

Modelling structured trial-by-trial variability in evidence accumulation

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Introduction

In this tutorial, we will demonstrate how to design dynamic evidence accumulation models and fit them to data using hierarchical Bayesian methods. We will utilize the *EMC2* package, assuming some prior knowledge of its functionalities (for reference, see the *EMC2* tutorial). Specifically, we will fit models to dataset 1 from Miletić et al. (2025), which corresponds to the ‘choice, short [CS]’ condition from Wagenmakers et al. (2004). In this experiment, participants were presented with a single digit and required to determine whether the digit was even or odd.

First, let’s load the required packages and data:

```
rm(list = ls())
# TMP -- install the right branch
# remotes::install_github("ampl-psych/EMC2@RL", dependencies=TRUE, Ncpus=8); .rs.restartR()
# END TMP
library(EMC2)
set.seed(1) # for reproducibility

# This is some code that contains plotting functions used later on in this tutorial
source('./plotting_utils.R')

# Load in the data
load("datasets/dataset_1.RData")

# Inspect the data
print(head(dat))
```

	subjects	S	R	rt
1	1	even	even	0.542
2	1	even	even	0.426
3	1	even	even	0.501
4	1	even	even	0.403
5	1	odd	odd	0.497
6	1	even	even	0.518

Here, **subjects** refers to subject number, **S** to the presented stimulus (even/odd), **R** the response (even/odd), and **rt** the response time in seconds.

Baseline models

We begin by setting up the ‘static’ baseline models without structured trial-by-trial variability. For a comprehensive tutorial on specifying designs in *EMC2*, please refer to the *EMC2* tutorial [ref]. We will set up two baseline models: first using a racing diffusion model (RDM), and then using a diffusion decision model (DDM). In the RDM, we model drift rates with a mean-difference parametrization. The `mapped_pars()` function is useful for tracking how parameter vectors are mapped onto each design cell:

```
# set up contrast matrix for mean-difference parametrisation
ADmat <- matrix(c(-.5,.5), ncol=1, dimnames=list(NULL,'d'))
design_RDM <- design(model=RDM,
                    data=dat,
                    contrast=list(lM=ADmat),
                    matchfun=function(d) d$S==d$lR,
                    formula=list(B ~ 1, v ~ lM, t0 ~ 1))
```

Sampled Parameters:

```
[1] "B"      "v"      "v_lMd" "t0"
```

Design Matrices:

\$B

B

1

\$v

	lM	v	v_lMd
TRUE	1		0.5
FALSE	1		-0.5

\$t0

t0

1

\$A

A

1

\$s

s

1

```
mapped_pars(design_RDM)
```

\$v

lM

TRUE : $\exp(v + 0.5 * v_lMd)$

FALSE : $\exp(v - 0.5 * v_lMd)$

In the DDM, we need to remember to flip the sign of the drift rate for one of the two stimulus types (in this case, even):

```
Smat <- matrix(c(-1,1), nrow = 2,dimnames=list(NULL,"dif"))
design_DDM <- design(model=DDM,
                    data=dat,
                    contrasts=list(S=Smat),
                    formula=list(Z ~ 1, v ~ S, a~1, t0 ~ 1))
```

```
Sampled Parameters:
[1] "Z"      "v"      "v_Sdif" "a"      "t0"
```

```
Design Matrices:
```

```
$Z
```

```
Z
```

```
1
```

```
$v
```

```
  S v v_Sdif
```

```
even 1      -1
```

```
odd 1       1
```

```
$a
```

```
a
```

```
1
```

```
$t0
```

```
t0
```

```
1
```

```
$s
```

```
s
```

```
1
```

```
$st0
```

```
st0
```

```
1
```

```
$sv
```

```
sv
```

```
1
```

```
$SZ
```

```
SZ
```

```
1
```

```
mapped_pars(design_DDM)
```

```
$v
```

```
S
```

```
even : v - v_Sdif
```

```
odd  : v + v_Sdif
```

Trend specification

Both the descriptive trends and the formal mechanisms of dynamics work through **trend** objects in *EMC2*. In this object, you specify (1) the covariate of interest (e.g., time on task), (2) a kernel to apply to the covariate (e.g., linear, power, exponential, polynomial, or delta rule), and (3) which decision parameter is informed by the resulting covariate, and (4) the functional form of the mapping between the resulting covariate and the decision parameters, referred to as the ‘base’. The **trend_help()** function gives an overview of the options:

```
trend_help()
```

Available kernels:

```
lin_decr: Decreasing linear kernel:  $k = -c$ 
lin_incr: Increasing linear kernel:  $k = c$ 
exp_decr: Decreasing exponential kernel:  $k = \exp(-d_{ed} * c)$ 
exp_incr: Increasing exponential kernel:  $k = 1 - \exp(-d_{ei} * c)$ 
pow_decr: Decreasing power kernel:  $k = (1 + c)^{-d_{pd}}$ 
pow_incr: Increasing power kernel:  $k = 1 - (1 + c)^{-d_{pi}}$ 
poly2: Quadratic polynomial:  $k = d_1 * c + d_2 * c^2$ 
poly3: Cubic polynomial:  $k = d_1 * c + d_2 * c^2 + d_3 * c^3$ 
poly4: Quartic polynomial:  $k = d_1 * c + d_2 * c^2 + d_3 * c^3 + d_4 * c^4$ 
delta: Standard delta rule kernel:  $k = q[i]$ .
      Updates  $q[i] = q[i-1] + \alpha * (c[i-1] - q[i-1])$ .
      Parameters:  $q_0$  (initial value),  $\alpha$  (learning rate).
delta2: Dual kernel delta rule:  $k = q[i]$ .
      Combines fast and slow learning rates
      and switches between them based on  $dSwitch$ .
      Parameters:  $q_0$  (initial value),  $\alpha_{Fast}$  (fast learning rate),
       $\alpha_{Slow}$  ( $\alpha_{Slow} = \alpha_{Fast} * propSlow$ ),  $dSwitch$  (switch threshold).
deltab: Threshold learning delta rule kernel:  $k = q_{FM}[i]$ .
      Updates  $q[i] = q[i-1] + \alpha * (B[i]/c[i-1] - q[i-1])$ .
      Parameters:  $q_0$  (initial value),  $\alpha$  (learning rate).
```

Available base types:

```
lin: Linear base:  $parameter + w * k$ 
exp_lin: Exponential linear base:  $\exp(parameter) + \exp(w) * k$ 
centered: Centered mapping:  $parameter + w * (k - 0.5)$ 
add: Additive base:  $parameter + k$ 
identity: Identity base:  $k$ 
```

Trend options:

```
premap: Trend is applied before parameter mapping. This means the trend parameters
        are mapped first, then used to transform cognitive model parameters before
        their mapping.
pretransform: Trend is applied after parameter mapping but before transformations.
              Cognitive model parameters are mapped first, then trend is applied,
              followed by transformations.
posttransform: Trend is applied after both mapping and transformations.
               Cognitive model parameters are mapped and transformed first,
               then trend is applied.
```

The last section, ‘trend options’, warrants some extra attention. In *EMC2*, the user can define parameters using model formula language, as we did above when defining the designs. *EMC2* uses these to create a design matrix by mapping the relevant factors to each design cell. In the case of the RDM, once mapped,

in each design cell, only the v , B , t_0 , s , (and optionally A) parameters per accumulator remain. However, in many applications, the parameter of interest is defined as a between-accumulator difference (e.g., v_lM_d in the RDM example above), or a between-condition difference (e.g., the effect of speed-accuracy trade-off cues on thresholds). These parameters only exist pre-mapping, and thus, the trend should be applied prior to mapping by setting `premap` to `TRUE`.

There is an important caveat here. By default, *EMC2* estimates parameters with a lower bound (e.g., non-decision time, thresholds, RDM's drift rates) on the log scale, and parameters with both a lower and upper bound on the probit scale. Parameters are *mapped* on the scale on which they are estimated, and *then* transformed. This also implies that if a trend is applied prior to mapping, the resulting parameters might later be transformed, leading to a potentially unwanted non-linear effect of the covariate on the parameter.

Let's clarify with an example. Let's try to impose a linear trend on thresholds in case of the RDM:

```
# Add a 'trials' column specifying trial number
dat <- EMC2::add_trials(dat)

# Rescale the effect of this covariate to a larger parameter range to help sampling
dat$trials2 <- dat$trials/1000
lin_trend <- make_trend(cov_names='trials2',
                       kernels = 'lin_incr',
                       par_names='B',
                       bases='lin',
                       premap=TRUE)

design_RDM_lin_B <- design(model=RDM,
                          data=dat,
                          contrast=list(lM=ADmat),
                          covariates='trials2', # specify relevant covariate columns
                          matchfun=function(d) d$S==d$lR,
                          formula=list(B ~ 1, v ~ lM, t0 ~ 1),
                          trend=lin_trend) # add trend
```

Sampled Parameters:

```
[1] "B"      "v"      "v_lMd" "t0"     "B.w"
```

Design Matrices:

```
$B
```

```
B
```

```
1
```

```
$v
```

```
lM v v_lMd
```

```
TRUE 1 0.5
```

```
FALSE 1 -0.5
```

```
$t0
```

```
t0
```

```
1
```

```
$B.w
```

```
B.w
```

```
1
```

```
$A
```

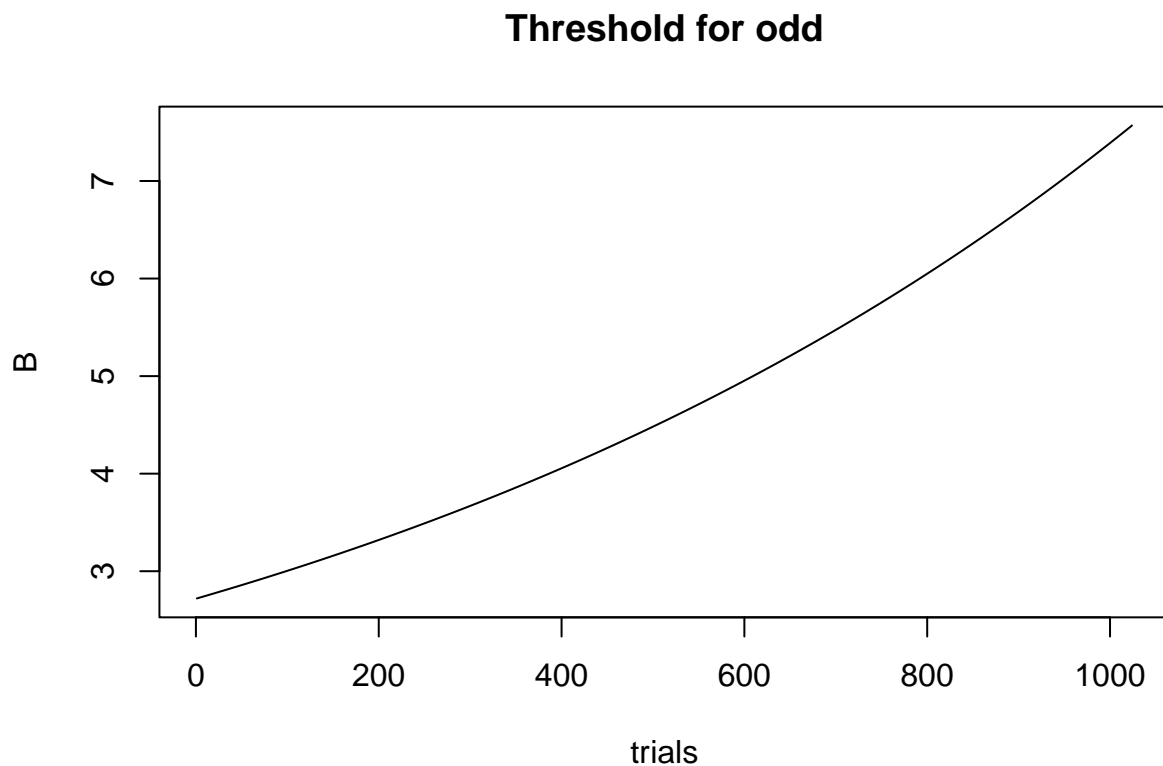
```
A
1

$s
s
1
```

Note that we are now sampling one extra parameter compared to before, $B.w$, which is the weight of the influence of trial number on thresholds. In $B_t = B_0 + B.w * trial$. Let's define a set of parameters and look at the resulting trial-by-trial thresholds:

```
samplers <- make_emc(dat, design=design_RDM_lin_B)
p_vector <- c('B'=1, 'v'=1, 'v_lMd'=1, 't0'=0.1, 'B.w'=1)

# Visualize trend
plot_trend(p_vector, samplers=samplers,
           par_name='B', subject=1,
           lR_filter='odd', main='Threshold for odd')
```



