

The influence of polarity items on inferential judgments

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Statistical analyses

NPI vs. no PI in NM environments

#contrast coding: N:1, O:-1

Experiment 1

Full model

```
a1 = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ PI+ Increasing+ Quantifier| subject),
  iter = 8000, data = a1df, save_pars = save_pars(all = TRUE))
summary(a1)
```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content) + (1 + PI + Increasing + Quantifier | subject)

Data: a1df (Number of observations: 1872)

Samples: 4 chains, each with iter = 8000; warmup = 4000; thin = 1;
total post-warmup samples = 16000

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	1.14	0.80	0.05	2.97	1.00	5820	7459
sd(PI1)	0.74	0.59	0.03	2.20	1.00	8312	7363
sd(Quantifier1)	0.84	0.65	0.03	2.40	1.00	7121	6586
sd(Increasing1)	0.92	0.69	0.04	2.58	1.00	8565	7873
cor(Intercept,PI1)	0.03	0.45	-0.80	0.83	1.00	18658	11387
cor(Intercept,Quantifier1)	0.02	0.44	-0.79	0.81	1.00	16253	11606
cor(PI1,Quantifier1)	-0.07	0.44	-0.84	0.77	1.00	13045	12659
cor(Intercept,Increasing1)	-0.01	0.45	-0.81	0.81	1.00	17443	11992
cor(PI1,Increasing1)	-0.03	0.45	-0.83	0.81	1.00	13458	12187
cor(Quantifier1,Increasing1)	0.06	0.44	-0.78	0.83	1.00	13489	13446

~subject (Number of levels: 66)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	9.79	1.01	7.98	11.97	1.00	4646	7845
sd(PI1)	1.55	0.88	0.08	3.34	1.00	1906	2526
sd(Increasing1)	19.26	1.80	16.09	23.15	1.00	5739	8872
sd(Quantifier1)	1.50	0.82	0.10	3.18	1.00	3465	4837

```

cor(Intercept,PI1)          -0.13    0.33   -0.74    0.54 1.00   14372   7414
cor(Intercept,Increasing1) -0.52    0.10   -0.70   -0.30 1.00   5558   8558
cor(PI1,Increasing1)        0.35    0.32   -0.42    0.86 1.00    693   1018
cor(Intercept,Quantifier1)  0.42    0.31   -0.32    0.90 1.00   12705   9185
cor(PI1,Quantifier1)        -0.25    0.41   -0.89    0.65 1.00   5359   9102
cor(Increasing1,Quantifier1) -0.23    0.31   -0.79    0.45 1.00   18380  10655

```

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	57.73	1.37	54.95	60.41	1.00	3122	6090
PI1	-2.18	0.61	-3.37	-1.00	1.00	16171	11829
Quantifier1	2.37	0.62	1.14	3.58	1.00	15401	11337
Increasing1	14.47	2.40	9.73	19.26	1.00	4732	7557

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	21.20	0.37	20.49	21.95	1.00	19256	11886

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`).

Probability that the presence of NPI lowers the directional ratings

```

post_samples_a1 = posterior_samples(a1)
mean(post_samples_a1$b_PI1 < 0)
[1] 0.99975

```

Experiment 2

Full model

```

b1 = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ PI+ Increasing+ Quantifier| subject),
  data = b1df,
  iter = 12000, save_pars = save_pars(all = TRUE), control = list(max_treedepth = 15))
summary(b1)

```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content) + (1 + PI + Increasing + Quantifier | subject)

Data: b1df (Number of observations: 1722)

Samples: 4 chains, each with iter = 12000; warmup = 6000; thin = 1; total post-warmup samples = 24000

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	0.64	0.52	0.02	1.91	1.00	14092	10361
sd(PI1)	0.65	0.53	0.02	1.98	1.00	14031	11187
sd(Quantifier1)	0.78	0.61	0.03	2.24	1.00	12020	11361

```
sd(Increasing1)          2.03      1.02      0.25      4.30 1.00      9230      7190
cor(Intercept,PI1)      -0.00      0.45     -0.81      0.81 1.00     26950     16950
cor(Intercept,Quantifier1) -0.00      0.45     -0.82      0.81 1.00     21261     16929
cor(PI1,Quantifier1)     -0.01      0.45     -0.81      0.81 1.00     20956     18669
cor(Intercept,Increasing1) -0.09      0.45     -0.85      0.77 1.00      9096     13639
cor(PI1,Increasing1)      0.05      0.44     -0.78      0.83 1.00     11234     15923
cor(Quantifier1,Increasing1) -0.16      0.43     -0.87      0.72 1.00     11391     16752
```

~subject (Number of levels: 64)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	12.40	1.25	10.20	15.09	1.00	5512	9566
sd(PI1)	1.71	0.84	0.16	3.39	1.00	3625	5377
sd(Increasing1)	20.85	2.02	17.31	25.20	1.00	6936	12436
sd(Quantifier1)	1.52	0.93	0.08	3.44	1.00	4374	7029
cor(Intercept,PI1)	-0.45	0.29	-0.90	0.23	1.00	16760	11926
cor(Intercept,Increasing1)	-0.27	0.13	-0.50	-0.01	1.00	6125	9919
cor(PI1,Increasing1)	0.27	0.31	-0.40	0.82	1.01	457	1210
cor(Intercept,Quantifier1)	0.17	0.33	-0.56	0.77	1.00	19631	11876
cor(PI1,Quantifier1)	-0.11	0.41	-0.83	0.71	1.00	6475	11165
cor(Increasing1,Quantifier1)	0.16	0.33	-0.57	0.77	1.00	22856	12599

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	57.43	1.67	54.07	60.76	1.00	3488	6374
PI1	-2.25	0.63	-3.48	-1.02	1.00	21008	17400
Quantifier1	2.72	0.63	1.47	3.97	1.00	24052	17590
Increasing1	10.55	2.77	5.08	15.97	1.00	5810	9937

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	21.48	0.39	20.73	22.27	1.00	25759	17317

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`).

Probability that the presence of NPI lowers the directional ratings

```
post_samples_b1 = posterior_samples(b1)
mean(post_samples_b1$b_PI1 < 0)
[1] 0.9993333
```

Experiment 3

Full model

```
c1 = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ PI+ Increasing+ Quantifier| subject),
  data = cldf,
  iter = 8000, save_pars = save_pars(all = TRUE))
summary(c1)
```

```

Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content)
+ (1 + PI + Increasing + Quantifier | subject)
Data: c1df (Number of observations: 2425)
Samples: 4 chains, each with iter = 8000; warmup = 4000; thin = 1;
         total post-warmup samples = 16000

```

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	1.03	0.70	0.05	2.68	1.00	6313	6414
sd(PI1)	1.11	0.74	0.05	2.81	1.00	4740	6125
sd(Quantifier1)	0.80	0.61	0.03	2.28	1.00	7435	6447
sd(Increasing1)	2.60	0.95	1.07	4.81	1.00	7968	7188
cor(Intercept,PI1)	0.02	0.43	-0.79	0.80	1.00	10352	10623
cor(Intercept,Quantifier1)	0.02	0.44	-0.80	0.81	1.00	16256	11994
cor(PI1,Quantifier1)	-0.01	0.44	-0.82	0.81	1.00	15220	12654
cor(Intercept,Increasing1)	-0.21	0.41	-0.87	0.65	1.00	5182	7669
cor(PI1,Increasing1)	0.29	0.40	-0.60	0.90	1.00	5930	7747
cor(Quantifier1,Increasing1)	-0.07	0.42	-0.82	0.75	1.00	8123	11854

~subject (Number of levels: 91)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	10.60	0.95	8.88	12.60	1.00	4471	8416
sd(PI1)	1.56	0.74	0.17	3.05	1.00	2522	2107
sd(Increasing1)	19.14	1.53	16.42	22.42	1.00	6058	9545
sd(Quantifier1)	2.37	0.85	0.55	3.92	1.00	3131	2669
cor(Intercept,PI1)	0.27	0.29	-0.39	0.77	1.00	13209	7608
cor(Intercept,Increasing1)	-0.31	0.11	-0.50	-0.09	1.00	6363	8921
cor(PI1,Increasing1)	0.33	0.28	-0.29	0.82	1.01	580	805
cor(Intercept,Quantifier1)	0.39	0.23	-0.06	0.82	1.00	9161	7230
cor(PI1,Quantifier1)	0.15	0.38	-0.64	0.81	1.00	2054	4215
cor(Increasing1,Quantifier1)	-0.24	0.23	-0.68	0.22	1.00	14872	9929

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	56.10	1.27	53.61	58.60	1.00	3405	5824
PI1	-1.11	0.62	-2.35	0.11	1.00	14245	11182
Quantifier1	2.76	0.60	1.60	3.94	1.00	13609	10769
Increasing1	17.39	2.21	13.07	21.75	1.00	6364	8721

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	22.01	0.33	21.36	22.68	1.00	15165	11496

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).

Probability that the presence of NPI lowers the directional ratings

```

post_samples_c1 = posterior_samples(c1)
mean(post_samples_c1$b_PI1 < 0)

```

[1] 0.96525

Experiment 4

Full model

```
d1 = brm(  
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)  
  + (1+ Increasing+ Quantifier| subject),  
  data = d1df,  
  iter = 8000, save_pars = save_pars(all = TRUE))  
summary(d1)
```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content)
+ (1 + Increasing + Quantifier | subject)

Data: d1df (Number of observations: 1672)

Samples: 4 chains, each with iter = 8000; warmup = 4000; thin = 1;
total post-warmup samples = 16000

Group-Level Effects:

~Content (Number of levels: 10)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	1.44	0.94	0.08	3.66	1.00	5385	6240
sd(PI1)	0.83	0.66	0.03	2.47	1.00	7563	6776
sd(Quantifier1)	0.67	0.57	0.02	2.13	1.00	9558	8033
sd(Increasing1)	1.24	0.87	0.05	3.26	1.00	6713	6163
cor(Intercept,PI1)	0.13	0.44	-0.74	0.86	1.00	17256	11598
cor(Intercept,Quantifier1)	-0.01	0.45	-0.82	0.81	1.00	21920	10960
cor(PI1,Quantifier1)	-0.00	0.45	-0.81	0.82	1.00	16839	12415
cor(Intercept,Increasing1)	-0.11	0.43	-0.85	0.74	1.00	14131	11738
cor(PI1,Increasing1)	0.01	0.45	-0.81	0.82	1.00	13019	11614
cor(Quantifier1,Increasing1)	-0.01	0.45	-0.83	0.80	1.00	10819	12326

~subject (Number of levels: 70)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	11.91	1.23	9.75	14.57	1.00	4283	7143
sd(Increasing1)	20.80	1.95	17.33	25.00	1.00	2850	5948
sd(Quantifier1)	1.25	0.99	0.04	3.58	1.00	2656	4220
cor(Intercept,Increasing1)	-0.44	0.11	-0.63	-0.20	1.00	2261	4149
cor(Intercept,Quantifier1)	0.03	0.42	-0.80	0.82	1.00	16009	8830
cor(Increasing1,Quantifier1)	-0.05	0.42	-0.83	0.79	1.00	15222	9229

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	57.56	1.68	54.28	60.91	1.00	3041	5086
PI1	-1.64	0.73	-3.08	-0.19	1.00	14390	11297
Quantifier1	2.54	0.71	1.17	3.98	1.00	12492	10709
Increasing1	13.65	2.61	8.42	18.81	1.00	2111	4486

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	20.34	0.37	19.62	21.07	1.00	19997	12415

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`).

Probability that the presence of NPI lowers the directional ratings

```
post_samples_d1 = posterior_samples(d1)
mean(post_samples_d1$b_PI1 < 0)
[1] 0.9841875
```

NPI vs. no PI in DN environments

```
#contrast coding: N:1, 0:-1
```

Experiment 3

Full model

```
e1 = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ PI+ Increasing+ Quantifier| subject),
  data = e1df,
  iter = 15000, save_pars = save_pars(all = TRUE))
summary(e1)
```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content) + (1 + PI + Increasing + Quantifier | subject)

Data: e1df (Number of observations: 2134)

Samples: 4 chains, each with iter = 15000; warmup = 7500; thin = 1; total post-warmup samples = 30000

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	2.12	1.20	0.18	4.84	1.00	8658	10113
sd(PI1)	1.02	0.81	0.04	2.99	1.00	14141	14459
sd(Quantifier1)	1.70	1.05	0.12	4.05	1.00	10395	11799
sd(Increasing1)	3.14	1.24	1.08	5.97	1.00	13647	11986
cor(Intercept,PI1)	0.02	0.44	-0.79	0.81	1.00	31418	22960
cor(Intercept,Quantifier1)	-0.00	0.42	-0.77	0.78	1.00	20614	20815
cor(PI1,Quantifier1)	0.05	0.44	-0.78	0.83	1.00	15867	20902
cor(Intercept,Increasing1)	0.02	0.39	-0.72	0.74	1.00	13532	15947
cor(PI1,Increasing1)	0.03	0.43	-0.78	0.80	1.00	9988	17125
cor(Quantifier1,Increasing1)	0.30	0.38	-0.55	0.89	1.00	14245	18562

~subject (Number of levels: 92)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	11.37	1.10	9.36	13.68	1.00	10441	18522
sd(PI1)	1.07	0.72	0.05	2.70	1.00	4858	9925
sd(Increasing1)	11.90	1.14	9.82	14.29	1.00	13051	18948
sd(Quantifier1)	8.91	1.01	7.08	11.02	1.00	13237	20802
cor(Intercept,PI1)	0.32	0.39	-0.59	0.89	1.00	30301	18976
cor(Intercept,Increasing1)	0.28	0.12	0.02	0.50	1.00	11409	17104
cor(PI1,Increasing1)	0.24	0.39	-0.63	0.86	1.00	449	1290
cor(Intercept,Quantifier1)	-0.23	0.13	-0.48	0.04	1.00	13729	18313
cor(PI1,Quantifier1)	0.02	0.40	-0.74	0.76	1.01	547	1778
cor(Increasing1,Quantifier1)	-0.11	0.14	-0.37	0.17	1.00	16555	22634

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	53.61	1.53	50.59	56.59	1.00	9846	14571
PI1	-0.85	0.72	-2.27	0.59	1.00	30915	21436
Quantifier1	-16.07	1.26	-18.59	-13.62	1.00	19356	20806
Increasing1	2.94	1.70	-0.42	6.24	1.00	15404	19234

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	27.48	0.46	26.59	28.39	1.00	31629	23101

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`).

