

Stan code for Husain et al paper, PLoS ONE 2014

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1 Paper reference

This code is for the paper:

Samar Husain, Shravan Vasishth, and Narayanan Srinivasan. Strong Expectations Cancel Locality Effects: Evidence from Hindi. PLoS ONE, 9(7):1-14, 2014.

Available from: <http://tinyurl.com/pnaykvs>.

2 Abstract

Expectation-driven facilitation (Hale, 2001; Levy, 2008) and locality-driven retrieval difficulty (Gibson, 1998, 2000; Lewis & Vasishth, 2005) are widely recognized to be two critical factors in incremental sentence processing; there is accumulating evidence that both can influence processing difficulty. However, it is unclear whether and how expectations and memory interact. We first confirm a key prediction of the expectation account: a Hindi self-paced reading study shows that when an expectation for an upcoming part of speech is dashed, building a rarer structure consumes more processing time than building a less rare structure. This is a strong validation of the expectation-based account. In a second study, we show that when expectation is strong, i.e., when a particular verb is predicted, strong facilitation effects are seen when the appearance of the verb is delayed; however, when expectation is weak, i.e., when only the part of speech is predicted but a particular verb is not predicted, the facilitation disappears and a tendency towards a locality effect is seen. The interaction seen between expectation strength and distance shows that strong expectations cancel locality effects, and that weak expectations allow locality effects to emerge.

3 Session Info

- R version 3.1.1 (2014-07-10), x86_64-apple-darwin13.1.0
- Locale:
en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

- Base packages:
- Other packages: rstan 2.4.0
- Loaded via a namespace (and not attached): base 3.1.1, datasets 3.1.1, graphics 3.1.1, grDevices 3.1.1, inline 0.3.13, methods 3.1.1, Rcpp 0.11.2, stats 3.1.1, stats4 3.1.1, tools 3.1.1, utils 3.1.1

4 Experiment 1

4.1 Data preparation

Load data and format for Stan:

```
> RC1<-read.table("expt1critdata.txt",header=T)
> e1data <- list(mu_prior=c(0,0,0,0),
+               subj=sort(as.integer(factor(RC1$subj))),
+               item=sort(as.integer(factor(RC1$item))),
+               lrt=RC1$lrt,
+               dist = RC1$dist,
+               rctype = RC1$RCTYPE,
+               interaction = RC1$int,
+               N = nrow(RC1),
+               I = length(unique(RC1$subj)),
+               K = length(unique(RC1$item))
+ )
```

4.2 Define model (method 1)

```
> expt1_code <-
+ 'data {
+   int<lower=1> N;
+   real lrt[N];
+   real<lower=-1,upper=1> dist[N];
+   real rctype[N];
+   real interaction[N];
+   int<lower=1> I;
+   int<lower=1> K;
+   int<lower=1, upper=I> subj[N];
+   int<lower=1, upper=K> item[N];
+   vector[4] mu_prior;
+ }
+ transformed data {
+   real ZERO;
+   ZERO <- 0.0;
+ }
```

```

+ parameters {
+   vector[4] beta;           // intercept and slope
+   vector[4] u[I];          // random intercept and slopes subj
+   vector[4] w[K];
+   real<lower=0> sigma_e;     // residual sd
+   vector<lower=0>[4] sigma_u; // subj sd
+   vector<lower=0>[4] sigma_w; // item sd
+   corr_matrix[4] Omega_u;   // correlation matrix for random intercepts and slopes s
+   corr_matrix[4] Omega_w;   // correlation matrix for random intercepts and slopes i
+ }
+ transformed parameters {
+   matrix[4,4] D_u;
+   matrix[4,4] D_w;
+   D_u <- diag_matrix(sigma_u);
+   D_w <- diag_matrix(sigma_w);
+ }
+ model {
+   matrix[4,4] L_u;
+   matrix[4,4] DL_u;
+   matrix[4,4] L_w;
+   matrix[4,4] DL_w;
+   real mu[N]; // mu for likelihood
+   //priors:
+   beta ~ normal(0,10);
+   sigma_e ~ normal(0,10);
+   sigma_u ~ normal(0,10);
+   sigma_w ~ normal(0,10);
+   Omega_u ~ lkj_corr(4.0);
+   Omega_w ~ lkj_corr(4.0);
+   L_u <- cholesky_decompose(Omega_u);
+   L_w <- cholesky_decompose(Omega_w);
+   for (m in 1:4) {
+     for (n in 1:m) {
+       DL_u[m,n] <- L_u[m,n] * sigma_u[m];
+     }
+   }
+   for (m in 1:4){
+     for (n in (m+1):4){
+       DL_u[m,n] <- ZERO;
+     }
+   }
+   for (m in 1:4){
+     for (n in 1:m){
+       DL_w[m,n] <- L_w[m,n] * sigma_w[m];
+     }
+   }
+ }