Clearly, this is not a linear increase. This happens because the threshold is sampled on the log scale, so an exponential transform is applied after mapping the parameter vector to the design cells. Since the linear trend was applied prior to mapping, this linear effect becomes non-linear. `mapped_pars()` demonstrates this:

```
mapped_pars(design_RDM_lin_B)
```

```
$B
```

```

      : exp(B_t)
Trends:
  B_t = B + B.w * trials2

$v
  LM
  TRUE  : exp(v + 0.5 * v_lMd)
  FALSE  : exp(v - 0.5 * v_lMd)

```

One option to prevent this from happening is to apply the trend after mapping and transformation, as follows:

```

lin_trend2 <- make_trend(cov_names='trials2',
                        kernels = 'lin_incr',
                        par_names='B',
                        bases='lin',
                        premap=FALSE, pretransform=FALSE)
design_RDM_lin_B2 <- design(model=RDM,
                          data=dat,
                          contrast=list(LM=ADmat),
                          covariates='trials2', # specify relevant covariate columns
                          matchfun=function(d) d$S==d$LR,
                          formula=list(B ~ 1, v ~ LM, t0 ~ 1),
                          trend=lin_trend2) # add trend

```

```

Sampled Parameters:
[1] "B"      "v"      "v_lMd" "t0"     "B.w"

```

Design Matrices:

```

$B
B
1

$v
  LM v v_lMd
  TRUE 1 0.5
  FALSE 1 -0.5

$t0
t0
1

$B.w
B.w
1

$A
A
1

$s
s
1

```

```
# note how the trend is added after the transformation
mapped_pars(design_RDM_lin_B2)
```

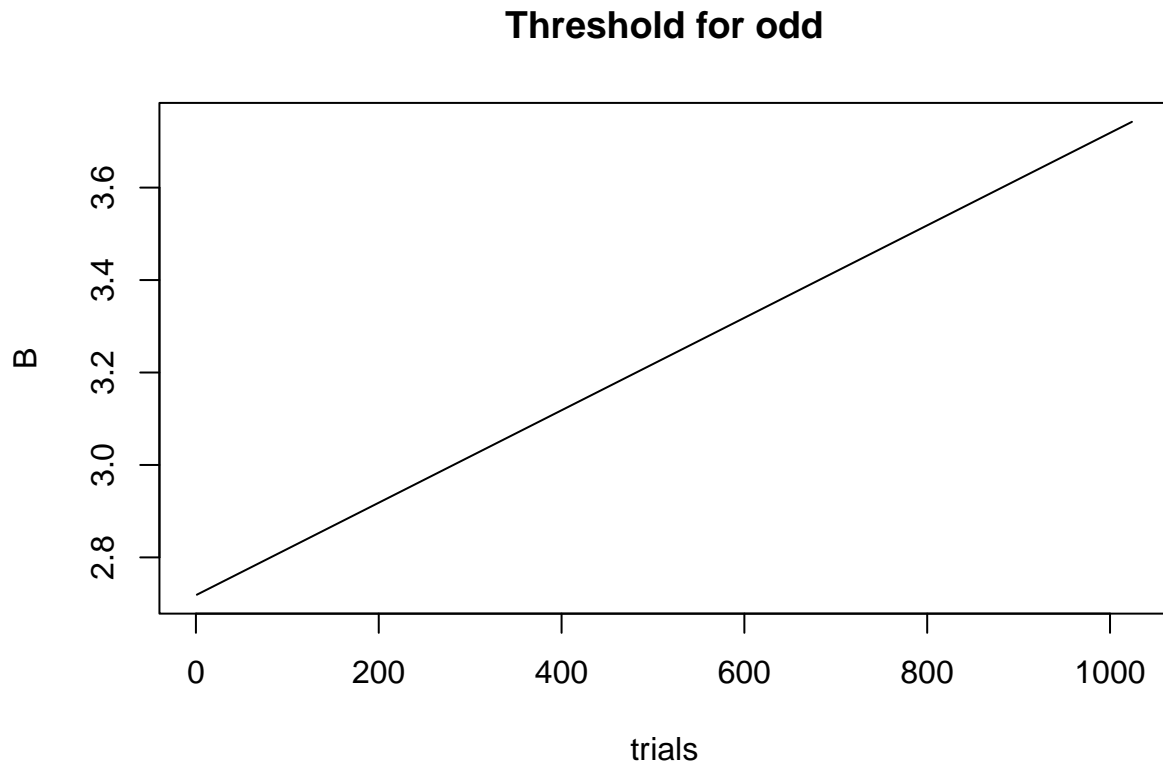
```
$B
```

```
      : exp(B) + B_t
Trends:
  B_t = B.w * trials2
```

```
$v
```

```
  lM
TRUE  : exp(v + 0.5 * v_lMd)
FALSE : exp(v - 0.5 * v_lMd)
```

```
samplers <- make_emc(dat, design=design_RDM_lin_B2)
p_vector <- c('B'=1, 'v'=1, 'v_lMd'=1, 't0'=0.1, 'B.w'=1)
# Visualize trend
plot_trend(p_vector, samplers=samplers,
            par_name='B', subject=1,
            lR_filter='odd', main='Threshold for odd')
```



However, `posttransform` implies `postmap`, and many parameters of interest are defined only prior to mapping. So applying trends to those premap parameter types is not possible in combination with `posttransform`. Instead, the user can tell *EMC2* to estimate parameters on their natural scales by turning off transformations of the relevant parameters. For example:


```

lin_trend3 <- make_trend(cov_names='trials2',
                        kernels = 'lin_incr',
                        par_names='B',
                        bases='lin',
                        premap=TRUE) # back to premap
design_RDM_lin_B3 <- design(model=RDM,
                           data=dat,
                           contrast=list(lM=ADmat),
                           covariates='trials2',
                           matchfun=function(d) d$S==d$Lr,
                           # here, we tell EMC2 to sample the threshold on the natural scale
                           transform=list(func=c('B'='identity')),
                           formula=list(B ~ 1, v ~ lM, t0 ~ 1),
                           trend=lin_trend3) # add trend

```

Sampled Parameters:

```
[1] "B"      "v"      "v_lMd" "t0"     "B.w"
```

Design Matrices:

\$B

B

1

\$v

lM v v_lMd

TRUE 1 0.5

FALSE 1 -0.5

\$t0

t0

1

\$B.w

B.w

1

\$A

A

1

\$s

s

1

```

# note how the transformation is no longer applied at all
mapped_pars(design_RDM_lin_B3)

```

\$B

: B_t

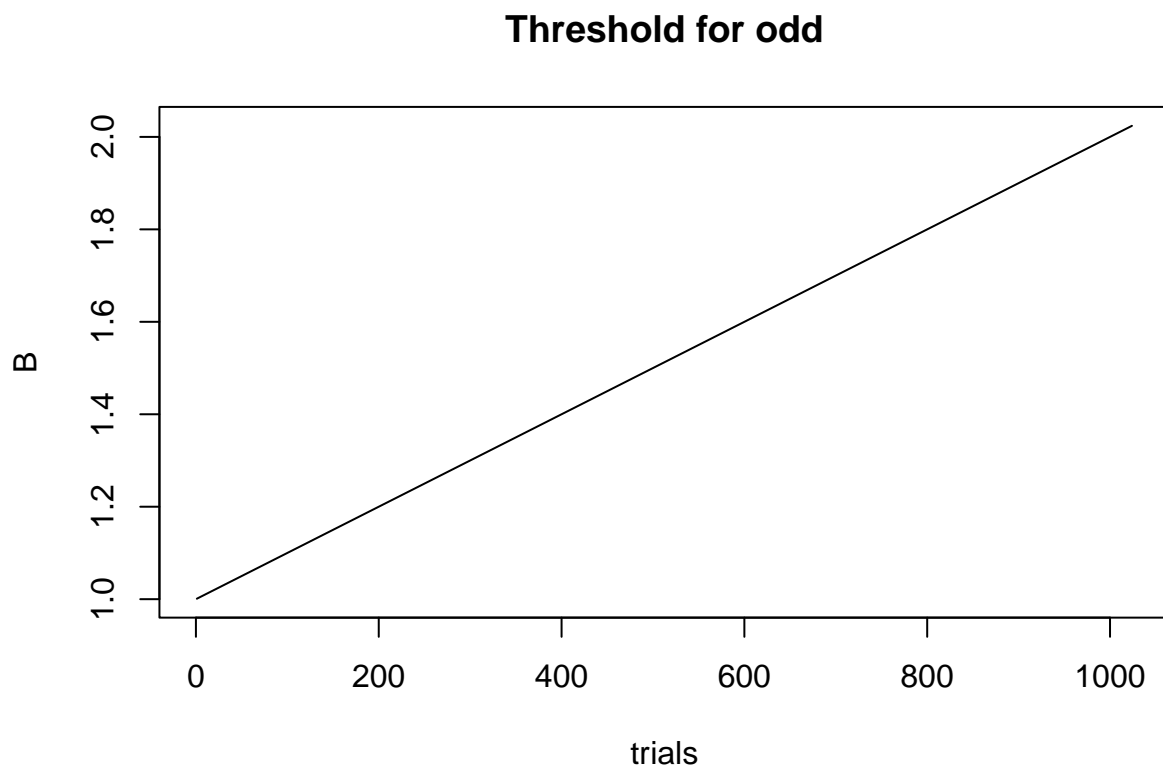
Trends:

B_t = B + B.w * trials2

```
$v
  lM
TRUE  : exp(v + 0.5 * v_lMd)
FALSE : exp(v - 0.5 * v_lMd)
```

```
samplers <- make_emc(dat, design=design_RDM_lin_B3)
p_vector <- c('B'=1, 'v'=1, 'v_lMd'=1, 't0'=0.1, 'B.w'=1)

# visualize trend
plot_trend(p_vector, samplers=samplers,
           par_name='B', subject=1,
           lR_filter='odd', main='Threshold for odd')
```

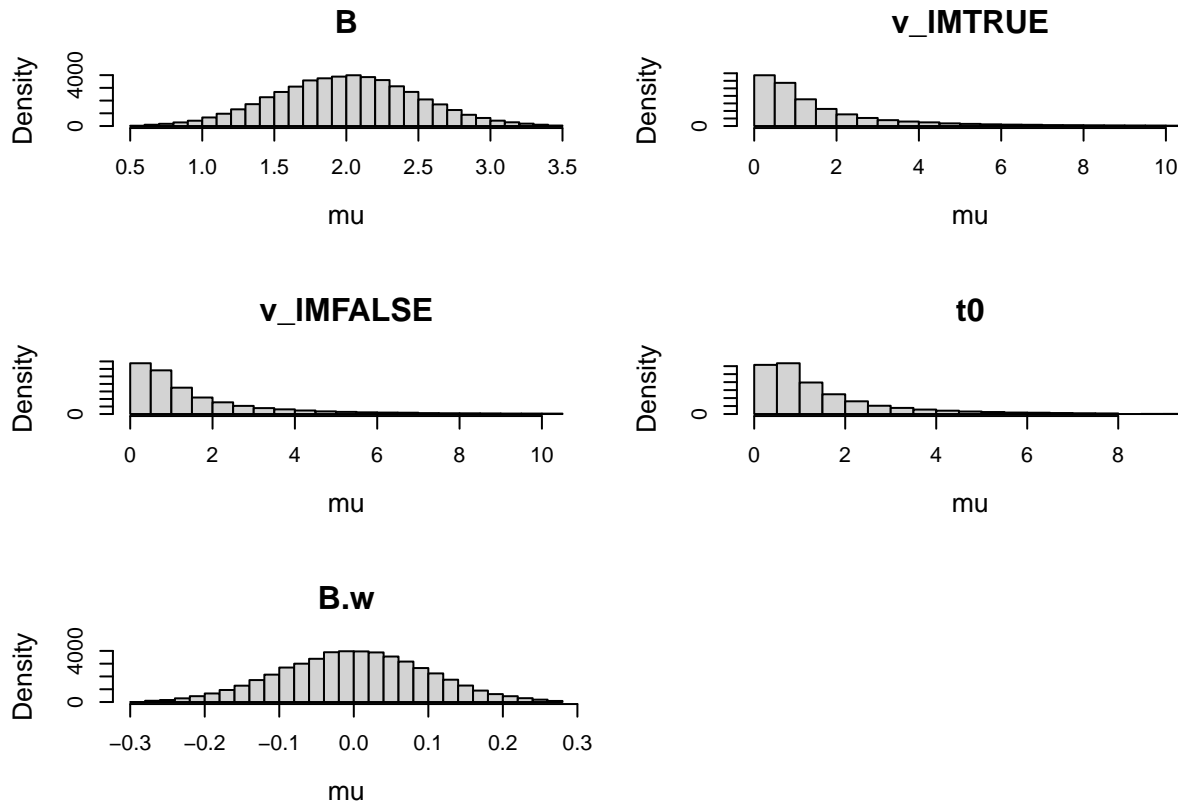


This leads to the expected effect. As a cautionary note, keep in mind that the default priors in *EMC2* are Gaussian distributions centered on 0 with unit variance. Since many cognitive model parameters cannot be negative, a $N(0,1)$ prior is poorly chosen for those parameters that do not have support on the real line. For estimation and sampling, this usually has little influence in practice, but it may be important when estimating Bayes Factors.

