Supplement 2: Case Study — Inverse Probability Weights for Quasi-Continuous Ordinal Exposures with a Binary Outcome: Method Comparison and Case Study

Sack, Daniel E, Shepherd, Bryan E, Audet, Carolyn M, De Schact, Caroline, Samuels, Lauren R

Updated 2022-08-18 for American Journal of Epidemiology

Setup

```
# full code available at https://github.com/dannysack/gen_prop_wts

source("../Code/orm.wt.R") # loads tidyverse, rms, and mice libraries
```

```
library(WeightIt)
library(MatchThem)
```

```
library(cobalt)
```

```
library(lme4)
```

```
library(kableExtra)
```

```
library(ggpubr)
library(parallel)
library(foreach)
```

```
library(doParallel)
```

```
library(extrafont)
```

```
library(ggdist)
library(table1)
```

```
library(gridExtra)
```

```
library(gtable)
library(grid)
library(broom.mixed)
```

```
library(forestplot)
```

```
library(DiagrammeR)
library(DiagrammeRsvg)
library(rsvg)
```

```
library(ggeffects)
loadfonts()
```

```
knitrSet(lang='markdown', fig.path='png2_pdf/', fig.align='center', w=9, h=8, cache=TRUE)
options(knitr.kable.NA = '')

# set seed
set.seed(1111)

# set theme for plots
theme <- theme_pubr() +
  theme(legend.position = "bottom",
                legend.key = element_rect(fill = NA, color = NA),
                text = element_text(family = "Arial"),
                axis.line = element_line(),
                axis.text = element_text(family = "Arial", color = "black"),
                strip.background = element_rect(fill = "grey95"))
```

Load Data

```
# start by loading hops+ data
# load cleaned data
load("/Users/sackd/Library/CloudStorage/Box-Box/Vanderbilt University/PhD/Dissertation/Thesis/Analysis/

# start by removing variables not relevant to the imputations or analyses
data <- quant %>%
  select(district.female, age.female, day.female, group.female, clinic.female,
         rel_stat.female, edu_cat.female, job_cat.female,
         stigma_com.female:peer_prop.female, who_stage, who_stage.male,
         district.male, age.male, day.male, group.male, rel_stat.male, edu_cat.male,
         job_cat.male, stigma_com.male:peer_prop.male, fem_int_tot:m_prop_int,
         time_to_fp, FP_method_final, Y_lc:covid_sens) %>%
  mutate(clinic.female = as.numeric(clinic.female)) %>% # required for imputations
  arrange(clinic.female) %>%
  mutate(who_stage = factor(who_stage, levels = c("I", "II", "III", "IV")),
         who_stage.male = factor(who_stage.male, levels = c("I", "II", "III", "IV"))) %>%
  filter(group.female == "Intervention") %>% # only want folks in the intervention group
  filter(!is.na(Y_raw)) %>% # only want folks with complete outcome data
  select(district.female:phq9.female, skills_comp.female, peer_comp.female,
         who_stage:phq9.male, skills_comp.male, peer_comp.male,
         FP_method_final, Y_raw) %>% # remove excess columns
  mutate(exp.female = skills_comp.female + peer_comp.female,
         exp.male = skills_comp.male + peer_comp.male)
```

