Model reporting template

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Contents

Table 1: CAPTION A

Parameter	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Group-Level Effects:							
fkClientID (Number of levels: 1034)							
sd(Intercept)	0.27	0.01	0.25	0.29	1.01	1 218	2 564
Population-Level Effects:							
Intercept	0.91	0.08	0.76	1.07	1.00	2 860	4 477
PHQ9_baseline	-7.73	0.17	-8.06	-7.38	1.00	2 643	4 098
PHQ9_change	-4.48	0.22	-4.90	-4.05	1.00	2 872	5 188
SOFAS_baseline	0.02	0.12	-0.20	0.25	1.00	2 874	4 790
SOFAS_change	1.04	0.14	0.77	1.31	1.00	4 486	5 491
Family Specific Parameters:							
sigma	0.26	0.01	0.24	0.27	1.00	1 317	3 036

Formula: aqol6d_total_w_cloglog ~PHQ9_baseline + PHQ9_change + SOFAS_baseline + SOFAS_change + (1 | fkClientID)

Family: gaussian

Links: mu = identity; sigma = identity

Data: data_tb (Number of observations: 1651)

Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;

total post-warmup samples = 8000

Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS

and Tail_ESS are effective sample size measures, and Rhat is the potential

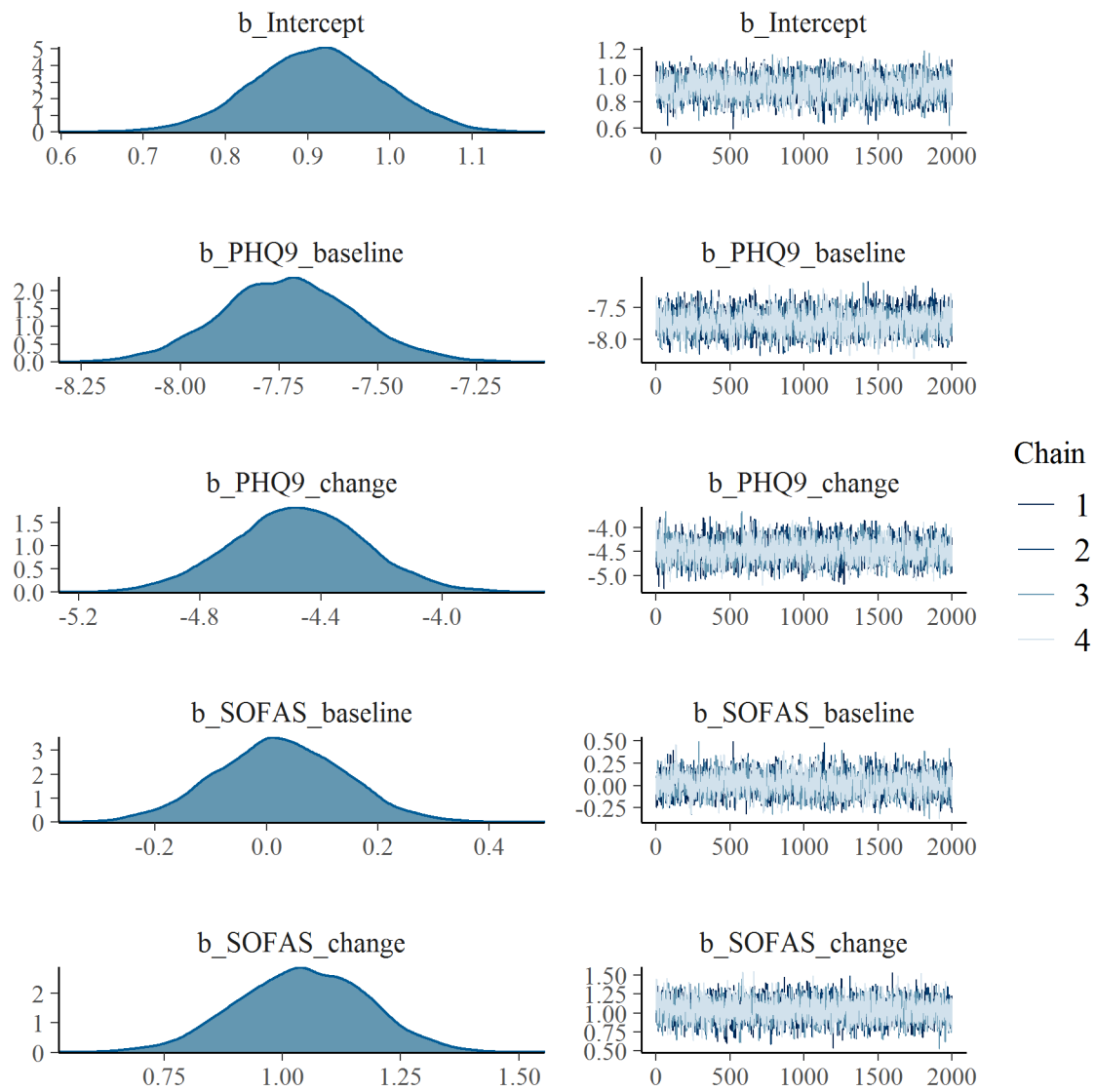scale reduction factor on split chains (at convergence, Rhat = 1).
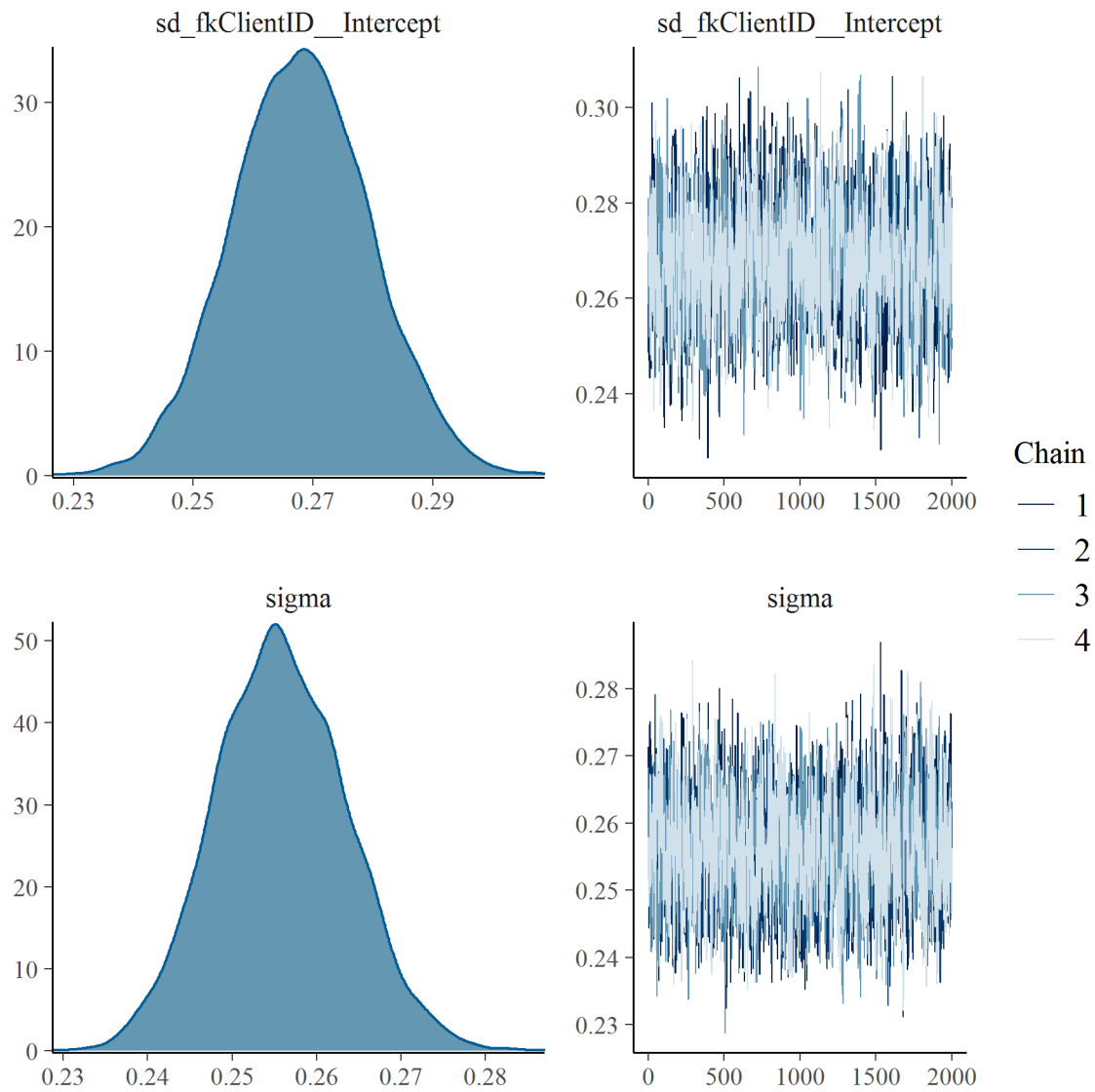
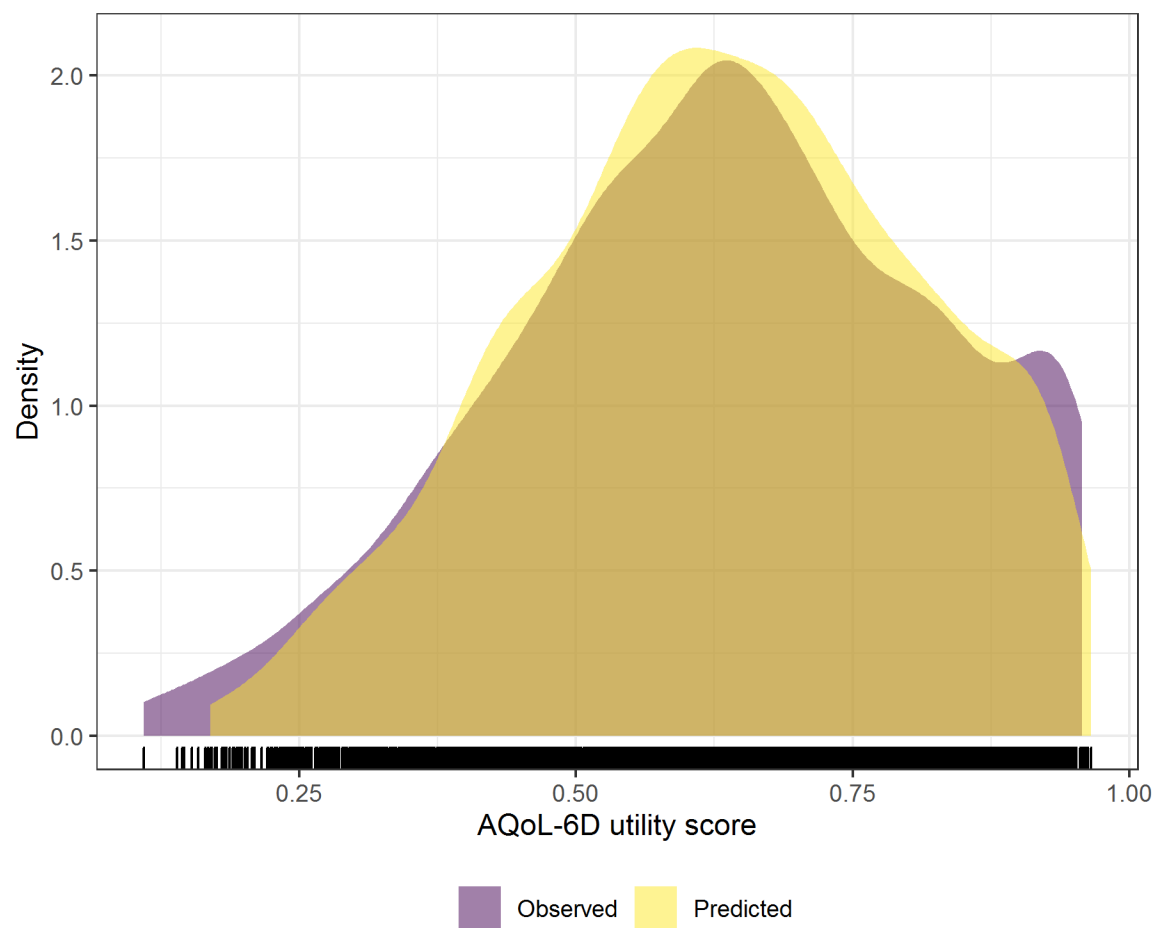Figure 1: Caption A