Probability that the presence of NPI lowers the directional ratings

```
post_samples_e1 = posterior_samples(e1)
mean(post_samples_e1$b_PI1 < 0)
[1] 0.8836333
```

Experiment 4

Full model

```
f1 = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ Increasing+ Quantifier| subject),
  data = f1df,
  iter = 8000, save_pars = save_pars(all = TRUE))
summary(f1)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content)
+ (1 + Increasing + Quantifier | subject)
Data: f1df (Number of observations: 1521)
Samples: 4 chains, each with iter = 8000; warmup = 4000; thin = 1;
         total post-warmup samples = 16000
```

Group-Level Effects:

```

~Content (Number of levels: 10)
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)      0.81      0.67      0.03      2.50 1.00      12013      9293
sd(PI1)            1.26      0.96      0.05      3.58 1.00      8057      8446
sd(Quantifier1)    0.91      0.74      0.03      2.77 1.00      11230      9088
sd(Increasing1)    1.15      0.89      0.05      3.31 1.00      10829      9958
cor(Intercept,PI1) 0.07      0.45     -0.78      0.84 1.00      18707      13302
cor(Intercept,Quantifier1) 0.00      0.45     -0.82      0.81 1.00      24965      11998
cor(PI1,Quantifier1) 0.07      0.45     -0.79      0.85 1.00      18932      13257
cor(Intercept,Increasing1) 0.05      0.45     -0.79      0.83 1.00      20126      12726
cor(PI1,Increasing1) 0.08      0.45     -0.77      0.85 1.00      18005      13996
cor(Quantifier1,Increasing1) 0.06      0.45     -0.79      0.84 1.00      13782      13755

~subject (Number of levels: 71)
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     12.52      1.62      9.67     16.00 1.00      5761     10200
sd(Increasing1)    12.61      1.43     10.08     15.64 1.00      5769     9880
sd(Quantifier1)    11.52      1.61      8.69     14.97 1.00      5834     9194
cor(Intercept,Increasing1) 0.06      0.17     -0.27      0.37 1.00      3184     6437
cor(Intercept,Quantifier1) 0.08      0.16     -0.24      0.39 1.00      5904     9200
cor(Increasing1,Quantifier1) -0.14      0.17     -0.46      0.20 1.00      6428     9948

Population-Level Effects:
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept      54.56      2.01     50.61     58.46 1.00      5642     8480
PI1             -2.72      1.90     -6.45      1.09 1.00      7535     9650
Quantifier1    -14.74      1.81    -18.28    -11.13 1.00      8516    10664
Increasing1     -1.45      1.75     -4.88      2.00 1.00      6369     9209

Family Specific Parameters:
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma      25.39      0.49     24.46     26.38 1.00      24716    12130

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).

```

Probability that the presence of NPI lowers the directional ratings

```

post_samples_f1 = posterior_samples(f1)
mean(post_samples_f1$b_PI1 < 0)
[1] 0.923625

```

PPI vs. no PI in NM environments

```
#contrast coding: P:1, 0:-1
```

Experiment 1

Full model


```
g1 = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ PI+ Increasing+ Quantifier| subject),
  data = g1df,
  iter = 8000, save_pars = save_pars(all = TRUE))
summary(g1)
```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content)
+ (1 + PI + Increasing + Quantifier | subject)

Data: g1df (Number of observations: 1877)

Samples: 4 chains, each with iter = 8000; warmup = 4000; thin = 1;
total post-warmup samples = 16000

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	1.48	0.88	0.09	3.47	1.00	5565	6600
sd(PI1)	0.99	0.71	0.05	2.66	1.00	7376	8375
sd(Quantifier1)	0.92	0.69	0.04	2.61	1.00	8045	8734
sd(Increasing1)	2.82	1.03	1.19	5.28	1.00	10821	10053
cor(Intercept,PI1)	0.16	0.43	-0.70	0.86	1.00	16491	11932
cor(Intercept,Quantifier1)	-0.04	0.44	-0.82	0.79	1.00	21455	12583
cor(PI1,Quantifier1)	-0.04	0.44	-0.83	0.79	1.00	15854	13437
cor(Intercept,Increasing1)	-0.34	0.37	-0.90	0.50	1.00	7672	8166
cor(PI1,Increasing1)	-0.32	0.41	-0.91	0.60	1.00	7253	9255
cor(Quantifier1,Increasing1)	0.16	0.42	-0.69	0.85	1.00	10670	12666

~subject (Number of levels: 66)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	10.03	1.06	8.15	12.28	1.00	6024	9864
sd(PI1)	1.64	0.80	0.15	3.27	1.00	2930	2705
sd(Increasing1)	17.93	1.70	14.94	21.62	1.00	7977	11031
sd(Quantifier1)	1.62	0.97	0.09	3.58	1.00	3194	7131
cor(Intercept,PI1)	-0.10	0.31	-0.70	0.55	1.00	20201	10084
cor(Intercept,Increasing1)	-0.47	0.11	-0.66	-0.23	1.00	10214	11326
cor(PI1,Increasing1)	0.46	0.29	-0.23	0.89	1.00	1197	1329
cor(Intercept,Quantifier1)	0.15	0.33	-0.54	0.77	1.00	19490	10071
cor(PI1,Quantifier1)	-0.27	0.41	-0.89	0.63	1.00	6025	9223
cor(Increasing1,Quantifier1)	-0.19	0.31	-0.77	0.49	1.00	20047	10503

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	60.02	1.44	57.15	62.88	1.00	4942	8278
PI1	0.09	0.67	-1.23	1.40	1.00	20364	13117
Quantifier1	3.24	0.66	1.94	4.54	1.00	22423	12273
Increasing1	13.44	2.47	8.61	18.29	1.00	8627	9827

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	22.05	0.38	21.32	22.82	1.00	19663	11797

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`).

Probability that the presence of PPI increases the directional ratings

```
post_samples_g1 = posterior_samples(g1)
mean(post_samples_g1$b_PI1 > 0)
[1] 0.551625
```

Experiment 2

Full model

```
h1 = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ PI+ Increasing+ Quantifier| subject),
  data = h1df,
  iter = 20000, save_pars = save_pars(all = TRUE), control = list(max_treedepth = 15))
summary(h1)
```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content)
+ (1 + PI + Increasing + Quantifier | subject)

Data: `h1df` (Number of observations: 1733)

Samples: 4 chains, each with iter = 20000; warmup = 10000; thin = 1;
total post-warmup samples = 40000

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	0.95	0.72	0.04	2.66	1.00	16374	17797
sd(PI1)	0.85	0.68	0.04	2.54	1.00	18251	18641
sd(Quantifier1)	0.90	0.68	0.04	2.52	1.00	18793	18300
sd(Increasing1)	1.67	0.95	0.13	3.78	1.00	14679	13655
cor(Intercept,PI1)	0.06	0.45	-0.79	0.84	1.00	36646	30278
cor(Intercept,Quantifier1)	0.09	0.45	-0.77	0.85	1.00	32725	27770
cor(PI1,Quantifier1)	0.08	0.45	-0.78	0.85	1.00	30825	30627
cor(Intercept,Increasing1)	-0.12	0.44	-0.85	0.74	1.00	21463	26000
cor(PI1,Increasing1)	0.03	0.44	-0.80	0.81	1.00	22608	28531
cor(Quantifier1,Increasing1)	-0.14	0.43	-0.86	0.73	1.00	23728	32992

~subject (Number of levels: 64)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	13.36	1.37	10.96	16.29	1.00	8421	15536
sd(PI1)	1.26	0.91	0.05	3.29	1.00	4315	14256
sd(Increasing1)	20.64	1.98	17.17	24.96	1.00	11282	19204
sd(Quantifier1)	1.76	0.80	0.23	3.39	1.00	11582	9768
cor(Intercept,PI1)	-0.07	0.36	-0.76	0.68	1.00	45065	23033
cor(Intercept,Increasing1)	-0.28	0.12	-0.50	-0.02	1.00	10340	17476
cor(PI1,Increasing1)	0.12	0.36	-0.64	0.79	1.01	479	1519

```
cor(Intercept,Quantifier1)      -0.19      0.29      -0.73      0.42 1.00      35270      23791
cor(PI1,Quantifier1)            0.09      0.42      -0.73      0.83 1.00      2720      9330
cor(Increasing1,Quantifier1)    0.54      0.27      -0.09      0.92 1.00      27449      19288
```

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	60.19	1.82	56.64	63.77	1.00	5428	10850
PI1	0.63	0.65	-0.64	1.92	1.00	34585	27732
Quantifier1	2.89	0.67	1.57	4.21	1.00	34325	28512
Increasing1	7.71	2.70	2.36	13.05	1.00	10654	17462

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	21.90	0.39	21.15	22.67	1.00	40808	30182

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`).

Probability that the presence of PPI increases the directional ratings

```
post_samples_h1 = posterior_samples(h1)
mean(post_samples_h1$b_PI1 > 0)
[1] 0.841675
```

Experiment 3

Full model

```
i1 = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ PI+ Increasing+ Quantifier| subject),
  data = iidf,
  iter = 20000, save_pars = save_pars(all = TRUE), control = list(max_treedepth = 15))
summary(i1)
```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content) + (1 + PI + Increasing + Quantifier | subject)

Data: iidf (Number of observations: 2437)

Samples: 4 chains, each with iter = 20000; warmup = 10000; thin = 1;
total post-warmup samples = 40000

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat
sd(Intercept)	1.56	0.74	0.27	3.22	1.00
sd(PI1)	0.67	0.55	0.03	2.06	1.00
sd(Quantifier1)	1.31	0.79	0.08	3.10	1.00
sd(Increasing1)	2.72	0.90	1.34	4.83	1.00
cor(Intercept,PI1)	0.01	0.44	-0.79	0.81	1.00
cor(Intercept,Quantifier1)	0.14	0.40	-0.67	0.83	1.00

cor(PI1,Quantifier1)	0.01	0.44	-0.80	0.81	1.00
cor(Intercept,Increasing1)	-0.53	0.31	-0.94	0.24	1.00
cor(PI1,Increasing1)	0.04	0.43	-0.76	0.80	1.00
cor(Quantifier1,Increasing1)	-0.16	0.38	-0.82	0.62	1.00

	Bulk_ESS	Tail_ESS
sd(Intercept)	16110	12594
sd(PI1)	23475	23849
sd(Quantifier1)	15218	20013
sd(Increasing1)	27122	26698
cor(Intercept,PI1)	67897	30105
cor(Intercept,Quantifier1)	42259	31940
cor(PI1,Quantifier1)	31988	33260
cor(Intercept,Increasing1)	20665	18988
cor(PI1,Increasing1)	28186	32407
cor(Quantifier1,Increasing1)	31920	32689

~subject (Number of levels: 91)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat
sd(Intercept)	10.94	0.95	9.23	12.95	1.00
sd(PI1)	0.94	0.62	0.04	2.31	1.00
sd(Increasing1)	20.29	1.62	17.39	23.72	1.00
sd(Quantifier1)	2.31	0.81	0.53	3.78	1.00
cor(Intercept,PI1)	0.33	0.36	-0.53	0.88	1.00
cor(Intercept,Increasing1)	-0.41	0.10	-0.59	-0.21	1.00
cor(PI1,Increasing1)	-0.17	0.37	-0.82	0.61	1.00
cor(Intercept,Quantifier1)	0.38	0.23	-0.08	0.80	1.00
cor(PI1,Quantifier1)	0.27	0.41	-0.63	0.89	1.00
cor(Increasing1,Quantifier1)	-0.06	0.23	-0.52	0.39	1.00

	Bulk_ESS	Tail_ESS
sd(Intercept)	14757	25186
sd(PI1)	8144	19010
sd(Increasing1)	19633	28564
sd(Quantifier1)	9681	10489
cor(Intercept,PI1)	59452	28236
cor(Intercept,Increasing1)	21796	28265
cor(PI1,Increasing1)	623	1940
cor(Intercept,Quantifier1)	32384	21758
cor(PI1,Quantifier1)	7094	16627
cor(Increasing1,Quantifier1)	46010	24914

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS
Intercept	57.63	1.33	54.98	60.27	1.00	13940
PI1	0.59	0.51	-0.42	1.59	1.00	64448
Quantifier1	2.99	0.67	1.66	4.33	1.00	47339
Increasing1	16.42	2.34	11.82	21.01	1.00	22725

	Tail_ESS
Intercept	22835
PI1	31354
Quantifier1	31466
Increasing1	27760

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	21.18	0.33	20.55	21.84	1.00	53805	29880

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`).

Probability that the presence of PPI increases the directional ratings

```
post_samples_i1 = posterior_samples(i1)
mean(post_samples_i1$b_PI1 > 0)
[1] 0.87965
```

Experiment 4

Full model

```
j1 = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ Increasing+ Quantifier| subject),
  data = j1df,
  iter = 8000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(j1)
```

```
j1 = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ PI+ Increasing+ Quantifier| subject),
  data = j1df,
  iter = 20000, save_pars = save_pars(all = TRUE))
summary(j1)
```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content) + (1 + PI + Increasing + Quantifier | subject)

Data: j1df (Number of observations: 1691)

Samples: 4 chains, each with iter = 20000; warmup = 10000; thin = 1; total post-warmup samples = 40000

Group-Level Effects:

~Content (Number of levels: 10)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	0.92	0.67	0.04	2.53	1.00	19278	20508
sd(PI1)	1.05	0.78	0.05	2.93	1.00	18586	20343
sd(Quantifier1)	1.08	0.81	0.04	3.02	1.00	18071	19370
sd(Increasing1)	2.55	1.07	0.87	5.07	1.00	19150	15391
cor(Intercept,PI1)	0.09	0.44	-0.77	0.85	1.00	37144	29948
cor(Intercept,Quantifier1)	0.03	0.44	-0.79	0.82	1.00	39298	31101
cor(PI1,Quantifier1)	-0.01	0.44	-0.81	0.80	1.00	36421	33542
cor(Intercept,Increasing1)	-0.29	0.42	-0.91	0.63	1.00	17699	20835
cor(PI1,Increasing1)	-0.15	0.42	-0.85	0.70	1.00	23321	28276
cor(Quantifier1,Increasing1)	-0.09	0.42	-0.82	0.73	1.00	26267	30754

~subject (Number of levels: 71)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	11.41	1.18	9.27	13.90	1.00	12580	20543
sd(PI1)	1.05	0.73	0.05	2.72	1.00	12103	20372
sd(Increasing1)	20.46	1.87	17.16	24.49	1.00	14014	24265
sd(Quantifier1)	0.99	0.71	0.04	2.61	1.00	14535	19895
cor(Intercept,PI1)	-0.29	0.40	-0.89	0.61	1.00	39647	29114
cor(Intercept,Increasing1)	-0.45	0.11	-0.64	-0.22	1.00	15084	22195
cor(PI1,Increasing1)	0.09	0.40	-0.71	0.81	1.00	876	2214
cor(Intercept,Quantifier1)	0.19	0.40	-0.66	0.85	1.00	41688	29968
cor(PI1,Quantifier1)	-0.06	0.44	-0.83	0.77	1.00	16905	28582
cor(Increasing1,Quantifier1)	0.08	0.41	-0.72	0.80	1.00	46909	31791

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	58.05	1.56	55.00	61.09	1.00	9729	17584
PI1	-1.00	0.78	-2.54	0.55	1.00	40158	31068
Quantifier1	2.76	0.79	1.17	4.31	1.00	25033	27402
Increasing1	13.54	2.66	8.31	18.76	1.00	17387	24382

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	20.37	0.37	19.65	21.11	1.00	56091	29463

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`).