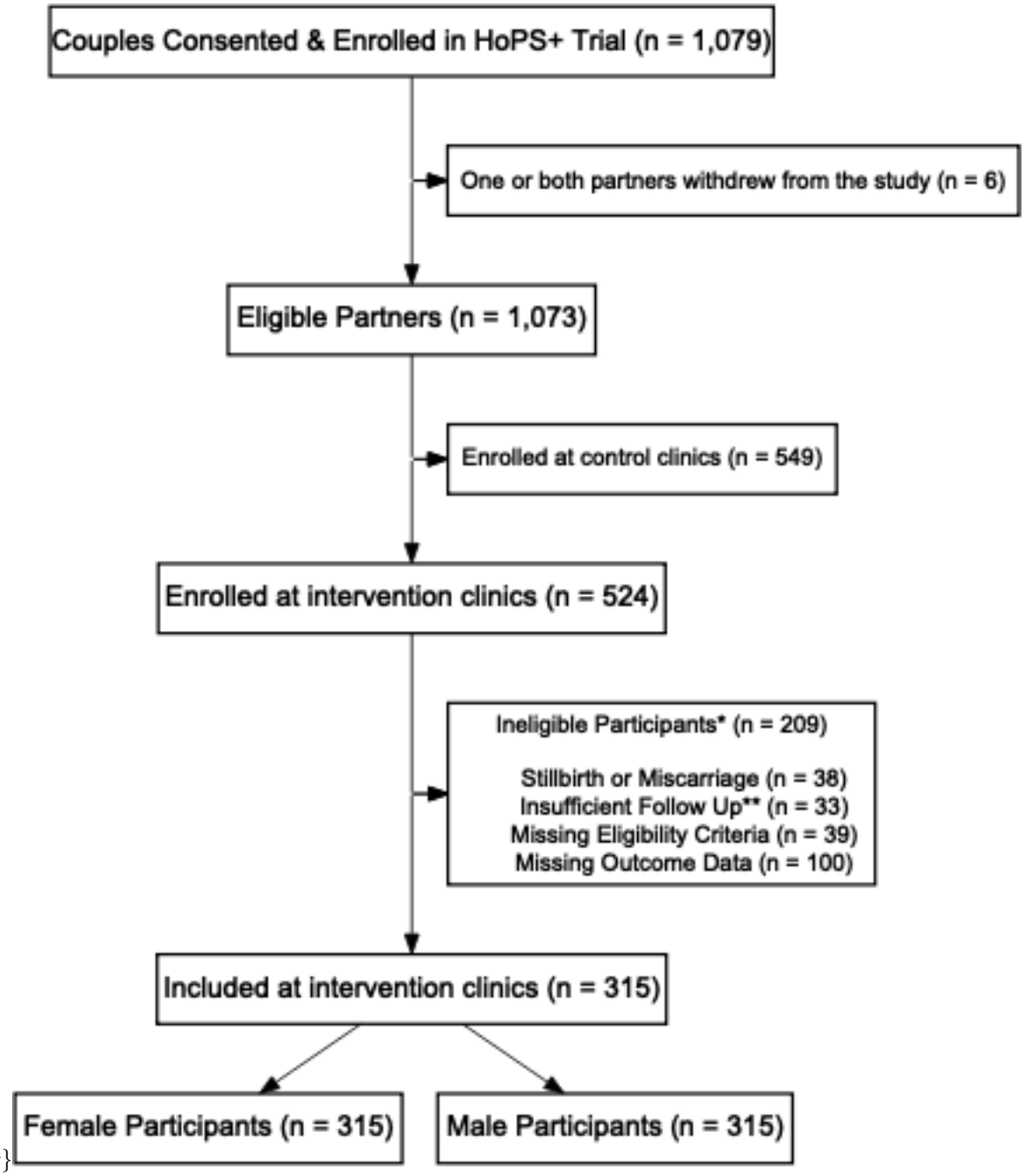
Describe Data

Given that the intervention consisted of six couples counseling and skills sessions focused on building communication skills, nine peer support sessions (with peer couples) focused on navigating pregnancy and the postpartum period, and joint couples antenatal and postnatal HIV care, we were interested whether intervention adherence (among female and male participants separately) impacted a secondary outcome (postpartum contraceptive uptake) among female participants in the intervention arm (1).

Supplemental Figure 2.1 - Enrollment Flow Chart

```
# create study flow chart

# set font
par(family = "Arial")

flow <- grViz("digraph flowchart {
      # main nodes
      node [fontname = Arial, shape = rectangle, penwidth = 1.5, fontsize = 14]
      consented [label = 'Couples Consented & Enrolled in HoPS+ Trial (n = 1,079)']
      enrolled [label = 'Eligible Partners (n = 1,073)']
      intclin [label = 'Enrolled at intervention clinics (n = 524)']
      finint [label = 'Included at intervention clinics (n = 315)']
      females [label= 'Female Participants (n = 315)']
      males [label = 'Male Participants (n = 315)']

      # exclusion nodes (smaller fontsize)
      node [fontname = Arial, shape = rectangle, penwidth = 1.5, fontsize = 12]
      excall [label = 'One or both partners withdrew from the study (n = 6)']
      exccont [label = 'Enrolled at control clinics (n = 549)']
      excint [label = 'Ineligible Participants* (n = 209)\\n
        Stillbirth or Miscarriage (n = 38)
        Insufficient Follow Up** (n = 33)
        Missing Eligibility Criteria (n = 39)
        Missing Outcome Data (n = 100)']

      # dummy nodes
      node [shape=none, width=0, height=0, label='']
      n1
      n2
      n3

      # edge definitions with the node IDs
      n1 -> excall
      n2 -> exccont
      n1 -> enrolled
      n2 -> intclin
      n3 -> excint
      n3 -> finint
      finint -> females
      finint -> males
      {rank = same; n1 -> excall}
      {rank = same; n2 -> exccont}
      {rank = same; n3 -> excint}
      {rank = same; females; males}

      edge[dir = none]
      consented -> n1
      enrolled -> n2
      intclin -> n3
      }
      ")
```

```
flow
```



\begin{center}

```
# export
# flow %>%
#   export_svg() %>%
#   charToRaw() %>%
#   rsvg_pdf("fig1.pdf")
# # embed fonts
# embedFonts("fig1.pdf", fontpaths = "/Library/Fonts/Microsoft/Arial.ttf")

# * indicates that individuals could share more than one reason
```

```
# **Delivery less than 1 year before Nov. 30, 2021
```

*indicates that individuals could share more than one reason

**Delivery less than 1 year before Nov. 30, 2021

Supplemental Figure 2.2 - Directed Acyclic Graph

To calculate each type of sIPW, we adjusted for the available minimally sufficient set of available confounding variables. These included: participant depression (continuous, measured via the Patient Health Questionaire-9)(2), female and male education (no education, some primary, completed primary, some secondary, completed secondary, college/higher education), participant WHO clinical stage (ordinal), participant social support (continuous, measured via adapted Berlin Social Support Scales)(3), partner HoPS+ engagement (continuous), participant age (continuous), and participant enrollment date (continuous). As this is merely a proof-of-concept analysis, we recognize that we are likely missing other potentially important confounders such as participant fertility intentions (which is part of the minimally sufficient set of theorized covariates), which were not available at the time of this analysis. The directed acyclic graph is shown below.

```
knitr::include_graphics("dag.pdf")
```