```

```

+ for (m in 1:4){
+   for (n in (m+1):4){
+     DL_w[m,n] <- ZERO;
+   }
+ }
+ for (i in 1:I)           // loop for subj random effects
+ u[i] ~ multi_normal_cholesky(mu_prior, DL_u);
+ for (k in 1:K)           // loop for item random effects
+ w[k] ~ multi_normal_cholesky(mu_prior, DL_w);
+ for (n in 1:N) {
+ mu[n] <- beta[1] + beta[2]*dist[n] + beta[3]*rctype[n] + beta[4]*interaction[n] + u[subj[n]]
+ }
+ lrt ~ normal(mu,sigma_e);      // likelihood
+ }
+ generated quantities {
+ cov_matrix[4] Sigma_u;
+ cov_matrix[4] Sigma_w;
+ Sigma_u <- D_u * Omega_u * D_u;
+ Sigma_w <- D_w * Omega_w * D_w;
+ }
+ '

```

Fit data:

```

> set_cppo('fast')
> fit <- stan(model_code = expt1_code, data = e1data,
+           iter = 500, chains = 4)

```

TRANSLATING MODEL 'expt1_code' FROM Stan CODE TO C++ CODE NOW.
 COMPILING THE C++ CODE FOR MODEL 'expt1_code' NOW.

SAMPLING FOR MODEL 'expt1_code' NOW (CHAIN 1).

```

Iteration: 1 / 500 [ 0%] (Warmup)
Iteration: 50 / 500 [ 10%] (Warmup)
Iteration: 100 / 500 [ 20%] (Warmup)
Iteration: 150 / 500 [ 30%] (Warmup)
Iteration: 200 / 500 [ 40%] (Warmup)
Iteration: 250 / 500 [ 50%] (Warmup)
Iteration: 251 / 500 [ 50%] (Sampling)
Iteration: 300 / 500 [ 60%] (Sampling)
Iteration: 350 / 500 [ 70%] (Sampling)
Iteration: 400 / 500 [ 80%] (Sampling)
Iteration: 450 / 500 [ 90%] (Sampling)
Iteration: 500 / 500 [100%] (Sampling)
# Elapsed Time: 12.7522 seconds (Warm-up)
#               5.3349 seconds (Sampling)

```

18.0871 seconds (Total)

SAMPLING FOR MODEL 'expt1_code' NOW (CHAIN 2).

Iteration: 1 / 500 [0%] (Warmup)
Iteration: 50 / 500 [10%] (Warmup)
Iteration: 100 / 500 [20%] (Warmup)
Iteration: 150 / 500 [30%] (Warmup)
Iteration: 200 / 500 [40%] (Warmup)
Iteration: 250 / 500 [50%] (Warmup)
Iteration: 251 / 500 [50%] (Sampling)
Iteration: 300 / 500 [60%] (Sampling)
Iteration: 350 / 500 [70%] (Sampling)
Iteration: 400 / 500 [80%] (Sampling)
Iteration: 450 / 500 [90%] (Sampling)
Iteration: 500 / 500 [100%] (Sampling)
Elapsed Time: 14.4072 seconds (Warm-up)
24.3153 seconds (Sampling)
38.7225 seconds (Total)

SAMPLING FOR MODEL 'expt1_code' NOW (CHAIN 3).

