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| Title |  |
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| Author: |  |
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| Reviewed: |  |
|  |  |
| Approved: |  |
|  |  |

1. Import demographic and laboratory data as dataframes:

url <- "https://raw.githubusercontent.com/RConsortium/submissions-pilot3-adam-to-fda/main/m5/datasets/rconsortiumpilot3/tabulations/sdtm/"  
  
# Read the DM data from public github  
dm\_url <- glue::glue(url, "dm.xpt")  
dm\_data <- haven::read\_xpt(readr::read\_file\_raw(dm\_url))  
  
dm\_data <- dm\_data %>%   
 dplyr::mutate(COUNTRY = factor(COUNTRY, levels = c("USA", "NOT USA"))) %>%  
 dplyr::arrange(USUBJID)  
  
  
# Read the LB data from public github  
lb\_url <- glue::glue(url, "lb.xpt")  
lb\_data <- haven::read\_xpt(readr::read\_file\_raw(lb\_url))  
  
lb\_data <- lb\_data %>%   
 arrange(USUBJID, LBSEQ)  
  
rm(url, dm\_url, lb\_url)  
  
if (is.data.frame(dm\_data)) {  
 message("The data is a data frame.")  
} else {  
 message("The data is not a data frame.")  
}

## The data is a data frame.

## # A tibble: 6 × 25  
## STUDYID DOMAIN USUBJID SUBJID RFSTDTC RFENDTC RFXSTDTC RFXENDTC RFICDTC  
## <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr>   
## 1 CDISCPILOT01 DM 01-701-1… 1015 2014-0… 2014-0… 2014-01… 2014-07… ""   
## 2 CDISCPILOT01 DM 01-701-1… 1023 2012-0… 2012-0… 2012-08… 2012-09… ""   
## 3 CDISCPILOT01 DM 01-701-1… 1028 2013-0… 2014-0… 2013-07… 2014-01… ""   
## 4 CDISCPILOT01 DM 01-701-1… 1033 2014-0… 2014-0… 2014-03… 2014-03… ""   
## 5 CDISCPILOT01 DM 01-701-1… 1034 2014-0… 2014-1… 2014-07… 2014-12… ""   
## 6 CDISCPILOT01 DM 01-701-1… 1047 2013-0… 2013-0… 2013-02… 2013-03… ""   
## # ℹ 16 more variables: RFPENDTC <chr>, DTHDTC <chr>, DTHFL <chr>, SITEID <chr>,  
## # AGE <dbl>, AGEU <chr>, SEX <chr>, RACE <chr>, ETHNIC <chr>, ARMCD <chr>,  
## # ARM <chr>, ACTARMCD <chr>, ACTARM <chr>, COUNTRY <fct>, DMDTC <chr>,  
## # DMDY <dbl>

if (is.data.frame(lb\_data)) {  
 message("The data is a data frame.")  
} else {  
 message("The data is not a data frame.")  
}

## The data is a data frame.

## # A tibble: 6 × 23  
## STUDYID DOMAIN USUBJID LBSEQ LBTESTCD LBTEST LBCAT LBORRES LBORRESU LBORNRLO  
## <chr> <chr> <chr> <dbl> <chr> <chr> <chr> <chr> <chr> <chr>   
## 1 CDISCPIL… LB 01-701… 1 ALB Album… CHEM… 3.8 g/dL "3.3"   
## 2 CDISCPIL… LB 01-701… 2 ALP Alkal… CHEM… 34 U/L "35"   
## 3 CDISCPIL… LB 01-701… 3 ALT Alani… CHEM… 27 U/L "6"   
## 4 CDISCPIL… LB 01-701… 4 ANISO Aniso… HEMA… 1 NO UNITS ""   
## 5 CDISCPIL… LB 01-701… 5 AST Aspar… CHEM… 40 U/L "9"   
## 6 CDISCPIL… LB 01-701… 6 BASO Basop… HEMA… 0.05 THOU/uL "0"   
## # ℹ 13 more variables: LBORNRHI <chr>, LBSTRESC <chr>, LBSTRESN <dbl>,  
## # LBSTRESU <chr>, LBSTNRLO <dbl>, LBSTNRHI <dbl>, LBNRIND <chr>,  
## # LBBLFL <chr>, VISITNUM <dbl>, VISIT <chr>, VISITDY <dbl>, LBDTC <chr>,  
## # LBDY <dbl>