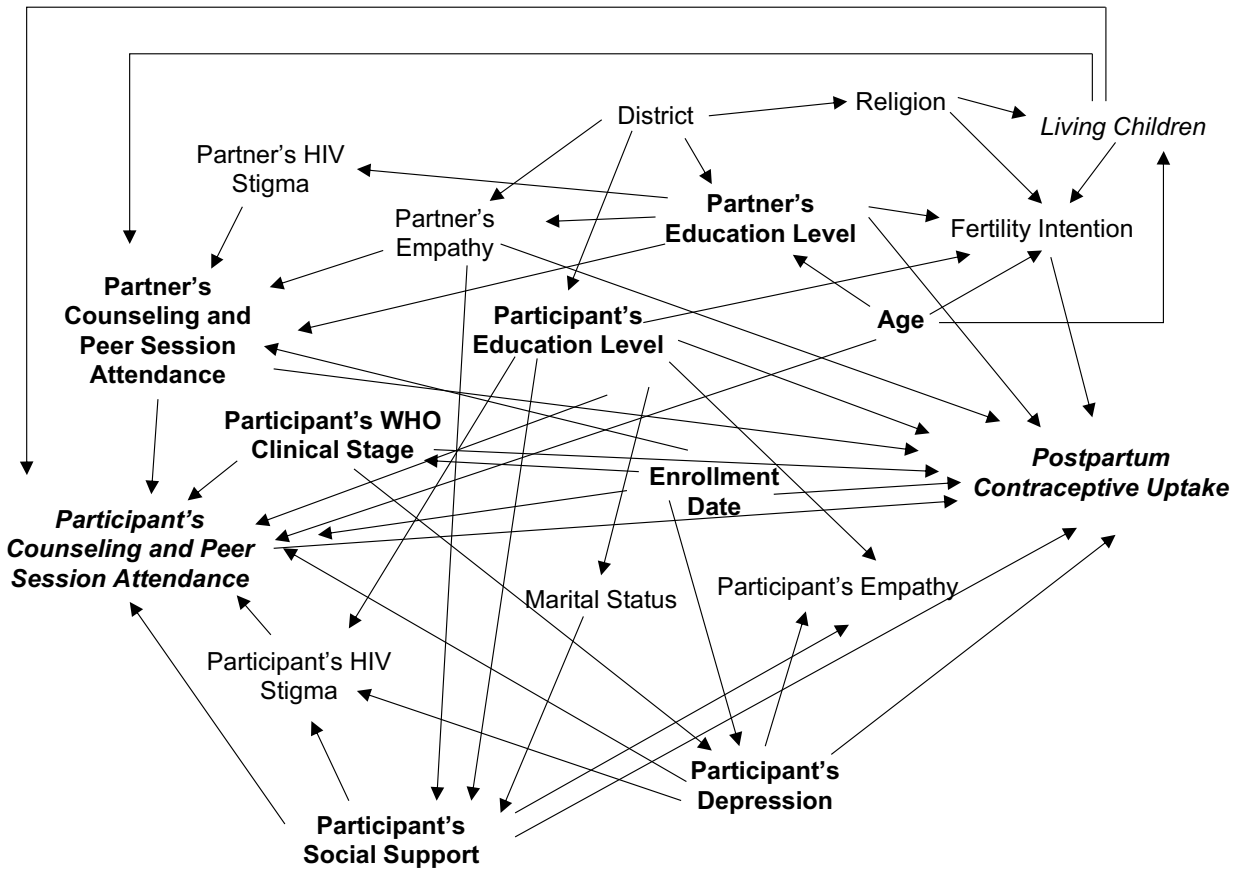


Table 3 - HoPS+ Descriptive Data

```
# code to generate table 1

# first split and combine female datasets
fem <- data %>% select(ends_with(".female"), who_stage, FP_method_final, Y_raw) %>%
  mutate(sex = "Female")
male <- data %>% select(ends_with(".male")) %>% mutate(sex = "Male")

# remove suffix
names(fem) <- gsub(".female", "", names(fem))
names(male) <- gsub(".male", "", names(male))

# now rowbind
tab1 <- bind_rows(fem, male) %>%
  mutate(sex = factor(sex, levels = c("Female", "Male")),
         skills_fac = factor(skills_comp),
         peer_fac = factor(peer_comp),
         exp_fac = factor(exp),
         fp_use = factor(Y_raw, labels = c("No", "Yes")))

# add some labels
label(tab1$exp) <- "Total Sessions Attended"
label(tab1$district) <- "District"
label(tab1$rel_stat) <- "Relationship Status"
label(tab1$edu_cat) <- "Education"
label(tab1$job_cat) <- "Occupation"
label(tab1$who_stage) <- "World Health Organization HIV Stage"
label(tab1$skills_fac) <- ""
label(tab1$peer_fac) <- ""
label(tab1$exp_fac) <- ""
label(tab1$fp_use) <- "Postpartum Contraceptive Use"
label(tab1$FP_method_final) <- "Method Type"

# table 1
table1(~ age + district + rel_stat +
         edu_cat + job_cat +
         stigma_com + stigma_pt +
         trust + cog_emp + aff_emp +
         soc_sup_ps + soc_sup_ns + # still need to add in clinical data (ART status, clinical stage, BM
         hivk + phq9 + who_stage +
         skills_comp + skills_fac +
         peer_comp +peer_fac +
         exp + exp_fac +  fp_use +
         FP_method_final | sex, data = tab1,
       render.continuous = c(.="Median [Q1, Q3]"), overall = FALSE)

# final data (do not need method type in imputation since all missing for males)
data <- data %>% select(-FP_method_final)
```

Table 1 describes baseline covariates among female and male HoPS+ participants. Female participants were younger (median age 23 years, interquartile range [IQR] 19.5, 27 years) than males (median age 27 years, IQR 24, 32 years) and less likely to have received any education (15.9% versus 6.0%). Female participants were far more likely to work as a domestic worker (50.2% versus 16.2% of male participants) and less likely to

work as a trader or fisherman (0.6% and 0% versus 13.7% and 19% among males respectively). Psychometric scale scores were similar in female and male participants.

Figure 4 - HoPS+ Exposure Distribution

```
# code to generate figure 4

fem_exp <- ggplot(data, aes(x = exp.female)) +
  geom_histogram(aes(y = ..count..),binwidth = 1, alpha = 0.5, color = "grey50") +
  # geom_density(adjust = 2) +
  ylab("Participants") +
  ylim(0, 90) +
  xlab("Female Session Attendance") +
  theme

m_exp <- ggplot(data, aes(x = exp.male)) +
  geom_histogram(aes(y = ..count..), binwidth = 1, alpha = 0.5, color = "grey50") +
  # geom_density(adjust = 2) +
  ylab("") +
  ylim(0, 90) +
  xlab("Male Session Attendance") +
  theme

ggarrange(fem_exp, m_exp,
          labels = c("A)", "B)"))

# save plot
ggsave("figs/fig4.pdf", width = 6, height = 4)
# embed the font
embed_fonts("figs/fig4.pdf")
```

Imputations

```
# create predictor matrix
predmat <- make.predictorMatrix(data)

# now edit predictor matrix, from "mice" documentation
# "Each row corresponds to a variable block, i.e., a set of variables to be imputed.
# A value of 1 means that the column variable is used as a predictor for
  # the target block (in the rows)."
# my understanding is that the column then denotes whether that variable
  #will be used to predict the row variable

# first make clinic the cluster variable for all predictions (except it's own)
# only need to do it in the column because it is not missing in the rows
predmat[, "clinic.female"] <- -2
predmat["clinic.female", "clinic.female"] <- 0

# 25 imputations
# update default for binary variables (outcome) to account for clustering in "defaultMethod"
```

```
imp <- mice(data, m = 25,
                predictorMatrix = predmat,
                defaultMethod = c("pmm", "2l.bin", "polyreg", "polr"),
                seed = 1111)

# now save for future analyses
Save(imp)

# now check some diagnostics
# stripplots to check distributions of imputed data
stripplot(imp)

# bwplots to re-check distributions of imputed data
bwplot(imp)
```

