P-Value Adjustment

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## Purpose

To adjust the raw p-values from the PCR results.

## Data

Human and mouse PCR p-values.

knitr::opts\_chunk$set(warning = FALSE, message = FALSE)

library(dplyr)  
source(here::here("scripts", "functions.R"))

pvalues = readxl::read\_excel(here::here("data", "inputs", "Liver-Kinome\_RTPCR-mRNA and p-values\_11-7-21.xlsx"))  
  
human\_cols = c(2, 3)  
mouse\_cols = c(6, 7)

get\_and\_adjust = function(full\_data, use\_cols){  
 #full\_data = pvalues  
 #use\_cols = human\_cols  
 org\_data = as.data.frame(full\_data[3:nrow(full\_data), use\_cols])  
 names(org\_data) = c("Gene Name", "p-value")  
 org\_data = org\_data %>%  
 dplyr::filter(!is.na(`Gene Name`)) %>%  
 unique()  
 numeric\_data = org\_data %>%  
 dplyr::mutate(`p-value` = dplyr::case\_when(  
 grepl("<0.0001", `p-value`) ~ as.numeric("0.0001"),  
 TRUE ~ as.numeric(`p-value`)  
 )) %>%  
 dplyr::mutate(`adjusted-p-value` = stats::p.adjust(`p-value`, method = "BH")) %>%  
 dplyr::mutate(`adjusted-p-value` = format(`adjusted-p-value`, nsmall = 4, digits = 1))  
 numeric\_data  
}  
  
human\_adjusted = get\_and\_adjust(pvalues, human\_cols)  
mouse\_adjusted = get\_and\_adjust(pvalues, mouse\_cols)

And now put the adjusted p-values back into the table.

pvalues\_human = pvalues[, c(1, 2, 3)]  
pvalues\_mouse = pvalues[, c(5, 6, 7)]  
add\_adjusted = function(org\_data, adjusted\_data, new\_name = NULL){  
 #org\_data = pvalues\_human  
 #adjusted\_data = human\_adjusted  
   
 new\_data = org\_data  
 new\_data[[new\_name]] = character(nrow(new\_data))  
 gene\_loc = which(grepl("Gene Name", new\_data[1, ]))  
 for (irow in seq\_len(nrow(adjusted\_data))) {  
 match\_loc = grepl(adjusted\_data$`Gene Name`[irow], new\_data[[gene\_loc]])  
 new\_data[[4]][match\_loc] = adjusted\_data$`adjusted-p-value`[irow]  
 }  
 new\_data[[4]][1] = "adjusted-p-value"  
 new\_data  
}  
  
adjusted\_data\_human = add\_adjusted(pvalues\_human, human\_adjusted, "...4")  
adjusted\_data\_mouse = add\_adjusted(pvalues\_mouse, mouse\_adjusted, "...8")  
  
all\_adjusted = cbind(adjusted\_data\_human, data.frame(...5 = character(nrow(pvalues))), adjusted\_data\_mouse)

openxlsx::write.xlsx(all\_adjusted, file = here::here("data", "outputs", "tables", "Liver-Kinome\_RTPCR-mRNA and p-values\_11-7-21\_adjusted.xlsx"), overwrite = TRUE)

## Methods

Raw PCR p-values were adjusted for each organism separately, using the Benjamini-Hochberg method (Benjamini and Hochberg 1995) in R (R Core Team 2021).

Benjamini, Yoav, and Yosef Hochberg. 1995. “Controlling the False Discovery Rate: A Practical and Powerful Approach to Multiple Testing.” *Journal of the Royal Statistical Society. Series B (Methodological)* 57 (1): 289–300. <https://www.jstor.org/stable/2346101>.

R Core Team. 2021. *R: A Language and Environment for Statistical Computing* (version 4.1.0). Vienna, Austria. <https://www.R-project.org/>.