1. Data integrity checks

2.1. Validate that all 25 variables and 306 rows are intact for demographic data:

if (nrow(dm\_data) == 306 & ncol(dm\_data) == 25) {  
 message("OK: The dataset has 306 rows and 25 columns, as expected.")  
} else {  
 message("ERROR: The dataset does not have the expected number of rows or columns.")  
}

## OK: The dataset has 306 rows and 25 columns, as expected.

2.2. Validate that all 23 variables and 59580 rows are intact for laboratory data:

if (nrow(lb\_data) == 59580 & ncol(lb\_data) == 23) {  
 message("OK: The dataset has 59580 rows and 23 columns, as expected.")  
} else {  
 message("ERROR: The dataset does not have the expected number of rows or columns.")  
}

## OK: The dataset has 59580 rows and 23 columns, as expected.

2.3. Validate that the join between demographic and laboratory data is successful:

# Merge demographic and laboratory data  
data <- lb\_data %>% select(-DOMAIN) %>%  
 left\_join(dm\_data %>% select(-DOMAIN, -SUBJID), by = c("USUBJID", "STUDYID")) %>%  
 dplyr::mutate(ARM = factor(ARM)) %>%  
 dplyr::select(!starts\_with("LB"), starts\_with("LB"))  
  
# check if join is correct  
if (nrow(data) == nrow(lb\_data) & ncol(data) == ncol(dm\_data) + ncol(lb\_data) - 5) {  
 message("The join was successful.")  
} else {  
 message("The join was unsuccessful.")  
}

## The join was successful.

1. Data cleaning and summaries

3.1. Data cleaning

# Define allowed visit levels  
visits <- unique(data$VISIT)  
ordered\_visits <- visits[grepl("SCREENING|WEEK", visits)]  
  
# Store original labels before modification  
labels <- lapply(data, attr, "label")  
  
# Data filtering and cleaning  
data\_clean <- data %>%  
 select(USUBJID, ARM, VISIT, AGE, SEX, LBORRES, LBTEST) %>%  
 filter(LBTEST == "Albumin", VISIT %in% ordered\_visits) %>%  
 mutate(  
 LBORRES = as.numeric(LBORRES),  
 VISIT = factor(VISIT, levels = unique(c(ordered\_visits, VISIT))),  
 ARM = factor(ARM, levels = unique(ARM))  
 )  
  
# Restore labels  
for (col in names(labels)) {  
 if (!is.null(labels[[col]]) && col %in% names(data\_clean)) {  
 attr(data\_clean[[col]], "label") <- labels[[col]]  
 }  
 }

3.2. Baseline summary table is generated correctly by arm:

baseline\_summary <- data %>%  
 dplyr::distinct(USUBJID, ARM, SEX, RACE, ETHNIC, COUNTRY) %>%   
 dplyr::mutate(RACE = fct\_infreq(RACE),  
 ETHNIC = fct\_infreq(ETHNIC)) %>%  
 gtsummary::tbl\_summary(  
 by = ARM,  
 include = -USUBJID,  
 digits = list(  
 all\_continuous() ~ c(1, 1, 1),  
 all\_categorical() ~ c(0,1 )),  
 statistic = list(  
 all\_continuous() ~ "{mean} ({sd})",  
 all\_categorical() ~ "{n} ({p}%)"  
 ),  
 missing = "no"  
 ) %>%  
 gtsummary::add\_p(pvalue\_fun = label\_style\_pvalue(digits = 3)) %>%  
 gtsummary::add\_overall() %>%  
 gtsummary::modify\_header(label = "\*\*Variable\*\*") %>%  
 gtsummary::bold\_labels() %>%   
 gtsummary::as\_flex\_table() %>%  
 flextable::theme\_vanilla() %>%   
 flextable::set\_table\_properties(width = 1.0, layout = "autofit") %>%  
 flextable::align(align = "left", part = "body") %>%   
 flextable::align(align = "left", part = "header")   
  
