Example analysis

Linear model, smoking is the exposure, birthweight in grams the outcome

```
infunc_confint <- function(ofit, wfit, exposurename, outcomename) {</pre>
  data <- ofit$data
  data1 <- data0 <- data
  data1[[exposurename]] <- 1</pre>
  data0[[exposurename]] <- 0</pre>
 n <- nrow(data1)</pre>
  est1f <- mean(predict(ofit, newdata = data1, type = "response"))</pre>
  estOf <- mean(predict(ofit, newdata = data0, type = "response"))</pre>
  # refit using unweighted eeqs
  ofitunwt <- glm(ofit$formula, family = ofit$family,
                  data = data)
  phat <- predict(wfit, type = "response")</pre>
  est1 <- predict(ofitunwt, newdata = data1, type = "response")</pre>
  est0 <- predict(ofitunwt, newdata = data0, type = "response")</pre>
  XXw <- model.matrix(wfit)</pre>
  XXo <- XXo1 <- XXo0 <- model.matrix(ofitunwt)</pre>
  XXo1[,exposurename] <- 1</pre>
  XXo0[,exposurename] <- 0</pre>
  ifweight <- t(vcov(wfit) %*% t(sandwich::estfun(wfit)))</pre>
```

```
ifout <- t(vcov(ofit) %*% t(sandwich::estfun(ofitunwt)))</pre>
  eifterms1 <- (data[[exposurename]] / phat * (data[[outcomename]] - est1) + (est1 - est1f
  eifterms0 <- ((1 - data[[exposurename]]) / (1 - phat) * (data[[outcomename]] - est0) + (</pre>
  hdot <- family(wfit)$mu.eta(predict(wfit, type = "link"))</pre>
  gdot0 <- family(ofit)$mu.eta(predict(ofitunwt, newdata = data0, type = "link"))</pre>
  gdot1 <- family(ofit)$mu.eta(predict(ofitunwt, newdata = data1, type = "link"))</pre>
  (data[[outcomename]] - est1), nrow = 1, ncol = n) %*%
  Kterm0 <- (1/n) * matrix((((1 - data[[exposurename]]) * hdot) / (1 - phat)^2) *
                             (data[[outcomename]] - est0), nrow = 1, ncol = n) %*%
    XXw
  Lterm1 <- (1/ n) * matrix(gdot1 * (1 - data[[exposurename]]/phat), nrow = 1, ncol = n) %
    XXo1
  Lterm0 <- (1/n) * matrix(gdot0 * ((1 - data[[exposurename]])/(1 - phat) - 1), nrow = 1,
    XX<sub>0</sub>0
  fullif1 <- cbind(eifterms1, (ifweight %*% t(Kterm1)), (ifout %*% t(Lterm1)))</pre>
  fullif0 <- cbind(eifterms0, (ifweight %*% t(Kterm0)), (ifout %*% t(Lterm0)))</pre>
  estse <- sqrt(sum((rowSums(fullif1) - rowSums(fullif0))^2))</pre>
  est <- est1f - est0f
  c(lower = est - 1.96 * estse, upper = est + 1.96 * estse)
}
data <- AF::clslowbwt
head(data)
                   race age lwt bwt
id birth smoke
                                        low lbw smoker
      1 1. Yes 3. Other 28 120 2865 0. No
```

```
3 2
         1 O. No 1. White 29 130 2613 O. No
4 2
         2 0. No 1. White 34 151 3125 0. No
                                                  0
                                                          0
5 2
         3 0. No 1. White 37 144 2481 1. Yes
                                                         0
         1 1. Yes 2. Black 31 187 1841 1. Yes
                                                          1
  ## propensity score fit
  pwfit <- glm(smoker ~ race * age * lwt + I(age^2) + I(lwt^2), data = data,</pre>
                family = "binomial")
  phat <- predict(pwfit, type = "response")</pre>
  data$weight <- data$smoker / phat + (1 - data$smoker) / (1 - phat)</pre>
  ## outcome model
  outfit <- glm(bwt \sim smoker * (race + age + lwt) + I(age^2) + I(lwt^2),
                 data = data, family = "gaussian", weights = weight)
  ## dummy data, where we set X to O and 1
  data0 <- data1 <- data
  dataO$smoker <- 0
  data1$smoker <- 1
  ## predicted couterfactuals
  Yhat0 <- predict(outfit, newdata = data0, type = "response")</pre>
  Yhat1 <- predict(outfit, newdata = data1, type = "response")</pre>
  ATEmean <- mean(Yhat1) - mean(Yhat0)
  ATEmean
[1] -223.6736
  infunc_confint(outfit, pwfit, "smoker", "bwt")
      lower
                  upper
-446.081852
              -1.265258
```

1

2 1. Yes 3. Other 33 141 2609 0. No

2 1

[1] -225.5489

Bootstrap for confidence interval, not echoed

```
2.5% 97.5% -387.12347 -46.48662
```

Logistic model, smoking is the exposure, low birthweight (birth weight $< 2500 \mathrm{g}$) the outcome

```
outfit <- glm(lbw ~ smoker * (race + age + lwt) + I(age<sup>2</sup>) + I(lwt<sup>2</sup>),
                 data = data, family = "binomial", weights = weight)
Warning in eval(family$initialize): non-integer #successes in a binomial glm!
  ## dummy data, where we set X to O and 1
  data0 <- data1 <- data
  data0$smoker <- 0
  data1$smoker <- 1
  ## predicted couterfactuals
  Yhat0 <- predict(outfit, newdata = data0, type = "response")</pre>
  Yhat1 <- predict(outfit, newdata = data1, type = "response")</pre>
  ATEmean <- mean(Yhat1) - mean(Yhat0)
  ATEmean
[1] 0.134932
  infunc_confint(outfit, pwfit, "smoker", "lbw")
       lower
                     upper
0.0009662041 0.2688977028
  RRmean <- mean(Yhat1) / mean(Yhat0)
  RRmean
[1] 1.478392
  ## separate outcome models, unweighted
  ofit1 <- glm(lbw \sim (race + age + lwt) + I(age^2) + I(lwt^2),
                 data = subset(data, smoker == 1), family = "binomial")
```

data = subset(data, smoker == 0), family = "binomial")

ofit0 <- $glm(lbw \sim (race + age + lwt) + I(age^2) + I(lwt^2)$,

```
dr1 <- data$lbw * (data$smoker == 1) / phat -
    predict(ofit1, newdata = data1, type = "response") *
    ((data$smoker == 1) - phat) / phat
dr0 <- data$lbw * (data$smoker == 0) / (1 - phat) +
    predict(ofit0, newdata = data0, type = "response") *
    ((data$smoker == 1) - phat) / (1 - phat)

ATEfunk <- mean(dr1) - mean(dr0)
RRfunk <- mean(dr1) / mean(dr0)
ATEfunk</pre>
```

[1] 0.1372512

RRfunk

[1] 1.488187

Bootstrap for confidence interval, not echoed

2.5% 97.5% 0.0279252 0.2411590

2.5% 97.5% 1.082286 2.004029