With all that in mind, we can now start sampling our first model. We set a $N(2,0.5)$ prior on the threshold B to reduce the prior density on negative thresholds. This is a somewhat subjective choice based on earlier experience, so it reflects my (but perhaps not your) prior belief. The rest of the priors are left to their default $N(0,1)$ – on the scale on which they are sampled.

```
prior_linB <- prior(design_RDM_lin_B3, mu_mean=c(B=2, B.w=0), mu_sd=c(B=0.5,B.w=0.1))
samplers <- make_emc(dat, design=design_RDM_lin_B3, prior_list = prior_linB)
```

```
plot(samplers, prior=TRUE)
```



```
samplers <- fit(samplers, cores_per_chain=6, cores_for_chains=3,
  fileName='./samples/ds1_linB.RData')
```

Time difference of 2.511284 mins

```
check(samplers)
```

Iterations:

	preburn	burn	adapt	sample
[1,]	0	0	0	1000
[2,]	0	0	0	1000
[3,]	0	0	0	1000

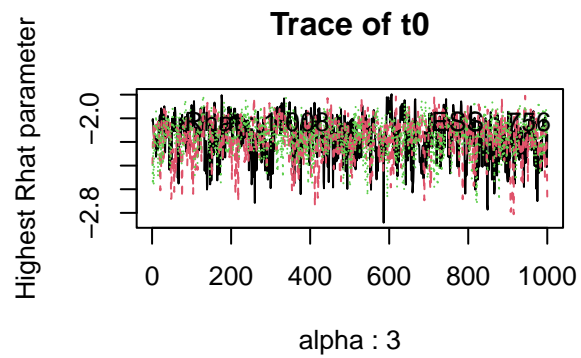
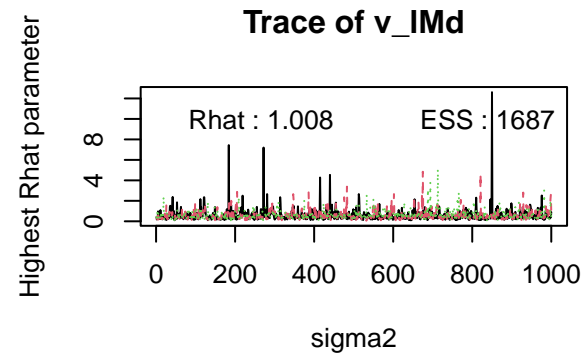
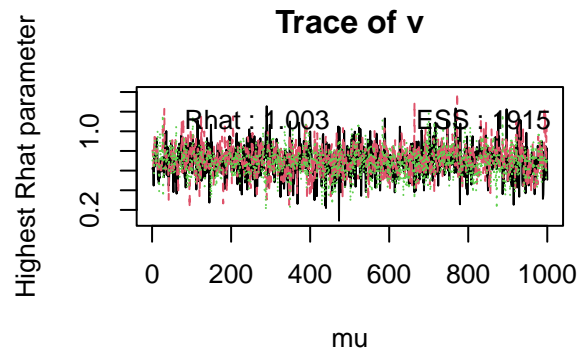
	B	v	v_lMd	t0	B.w
Rhat	1.001	1.003	1.002	1.002	1
ESS	2288.000	1915.000	1785.000	2089.000	1951

	B	v	v_lMd	t0	B.w
Rhat	1.002	1.007	1.008	1.002	1.006
ESS	1941.000	1550.000	1687.000	1556.000	1279.000

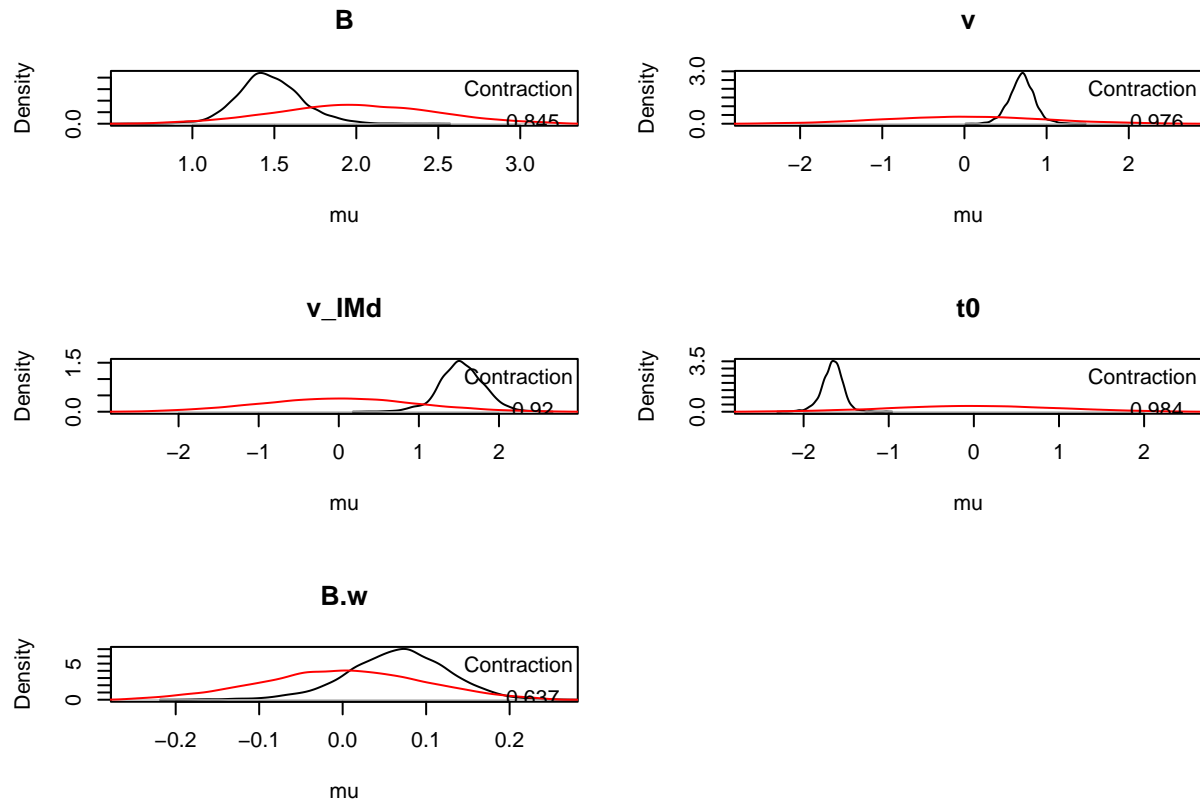
```

alpha highest Rhat : 3
      B      v    v_lMd    t0  B.w
Rhat  1.005  1.003  1.002  1.008  1
ESS   896.000 1153.000 1438.000 756.000 1552

```



```
plot_pars(samplers)
```



```
credint(samplers)
```

```
$mu
      2.5%   50%  97.5%
B      1.112  1.460  1.881
v      0.382  0.700  1.012
v_lMd  0.945  1.529  2.089
t0     -1.937 -1.657 -1.430
B.w    -0.062  0.068  0.178
```

On a group-level, we find a small (not credible) positive $B.w$ – on average, in this dataset, thresholds appear to increase by ~ 0.070 over the course of 1000 trials.

Exponential and power laws

Practice effects tend to be large initially and then gradually decay. Asymptotic functions like exponential or power functions can be used to model such effects. *EMC2* offers increasing and decreasing kernels in both cases. To demonstrate these functional forms:

```
trend_exp_incr <- make_trend(par_names='B', cov_names = 'trials2',
                             kernels = 'exp_incr', bases = 'lin')
trend_exp_decr <- make_trend(par_names='B', cov_names = 'trials2',
                             kernels = 'exp_decr', bases = 'lin')
design_exp_incr <- design(model=RDM,
                          data=dat,
                          contrast=list(lM=ADmat),
```

```

covariates='trials2',
matchfun=function(d) d$S==d$LR,
transform=list(func=c('B'='identity')),
formula=list(B ~ 1, v ~ 1M, t0 ~ 1),
trend=trend_exp_incr)

```

Sampled Parameters:

```

[1] "B"      "v"      "v_1Md"  "t0"     "B.w"    "B.d_ei"

```

Design Matrices:

```

$B
B
1

$v
      1M v v_1Md
TRUE 1   0.5
FALSE 1  -0.5

$t0
t0
1

$B.w
B.w
1

$B.d_ei
B.d_ei
1

$A
A
1

$s
s
1

```

```

design_exp_decr <- design(model=RDM,
                          data=dat,
                          contrast=list(1M=ADmat),
                          covariates='trials2',
                          matchfun=function(d) d$S==d$LR,
                          transform=list(func=c('B'='identity')),
                          formula=list(B ~ 1, v ~ 1M, t0 ~ 1),
                          trend=trend_exp_decr)

```

Sampled Parameters:

```

[1] "B"      "v"      "v_1Md"  "t0"     "B.w"    "B.d_ed"

```

Design Matrices:

```

$B

```

```

B
1

$v
  1M v v_lMd
  TRUE 1 0.5
  FALSE 1 -0.5

$t0
t0
1

$B.w
B.w
1

$B.d_ed
B.d_ed
1

$A
A
1

$s
s
1

```

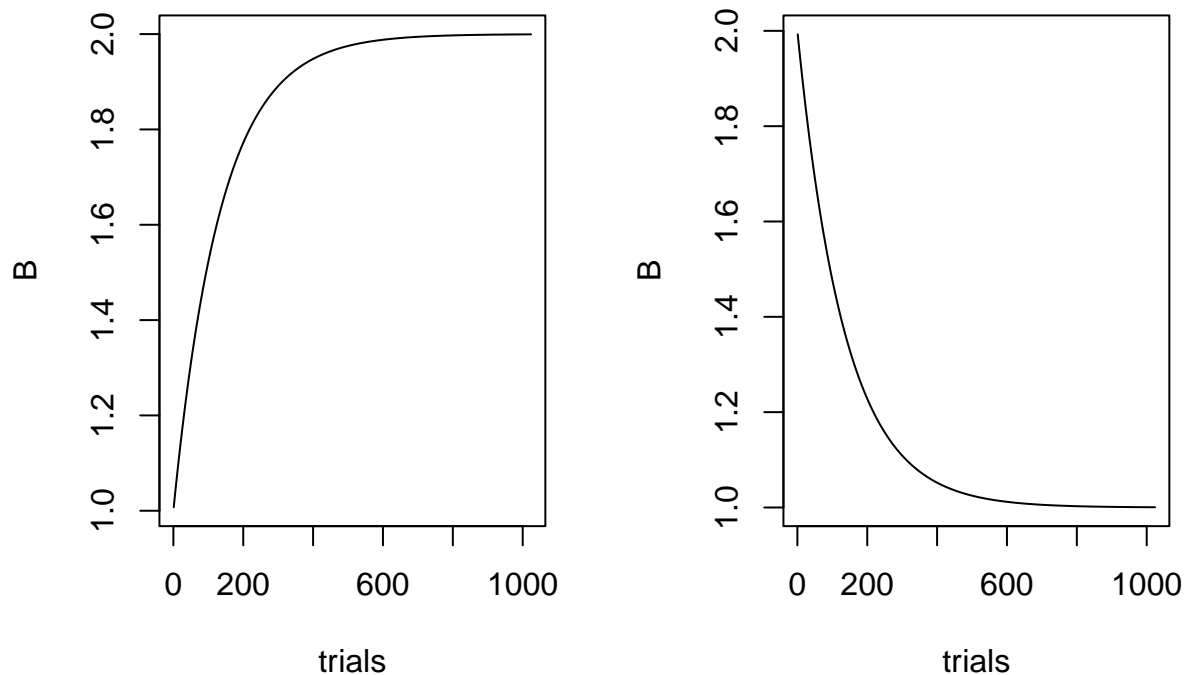
```

samlers_incr <- make_emc(dat, design_exp_incr)
samlers_decr <- make_emc(dat, design_exp_decr)

p_vector_incr <- c('B'=1, 'v'=1, 'v_lMd'=1, 't0'=0.1, 'B.w'=1, 'B.d_ei'=2)
p_vector_decr <- c('B'=1, 'v'=1, 'v_lMd'=1, 't0'=0.1, 'B.w'=1, 'B.d_ed'=2)

par(mfrow=c(1,2))
plot_trend(p_vector_incr, samplers=samlers_incr,
           par_name='B', subject=1, lR_filter='odd')
plot_trend(p_vector_decr, samplers=samlers_decr,
           par_name='B', subject=1, lR_filter='odd')

```



Note that the interpretation of the exponent (`B.e_ei` or `B.e_ed`) depends on the direction: In the increasing case, it corresponds to the asymptote; in the decreasing case, to the intercept.

