# Based on Van Krugten et al., Medical Decision Making, 2023.

# Create new variable NL\_MHQOL

# If data is missing for one of the individual dimensions, set NL\_MHQOL to missing

# Otherwise set to 1

MHQOL <- MHQOL %>%

 mutate(NL\_MHQOL = ifelse(

 is.na(MHQOL\_SI) |

 is.na(MHQOL\_ID) |

 is.na(MHQOL\_MO) |

 is.na(MHQOL\_RE) |

 is.na(MHQOL\_DA) |

 is.na(MHQOL\_PH) |

 is.na(MHQOL\_FU),

 NA, #value if true, NA

 1)) #value if false, set to 1

# Assign values manually

# As levels 2, 3 and 4 are worse than 1, subtract specified value from existing NL\_MHQOL value

# Consecutively do so for every dimension

MHQOL <- MHQOL %>%

 mutate(NL\_MHQOL = case\_when(

 MHQOL\_SI == 1 ~ NL\_MHQOL,

 MHQOL\_SI == 2 ~ NL\_MHQOL - .0070746,

 MHQOL\_SI == 3 ~ NL\_MHQOL - .13724,

 MHQOL\_SI == 4 ~ NL\_MHQOL - .21064))

MHQOL <- MHQOL %>%

 mutate(NL\_MHQOL = case\_when(

 MHQOL\_ID == 1 ~ NL\_MHQOL,

 MHQOL\_ID == 2 ~ NL\_MHQOL - .017728,

 MHQOL\_ID == 3 ~ NL\_MHQOL - .11807,

 MHQOL\_ID == 4 ~ NL\_MHQOL - .18415))

MHQOL <- MHQOL %>%

 mutate(NL\_MHQOL = case\_when(

 MHQOL\_MO == 1 ~ NL\_MHQOL,

 MHQOL\_MO == 2 ~ NL\_MHQOL - .062768,

 MHQOL\_MO == 3 ~ NL\_MHQOL - .17946,

 MHQOL\_MO == 4 ~ NL\_MHQOL - .31055))

MHQOL <- MHQOL %>%

 mutate(NL\_MHQOL = case\_when(

 MHQOL\_RE == 1 ~ NL\_MHQOL,

 MHQOL\_RE == 2 ~ NL\_MHQOL - .015094,

 MHQOL\_RE == 3 ~ NL\_MHQOL - .1721,

 MHQOL\_RE == 4 ~ NL\_MHQOL - .26913))

MHQOL <- MHQOL %>%

 mutate(NL\_MHQOL = case\_when(

 MHQOL\_DA == 1 ~ NL\_MHQOL,

 MHQOL\_DA == 2 ~ NL\_MHQOL - .021342,

 MHQOL\_DA == 3 ~ NL\_MHQOL - .14039,

 MHQOL\_DA == 4 ~ NL\_MHQOL - .21338))

MHQOL <- MHQOL %>%

 mutate(NL\_MHQOL = case\_when(

 MHQOL\_PH == 1 ~ NL\_MHQOL,

 MHQOL\_PH == 2 ~ NL\_MHQOL - .06381,

 MHQOL\_PH == 3 ~ NL\_MHQOL - .24316,

 MHQOL\_PH == 4 ~ NL\_MHQOL - .38251))

MHQOL <- MHQOL %>%

 mutate(NL\_MHQOL = case\_when(

 MHQOL\_FU == 1 ~ NL\_MHQOL,

 MHQOL\_FU == 2 ~ NL\_MHQOL,

 MHQOL\_FU == 3 ~ NL\_MHQOL - .10564,

 MHQOL\_FU == 4 ~ NL\_MHQOL - .17028

 ))

# See summary statistics

MHQOL %>% summary()