baseline\_summary

| **Variable** | **Overall  N = 2541** | **Placebo  N = 861** | **Xanomeline High Dose  N = 841** | **Xanomeline Low Dose  N = 841** | **p-value2** |
| --- | --- | --- | --- | --- | --- |
| **Sex** |  |  |  |  | 0.141 |
| F | 143 (56.3%) | 53 (61.6%) | 40 (47.6%) | 50 (59.5%) |  |
| M | 111 (43.7%) | 33 (38.4%) | 44 (52.4%) | 34 (40.5%) |  |
| **RACE** |  |  |  |  | 0.680 |
| WHITE | 230 (90.6%) | 78 (90.7%) | 74 (88.1%) | 78 (92.9%) |  |
| BLACK OR AFRICAN AMERICAN | 23 (9.1%) | 8 (9.3%) | 9 (10.7%) | 6 (7.1%) |  |
| AMERICAN INDIAN OR ALASKA NATIVE | 1 (0.4%) | 0 (0.0%) | 1 (1.2%) | 0 (0.0%) |  |
| **ETHNIC** |  |  |  |  | 0.570 |
| NOT HISPANIC OR LATINO | 242 (95.3%) | 83 (96.5%) | 81 (96.4%) | 78 (92.9%) |  |
| HISPANIC OR LATINO | 12 (4.7%) | 3 (3.5%) | 3 (3.6%) | 6 (7.1%) |  |
| **COUNTRY** |  |  |  |  | >0.999 |
| USA | 254 (100.0%) | 86 (100.0%) | 84 (100.0%) | 84 (100.0%) |  |
| NOT USA | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) |  |
| 1n (%) | | | | | |
| 2Pearson's Chi-squared test; Fisher's exact test | | | | | |

3.3. Summaries by ARM and VISIT:

ALB\_summary <- data\_clean %>%   
 dplyr::group\_by(ARM, VISIT) %>%  
 dplyr::summarise(n = n(),  
 mean = round(mean(LBORRES, na.rm = TRUE), 2),  
 sd = round(sd(LBORRES, na.rm = TRUE), 2),  
 median = median(LBORRES, na.rm = TRUE),  
 min = min(LBORRES, na.rm = TRUE),  
 max = max(LBORRES, na.rm = TRUE),  
 .groups = "drop") %>%  
 flextable::flextable() %>%  
 flextable::theme\_booktabs() %>%  
 flextable::autofit()  
  