Probability that the presence of PPI increases the directional ratings

```
post_samples_j1 = posterior_samples(j1)
mean(post_samples_j1$b_PI1 > 0)
[1] 0.1043125
```

PPI vs. no PI in DN environments

```
#contrast coding: P:1, 0:-1
```

Experiment 3

Full model

```
k1 = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ PI+ Increasing+ Quantifier| subject),
  data = kldf,
  iter = 15000, save_pars = save_pars(all = TRUE))
summary(k1)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content)
```

```
+ (1 + PI + Increasing + Quantifier | subject)
```

```
Data: k1df (Number of observations: 2130)
```

```
Samples: 4 chains, each with iter = 15000; warmup = 7500; thin = 1;
         total post-warmup samples = 30000
```

Group-Level Effects:

```
~Content (Number of levels: 12)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	2.15	1.17	0.18	4.75	1.00	8704	10167
sd(PI1)	0.82	0.67	0.03	2.48	1.00	17453	17192
sd(Quantifier1)	1.77	1.02	0.15	4.05	1.00	11581	11913
sd(Increasing1)	3.95	1.29	1.97	6.98	1.00	18950	21857
cor(Intercept,PI1)	0.01	0.45	-0.81	0.81	1.00	41590	21009
cor(Intercept,Quantifier1)	0.10	0.41	-0.71	0.81	1.00	24431	22185
cor(PI1,Quantifier1)	0.01	0.44	-0.80	0.82	1.00	16015	22799
cor(Intercept,Increasing1)	-0.16	0.37	-0.79	0.59	1.00	14350	17514
cor(PI1,Increasing1)	0.00	0.44	-0.79	0.80	1.00	9018	16874
cor(Quantifier1,Increasing1)	0.39	0.36	-0.45	0.91	1.00	12907	15016

```
~subject (Number of levels: 91)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	9.76	1.01	7.93	11.89	1.00	12921	18030
sd(PI1)	0.73	0.55	0.03	2.07	1.00	14214	14966
sd(Increasing1)	12.29	1.18	10.17	14.77	1.00	13504	21556
sd(Quantifier1)	9.71	1.02	7.86	11.85	1.00	16026	20713
cor(Intercept,PI1)	-0.14	0.42	-0.85	0.72	1.00	47657	21752
cor(Intercept,Increasing1)	0.21	0.13	-0.06	0.45	1.00	11416	17612
cor(PI1,Increasing1)	-0.01	0.43	-0.82	0.78	1.01	504	1476
cor(Intercept,Quantifier1)	-0.25	0.14	-0.50	0.02	1.00	13504	19373
cor(PI1,Quantifier1)	-0.01	0.42	-0.79	0.78	1.01	602	1765
cor(Increasing1,Quantifier1)	-0.10	0.13	-0.36	0.17	1.00	18512	23644

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	56.80	1.40	54.07	59.58	1.00	14547	19658
PI1	2.06	0.67	0.77	3.38	1.00	40209	23035
Quantifier1	-16.05	1.34	-18.71	-13.41	1.00	23415	21738
Increasing1	2.50	1.87	-1.17	6.24	1.00	19629	20625

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	26.98	0.45	26.12	27.88	1.00	39736	23077

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`).

Probability that the presence of PPI increases the directional ratings

```
post_samples_k1 = posterior_samples(k1)
mean(post_samples_k1$b_PI1 > 0)
[1] 0.9984667
```

Experiment 4

Full model

```
l1 = brm(  
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)  
  + (1+ Increasing+ Quantifier| subject),  
  data = l1df,  
  iter = 8000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))  
summary(l1)
```

Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content)
+ (1 + Increasing + Quantifier | subject)
Data: l1df (Number of observations: 1522)
Samples: 4 chains, each with iter = 8000; warmup = 4000; thin = 1;
total post-warmup samples = 16000

Group-Level Effects:

~Content (Number of levels: 10)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	0.98	0.80	0.04	2.96	1.00	8208	7733
sd(PI1)	0.98	0.79	0.04	2.95	1.00	8693	7541
sd(Quantifier1)	0.83	0.69	0.03	2.59	1.00	11437	8603
sd(Increasing1)	2.05	1.25	0.13	4.93	1.00	5076	4968
cor(Intercept,PI1)	0.08	0.45	-0.79	0.85	1.00	15459	11899
cor(Intercept,Quantifier1)	-0.01	0.45	-0.82	0.82	1.00	15765	10955
cor(PI1,Quantifier1)	0.04	0.45	-0.79	0.83	1.00	14001	11659
cor(Intercept,Increasing1)	-0.12	0.44	-0.86	0.75	1.00	7568	9950
cor(PI1,Increasing1)	-0.03	0.44	-0.82	0.79	1.00	9011	11862
cor(Quantifier1,Increasing1)	-0.04	0.45	-0.83	0.79	1.00	9709	11632

~subject (Number of levels: 70)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	8.80	1.53	6.15	12.11	1.00	3631	6668
sd(Increasing1)	12.86	1.43	10.30	15.87	1.00	4442	7896
sd(Quantifier1)	12.39	1.68	9.30	15.91	1.00	4191	7183
cor(Intercept,Increasing1)	-0.09	0.19	-0.45	0.29	1.00	1382	2848
cor(Intercept,Quantifier1)	0.09	0.18	-0.27	0.43	1.00	2462	4601
cor(Increasing1,Quantifier1)	0.04	0.16	-0.28	0.35	1.00	4022	6722

Population-Level Effects:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	59.31	1.65	56.15	62.62	1.00	4346	7393
PI1	1.92	1.95	-1.90	5.66	1.00	4204	6916
Quantifier1	-12.78	1.84	-16.37	-9.13	1.00	5056	7624
Increasing1	0.46	1.86	-3.23	4.14	1.00	4207	7259

Family Specific Parameters:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	25.45	0.49	24.51	26.45	1.00	15747	12575

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`).

Probability that the presence of PPI increases the directional ratings

```
post_samples_l1 = posterior_samples(l1)
mean(post_samples_l1$b_PI1 > 0)
[1] 0.838
```

Meta-analysis

NPI in NM

```
#contrast coding: N:1, 0:-1
```

Full model

```
maal = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ Increasing+ Quantifier| subject),
  data = maaldf,
  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(maal)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content)
+ (1 + Increasing + Quantifier | subject)
Data: maaldf (Number of observations: 7691)
Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
total post-warmup samples = 20000
```

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	0.97	0.46	0.17	1.99	1.00	6647	5458
sd(PI1)	0.46	0.34	0.02	1.29	1.00	7570	8550
sd(Quantifier1)	0.48	0.35	0.02	1.31	1.00	8482	9351
sd(Increasing1)	2.00	0.60	1.09	3.40	1.00	10862	12581
cor(Intercept,PI1)	-0.00	0.43	-0.79	0.78	1.00	19516	14430
cor(Intercept,Quantifier1)	0.15	0.42	-0.69	0.86	1.00	18525	14061
cor(PI1,Quantifier1)	-0.08	0.44	-0.84	0.77	1.00	14974	14869
cor(Intercept,Increasing1)	-0.37	0.33	-0.88	0.36	1.00	6648	9692
cor(PI1,Increasing1)	0.22	0.42	-0.67	0.88	1.00	5817	8062
cor(Quantifier1,Increasing1)	-0.17	0.41	-0.84	0.67	1.00	8515	12174

~subject (Number of levels: 291)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	10.88	0.53	9.89	11.97	1.00	5253	9871
sd(Increasing1)	19.67	0.86	18.06	21.43	1.00	2501	5355
sd(Quantifier1)	1.90	0.57	0.65	2.90	1.00	2517	3006

```
cor(Intercept,Increasing1)    -0.40    0.06   -0.50   -0.28 1.00    1746    3439
cor(Intercept,Quantifier1)    0.40    0.18    0.08    0.83 1.00    4942    3473
cor(Increasing1,Quantifier1) -0.15    0.17   -0.51    0.17 1.00    9050    5057
```

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	57.07	0.75	55.61	58.55	1.00	3805	7447
PI1	-1.73	0.31	-2.34	-1.13	1.00	19577	13844
Quantifier1	2.62	0.33	1.98	3.28	1.00	16267	14565
Increasing1	14.32	1.34	11.70	16.96	1.00	2322	4719

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	21.36	0.18	21.00	21.73	1.00	20758	14835

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`).

Probability that the presence of NPI decreases the directional ratings

```
post_samples_maa1 = posterior_samples(maa1)
mean(post_samples_maa1$b_PI1 < 0)
[1] 0.99995
```

PPI in NM

#contrast coding: P:1, 0:-1

Full model

```
mab1 = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ Increasing+ Quantifier| subject),
  data = mab1df,
  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(mab1)
```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content) + (1 + Increasing + Quantifier | subject)

Data: mab1df (Number of observations: 7738)

Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1; total post-warmup samples = 20000

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	1.19	0.42	0.51	2.15	1.00	11378	11368
sd(PI1)	0.44	0.36	0.02	1.32	1.00	8230	11067
sd(Quantifier1)	0.56	0.40	0.03	1.49	1.00	7754	10154
sd(Increasing1)	2.50	0.68	1.49	4.15	1.00	12089	14278

```
cor(Intercept,PI1)          0.13      0.43    -0.72     0.85 1.00    23187    14298
cor(Intercept,Quantifier1)  0.16      0.41    -0.67     0.84 1.00    22338    14787
cor(PI1,Quantifier1)       -0.01      0.45    -0.81     0.80 1.00    14412    16257
cor(Intercept,Increasing1) -0.64      0.24    -0.96    -0.04 1.00     9614    13073
cor(PI1,Increasing1)       -0.12      0.42    -0.83     0.71 1.00    10980    13186
cor(Quantifier1,Increasing1) 0.05      0.40    -0.72     0.76 1.00    13172    13914
```

~subject (Number of levels: 292)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	11.28	0.55	10.27	12.40	1.00	5721	9934
sd(Increasing1)	19.73	0.87	18.12	21.50	1.00	3282	6948
sd(Quantifier1)	1.63	0.62	0.28	2.71	1.00	2130	2734
cor(Intercept,Increasing1)	-0.42	0.06	-0.53	-0.31	1.00	2101	4102
cor(Intercept,Quantifier1)	0.28	0.21	-0.09	0.76	1.00	7025	4141
cor(Increasing1,Quantifier1)	0.09	0.21	-0.31	0.52	1.00	12117	6143

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	58.95	0.80	57.39	60.52	1.00	4274	7666
PI1	0.26	0.30	-0.32	0.86	1.00	23664	15739
Quantifier1	3.02	0.34	2.35	3.70	1.00	19823	15482
Increasing1	13.15	1.43	10.30	15.96	1.00	3343	6632

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	21.42	0.18	21.07	21.79	1.00	21094	14682

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`).

Probability that the presence of PPI increases the directional ratings

```
post_samples_mab1 = posterior_samples(mab1)
mean(post_samples_mab1$b_PI1 > 0)
[1] 0.8167
```

NPI in DD

#contrast coding: N:1, 0:-1

Full model

```
mac1 = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ Increasing+ Quantifier| subject),
  data = mac1df,
  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(mac1)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content)
```

```

+ (1 + Increasing + Quantifier | subject)
  Data: mac1df (Number of observations: 3655)
Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup samples = 20000

Group-Level Effects:
~Content (Number of levels: 12)

```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
<code>sd(Intercept)</code>	0.86	0.67	0.04	2.47	1.00	8814	9032
<code>sd(PI1)</code>	0.91	0.66	0.04	2.49	1.00	7684	9526
<code>sd(Quantifier1)</code>	0.91	0.66	0.04	2.47	1.00	8301	8313
<code>sd(Increasing1)</code>	2.28	0.93	0.73	4.39	1.00	9450	7129
<code>cor(Intercept,PI1)</code>	0.09	0.44	-0.76	0.85	1.00	14602	14025
<code>cor(Intercept,Quantifier1)</code>	0.01	0.44	-0.80	0.81	1.00	17586	14540
<code>cor(PI1,Quantifier1)</code>	0.15	0.44	-0.74	0.87	1.00	14319	14641
<code>cor(Intercept,Increasing1)</code>	0.01	0.43	-0.77	0.78	1.00	7404	11131
<code>cor(PI1,Increasing1)</code>	0.21	0.42	-0.67	0.88	1.00	7255	10802
<code>cor(Quantifier1,Increasing1)</code>	0.21	0.41	-0.67	0.87	1.00	9474	13058

```

~subject (Number of levels: 163)

```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
<code>sd(Intercept)</code>	11.65	0.89	10.03	13.50	1.00	6986	12284
<code>sd(Increasing1)</code>	12.10	0.86	10.51	13.90	1.00	7037	11890
<code>sd(Quantifier1)</code>	9.74	0.83	8.19	11.45	1.00	6854	12043
<code>cor(Intercept,Increasing1)</code>	0.19	0.10	-0.01	0.38	1.00	3745	7542
<code>cor(Intercept,Quantifier1)</code>	-0.08	0.11	-0.28	0.13	1.00	5293	10804
<code>cor(Increasing1,Quantifier1)</code>	-0.14	0.11	-0.34	0.08	1.00	5827	10387

```

Population-Level Effects:

```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	54.08	1.12	51.91	56.29	1.00	6111	10058
PI1	-1.13	0.65	-2.42	0.15	1.00	18326	14817
Quantifier1	-15.56	1.00	-17.53	-13.58	1.00	8235	11137
Increasing1	1.15	1.29	-1.39	3.68	1.00	5855	10564

```

Family Specific Parameters:

```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	26.67	0.33	26.02	27.33	1.00	24312	15901

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`).

Probability that the presence of NPI decreases the directional ratings

```

post_samples_mac1 = posterior_samples(mac1)
mean(post_samples_mac1$b_PI1 < 0)
[1] 0.96045

```

PPI in DD

```
#contrast coding: P:1, 0:-1
```

Full model

```
mad1 = brm(
  formula = Irep ~ PI + Quantifier + Increasing+ (1+PI + Quantifier + Increasing| Content)
  + (1+ Increasing+ Quantifier| subject),
  data = mad1df,
  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(mad1)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI + Quantifier + Increasing + (1 + PI + Quantifier + Increasing | Content)
+ (1 + Increasing + Quantifier | subject)
Data: mad1df (Number of observations: 3652)
Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup samples = 20000
```

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	1.51	0.84	0.13	3.42	1.00	5973	5668
sd(PI1)	0.57	0.47	0.02	1.73	1.00	11126	9467
sd(Quantifier1)	0.85	0.62	0.04	2.29	1.00	8413	8056
sd(Increasing1)	3.04	1.01	1.52	5.45	1.00	10588	12810
cor(Intercept,PI1)	0.08	0.45	-0.78	0.84	1.00	21439	13476
cor(Intercept,Quantifier1)	0.07	0.43	-0.76	0.83	1.00	17321	14144
cor(PI1,Quantifier1)	0.07	0.45	-0.78	0.84	1.00	14119	15009
cor(Intercept,Increasing1)	-0.19	0.37	-0.82	0.58	1.00	6539	8641
cor(PI1,Increasing1)	0.08	0.44	-0.77	0.83	1.00	5230	9995
cor(Quantifier1,Increasing1)	0.20	0.41	-0.65	0.87	1.00	7117	9845

~subject (Number of levels: 161)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	9.61	0.85	8.06	11.38	1.00	6008	10140
sd(Increasing1)	12.34	0.87	10.74	14.16	1.00	5869	11288
sd(Quantifier1)	10.50	0.87	8.90	12.33	1.00	6200	10164
cor(Intercept,Increasing1)	0.12	0.11	-0.09	0.33	1.00	2607	4994
cor(Intercept,Quantifier1)	-0.09	0.11	-0.30	0.12	1.00	4171	7579
cor(Increasing1,Quantifier1)	-0.07	0.11	-0.28	0.14	1.00	4676	8855

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	57.78	1.07	55.68	59.87	1.00	6545	11365
PI1	2.02	0.58	0.88	3.16	1.00	17554	15406
Quantifier1	-14.82	1.03	-16.89	-12.80	1.00	6566	9914
Increasing1	1.70	1.43	-1.09	4.54	1.00	6437	10376

