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| Table 1. Comparison Between One at a Time and Vectorized Approach | |
| One at a time approach | Vectorized approach |
| biomarker <- function(  m\_ind\_traits,  a\_coef\_ukpds\_ind\_traits,  biomarker\_eq,  time\_step) {    # Calculate patient-specific factors using model coefficients and patient data  updated\_biomarker <- (m\_ind\_traits[max(1,time\_step-1),] %\*% a\_coef\_ukpds\_ind\_traits[, biomarker\_eq, 1] +  a\_coef\_ukpds\_other\_ind\_traits["lambda", biomarker\_eq, 1] )    return(updated\_biomarker)  } | biomarker <- function(  m\_ind\_traits,  a\_coef\_ukpds\_ind\_traits,  a\_coef\_ukpds\_other\_ind\_traits,  biomarker\_eq) {    # Calculate patient-specific factors using model coefficients and patient data  m\_updated\_biomarker <- m\_ind\_traits %\*%  a\_coef\_ukpds\_ind\_traits[, biomarker\_eq, 1] +  a\_coef\_ukpds\_other\_ind\_traits["lambda", biomarker\_eq, 1]    return(m\_updated\_biomarker)  } |