Discussion Assignment 2: Causal Parameters & Simulations in R

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```
## -- Attaching packages ------------------------------------- tidyverse 1.3.1 --

## v ggplot2 3.3.3     v purrr   0.3.4
## v tibble  3.1.2     v dplyr   1.0.6
## v tidyr   1.1.3     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.1

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()

##
## Attaching package: 'ggdag'

## The following object is masked from 'package:stats':
##
##     filter

## here() starts at /Users/ajcr./OneDrive - University of Massachusetts/micokoch/R/biostats683_causal
```

4

```r
circum_hiv <- dagify(y ~ w + a + z + U,
                     z ~ w + a + U,
                     a ~ w + U,
                     w ~ U,
                     labels = c("y" = "HIV status",
                                "a" = "male circumcision",
                                "z" = "STI & sexual behavior",
                                "w" = "tribe & religion",
                                "U" = "Unmeasured all"),
                     exposure = "a",
                     outcome = "y",
                     coords = list(x = c(y = 5, a = 2, w = 1, z = 3, U = 3),
                                   y = c(y = 1, a = 1, w = 2, z = 2, U = 3))) %>%
  tidy_dagitty() %>%
  dplyr::mutate(Variable = case_when(
    name == "y" ~ "HIV Status",
```

```
    name == "a" ~ "Male Circumcision",
name == "z" ~ "STI & Sexual Behavior",
    name == "w" ~ "Tribe & Religion",
    name == "U" ~ "Unmeasured (all)"))

circum_hiv_dag <- circum_hiv %>%
  ggplot(aes(
    x = x,
    y = y,
    xend = xend,
    yend = yend
  )) +
  geom_dag_point(aes(color = Variable)) +
  geom_dag_edges() +
  geom_dag_text() +
  theme_dag() +
  scale_color_viridis_d()+
  ggtitle("Causal DAG \nEffect of male circumcision on risk of HIV acquisition") +
  theme(plot.title = element_text(hjust = 0.5, face = "bold")) +
  guides(color = guide_legend(override.aes = list(size = 8)))

circum_hiv_dag
```
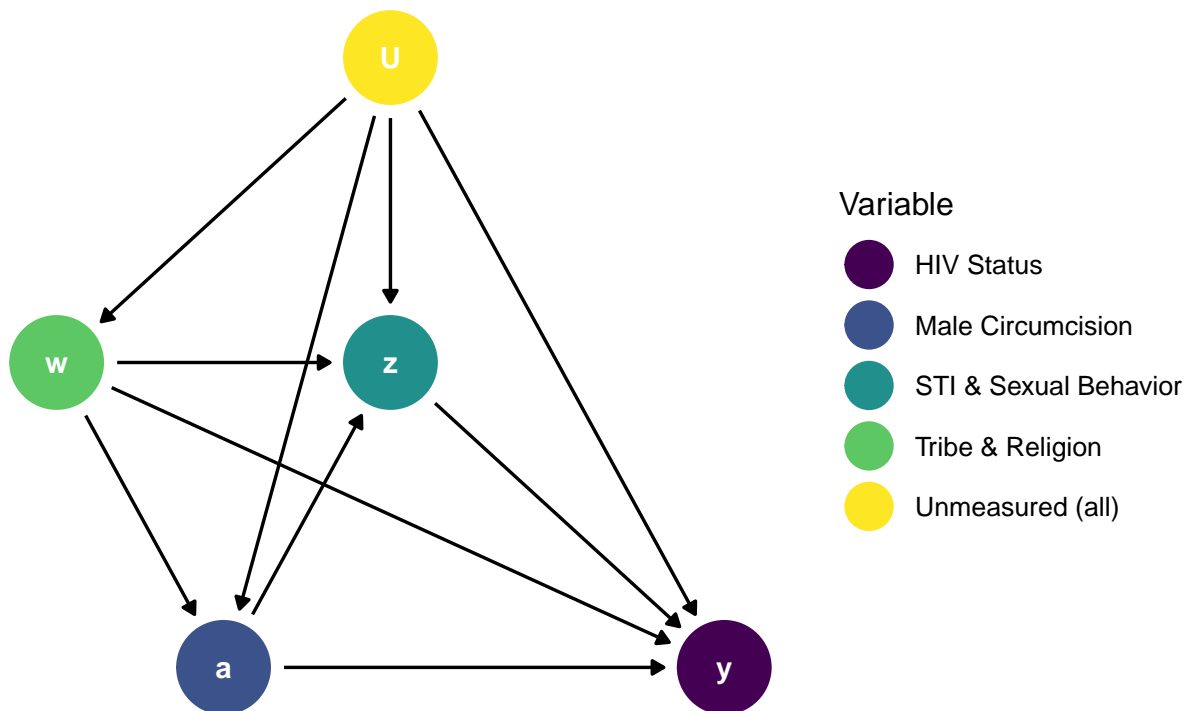
Causal DAG
ect of male circumcision on risk of HIV acquisition


