Chick Embryo Data Exploration

ABB

2025-01-31

## Identifying inclduded studies

Looking at which studies have discrepant screening decisions.

# Identify studyIDs with discrepancies  
discrepant\_studyIDs <- Annotation\_data\_2025\_01\_30\_Wide\_format %>%  
 group\_by(StudyId) %>%  
 summarize(unique\_values = n\_distinct(`Exclusion of article?\_fabf514a-b197-40d4-ae77-b9f24f3981f0\_Answer`)) %>%  
 filter(unique\_values > 1) %>%  
 pull(StudyId)  
  
# Filter and display the rows with discrepancies  
discrepant\_rows <- Annotation\_data\_2025\_01\_30\_Wide\_format %>% filter(StudyId %in% discrepant\_studyIDs)  
  
# number of unique IDs with discrepant inclusion decisions  
length(unique(discrepant\_rows$StudyId))

## [1] 176

#176

## Majority Screening decision

Then determining what the majority decision is where there are discrrepancies an how many studies have a majority decision for include.

# Determine the majority response when there are three or more occurrences  
df\_majority <- Annotation\_data\_2025\_01\_30\_Wide\_format %>%  
 group\_by(StudyId, `Exclusion of article?\_fabf514a-b197-40d4-ae77-b9f24f3981f0\_Answer`) %>%  
 summarize(count = n(), .groups = "drop") %>%  
 group\_by(StudyId) %>%  
 filter(count == max(count)) %>%  
 ungroup()  
  
summary(df\_majority$`Exclusion of article?\_fabf514a-b197-40d4-ae77-b9f24f3981f0\_Answer`)

## Length Class Mode   
## 1758 character character

df\_majority\_incl <- df\_majority %>% filter(`Exclusion of article?\_fabf514a-b197-40d4-ae77-b9f24f3981f0\_Answer` == "no")  
  
length(unique(df\_majority\_incl$StudyId))

## [1] 1021

# Code to generate data set of included studies (all decisions)  
# Filter the entire dataframe to retain majority responses and previous information  
df\_incl\_filtered <- Annotation\_data\_2025\_01\_30\_Wide\_format %>%  
 left\_join(df\_majority\_incl, by = c("StudyId", "Exclusion of article?\_fabf514a-b197-40d4-ae77-b9f24f3981f0\_Answer")) %>%  
 filter(!is.na(count) | StudyId %in% discrepant\_studyIDs) %>%  
 select(-count) # Remove count column if not needed

## Experimental Data

You can also embed plots, for example:

# Identify discrepancies in answers for each StudyId and Question  
discrepant\_questions <- Annotation\_data\_Experimentlevel %>%  
 group\_by(StudyId, Question, QuestionId) %>%  
 summarize(unique\_answers = n\_distinct(Answer), .groups = "drop") %>%  
 filter(unique\_answers > 1)  
  
# Count discrepancies for each question  
discrepant\_question\_counts <- discrepant\_questions %>%  
 count(Question, sort = TRUE)  
  
  
# Print all rows  
print(discrepant\_question\_counts, n = nrow(discrepant\_question\_counts))

## # A tibble: 23 × 2  
## Question n  
## <chr> <int>  
## 1 Type of intervention 1410  
## 2 Reporting quality: incubation conditions 706  
## 3 Experiment label? 668  
## 4 Killing of the embryos 640  
## 5 Adverse effects 614  
## 6 Anatomical structure used for intervention 576  
## 7 Age of chicken embryos at end of study or when being killed 547  
## 8 Control group 465  
## 9 Age of chicken embryos at beginning of the manipulation 443  
## 10 Randomization 411  
## 11 Reporting quality: dosage of injected substance / agent / cells or oth… 357  
## 12 Killing of the embryo 352  
## 13 Reporting quality: number of chicken embryos / embryonated chicken eggs 346  
## 14 Blinding 310  
## 15 Reporting quality: drop-outs 281  
## 16 Reporting quality: origin of the eggs / chicken embryos 163  
## 17 Reporting quality: chicken line, hybrid or breed 101  
## 18 Reporting quality: hygienic status (e.g., SPF) 87  
## 19 Reporting quality: sex 40  
## 20 Reporting quality: genetic status (e.g., genetically altered) 26  
## 21 Reporting quality: reasons for drop-outs 10  
## 22 Anesthesia and / or analgesia that has / have been used 9  
## 23 Reporting of anesthesia or analgesia 9