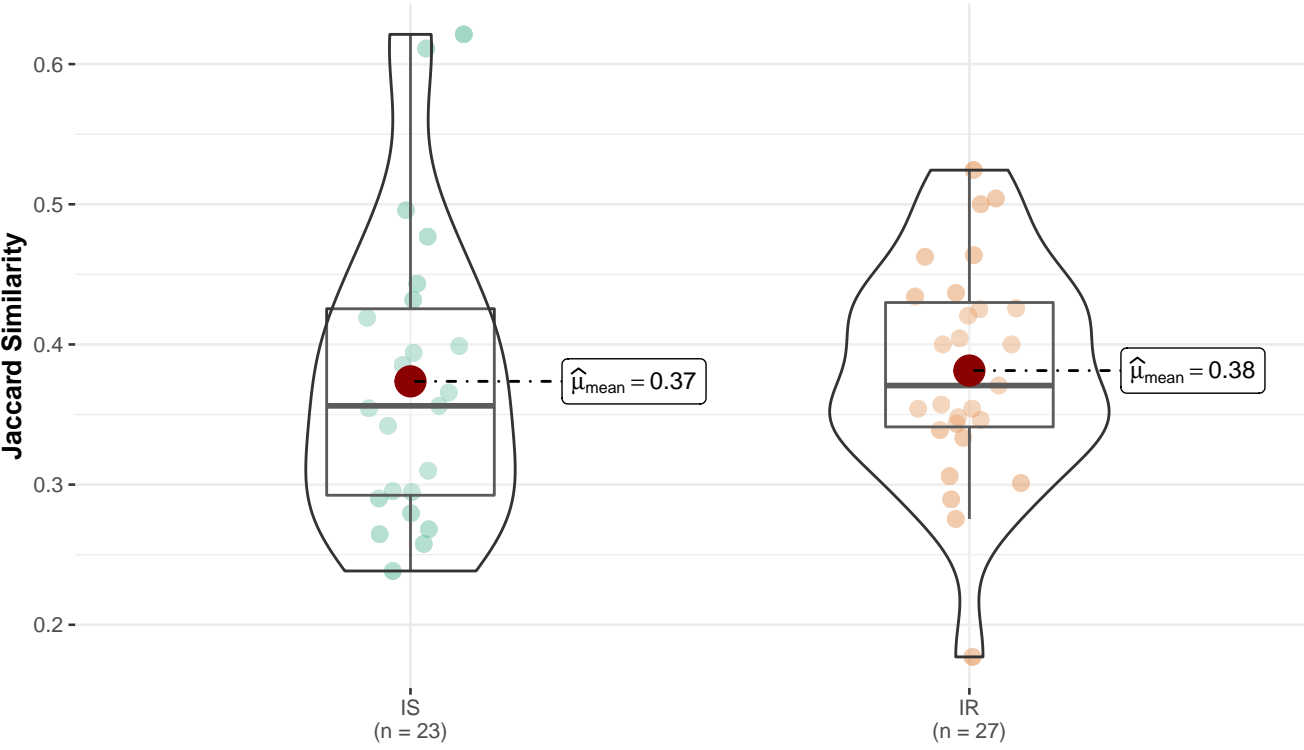


Stool Microbiome

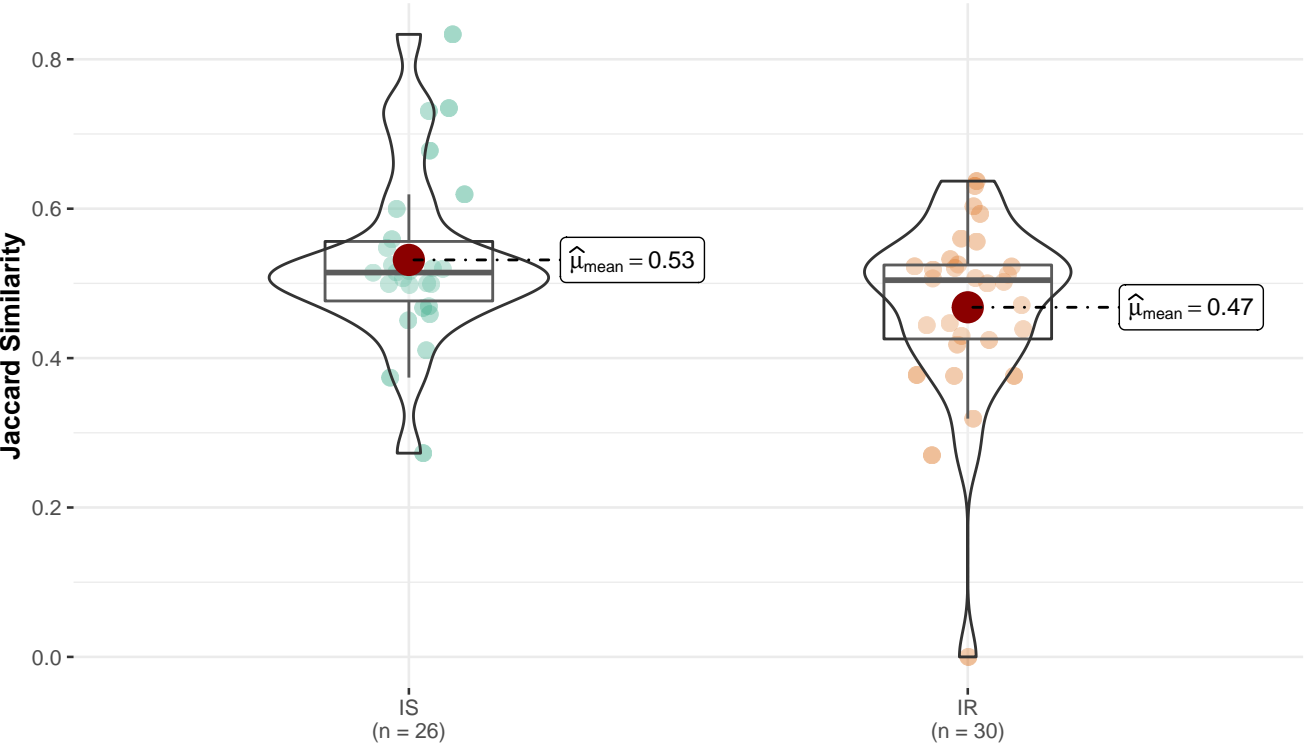
$t_{\text{Welch}}(40.07) = -0.29, p = 0.77, \hat{g}_{\text{Hedges}} = -0.08, \text{CI}_{95\%} [-0.63, 0.47], n_{\text{obs}} = 50$



