# Propensity Score Diagnostics

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# Checking balance

Love plots (Standardized Mean Difference)

**ECDF** plots

# Standardized Mean Difference (SMD)

$$d = rac{ar{x}_{treatment} - ar{x}_{control}}{\sqrt{rac{s_{treatment}^2 + s_{control}^2}{2}}}$$

# Create a "design object" to incorporate the weights

```
library(survey)

svy_des <- svydesign(
  ids = ~ 1,
  data = df,
  weights = ~ wts
)</pre>
```

# 2 Calculate the unweighted standardized mean differences

```
library(tableone)
library(tidyverse)

smd_table_unweighted <- CreateTableOne(
  vars = c("confounder_1", "confounder_1", ...),
  strata = "exposure",
  data = df,
  test = FALSE)</pre>
```

# 3 Calculate the weighted standardized mean differences

```
smd_table <- svyCreateTableOne(
  vars = c("confounder_1", "confounder_1", ...),
  strata = "exposure",
  data = svy_des,
  test = FALSE)</pre>
```

# 3 Calculate the weighted standardized mean differences

```
smd_table <- svyCreateTableOne(
  vars = c("confounder_1", "confounder_1", ...),
  strata = "exposure",
  data = svy_des,
  test = FALSE)</pre>
```



```
plot_df <- data.frame(
  var = rownames(ExtractSmd(smd_table)),
  Unadjusted = as.numeric(ExtractSmd(smd_table_unweighted)),
  Weighted = as.numeric(ExtractSmd(smd_table))) %>%
  pivot_longer(-var, names_to = "Method", values_to = "SMD")
```



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    var = rownames(ExtractSmd(smd_table)),
    Unadjusted = as.numeric(ExtractSmd(smd_table_unweighted)),
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    pivot_longer(-var, names_to = "Method", values_to = "SMD")

rownames(EXtractSMD(smd_table))

#> [1] "confounder_1" "confounder_2"
```



```
plot_df <- data.frame(
   var = rownames(ExtractSmd(smd_table)),
   Unadjusted = as.numeric(ExtractSmd(smd_table_unweighted)),
   Weighted = as.numeric(ExtractSmd(smd_table))) %>%
   pivot_longer(-var, names_to = "Method", values_to = "SMD")

as.numeric(ExtractSmd(smd_table_unweighted))
#> [1] 0.160 0.177
```



```
plot_df <- data.frame(
  var = rownames(ExtractSmd(smd_table)),
  Unadjusted = as.numeric(ExtractSmd(smd_table_unweighted)),
  Weighted = as.numeric(ExtractSmd(smd_table))) %>%
  pivot_longer(-var, names_to = "Method", values_to = "SMD")

as.numeric(ExtractSmd(smd_table))

#> [1] 0.002 0.007
```



```
plot_df <- data.frame(
  var = rownames(ExtractSmd(smd_table)),
  Unadjusted = as.numeric(ExtractSmd(smd_table_unweighted)),
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  pivot_longer(-var, names_to = "Method", values_to = "SMD")
```

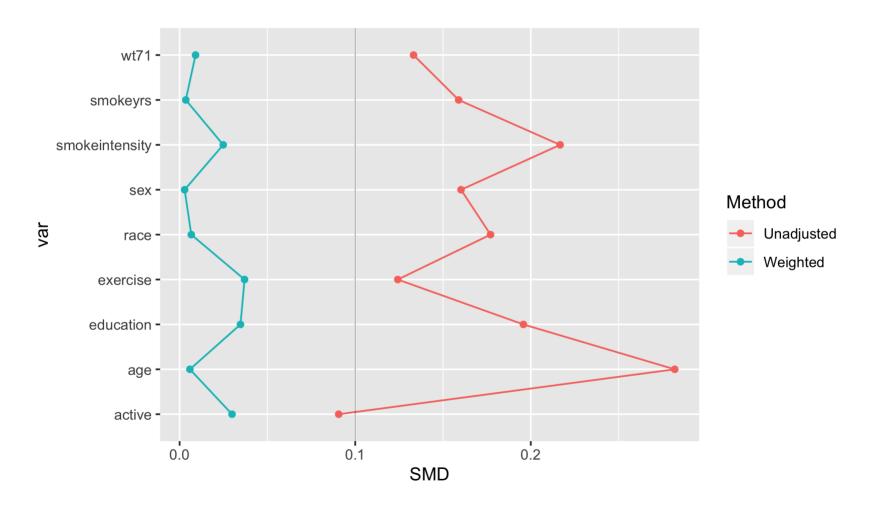
# 5

# 5

# 5