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	26.36	0.33	25.72	27.02	1.00	23128	15902

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).
```

Probability that the presence of PPI increases the directional ratings

```
post_samples_mad1 = posterior_samples(mad1)
mean(post_samples_mad1$b_PI1 > 0)
[1] 0.9995
```

META-ANALYSIS ON UPWARD AND DOWNWARD INFERENCES SEPARATELY

```
#contrast coding for models with NPI vs. 0: N:1, 0:-1
#contrast coding for models with PPI vs. 0: P:1, 0:-1
```

NPI in NM D

Full model

```
dema1 = brm(
  formula = Ireponse ~ PI + Quantifier + (1+PI + Quantifier | Content)
  + (1+ Quantifier| subject),
  data = dema1df,
  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(dema1)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Ireponse ~ PI + Quantifier + (1 + PI + Quantifier | Content)
+ (1 + Quantifier | subject)
Data: dema1df (Number of observations: 3884)
Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup samples = 20000
```

Group-Level Effects:

`~Content` (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
<code>sd</code> (Intercept)	1.53	0.63	0.47	3.01	1.00	5027	4070
<code>sd</code> (PI1)	0.90	0.61	0.05	2.33	1.00	4576	7912
<code>sd</code> (Quantifier1)	0.80	0.50	0.05	1.93	1.00	7239	7708
<code>cor</code> (Intercept,PI1)	0.02	0.44	-0.81	0.82	1.00	16248	12530
<code>cor</code> (Intercept,Quantifier1)	0.18	0.43	-0.72	0.89	1.00	17896	11669
<code>cor</code> (PI1,Quantifier1)	-0.17	0.48	-0.92	0.79	1.00	10557	13953

`~subject` (Number of levels: 290)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
<code>sd</code> (Intercept)	18.53	0.84	16.99	20.26	1.00	3482	6836
<code>sd</code> (Quantifier1)	1.10	0.74	0.04	2.58	1.00	2510	7111
<code>cor</code> (Intercept,Quantifier1)	-0.07	0.37	-0.85	0.77	1.00	16266	7111

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
--	----------	-----------	----------	----------	------	----------	----------

Intercept	28.36	1.21	25.97	30.74	1.00	2256	5210
PI1	0.93	0.43	0.07	1.81	1.00	16126	12676
Quantifier1	-0.78	0.41	-1.58	0.02	1.00	18892	15100

Family Specific Parameters:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	17.72	0.21	17.30	18.15	1.00	20482	13758

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`).

Probability that the presence of NPI increases DE-rating

```
post_samples_dema1 = posterior_samples(dema1)
mean(post_samples_dema1$b_PI1 > 0)
[1] 0.9816
```

NPI in NM U

Full model

```
uema1 = brm(
  formula = Ireponse ~ PI + Quantifier + (1+PI + Quantifier | Content)
  + (1+ Quantifier| subject),
  data = uema1df,
  iter = 8000, save_pars = save_pars(all = TRUE))
summary(uema1)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Ireponse ~ PI + Quantifier + (1 + PI + Quantifier | Content)
+ (1 + Quantifier | subject)
Data: uema1df (Number of observations: 3807)
Samples: 4 chains, each with iter = 8000; warmup = 4000; thin = 1;
total post-warmup samples = 16000
```

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	2.74	0.90	1.36	4.83	1.00	6070	9029
sd(PI1)	0.67	0.50	0.03	1.90	1.00	6848	8011
sd(Quantifier1)	0.61	0.47	0.02	1.78	1.00	9367	8673
cor(Intercept,PI1)	-0.28	0.46	-0.94	0.74	1.00	17757	11646
cor(Intercept,Quantifier1)	0.15	0.48	-0.80	0.91	1.00	19076	11589
cor(PI1,Quantifier1)	-0.04	0.50	-0.89	0.87	1.00	13755	12692

~subject (Number of levels: 291)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	25.49	1.15	23.36	27.85	1.00	3076	5214
sd(Quantifier1)	3.62	0.78	1.92	5.02	1.00	3857	4151
cor(Intercept,Quantifier1)	0.28	0.14	0.01	0.58	1.00	8638	5798

Population-Level Effects:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	42.43	1.73	39.02	45.85	1.00	2863	5474
PI1	-2.54	0.49	-3.51	-1.59	1.00	18665	12230
Quantifier1	4.53	0.52	3.51	5.55	1.00	16207	11798

Family Specific Parameters:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	24.22	0.30	23.64	24.82	1.00	14312	11092

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`).

Probability that the presence of NPI decreases UE-rating

```
post_samples_uema1 = posterior_samples(uema1)
mean(post_samples_uema1$b_PI1 < 0)
[1] 1
```

PPI in NM D

Full model

```
demb1 = brm(
  formula = Ireponse ~ PI + Quantifier + (1+PI + Quantifier | Content)
  + (1+ Quantifier| subject),
  data = demb1df,
  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(demb1)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Ireponse ~ PI + Quantifier + (1 + PI + Quantifier | Content)
+ (1 + Quantifier | subject)
Data: demb1df (Number of observations: 3875)
Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
total post-warmup samples = 20000
```

Group-Level Effects:

`~Content` (Number of levels: 12)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	1.45	0.54	0.56	2.70	1.00	7190	8526
sd(PI1)	0.45	0.36	0.02	1.33	1.00	8533	10084
sd(Quantifier1)	0.63	0.41	0.03	1.56	1.00	8109	7902
cor(Intercept,PI1)	-0.14	0.48	-0.91	0.80	1.00	23821	14213
cor(Intercept,Quantifier1)	0.36	0.43	-0.62	0.95	1.00	17754	13537
cor(PI1,Quantifier1)	-0.15	0.49	-0.92	0.82	1.00	14346	15789

`~subject` (Number of levels: 292)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	18.45	0.82	16.95	20.14	1.00	2711	6141
sd(Quantifier1)	1.08	0.65	0.06	2.39	1.00	2365	5377


```
cor(Intercept,Quantifier1)      0.29      0.34     -0.52      0.93 1.00     13143     8041
```

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	27.93	1.20	25.51	30.25	1.00	1869	3881
PI1	0.24	0.32	-0.40	0.88	1.00	22990	15491
Quantifier1	-0.60	0.36	-1.31	0.11	1.00	19814	15321

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	16.70	0.20	16.31	17.10	1.00	20742	14578

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`).

Probability that the presence of PPI decreases DE-rating

```
post_samples_demb1 = posterior_samples(demb1)
mean(post_samples_demb1$b_PI1 < 0)
[1] 0.22665
```

PPI in NM U

Full model

```
uemb1 = brm(
  formula = Ireponse ~ PI + Quantifier + (1+PI + Quantifier | Content)
  + (1+ Quantifier| subject),
  data = uemb1df,
  iter = 10000, save_pars = save_pars(all = TRUE))
summary(uemb1)
```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Ireponse ~ PI + Quantifier + (1 + PI + Quantifier | Content)
+ (1 + Quantifier | subject)

Data: `uemb1df` (Number of observations: 3863)

Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
total post-warmup samples = 20000

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	3.83	1.15	2.15	6.59	1.00	8685	13540
sd(PI1)	0.67	0.55	0.02	2.05	1.00	9253	11237
sd(Quantifier1)	0.83	0.59	0.04	2.25	1.00	9123	11746
cor(Intercept,PI1)	0.03	0.47	-0.85	0.86	1.00	30935	14006
cor(Intercept,Quantifier1)	0.21	0.44	-0.72	0.91	1.00	29708	14498
cor(PI1,Quantifier1)	0.09	0.51	-0.85	0.91	1.00	16572	16895

~subject (Number of levels: 290)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
--	----------	-----------	----------	----------	------	----------	----------

sd(Intercept)	26.20	1.18	23.99	28.62	1.00	4478	8136
sd(Quantifier1)	3.56	0.81	1.73	4.98	1.00	4561	4859
cor(Intercept,Quantifier1)	0.26	0.15	-0.01	0.59	1.00	9761	6043

Population-Level Effects:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	45.55	1.94	41.76	49.35	1.00	4320	7832
PI1	0.92	0.49	-0.05	1.89	1.00	28890	14491
Quantifier1	5.47	0.55	4.38	6.56	1.00	22893	16249

Family Specific Parameters:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	24.89	0.31	24.29	25.51	1.00	21088	13520

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`).

Probability that the presence of PPI increases UE-rating

```
post_samples_uemb1 = posterior_samples(uemb1)
mean(post_samples_uemb1$b_PI1 > 0)
[1] 0.9697
```

NPI in DD D

Full model

```
demc1 = brm(
  formula = Ireponse ~ PI + Quantifier + (1+PI + Quantifier | Content)
  + (1+ Quantifier| subject),
  data = demc1df,
  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(demc1)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Ireponse ~ PI + Quantifier + (1 + PI + Quantifier | Content)
+ (1 + Quantifier | subject)
Data: demc1df (Number of observations: 1825)
Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
total post-warmup samples = 20000
```

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	2.06	1.21	0.15	4.82	1.00	5508	8022
sd(PI1)	0.84	0.67	0.03	2.50	1.00	11022	10181
sd(Quantifier1)	1.18	0.86	0.05	3.18	1.00	9537	10186
cor(Intercept,PI1)	0.12	0.50	-0.84	0.91	1.00	24914	14831
cor(Intercept,Quantifier1)	0.12	0.48	-0.81	0.90	1.00	19691	13858
cor(PI1,Quantifier1)	0.12	0.50	-0.84	0.92	1.00	13895	16128

```

~subject (Number of levels: 161)
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)      18.93      1.32    16.49    21.66 1.00     5751     9926
sd(Quantifier1)     10.45      1.01     8.55    12.52 1.00     7844    12568
cor(Intercept,Quantifier1) 0.30      0.11     0.08     0.50 1.00     8522    13380

```

Population-Level Effects:

```

      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept      44.18      1.82    40.59    47.74 1.00     4943     8906
PI1              1.39      0.81    -0.22     3.00 1.00    20098    14713
Quantifier1     10.90      1.19     8.58    13.25 1.00    10712    12858

```

Family Specific Parameters:

```

      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma      25.61      0.46    24.72    26.53 1.00    23246    15850

```

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`).

Probability that the presence of NPI increases DE-rating

```

post_samples_demc1 = posterior_samples(demc1)
mean(post_samples_demc1$b_PI1 > 0)
[1] 0.95605

```

NPI in DD U

Full model

```

uemc1 = brm(
  formula = Ireponse ~ PI + Quantifier + (1+PI + Quantifier | Content)
  + (1+ Quantifier| subject),
  data = uemc1df,
  iter = 8000, save_pars = save_pars(all = TRUE))
summary(uemc1)

```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Ireponse ~ PI + Quantifier + (1 + PI + Quantifier | Content)
+ (1 + Quantifier | subject)

Data: `uemc1df` (Number of observations: 1830)

Samples: 4 chains, each with iter = 8000; warmup = 4000; thin = 1;
total post-warmup samples = 16000

Group-Level Effects:

```

~Content (Number of levels: 12)
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)      2.19      1.15     0.22     4.77 1.00     5242     5977
sd(PI1)              1.54      1.02     0.08     3.93 1.00     6806     9540
sd(Quantifier1)      1.06      0.81     0.05     3.01 1.00    10396    11501
cor(Intercept,PI1)   -0.18      0.46    -0.91     0.76 1.00    16696    11520
cor(Intercept,Quantifier1) -0.18      0.48    -0.92     0.80 1.00    21186    11794

```

```
cor(PI1,Quantifier1)          0.05      0.49    -0.85      0.89 1.00      16490      13546
```

```
~subject (Number of levels: 163)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	14.86	1.19	12.68	17.32	1.00	5988	9218
sd(Quantifier1)	12.49	1.08	10.47	14.71	1.00	6558	11152
cor(Intercept,Quantifier1)	-0.04	0.11	-0.26	0.17	1.00	6060	9559

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	52.44	1.57	49.38	55.51	1.00	9448	11706
PI1	-1.15	0.92	-2.98	0.63	1.00	20880	12218
Quantifier1	-20.09	1.30	-22.64	-17.50	1.00	11201	12147

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	25.54	0.46	24.66	26.46	1.00	19543	12435

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`).

Probability that the presence of NPI decreases UE-rating

```
[1] 0.902875
```

PPI in DD D

Full model

```
demd1 = brm(
  formula = Ireponse ~ PI + Quantifier + (1+PI + Quantifier | Content)
  + (1+ Quantifier| subject),
  data = demd1df,
  iter = 8000, save_pars = save_pars(all = TRUE))
summary(demd1)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Ireponse ~ PI + Quantifier + (1 + PI + Quantifier | Content)
+ (1 + Quantifier | subject)
Data: demd1df (Number of observations: 1847)
Samples: 4 chains, each with iter = 8000; warmup = 4000; thin = 1;
         total post-warmup samples = 16000
```

Group-Level Effects:

```
~Content (Number of levels: 12)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	2.78	1.14	0.78	5.35	1.00	5397	4643
sd(PI1)	1.29	0.87	0.06	3.31	1.00	7238	8860
sd(Quantifier1)	0.90	0.72	0.03	2.71	1.00	10275	9852
cor(Intercept,PI1)	0.36	0.44	-0.65	0.95	1.00	16038	12155
cor(Intercept,Quantifier1)	0.06	0.48	-0.84	0.88	1.00	22505	10890

```
cor(PI1,Quantifier1)          0.08      0.50     -0.84      0.91 1.00      16028      13757
```

```
~subject (Number of levels: 161)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	17.12	1.26	14.83	19.75	1.00	5769	9260
sd(Quantifier1)	11.35	1.04	9.43	13.50	1.00	6485	10275
cor(Intercept,Quantifier1)	0.19	0.11	-0.02	0.39	1.00	7129	10277

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	39.69	1.76	36.23	43.16	1.00	6886	9512
PI1	-2.10	0.84	-3.74	-0.45	1.00	18705	12748
Quantifier1	9.58	1.21	7.17	11.97	1.00	10635	11247

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	24.90	0.45	24.05	25.81	1.00	19856	12889

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`).

Probability that the presence of PPI decreases DE-rating

```
post_samples_demd1 = posterior_samples(demd1)
mean(post_samples_demd1$b_PI1 < 0)
[1] 0.9930625
```

PPI in DD U

Full model

```
uemd1 = brm(
  formula = Ireponse ~ PI + Quantifier + (1+PI + Quantifier | Content)
  + (1+ Quantifier| subject),
  data = uemd1df,
  iter = 8000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(uemd1)
```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Ireponse ~ PI + Quantifier + (1 + PI + Quantifier | Content)
+ (1 + Quantifier | subject)

Data: uemd1df (Number of observations: 1805)

Samples: 4 chains, each with iter = 8000; warmup = 4000; thin = 1;
total post-warmup samples = 16000

Group-Level Effects:

```
~Content (Number of levels: 12)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	3.99	1.34	1.95	7.18	1.00	6101	9221
sd(PI1)	0.77	0.64	0.03	2.34	1.00	9390	7577
sd(Quantifier1)	1.29	0.97	0.05	3.60	1.00	5812	6454

```
cor(Intercept,PI1)          -0.03      0.49    -0.88      0.86 1.00      20173      10162
cor(Intercept,Quantifier1)   0.02      0.45    -0.83      0.84 1.00      17061      11105
cor(PI1,Quantifier1)        -0.05      0.50    -0.89      0.87 1.00       9714      11939
```

```
~subject (Number of levels: 161)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	14.85	1.20	12.66	17.32	1.00	4987	9388
sd(Quantifier1)	12.63	1.13	10.50	14.94	1.00	5593	10131
cor(Intercept,Quantifier1)	0.04	0.11	-0.18	0.26	1.00	3634	6800

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	55.75	1.89	51.99	59.50	1.00	4244	7277
PI1	2.03	0.80	0.45	3.59	1.00	16816	13011
Quantifier1	-20.17	1.33	-22.83	-17.53	1.00	6005	9636

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	25.27	0.46	24.39	26.19	1.00	19448	12308

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`).