$\log_e(\text{BF}_{01}) = 1.22, \hat{\sigma}_{\text{difference}}^{\text{posterior}} = -5.71\text{e-}03, \text{CI}_{95\%}^{\text{HDI}} [-0.05, 0.04], r_{\text{Cauchy}}^{\text{JZS}} = 0.71$

Skin Microbiome

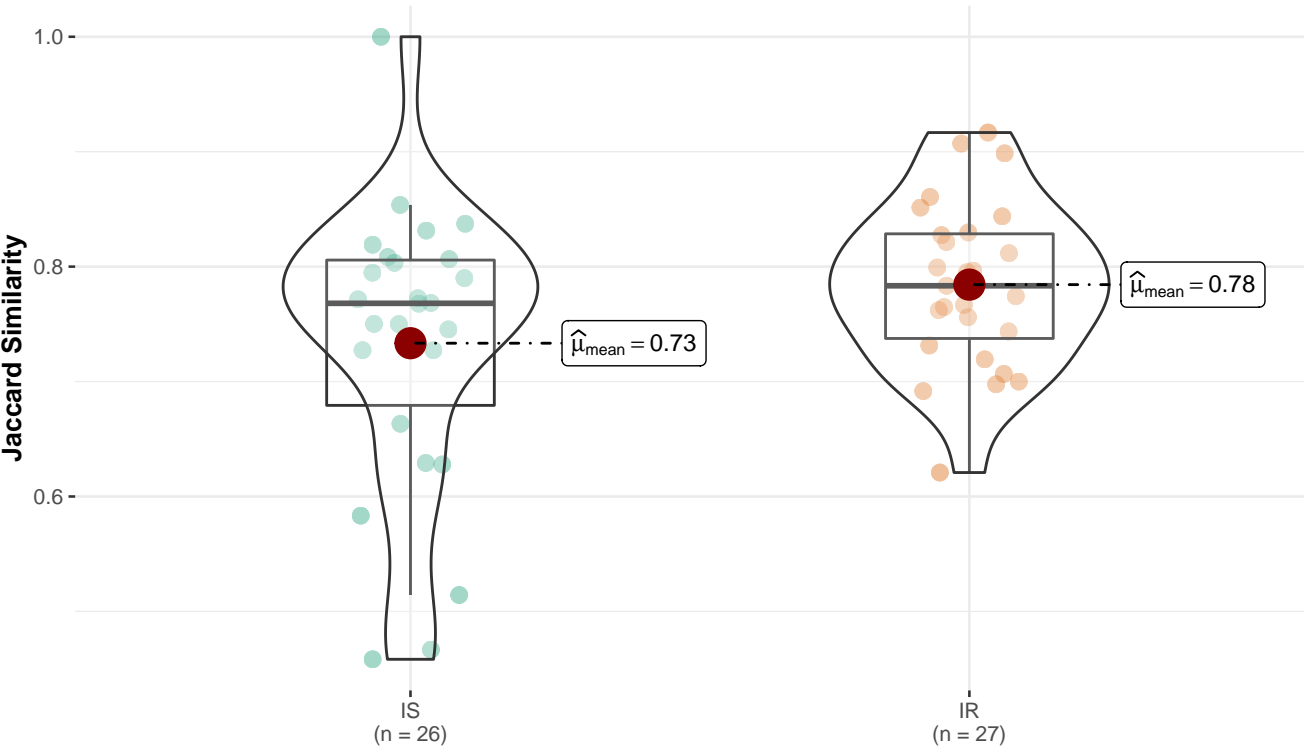
$t_{\text{Welch}}(53.61) = 1.97, p = 0.05, \hat{g}_{\text{Hedges}} = 0.52, \text{CI}_{95\%} [-7.85\text{e-}03, 1.04], n_{\text{obs}} = 56$