ALB\_summary

| ARM | Visit Name | n | mean | sd | median | min | max |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Placebo | SCREENING 1 | 86 | 3.98 | 0.28 | 4.00 | 3.2 | 4.6 |
| Placebo | WEEK 2 | 83 | 3.89 | 0.31 | 3.90 | 3.1 | 4.6 |
| Placebo | WEEK 4 | 79 | 3.88 | 0.33 | 3.90 | 2.9 | 4.7 |
| Placebo | WEEK 6 | 73 | 3.91 | 0.26 | 3.90 | 3.4 | 4.5 |
| Placebo | WEEK 8 | 72 | 3.98 | 0.35 | 4.00 | 2.8 | 4.9 |
| Placebo | WEEK 12 | 67 | 3.95 | 0.35 | 4.00 | 2.8 | 4.7 |
| Placebo | WEEK 16 | 68 | 4.04 | 0.30 | 4.00 | 3.3 | 4.8 |
| Placebo | WEEK 20 | 65 | 3.96 | 0.35 | 4.00 | 2.6 | 4.6 |
| Placebo | WEEK 24 | 57 | 3.97 | 0.33 | 4.00 | 2.9 | 4.6 |
| Placebo | WEEK 26 | 57 | 3.98 | 0.30 | 4.00 | 3.3 | 4.7 |
| Xanomeline High Dose | SCREENING 1 | 84 | 4.03 | 0.28 | 4.00 | 3.2 | 4.9 |
| Xanomeline High Dose | WEEK 2 | 78 | 3.89 | 0.28 | 3.90 | 3.3 | 4.6 |
| Xanomeline High Dose | WEEK 4 | 72 | 3.91 | 0.30 | 3.90 | 3.0 | 4.8 |
| Xanomeline High Dose | WEEK 6 | 66 | 3.95 | 0.28 | 3.90 | 3.4 | 4.5 |
| Xanomeline High Dose | WEEK 8 | 56 | 3.98 | 0.23 | 4.00 | 3.6 | 4.5 |
| Xanomeline High Dose | WEEK 12 | 50 | 3.98 | 0.24 | 3.95 | 3.5 | 4.4 |
| Xanomeline High Dose | WEEK 16 | 37 | 3.99 | 0.19 | 4.00 | 3.6 | 4.4 |
| Xanomeline High Dose | WEEK 20 | 31 | 3.96 | 0.19 | 4.00 | 3.5 | 4.4 |
| Xanomeline High Dose | WEEK 24 | 30 | 4.05 | 0.21 | 4.10 | 3.5 | 4.4 |
| Xanomeline High Dose | WEEK 26 | 27 | 4.00 | 0.23 | 4.00 | 3.5 | 4.5 |
| Xanomeline Low Dose | SCREENING 1 | 82 | 3.98 | 0.26 | 4.00 | 3.2 | 4.6 |
| Xanomeline Low Dose | WEEK 2 | 80 | 3.87 | 0.32 | 3.90 | 3.1 | 4.6 |
| Xanomeline Low Dose | WEEK 4 | 72 | 3.86 | 0.28 | 3.85 | 3.1 | 4.5 |
| Xanomeline Low Dose | WEEK 6 | 62 | 3.84 | 0.26 | 3.80 | 3.2 | 4.4 |
| Xanomeline Low Dose | WEEK 8 | 60 | 3.91 | 0.29 | 3.90 | 3.3 | 5.1 |
| Xanomeline Low Dose | WEEK 12 | 51 | 3.89 | 0.22 | 3.90 | 3.1 | 4.4 |
| Xanomeline Low Dose | WEEK 16 | 42 | 3.91 | 0.30 | 3.90 | 3.2 | 4.5 |
| Xanomeline Low Dose | WEEK 20 | 30 | 3.86 | 0.27 | 3.90 | 2.8 | 4.2 |
| Xanomeline Low Dose | WEEK 24 | 26 | 4.04 | 0.25 | 4.05 | 3.2 | 4.5 |
| Xanomeline Low Dose | WEEK 26 | 25 | 3.92 | 0.24 | 3.90 | 3.5 | 4.4 |

1. Statistical modeling

4.1 LM model

# LM model ----  
lm\_model <- lm(LBORRES ~ ARM \* VISIT + AGE,   
 data = data\_clean)  
  
lm\_model\_results <- broom.mixed::tidy(lm\_model) %>%   
 mutate(across(where(is.numeric), ~ round(.x, 3)))  
  
lm\_numeric\_cols <- names(lm\_model\_results)[sapply(lm\_model\_results, is.numeric)]  
  
lm\_model\_table <- lm\_model\_results %>%  
 flextable() %>%  
 colformat\_num(j = lm\_numeric\_cols, digits = 3) %>% # Ensure 3-digit precision  
 theme\_booktabs() %>% # Optional: Clean table style  
 autofit() # Adjust column widths  
lm\_model\_table