Probability that the presence of PPI increases UE-rating

```
[1] 0.9933125
```

Looking at environment-PI interactions

NPI in DE vs. NM

```
#contrast coding for models with NPI vs. 0: N:1, 0:-1; DE:1, NM:-1
```

Full model

```
envpia1 = brm(
  formula = Irep ~ PI*Monotonicity + Increasing + (1|Quantifier)
  + (1+ PI*Monotonicity + Increasing| Content)
  + (1+ Monotonicity + Increasing| subject),
  data = envpia1df,
  iter = 2000, save_pars = save_pars(all = TRUE),
  control = list(adapt_delta = 0.999, max_treedepth = 15))
summary(envpia1)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI * Monotonicity + Increasing + (1 | Quantifier)
+ (1 + PI * Monotonicity + Increasing | Content)
+ (1 + Monotonicity + Increasing | subject)
Data: envpia1df (Number of observations: 20314)
Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
```

```

total post-warmup samples = 4000

Group-Level Effects:
~Content (Number of levels: 12)
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)      1.13    0.40    0.51    2.04 1.00    1815    2285
sd(PI1)             0.28    0.23    0.01    0.85 1.00    1906    1991
sd(Monotonicity1)   0.54    0.33    0.04    1.30 1.00    1709    1995
sd(Increasing1)     2.06    0.59    1.22    3.52 1.00    2212    2868
sd(PI1:Monotonicity1) 0.52    0.33    0.03    1.27 1.00    1085    1389
cor(Intercept,PI1)  -0.07    0.40   -0.78    0.70 1.00    6372    2592
cor(Intercept,Monotonicity1) 0.22    0.37   -0.54    0.83 1.00    4839    2647
cor(PI1,Monotonicity1) -0.12    0.41   -0.81    0.71 1.00    2695    2791
cor(Intercept,Increasing1) -0.30    0.29   -0.79    0.30 1.00    1997    2401
cor(PI1,Increasing1)  -0.03    0.40   -0.76    0.75 1.01     867    2125
cor(Monotonicity1,Increasing1) -0.04    0.36   -0.72    0.63 1.00    1465    2165
cor(Intercept,PI1:Monotonicity1) -0.20    0.36   -0.81    0.56 1.00    3880    3076
cor(PI1,PI1:Monotonicity1)  0.06    0.41   -0.71    0.81 1.00    2033    2587
cor(Monotonicity1,PI1:Monotonicity1) -0.19    0.39   -0.83    0.62 1.00    2940    2989
cor(Increasing1,PI1:Monotonicity1) -0.24    0.35   -0.81    0.51 1.00    4359    3330

~Quantifier (Number of levels: 5)
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)    10.18     6.99     3.70    29.08 1.00    1045     930

~subject (Number of levels: 293)
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)    10.28     0.50     9.38    11.30 1.00     971    1767
sd(Monotonicity1)  6.82     0.37     6.15     7.57 1.00    1855    2533
sd(Increasing1)   12.46     0.57    11.42    13.62 1.00    1012    1888
cor(Intercept,Monotonicity1)  0.29     0.07     0.16     0.41 1.01    1031    1951
cor(Intercept,Increasing1) -0.49     0.05   -0.58   -0.39 1.01     770    1261
cor(Monotonicity1,Increasing1) -0.41     0.06   -0.53   -0.29 1.00     654    1215

Population-Level Effects:
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept      41.69     5.26    30.46    50.97 1.00    1636    1211
PI1             -1.11     0.23   -1.55   -0.66 1.00    5240    2984
Monotonicity1   -14.74     5.74   -25.17   -3.94 1.00    1233    1084
Increasing1      1.42     1.00   -0.53     3.39 1.00     993    1578
PI1:Monotonicity1  0.56     0.27     0.02     1.06 1.00    3683    2534

Family Specific Parameters:
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma      27.03     0.14    26.76    27.30 1.00     8106    2871

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).

Probability that the PI has a larger effect in one environment

post_samples_envpia1 = posterior_samples(envpia1)
mean(post_samples_envpia1$b_PI1:Monotonicity1` > 0)

```

```
[1] 0.9765
```

NPI in DN vs. DE

```
#contrast coding for models with NPI vs. 0: N:1, 0:-1; DD:1, DE:-1
```

Full model

```
envpib1 = brm(  
  formula = Irep ~ PI*Monotonicity + Increasing + (1|Quantifier)  
  + (1+ PI*Monotonicity + Increasing| Content)  
  + (1+ Monotonicity + Increasing| subject),  
  data = envpib1df,  
  iter = 4000, save_pars = save_pars(all = TRUE),  
  control = list(adapt_delta = 0.99, max_treedepth = 15))  
summary(envpib1)
```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Irep ~ PI * Monotonicity + Increasing + (1 | Quantifier)
+ (1 + PI * Monotonicity + Increasing | Content)
+ (1 + Monotonicity + Increasing | subject)

Data: envpib1df (Number of observations: 16278)

Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
total post-warmup samples = 8000

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	0.76	0.44	0.06	1.77	1.00	2871	3385
sd(PI1)	0.43	0.33	0.02	1.19	1.00	3106	3738
sd(Monotonicity1)	1.19	0.47	0.42	2.27	1.00	3786	3959
sd(Increasing1)	2.19	0.62	1.29	3.67	1.00	4421	5188
sd(PI1:Monotonicity1)	0.69	0.40	0.04	1.61	1.00	2588	2397
cor(Intercept,PI1)	0.00	0.41	-0.76	0.75	1.00	8890	6058
cor(Intercept,Monotonicity1)	-0.12	0.37	-0.78	0.61	1.00	3297	4858
cor(PI1,Monotonicity1)	0.16	0.39	-0.65	0.82	1.00	2724	4173
cor(Intercept,Increasing1)	-0.15	0.35	-0.77	0.54	1.00	2374	3404
cor(PI1,Increasing1)	-0.07	0.38	-0.76	0.68	1.00	2128	3526
cor(Monotonicity1,Increasing1)	0.29	0.29	-0.33	0.78	1.00	3628	5027
cor(Intercept,PI1:Monotonicity1)	0.16	0.39	-0.65	0.81	1.00	4922	4849
cor(PI1,PI1:Monotonicity1)	0.02	0.40	-0.74	0.76	1.00	4042	5113
cor(Monotonicity1,PI1:Monotonicity1)	-0.25	0.36	-0.83	0.50	1.00	5560	5406
cor(Increasing1,PI1:Monotonicity1)	0.23	0.34	-0.50	0.80	1.00	6028	5532

~Quantifier (Number of levels: 5)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	18.54	8.95	8.20	42.30	1.00	3105	4143

~subject (Number of levels: 293)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
--	----------	-----------	----------	----------	------	----------	----------

sd(Intercept)	8.42	0.53	7.45	9.51	1.00	1962	3929
sd(Monotonicity1)	10.27	0.58	9.19	11.46	1.00	2015	3605
sd(Increasing1)	10.40	0.50	9.48	11.42	1.00	2021	3574
cor(Intercept, Monotonicity1)	-0.10	0.08	-0.26	0.05	1.00	1048	1898
cor(Intercept, Increasing1)	-0.11	0.08	-0.27	0.05	1.01	610	1331
cor(Monotonicity1, Increasing1)	0.29	0.07	0.14	0.42	1.00	716	1706

Population-Level Effects:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	38.87	8.72	20.20	55.26	1.00	3685	4318
PI1	-1.40	0.30	-1.99	-0.80	1.00	7514	6001
Monotonicity1	13.77	9.27	-3.95	33.41	1.00	3750	3656
Increasing1	-4.98	0.96	-6.82	-3.06	1.00	1802	3243
PI1:Monotonicity1	-0.79	0.35	-1.49	-0.08	1.00	6029	5250

Family Specific Parameters:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	26.04	0.15	25.75	26.33	1.00	14807	5997

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`).

Probability that the PI has a larger effect in one environment

```
> mean(post_samples_envpic1$b_PI1:Monotonicity1 < 0)
[1] 0.985625
```

PPI in NM vs. UE

Full model

```
#contrast coding P:1, 0:-1; NM:1, UE:-1
```

```
envpic1 = brm(
  formula = Irep ~ PI*Monotonicity + Increasing + (1|Quantifier)
  + (1+ PI*Monotonicity + Increasing| Content)
  + (1+ Monotonicity + Increasing| subject),
  data = envpic1df,
  iter = 4000, save_pars = save_pars(all = TRUE),
  control = list(adapt_delta = 0.99, max_treedepth = 15))
summary(envpic1)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI * Monotonicity + Increasing + (1 | Quantifier)
+ (1 + PI * Monotonicity + Increasing | Content)
+ (1 + Monotonicity + Increasing | subject)
Data: envpic1df (Number of observations: 20537)
Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
total post-warmup samples = 8000
```

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	1.45	0.42	0.83	2.44	1.00	3934	5437
sd(PI1)	0.32	0.25	0.01	0.92	1.00	3327	4278
sd(Monotonicity1)	0.45	0.29	0.02	1.12	1.00	3452	4013
sd(Increasing1)	2.77	0.71	1.76	4.49	1.00	4129	4907
sd(PI1:Monotonicity1)	0.42	0.25	0.03	1.00	1.00	4153	4068
cor(Intercept,PI1)	-0.11	0.38	-0.80	0.66	1.00	11192	5734
cor(Intercept,Monotonicity1)	-0.24	0.36	-0.84	0.51	1.00	10726	6061
cor(PI1,Monotonicity1)	0.11	0.40	-0.67	0.80	1.00	6677	6474
cor(Intercept,Increasing1)	-0.39	0.25	-0.80	0.17	1.00	6355	4757
cor(PI1,Increasing1)	0.16	0.38	-0.62	0.80	1.00	2829	4359
cor(Monotonicity1,Increasing1)	-0.03	0.35	-0.68	0.66	1.00	3464	5158
cor(Intercept,PI1:Monotonicity1)	0.31	0.36	-0.48	0.87	1.00	10183	6182
cor(PI1,PI1:Monotonicity1)	-0.07	0.40	-0.77	0.70	1.00	7233	6712
cor(Monotonicity1,PI1:Monotonicity1)	-0.12	0.39	-0.80	0.67	1.00	6712	6162
cor(Increasing1,PI1:Monotonicity1)	-0.36	0.35	-0.88	0.45	1.00	6875	6731

~Quantifier (Number of levels: 5)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	5.35	3.87	1.86	15.77	1.00	2370	2882

~subject (Number of levels: 293)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	9.30	0.43	8.50	10.18	1.00	1956	3341
sd(Monotonicity1)	7.45	0.36	6.79	8.21	1.00	2969	5076
sd(Increasing1)	11.53	0.51	10.58	12.57	1.00	2348	3994
cor(Intercept,Monotonicity1)	-0.08	0.07	-0.21	0.05	1.00	2018	3531
cor(Intercept,Increasing1)	0.24	0.06	0.12	0.36	1.00	1886	3333
cor(Monotonicity1,Increasing1)	-0.61	0.04	-0.69	-0.52	1.00	1665	2982

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	68.97	2.95	63.35	75.54	1.00	4275	3389
PI1	0.27	0.21	-0.15	0.68	1.00	9491	6190
Monotonicity1	-9.87	3.06	-16.09	-3.93	1.00	3851	3280
Increasing1	-0.63	1.09	-2.73	1.52	1.00	3183	4420
PI1:Monotonicity1	-0.01	0.23	-0.47	0.43	1.00	8936	6091

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	23.72	0.12	23.48	23.96	1.00	15181	6020

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).

Probability that the PI has a larger effect in one environment

```
> post_samples_envpic1 = posterior_samples(envpic1)
> mean(post_samples_envpic1$b_PI1:Monotonicity1 > 0)
[1] 0.475125
```

PPIs in DD vs. UE

#contrast coding P:1, 0:-1; DD:1, UE:-1

Full model

```
envpid1 = brm(
  formula = Irep ~ PI*Monotonicity + Increasing + (1|Quantifier)
  +(1+ PI*Monotonicity + Increasing| Content)
  + (1+ Monotonicity + Increasing| subject),
  data = envpid1df,
  iter = 8000, save_pars = save_pars(all = TRUE),
  control = list(adapt_delta = 0.999, max_tredepth = 15))
summary(envpid1)
```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Irep ~ PI * Monotonicity + Increasing + (1 | Quantifier)
 + (1 + PI * Monotonicity + Increasing | Content)
 + (1 + Monotonicity + Increasing | subject)

Data: envpid1df (Number of observations: 16451)

Samples: 4 chains, each with iter = 8000; warmup = 4000; thin = 1;
 total post-warmup samples = 16000

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat
sd(Intercept)	1.69	0.51	0.94	2.94	1.00
sd(PI1)	0.66	0.32	0.09	1.39	1.00
sd(Monotonicity1)	0.92	0.40	0.21	1.81	1.00
sd(Increasing1)	2.99	0.78	1.88	4.92	1.00
sd(PI1:Monotonicity1)	0.28	0.23	0.01	0.86	1.00
cor(Intercept,PI1)	-0.28	0.33	-0.83	0.41	1.00
cor(Intercept,Monotonicity1)	0.01	0.32	-0.63	0.60	1.00
cor(PI1,Monotonicity1)	0.31	0.34	-0.45	0.85	1.00
cor(Intercept,Increasing1)	-0.15	0.27	-0.64	0.40	1.00
cor(PI1,Increasing1)	0.44	0.30	-0.26	0.89	1.00
cor(Monotonicity1,Increasing1)	0.29	0.30	-0.34	0.79	1.00
cor(Intercept,PI1:Monotonicity1)	0.10	0.40	-0.69	0.81	1.00
cor(PI1,PI1:Monotonicity1)	0.03	0.41	-0.74	0.76	1.00
cor(Monotonicity1,PI1:Monotonicity1)	0.05	0.40	-0.73	0.77	1.00
cor(Increasing1,PI1:Monotonicity1)	-0.06	0.40	-0.77	0.71	1.00

	Bulk_ESS	Tail_ESS
sd(Intercept)	7462	10653
sd(PI1)	5330	3685
sd(Monotonicity1)	5896	5199
sd(Increasing1)	8181	11330
sd(PI1:Monotonicity1)	8958	9564
cor(Intercept,PI1)	15588	12539
cor(Intercept,Monotonicity1)	15238	12785
cor(PI1,Monotonicity1)	8831	9460
cor(Intercept,Increasing1)	11692	12255
cor(PI1,Increasing1)	5498	6451

```

cor(Monotonicity1,Increasing1)      10155    10834
cor(Intercept,PI1:Monotonicity1)    21050    11704
cor(PI1,PI1:Monotonicity1)          18944    12510
cor(Monotonicity1,PI1:Monotonicity1) 16343    13856
cor(Increasing1,PI1:Monotonicity1)   17567    12532

~Quantifier (Number of levels: 5)
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)    15.63     7.14    7.19   34.16 1.00    7282    9688

~subject (Number of levels: 293)
      Estimate Est.Error l-95% CI u-95% CI Rhat
sd(Intercept)    10.28     0.54    9.28   11.38 1.00
sd(Monotonicity1)  6.53     0.43    5.72    7.41 1.00
sd(Increasing1)   9.92     0.46    9.07   10.89 1.00
cor(Intercept,Monotonicity1) -0.05     0.08   -0.21    0.12 1.00
cor(Intercept,Increasing1)  0.20     0.07    0.07    0.33 1.00
cor(Monotonicity1,Increasing1) -0.31     0.08   -0.46   -0.14 1.00
      Bulk_ESS Tail_ESS
sd(Intercept)    3884    7118
sd(Monotonicity1) 4959    9041
sd(Increasing1)   4596    7567
cor(Intercept,Monotonicity1) 4603    7940
cor(Intercept,Increasing1)  1735    3792
cor(Monotonicity1,Increasing1) 1127    2762

Population-Level Effects:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept    70.33     7.31   56.17   85.68 1.00    9967    9456
PI1           1.43     0.30    0.83    2.02 1.00   11340    9850
Monotonicity1 -10.23     7.72  -26.28    5.14 1.00    8091    8008
Increasing1   -7.11     1.09   -9.26   -4.98 1.00    5660    9285
PI1:Monotonicity1 1.15     0.24    0.69    1.62 1.00   18671   12158

Family Specific Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma    21.11     0.12   20.88   21.34 1.00   29497   11739

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).