```
ggsave(here("r_labs/disc_hw2/circum_hiv_dag.jpg"), width = 8, height = 6, units = "in")

# ggdag(circum_hiv_dag, text = FALSE, use_labels = "label")
```

```r
circum_hiv_2 <- dagify(y ~ w + a + z + Uy,
                       z ~ w + a + U,
                       a ~ w + U,
                       w ~ U,
                       labels = c("y" = "HIV status",
                                  "a" = "male circumcision",
                                  "z" = "STI & sexual behavior",
                                  "w" = "tribe & religion",
                                  "U" = "Unmeasured w,a,z",
                                  "Uy" = "Unmeasured y"),
                       exposure = "a",
                       outcome = "y",
                       coords = list(x = c(y = 5, a = 2, w = 1, z = 3, U = 3, Uy = 5),
                                     y = c(y = 1, a = 1, w = 2, z = 2, U = 3, Uy = 3))) %>%
  tidy_dagitty() %>%
  dplyr::mutate(Variable = case_when(
    name == "y" ~ "HIV Status",
    name == "a" ~ "Male Circumcision",
    name == "z" ~ "STI & Sexual Behavior",
    name == "w" ~ "Tribe & Religion",
    name == "U" ~ "Unmeasured for w, a, z",
    name == "Uy" ~ "Unmeasured for y"))

circum_hiv_dag_2 <- circum_hiv_2 %>%
  ggplot(aes(
    x = x,
    y = y,
    xend = xend,
    yend = yend
  )) +
  geom_dag_point(aes(color = Variable)) +
  geom_dag_edges() +
  geom_dag_text() +
  theme_dag() +
  scale_color_viridis_d() +
  ggtitle("Identifiable DAG \nEffect of male circumcision on risk of HIV acquisition") +
  theme(plot.title = element_text(hjust = 0.5, face = "bold")) +
  guides(color = guide_legend(override.aes = list(size = 8)))

circum_hiv_dag_2
```
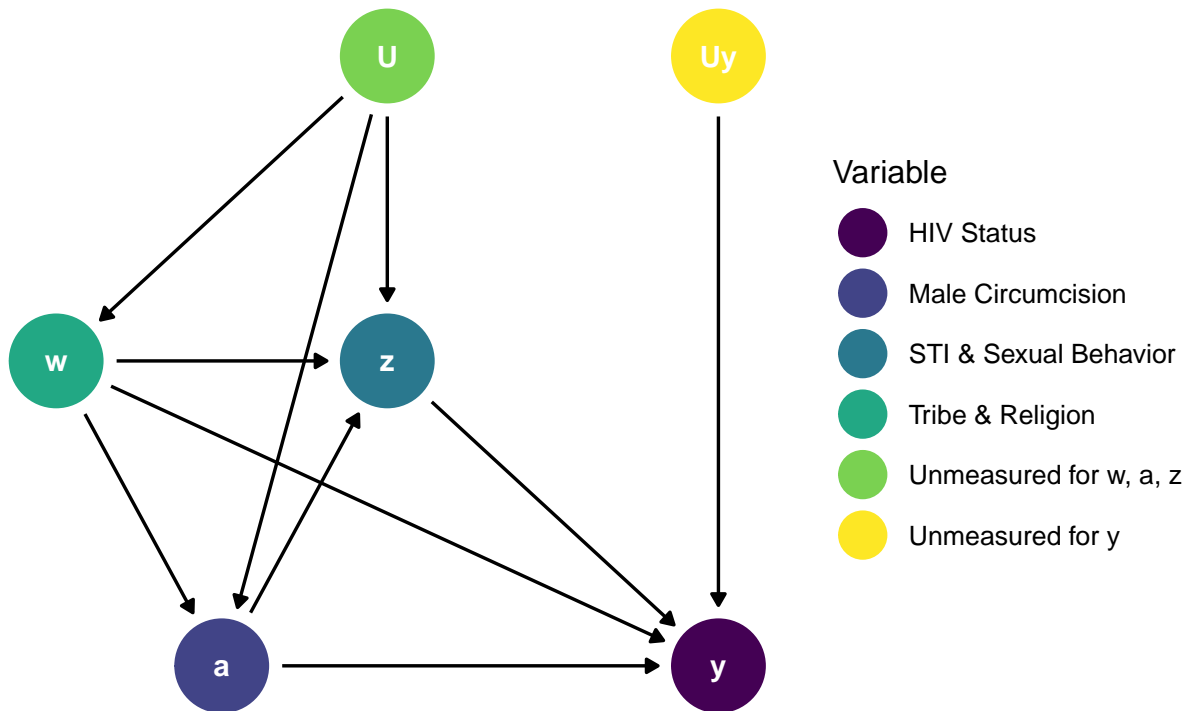
Identifiable DAG
ect of male circumcision on risk of HIV acquisition


