```{r, fig-deli}

#| label: fig-results

#| fig.cap: "Results for L. delicata. A) Predicted probability of choosing the correct feeder first over trials. The lines represent the mean predicted probability of choosing the correct feeder first, and the shaded areas represent the standard deviation of the mean; both obtained by using the slope and intercept estimates from the posterior distributions. The different colours represent the different treatments. B) Distribution of the estimates of the slopes per each treatment. The x-axis represents the estimates of the slopes, and the y-axis represents the density of the estimates. The different colours represent the different treatments."

source(here("R", "func.R"))

# First step, create the dfs for the first plot

## 1) L. delicata

df\_deli <- df\_fig(as.data.frame(deli), "L. delicata") %>%

mutate(Trial = gsub("X", "", Trial)) %>%

mutate(Trial = as.numeric(Trial)) %>%

group\_by(Trial, Treatment, Species) %>%

summarize(

Mean\_Predicted\_prob = mean(Value),

SE\_Predicted\_prob = sd(Value)

) %>%

ungroup() %>%

mutate(

Treatment = factor(Treatment,

levels = c("CORT-Cold", "Control-Cold", "CORT-Hot", "Control-Hot")),

) %>%

data.frame()

write.csv(df\_deli, file= "./output/Checking/df\_deli.csv")

## 2) L. guichenoti

df\_guich <- df\_fig(as.data.frame(guich), "L. guichenoti")

#

# Second step, merge the df into a big Fig\_df

Fig\_df <- rbind(df\_deli, df\_guich) %>%

mutate(Trial = gsub("X", "", Trial)) %>%

mutate(Trial = as.numeric(Trial)) %>%

group\_by(Trial, Treatment, Species) %>%

summarize(

Mean\_Predicted\_prob = mean(Value),

SE\_Predicted\_prob = sd(Value)

) %>%

ungroup() %>%

mutate(

Treatment = factor(Treatment,

levels = c("CORT-Cold", "Control-Cold", "CORT-Hot", "Control-Hot")),

) %>%

data.frame()

write.csv(Fig\_df, file= "./output/Checking/Fig\_df.csv")

# Make the plot

figure\_results <- plotting(Fig\_df)

ggsave("./output/figures/figure\_results.png", plot=figure\_results, width = 18, height = 20, units = "cm", dpi = 3000)

knitr::include\_graphics("./output/figures/figure\_results.png")

```

####################

####################

# Function to create the prob\_plot

#' @title plotting

#' @param df to select the df

plotting <- function(df){

plot <- ggplot(df, aes(x = Trial, y = Mean\_Predicted\_prob, color = Treatment)) +

geom\_line(linewidth = 1) +

scale\_color\_manual(values = c("CORT-Cold"="darkblue", "Control-Cold"="cyan", "CORT-Hot"="black", "Control-Hot"="#616161")) +

geom\_ribbon(aes(ymin = Mean\_Predicted\_prob - SE\_Predicted\_prob, ymax = Mean\_Predicted\_prob + SE\_Predicted\_prob, fill = Treatment), color = NA, alpha = 0.075) +

scale\_fill\_manual(values = c("CORT-Cold"="darkblue", "Control-Cold"="cyan", "CORT-Hot"="black", "Control-Hot"="#616161")) +

theme\_classic() +

facet\_wrap(Species ~ ., scale = "free\_x", ncol= 1, strip.position = "right") +

theme(strip.placement = "outside") +

theme(strip.background = element\_blank()) +

labs(y = "Predicted probability of correct choice", x = "Trial") +

theme(plot.margin = margin(5.5, 5.5, 5.5, 5.5, "mm")) +

theme(

axis.title = element\_text(size = 15, family = "Times"),

axis.text = element\_text(size = 10, family = "Times"),

legend.title = element\_text(size = 12, family = "Times"),

legend.text = element\_text(size = 10, family = "Times"),

strip.text = element\_text(size = 14, family = "Times", face = "italic")

)

return(plot)

