

Appendix 1: Details of estimation procedure

Our final analysis was comprised of one estimation for each condition-race-outcome triple, or 3 conditions * 2 outcomes * 2 race/ethnicities (hereafter “Minority”) = 12 models. The mixed logistic was estimated in Stata 10.0 (College Station, TX) using the **xtmelogit** command. Thus, the procedure for each model was as follows:

1. Estimate the mixed logistic model, including the specified covariates as well as a race indicator, saving the coefficient estimates and associated variance-covariance matrix for the “fixed effect” estimates and the Bayesian (modal) estimate for the hospital-specific random effects (and associated estimated standard errors).
2. Replicate the following loop 1000 times:
 - a. Perform a parametric bootstrap of the coefficients using the fixed effect (regression parameter) variance-covariance matrix (using Stata’s **drawnorm**) and the hospital-specific random intercepts using the Bayesian estimate and the estimated standard errors (in the latter case, ensuring the same replicated value is drawn for all subjects discharged from the same hospital). Both the regression estimates and random intercepts are assumed to be distributed normally.
 - b. Sample (with replacement) from the sample of Whites a number equal to the number of Minorities
 - c. Calculate predicted probabilities based on the parameter estimates, including the hospital-specific random effects, but ignoring the race coefficient (treating all as White)
 - d. Sort the White and Minority sample by predicted probability, and match observations based on their percentile (e.g. the White with the smallest predicted probability is matched to the Minority with the smallest predicted probability; the White with the

second lowest predicted probability is matched to the Minority with the second lowest predicted probability, etc.)

- e. Randomize the order of the included variables (including hospital-specific random effect). That is, of the $k+1$ variables used as covariates (including the hospital-specific random intercept), place the variable names in random order (e.g. age, diabetes comorbidity, nonmetro location, female, PTs per resident of the county, etc.). (This step is necessary because the order of the allocation will determine the estimated magnitude of the adjustment due to the variable; reordering at each replicate minimizes this effect.)
 - f. For each variable, perform the following loop:
 - i. Assign the value of the variable of the Minority subject to its matched White subject
 - ii. Recalculate the predicted probability for the White subject
 - iii. Calculate the difference in predicted probability due to the “allocation” of this variable
3. Compute the sum of decomposition effects for a given domain of characteristics (e.g. clinical characteristics)
 4. Calculate the average of the sums
 5. Determine statistical significance using 2.5th and 97.5th percentiles of the bootstrapped values of the individual variables and the variable domain (e.g. clinical characteristics)