```
ggsave(here("r_labs/disc_hw2/circum_hiv_dag_2.jpg"), width = 8, height = 6, units = "in")
```

```
circum_hiv_3 <- dagify(y ~ w + a + z + Uy,
                       z ~ w + a + U,
                       a ~ w + Ua,
                       w ~ U,
                       labels = c("y" = "HIV status",
                                  "a" = "male circumcision",
                                  "z" = "STI & sexual behavior",
                                  "w" = "tribe & religion",
                                  "U" = "Unmeasured w,z",
                                  "Ua" = "Unmeasured a",
                                  "Uy" = "Unmeasured y"),
                       exposure = "a",
                       outcome = "y",
                       coords = list(x = c(y = 5, a = 2, w = 1, z = 3, U = 3, Ua = 2, Uy = 5),
                                     y = c(y = 1, a = 1, w = 2, z = 2, U = 3, Ua = 3, Uy = 3))) %>%
  tidy_dagitty() %>%
  dplyr::mutate(Variable = case_when(
    name == "y" ~ "HIV Status",
    name == "a" ~ "Male Circumcision",
    name == "z" ~ "STI & Sexual Behavior",
    name == "w" ~ "Tribe & Religion",
    name == "U" ~ "Unmeasured for w, z",
    name == "Ua" ~ "Unmeasured for a",
    name == "Uy" ~ "Unmeasured for y"))
```

```
circum_hiv_dag_3 <- circum_hiv_3 %>%
  ggplot(aes(
    x = x,
    y = y,
    xend = xend,
    yend = yend
  )) +
  geom_dag_point(aes(color = Variable)) +
  geom_dag_edges() +
  geom_dag_text() +
  theme_dag() +
  scale_color_viridis_d() +
  ggtitle("Q. 4: DAG requiring W adjustment
          \nEffect of male circumcision on risk of HIV acquisition") +
  theme(plot.title = element_text(hjust = 0.5, face = "bold")) +
  guides(color = guide_legend(override.aes = list(size = 8)))

