caf_diet

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Load libraries

```
pacman::p_load(
  ggplot2,
  tidyverse,
  googlesheets4,
  ggpubr,
  ggrepel
)
```

Load data

```
# 2h daily exposure to cafeteria diet
caf_diet_intake_raw <- read_sheet("https://docs.google.com/spreadsheets/d/1yN0byHvCX7_lhpqhMryK8NE82710</pre>
## ! Using an auto-discovered, cached token.
##
     To suppress this message, modify your code or options to clearly consent to
     the use of a cached token.
##
##
     See gargle's "Non-interactive auth" vignette for more details:
##
     <https://gargle.r-lib.org/articles/non-interactive-auth.html>
## i The googlesheets4 package is using a cached token for 'l.luarte@uc.cl'.
## v Reading from "ingesta_caf".
## v Range 'ingesta_caf'.
# 22 hour chow (standard diet) intake
chow_diet_intake_raw <- read_sheet("https://docs.google.com/spreadsheets/d/1LhdjUG9xIxbZ3kmRWPWzSAUHyMc</pre>
## v Reading from "ingesta_chow_22hr".
## v Range 'Hoja 1'.
# cafeteria diet macronutrient information
macronutrients_info <- read_sheet("https://docs.google.com/spreadsheets/u/1/d/1a7jy9vIBOiPlJYsKFF4vUyEt</pre>
## v Reading from "macronutrientes".
## v Range 'macronutrientes'.
```

Data preproc

```
# daily cafeteria dieta intake
caf_diet_intake <- caf_diet_intake_raw %>%
  # fix hour in and hour out format
 mutate(
   hour_in = hms::as_hms(hour_in),
   hour out = hms::as hms(hour out),
   # corrected intake
   # criollitas
   criollitas_intake = criollitas_in_gr - (criollitas_out_gr + criollitas_sp_gr),
    # trencito
   trencito_intake = trencito_in_gr - (trencito_out_gr + trencito_sp_gr),
   cheetos_intake = cheetos_in_gr - (cheetos_out_gr + cheetos_sp_gr),
   # papas
   papas_intake = papas_in_gr - (papas_out_gr + papas_sp_gr),
    # chow
    chow_intake = chow_in_gr - (chow_out_gr + chow_sp_gr)
  ) %>%
  pivot_longer(
   cols = contains("intake"),
   names_to = "food_name",
   values_to = "corrected_intake_gr"
  ) %>%
 mutate(
   food_name = str_extract(food_name, "[^_]*")
  )
# isolate caja control to obtain percentage increase/decrease of food
# without a mice
caja_control <- caf_diet_intake_raw %>%
 filter(
    exp_tag == "caja_control"
  ) %>%
  mutate(
    # fix hour format
   hour_in = hms::as_hms(hour_in),
   hour_out = hms::as_hms(hour_out),
    # criollitas
   criollitas_percent_diff = ((criollitas_out_gr + criollitas_sp_gr) - criollitas_in_gr) /
     criollitas in gr,
    # cheetos
   cheetos_percent_diff = ((cheetos_out_gr + cheetos_sp_gr) - cheetos_in_gr) /
     cheetos_in_gr,
    # trencito
   trencito_percent_diff = ((trencito_out_gr + trencito_sp_gr) - trencito_in_gr) /
     trencito_in_gr,
    # papas
   papas_percent_diff = ((papas_out_gr + papas_sp_gr) - papas_in_gr) /
     papas_in_gr,
   chow_percent_diff = ((chow_out_gr + chow_sp_gr) - chow_in_gr) /
     chow_in_gr
```

```
) %>%
  select(ID:hour_out, criollitas_percent_diff:chow_percent_diff) %>%
  pivot_longer(
   cols = contains("percent_diff"),
   names_to = "food_name",
   values_to = "control_percent_diff"
 ) %>%
 mutate(
   food_name = str_extract(food_name, "[^_]*")
# add back caja control percent difference per food into caf_diet_intake
caf_diet_intake_cr <- caf_diet_intake %>%