Iteration: 1 / 500 [0%] (Warmup)
Iteration: 50 / 500 [10%] (Warmup)
Iteration: 100 / 500 [20%] (Warmup)
Iteration: 150 / 500 [30%] (Warmup)
Iteration: 200 / 500 [40%] (Warmup)
Iteration: 250 / 500 [50%] (Warmup)
Iteration: 251 / 500 [50%] (Sampling)
Iteration: 300 / 500 [60%] (Sampling)
Iteration: 350 / 500 [70%] (Sampling)
Iteration: 400 / 500 [80%] (Sampling)
Iteration: 450 / 500 [90%] (Sampling)
Iteration: 500 / 500 [100%] (Sampling)
Elapsed Time: 10.2164 seconds (Warm-up)
10.2089 seconds (Sampling)
20.4253 seconds (Total)

SAMPLING FOR MODEL 'expt1_code' NOW (CHAIN 4).

Iteration: 1 / 500 [0%] (Warmup)
Iteration: 50 / 500 [10%] (Warmup)
Iteration: 100 / 500 [20%] (Warmup)

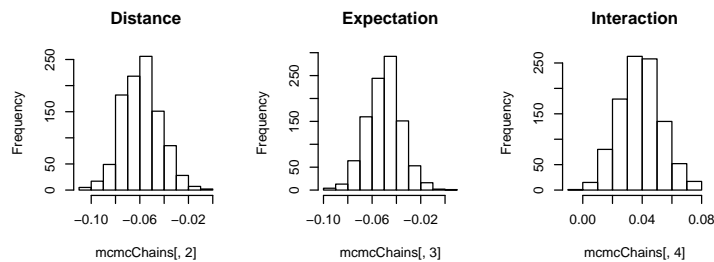
```

Iteration: 150 / 500 [ 30%] (Warmup)
Iteration: 200 / 500 [ 40%] (Warmup)
Iteration: 250 / 500 [ 50%] (Warmup)
Iteration: 251 / 500 [ 50%] (Sampling)
Iteration: 300 / 500 [ 60%] (Sampling)
Iteration: 350 / 500 [ 70%] (Sampling)
Iteration: 400 / 500 [ 80%] (Sampling)
Iteration: 450 / 500 [ 90%] (Sampling)
Iteration: 500 / 500 [100%] (Sampling)
# Elapsed Time: 10.877 seconds (Warm-up)
#               10.9669 seconds (Sampling)
#               21.844 seconds (Total)

> ## not run, too verbose:
> #print(fit)

```

Plot the posterior distributions of the three coefficients of interest:



4.3 Run model (Method 2)

```

> library(parallel)
> ## uncomment to save results to a file:
> #sink("expt1resultsrun2.txt")

```

```
>
> ## the model is defined in a separate file:
> e1.sm <- stan_model("expt1subjitem.stan", model_name = "e1subjitem")
```

```
TRANSLATING MODEL 'e1subjitem' FROM Stan CODE TO C++ CODE NOW.
COMPILING THE C++ CODE FOR MODEL 'e1subjitem' NOW.
```

```
> sflist <- mclapply(1:4, mc.cores = detectCores(),
+                   function(i) sampling(e1.sm, data = e1data,
+                                       chains = 1, chain_id = i,
+                                       seed = 12345))
> e1.sf <- sflist2stanfit(sflist)
> #print(e1.sf,digits=4)
```

Comparison with lmer:

```
> library(lme4)
> m1<-lmer(lrt~dist+RCType+int+(1+dist+RCType+int/subj)+(1+dist+RCType+int/item),RC1)
> summary(m1)
```

Linear mixed model fit by REML ['lmerMod']

Formula: lrt ~ dist + RCType + int + (1 + dist + RCType + int | subj) +
(1 + dist + RCType + int | item)

Data: RC1

REML criterion at convergence: 2051.9

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-5.6366	-0.6089	-0.1853	0.4630	4.6925

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
subj	(Intercept)	0.0901560	0.30026	
	dist	0.0031861	0.05645	-0.60
	RCType	0.0005826	0.02414	-0.56 0.70
	int	0.0018562	0.04308	0.74 -0.94 -0.88
item	(Intercept)	0.0034894	0.05907	
	dist	0.0018261	0.04273	-0.39
	RCType	0.0007440	0.02728	0.60 -0.35
	int	0.0010803	0.03287	-0.61 -0.38 0.05
Residual		0.2089150	0.45707	