circum_hiv_dag_3
```

Q. 4: DAG requiring W adjustment

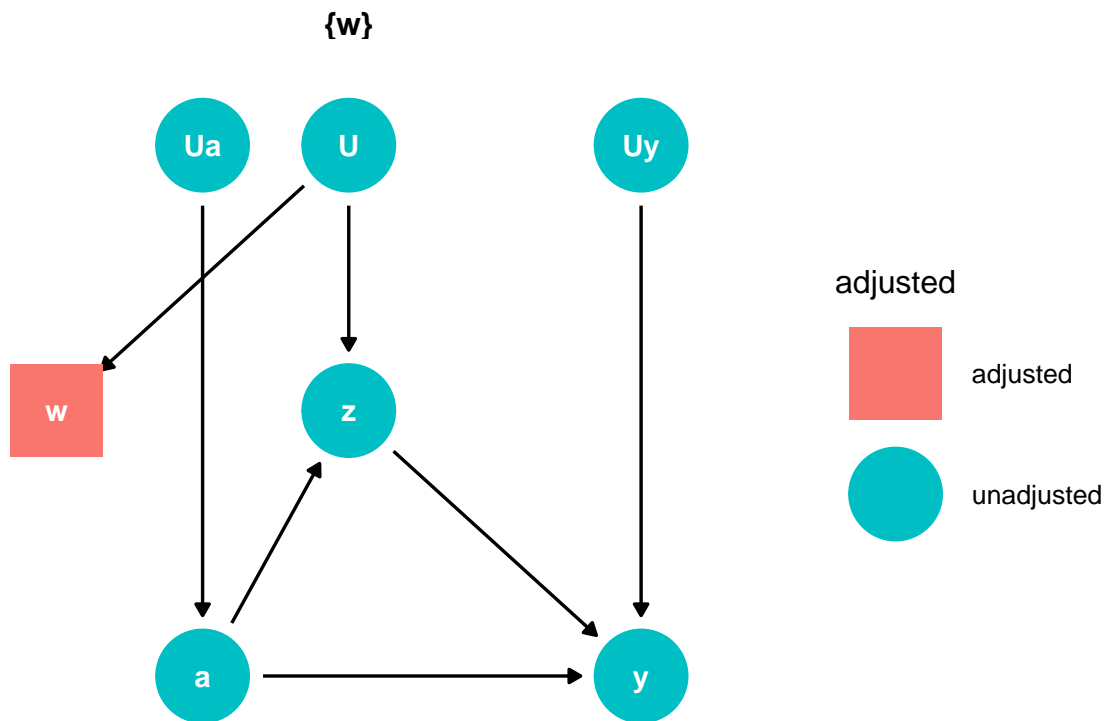## ect of male circumcision on risk of HIV acquisition
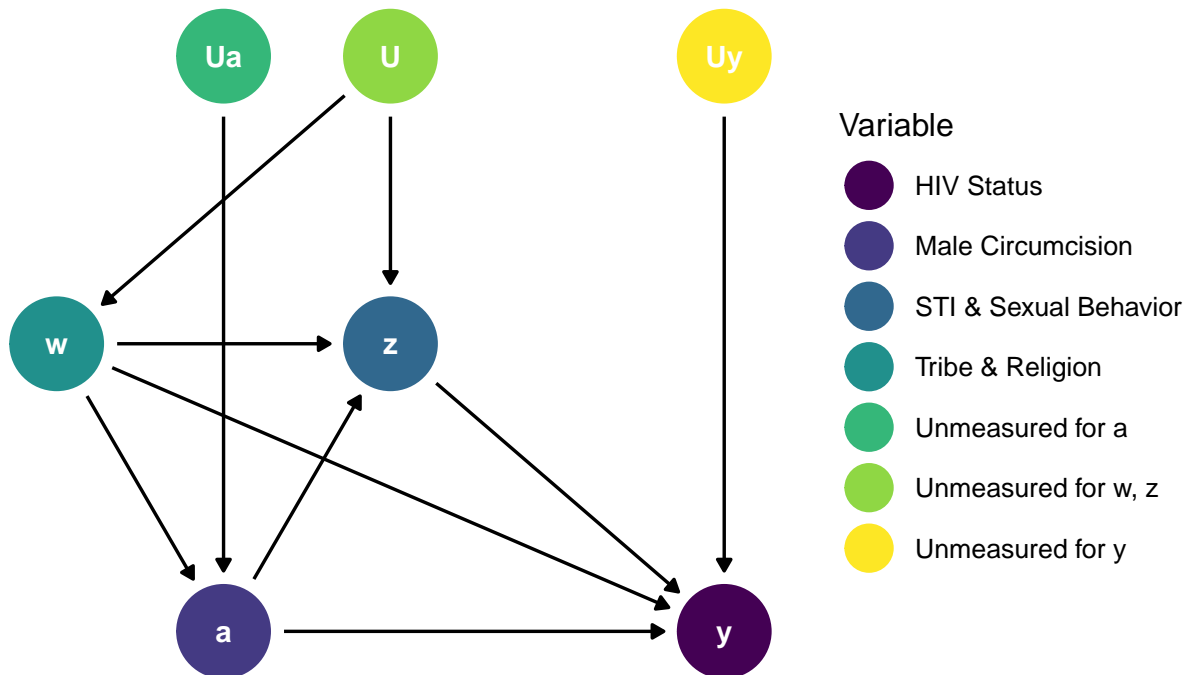