Supplemental Figure 2.3 - Covariate Balance

```
# pull in imputations
Load(imp)

# first need to make clinic.female a factor in all iterations
long <- complete(imp, action = "long", include = TRUE)
long$clinic.female <- factor(long$clinic.female)
# now make it back into a mids object
imp <- as.mids(long)
```

```
# create model formula to assess female and male participation per DAG
f_form <- formula(exp.female ~ skills_comp.male + peer_comp.male +
                    rcs(age.female, 4) + who_stage + edu_cat.female +
                    edu_cat.male + rcs(day.female, 4) + rcs(phq9.female, 4) +
                    clinic.female + rcs(soc_sup_ps.female, 4) + rcs(soc_sup_ns.female, 4))
m_form <- formula(exp.male ~ skills_comp.female + peer_comp.female +
                    rcs(age.male, 4) + who_stage.male + edu_cat.female +
                    edu_cat.male + rcs(day.male, 4) + rcs(phq9.male, 4) +
                    clinic.female +  rcs(soc_sup_ps.male, 4) + rcs(soc_sup_ns.male, 4))


# Now assess weights across imputations
f_w_ols <- weightthem(f_form, datasets = imp, approach = "within", method = "ps")
```

```
f_w_cbps <- weightthem(f_form, datasets = imp, approach = "within", method = "cbps",
                       over = FALSE)
```

```
m_w_ols <- weightthem(m_form, datasets = imp, approach = "within", method = "ps")
```

```
m_w_cbps <- weightthem(m_form, datasets = imp, approach = "within", method = "cbps",
                       over = FALSE)
```

```
# create olr weights from my own function
f_w_olr <- orm.wt(object = imp,
                  exposure = "exp.female",
                  cov_form = "~ skills_comp.male + peer_comp.male + rcs(age.female, 4) +
                  who_stage + edu_cat.female + edu_cat.male + rcs(day.female, 4) +
```

```
                  rcs(phq9.female, 4) + clinic.female +
                  rcs(soc_sup_ps.female, 4) + rcs(soc_sup_ns.female, 4)")
```