 left_join(
    caja_control %>% select(
     date,
     food_name,
     control_percent_diff
   ),
   bv = c(
     "date",
     "food_name"
   )
  ) %>%
  group by(
   date,
   food name,
   ID
  ) %>%
  summarise(
    # corrected intake by spillage AND control cage
    # criollitas
   criollitas_intake_cr = (criollitas_in_gr + (criollitas_in_gr * control_percent_diff))
   - (criollitas_out_gr + criollitas_sp_gr),
   # trencito
   trencito_intake_cr = (trencito_in_gr + (trencito_in_gr * control_percent_diff))
   - (trencito_out_gr + trencito_sp_gr),
   papas_intake_cr = (papas_in_gr + (papas_in_gr * control_percent_diff))
    - (papas_out_gr + papas_sp_gr),
   # cheetos
   cheetos_intake_cr = (cheetos_in_gr + (cheetos_in_gr * control_percent_diff))
   - (cheetos_out_gr + cheetos_sp_gr),
    # chow
   chow_intake_cr = (chow_in_gr + (chow_in_gr * control_percent_diff))
    - (chow_out_gr + chow_sp_gr)
  ) %>%
   pivot_longer(
   cols = contains("intake_cr"),
   names_to = "food_name_cr",
   values_to = "corrected_intake_gr_cr"
  ) %>%
  mutate(
```

```
food_name = str_extract(food_name_cr, "[^_]*"),
    # if its less than 0.01 this cannot be measured by the scale
    corrected intake_gr_cr = if_else(corrected_intake_gr_cr < 0.01, 0, corrected_intake_gr_cr)</pre>
## `summarise()` has grouped output by 'date', 'food_name'. You can override using
## the `.groups` argument.
# macronutrient information
macronutrients info long <- macronutrients info %>%
 pivot_longer(
   cols = !macronutriente,
   names_to = "food_name",
   values to = "kcal per gr"
  )
# 22 hour chow intake
chow_diet_intake <- chow_diet_intake_raw %>%
  mutate(
   corrected intake gr = chow_22_in_gr - (chow_22_out_gr + chow_22_sp_gr),
   hour_in = hms::as_hms(hour_in),
   hour_out = hms::as_hms(hour_out)
 mutate(food_name = "chow", time = "22_hr")
# TODO correct by percent difference
chow 22 control <- chow diet intake raw %>%
  filter(
    exp_tag == "caja_control"
  ) %>%
 mutate(
   hour_in = hms::as_hms(hour_in),
   hour out = hms::as hms(hour out),
    # percent diff in control chow
   chow_22_percent_diff = ((chow_22_out_gr + chow_22_sp_gr) - chow_22_in_gr) /
      chow_22_in_gr,
  ) %>%
  select(ID:hour_out, chow_22_percent_diff) %>%
  pivot_longer(
   cols = contains("percent_diff"),
   names_to = "food_name",
   values_to = "control_percent_diff"
 ) %>%
  mutate(
   food_name = str_extract(food_name, "[^_]*")
chow_diet_intake_cr <- chow_diet_intake %>%
  left join(
    chow_22_control %>% select(
      date,
      food_name,
      control_percent_diff
   ),
```

```
by = c(
    "date",
    "food_name"
  )
) %>%
group_by(
  date,
  food name,
  ID
) %>%
summarise(
  # corrected intake by spillage AND control cage
  chow_22_intake_cr = (chow_22_in_gr + (chow_22_in_gr * control_percent_diff))
  - (chow_22_out_gr + chow_22_sp_gr)
) %>%
  pivot_longer(
  cols = contains("intake_cr"),
  names_to = "food_name_cr",
 values_to = "corrected_intake_gr_cr"
) %>%
mutate(
  food_name = str_extract(food_name_cr, "[^_]*"),
  # if its less than 0.01 this cannot be measured by the scale
  corrected_intake_gr_cr = if_else(corrected_intake_gr_cr < 0.01, 0, corrected_intake_gr_cr)</pre>
)
```