Advanced note: Enforcing a direction

Having both increasing and decreasing kernels may appear redundant, since the direction of the effect can also be flipped by the `w` parameter in the `lin` base. However, having both increasing and decreasing kernels facilitates enforcing a directional effect. For example, one might hypothesize that `v_lMd` increases sharply over the first few trials due to practice effects, and then stabilizes. An increase could be implemented with `exp_incr`, but if the sampler converges on negative values of `w` of the base, the resulting trend is actually decreasing rather than increasing.

We can force the sampler to sample only increasing trends by restricting the range of `w`. This can be done by sampling `w` on the log-scale, and transforming it to the natural scale. Note that transformations applied to parameters relating to the trends are always applied prior to estimating the trend.

```
trend_exp_incr <- make_trend(par_names='v_lMd', cov_names = 'trials2',
                             kernels = 'exp_incr', bases = 'lin')
design_exp_incr <- design(model=RDM,
                          data=dat,
                          contrast=list(lM=ADmat),
                          covariates='trials2',
                          matchfun=function(d) d$S==d$lR,
                          transform=list(func=c('v'='identity',
                                                  'v_lMd.w'='exp')),
                          formula=list(B ~ 1, v ~ lM, t0 ~ 1),
                          trend=trend_exp_incr)
```



```

Sampled Parameters:
[1] "B"          "v"          "v_lMd"      "t0"          "v_lMd.w"
[6] "v_lMd.d_ei"

Design Matrices:
$B
B
1

$v
lm v v_lMd
TRUE 1 0.5
FALSE 1 -0.5

$t0
t0
1

$v_lMd.w
v_lMd.w
1

$v_lMd.d_ei
v_lMd.d_ei
1

$A
A
1

$s
s
1

mapped_pars(design_exp_incr)

$v
lm
TRUE : v + 0.5 * v_lMd_t
FALSE : v - 0.5 * v_lMd_t
Trends:
v_lMd_t = v_lMd + exp(v_lMd.w) * (1 - exp(-exp(v_lMd.d_ei) * trials2))

```

```

samlers_incr <- make_emc(dat, design_exp_incr)
p_vector1 <- c('B'=1, 'v'=3, 'v_lMd'=1, 't0'=0.1, 'v_lMd.w'=-1, 'v_lMd.d_ei'=2)
p_vector2 <- c('B'=1, 'v'=3, 'v_lMd'=1, 't0'=0.1, 'v_lMd.w'=0, 'v_lMd.d_ei'=2)
p_vector3 <- c('B'=1, 'v'=3, 'v_lMd'=1, 't0'=0.1, 'v_lMd.w'=1, 'v_lMd.d_ei'=2)

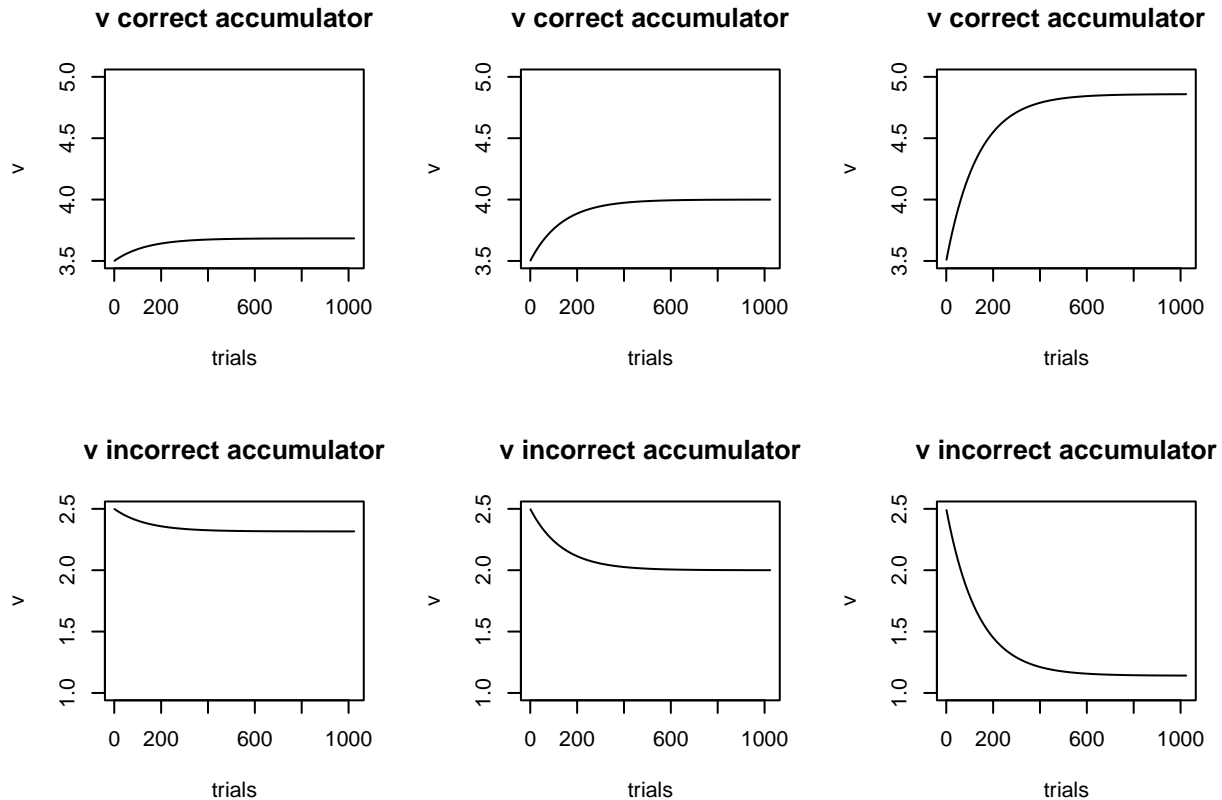
par(mfcol=c(2,3))
plot_trend(p_vector1, samplers=samlers_incr, par_name='v',
            subject=1, lm_filter=TRUE, main='v correct accumulator', ylim=c(3.5,5))
plot_trend(p_vector1, samplers=samlers_incr, par_name='v',
            subject=1, lm_filter=FALSE, main='v incorrect accumulator', ylim=c(1, 2.5))

```

```

plot_trend(p_vector2, samplers=samplers_incr, par_name='v',
           subject=1, lM_filter=TRUE, main='v correct accumulator', ylim=c(3.5,5))
plot_trend(p_vector2, samplers=samplers_incr, par_name='v',
           subject=1, lM_filter=FALSE, main='v incorrect accumulator', ylim=c(1, 2.5))
plot_trend(p_vector3, samplers=samplers_incr, par_name='v',
           subject=1, lM_filter=TRUE, main='v correct accumulator', ylim=c(3.5,5))
plot_trend(p_vector3, samplers=samplers_incr, par_name='v',
           subject=1, lM_filter=FALSE, main='v incorrect accumulator', ylim=c(1, 2.5))

```



In this set-up, no matter the value of `v_LMd.w` the between-accumulator difference in drift rates increases over time. Using the same logic, we can also enforce a decrease by using `exp_decr` as a kernel and applying an exponential transform to `w`.

So far, we only inspected time on task as defined by trial number. Other options include time on task within block (e.g., short breaks between trials could cause an increased threshold for the first few trials in each block), or the number of times a stimulus type has been shown. Furthermore, the parameters describing the trend could differ between blocks and stimulus types. To test such hypotheses, we can allow the trend parameters themselves to vary with experimental factors, as defined in `formula` in `design()`. The example data does not have stimulus type recorded, and all trials were run in a single block, but for demonstrative purposes we can simulate such effects:

```

# simulate block number (assume 3 blocks)
dat$block <- as.factor(as.numeric(cut(dat$trials, breaks=3)))
for(subject in unique(dat$subjects)) {
  dat[dat$subjects==subject, 'trial_in_block'] <- ave(

```

```

    seq_along(dat[dat$subjects==subject,'block']),
    dat[dat$subjects==subject,'block'], FUN = seq_along)/1000
}
# simulate presented digit
dat$stimulus_repetition <- ave(seq_along(dat$S),
                              dat$S, FUN = seq_along)

# combine two trends
trends <- make_trend(par_names=c('B', 'v_lMd'),
                     cov_names=c('trial_in_block', 'stimulus_repetition'),
                     kernels = c('exp_decr', 'exp_incr'),
                     bases = c('lin', 'lin'), )
design_multitrend <- design(model=RDM,
                           data=dat,
                           contrast=list(lM=ADmat),
                           covariates=c('trial_in_block', 'stimulus_repetition'),
                           matchfun=function(d) d$S==d$LR,
                           transform=list(func=c('v_lMd.w'='exp',
                                                  'B.w'='exp',
                                                  'v'='identity',
                                                  'B'='identity')),
                           formula=list(B ~ 1, v ~ lM, t0 ~ 1, `B.d_ed`~block),
                           trend=trends)

```

Sampled Parameters:

```

[1] "B"          "v"          "v_lMd"      "t0"
[5] "B.d_ed"     "B.d_ed_block2" "B.d_ed_block3" "B.w"
[9] "v_lMd.w"    "v_lMd.d_ei"

```

Design Matrices:

\$B

B

1

\$v

lM v v_lMd

TRUE 1 0.5

FALSE 1 -0.5

\$t0

t0

1

\$B.d_ed

block B.d_ed B.d_ed_block2 B.d_ed_block3

1 1 0 0

2 1 1 0

3 1 0 1

\$B.w

B.w

1

\$v_lMd.w

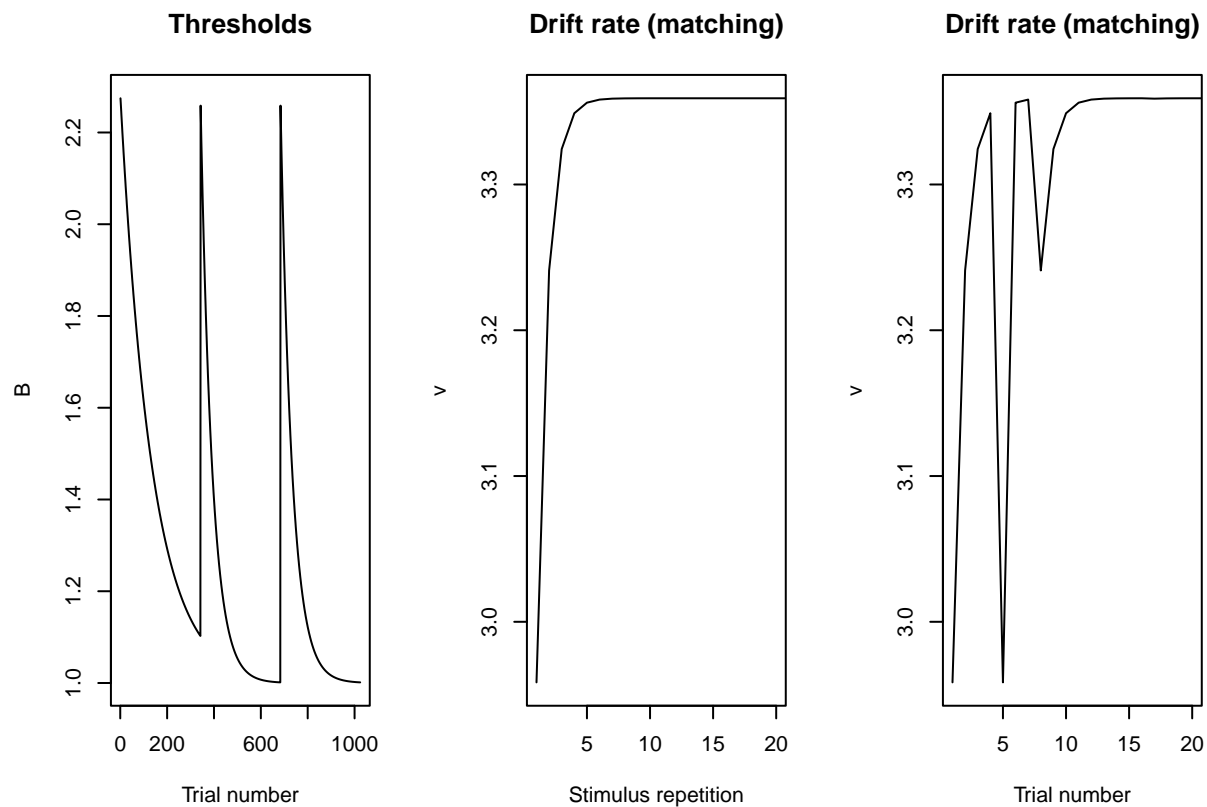
```
v_lMd.w  
1
```

```
$v_lMd.d_ei  
v_lMd.d_ei  
1
```

```
$A  
A  
1
```

```
$s  
s  
1
```

```
samplers_multitrend <- make_emc(dat, design_multitrend)  
  
# thresholds  
p_vector <- c('B'=1, 'v'=1, 'v_lMd'=2, 't0'=0.1,  
              'B.d_ed'=2, 'B.d_ed_block2'=1, 'B.d_ed_block3'=1, 'B.w'=.25,  
              'v_lMd.w'=1, 'v_lMd.d_ei'=.2)  
  
par(mfcol=c(1,3))  
plot_trend(p_vector, samplers=samplers_multitrend, par_name='B',  
           subject=1, lR_filter='odd', main='Thresholds',  
           xlab='Trial number')  
plot_trend(p_vector, samplers=samplers_multitrend, par_name='v',  
           subject=1, lM_filter=TRUE, main='Drift rate (matching)',  
           on_x_axis='stimulus_repetition',  
           xlab='Stimulus repetition', xlim=c(1,20))  
plot_trend(p_vector, samplers=samplers_multitrend, par_name='v',  
           subject=1, lM_filter=TRUE, main='Drift rate (matching)',  
           xlab='Trial number', xlim=c(1,20))
```



```
mapped_pars(design_multitrend)
```

```
$B
```

```
      : B_t
Trends:
  B_t = B + exp(B.w) * exp(-exp(B.d_ed) * trial_in_block)
```

```
$v
```

```
  lM
  TRUE  : v + 0.5 * v_lMd_t
  FALSE : v - 0.5 * v_lMd_t
Trends:
  v_lMd_t = v_lMd + exp(v_lMd.w) * (1 - exp(-exp(v_lMd.d_ei) * stimulus_repetition))
```

```
$B.d_ed
```

```
  block
  1      : exp(B.d_ed)
  2      : exp(B.d_ed + B.d_ed_block2)
  3      : exp(B.d_ed + B.d_ed_block3)
```

The left panel illustrate how the thresholds decrease within each block (at different rates), but then reset to the same asymptote after every break. The middle panel shows the drift rate for the correct accumulator as a function of how often a stimulus has been presented. Note that, when plotted against trial number (right panel), this leads to strong variability in rates across trials.

Polynomials

When a researcher has no strong prior assumptions about the shape of the trend but wishes to capture gradual changes, it is possible to fit a set of basis functions, such as polynomials. EMC2 currently includes second-, third-, and fourth-order polynomials as available kernels. This approach follows the logic of a Taylor expansion: any function can be approximated with increasing accuracy by summing polynomials of increasing order. However, the increased accuracy comes at a cost of increased sampling uncertainty, since more parameters need to be estimated. As such, it may be possible to estimate only a few polynomials.

```
trend_help(kernel='poly4')
```

Description:

Quartic polynomial: $k = d1 * c + d2 * c^2 + d3 * c^3 + d4 * c^4$

Default transformations (in order):

```
list(d1 = "identity", d2 = "identity", d3 = "identity", d4 = "identity")
```

Available bases, first is the default:

```
add, identity
```

Note that the kernel parameters (`d1`, `d2`, `d3`, `d4`) already weigh the contributions of the individual polynomial terms. As such, this kernel should not be combined with a linear base (`base = 'lin'`), but instead with an additive base (`base = 'add'`). Additionally, we should center the Taylor expansion around the mean of the covariate. The following demonstrates the flexibility of a 4th order polynomial with a few randomly chosen parameter sets:

```
dat$tctrd <- dat$trials2 - mean(dat$trials2)
trend_poly <- make_trend(par_names='B',
                        cov_names='tctrd',
                        kernels='poly4',
                        bases='add')
design_poly <- design(model=RDM,
                    data=dat,
                    contrast=list(lm=ADmat),
                    covariates='tctrd',
                    matchfun=function(d) d$S==d$LR,
                    transform=list(func=c('B'='identity')),
                    formula=list(B ~ 1, v ~ 1M, t0 ~ 1),
                    trend=trend_poly)
```

Sampled Parameters:

```
[1] "B"      "v"      "v_1Md"  "t0"     "B.d1"   "B.d2"   "B.d3"   "B.d4"
```

Design Matrices:

```
$B
```

```
B
```

```
1
```

```
$v
```

```
1M v v_1Md
```

```
TRUE 1 0.5
```

```
FALSE 1 -0.5
```

```

$t0
  t0
  1

$B.d1
  B.d1
  1

$B.d2
  B.d2
  1

$B.d3
  B.d3
  1

$B.d4
  B.d4
  1

$A
  A
  1

$s
  s
  1

```

```
mapped_pars(design_poly)
```

```

$B

      : B_t
Trends:
  B_t = B + (B.d1 * tctrd + B.d2 * tctrd^2 + B.d3 * tctrd^3 + B.d4 * tctrd^4)

$v
  lM
  TRUE   : exp(v + 0.5 * v_lMd)
  FALSE  : exp(v - 0.5 * v_lMd)

```

```

samplers_poly <- make_emc(dat, design_poly)

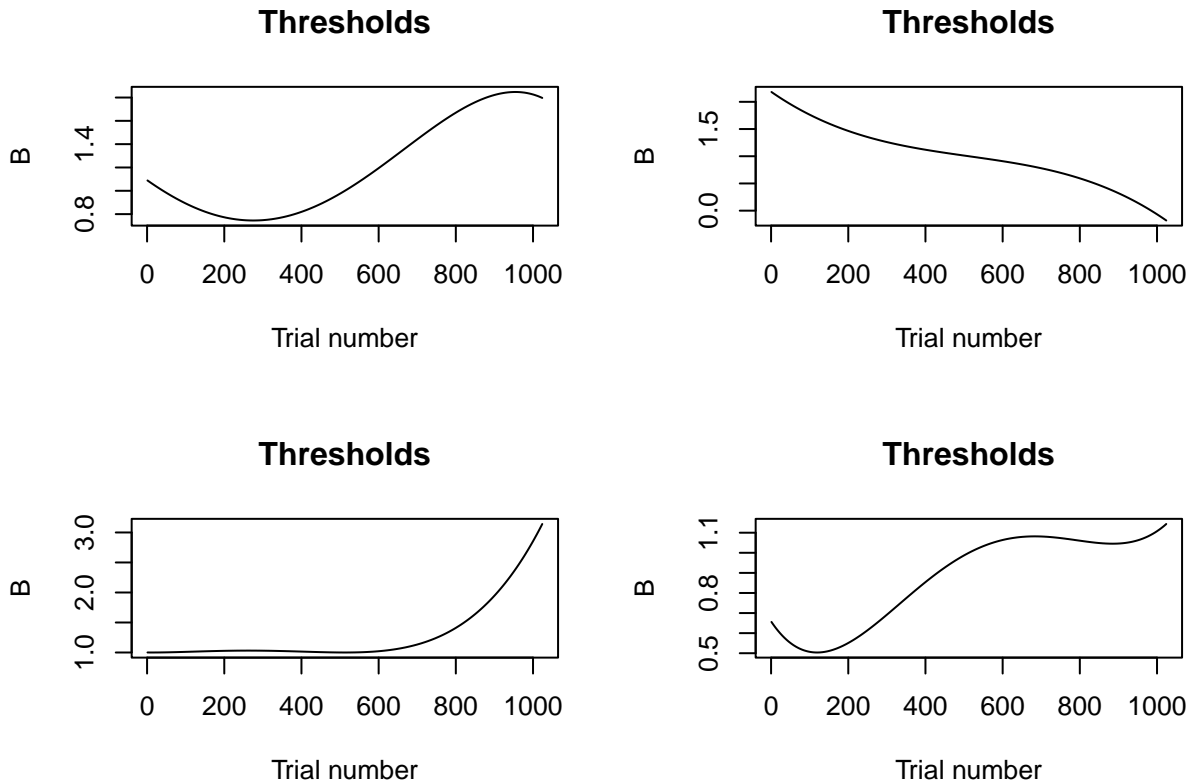
p_vector1 <- c('B'=1, 'v'=1, 'v_lMd'=2, 't0'=0.1,
               'B.d1'=2, 'B.d2'=3, 'B.d3'=-5, 'B.d4'=-5)
p_vector2 <- c('B'=1, 'v'=1, 'v_lMd'=2, 't0'=0.1,
               'B.d1'=-1, 'B.d2'=0, 'B.d3'=-5, 'B.d4'=0)
p_vector3 <- c('B'=1, 'v'=1, 'v_lMd'=2, 't0'=0.1,
               'B.d1'=0, 'B.d2'=2, 'B.d3'=8, 'B.d4'=8)
p_vector4 <- c('B'=1, 'v'=1, 'v_lMd'=2, 't0'=0.1,
               'B.d1'=1, 'B.d2'=-3, 'B.d3'=-2, 'B.d4'=10)

```

```

par(mfrow=c(2,2))
plot_trend(p_vector1, samplers=samplers_poly, par_name='B',
           subject=1, lR_filter='odd', main='Thresholds',
           xlab='Trial number')
plot_trend(p_vector2, samplers=samplers_poly, par_name='B',
           subject=1, lR_filter='odd', main='Thresholds',
           xlab='Trial number')
plot_trend(p_vector3, samplers=samplers_poly, par_name='B',
           subject=1, lR_filter='odd', main='Thresholds',
           xlab='Trial number')
plot_trend(p_vector4, samplers=samplers_poly, par_name='B',
           subject=1, lR_filter='odd', main='Thresholds',
           xlab='Trial number')

```



Mechanisms of dynamics: Stimulus memory

Models with formal mechanisms of dynamics rely on delta rules. To implement delta rules, we follow the same general logic as above—the delta rule is implemented as a kernel in `make_trend`. Let’s implement the stimulus memory mechanism proposed by Miletic et al. (2025). Here, the decision maker keeps track of the probability that a stimulus is even (or odd). The covariate in this case is the stimulus, which we can recode as 1 (even) and -1 (odd). With the delta rule:

$$Q_{SM,t+1} = Q_{SM,t} + \alpha_{SM} \cdot (S_t - Q_{SM,t}), \quad S \in \{-1, 1\}$$

The delta rule introduces two extra parameters: a learning rate α_{SM} , and a value for Q at the start of the experiment $Q_{SM,0}$. The latter is hard to estimate, and we tend to fix it to a constant—for this rule, a constant of 0 implies equal beliefs in both stimuli.

For now, let us assume that stimulus memory influences the relative thresholds: the even threshold increases, and the odd threshold decreases (by the same amount). To achieve this, we need to parameterize thresholds with the same mean-difference parameterization as we used for drift rates. That is,

$$B_{odd} = B_{mean} + B_{lRd}$$

$$B_{even} = B_{mean} - B_{lRd}$$

The B_{lRd} term is the parameter influenced by the updated covariate—however, since we do not necessarily expect an across-trial *mean* difference between thresholds, we set B_{lRd} as a constant to 0.