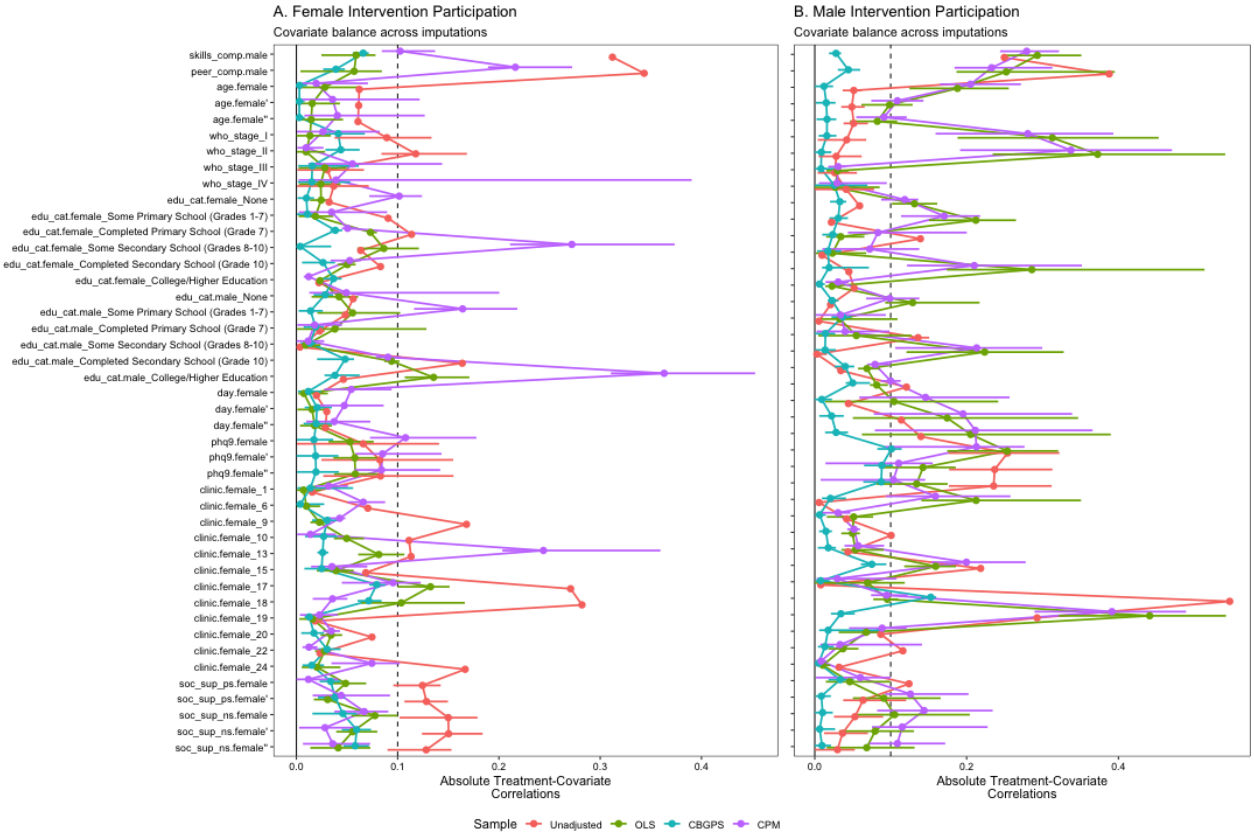
```
m_w_olr <- orm.wt(object = imp,
                  exposure = "exp.male",
                  cov_form = "~ skills_comp.female + peer_comp.female + rcs(age.male, 4) +
                  who_stage.male + edu_cat.female + edu_cat.male + rcs(day.male, 4) +
                  rcs(phq9.male, 4) + clinic.female +
                  rcs(soc_sup_ps.male, 4) + rcs(soc_sup_ns.male, 4)")
```

```
# Make female and male plot side by side
# make theme for tables
tt_theme <- ttheme_minimal(base_family = "Arial",
                           base_size = 10,
                           core = list(fg_params = list(hjust = 0, x = 0.1)),
                           colhead = list(fg_params = list(hjust = 0, x = 0.1)))

# female
# first make table
fem_bal_tab <- bal.tab(f_form, data = imp,
        weights = list(OLS = get.w(f_w_ols),
                       CBGPS = get.w(f_w_cbps),
                       OLR = unname(unlist(f_w_olr))),
        stats = c("c"),
        un = TRUE, thresholds = c(cor = .1))

# get effective sample size
bal_fem_obs <- tibble(All = rep(NA, 25),
                      OLS = rep(NA, 25),
                      CBGPS = rep(NA, 25),
                      OLR = rep(NA, 25))
for(i in 1:25) {
    bal_fem_obs[i, ] <- t(fem_bal_tab$Imputation.Balance[[i]]$Observations)
}

# get list of mean number of balanced covariates
bal_fem_cor <- tibble(OLS = rep(NA, 25),
                      CBGPS = rep(NA, 25),
                      OLR = rep(NA, 25))
for(i in 1:25) {
    bal_fem_cor[i, ] <- fem_bal_tab$Imputation.Balance[[i]]$Balanced.correlations[2, ]
}

# create bal_fem table for plot
bal_fem <- tibble(Sample = c("Unadjusted",
                             "OLS",
                             "CBGPS",
                             "CPM"),
                  `Correlation > 0.1` = c("",
                                          paste0(mean(bal_fem_cor$OLS), " (",
                                                 min(bal_fem_cor$OLS), ", ",
                                                 max(bal_fem_cor$OLS), ")"),
                                          paste0(mean(bal_fem_cor$CBGPS), " (",
                                                 min(bal_fem_cor$CBGPS), ", ",
```

```
                                          max(bal_fem_cor$CBGPS), ")"),
                                    paste0(mean(bal_fem_cor$OLR), " (",
                                          min(bal_fem_cor$OLR), ", ",
                                          max(bal_fem_cor$OLR), ")")),
                `sIPW Distribution` = c("",
                                    paste0(round(mean(get.w(f_w_ols)), 2), " (",
                                          round(min(get.w(f_w_ols)), 2), ", ",
                                          round(max(get.w(f_w_ols)), 2), ")"),
                                    paste0(round(mean(get.w(f_w_cbps)), 2), " (",
                                          round(min(get.w(f_w_cbps)), 2), ", ",
                                          round(max(get.w(f_w_cbps)), 2), ")"),
                                    paste0(round(mean(unlist(f_w_olr)), 2), " (",
                                          round(min(unlist(f_w_olr)), 2), ", ",
                                          round(max(unlist(f_w_olr)), 2), ")")))

# make into grob
fem_tab <- tableGrob(bal_fem, theme = tt_theme, rows = NULL)
fem_tab <- gtable_add_grob(fem_tab,
                           grobs = rectGrob(gp = gpar(fill= NA, lwd = 2)),
                           t = 1, b = nrow(fem_tab), l = 1, r = ncol(fem_tab))

# now make plot
fem_love <- love.plot(f_form, data = imp,
        weights = list(OLS = get.w(f_w_ols),
                       CBGPS = get.w(f_w_cbps),
                       CPM = unname(unlist(f_w_olr))),
          stats = c("c"), thresholds = c(cor = .1),
          abs = TRUE, line = TRUE) +
  # annotation_custom(fem_tab,
  #                   xmin = 0.18, ymin = 2, ymax = 8) +
  labs(title = "A. Female Intervention Participation",
       subtitle = "Covariate balance across imputations") +
  theme(text = element_text(family = "Arial"),
        plot.title = element_text(hjust = 0),
        plot.subtitle = element_text(hjust = 0))

# male
# first make table
m_bal_tab <- bal.tab(m_form, data = imp,
        weights = list(OLS = get.w(m_w_ols),
                       CBGPS = get.w(m_w_cbps),
                       OLR = unname(unlist(m_w_olr))),
        stats = c("c"),
        un = TRUE, thresholds = c(cor = .1))

# get effective sample size
bal_m_obs <- tibble(All = rep(NA, 25),
                    OLS = rep(NA, 25),
                    CBGPS = rep(NA, 25),
                    OLR = rep(NA, 25))
for(i in 1:25) {
    bal_m_obs[i, ] <- t(m_bal_tab$Imputation.Balance[[i]]$Observations)
}
```

```r
# get list of mean number of balanced covariates
bal_m_cor <- tibble(OLS = rep(NA, 25),
                    CBGPS = rep(NA, 25),
                    OLR = rep(NA, 25))
for(i in 1:25) {
    bal_m_cor[i, ] <- m_bal_tab$Imputation.Balance[[i]]$Balanced.correlations[2, ]
}

# create bal_fem table for plot
bal_male <- tibble(Sample = c("Unadjusted",
                              "OLS",
                              "CBGPS",
                              "CPM"),
                   `Correlation > 0.1` = c("",
                                           paste0(mean(bal_m_cor$OLS), " (",
                                                  min(bal_m_cor$OLS), ", ",
                                                  max(bal_m_cor$OLS), ")"),
                                           paste0(mean(bal_m_cor$CBGPS), " (",
                                                  min(bal_m_cor$CBGPS), ", ",
                                                  max(bal_m_cor$CBGPS), ")"),
                                           paste0(mean(bal_m_cor$OLR), " (",
                                                  min(bal_m_cor$OLR), ", ",
                                                  max(bal_m_cor$OLR), ")")),
                   `sIPW Distribution` = c("",
                                           paste0(round(mean(get.w(m_w_ols)), 2), " (",
                                                  round(min(get.w(m_w_ols)), 2), ", ",
                                                  round(max(get.w(m_w_ols)), 2), ")"),
                                           paste0(round(mean(get.w(m_w_cbps)), 2), " (",
                                                  round(min(get.w(m_w_cbps)), 2), ", ",
                                                  round(max(get.w(m_w_cbps)), 2), ")"),
                                           paste0(round(mean(unlist(m_w_olr)), 2), " (",
                                                  round(min(unlist(m_w_olr)), 2), ", ",
                                                  round(max(unlist(m_w_olr)), 2), ")")))

# make into grob
male_tab <- tableGrob(bal_male, theme = tt_theme, rows = NULL)
male_tab <- gtable_add_grob(male_tab,
                            grobs = rectGrob(gp = gpar(fill= NA, lwd = 2)),
                            t = 1, b = nrow(male_tab), l = 1, r = ncol(male_tab))

# now make plot
male_love <- love.plot(m_form, data = imp,
        weights = list(OLS = get.w(m_w_ols),
                       CBGPS = get.w(m_w_cbps),
                       CPM = unname(unlist(m_w_olr))),
          stats = c("c"), thresholds = c(cor = .1),
          abs = TRUE, line = TRUE) +
  # annotation_custom(male_tab,
  #                   xmin = 0.15, ymin = 2, ymax = 8) +
  labs(title = "B. Male Intervention Participation",
       subtitle = "Covariate balance across imputations") +
  theme(text = element_text(family = "Arial"),
        axis.text.y = element_blank(),
```

```
        plot.title = element_text(hjust = 0),
        plot.subtitle = element_text(hjust = 0))
# combine
ggarrange(fem_love, male_love, nrow = 1,
          widths = c(1, 0.6),
          common.legend = TRUE,
          legend = "bottom")
```