```

Probability that the PI has a larger effect in one environment

```

post_samples_envpid1 = posterior_samples(envpid1)
mean(post_samples_envpid1$b_PI1:Monotonicity1` > 0)
[1] 0.999875

```

NPIs in DD vs. NM

```
#contrast coding for models with NPI vs. 0: N:1, 0:-1; DD:1, NM:-1
```

Full model

```

Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI * Monotonicity + Increasing + (1 | Quantifier) + (1 + PI * Monotonicity + Increasing
Data: envpie1df (Number of observations: 11346)
Samples: 4 chains, each with iter = 8000; warmup = 4000; thin = 1;
         total post-warmup samples = 16000

```

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat
sd(Intercept)	0.44	0.34	0.02	1.26	1.00
sd(PI1)	0.43	0.31	0.02	1.16	1.00
sd(Monotonicity1)	0.69	0.43	0.04	1.67	1.00
sd(Increasing1)	2.18	0.64	1.24	3.72	1.00
sd(PI1:Monotonicity1)	0.44	0.34	0.02	1.28	1.00
cor(Intercept,PI1)	-0.04	0.41	-0.77	0.73	1.00
cor(Intercept,Monotonicity1)	-0.00	0.40	-0.74	0.74	1.00
cor(PI1,Monotonicity1)	-0.06	0.41	-0.79	0.72	1.00
cor(Intercept,Increasing1)	-0.17	0.39	-0.82	0.63	1.00
cor(PI1,Increasing1)	0.26	0.39	-0.58	0.87	1.00
cor(Monotonicity1,Increasing1)	-0.22	0.35	-0.82	0.52	1.00
cor(Intercept,PI1:Monotonicity1)	0.00	0.41	-0.75	0.75	1.00
cor(PI1,PI1:Monotonicity1)	-0.08	0.41	-0.80	0.72	1.00
cor(Monotonicity1,PI1:Monotonicity1)	0.13	0.40	-0.67	0.81	1.00
cor(Increasing1,PI1:Monotonicity1)	-0.04	0.39	-0.75	0.70	1.00

	Bulk_ESS	Tail_ESS
sd(Intercept)	8203	8843
sd(PI1)	7763	8454
sd(Monotonicity1)	6284	7342
sd(Increasing1)	9841	12306
sd(PI1:Monotonicity1)	8362	9188
cor(Intercept,PI1)	17765	12459
cor(Intercept,Monotonicity1)	12823	12742
cor(PI1,Monotonicity1)	11929	12589
cor(Intercept,Increasing1)	5311	7037
cor(PI1,Increasing1)	6010	9384
cor(Monotonicity1,Increasing1)	9132	11033
cor(Intercept,PI1:Monotonicity1)	19893	12260
cor(PI1,PI1:Monotonicity1)	15964	13094
cor(Monotonicity1,PI1:Monotonicity1)	13552	13612
cor(Increasing1,PI1:Monotonicity1)	17887	13774

~Quantifier (Number of levels: 4)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	25.79	16.13	8.91	68.11	1.00	7555	9753

~subject (Number of levels: 293)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat
sd(Intercept)	8.60	0.54	7.59	9.70	1.00
sd(Monotonicity1)	8.07	0.55	7.06	9.22	1.00
sd(Increasing1)	17.04	0.78	15.61	18.65	1.00
cor(Intercept,Monotonicity1)	-0.19	0.08	-0.35	-0.02	1.00
cor(Intercept,Increasing1)	-0.03	0.09	-0.19	0.14	1.00

```
cor(Monotonicity1,Increasing1)    -0.45      0.07    -0.59    -0.30  1.00
                                Bulk_ESS Tail_ESS
sd(Intercept)                    4740      9212
sd(Monotonicity1)                 4993      8314
sd(Increasing1)                   4174      7153
cor(Intercept,Monotonicity1)      4119      6662
cor(Intercept,Increasing1)        1565      3351
cor(Monotonicity1,Increasing1)    1447      3112
```

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	56.47	13.28	29.17	84.51	1.00	11414	8955
PI1	-1.79	0.31	-2.39	-1.18	1.00	19464	13665
Monotonicity1	1.74	14.68	-27.70	33.06	1.00	10178	8201
Increasing1	10.60	1.22	8.20	12.99	1.00	5402	8588
PI1:Monotonicity1	0.14	0.32	-0.48	0.76	1.00	17907	12681

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	25.41	0.17	25.07	25.76	1.00	25292	10900

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`).

Probability that the PI has a larger effect in one environment

```
post_samples_envpie1 = posterior_samples(envpie1)
mean(post_samples_envpie1$b_PI1:Monotonicity1` < 0)
[1] 0.32925
```

PPIs in DD vs. NM

```
#contrast coding: P:1, 0:-1; DD:1, NM:-1
```

Full model

```
envpif1 = brm(
  formula = Irep ~ PI*Monotonicity + Increasing + (1|Quantifier)
  + (1+ PI*Monotonicity + Increasing| Content)
  + (1+ Monotonicity + Increasing| subject),
  data = envpif1df,
  iter = 8000, save_pars = save_pars(all = TRUE),
  control = list(adapt_delta = 0.999, max_treedepth = 15))
summary(envpif1)

Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI * Monotonicity + Increasing + (1 | Quantifier)
+ (1 + PI * Monotonicity + Increasing | Content)
+ (1 + Monotonicity + Increasing | subject)
Data: envpif1df (Number of observations: 11390)
Samples: 4 chains, each with iter = 8000; warmup = 4000; thin = 1;
total post-warmup samples = 16000
```

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat
sd(Intercept)	1.23	0.46	0.47	2.26	1.00
sd(PI1)	0.29	0.24	0.01	0.89	1.00
sd(Monotonicity1)	0.59	0.39	0.03	1.48	1.00
sd(Increasing1)	2.69	0.73	1.62	4.44	1.00
sd(PI1:Monotonicity1)	0.45	0.36	0.02	1.33	1.00
cor(Intercept,PI1)	0.05	0.41	-0.74	0.78	1.00
cor(Intercept,Monotonicity1)	0.16	0.37	-0.63	0.79	1.00
cor(PI1,Monotonicity1)	0.04	0.41	-0.73	0.79	1.00
cor(Intercept,Increasing1)	-0.44	0.27	-0.87	0.18	1.00
cor(PI1,Increasing1)	0.04	0.41	-0.74	0.77	1.00
cor(Monotonicity1,Increasing1)	0.19	0.36	-0.57	0.80	1.00
cor(Intercept,PI1:Monotonicity1)	-0.06	0.39	-0.77	0.70	1.00
cor(PI1,PI1:Monotonicity1)	0.03	0.41	-0.74	0.77	1.00
cor(Monotonicity1,PI1:Monotonicity1)	0.10	0.40	-0.70	0.80	1.00
cor(Increasing1,PI1:Monotonicity1)	0.13	0.38	-0.65	0.79	1.00

Bulk_ESS Tail_ESS

sd(Intercept)	7725	8489
sd(PI1)	10691	8226
sd(Monotonicity1)	6999	9176
sd(Increasing1)	8630	11201
sd(PI1:Monotonicity1)	7651	8821
cor(Intercept,PI1)	26502	11809
cor(Intercept,Monotonicity1)	17091	11574
cor(PI1,Monotonicity1)	12644	13127
cor(Intercept,Increasing1)	11073	11581
cor(PI1,Increasing1)	7024	10521
cor(Monotonicity1,Increasing1)	9392	11571
cor(Intercept,PI1:Monotonicity1)	21968	12916
cor(PI1,PI1:Monotonicity1)	14742	12972
cor(Monotonicity1,PI1:Monotonicity1)	15078	12969
cor(Increasing1,PI1:Monotonicity1)	17708	13092

~Quantifier (Number of levels: 4)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	24.26	15.21	8.58	65.89	1.00	7485	9051

~subject (Number of levels: 292)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat
sd(Intercept)	8.20	0.54	7.19	9.30	1.00
sd(Monotonicity1)	7.96	0.53	6.97	9.04	1.00
sd(Increasing1)	16.80	0.77	15.40	18.39	1.00
cor(Intercept,Monotonicity1)	0.06	0.09	-0.11	0.22	1.00
cor(Intercept,Increasing1)	-0.06	0.09	-0.22	0.11	1.00
cor(Monotonicity1,Increasing1)	0.44	0.07	0.30	0.58	1.00

Bulk_ESS Tail_ESS

sd(Intercept)	5701	9391
sd(Monotonicity1)	6055	9879
sd(Increasing1)	4541	8450
cor(Intercept,Monotonicity1)	4641	8372
cor(Intercept,Increasing1)	1521	2935

```
cor(Monotonicity1,Increasing1)      1460      2235
```

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	59.93	12.49	35.84	86.38	1.00	12273	9671
PI1	1.41	0.30	0.83	1.99	1.00	21185	12960
Monotonicity1	-0.61	14.42	-30.19	28.46	1.00	10150	7873
Increasing1	9.67	1.30	7.10	12.21	1.00	6412	10369
PI1:Monotonicity1	1.15	0.32	0.52	1.77	1.00	18635	13304

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	25.41	0.17	25.07	25.75	1.00	23123	11402

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`).

Probability that the PI has a larger effect in one environment

```
post_samples_envpif1 = posterior_samples(envpif1)
mean(post_samples_envpif1$b_PI1:Monotonicity1` > 0)
[1] 0.9989375
```

Appendix A: effect of monotonicity on inferential judgments

DE ratings

NM vs. UE

```
#contrast coding: NM:1, UE:-1
```

Full model

```
envinfa1 = brm(
  formula = Ireponse ~ Monotonicity + (1+ Monotonicity| subject),
  data = envinfadf,
  iter = 4000, save_pars = save_pars(all = TRUE))
summary(envinfa1)
```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Ireponse ~ Monotonicity + (1 + Monotonicity | subject)

Data: envinfadf (Number of observations: 12055)

Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
total post-warmup samples = 8000

Group-Level Effects:

~subject (Number of levels: 293)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	17.76	0.77	16.29	19.29	1.00	913
sd(Monotonicity1)	4.27	0.26	3.78	4.78	1.00	3892


```
cor(Intercept,Monotonicity1)      0.09      0.07      -0.05      0.23 1.00      4896
                                Tail_ESS
sd(Intercept)                    1904
sd(Monotonicity1)                5776
cor(Intercept,Monotonicity1)      6247
```

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	29.35	1.06	27.22	31.38	1.01	492	889
Monotonicity1	-0.96	0.31	-1.56	-0.38	1.00	4699	5665

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	17.58	0.12	17.35	17.82	1.00	18931	6198

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`).

Probability that NM environments have lower DE-ratings than UE environments

```
post_samples_envinfa1 = posterior_samples(envinfa1)
mean(post_samples_envinfa1$b_Monotonicity1` < 0)
[1] 0.999
```

UE vs. DN

#contrast coding: DN: 1, UE:-1

Full model

```
envinfb1 = brm(
  formula = Ireponse ~ Monotonicity + (1+ Monotonicity| subject),
  data = envinfbdf,
  iter = 4000, save_pars = save_pars(all = TRUE))
summary(envinfb1)
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Ireponse ~ Monotonicity + (1 + Monotonicity | subject)
Data: envinfbdf (Number of observations: 9001)
Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
         total post-warmup samples = 8000
```

Group-Level Effects:

`~subject` (Number of levels: 293)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	16.59	0.81	15.09	18.27	1.00	1961
sd(Monotonicity1)	6.42	0.47	5.53	7.38	1.00	2827
cor(Intercept,Monotonicity1)	0.04	0.09	-0.14	0.21	1.00	3661

	Tail_ESS
sd(Intercept)	3013
sd(Monotonicity1)	5115
cor(Intercept,Monotonicity1)	5452

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	35.84	1.03	33.81	37.82	1.00	1295	2687
Monotonicity1	5.58	0.56	4.47	6.68	1.00	4194	5543

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	21.68	0.16	21.35	22.00	1.00	16764	5387

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`).

Probability that DN environments have lower DE-ratings than UE environments

```
post_samples_envinfb1 = posterior_samples(envinfb1)
mean(post_samples_envinfb1$b_Monotonicity1 < 0)
[1] 0
```

DN vs. DE

#contrast coding: DN: 1, DE:-1

Full model

```
envinfc1 = brm(
  formula = Ireponse ~ Monotonicity + (1+ Monotonicity| subject),
  data = envinfcdf,
  iter = 4000, save_pars = save_pars(all = TRUE))
summary(envinfc1)
```

Family: gaussian

Links: mu = identity; sigma = identity

Formula: Ireponse ~ Monotonicity + (1 + Monotonicity | subject)

Data: `envinfcdf` (Number of observations: 8909)

Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
total post-warmup samples = 8000

Group-Level Effects:

`~subject` (Number of levels: 293)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	11.88	0.72	10.55	13.34	1.00	3042
sd(Monotonicity1)	11.15	0.72	9.85	12.64	1.00	2512
cor(Intercept,Monotonicity1)	0.18	0.08	0.03	0.33	1.00	2273

	Tail_ESS
sd(Intercept)	4416
sd(Monotonicity1)	4800
cor(Intercept,Monotonicity1)	3841

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	59.96	0.91	58.14	61.73	1.00	3240	4097
Monotonicity1	-19.00	0.88	-20.75	-17.31	1.00	3658	4843

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	27.85	0.21	27.43	28.27	1.00	13346	5369

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`).