```
ggplot(data = plot_df, mapping = aes(x = var, y = SMD, group = Method
geom_line() +
geom_point() +
geom_hline(yintercept = 0.1, color = "black", size = 0.1) +
coord_flip()
```

# Love plot



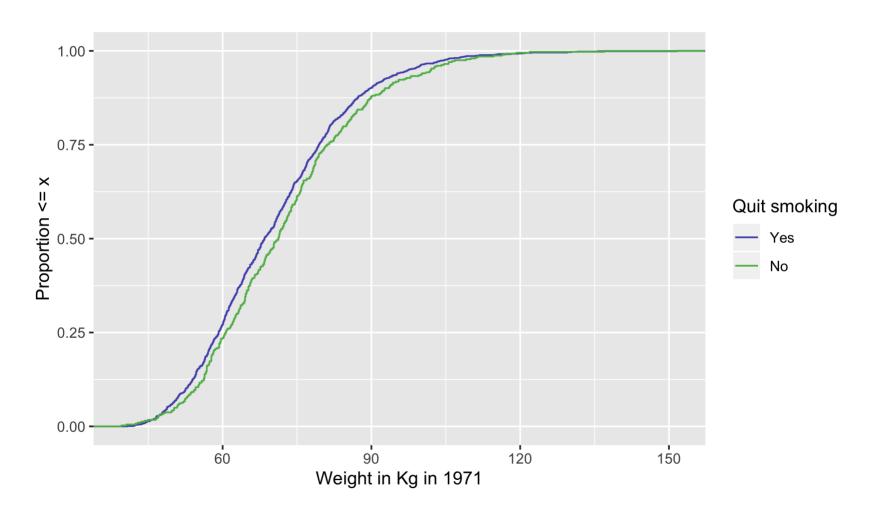
#### Your turn 1

1 Create a Love Plot for the propensity score weighting you created in the previous exercise

07:00

### **ECDF**

For continuous variables, it can be helpful to look at the **whole** distribution pre and post-weighting rather than a single summary measure



```
ecdf 1 <- df %>%
  filter(qsmk == 1) %>%
  arrange(wt71) %>%
  mutate(cum pct = cumsum(w ate) / sum(w ate))
ecdf 0 <- df %>%
  filter(qsmk == 0) %>%
  arrange(wt71) %>%
  mutate(cum pct = cumsum(w ate) / sum(w ate))
ggplot(ecdf_1, aes(x = wt71, y = cum_pct)) +
  geom line( color = "#5DB854") +
  geom_line(data = ecdf_0, aes(x = wt71, y = cum_pct), color = \#515
  xlab("Weight in Kg in 1971") +
  ylab("Proportion <= x")</pre>
```

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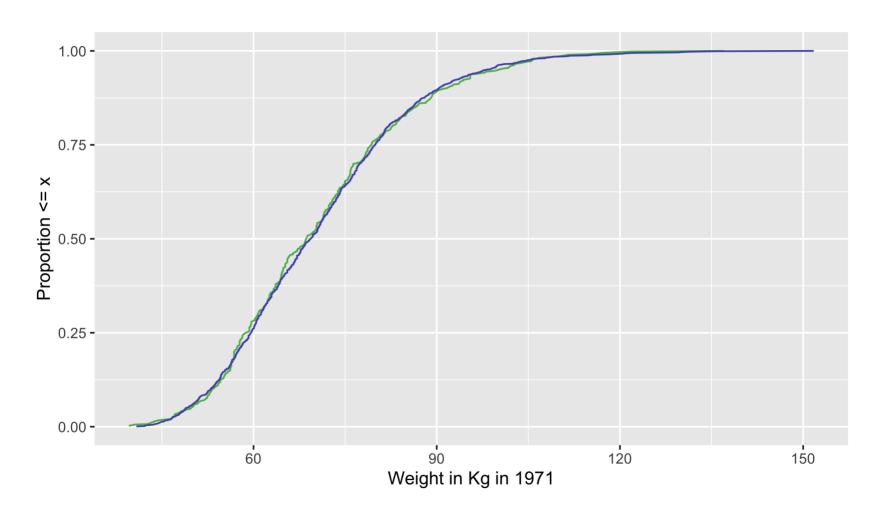
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  geom line( color = "#5DB854") +
  geom line(data = ecdf 0, aes(x = wt71, y = cum pct), color = \frac{1}{5}
  xlab("Weight in Kg in 1971") +
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```

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  xlab("Weight in Kg in 1971") +
  ylab("Proportion <= x")</pre>
```



#### Your turn 2

- 1 Create an unweighted ECDF
  examining the smokeyrs confounder
  for those that quit smoking and
  those that did not
- Create a weighted ECDF examining the smokeyrs confounder

07:00