| term | estimate | std.error | statistic | p.value |
| --- | --- | --- | --- | --- |
| (Intercept) | 4.512 | 0.069 | 65.619 | 0.000 |
| ARMXanomeline High Dose | 0.039 | 0.043 | 0.903 | 0.367 |
| ARMXanomeline Low Dose | -0.004 | 0.044 | -0.102 | 0.919 |
| VISITWEEK 2 | -0.096 | 0.043 | -2.207 | 0.027 |
| VISITWEEK 4 | -0.109 | 0.044 | -2.489 | 0.013 |
| VISITWEEK 6 | -0.078 | 0.045 | -1.735 | 0.083 |
| VISITWEEK 8 | -0.010 | 0.045 | -0.212 | 0.832 |
| VISITWEEK 12 | -0.040 | 0.046 | -0.872 | 0.383 |
| VISITWEEK 16 | 0.052 | 0.046 | 1.128 | 0.259 |
| VISITWEEK 20 | -0.030 | 0.046 | -0.646 | 0.518 |
| VISITWEEK 24 | -0.021 | 0.048 | -0.436 | 0.663 |
| VISITWEEK 26 | -0.005 | 0.048 | -0.109 | 0.914 |
| AGE | -0.007 | 0.001 | -8.561 | 0.000 |
| ARMXanomeline High Dose:VISITWEEK 2 | -0.042 | 0.062 | -0.675 | 0.500 |
| ARMXanomeline Low Dose:VISITWEEK 2 | -0.013 | 0.062 | -0.217 | 0.828 |
| ARMXanomeline High Dose:VISITWEEK 4 | -0.014 | 0.063 | -0.218 | 0.827 |
| ARMXanomeline Low Dose:VISITWEEK 4 | -0.007 | 0.063 | -0.104 | 0.917 |
| ARMXanomeline High Dose:VISITWEEK 6 | -0.008 | 0.065 | -0.120 | 0.904 |
| ARMXanomeline Low Dose:VISITWEEK 6 | -0.056 | 0.065 | -0.860 | 0.390 |
| ARMXanomeline High Dose:VISITWEEK 8 | -0.039 | 0.066 | -0.584 | 0.559 |
| ARMXanomeline Low Dose:VISITWEEK 8 | -0.050 | 0.066 | -0.763 | 0.446 |
| ARMXanomeline High Dose:VISITWEEK 12 | -0.010 | 0.068 | -0.150 | 0.881 |
| ARMXanomeline Low Dose:VISITWEEK 12 | -0.054 | 0.068 | -0.800 | 0.424 |
| ARMXanomeline High Dose:VISITWEEK 16 | -0.093 | 0.072 | -1.291 | 0.197 |
| ARMXanomeline Low Dose:VISITWEEK 16 | -0.118 | 0.070 | -1.683 | 0.093 |
| ARMXanomeline High Dose:VISITWEEK 20 | -0.031 | 0.075 | -0.408 | 0.683 |
| ARMXanomeline Low Dose:VISITWEEK 20 | -0.093 | 0.076 | -1.231 | 0.219 |
| ARMXanomeline High Dose:VISITWEEK 24 | 0.042 | 0.077 | 0.551 | 0.582 |
| ARMXanomeline Low Dose:VISITWEEK 24 | 0.064 | 0.080 | 0.798 | 0.425 |
| ARMXanomeline High Dose:VISITWEEK 26 | -0.034 | 0.079 | -0.437 | 0.662 |
| ARMXanomeline Low Dose:VISITWEEK 26 | -0.069 | 0.080 | -0.863 | 0.388 |

4.2 LMM model

# LMM model ----  
# fixed effects: ARM, VISIT, AGE  
# random effect: USUBJID  
lmm\_model <- lmer(LBORRES ~ ARM \* VISIT + AGE + (1 | USUBJID),   
 data = data\_clean)  
  
lmm\_model\_results <- broom.mixed::tidy(lmm\_model) %>%  
 mutate(across(where(is.numeric), ~ round(.x, 1))) %>%   
 select(-group) %>%   
 filter(term %in% c("VISITWEEK 2", "VISITWEEK 4", " VISITWEEK 6", "VISITWEEK 8", "VISITWEEK 12", "VISITWEEK 16", "VISITWEEK 20", "VISITWEEK 24", "VISITWEEK 26", "AGE"))  
  
lmm\_numeric\_cols <- names(lmm\_model\_results)[sapply(lmm\_model\_results, is.numeric)]  
  
lmm\_model\_table <- lmm\_model\_results %>%  
 flextable() %>%  
 colformat\_num(j = lmm\_numeric\_cols, digits = 1) %>% # Ensure 3-digit precision  
 theme\_booktabs() %>% # Optional: Clean table style  
 autofit() # Adjust column widths  
lmm\_model\_table