Probability that DN environments have lower DE-ratings than DE environments

```
post_samples_envinfc1 = posterior_samples(envinfc1)
mean(post_samples_envinfc1$b_Monotonicity1 < 0)
[1] 1
```

UE ratings

DE vs. NM

#contrast coding: : DE:1, NM:-1

Full model

```
envinfd1 = brm(
  formula = Ireponse ~ Monotonicity + (1 + Monotonicity | subject),
  data = envinfd1,
  iter = 4000, save_pars = save_pars(all = TRUE))
summary(envinfd1)
```

Family: gaussian
 Links: mu = identity; sigma = identity
 Formula: Ireponse ~ Monotonicity + (1 + Monotonicity | subject)
 Data: envinfd1 (Number of observations: 11901)
 Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
 total post-warmup samples = 8000

Group-Level Effects:

~subject (Number of levels: 293)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	21.12	0.93	19.34	22.93	1.00	1212
sd(Monotonicity1)	8.58	0.43	7.78	9.46	1.00	3189
cor(Intercept, Monotonicity1)	-0.39	0.06	-0.50	-0.27	1.00	2978

	Tail_ESS
sd(Intercept)	2366
sd(Monotonicity1)	5211
cor(Intercept, Monotonicity1)	4647

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	38.88	1.23	36.42	41.40	1.01	406	1331
Monotonicity1	-5.11	0.55	-6.21	-4.05	1.00	2280	4573

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	24.85	0.16	24.53	25.17	1.00	15445	6115

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`).

Probability that DE environments have lower UE-ratings than NM environments

```
post_samples_envinfdf1 = posterior_samples(envinfdf1)
mean(post_samples_envinfdf1$b_Monotonicity1` < 0)
[1] 1
```

DN vs. NM

#contrast coding: : DN:1, NM:-1

Full model

```
envinfef1 = brm(
  formula = Ireponse ~ Monotonicity + (1+ Monotonicity| subject),
  data = envinfedf,
  iter = 4000, save_pars = save_pars(all = TRUE))
summary(envinfef1)
```

Family: gaussian
 Links: mu = identity; sigma = identity
 Formula: Ireponse ~ Monotonicity + (1 + Monotonicity | subject)
 Data: envinfedf (Number of observations: 8180)
 Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
 total post-warmup samples = 8000

Group-Level Effects:

~subject (Number of levels: 293)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	16.03	0.86	14.42	17.80	1.00	2448	
sd(Monotonicity1)	13.57	0.78	12.11	15.16	1.00	2631	
cor(Intercept,Monotonicity1)	-0.46	0.07	-0.59	-0.33	1.00	1958	
							Tail_ESS
sd(Intercept)							4147
sd(Monotonicity1)							4900
cor(Intercept,Monotonicity1)							3490

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	50.20	1.09	48.05	52.34	1.00	1866	3355
Monotonicity1	6.30	0.97	4.40	8.19	1.00	2486	3941

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	28.97	0.23	28.53	29.43	1.00	17642	5912

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`).

Probability that DN environments have lower UE-ratings than NM environments

```
post_samples_envinfe1 = posterior_samples(envinfe1)
mean(post_samples_envinfe1$b_Monotonicity1 < 0)
[1] 0
```

DN vs. UE

```
#contrast coding: : DN:1, UE:-1
```

Full model

```
envinff1 = brm(
  formula = Ireponse ~ Monotonicity + (1+ Monotonicity| subject),
  data = envinffdf,
  iter = 4000, save_pars = save_pars(all = TRUE))
summary(envinff1)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Ireponse ~ Monotonicity + (1 + Monotonicity | subject)
Data: envinffdf (Number of observations: 8989)
Samples: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
        total post-warmup samples = 8000
```

Group-Level Effects:

```
~subject (Number of levels: 293)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	12.18	0.67	10.96	13.55	1.00	2396
sd(Monotonicity1)	7.43	0.54	6.42	8.58	1.00	2753
cor(Intercept,Monotonicity1)	0.23	0.08	0.07	0.38	1.00	3336
	Tail_ESS					
sd(Intercept)	4093					
sd(Monotonicity1)	4554					
cor(Intercept,Monotonicity1)	4299					

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	72.27	0.86	70.57	73.94	1.00	2553	3854
Monotonicity1	-15.28	0.66	-16.55	-13.99	1.00	4149	5383

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	24.61	0.19	24.25	24.98	1.00	13103	5979

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`).

Probability that DN environments have lower UE-ratings than UE environments

```
post_samples_envinff1 = posterior_samples(envinff1)
mean(post_samples_envinff1$b_Monotonicity1` < 0)
```

```
[1] 1
```

NEW: Quantifier-PI interaction-Appendix B

NPI in NM

```
#contrast coding: : N=1, 0=-1, Exactly12 = 1, Only12 = -1
```

Full model

```
maalappb = brm(
  formula = Irep ~ PI*Quantifier + Increasing
  + (1+PI*Quantifier + Increasing| Content)
  + (1+ Increasing+ Quantifier| subject),
  data = maalappbdf,
  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(maalappb)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI * Quantifier + Increasing
+ (1 + PI * Quantifier + Increasing | Content)
+ (1 + Increasing + Quantifier | subject)
Data: maalappbdf (Number of observations: 7691)
Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
total post-warmup samples = 20000
```

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat
sd(Intercept)	0.97	0.46	0.16	2.01	1.00
sd(PI1)	0.46	0.35	0.02	1.30	1.00
sd(Quantifier1)	0.49	0.35	0.02	1.31	1.00
sd(Increasing1)	2.01	0.62	1.08	3.48	1.00
sd(PI1:Quantifier1)	0.34	0.28	0.01	1.02	1.00
cor(Intercept,PI1)	0.00	0.39	-0.74	0.73	1.00
cor(Intercept,Quantifier1)	0.13	0.39	-0.66	0.82	1.00
cor(PI1,Quantifier1)	-0.07	0.40	-0.79	0.71	1.00
cor(Intercept,Increasing1)	-0.32	0.32	-0.84	0.38	1.00
cor(PI1,Increasing1)	0.19	0.38	-0.62	0.83	1.00
cor(Quantifier1,Increasing1)	-0.14	0.38	-0.80	0.62	1.00
cor(Intercept,PI1:Quantifier1)	0.10	0.40	-0.68	0.79	1.00
cor(PI1,PI1:Quantifier1)	-0.06	0.41	-0.78	0.73	1.00
cor(Quantifier1,PI1:Quantifier1)	0.06	0.41	-0.71	0.78	1.00
cor(Increasing1,PI1:Quantifier1)	-0.13	0.40	-0.82	0.67	1.00
	Bulk_ESS	Tail_ESS			
sd(Intercept)	5667	5325			
sd(PI1)	7696	9625			
sd(Quantifier1)	8358	8000			

```
sd(Increasing1)          10523    13210
sd(PI1:Quantifier1)      12513    11822
cor(Intercept,PI1)       21849    14687
cor(Intercept,Quantifier1) 20969    14399
cor(PI1,Quantifier1)      16560    15982
cor(Intercept,Increasing1) 7325     8794
cor(PI1,Increasing1)      6827    10307
cor(Quantifier1,Increasing1) 8370    12974
cor(Intercept,PI1:Quantifier1) 23992    14525
cor(PI1,PI1:Quantifier1)  21160    15965
cor(Quantifier1,PI1:Quantifier1) 18132    17083
cor(Increasing1,PI1:Quantifier1) 21599    17086
```

~subject (Number of levels: 291)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	10.83	0.52	9.85	11.91	1.00	5723
sd(Increasing1)	19.63	0.85	18.05	21.41	1.00	2923
sd(Quantifier1)	1.88	0.56	0.66	2.86	1.00	2475
cor(Intercept,Increasing1)	-0.39	0.06	-0.50	-0.28	1.00	1612
cor(Intercept,Quantifier1)	0.40	0.18	0.08	0.84	1.00	4579
cor(Increasing1,Quantifier1)	-0.15	0.17	-0.52	0.17	1.00	7769

Tail_ESS

```
sd(Intercept)          9259
sd(Increasing1)        5580
sd(Quantifier1)        2683
cor(Intercept,Increasing1) 3734
cor(Intercept,Quantifier1) 3144
cor(Increasing1,Quantifier1) 5341
```

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	57.08	0.76	55.61	58.59	1.00	4029	7397
PI1	-1.73	0.31	-2.32	-1.14	1.00	20529	15300
Quantifier1	2.60	0.33	1.94	3.25	1.00	16755	15185
Increasing1	14.33	1.32	11.75	16.95	1.00	2912	6224
PI1:Quantifier1	-0.51	0.30	-1.10	0.09	1.00	19810	14720

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	21.36	0.18	21.01	21.72	1.00	19244	14742

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).

Probability that the PI has a larger effect with one quantifier

```
post_samples_maa1appb = posterior_samples(maa1appb)
mean(post_samples_maa1appb$b_PI1:Quantifier1 < 0)
[1] 0.954
```

NPI in DN

#contrast coding: : N=1, O=-1; Ew=1, Nw=-1

Full model

```
macIappb = brm(
  formula = Irep ~ PI*Quantifier + Increasing
  + (1+PI*Quantifier + Increasing| Content)
  + (1+ Increasing+ Quantifier| subject),
  data = macIappbdf,
  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(macIappb)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI * Quantifier + Increasing
+ (1 + PI * Quantifier + Increasing | Content)
+ (1 + Increasing + Quantifier | subject)
Data: macIappbdf (Number of observations: 3655)
Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
total post-warmup samples = 20000
```

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat
sd(Intercept)	0.86	0.67	0.03	2.50	1.00
sd(PI1)	0.86	0.65	0.04	2.43	1.00
sd(Quantifier1)	0.88	0.64	0.04	2.38	1.00
sd(Increasing1)	2.27	0.90	0.77	4.29	1.00
sd(PI1:Quantifier1)	0.90	0.64	0.04	2.42	1.00
cor(Intercept,PI1)	0.07	0.41	-0.73	0.80	1.00
cor(Intercept,Quantifier1)	0.01	0.41	-0.75	0.76	1.00
cor(PI1,Quantifier1)	0.12	0.40	-0.68	0.81	1.00
cor(Intercept,Increasing1)	0.01	0.39	-0.73	0.74	1.00
cor(PI1,Increasing1)	0.17	0.39	-0.63	0.82	1.00
cor(Quantifier1,Increasing1)	0.16	0.39	-0.64	0.81	1.00
cor(Intercept,PI1:Quantifier1)	-0.01	0.41	-0.76	0.74	1.00
cor(PI1,PI1:Quantifier1)	-0.05	0.40	-0.78	0.72	1.00
cor(Quantifier1,PI1:Quantifier1)	-0.03	0.40	-0.76	0.73	1.00
cor(Increasing1,PI1:Quantifier1)	-0.20	0.39	-0.84	0.60	1.00

	Bulk_ESS	Tail_ESS
sd(Intercept)	9490	10496
sd(PI1)	8548	10213
sd(Quantifier1)	10084	10524
sd(Increasing1)	9555	7987
sd(PI1:Quantifier1)	10288	9238
cor(Intercept,PI1)	22238	15143
cor(Intercept,Quantifier1)	24302	16227
cor(PI1,Quantifier1)	17092	15994
cor(Intercept,Increasing1)	9940	13792
cor(PI1,Increasing1)	9203	13540
cor(Quantifier1,Increasing1)	9805	13681
cor(Intercept,PI1:Quantifier1)	24042	16269


```
cor(PI1,PI1:Quantifier1)          19473    15854
cor(Quantifier1,PI1:Quantifier1)   17393    16765
cor(Increasing1,PI1:Quantifier1)   19234    17241

~subject (Number of levels: 163)
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS
sd(Intercept)      11.73      0.89   10.07   13.58 1.00    7157
sd(Increasing1)     12.13      0.88   10.49   13.98 1.00    7059
sd(Quantifier1)      9.75      0.82    8.22   11.46 1.00    7416
cor(Intercept,Increasing1)    0.19      0.10   -0.01    0.38 1.00    3982
cor(Intercept,Quantifier1)   -0.08      0.11   -0.28    0.13 1.00    5578
cor(Increasing1,Quantifier1) -0.13      0.11   -0.34    0.08 1.00    6758

      Tail_ESS
sd(Intercept)    12989
sd(Increasing1)  11561
sd(Quantifier1)  12565
cor(Intercept,Increasing1)    8376
cor(Intercept,Quantifier1)   10354
cor(Increasing1,Quantifier1)  10871

Population-Level Effects:
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept      54.13      1.13   51.93   56.33 1.00    6344   11491
PI1             -1.08      0.63   -2.32    0.17 1.00   24512   14800
Quantifier1     -15.50      1.00  -17.46  -13.54 1.00    8914   12841
Increasing1       1.14      1.28   -1.36    3.67 1.00    7958   11891
PI1:Quantifier1   0.71      0.64   -0.55    1.96 1.00   23249   16507

Family Specific Parameters:
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     26.66      0.33   26.00   27.31 1.00   30977   14684
```

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`).

Probability that the PI has a larger effect with one quantifier

```
post_samples_mac1appb = posterior_samples(mac1appb)
mean(post_samples_mac1appb$b_PI1:Quantifier1 < 0)

[1] 0.1312
```

PPI in NM

```
#contrast coding: :P=1, O=-1; Ex=1, On=-1
```

Full model

```
mablappb = brm(
  formula = Irep ~ PI*Quantifier + Increasing
  + (1+PI*Quantifier + Increasing| Content)
  + (1+ Increasing+ Quantifier| subject),
  data = mablappbdf,
```

```

  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(mablappb)

```

```

Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI * Quantifier + Increasing
+ (1 + PI * Quantifier + Increasing | Content)
+ (1 + Increasing + Quantifier | subject)
Data: mablappbdf (Number of observations: 7738)
Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup samples = 20000

```

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat
sd(Intercept)	1.18	0.43	0.48	2.16	1.00
sd(PI1)	0.45	0.36	0.02	1.34	1.00
sd(Quantifier1)	0.57	0.40	0.03	1.50	1.00
sd(Increasing1)	2.51	0.68	1.51	4.15	1.00
sd(PI1:Quantifier1)	0.36	0.29	0.01	1.08	1.00
cor(Intercept,PI1)	0.11	0.39	-0.67	0.79	1.00
cor(Intercept,Quantifier1)	0.13	0.37	-0.63	0.78	1.00
cor(PI1,Quantifier1)	-0.01	0.41	-0.75	0.76	1.00
cor(Intercept,Increasing1)	-0.58	0.25	-0.93	0.02	1.00
cor(PI1,Increasing1)	-0.11	0.39	-0.78	0.66	1.00
cor(Quantifier1,Increasing1)	0.05	0.37	-0.66	0.71	1.00
cor(Intercept,PI1:Quantifier1)	-0.01	0.40	-0.74	0.74	1.00
cor(PI1,PI1:Quantifier1)	-0.01	0.41	-0.77	0.75	1.00
cor(Quantifier1,PI1:Quantifier1)	0.07	0.40	-0.72	0.78	1.00
cor(Increasing1,PI1:Quantifier1)	0.06	0.39	-0.69	0.76	1.00

	Bulk_ESS	Tail_ESS
sd(Intercept)	8668	6182
sd(PI1)	8674	11293
sd(Quantifier1)	7058	9893
sd(Increasing1)	11498	13449
sd(PI1:Quantifier1)	12200	11779
cor(Intercept,PI1)	23118	14464
cor(Intercept,Quantifier1)	20055	15480
cor(PI1,Quantifier1)	16193	16075
cor(Intercept,Increasing1)	10031	10206
cor(PI1,Increasing1)	10494	14048
cor(Quantifier1,Increasing1)	12903	14131
cor(Intercept,PI1:Quantifier1)	29891	13569
cor(PI1,PI1:Quantifier1)	22490	15155
cor(Quantifier1,PI1:Quantifier1)	18364	17351
cor(Increasing1,PI1:Quantifier1)	25567	16527

~subject (Number of levels: 292)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	11.27	0.54	10.27	12.38	1.00	5419
sd(Increasing1)	19.72	0.88	18.09	21.50	1.00	3551
sd(Quantifier1)	1.63	0.62	0.32	2.69	1.00	2694
cor(Intercept,Increasing1)	-0.42	0.05	-0.53	-0.31	1.00	2246