Number of obs: 1440, groups: subj, 60; item, 24

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	6.65832	0.04234	157.24

dist	-0.05746	0.01656	-3.47
RCType	-0.04974	0.01363	-3.65
int	0.03712	0.01487	2.50

Correlation of Fixed Effects:

	(Intr)	dist	RCType
dist	-0.301		
RCType	-0.047	-0.005	
int	0.176	-0.245	-0.067

5 Experiment 2

5.1 Data preparation

Load data:

```
> CP1<-read.table("expt2critdata.txt",header=T)
> e2data <- list(mu_prior=c(0,0,0,0),
+               subj=sort(as.integer(factor(CP1$subj))),
+               item=sort(as.integer(factor(CP1$item))),
+               lrt = log(CP1$rt),
+               dist = CP1$dist,
+               expectation = CP1$exp,
+               interaction = CP1$int,
+               N = nrow(CP1),
+               I = length(unique(CP1$subj)),
+               K = length(unique(CP1$item))
+ )
```

5.2 Define model

```
> expt2_code <-'
+ data {
+   int<lower=0> N;
+   real lrt[N];
+   real dist[N];
+   real expectation[N];
+   real interaction[N];
+   int<lower=1> I;
+   int<lower=1> K;
+   int<lower=1, upper=I> subj[N];
+   int<lower=1, upper=K> item[N];
+   vector[4] mu_prior;
+ }
+ transformed data {
+   real ZERO;
+   //outcome
+   //predictor
+   //predictor
+   //predictor
+   //number of subjects
+   //number of items
+   //subject id
+   //item id
+   //vector of zeros passed in from R
+   // like #define ZERO 0 in C/C++
```



```

+ ZERO <- 0.0;
+ }
+ parameters {
+   vector[4] beta;           // intercept and slope
+   vector[4] u[I];           // random intercept and slopes subj
+   vector[4] w[K];
+   real<lower=0> sigma_e;     // residual sd
+   vector<lower=0>[4] sigma_u; // subj sd
+   vector<lower=0>[4] sigma_w; // item sd
+   corr_matrix[4] Omega_u;   // correlation matrix for random intercepts and slopes s
+   corr_matrix[4] Omega_w;   // correlation matrix for random intercepts and slopes i
+ }
+ transformed parameters {
+   matrix[4,4] D_u;
+   matrix[4,4] D_w;
+   D_u <- diag_matrix(sigma_u);
+   D_w <- diag_matrix(sigma_w);
+ }
+ model {
+   matrix[4,4] L_u;
+   matrix[4,4] DL_u;
+   matrix[4,4] L_w;
+   matrix[4,4] DL_w;
+   real mu[N]; // mu for likelihood
+   //priors:
+   beta ~ normal(0,10);
+   sigma_e ~ normal(0,10);
+   sigma_u ~ normal(0,10);
+   sigma_w ~ normal(0,10);
+   Omega_u ~ lkj_corr(4.0);
+   Omega_w ~ lkj_corr(4.0);
+   L_u <- cholesky_decompose(Omega_u);
+   L_w <- cholesky_decompose(Omega_w);
+   for (m in 1:4) {
+     for (n in 1:m) {
+       DL_u[m,n] <- L_u[m,n] * sigma_u[m];
+     }
+   }
+   for (m in 1:4){
+     for (n in (m+1):4){
+       DL_u[m,n] <- ZERO;
+     }
+   }
+   for (m in 1:4){
+     for (n in 1:m){
+       DL_w[m,n] <- L_w[m,n] * sigma_w[m];

```

```

+ }
+ }
+ for (m in 1:4){
+ for (n in (m+1):4){
+ DL_w[m,n] <- ZERO;
+ }
+ }
+ for (i in 1:I)           // loop for subj random effects
+ u[i] ~ multi_normal_cholesky(mu_prior, DL_u);
+ for (k in 1:K)           // loop for item random effects
+ w[k] ~ multi_normal_cholesky(mu_prior, DL_w);
+ for (n in 1:N) {
+ mu[n] <- beta[1] + beta[2]*dist[n] + beta[3]*expectation[n] + beta[4]*interaction[n]
+ + u[subj[n], 1] + u[subj[n], 2]*dist[n] + u[subj[n], 3]*expectation[n] + u[subj[n], 4]*int
+ }
+ lrt ~ normal(mu,sigma_e);           // likelihood
+ }
+ generated quantities {
+ cov_matrix[4] Sigma_u;
+ cov_matrix[4] Sigma_w;
+ Sigma_u <- D_u * Omega_u * D_u;
+ Sigma_w <- D_w * Omega_w * D_w;
+ }
+ '