| effect | term | estimate | std.error | statistic | df | p.value |
| --- | --- | --- | --- | --- | --- | --- |
| fixed | VISITWEEK 2 | -0.1 | 0 | -3.4 | 1,502.6 | 0.0 |
| fixed | VISITWEEK 4 | -0.1 | 0 | -3.7 | 1,504.8 | 0.0 |
| fixed | VISITWEEK 8 | 0.0 | 0 | -1.3 | 1,512.8 | 0.2 |
| fixed | VISITWEEK 12 | -0.1 | 0 | -2.1 | 1,514.3 | 0.0 |
| fixed | VISITWEEK 16 | 0.0 | 0 | 1.0 | 1,514.4 | 0.3 |
| fixed | VISITWEEK 20 | 0.0 | 0 | -1.6 | 1,514.7 | 0.1 |
| fixed | VISITWEEK 24 | 0.0 | 0 | -0.7 | 1,515.0 | 0.5 |
| fixed | VISITWEEK 26 | 0.0 | 0 | -0.1 | 1,515.1 | 0.9 |
| fixed | AGE | 0.0 | 0 | -4.3 | 251.0 | 0.0 |

4.3. LMM model with nesting and map function

data\_perf <- data %>%  
 select(USUBJID, ARM, VISIT, AGE, LBORRES, LBTEST) %>%  
 filter(VISIT %in% ordered\_visits) %>%  
 mutate(  
 LBORRES = as.numeric(LBORRES),  
 VISIT = factor(VISIT, levels = unique(c(ordered\_visits, VISIT))),  
 ARM = factor(ARM, levels = unique(ARM))  
 ) %>%  
 filter(!is.na(LBORRES))

## Warning: There was 1 warning in `mutate()`.  
## ℹ In argument: `LBORRES = as.numeric(LBORRES)`.  
## Caused by warning:  
## ! NAs introduced by coercion

tests <- unique(data\_perf$LBTEST)[1:5]  
   
data\_perf\_filtered <- data\_perf %>% filter(LBTEST %in% tests)  
   
# Analysis with nesting and map function (replacement for for loop)  
data\_analysis <- data\_perf\_filtered %>%  
 group\_by(LBTEST) %>%  
 nest() %>%  
 mutate(  
 model = map(.x = data, ~ lmer(LBORRES ~ ARM \* VISIT + AGE + (1 | USUBJID), data = .)), # Fit the model once  
 test\_results = map(model, tidy), # Extract tidy results  
 tables = map(model, ~ tbl\_regression(., exponentiate = FALSE) # Generate regression table  
 )  
 )

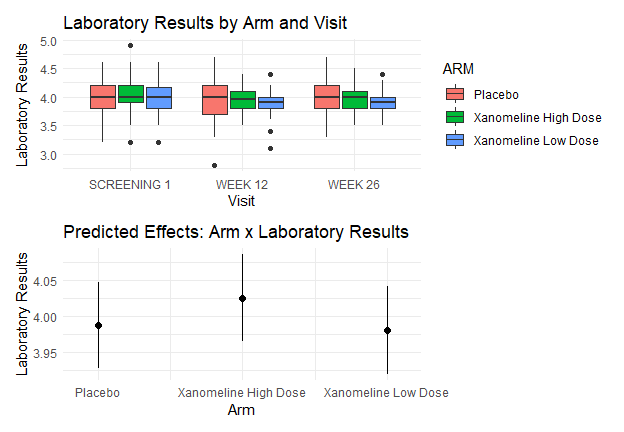
## Warning: There were 2 warnings in `mutate()`.  
## The first warning was:  
## ℹ In argument: `model = map(...)`.  
## ℹ In group 4: `LBTEST = "Anisocytes"`.  
## Caused by warning in `checkConv()`:  
## ! Model failed to converge with max|grad| = 13.7337 (tol = 0.002, component 1)  
## ℹ Run `dplyr::last\_dplyr\_warnings()` to see the 1 remaining warning.