All tables are mean (min, max). The points represent the mean absolute treatment-covariate correlation across the 25 imputed datasets and the error bars show the range of correlations across datasets.

Model Fitting

```
# ols
f_ols_mod <- with(f_w_ols,
                  glmer(Y_raw ~ exp.female + (1 | clinic.female),
                        family = binomial)) %>%
  pool() %>%
  summary()

# cbgps
f_cbgps_mod <- with(f_w_cbps,
                  glmer(Y_raw ~ exp.female + (1 | clinic.female),
                        family = binomial)) %>%
  pool() %>%
```

```
  summary()

# olr
f_olr_mod <- map2(complete(imp, "all"), f_w_olr, ~
                    glmer(Y_raw ~ exp.female + (1 | clinic.female),
                          family = binomial,
                          data = .x,
                          weights = .y)) %>%
  as.mira() %>%
  pool() %>%
  summary()
```

```
# ols
m_ols_mod <- with(m_w_ols,
                  glmer(Y_raw ~ exp.male + (1 | clinic.female),
                        family = binomial)) %>%
  pool() %>%
  summary()

# cbgps
m_cbgps_mod <- with(m_w_cbps,
                  glmer(Y_raw ~ exp.male + (1 | clinic.female),
                        family = binomial)) %>%
  pool() %>%
  summary()

# olr
m_olr_mod <- map2(complete(imp, "all"), m_w_olr, ~
                    glmer(Y_raw ~ exp.male + (1 | clinic.female),
                          family = binomial,
                          data = .x,
                          weights = .y)) %>%
  as.mira() %>%
  pool() %>%
  summary()
```

Figure 5 - Dose Response Plot

```
# females
# ols
f_ols_pp <- with(f_w_ols,
                 glmer(Y_raw ~ exp.female + (1 | clinic.female),
                       family = binomial))$analyses %>%
  map(~ ggpredict(.x, terms = "exp.female")) %>%
  pool_predictions() %>%
  tibble() %>%
  mutate(IPW = "OLS")

# cbgps
f_cbgps_pp <- with(f_w_cbps,
                  glmer(Y_raw ~ exp.female + (1 | clinic.female),
```

```
                        family = binomial))$analyses %>%
  map(~ ggpredict(.x, terms = "exp.female")) %>%
  pool_predictions() %>%
  tibble() %>%
  mutate(IPW = "CBGPS")

# olr
f_olr_pp <- map2(complete(imp, "all"), f_w_olr, ~
                   glmer(Y_raw ~ exp.female + (1 | clinic.female),
                         family = binomial,
                         data = .x,
                         weights = .y)) %>%
  map(~ ggpredict(.x, terms = "exp.female")) %>%
  pool_predictions() %>%
  tibble() %>%
  mutate(IPW = "CPM")

# combine all three into one df
fem_pp <- f_ols_pp %>%
  bind_rows(f_cbgps_pp) %>%
  bind_rows(f_olr_pp) %>%
  mutate(IPW = factor(IPW, levels = c("OLS", "CBGPS", "CPM")),
         x_new = ifelse(IPW == "OLS", x - 0.2, x),
         x_new = ifelse(IPW == "CPM", x + 0.2, x_new))

# combine into one plot
fem_pp_plot <- ggplot(fem_pp) +
  geom_errorbarh(aes(y = x_new, xmin = conf.low, xmax = conf.high, color = IPW),
                 alpha = 0.25, height = 0.25) +
  geom_point(aes(x = predicted, y = x_new, color = IPW, shape = IPW), size = 1) +
  scale_color_manual(values = c("#606060", "#919191", "#C4C4C4")) +
  ylab("Completed Sessions") +
  xlab("Probability of Female Postpartum \nContraceptive Use") +
  ggtitle("A) Female Attendance") +
  xlim(0, 1) +
  theme +
  theme(axis.text = element_text(size = 10))

# males
# ols
m_ols_pp <- with(m_w_ols,
                 glmer(Y_raw ~ exp.male + (1 | clinic.female),
                       family = binomial))$analyses %>%
  map(~ ggpredict(.x, terms = "exp.male")) %>%
  pool_predictions() %>%
  tibble() %>%
  mutate(IPW = "OLS")

# cbgps
m_cbgps_pp <- with(m_w_cbps,
                   glmer(Y_raw ~ exp.male + (1 | clinic.female),
                         family = binomial))$analyses %>%
  map(~ ggpredict(.x, terms = "exp.male")) %>%
```

```
  pool_predictions() %>%
  tibble() %>%
  mutate(IPW = "CBGPS")

# olr
m_olr_pp <- map2(complete(imp, "all"), m_w_olr, ~
                   glmer(Y_raw ~ exp.male + (1 | clinic.female),
                         family = binomial,
                         data = .x,
                         weights = .y)) %>%
  map(~ ggpredict(.x, terms = "exp.male")) %>%
  pool_predictions() %>%
  tibble() %>%
  mutate(IPW = "CPM")

# combine all three into one df
m_pp <- m_ols_pp %>%
  bind_rows(m_cbgps_pp) %>%
  bind_rows(m_olr_pp) %>%
  mutate(IPW = factor(IPW, levels = c("OLS", "CBGPS", "CPM")),
         x_new = ifelse(IPW == "OLS", x - 0.2, x),
         x_new = ifelse(IPW == "CPM", x + 0.2, x_new))

# combine into one plot
m_pp_plot <- ggplot(m_pp) +
  geom_errorbarh(aes(y = x_new, xmin = conf.low, xmax = conf.high, color = IPW),
                 alpha = 0.25, height = 0.25) +
  geom_point(aes(x = predicted, y = x_new, color = IPW, shape = IPW), size = 1) +
  scale_color_manual(values = c("#606060", "#919191", "#C4C4C4")) +
  ylab("") +
  xlab("Probability of Female Postpartum \nContraceptive Use") +
  ggtitle("B) Male Attendance") +
  xlim(0, 1) +
  theme +
  theme(axis.text = element_text(size = 10))

# combine
ggarrange(fem_pp_plot, m_pp_plot,
          common.legend = TRUE,
          legend = "bottom")

# save plot
ggsave("figs/fig5.pdf", width = 7, height = 5)
# embed the font
embed_fonts("figs/fig5.pdf")
```

