

# Quantitative Analysis

2025-04-13

## Forest plot comparing consent models

```
library(meta)
library(metafor)

# Study data
study <- c(
  "Ah Ra Lee et al. (2024)",
  "Antje Fischer-Rosinsky et al. (2025)",
  "Hans et al. (2024)",
  "Ewing et al. (2015)",
  "Thiel et al. (2014)",
  "Xiong et al. (2024)"
)

# Events = number of people who consented
events <- c(
  30,      # Ah Ra Lee: 100% of 30
  313,     # Antje: 313 consented
  68,      # Hans: 68 consented
  1161,    # Ewing Broad
  137,     # Thiel: 137 completed consent process
  59       # Xiong: 59 agreed to receive platform
)

# Total participants
n <- c(30, 1138, 151, 1528, 187, 99)

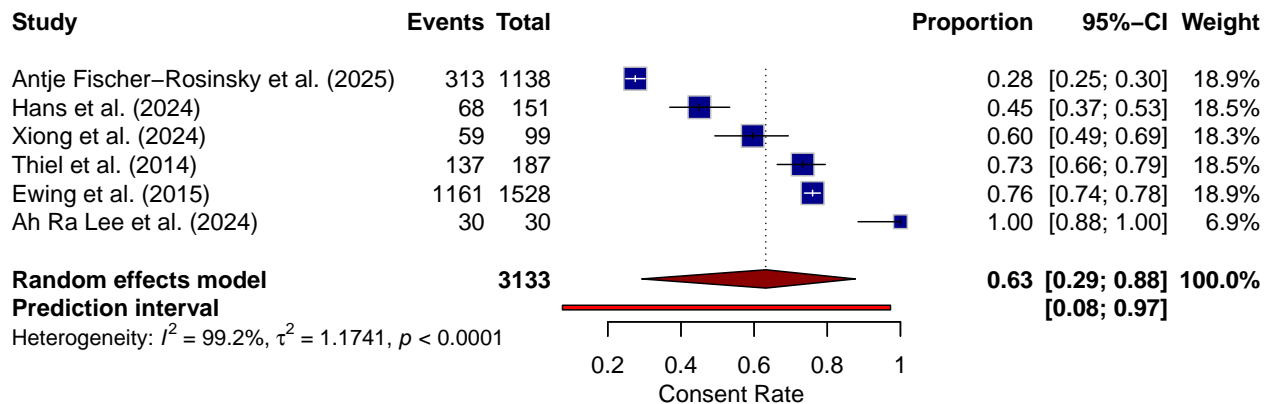
# Create meta-analysis object
meta_obj <- metaprop(
  event = events,
  n = n,
  studlab = study,
  sm = "PLOGIT",      # Logit transformation for proportions
  method = "Inverse", # Inverse variance method
  comb.fixed = FALSE,
  comb.random = TRUE,
  haki = TRUE,        # Hartung-Knapp adjustment
  prediction = TRUE,
  title = "Consent Rates by Study"
)

# Forest plot
forest()
```

```

meta_obj,
sortvar = events / n,
xlab = "Consent Rate",
leftcols = c("studlab", "event", "n"),
leftlabs = c("Study", "Events", "Total"),
print.tau2 = TRUE,
print.I2 = TRUE,
colgap.studlab = "2mm",
col.square = "darkblue",
col.diamond = "darkred",
col.diamond.lines = "black",
backtransf = TRUE
)

```



```

library(meta)
library(metafor)

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  "Ah Ra Lee et al. (2024)",
  "Antje Fischer-Rosinsky et al. (2025)",
  "Hans et al. (2024)",
  "Ewing et al. (2015)",
  "Thiel et al. (2014)",
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)

# Total participants
n <- c( 30, 1138, 151, 1528, 187, 99)

# Define study type (dynamic consent or broad consent)