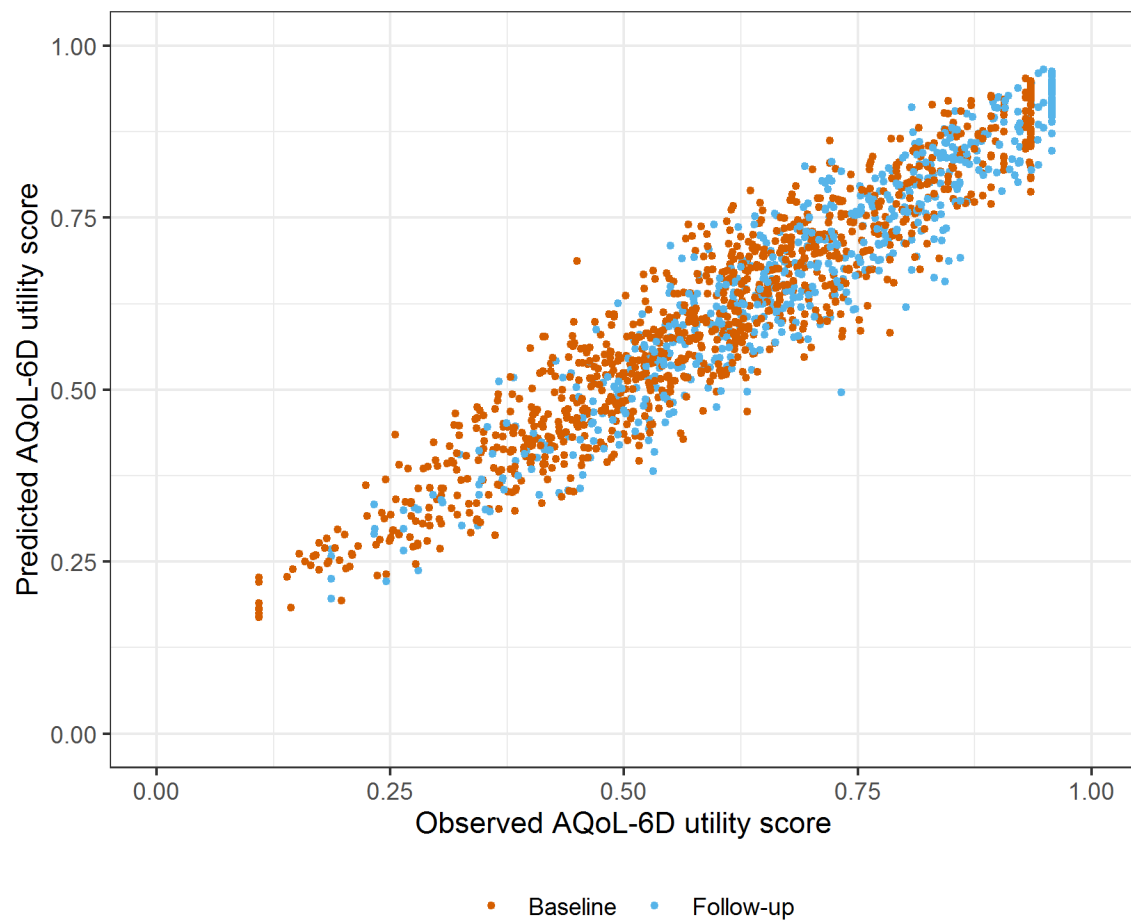Figure 2: Caption B

Figure 3: Caption C

Figure 4: Caption D

Table 2: CAPTION B

Parameter	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Group-Level Effects:							
fkClientID (Number of levels: 1034)							
sd(Intercept)	0.10	0.01	0.08	0.12	1.00	599	1 106
Population-Level Effects:							
Intercept	-0.03	0.04	-0.11	0.04	1.00	4 700	5 335
PHQ9_baseline	-3.86	0.08	-4.03	-3.70	1.00	3 647	4 904
PHQ9_change	-2.45	0.13	-2.70	-2.20	1.00	1 342	3 300
SOFAS_baseline	0.01	0.06	-0.10	0.12	1.00	4 767	5 393
SOFAS_change	0.41	0.07	0.27	0.55	1.00	6 621	6 049
Family Specific Parameters:							
sigma	0.10	0.00	0.09	0.10	1.01	661	1 473

Formula: aqol6d_total_w ~PHQ9_baseline + PHQ9_change + SOFAS_baseline + SOFAS_change + (1 | fkClientID)

Family: gaussian

Links: mu = log; sigma = identity

Data: data_tb (Number of observations: 1651)

Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;