```

cor(Intercept,Quantifier1)      0.28      0.21     -0.09      0.76 1.00      8766
cor(Increasing1,Quantifier1)    0.09      0.20     -0.31      0.52 1.00     16016
                                Tail_ESS
sd(Intercept)                  9953
sd(Increasing1)                6939
sd(Quantifier1)                3594
cor(Intercept,Increasing1)     4583
cor(Intercept,Quantifier1)     6179
cor(Increasing1,Quantifier1)    7785

```

Population-Level Effects:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	58.98	0.81	57.39	60.55	1.00	4136	7830
PI1	0.26	0.31	-0.33	0.87	1.00	25668	15744
Quantifier1	3.02	0.34	2.34	3.68	1.00	19225	14936
Increasing1	13.15	1.42	10.34	15.94	1.00	2999	6652
PI1:Quantifier1	-0.06	0.31	-0.67	0.53	1.00	24906	15660

Family Specific Parameters:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	21.43	0.18	21.07	21.79	1.00	21006	13401

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`).

Probability that the PI has a larger effect with one quantifier

```

post_samples_mablappb = posterior_samples(mablappb)
mean(post_samples_mablappb$b_PI1:Quantifier1` > 0)

```

```
[1] 0.4188
```

PPI in DN

```
#contrast coding: :P=1, 0=-1; Ew=1, Nw = -1
```

Full model

```

mablappb = brm(
  formula = Irep ~ PI*Quantifier + Increasing
  + (1+PI*Quantifier + Increasing| Content)
  + (1+ Increasing+ Quantifier| subject),
  data = mablappbdf,
  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(mablappb)

```

Family: gaussian

```

Links: mu = identity; sigma = identity
Formula: Irep ~ PI * Quantifier + Increasing
+ (1 + PI * Quantifier + Increasing | Content)
+ (1 + Increasing + Quantifier | subject)
Data: mablappbdf (Number of observations: 3652)

```

Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
total post-warmup samples = 20000

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat
sd(Intercept)	1.51	0.82	0.14	3.33	1.00
sd(PI1)	0.57	0.46	0.02	1.71	1.00
sd(Quantifier1)	0.87	0.64	0.04	2.39	1.00
sd(Increasing1)	3.07	1.00	1.54	5.42	1.00
sd(PI1:Quantifier1)	1.33	0.80	0.08	3.11	1.00
cor(Intercept,PI1)	0.06	0.41	-0.73	0.79	1.00
cor(Intercept,Quantifier1)	0.08	0.40	-0.69	0.78	1.00
cor(PI1,Quantifier1)	0.06	0.41	-0.73	0.79	1.00
cor(Intercept,Increasing1)	-0.17	0.34	-0.77	0.54	1.00
cor(PI1,Increasing1)	0.07	0.40	-0.71	0.78	1.00
cor(Quantifier1,Increasing1)	0.15	0.38	-0.64	0.80	1.00
cor(Intercept,PI1:Quantifier1)	0.21	0.38	-0.60	0.83	1.00
cor(PI1,PI1:Quantifier1)	-0.01	0.41	-0.76	0.75	1.00
cor(Quantifier1,PI1:Quantifier1)	0.09	0.40	-0.69	0.78	1.00
cor(Increasing1,PI1:Quantifier1)	-0.12	0.35	-0.75	0.59	1.00

	Bulk_ESS	Tail_ESS
sd(Intercept)	6310	5584
sd(PI1)	13106	10702
sd(Quantifier1)	8679	9959
sd(Increasing1)	12226	13797
sd(PI1:Quantifier1)	7031	7223
cor(Intercept,PI1)	29228	14969
cor(Intercept,Quantifier1)	21362	14562
cor(PI1,Quantifier1)	16287	15166
cor(Intercept,Increasing1)	8256	8903
cor(PI1,Increasing1)	6392	11063
cor(Quantifier1,Increasing1)	7647	11615
cor(Intercept,PI1:Quantifier1)	15345	13853
cor(PI1,PI1:Quantifier1)	14856	16573
cor(Quantifier1,PI1:Quantifier1)	14476	16041
cor(Increasing1,PI1:Quantifier1)	20284	17195

~subject (Number of levels: 161)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	9.62	0.84	8.06	11.36	1.00	6622
sd(Increasing1)	12.33	0.88	10.69	14.15	1.00	6340
sd(Quantifier1)	10.48	0.87	8.88	12.29	1.00	5977
cor(Intercept,Increasing1)	0.12	0.11	-0.09	0.32	1.00	2670
cor(Intercept,Quantifier1)	-0.09	0.11	-0.29	0.13	1.00	4053
cor(Increasing1,Quantifier1)	-0.06	0.10	-0.27	0.14	1.00	5370

	Tail_ESS
sd(Intercept)	11817
sd(Increasing1)	10861
sd(Quantifier1)	11188
cor(Intercept,Increasing1)	5616
cor(Intercept,Quantifier1)	8398
cor(Increasing1,Quantifier1)	10815

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	57.82	1.06	55.76	59.93	1.00	7957	11890
PI1	2.08	0.58	0.95	3.22	1.00	22082	16078
Quantifier1	-14.65	1.05	-16.72	-12.58	1.00	7231	11075
Increasing1	1.67	1.41	-1.13	4.45	1.00	6831	11277
PI1:Quantifier1	0.86	0.71	-0.56	2.23	1.00	16470	14779

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	26.34	0.33	25.70	26.99	1.00	27495	15901

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`).

Probability that the PI has a larger effect with one quantifier

```
post_samples_madlappb = posterior_samples(madlappb)
mean(post_samples_madlappb$`b_PI1:Quantifier1` > 0)
```

```
[1] 0.89555
```

Sub-analyses Appendix B

NPI vs no PI in NM: ‘Exactly 12’

```
#contrast coding: :N=1, 0=-1
```

Full model

```
maalappb = brm(
  formula = Irep ~ PI + Increasing + (1+PI + Increasing | Content) + (1 + Increasing | subject),
  data = maalappbdf,
  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(maalappb)
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI + Increasing + (1 + PI + Increasing | Content) + (1 + Increasing | subject)
Data: maalappbdf (Number of observations: 3912)
Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup samples = 20000
```

Group-Level Effects:

```
~Content (Number of levels: 12)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	1.30	0.66	0.16	2.77	1.00	6255
sd(PI1)	0.42	0.35	0.01	1.30	1.00	11902
sd(Increasing1)	2.30	0.79	1.09	4.17	1.00	10012
cor(Intercept,PI1)	0.04	0.50	-0.86	0.88	1.00	27526
cor(Intercept,Increasing1)	-0.30	0.38	-0.90	0.53	1.00	6925
cor(PI1,Increasing1)	0.05	0.49	-0.86	0.89	1.00	4908
Tail_ESS						

```
sd(Intercept)          5480
sd(PI1)                 8771
sd(Increasing1)        13634
cor(Intercept,PI1)     13777
cor(Intercept,Increasing1) 7794
cor(PI1,Increasing1)   10111

~subject (Number of levels: 275)
      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS
sd(Intercept)      11.76      0.63   10.57   13.04 1.00    7760
sd(Increasing1)     19.71      0.93   18.00   21.62 1.00    4307
cor(Intercept,Increasing1) -0.44      0.06   -0.55   -0.32 1.00    2835
      Tail_ESS
sd(Intercept)      12313
sd(Increasing1)     9161
cor(Intercept,Increasing1) 5245
```

Population-Level Effects:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	59.98	0.90	58.21	61.74	1.00	6258	9982
PI1	-2.15	0.42	-2.97	-1.32	1.00	22284	15509
Increasing1	12.14	1.43	9.35	14.93	1.00	4437	8304

Family Specific Parameters:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	21.87	0.27	21.36	22.40	1.00	24269	15660

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`).

Probability that the presence of NPI decreases the judgments

```
post_samples_maalappb = posterior_samples(maalappb)
mean(post_samples_maalappb$b_PI1` < 0)
mean(post_samples_maalappb$b_PI1` > 0)
[1] 1
[1] 0
```

NPI vs no PI in NM: ‘Only 12’

#contrast coding: :N=1, 0=-1

Full model

```
maalappb = brm(
  formula = Irep ~ PI + Increasing+ (1+PI + Increasing| Content)+(1+ Increasing| subject),
  data = maalappbdf,
  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(maalappb)
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI + Increasing + (1 + PI + Increasing | Content) + (1 + Increasing | subject)
Data: maalappbdf (Number of observations: 3779)
```

Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
total post-warmup samples = 20000

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	0.70	0.50	0.04	1.86	1.00	7788
sd(PI1)	0.74	0.52	0.04	1.94	1.00	7827
sd(Increasing1)	1.81	0.70	0.70	3.43	1.00	9328
cor(Intercept,PI1)	0.03	0.49	-0.86	0.88	1.00	14174
cor(Intercept,Increasing1)	-0.25	0.45	-0.93	0.74	1.00	5519
cor(PI1,Increasing1)	0.29	0.45	-0.70	0.94	1.00	7206

Tail_ESS

sd(Intercept)	9135
sd(PI1)	9633
sd(Increasing1)	9368
cor(Intercept,PI1)	14791
cor(Intercept,Increasing1)	8345
cor(PI1,Increasing1)	8988

~subject (Number of levels: 270)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	10.31	0.59	9.23	11.50	1.00	7934
sd(Increasing1)	19.33	0.92	17.60	21.21	1.00	4260
cor(Intercept,Increasing1)	-0.39	0.07	-0.51	-0.26	1.00	2228

Tail_ESS

sd(Intercept)	11992
sd(Increasing1)	8981
cor(Intercept,Increasing1)	4998

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	54.19	0.78	52.67	55.71	1.00	6552	9419
PI1	-1.26	0.45	-2.14	-0.38	1.00	20964	15079
Increasing1	16.98	1.37	14.32	19.64	1.00	3617	7717

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	20.41	0.25	19.92	20.91	1.00	26098	15956

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).

Probability that the presence of NPI decreases the judgments

```
post_samples_maa1appb = posterior_samples(maa1appb)
mean(post_samples_maa1appb$b_PI1 ~ < 0)
mean(post_samples_maa1appb$b_PI1 ~ > 0)
[1] 0.9962
[1] 0.0038
```

PPI vs no PI in DN: ‘Every not’

#contrast coding: :P=1, 0=-1

Full model

```
maalappb = brm(
  formula = Irep ~ PI + Increasing+ (1+PI + Increasing| Content)+(1+ Increasing| subject),
  data = maalappbdf,
  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(maalappb)
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI + Increasing + (1 + PI + Increasing | Content) + (1 + Increasing | subject)
Data: maalappbdf (Number of observations: 1718)
Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup samples = 20000
```

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	2.16	1.16	0.20	4.73	1.00	5348
sd(PI1)	1.40	0.94	0.07	3.56	1.00	7622
sd(Increasing1)	2.77	1.24	0.54	5.58	1.00	6355
cor(Intercept,PI1)	0.38	0.45	-0.69	0.96	1.00	10063
cor(Intercept,Increasing1)	-0.20	0.42	-0.88	0.67	1.00	7585
cor(PI1,Increasing1)	-0.22	0.45	-0.92	0.72	1.00	6750

Tail_ESS

sd(Intercept)	5292
sd(PI1)	8030
sd(Increasing1)	4001
cor(Intercept,PI1)	10024
cor(Intercept,Increasing1)	9660
cor(PI1,Increasing1)	11765

~subject (Number of levels: 142)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	13.60	1.10	11.57	15.90	1.00	7172
sd(Increasing1)	16.10	1.25	13.80	18.70	1.00	5560
cor(Intercept,Increasing1)	0.10	0.11	-0.11	0.32	1.00	2641

Tail_ESS

sd(Intercept)	12496
sd(Increasing1)	10285
cor(Intercept,Increasing1)	5432

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	43.10	1.51	40.13	46.08	1.00	5698	10089
PI1	2.92	0.92	1.12	4.72	1.00	13452	14536
Increasing1	7.32	1.77	3.78	10.79	1.00	4942	9296

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	25.74	0.49	24.79	26.71	1.00	18298	14877

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`).

Probability that the presence of PPI increases the judgments

```
post_samples_maalappb = posterior_samples(maalappb)
mean(post_samples_maalappb$`b_PI1` < 0)
mean(post_samples_maalappb$`b_PI1` > 0)
[1] 0.00185
[1] 0.99815
```

PPI vs no PI in DN: ‘No without’

#contrast coding: :P=1, 0=-1

Full model

```
maalappb = brm(
  formula = Irep ~ PI + Increasing+ (1+PI + Increasing| Content)+ (1+ Increasing| subject),
  data = maalappbdf,
  iter = 10000, save_pars = save_pars(all = TRUE), control = list(adapt_delta = 0.99))
summary(maalappb)
Family: gaussian
Links: mu = identity; sigma = identity
Formula: Irep ~ PI + Increasing + (1 + PI + Increasing | Content) + (1 + Increasing | subject)
Data: maalappbdf (Number of observations: 1934)
Samples: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
         total post-warmup samples = 20000
```

Group-Level Effects:

~Content (Number of levels: 12)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	1.24	0.86	0.06	3.22	1.00	7757
sd(PI1)	1.32	0.93	0.06	3.46	1.00	7615
sd(Increasing1)	3.29	1.23	1.31	6.13	1.00	6735
cor(Intercept,PI1)	-0.09	0.49	-0.90	0.83	1.00	12839
cor(Intercept,Increasing1)	-0.21	0.45	-0.91	0.74	1.00	5058
cor(PI1,Increasing1)	0.03	0.45	-0.81	0.84	1.00	6370

Tail_ESS

sd(Intercept)	9085
sd(PI1)	9012
sd(Increasing1)	5858
cor(Intercept,PI1)	12782
cor(Intercept,Increasing1)	7118
cor(PI1,Increasing1)	9677

~subject (Number of levels: 140)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS
sd(Intercept)	15.32	1.12	13.27	17.66	1.00	6353
sd(Increasing1)	10.98	0.97	9.18	12.99	1.00	8005
cor(Intercept,Increasing1)	-0.04	0.11	-0.25	0.18	1.00	6282

Tail_ESS

```
sd(Intercept)          11332
sd(Increasing1)        12786
cor(Intercept,Increasing1) 10710
```

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	72.66	1.48	69.78	75.55	1.00	5057	9345
PI1	1.19	0.84	-0.46	2.84	1.00	16394	14505
Increasing1	-2.85	1.49	-5.81	0.09	1.00	8861	12719

Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	24.49	0.43	23.66	25.35	1.00	24938	15210

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`).

Probability that the presence of PPI increases the judgments

```
post_samples_maa1appb = posterior_samples(maa1appb)
mean(post_samples_maa1appb$`b_PI1` < 0)
mean(post_samples_maa1appb$`b_PI1` > 0)
[1] 0.07635
[1] 0.92365
```