```
ggsave(here("r_labs/disc_hw2/circum_hiv_dag_3.jpg"), width = 8, height = 6, units = "in")

w_adj_dag <- ggdag_adjustment_set(circum_hiv_3, exposure = "a", outcome = "y", type = "minimal") +
  theme_dag() +
  labs(title = "Q. 4: DAG requiring W adjustment") +
  theme(plot.title = element_text(hjust = 0.5, face = "bold"))

w_adj_dag
```

Q. 4: DAG requiring W adjustment
{w}


```
ggsave(here("r_labs/disc_hw2/w_adj_dag.jpg"), width = 8, height = 6, units = "in")
```

```
circum_hiv_4 <- dagify(y ~ w + a + z + Uy,
                       z ~ U,
                       a ~ w + U,
                       w ~ Uw,
                       labels = c("y" = "HIV status",
                                  "a" = "male circumcision",
                                  "z" = "STI & sexual behavior",
                                  "w" = "tribe & religion",
                                  "U" = "Unmeasured a,z",
                                  "Uw" = "Unmeasured w",
                                  "Uy" = "Unmeasured y"),
                       exposure = "a",
                       outcome = "y",
                       coords = list(x = c(y = 5, a = 2, w = 1, z = 3, U = 3, Uw = 1, Uy = 5),
                                     y = c(y = 1, a = 1, w = 2, z = 2, U = 3, Uw = 3, Uy = 3))) %>%
  tidy_dagitty() %>%
  dplyr::mutate(Variable = case_when(
    name == "y" ~ "HIV Status",
    name == "a" ~ "Male Circumcision",
    name == "z" ~ "STI & Sexual Behavior",
    name == "w" ~ "Tribe & Religion",
    name == "U" ~ "Unmeasured for a, z",
    name == "Uw" ~ "Unmeasured for w",
    name == "Uy" ~ "Unmeasured for y"))
```

```
circum_hiv_dag_4 <- circum_hiv_4 %>%
  ggplot(aes(
    x = x,
    y = y,
    xend = xend,
    yend = yend
  )) +
  geom_dag_point(aes(color = Variable)) +
  geom_dag_edges() +
  geom_dag_text() +
  theme_dag() +
  scale_color_viridis_d() +
  ggtitle("Q. 4: DAG requiring W, Z adjustment
          \nEffect of male circumcision on risk of HIV acquisition") +
  theme(plot.title = element_text(hjust = 0.5, face = "bold")) +
  guides(color = guide_legend(override.aes = list(size = 8)))