`summarise()` has grouped output by 'date', 'food_name'. You can override using
the `.groups` argument.

merge tables

```
# this adds macro nutrients to each corrected food intake
caf_diet_intake_macros <- caf_diet_intake_cr %>%
 left_join(
   macronutrients_info_long,
   by = c("food_name")
 ) %>%
 mutate(time = "2_hr") %>%
# next we compute the real kcal eaten for each food
 mutate(
   kcal_intake = kcal_per_gr * corrected_intake_gr_cr
  )
chow_22_intake_macros <- chow_diet_intake_cr %>%
 left join(
   macronutrients_info_long,
   by = c("food_name")
 ) %>%
  mutate(
   kcal_intake = kcal_per_gr * corrected_intake_gr_cr
```

```
# we bind both data sets to add up normal chow intake to the caf diet
# chow intake
caf_diet_intake_macros <- bind_rows(caf_diet_intake_macros, chow_22_intake_macros)</pre>
```

summary tables

```
# add back session info
session <- caf diet intake raw %>%
  select(
   ID.
   date,
   session,
   exp_tag
caf_diet_intake_macros <- caf_diet_intake_macros %>%
  left_join(
    session,
   by = c("ID", "date")
 )
# this tables considers total chow intake
# normal chow + chow consumed during cafeteria diet
caf_chow_kcal <- caf_diet_intake_macros %>%
  group_by(
   ID,
   session,
   food name,
   macronutriente,
   exp_tag
  ) %>%
  summarise(
   kcal_intake = sum(kcal_intake)
## `summarise()` has grouped output by 'ID', 'session', 'food_name',
## 'macronutriente'. You can override using the `.groups` argument.
# normal + chow consumed during cafeteria diet vs caf diet in % of daily intake kcal
caf_chow_kcal_daily_ind <- caf_chow_kcal %>%
  group_by(
   ID,
   session,
   exp_tag,
   macronutriente
  ) %>%
  summarise(
   total_intake_sum_kcal = sum(kcal_intake)
  ) %>%
 right_join(
   caf chow kcal,
   by = c("ID", "session", "exp_tag", "macronutriente")
  ) %>%
 mutate(
   percent_of_daily_intake = (kcal_intake / total_intake_sum_kcal) * 100,
   type_of_food = if_else(food_name == "chow", "chow", "caf")
```

```
) %>%
  group_by(
   ID,
   session,
   macronutriente,
   exp_tag,
   type_of_food
  ) %>%
  summarise(
   percent_of_daily_intake_total = sum(percent_of_daily_intake)
  ) %>%
 ungroup()
## `summarise()` has grouped output by 'ID', 'session', 'exp_tag'. You can
## override using the `.groups` argument.`summarise()` has grouped output by 'ID',
## 'session', 'macronutriente', 'exp_tag'. You can override using the `.groups`
## argument.
# this is the same data but at a group level
caf_chow_kcal_daily_group <- caf_chow_kcal_daily_ind %>%
  filter(exp_tag != "caja_control", macronutriente == "total") %>%
  drop_na() %>%
 group_by(
   session,
   exp_tag,
   type of food
 ) %>%
  summarise(
   percent_of_daily_intake_total_group = mean(percent_of_daily_intake_total),
   err = sd(percent of daily intake total) / sqrt(n())
  ) %>%
 ungroup()
## `summarise()` has grouped output by 'session', 'exp_tag'. You can override using
## the `.groups` argument.
# intake by macro nutrient in kcal
# this considers only the 2hr intake
macro_intake_kcal_ind <- caf_diet_intake_macros %>%
 drop na() %>%
 filter(time == "2 hr") %>%
  group_by(
   ID,
   session,
   macronutriente,
   exp_tag
 ) %>%
  summarise(
   total_intake_kcal = sum(kcal_intake)
## `summarise()` has grouped output by 'ID', 'session', 'macronutriente'. You can
## override using the `.groups` argument.
macro_intake_kcal_group <- macro_intake_kcal_ind %>%
  # at this point we have the total intake per session
```

```
\# now we get the mean and std error
  ungroup() %>%
  group_by(
   session,
   macronutriente,
   exp_tag
 ) %>%
  summarise(
   mean_total_intake_kcal = mean(total_intake_kcal),
   err = sd(total_intake_kcal) / sqrt(n())
## `summarise()` has grouped output by 'session', 'macronutriente'. You can
## override using the `.groups` argument.
# intake in gr
# intake by macro nutrient in kcal
macro_intake_gr <- caf_diet_intake_macros %>%
  drop_na() %>%
  filter(time == "2_hr", macronutriente == "total") %>%
 group_by(
   ID,
   session,
   exp_tag,
   food_name
  ) %>%
  summarise(
   total_intake_gr = sum(corrected_intake_gr_cr)
  ) %>%
  # at this point we have the total intake per session
  # now we get the mean and std error
  ungroup() %>%
  group_by(
   session,
   exp_tag,
   food_name
 ) %>%
  summarise(
   mean_total_intake_gr = mean(total_intake_gr),
   err = sd(total_intake_gr) / sqrt(n())
 )
## `summarise()` has grouped output by 'ID', 'session', 'exp_tag'. You can override
## using the `.groups` argument.`summarise()` has grouped output by 'session',
## 'exp_tag'. You can override using the `.groups` argument.
```

Plots

2 hours kcal

x axis = experimental sessions y axis = kcal or grams

```
# macro intake in kcal
p1 <- macro_intake_kcal_ind %>%
  mutate(ID = as.factor(ID)) %>%
```

```
filter(
  macronutriente == "total",
  exp_tag != "caja_control"
ggplot(aes(
  session,
  total_intake_kcal,
 group = ID,
  color = exp_tag
geom_line(alpha = 0.2) +
geom_point(alpha = 0.2) +
geom label repel(aes(label = ID)) +
geom_line(
  data = macro_intake_kcal_group %>%
   filter(
      macronutriente == "total",
      exp_tag != "caja_control"
  inherit.aes = FALSE,
  aes(
    session,
   mean_total_intake_kcal,
   color = exp_tag
  )
) +
geom_point(
   data = macro_intake_kcal_group %>%
    filter(
      macronutriente == "total",
      exp_tag != "caja_control"
   ),
  inherit.aes = FALSE,
   session,
   mean_total_intake_kcal,
   color = exp_tag
  )
) +
geom_errorbar(
   data = macro_intake_kcal_group %>%
    filter(
      macronutriente == "total",
      exp_tag != "caja_control"
    ),
  inherit.aes = FALSE,
  aes(
    session,
   mean_total_intake_kcal,
    color = exp_tag,
   ymin = mean_total_intake_kcal - err,
   ymax = mean_total_intake_kcal + err
```

```
width = 0.01
) +
theme_pubr() +
labs(color = "Experimental condition") +
ylab("Mean intake (kcal)") +
xlab("Sessions") +
scale_x_continuous(breaks = seq(1, max(macro_intake_kcal_ind$session), 1))
```