$\log_e(\text{BF}_{01}) = -0.27, \hat{\sigma}_{\text{difference}}^{\text{posterior}} = 0.05, \text{CI}_{95\%}^{\text{HDI}} [-5.56\text{e-}03, 0.12], r_{\text{Cauchy}}^{\text{JZS}} = 0.71$

Oral Microbiome

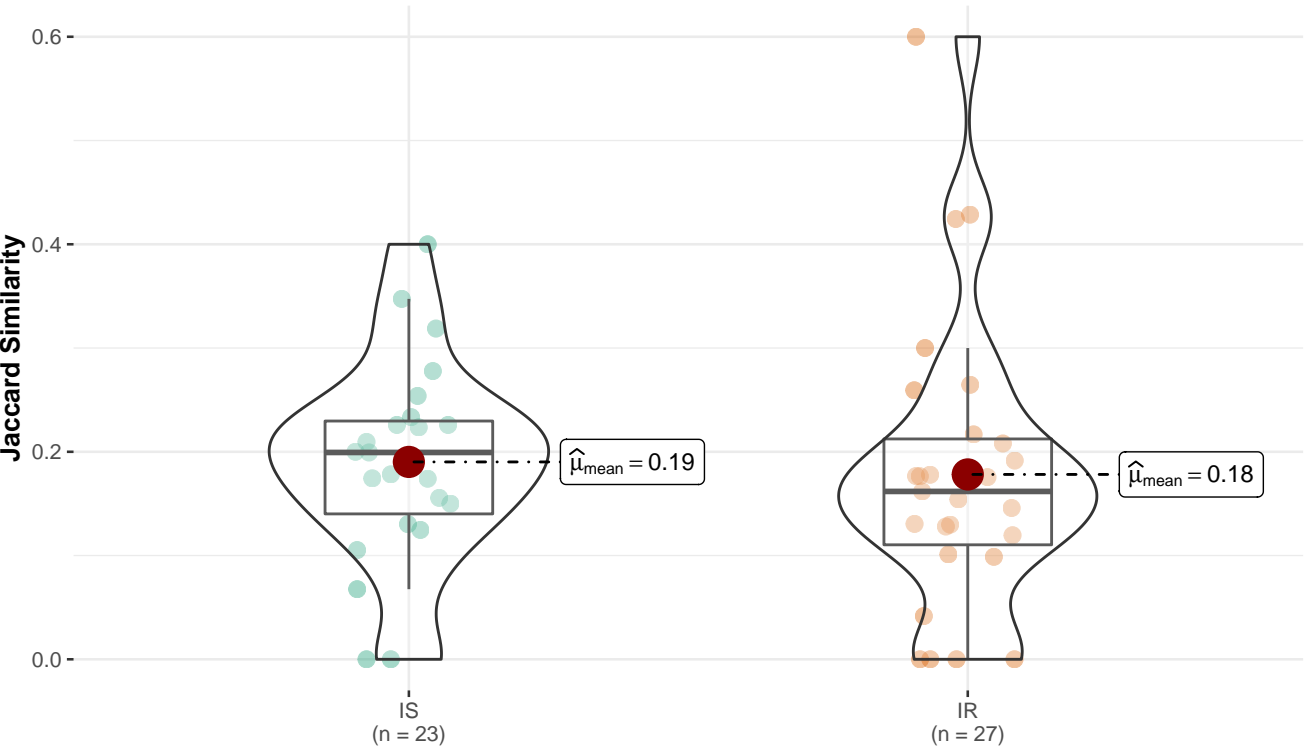
$t_{\text{Welch}}(39.58) = -1.82, p = 0.08, \hat{g}_{\text{Hedges}} = -0.49, \text{CI}_{95\%} [-1.03, 0.05], n_{\text{obs}} = 53$



$\log_e(\text{BF}_{01}) = -0.09, \hat{\sigma}_{\text{difference}}^{\text{posterior}} = -0.04, \text{CI}_{95\%}^{\text{HDI}} [-0.10, 8.45\text{e-}03], r_{\text{Cauchy}}^{\text{JZS}} = 0.71$

Nasal Microbiome

$t_{\text{Welch}}(46.39) = 0.36, p = 0.72, \hat{g}_{\text{Hedges}} = 0.10, \text{CI}_{95\%} [-0.44, 0.64], n_{\text{obs}} = 50$



$\log_e(\text{BF}_{01}) = 1.21, \hat{\sigma}_{\text{difference}}^{\text{posterior}} = 0.01, \text{CI}_{95\%}^{\text{HDI}} [-0.05, 0.07], r_{\text{Cauchy}}^{\text{JZS}} = 0.71$