Supplementary Material 1. The R code used for the study analyses.

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R code used for study modeling
# Propensity score matching
library(Matchit)
m_out <-
  matchit(
    formula = rheumart ~
      age + sex + race_ethnicity + comobes + comsmok + sdi_decile,
    data         = M,
    method     = "nearest",
    m.order     = "random",
    ratio         = 1,
    replace      = FALSE,
    calcclosest  = FALSE,
    caliper       = 0.2,
    distance     = "logit")
# Propensity matched pairs
matches <- get_matches(m_out)
# Propensity Scores
propensity <- m_out[["distance"]]
# Propensity adjusted multilevel logistic regression
library(lme4)
model <-
  glmer(
    formula  =  m_h ~
        age              +   sex          + race_ethnicity + insurance    + sdi_decile +
        deyo_index   +   deyolung   + deyocvd          + deyockd     + deyochf    +
        dm               +   chrliver     + malign           + oftotal       + year         +
        procimvall     +   prochd      + procbld          + rheumart    + teaching    +
        infection       + comsmok    + comobes        + propensity  + (1|thcic_id),
    data          = M,
    family        = binomial,
    control       = glmerControl(
    optimizer   = "nloptwrap",
    optCtrl       = list(maxfun = 1e6)),
    start          = NULL,
    verbose       = 0L,
    nAGQ          = 0,
    contrasts     = NULL,
    devFunOnly = FALSE)

# 95% Confidence intervals for adjusted odds ratios and p values
sepsis_rheum       <- summary(model)
estimates_rheum <- sepsis_rheum$coefficients[, 1]
std_rheum           <- sepsis_rheum$coefficients[, 2]
p_value_rheum     <- sepsis_rheum$coefficients[, 4]

M_rheum <-
  tibble(
    name    = rownames(sepsis_rheum$coefficients),
    L         = round(exp(estimates_rheum - 1.96 * std_rheum), digits = 4),
    OR       = round(exp(estimates_rheum), digits = 4),
    U         = round(exp(estimates_rheum + 1.96 * std_rheum), digits = 4),
    p_value = round(p_value_rheum, digits = 4))

## Display confidence intervals
M_rheum %>% kable(align = c("l", "c", "c", "c"))
## Write results to csv
write_csv(x = M_rheum, path = "mllr_rheum_all.csv")
```

```
# Multivariable logistic regression without propensity adjustment
model_glm <-
  glm(
    formula  =  m_h ~
        age             +   sex          + race_ethnicity + insurance   + sdi_decile +
        deyo_index   +   deyolung  + deyocvd         + deyockd     + deyochf   +
        dm              +   chrliver     + malign          + oftotal       + year        +
        procimvall    +   prochd     + procbld         + rheumart    + teaching   +
        infection       + comsmok    + comobes,
    family    = binomial,
    data      = M)
```