```

5.3 Run model (Method 1)

```

> set_cppo('fast')
> fit <- stan(model_code = expt2_code, data = e2data,
+             iter = 500, chains = 2)

```

TRANSLATING MODEL 'expt2_code' FROM Stan CODE TO C++ CODE NOW.
 COMPILING THE C++ CODE FOR MODEL 'expt2_code' NOW.

SAMPLING FOR MODEL 'expt2_code' NOW (CHAIN 1).

```

Iteration: 1 / 500 [ 0%] (Warmup)
Iteration: 50 / 500 [ 10%] (Warmup)
Iteration: 100 / 500 [ 20%] (Warmup)
Iteration: 150 / 500 [ 30%] (Warmup)
Iteration: 200 / 500 [ 40%] (Warmup)
Iteration: 250 / 500 [ 50%] (Warmup)
Iteration: 251 / 500 [ 50%] (Sampling)
Iteration: 300 / 500 [ 60%] (Sampling)
Iteration: 350 / 500 [ 70%] (Sampling)
Iteration: 400 / 500 [ 80%] (Sampling)

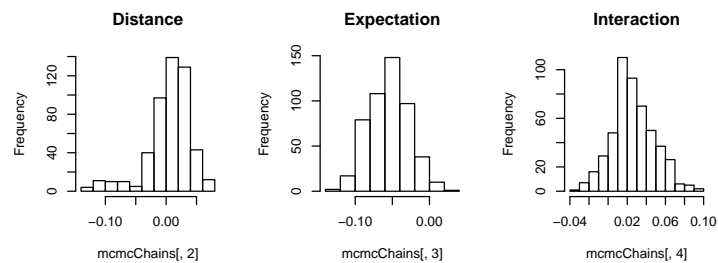
```

```
Iteration: 450 / 500 [ 90%] (Sampling)
Iteration: 500 / 500 [100%] (Sampling)
# Elapsed Time: 5.85641 seconds (Warm-up)
#               4.26557 seconds (Sampling)
#               10.122 seconds (Total)
```

SAMPLING FOR MODEL 'expt2_code' NOW (CHAIN 2).

```
Iteration:   1 / 500 [  0%] (Warmup)
Iteration:  50 / 500 [ 10%] (Warmup)
Iteration: 100 / 500 [ 20%] (Warmup)
Iteration: 150 / 500 [ 30%] (Warmup)
Iteration: 200 / 500 [ 40%] (Warmup)
Iteration: 250 / 500 [ 50%] (Warmup)
Iteration: 251 / 500 [ 50%] (Sampling)
Iteration: 300 / 500 [ 60%] (Sampling)
Iteration: 350 / 500 [ 70%] (Sampling)
Iteration: 400 / 500 [ 80%] (Sampling)
Iteration: 450 / 500 [ 90%] (Sampling)
Iteration: 500 / 500 [100%] (Sampling)
# Elapsed Time: 5.76126 seconds (Warm-up)
#               3.07824 seconds (Sampling)
#               8.8395 seconds (Total)
```

Plot posterior distributions:



5.4 Run model (Method 2)

```
> #sink("expt2resultsrun2.txt")
>
> e2.sm <- stan_model("expt2subjitem.stan", model_name = "e2subjitem")
```

TRANSLATING MODEL 'e2subjitem' FROM Stan CODE TO C++ CODE NOW.
 COMPILING THE C++ CODE FOR MODEL 'e2subjitem' NOW.

```
> sflist <- mclapply(1:4, mc.cores = detectCores(),
+                   function(i) sampling(e2.sm, data = e2data, chains = 1, chain_id = i, seed = i))
> e2.sf <- sflist2stanfit(sflist)
> #print(e2.sf, digits=4)
> #sink()
```