```

```
study_type <- c("Dynamic", "Broad", "Broad", "Broad", "Dynamic", "Dynamic")
```

```
# Create meta-analysis object
```

```
meta_obj <- metaprop(
  event = events,
  n = n,
  studlab = study,
  sm = "PLOGIT",          # Logit transformation for proportions
  method = "Inverse",    # Inverse variance method
  comb.fixed = FALSE,
  comb.random = TRUE,
  hakn = TRUE,           # Hartung-Knapp adjustment
  prediction = TRUE,
  title = "Consent Rates by Study"
)
```

```
# Define colors for dynamic and broad consent
```

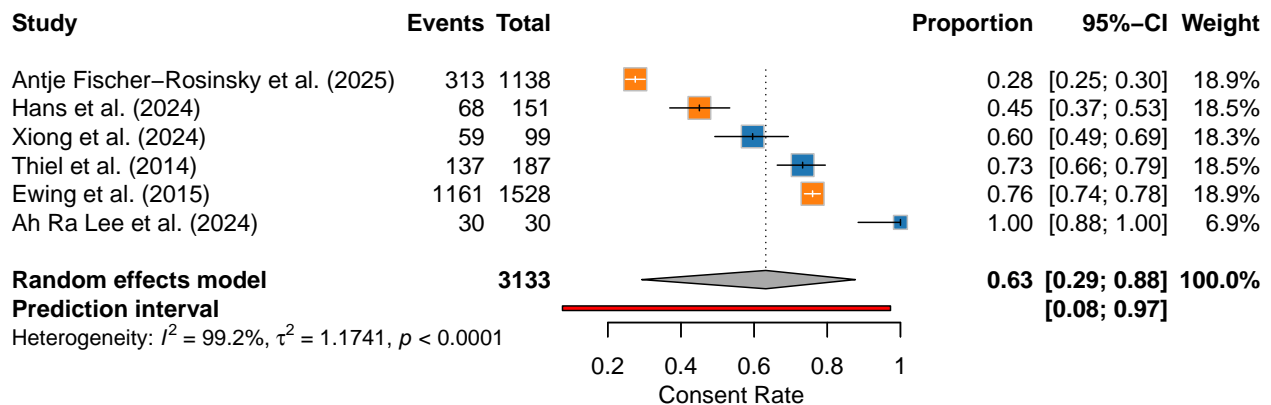
```
study_colors <- ifelse(study_type == "Dynamic", "#1f77b4", "#ff7f0e")
```

```
# Create the plot by explicitly calling plot.new()
```

```
#plot.new() # Initialize a new plot
```

```
# Plot the forest plot
```

```
forest(
  meta_obj,
  sortvar = events / n,
  xlab = "Consent Rate",
  leftcols = c("studlab", "event", "n"),
  leftlabs = c("Study", "Events", "Total"),
  print.tau2 = TRUE,
  print.I2 = TRUE,
  colgap.studlab = "2mm",
  col.square = study_colors, # Color for each square
  col.diamond = "darkgray", # Common color for the diamond
  col.diamond.lines = "black",
  backtransf = TRUE
)
```



```
# Add the legend manually
```

```
#legend("topright", legend = c("Dynamic Consent", "Broad Consent"),
#      fill = c("#1f77b4", "#ff7f0e"), cex = 1.2, horiz = TRUE)
```