# unnest the 'test\_results'  
test\_results <- data\_analysis %>%  
 select(LBTEST, test\_results) %>%  
 unnest(test\_results)  
test\_results

## # A tibble: 165 × 9  
## # Groups: LBTEST [5]  
## LBTEST effect group term estimate std.error statistic df p.value  
## <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl> <dbl> <dbl>  
## 1 Albumin fixed <NA> (Intercept) 4.56 0.136 33.6 260. 1.59e-96  
## 2 Albumin fixed <NA> ARMXanomeli… 0.0385 0.0434 0.889 553. 3.74e- 1  
## 3 Albumin fixed <NA> ARMXanomeli… -0.00623 0.0435 -0.143 559. 8.86e- 1  
## 4 Albumin fixed <NA> VISITWEEK 2 -0.0973 0.0282 -3.45 1503. 5.80e- 4  
## 5 Albumin fixed <NA> VISITWEEK 4 -0.105 0.0286 -3.66 1505. 2.65e- 4  
## 6 Albumin fixed <NA> VISITWEEK 6 -0.0991 0.0294 -3.37 1511. 7.71e- 4  
## 7 Albumin fixed <NA> VISITWEEK 8 -0.0382 0.0296 -1.29 1513. 1.97e- 1  
## 8 Albumin fixed <NA> VISITWEEK 12 -0.0641 0.0302 -2.12 1514. 3.42e- 2  
## 9 Albumin fixed <NA> VISITWEEK 16 0.0309 0.0301 1.03 1514. 3.05e- 1  
## 10 Albumin fixed <NA> VISITWEEK 20 -0.0487 0.0305 -1.60 1515. 1.11e- 1  
## # ℹ 155 more rows

1. Laboratory results by ARM and VISIT and predicted effects of ARM

plot1 <- data\_clean %>%  
 filter(VISIT %in% c("SCREENING 1", "WEEK 12", "WEEK 26")) %>%   
 ggplot(aes(x = VISIT, y = LBORRES, fill = ARM)) +  
 geom\_boxplot() +  
 labs(  
 title = "Laboratory Results by Arm and Visit",  
 x = "Visit",  
 y = "Laboratory Results"  
 ) +  
 theme\_minimal() +  
 coord\_cartesian()  
  
interaction\_effects <- ggeffects::ggpredict(lmm\_model, terms = c("ARM"))  
  
plot2 <- interaction\_effects %>%  
 plot() +  
 labs(  
 title = "Predicted Effects: Arm x Laboratory Results",  
 x = "Arm",  
 y = "Laboratory Results"  
 ) +  
 theme\_minimal()  
  
combined\_plot <- plot1 + plot2 + plot\_layout(ncol = 1)  
combined\_plot



Combined plot of laboratory results by arm and visit and predicted effects of arm on laboratory results.

1. Measure system response time for queries:

data\_perf <- data %>%  
 select(USUBJID, ARM, VISIT, AGE, LBORRES, LBTEST) %>%  
 filter(VISIT %in% ordered\_visits) %>%  
 mutate(  
 LBORRES = as.numeric(LBORRES),  
 VISIT = factor(VISIT, levels = unique(c(ordered\_visits, VISIT))),  
 ARM = factor(ARM, levels = unique(ARM))  
 ) %>%  
 filter(!is.na(LBORRES))  
  
tests <- unique(data\_perf$LBTEST)[1:30]  
  
start\_time <- Sys.time()  
  
data\_perf\_filtered <- data\_perf %>% filter(LBTEST %in% tests)  
  
# Analysis with nesting and map function (replacement for for loop)  
data\_analysis <- data\_perf\_filtered %>%  
 group\_by(LBTEST) %>%  
 nest() %>%  
 mutate(test\_results = map(.x=data, ~ lmer(LBORRES ~ ARM \* VISIT + AGE + (1 | USUBJID),  
 data = .) %>% tidy()  
 )  
 ) %>%  
 unnest(test\_results) %>%  
 select(-data)  
  
  
for (i in tests) {  
 lmer(LBORRES ~ ARM \* VISIT + AGE + (1 | USUBJID),  
 data = data\_perf %>% filter(LBTEST == i)) %>% na.omit()  
 #print(i)  
 }  
end\_time <- Sys.time()  
response\_time <- end\_time - start\_time  
print(paste("Total Time:", response\_time))

## [1] "Total Time: 6.88285207748413"