}

ALT RESULTS

There were not significant differences between treatments in *\_L. delicata\_* (Control-Cold - CORT-Cold = `r format\_dec(mean(deli\_ControlCold - deli\_CORTCold), 3)`, p- value = `r format\_dec(pmcmc(deli\_ControlCold - deli\_CORTCold), 3)`; Control-Hot - CORT-Hot = `r format\_dec(mean(deli\_ControlHot - deli\_CORTHot), 3)`, p- value = `r format\_dec(pmcmc(deli\_ControlHot - deli\_CORTHot), 3)`; Control-Hot - Control-Cold = `r format\_dec(mean(deli\_ControlHot - deli\_ControlCold), 3)`, p-value = `r format\_p(pmcmc(deli\_ControlHot - deli\_ControlCold), 3)`; CORT-Hot - CORT-Cold = `r format\_dec(mean(deli\_CORTHot - deli\_CORTCold), 3)`, p-value = `r format\_p(pmcmc(deli\_CORTHot - deli\_CORTCold), 3)`) (see @fig-results) or *\_L. guichenoti\_* (Control-Cold - CORT-Cold = `r format\_dec(mean(guich\_ControlCold - guich\_CORTCold), 3)`, p- value = `r format\_dec(pmcmc(guich\_ControlCold - guich\_CORTCold), 3)`; Control-Hot - CORT-Hot = `r format\_dec(mean(guich\_ControlHot - guich\_CORTHot), 3)`, p- value = `r format\_dec(pmcmc(guich\_ControlHot - guich\_CORTHot), 3)`; Control-Hot - Control-Cold = `r format\_dec(mean(guich\_ControlHot - guich\_ControlCold), 3)`, p-value = `r format\_p(pmcmc(guich\_ControlHot - guich\_ControlCold), 3)`; CORT-Hot - CORT-Cold = `r format\_dec(mean(guich\_CORTHot - guich\_CORTCold), 3)`, p-value = `r format\_p(pmcmc(guich\_CORTHot - guich\_CORTCold), 3)`) (see @fig-results).

We compared each factor (hormone and incubation temperature) separately by pooling together the observations for all the individuals from the same hormone treatment or the same incubation temperature. In this regard, we did not find any significant effect of the hormone treatment (*\_L. delicata\_*: Control learning slope - CORT learning slope = `r format\_dec(mean((deli\_ControlCold + deli\_ControlHot) - (deli\_CORTCold + deli\_CORTHot)), 3)`, p-value = `r format\_p(pmcmc((deli\_ControlCold + deli\_ControlHot) - (deli\_CORTCold + deli\_CORTHot)), 3)`; *\_L. guichenoti\_*: Control learning slope - CORT learning slope = `r format\_dec(mean((guich\_ControlCold + guich\_ControlHot)-(guich\_CORTCold + guich\_CORTHot)), 3)`, p-value = `r format\_p(pmcmc((guich\_ControlCold + guich\_ControlHot)-(guich\_CORTCold + guich\_CORTHot)), 3)`) or the incubation temperature (*\_L. delicata\_*: Hot learning slope - Cold learning slope = `r format\_dec(mean((deli\_CORTHot + deli\_ControlHot) - (deli\_CORTCold + deli\_ControlCold)),3)`, p-value = `r format\_p(pmcmc((deli\_CORTHot + deli\_ControlHot) - (deli\_CORTCold + deli\_ControlCold)),3)`; *\_L. guichenoti\_*: Hot learning slope - Cold learning slope = `r format\_dec(mean((guich\_CORTHot + guich\_ControlHot) - (guich\_CORTCold + guich\_ControlCold)),3)`, p-value = `r format\_p(pmcmc((guich\_CORTHot + guich\_ControlHot) -(guich\_CORTCold + guich\_ControlCold)),3)`) in either species.

Finally, when all individuals from all the treatments were pooled together and species were compared, there were not significant differences in the estimated slopes (*\_L. delicata\_* - *\_L. guichenoti\_* = `r format\_dec(mean((deli\_CORTCold + deli\_ControlCold + deli\_CORTHot + deli\_ControlHot) - (guich\_CORTCold + guich\_ControlCold + guich\_CORTHot + guich\_ControlHot)), 3)`, p-value = `r format\_p(pmcmc((deli\_CORTCold + deli\_ControlCold + deli\_CORTHot + deli\_ControlHot) - (guich\_CORTCold + guich\_ControlCold + guich\_CORTHot + guich\_ControlHot)), 3)`).