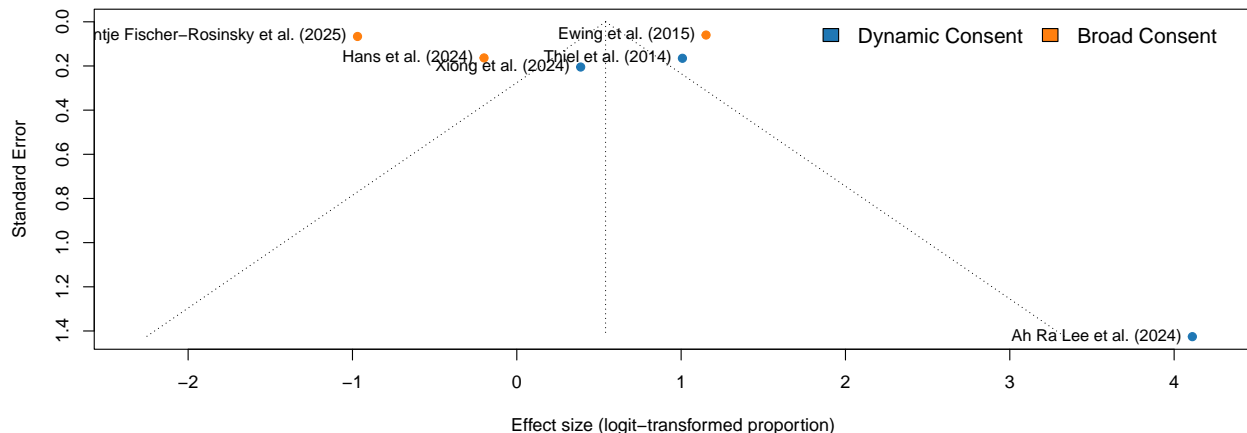
## Interpretation of the Forest Plot

The forest plot presents the pooled consent rates across six studies investigating either dynamic or broad consent models. Each study is represented by a square indicating the point estimate of the consent rate, with the horizontal line denoting the 95% confidence interval (CI). Notably, Ah Ra Lee et al. (2024) reported a perfect consent rate of 1.00, which skews high relative to other studies. In contrast, Antje Fischer-Rosinsky et al. (2025) showed the lowest consent rate at 0.28. The random-effects meta-analysis yielded a pooled consent rate of 0.63 (95% CI: 0.29–0.88), with a prediction interval of 0.08–0.97, suggesting wide variability in expected future results. The heterogeneity is considerable ( $I^2 = 99.2\%$ ,  $p < 0.0001$ ), indicating substantial differences among study populations, methodologies, or consent model implementations. The weighting of studies is roughly equal (~18%), except for Ah Ra Lee et al., whose smaller sample size reduced its weight (6.9%). These findings suggest that while dynamic consent models often yield higher consent rates, their effectiveness is highly context-dependent. Therefore, tailoring the model to participant demographics, technology familiarity, and healthcare setting may be critical for optimizing engagement and ethical research participation.

## Funnel Plot (Publication Bias)

```
# Funnel plot with colors
funnel(
  meta_obj,
  xlab = "Effect size (logit-transformed proportion)",
  ylab = "Standard Error",
  col = study_colors,
  pch = 19,
  studlab = TRUE,
  cex.studlab = 0.9
)

# Add horizontal legend at top right
legend("topright",
  legend = c("Dynamic Consent", "Broad Consent"),
  fill = c("#1f77b4", "#ff7f0e"),
  horiz = TRUE,
  cex = 1.2,
  bty = "n")
```



### Interpretation of the Funnel Plot

The funnel plot is used to assess potential publication bias in the included studies evaluating consent rates. In an unbiased scenario, studies with smaller standard errors (i.e., larger sample sizes) cluster near the average effect size at the top, and smaller studies with more variance should scatter symmetrically around the mean at the bottom. However, this plot reveals asymmetry, with most studies leaning toward the left and only one extreme outlier (Ah Ra Lee et al., 2024) on the right. This study, reporting a 100% consent rate, exhibits a high effect size and standard error, making it an outlier that potentially inflates the pooled estimate. The left-skewed distribution may suggest the absence of smaller studies with low consent rates, implying possible publication bias where studies with less favorable or non-significant outcomes are underreported. Moreover, the concentration of studies on one side of the plot could also reflect true heterogeneity rather than selective publication alone. Overall, while the presence of publication bias cannot be conclusively established without further statistical tests (e.g., Egger's test), the funnel plot highlights the importance of including and publishing studies across the full spectrum of consent outcomes to achieve balanced evidence synthesis.