Using a linear base, we then allow the threshold difference to vary on a trial-by-trial basis with

$$B_{lRd,t} = B_{lRd} + w_{SM} \cdot Q_{SM,t}$$

Note the extra parameter here: w_{SM} .

```
dat$Stim1 <- ifelse(dat$S=='even', 1, -1)
SM_trend <- make_trend(cov_names=c('Stim1'),
                      kernels = 'delta',
                      par_names='B_lRd',
                      bases='lin',
                      premap=TRUE,
                      filter_lR=TRUE)
# see advanced notes for an explanation filter_lR
design_RDM_SM <- design(model=RDM,
                      data=dat,
                      contrast=list(lM=ADmat, lR=ADmat),
                      covariates='Stim1',
                      matchfun=function(d) d$S==d$lR,
                      formula=list(B ~ lR, v ~ lM, t0 ~ 1),
                      trend=SM_trend,
                      constants=c('B_lRd'=0, 'B_lRd.q0'=0))
```

```
Sampled Parameters:
[1] "B"          "v"          "v_lMd"      "t0"         "B_lRd.w"
[6] "B_lRd.alpha"
```

Design Matrices:

```
$B
  lR B B_lRd
even 1 -0.5
odd 1  0.5
```

```
$v
  lM v v_lMd
TRUE 1  0.5
FALSE 1 -0.5
```

```
$t0
```

```

t0
1

$B_lRd.w
  B_lRd.w
    1

$B_lRd.q0
  B_lRd.q0
    1

$B_lRd.alpha
  B_lRd.alpha
    1

$A
  A
  1

$s
  s
  1

```

We can now apply a similar prior to B as above, and fit the model. Note data compression is turned off automatically, since the delta rule needs to be applied to the covariate on each trial individually.

```
prior_SMB <- prior(design_RDM_SM, mu_mean=c(B=2), mu_sd=c(B=0.5))
samplers <- make_emc(dat, design=design_RDM_SM, prior_list = prior_SMB, compress=FALSE)
```

```
samplers <- fit(samplers, cores_per_chain=6, cores_for_chains=3,
               fileName='./samples/ds1_SMB.RData')
```

Time difference of 5.253126 mins

```
check(samplers)
```

Iterations:

	preburn	burn	adapt	sample
[1,]	0	0	0	1000
[2,]	0	0	0	1000
[3,]	0	0	0	1000

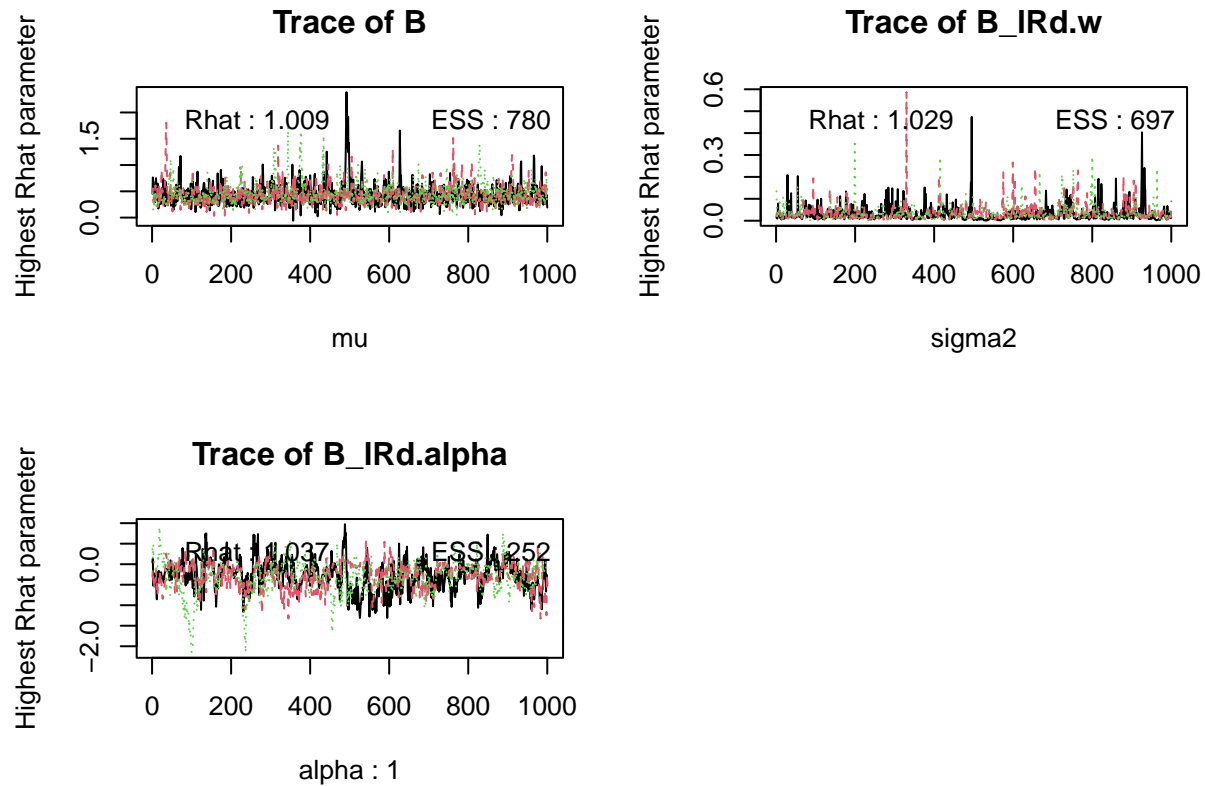
	mu		B		v	v_lMd	t0	B_lRd.w	B_lRd.alpha
Rhat	1.009	1	1	1.002	1.003	1.006			
ESS	780.000	1805	1691	1505.000	1408.000	911.000			

	sigma2		B		v	v_lMd	t0	B_lRd.w	B_lRd.alpha
Rhat	1.003	1.001	1	1.005	1.029	1.029			
ESS	630.000	1310.000	1471	1146.000	697.000	533.000			

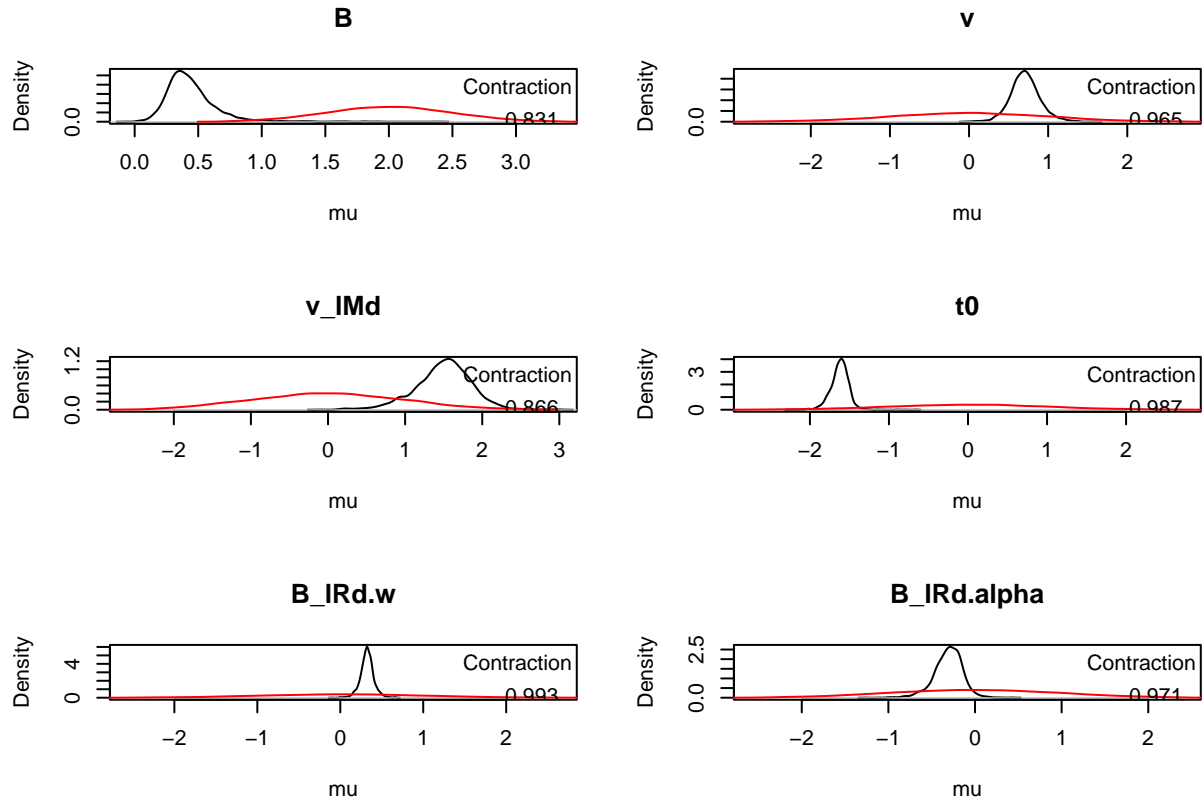
```

alpha highest Rhat : 1
      B      v    v_lMd      t0 B_lRd.w B_lRd.alpha
Rhat   1.002  1.005  1.005    1.002  1.031    1.037
ESS   1326.000 912.000 848.000 1324.000 350.000    252.000

```



```
plot_pars(samplers)
```



We find excellent convergence properties. Note that learning rates are by default sampled on the probit scale, so if we want to know the mean learning rate, we need to map and transform the parameters first:

```
credint(samplers, map=TRUE)
```

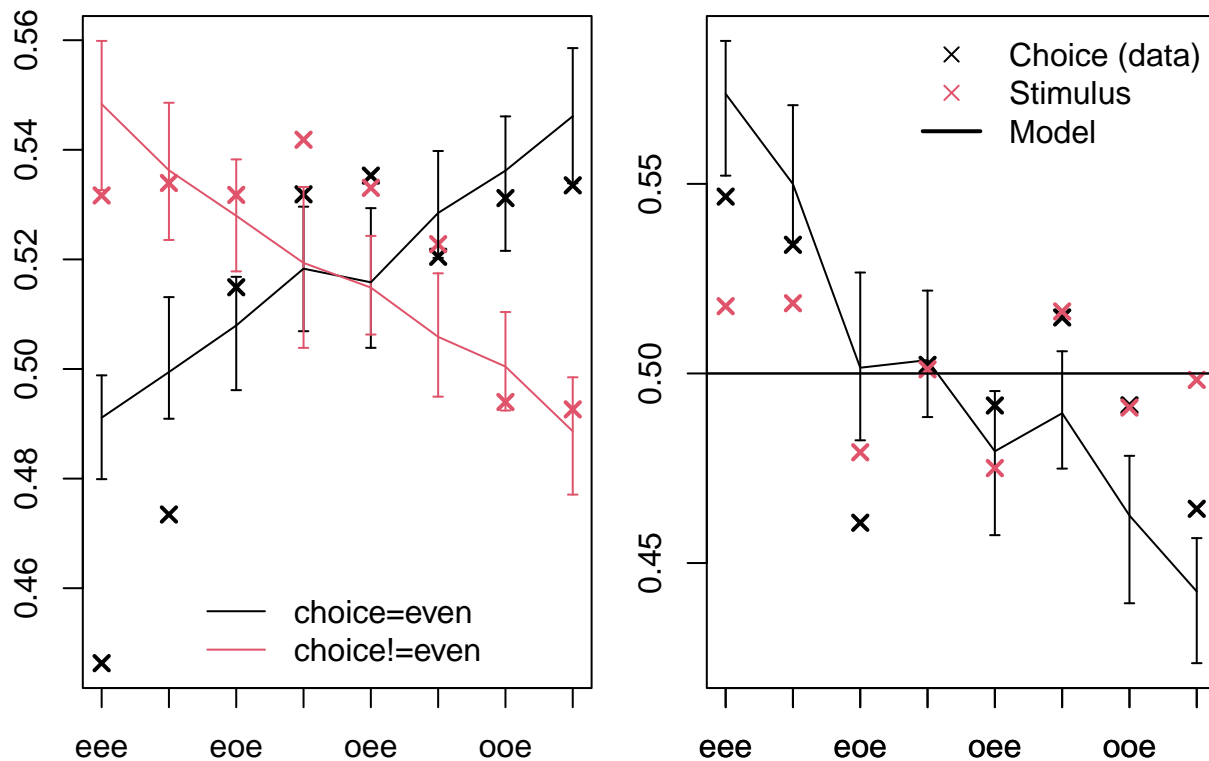
```
$mu
      2.5%  50% 97.5%
B_lReven  1.176 1.502 2.534
B_lRodd   1.176 1.502 2.534
v_lMTRUE  3.473 4.323 5.203
v_lMFALSE 0.492 0.946 2.038
t0         0.154 0.199 0.240
B_lRd.w    0.153 0.323 0.490
B_lRd.alpha 0.248 0.383 0.496
```

So we find a learning rate of ~ 0.368 , and the threshold of the odd accumulator is 0.333 lower than the threshold for the even accumulator if the participant has a Q_{SM} -value of 1.