total post-warmup samples = 8000

Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
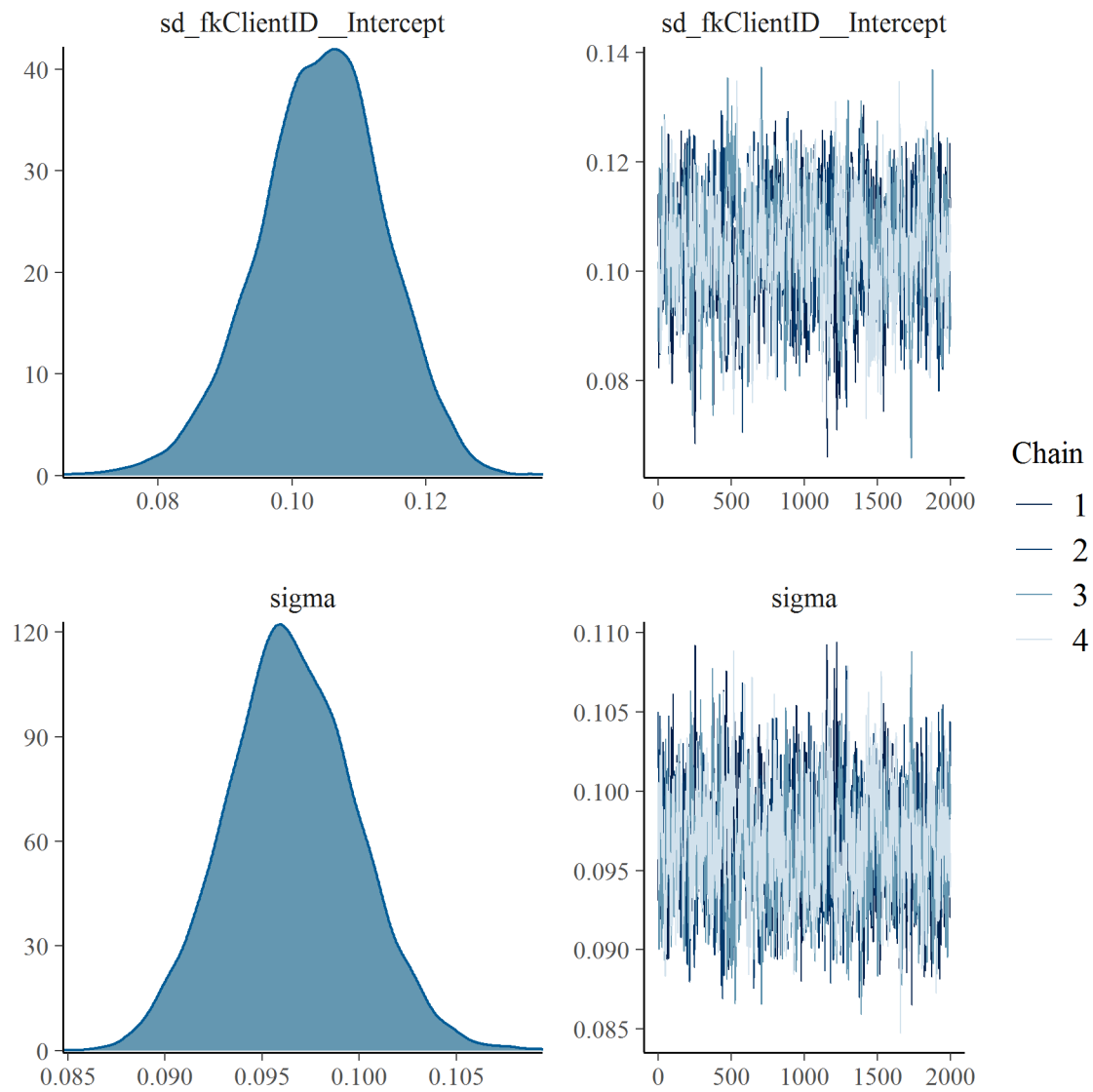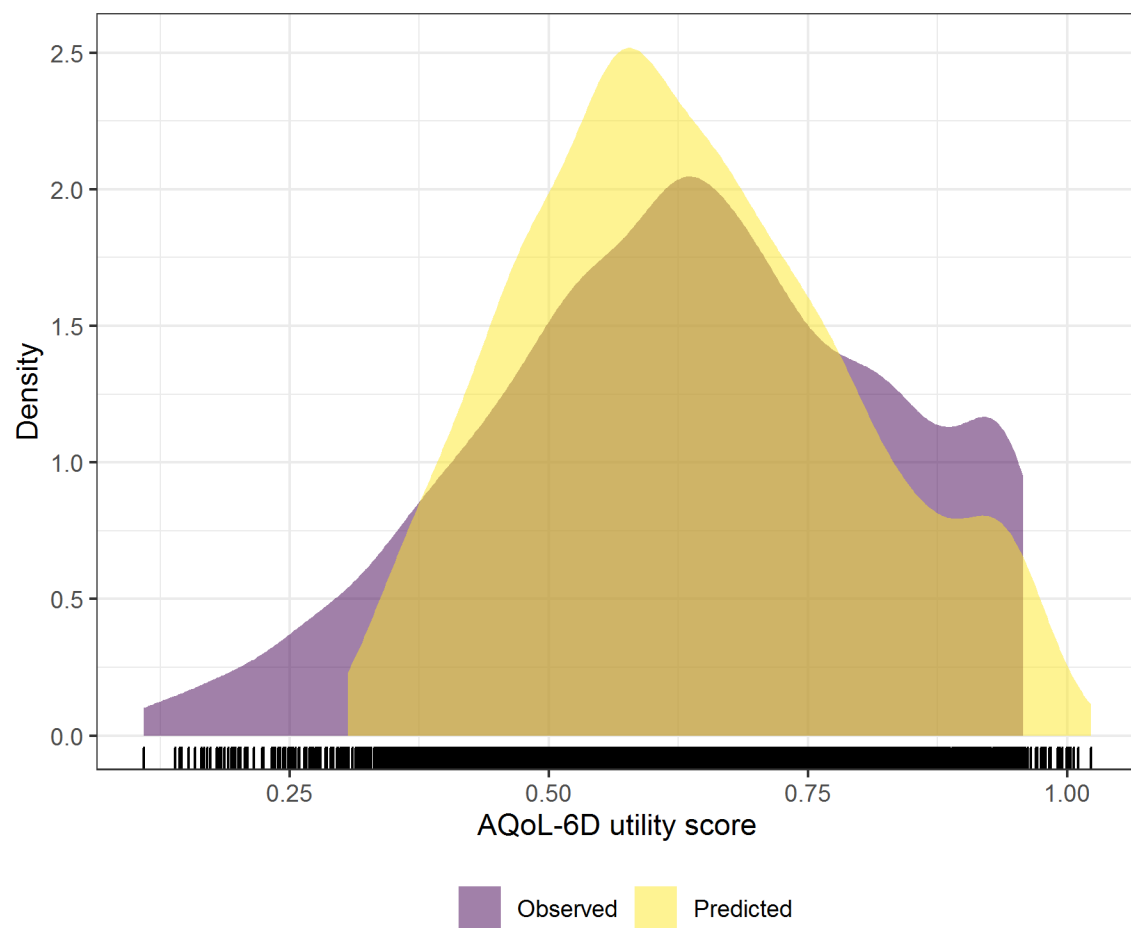scale reduction factor