circum_hiv_dag_4
```

Q. 4: DAG requiring W, Z adjustment

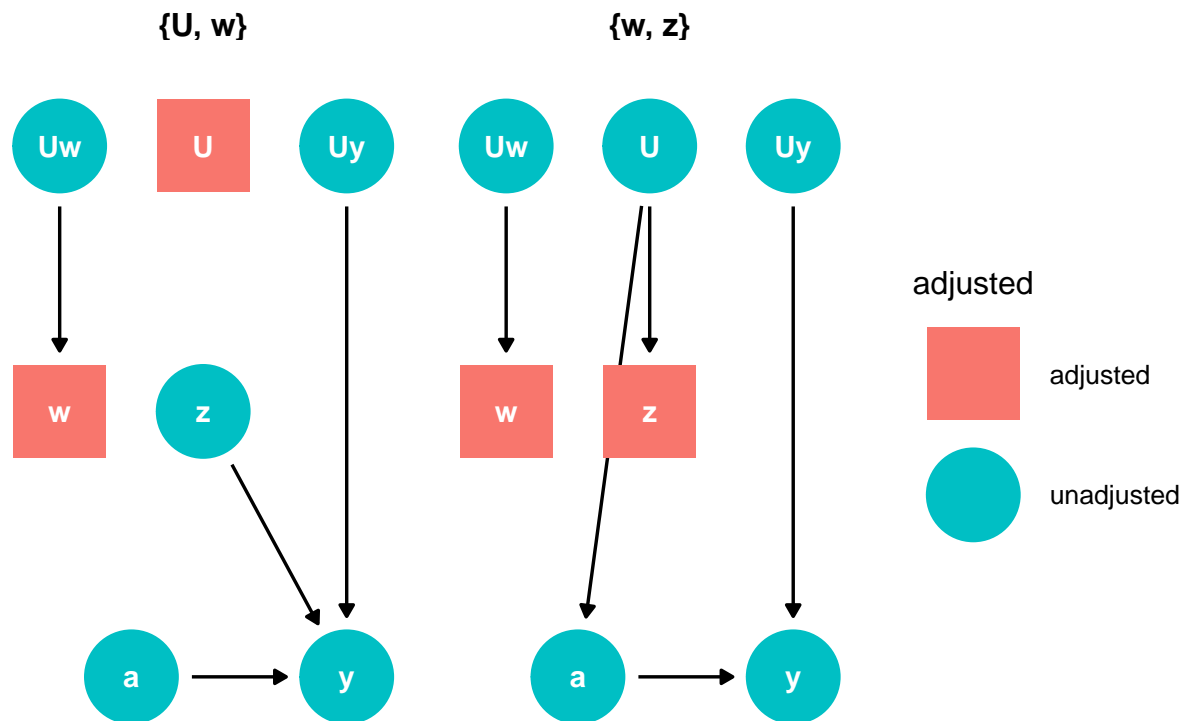## ect of male circumcision on risk of HIV acquisition
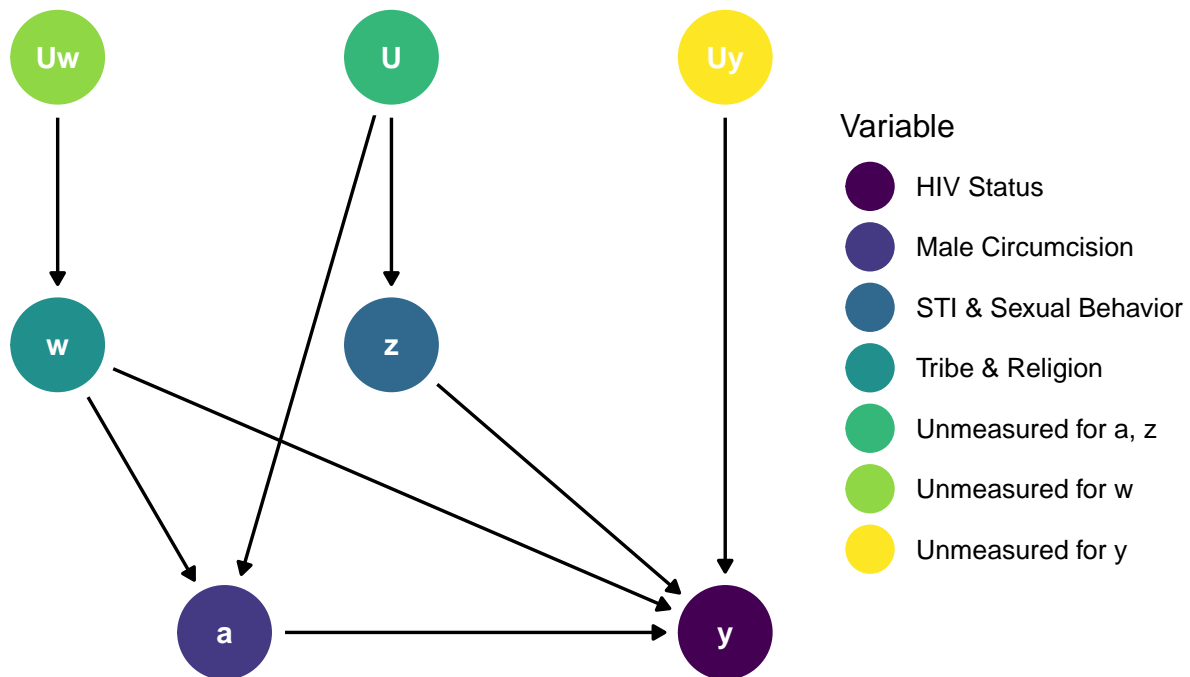

```
ggsave(here("r_labs/disc_hw2/circum_hiv_dag_4.jpg"), width = 8, height = 6, units = "in")

wz_adj_dag <- ggdag_adjustment_set(circum_hiv_4, exposure = "a", outcome = "y", type = "minimal") +
  theme_dag() +
  labs(title = "Q. 4: DAG requiring W, Z adjustment") +
  theme(plot.title = element_text(hjust = 0.5, face = "bold"))
```

Q. 4: DAG requiring W, Z adjustment

{U, w}   **{w, z}**

ggsave(here("r_labs/disc_hw2/wz_adj_dag.jpg"), width = 8, height = 6, units = "in")