We can now check whether the SM mechanism can explain stimulus-history effects by plotting the RTs (by choice) and the probability of choosing left as a function of the previous three presented stimuli. First, generate posterior predictives:

```
pp <- predict(samplers, n_cores=10)
save(pp, file='./ds1_SMB_pps.RData')
```

```
load('./ds1_SMB_pps.RData')
par(mar=c(3,2,2,1))
plot_history_effects(dat, pp, n_hist=3)
```



The left panel of this plot shows the mean RT as a function of the three previous trials' stimuli (ooo = odd, odd, odd; ooe = odd, odd, even; etc.). The data show a cross-over pattern, such that if the previous three stimuli were odd, 'odd' responses are faster than 'even' responses; and vice versa. The model tends to capture this cross-over pattern fairly well, with some misfits mostly due to an apparent asymmetry in the cross-over in the data.

The right panel shows the probability of choosing even (black) and the probability of the stimulus being even (red) as a function of local trial history. The black line demonstrates that participants are more likely (~ 0.55) to choose 'even' if the previous three trials were 'even'. The red crosses are important as a quality check. If the stimuli are generated truly randomly, the red crosses should be approximately 0.5 in all cases. However, some experiments use pseudorandomization, which can lead to negative correlations in local stimulus histories. This can confound any stimulus history effects present in the human data. True stimulus history effects are those that are larger than the ones present in the data, e.g., visible as 'slopes' in data that are steeper than the stimulus history contingencies in the experiment design.

Advanced note: filter_IR

Under the hood, EMC2 works with data-augmented design matrices (**dadms**). A **dadm** contains one row per accumulator per trial – so for race models applied to two-alternative forced choice tasks, this will typically result in two rows per trial. We can inspect the **dadm** for the first subject in the **samplers** object to see that the covariate **Stim1** is indeed the same across accumulators in each trial:

```
head(samplers[[1]]$data[[1]])
```

	subjects	S	R	rt	trials	trials2	block	trial_in_block
1	1	even	even	0.54	1	0.001	1	0.001
2	1	even	even	0.54	1	0.001	1	0.001
3	1	even	even	0.42	2	0.002	1	0.002
4	1	even	even	0.42	2	0.002	1	0.002
5	1	even	even	0.50	3	0.003	1	0.003
6	1	even	even	0.50	3	0.003	1	0.003

	stimulus_repetition	tctrd	Stim1	lR	lM	winner	Stim1_lRfiltered
1		1	-0.5115	1 even	TRUE	TRUE	1
2		1	-0.5115	1 odd	FALSE	FALSE	NA
3		2	-0.5105	1 even	TRUE	TRUE	1
4		2	-0.5105	1 odd	FALSE	FALSE	NA
5		3	-0.5095	1 even	TRUE	TRUE	1
6		3	-0.5095	1 odd	FALSE	FALSE	NA

The delta rule is applied to the covariate as it is specified in the `dadm`. Since, in the examples in this tutorial, the covariate is the same for both accumulators, blindly applying a delta rule to the covariate in the `dadm` would lead to *two* updates every trial: One for the first accumulator, and then another one for the second accumulator. The Q-values would then also differ between accumulators. The correct behavior is to update only once every trial (i.e., for the first accumulator), and then feed forward the updated Q-value to every second (and third, fourth, ...) accumulator. This can be done by setting the covariate for every second, third, fourth, etc accumulator to NA, since NA-values are ignored when updating. `filter_lR=TRUE` does this: it creates a new column `covariate_lRfiltered`, and applies the delta rule to that column, feeding forward updated Q-values when encountering an NA-value.

In many applications when using dynamic EAMs, this is likely the intended behavior. However, there are two exceptions: 1) The DDM only has one accumulator per trial, so no filtering has to be done (or can be done); and 2) when using RL-EAMs, applied to instrumental learning tasks, the covariate can differ between the two accumulators (feedback can be given to one specific option, for example). In such cases, more advanced handling of the covariate is required, and `filter_lR` should not be TRUE.

Stimulus memory: DDM and drift rate effects

The example above replicates Miletic et al. (2025) by assuming an RDM and assuming that stimulus memory causes a threshold (start point) bias. *EMC2* is flexibly designed to implement your own hypotheses. For example, we can propose a DDM instead and hypothesize that drift rates rather than start points are biased. This can be implemented as follows:

```
trend_SM_DDM <- make_trend(cov_names='Stim1',
                           kernels = 'delta',
                           par_names='v',
                           bases='lin',
                           premap=TRUE)
Smat <- matrix(c(-1,1), nrow = 2,dimnames=list(NULL,"dif"))
design_DDM <- design(model=DDM,
                    data=dat,
                    covariates=c('Stim1'),
                    contrasts=list(S=Smat),
                    formula=list(v ~ S, a~1, t0 ~ 1),
```

```
constants=c('v.q0'=0, 'v'=0),  
trend=trend_SM_DDM)
```

Sampled Parameters:

```
[1] "v_Sdif" "a"      "t0"      "v.w"      "v.alpha"
```

Design Matrices:

\$v

```
  S v v_Sdif  
even 1     -1  
odd 1      1
```

\$a

```
a  
1
```

\$t0

```
t0  
1
```

\$v.w

```
v.w  
1
```

\$v.q0

```
v.q0  
1
```

\$v.alpha

```
v.alpha  
1
```

\$s

```
s  
1
```

\$st0

```
st0  
1
```

\$sv

```
sv  
1
```

\$SZ

```
SZ  
1
```

\$Z

```
Z  
1
```

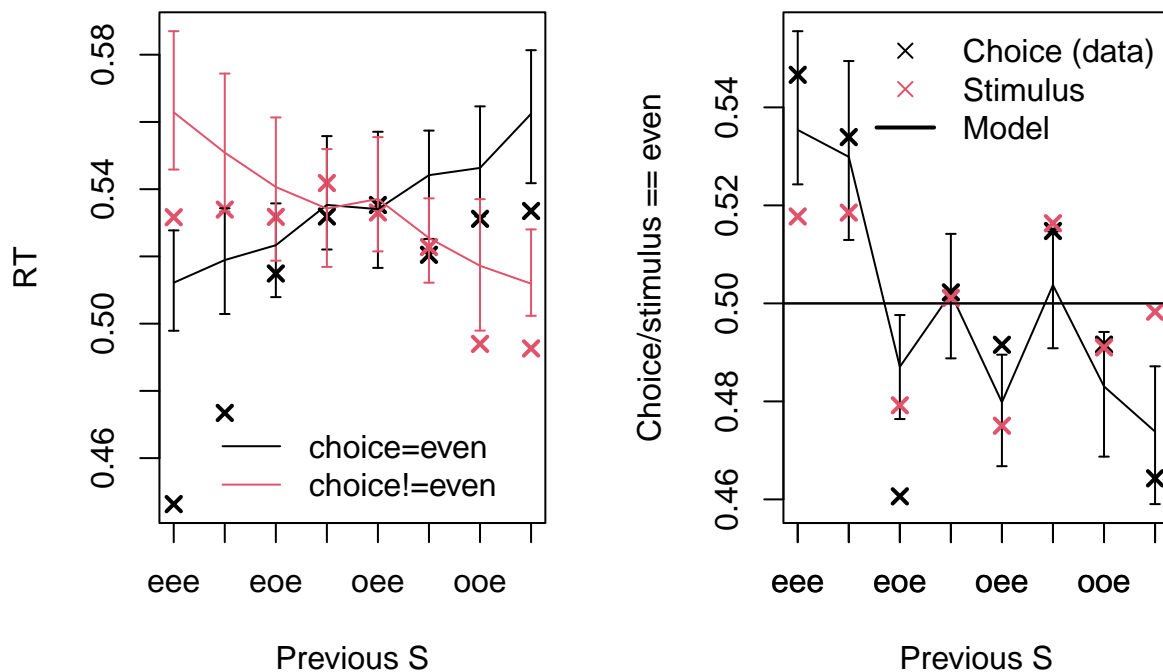
```
# since v is estimated on the natural scale (in case of the DDM),
# we do not need to change the transformations, and we can use the default priors.
samplers <- make_emc(dat, design=design_DDM, compress=FALSE)
samplers <- fit(samplers, cores_per_chain=6, cores_for_chains=3,
               fileName='./samples/ds1_SMv_DDM.RData')
```

Time difference of 3.331497 mins

However, this does not appear to fit as well qualitatively and loses model comparisons:

```
pp_ddm <- predict(samplers, n_cores=10)
save(pp_ddm, file='./samples/ds1_SMv_DDM_pps.RData')
```

```
plot_history_effects(dat, pp_ddm)
```



```
#compare(sList=list(rdm=get(load('./samples/ds1_SMB.RData')),
#                   ddm=get(load('./samples/ds1_SMv_DDM.RData'))))
```

Mechanisms of dynamics: Accuracy memory

Accuracy memory follows the same logic as above, with a different covariate (errors) and a different parameter (urgency, v). Errors are the inverse of accuracy; they are 0 when the response matches the stimulus, and 1 otherwise. Unlike the presented stimulus, accuracy/error is not a static property of the experimental design

but depends on the observed behavior. This also means that, when simulating behavior, accuracy needs to be re-calculated based on the newly simulated data.

For this reason, it is useful to have *EMC2* calculate accuracy with a function rather than specifying it in the dataframe (in which case it would be treated as a static experimental factor and assumed fixed across simulations). The same function is applied when generating posterior predictives, so the accuracy is correctly determined in that phase.

```
AM_trend <- make_trend(cov_names='error',
                      kernels = 'delta',
                      par_names='v',
                      bases='lin',
                      premap=TRUE,
                      filter_lR=TRUE)
design_RDM_AM <- design(model=RDM,
                      data=dat,
                      contrast=list(lM=ADmat, lR=ADmat),
                      functions=list(error=function(x) x$S!=x$R),
                      covariates='error',
                      matchfun=function(d) d$S==d$lR,
                      formula=list(B ~ 1, v ~ lM, t0 ~ 1, s~lM),
                      trend=AM_trend,
                      constants=c('v.q0'=0, 's'=1))
```

Sampled Parameters:

```
[1] "B"      "v"      "v_lMd"  "t0"     "s_lMd"  "v.w"    "v.alpha"
```

Design Matrices:

\$B

B

1

\$v

```
  lM v v_lMd
TRUE 1  0.5
FALSE 1 -0.5
```

\$t0

t0

1

\$s

```
  lM s s_lMd
TRUE 1  0.5
FALSE 1 -0.5
```

\$v.w

v.w

1

\$v.q0

v.q0

1

\$v.alpha

```
v.alpha  
1
```

```
$A  
A  
1
```

```
# note that 1) we allow within-trial noise  $s$  to vary with accumulator  
# match (correct/incorrect), which will allow us to capture the  
# relative speed of errors.  
  
# note that 2) in this case, we are not estimating  $v$  on the natural scale.  
# This is because the RDM has no known analytic likelihood for negative drift rates,  
# the AM mechanism can push drift rates on individual trials to negative values when  
# applied on the natural scale. In this specific case, this can lead to difficulties  
# sampling. Hence, the effect of errors on urgency as we implement it here,  
# is not strictly linear -- it is linear on the log-scale, and then exponentiated.  
# The cognitive interpretation is similar.  
  
samplers <- make_emc(dat, design=design_RDM_AM, compress=FALSE)  
samplers <- fit(samplers, cores_per_chain=6, cores_for_chains=3,  
               fileName='./samples/ds1_AM.RData')
```

Time difference of 10.04971 mins

```
credint(samplers)
```

```
$mu  
      2.5%   50%  97.5%  
B      1.021  1.303  1.547  
v      0.544  1.019  1.532  
v_lMd   2.020  2.884  3.742  
t0     -2.093 -1.748 -1.344  
s_lMd  -0.518 -0.359 -0.164  
v.w     -1.322 -0.732 -0.296  
v.alpha -1.440 -0.376  0.604
```