on split chains (at convergence, Rhat = 1).
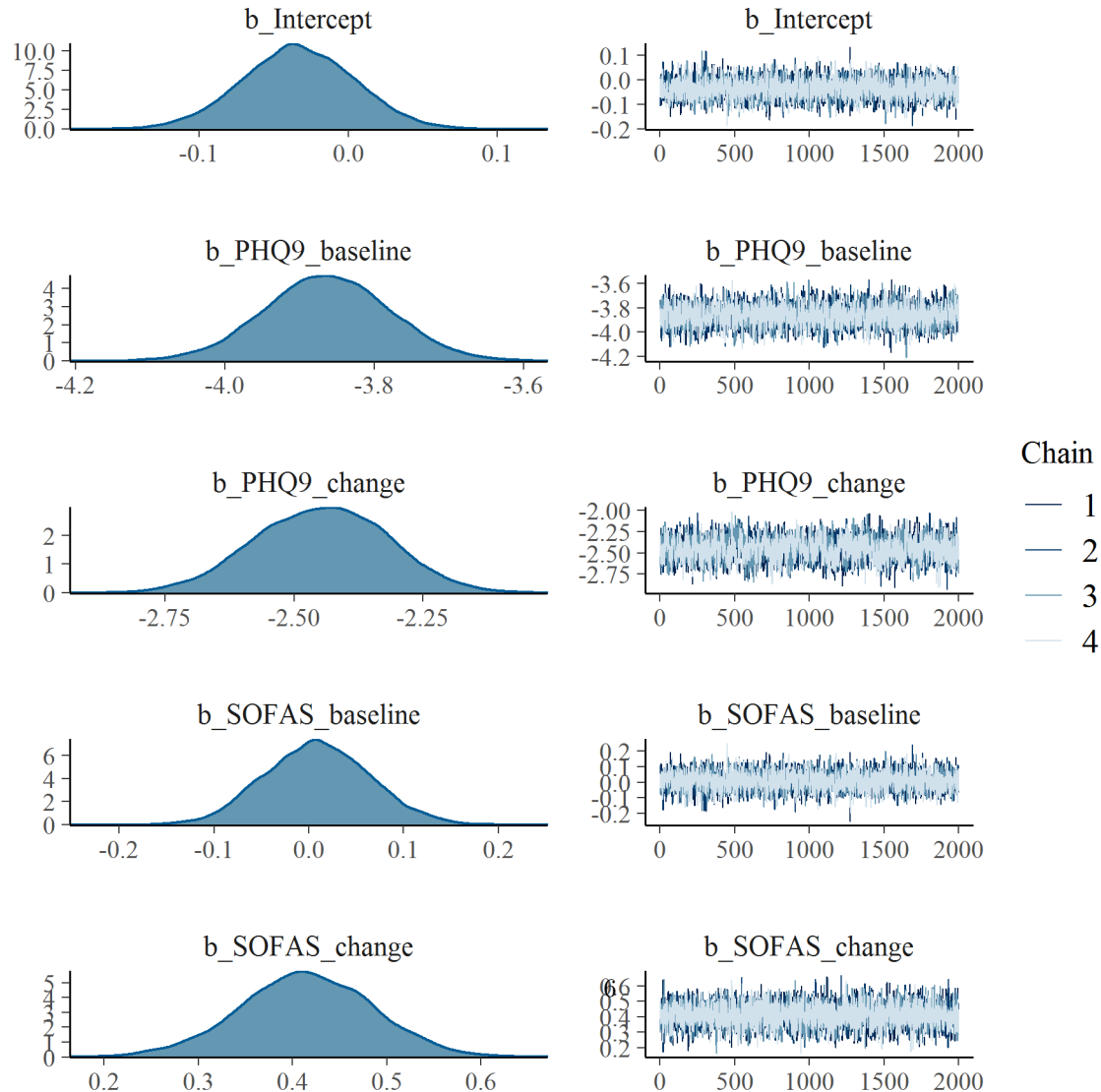
