
## F-statistic: 0.5434 on 1 and 23 DF,  p-value: 0.4685

# Get the summary of the model
mdl_summary <- summary(mdl)

# Extract the p-value
p_value <- mdl_summary$coefficients["transferability_efficiency", "Pr(>|t|)"]

# Set the desired significance level
alpha <- 0.05

# Check if the p-value is lower than the significance level
if (p_value < alpha) {
  # Null hypothesis rejected
  cat("The null hypothesis is rejected (p <", alpha, ")")
} else {
  # Null hypothesis not rejected

```

```
cat("The null hypothesis is not rejected (p >=", alpha, ")")  
}
```

```
## The null hypothesis is not rejected (p >= 0.05 )
```