Figure 6 - Forest Plot

```
# female participants
fem_fp <- tibble(Analysis = c("OLS",
                              "CBGPS",
```

```
                            "CPM"),
               coef = c(f_ols_mod$estimate[2],
                        f_cbgps_mod$estimate[2],
                        f_olr_mod$estimate[2]),
                  se = c(f_ols_mod$std.error[2],
                        f_cbgps_mod$std.error[2],
                        f_olr_mod$std.error[2])) %>%
  mutate(lb = coef - (1.96*se),
         ub = coef + (1.96*se),
         or = exp(coef),
         or_lb = exp(lb),
         or_ub = exp(ub),
         `Odds Ratio (95% Confidence Interval)` = paste0(round(or, 2), " (", round(or_lb, 3), ", ", rou

# male participants
m_fp <- tibble(Analysis = c("OLS",
                            "CBGPS",
                            "CPM"),
               coef = c(m_ols_mod$estimate[2],
                        m_cbgps_mod$estimate[2],
                        m_olr_mod$estimate[2]),
                  se = c(m_ols_mod$std.error[2],
                        m_cbgps_mod$std.error[2],
                        m_olr_mod$std.error[2])) %>%
  mutate(lb = coef - (1.96*se),
         ub = coef + (1.96*se),
         or = exp(coef),
         or_lb = exp(lb),
         or_ub = exp(ub),
         `Odds Ratio (95% Confidence Interval)` = paste0(round(or, 2), " (", round(or_lb, 3), ", ", rou

# now make a forestplot
tabletext <- bind_cols(c("", "Female Participants", "Mean sIPW (min, max)",
                         "Mean correlations > 0.1 (min, max)",
                         "+1 session [OR (95% CI)]",
                         "Male Participants", "Mean sIPW (min, max)",
                         "Mean correlations > 0.1 (min, max)",
                         "+1 session [OR (95% CI)]"),
                       c("OLS", "",
                         bal_fem$`sIPW Distribution`[2],
                         bal_fem$`Correlation > 0.1`[2],
                         fem_fp$`Odds Ratio (95% Confidence Interval)`[1],
                         "",
                         bal_male$`sIPW Distribution`[2],
                         bal_male$`Correlation > 0.1`[2],
                         m_fp$`Odds Ratio (95% Confidence Interval)`[1]),
                       c("CBGPS", "",
                         bal_fem$`sIPW Distribution`[3],
                         bal_fem$`Correlation > 0.1`[3],
                         fem_fp$`Odds Ratio (95% Confidence Interval)`[2],
                         "",
                         bal_male$`sIPW Distribution`[3],
                         bal_male$`Correlation > 0.1`[3],
```

```
                    m_fp$`Odds Ratio (95% Confidence Interval)`[2]),
                  c("CPM", "",
                    bal_fem$`sIPW Distribution`[4],
                    bal_fem$`Correlation > 0.1`[4],
                    fem_fp$`Odds Ratio (95% Confidence Interval)`[3],
                    "",
                    bal_male$`sIPW Distribution`[4],
                    bal_male$`Correlation > 0.1`[4],
                    m_fp$`Odds Ratio (95% Confidence Interval)`[3]))
pdf("figs/fig6.pdf", height = 3.5, width = 7)
forestplot(tabletext,
           mean = bind_cols(c(rep(NA, 4), fem_fp$or[1], rep(NA, 3), m_fp$or[1]),
                            c(rep(NA, 4), fem_fp$or[2], rep(NA, 3), m_fp$or[2]),
                            c(rep(NA, 4), fem_fp$or[3], rep(NA, 3), m_fp$or[3])),
           lower = bind_cols(c(rep(NA, 4), fem_fp$or_lb[1], rep(NA, 3), m_fp$or_lb[1]),
                             c(rep(NA, 4), fem_fp$or_lb[2], rep(NA, 3), m_fp$or_lb[2]),
                             c(rep(NA, 4), fem_fp$or_lb[3], rep(NA, 3), m_fp$or_lb[3])),
           upper = bind_cols(c(rep(NA, 4), fem_fp$or_ub[1], rep(NA, 3), m_fp$or_ub[1]),
                             c(rep(NA, 4), fem_fp$or_ub[2], rep(NA, 3), m_fp$or_ub[2]),
                             c(rep(NA, 4), fem_fp$or_ub[3], rep(NA, 3), m_fp$or_ub[3])),
           is.summary = c(rep(TRUE, 2), rep(FALSE, 3),
                          TRUE, rep(FALSE, 3)),
           xlog = TRUE,
           xlab = "Adjusted Odds Ratio",
           boxsize = 0.15,
           col = fpColors(box = c("#606060", "#919191", "#C4C4C4"),
                          line = c("#606060", "#919191", "#C4C4C4")),
           align = "l",
           legend = c("OLS", "CBGPS", "CPM"),
           legend_args = fpLegend(pos = list(x = 0.85, y = 0.8)),
           vertices = TRUE,
           vertices.height = 0.05,
           txt_gp = fpTxtGp(cex=0.7,
                            label=gpar(fontfamily="Arial"),
                            ticks=gpar(cex=0.6),
                            xlab=gpar(cex=0.7)))
dev.off()
# embed the font
embed_fonts("figs/fig6.pdf")
```