Figure 6: Caption 2
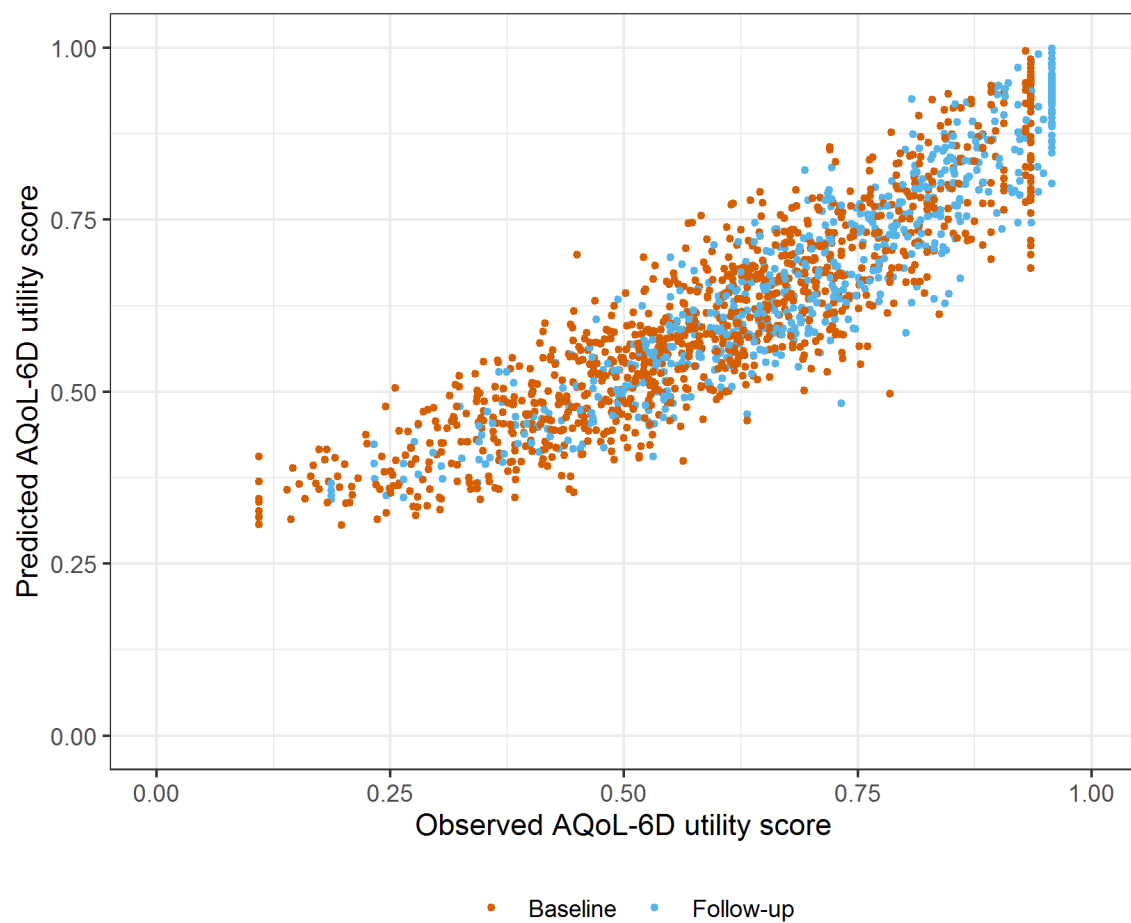
Figure 7: Caption 3

Figure 8: Caption 4