2 hours gr per food type

```
# macro intake in gr
p2 <- macro_intake_gr %>%
 filter(
    exp_tag != "caja_control"
  ) %>%
  ggplot(aes(
   as.factor(session),
   group = food_name,
   mean_total_intake_gr,
   color = food_name,
   ymin = mean_total_intake_gr - err,
   ymax = mean_total_intake_gr + err
  )) +
  geom_point() +
  geom_line() +
  geom_errorbar(width = 0.1) +
  theme_pubr() +
  labs(color = "Experimental condition") +
  ylab("Mean intake (gr)") +
  xlab("Sessions") +
  facet_wrap(~exp_tag)
```

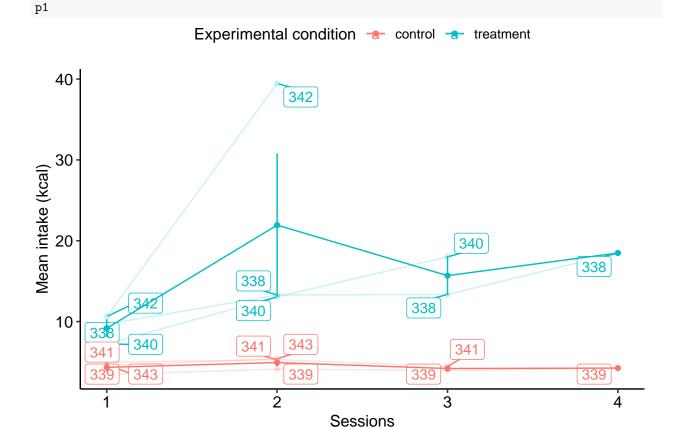
percent intake in 24 hours of cafeteria dieta vs chow

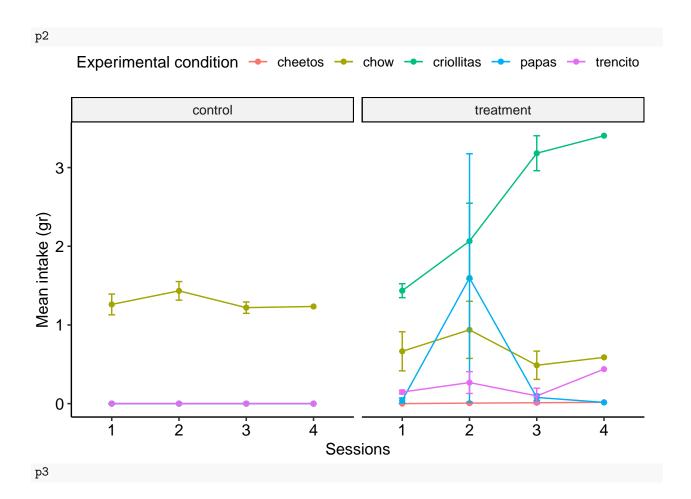
x axis = experimental sessions y axis = % of intake in kcal caf vs chow

```
p3 <- caf chow kcal daily group %>%
 filter(exp_tag != "caja_control") %>%
  ggplot(aes(
   session,
   percent_of_daily_intake_total_group,
    color = type_of_food
  geom_hline(yintercept = 50, color = "gray") +
  geom_point() +
  geom_line() +
  geom_errorbar(aes(
   ymin = percent_of_daily_intake_total_group - err,
   ymax = percent_of_daily_intake_total_group + err
   ), width = 0.01) +
   geom_point(
    inherit.aes = FALSE,
   data = caf_chow_kcal_daily_ind %>%
```

```
filter(macronutriente == "total", exp_tag != "caja_control"),
  aes(
    session,
    percent_of_daily_intake_total,
    color = type_of_food
  ), alpha = 0.3
) +
geom_label_repel(
  inherit.aes = FALSE,
  data = caf_chow_kcal_daily_ind %>%
    filter(macronutriente == "total", exp_tag != "caja_control"),
  aes(
    session,
   percent_of_daily_intake_total,
   color = type_of_food,
   label = ID
  ), size = 2
) +
facet_wrap(~exp_tag) +
ylab("Mean percent of daily intake") +
scale_x_continuous(breaks = seq(1, max(caf_chow_kcal_daily_group$session), 1)) +
theme_pubr()
```

save plots





type_of_food a caf a chow