Table 4 - Method Characteristics and Likelihood of Female Postpartum Contraceptive Uptake

```
kable(tabletext)
```

Session Info

```
sessionInfo()
```

```
R version 4.1.0 (2021-05-18)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS 12.4

Matrix products: default
BLAS:   /Library/Frameworks/R.framework/Versions/4.1-arm64/Resources/lib/libRblas.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.1-arm64/Resources/lib/libRlapack.dylib

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

attached base packages:
[1] grid      parallel  stats     graphics  grDevices utils     datasets
[8] methods   base

other attached packages:
 [1] ggeffects_1.1.1    rsvg_2.1.2         DiagrammeRsvg_0.1  DiagrammeR_1.0.6.1
 [5] forestplot_2.0.1   checkmate_2.0.0    magrittr_2.0.2     broom.mixed_0.2.7
 [9] gtable_0.3.0       gridExtra_2.3      table1_1.4.2       ggdist_3.0.0
[13] extrafont_0.17     doParallel_1.0.16  iterators_1.0.14   foreach_1.5.2
[17] ggpubr_0.4.0       kableExtra_1.3.4   lme4_1.1-27.1      Matrix_1.3-4
[21] cobalt_4.3.1       MatchThem_1.0.1    WeightIt_0.12.0    mice_3.13.0
[25] rms_6.2-0          SparseM_1.81       Hmisc_4.6-0        Formula_1.2-4
[29] survival_3.2-13    lattice_0.20-45    forcats_0.5.1      stringr_1.4.0
[33] dplyr_1.0.8        purrr_0.3.4        readr_2.0.2        tidyr_1.2.0
[37] tibble_3.1.6       ggplot2_3.3.5      tidyverse_1.3.1

loaded via a namespace (and not attached):
  [1] readxl_1.3.1         backports_1.3.0      systemfonts_1.0.3
  [4] plyr_1.8.6           splines_4.1.0        listenv_0.8.0
  [7] TH.data_1.1-0        digest_0.6.29        htmltools_0.5.2
 [10] magick_2.7.3         fansi_1.0.2          cluster_2.1.2
 [13] tzdb_0.2.0           recipes_0.1.17       globals_0.14.0
 [16] modelr_0.1.8         gower_0.2.2          matrixStats_0.61.0
 [19] extrafontdb_1.0      sandwich_3.0-1       svglite_2.0.0
 [22] jpeg_0.1-9           colorspace_2.0-3     rvest_1.0.2
 [25] mitools_2.4          haven_2.4.3          xfun_0.30
 [28] crayon_1.5.0         jsonlite_1.8.0       zoo_1.8-9
 [31] glue_1.6.2           ipred_0.9-12         webshot_0.5.2
 [34] MatrixModels_0.5-0   V8_3.6.0             distributional_0.2.2
 [37] car_3.0-12           Rttf2pt1_1.3.9       shape_1.4.6
 [40] future.apply_1.8.1   abind_1.4-5          scales_1.1.1
 [43] mvtnorm_1.1-3        DBI_1.1.1            rstatix_0.7.0
 [46] Rcpp_1.0.8.3         viridisLite_0.4.0    htmlTable_2.3.0
 [49] foreign_0.8-81       stats4_4.1.0         lava_1.6.10
 [52] survey_4.1-1         prodlim_2019.11.13   glmnet_4.1-2
 [55] htmlwidgets_1.5.4    httr_1.4.2           MatchIt_4.3.0
 [58] RColorBrewer_1.1-2   ellipsis_0.3.2       farver_2.1.0
 [61] pkgconfig_2.0.3      nnet_7.3-16          dbplyr_2.1.1
 [64] utf8_1.2.2           caret_6.0-90         labeling_0.4.2
 [67] tidyselect_1.1.2     rlang_1.0.2          reshape2_1.4.4
 [70] visNetwork_2.1.0     munsell_0.5.0        cellranger_1.1.0
 [73] tools_4.1.0          cli_3.2.0            generics_0.1.2
 [76] sjlabelled_1.1.8     broom_0.7.10         evaluate_0.15
```

```
 [79] fastmap_1.1.0        yaml_2.3.5           ModelMetrics_1.2.2.2
 [82] knitr_1.37           fs_1.5.2             future_1.23.0
 [85] nlme_3.1-153         quantreg_5.86        xml2_1.3.3
 [88] compiler_4.1.0       rstudioapi_0.13      curl_4.3.2
 [91] png_0.1-7            ggsignif_0.6.3       CBPS_0.22
 [94] reprex_2.0.1         stringi_1.7.6        nloptr_1.2.2.3
 [97] vctrs_0.3.8          pillar_1.7.0         lifecycle_1.0.1
[100] insight_0.14.5.1     cowplot_1.1.1        data.table_1.14.2
[103] conquer_1.2.1        R6_2.5.1             latticeExtra_0.6-29
[106] parallelly_1.28.1    codetools_0.2-18     polspline_1.1.19
[109] boot_1.3-28          MASS_7.3-54          assertthat_0.2.1
[112] withr_2.5.0          multcomp_1.4-17      hms_1.1.1
[115] rpart_4.1-15         timeDate_3043.102    class_7.3-19
[118] minqa_1.2.4          snakecase_0.11.0     rmarkdown_2.13
[121] carData_3.0-4        pROC_1.18.0          numDeriv_2016.8-1.1
[124] lubridate_1.8.0      base64enc_0.1-3
```

References

1. Audet CM, Graves E, Barreto E, et al. Partners-based HIV treatment for seroconcordant couples attending antenatal and postnatal care in rural Mozambique: A cluster randomized trial protocol. *Contemp Clin Trials*. 2018;71:63–69.
2. Kroenke K, Spitzer RL, Williams JB. The PHQ-9: Validity of a brief depression severity measure. *J Gen Intern Med* [electronic article]. 2001;16(9):606–13. (https://www.ncbi.nlm.nih.gov/pubmed/11556941)
3. Schulz U, Schwarzer R. Social support in coping with illness: The Berlin Social Support Scales (BSSS). *Diagnostica* [electronic article]. 2003;49(2):73–82. (://WOS:000182834400003)