Accuracy memory can help explain error-related effects, like post-error slowing. To visualize, we can generate posterior predictives and then use a convenience function to plot mean RT as a function of trial number relative to an error. Note that, since the covariate in this case depends on observed behavior, we need to simulate data and determine the covariate one trial at a time. *EMC2* detects whether the covariate is `rt`, `R`, or the output of one of the functions provided to `design`. If it is, it automatically simulates data trial-by-trial. As vectorisation is not possible in this case, this is slower.

```
samplers <- get(load('./samples/ds1_AM.RData'))  
  
pp <- predict(samplers, n_cores=10, conditional_on_data=FALSE)  
save(pp, file='./samples/ds1_AM_pps.RData')
```

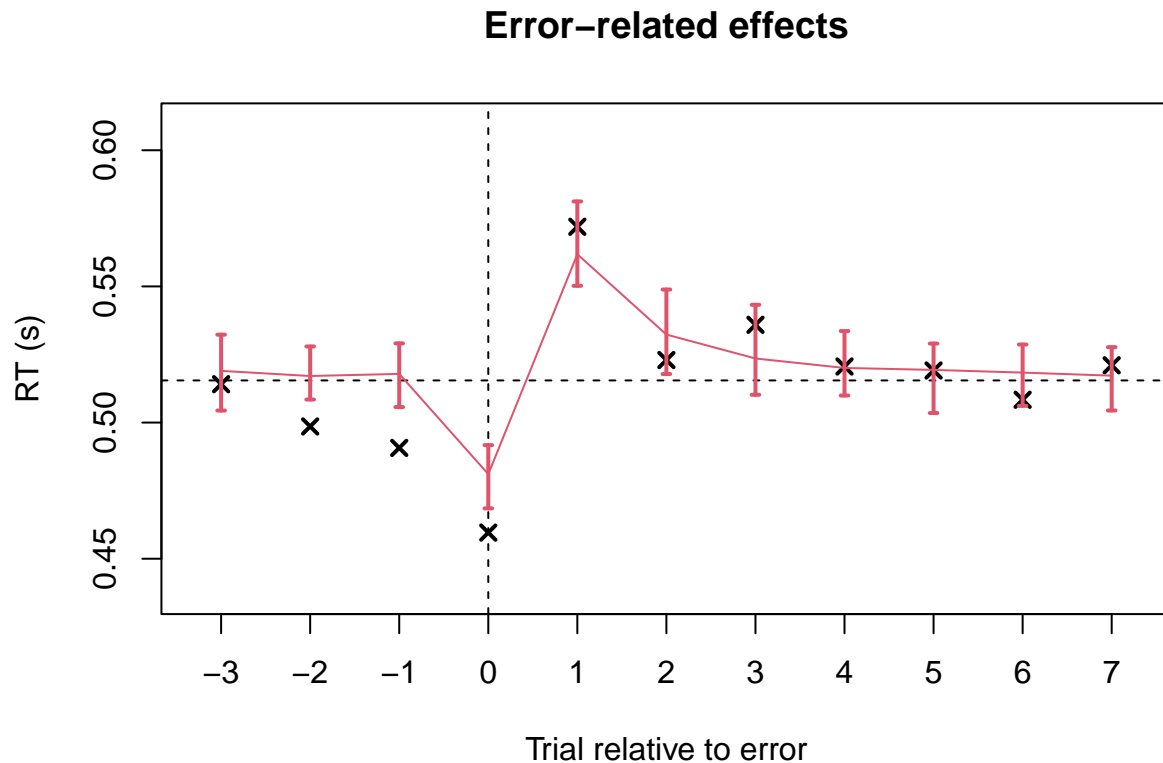
```
# needed for plotting  
pp$accuracy <- 1-pp$error  
dat$accuracy <- dat$S==dat$R  
  
# calculate post-error slowing statistics
```

```

data_PES <- getErrorEffects(dat)
pp_PES <- getErrorEffects(pp, mc.cores=10)

# and plot with convenience function
par(mfrow=c(1,1))
plotPES(data_PES=data_PES$average, pp_PES=pp_PES$average,
        mean_rt=mean(aggregate(rt~subjects,dat,mean)[,2]),
        main='Error-related effects')

```



Like in the case of stimulus memory, the accuracy memory mechanism can be adjusted to other EAMs like the DDM, and it can affect other parameters. The DDM does not have an urgency mechanism, but we could, for example, allow AM to affect thresholds. This trend can be specified as post-transform since the thresholds are the same across all design cells. So in this case, we can sample thresholds on the log scale, then transform to the natural scale, and then apply the trend.

```

trend_AM_DDM <- make_trend(cov_names='error',
                           kernels = 'delta',
                           par_names='a',
                           bases='lin',
                           premap=FALSE, pretransform=FALSE)
Smat <- matrix(c(-1,1), nrow = 2,dimnames=list(NULL,"dif"))
design_DDM <- design(model=DDM,
                    data=dat,
                    functions=list(error=function(x) x$S!=x$R),
                    covariates='error', # specify relevant covariate columns
                    contrasts=list(S=Smat),

```

```
formula=list(v ~ S, a~1, t0 ~ 1),
constants=c('a.q0'=0),
trend=trend_AM_DDM)
```

Sampled Parameters:

```
[1] "v"      "v_Sdif" "a"      "t0"     "a.w"    "a.alpha"
```

Design Matrices:

\$v

```
  S v v_Sdif
even 1   -1
odd 1    1
```

\$a

```
a
1
```

\$t0

```
t0
1
```

\$a.w

```
a.w
1
```

\$a.q0

```
a.q0
1
```

\$a.alpha

```
a.alpha
1
```

\$s

```
s
1
```

\$st0

```
st0
1
```

\$sv

```
sv
1
```

\$SZ

```
SZ
1
```

\$Z

```
Z
1
```

```
samplers <- make_emc(dat, design=design_DDM, compress=FALSE)
samplers <- fit(samplers, cores_per_chain=6, cores_for_chains=3,
               fileName='./samples/ds1_AMa_DDM.RData')
```

Time difference of 4.530009 mins

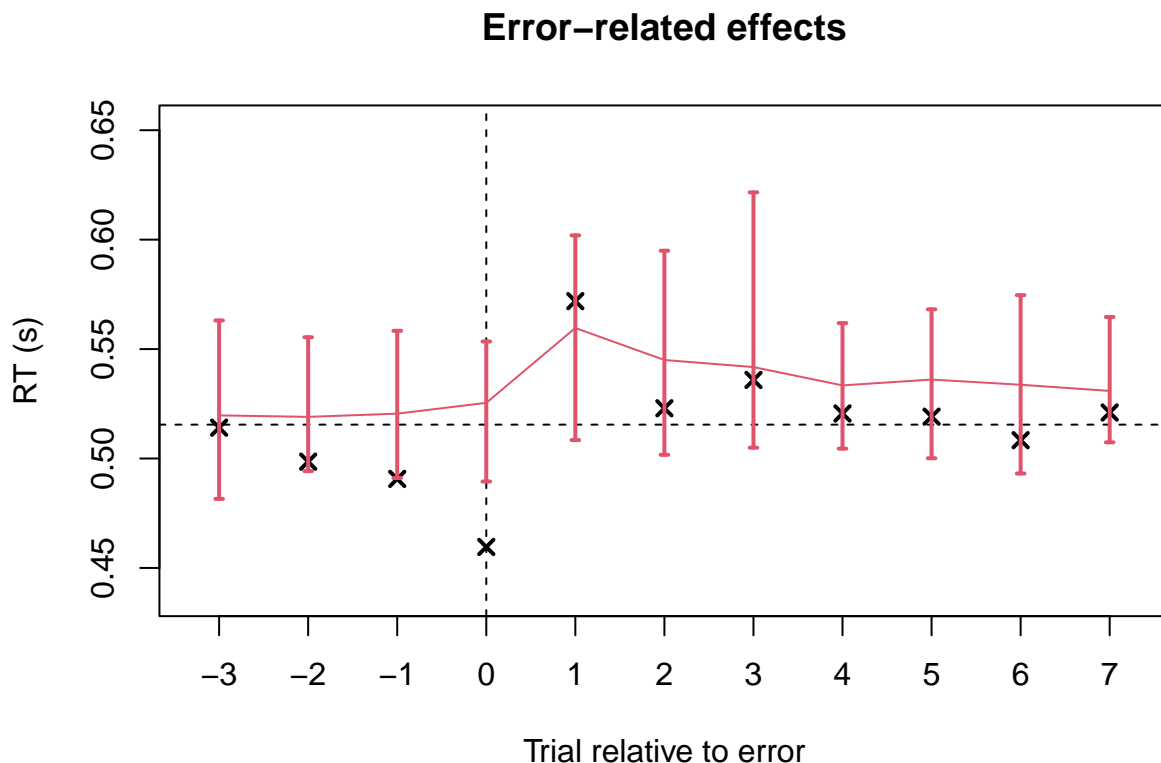
However, this again does not appear to fit as well qualitatively, and loses model comparisons:

```
samplers <- get(load('./samples/ds1_AMa_DDM.RData'))
pp_ddm <- predict(samplers, n_cores=10, conditional_on_data=FALSE)
save(pp_ddm, file='./samples/ds1_AMa_DDM_pps.RData')
```

```
# needed for plotting
pp_ddm$accuracy <- 1-pp_ddm$error
dat$accuracy <- dat$S==dat$R

# calculate post-error slowing statistics
data_PES <- getErrorEffects(dat)
pp_ddm_PES <- getErrorEffects(pp_ddm, mc.cores=10)

# and plot with convenience function
par(mfrow=c(1,1))
plotPES(data_PES=data_PES$average, pp_PES=pp_ddm_PES$average,
        mean_rt=mean(aggregate(rt~subjects,dat,mean)[,2]),
        main='Error-related effects')
```



```
# and loses model comparisons again
#compare(sList=list(rdm=get(load('./samples/ds1_AM.RData')),
#                   ddm=get(load('./samples/ds1_AMa_DDM.RData'))))
```

Special case: Fluency memory

Fluency memory is a formalization of the idea that participants adjust their behavior according to perceived difficulty. To estimate perceived difficulty, we rely on a few simplifying assumptions: participants can quantify (1) their thresholds, and (2) their response time. In race models, the ratio of threshold over response time constitutes a measure of mean speed, which can be used as a proxy for difficulty. After all, we expect processing efficiency to be lower for difficult trials than for easy trials. Formally, $Q_{FM,t+1} = Q_{FM,t} + \alpha_{FM}(b_t/rt_t - Q_{FM,t})$. Contrary to stimulus and accuracy memory, fluency memory is a very specific effect, and its implementation is not very flexible. It can only work for race models; it must influence thresholds; and the thresholds should be estimated on the natural scale. *EMC2* implements it as a separate kernel `deltab` with covariate `rt`:

```
trend_FM=make_trend(kernel='deltab',
                    base='lin',
                    cov_names='rt',
                    par_names='B', premap = TRUE, filter_LR=TRUE)

design_FM <- design(model=RDM,
                  data=dat,
                  contrast=list(lM=ADmat),
                  matchfun=function(d) d$S==d$lR,
                  formula=list(B ~ 1, v ~ lM, t0 ~ 1, s~lM),
                  transform=list(func=c(B='identity'),
                                   lower=c(B.alpha=0.05)),
                  constants=c('B.q0'=3, 's'=log(1)),
                  trend=trend_FM)
```

should also update prior in this case

Why 3? When fitting a static RDM, the

Sampled Parameters:

```
[1] "B"      "v"      "v_lMd"  "t0"     "s_lMd"  "B.w"    "B.alpha"
```

Design Matrices:

\$B

B

1

\$v

lM v v_lMd

TRUE 1 0.5

FALSE 1 -0.5

\$t0

t0

1

\$s

lM s s_lMd

TRUE 1 0.5

FALSE 1 -0.5

```
$B.w
  B.w
    1

$B.q0
  B.q0
    1

$B.alpha
  B.alpha
    1
```

```
$A
  A
  1
```

```
prior_FM <- prior(design_FM, mu_mean=c('B'=2), mu_sd=c('B'=0.5))
samplers <- make_emc(dat, design=design_FM, compress=FALSE, prior_list=prior_FM)

samplers <- fit(samplers, cores_per_chain=6, cores_for_chains=3,
               fileName='samples/ds1_FM.RData')
```

Time difference of 10.20095 mins

```
check(samplers)
```

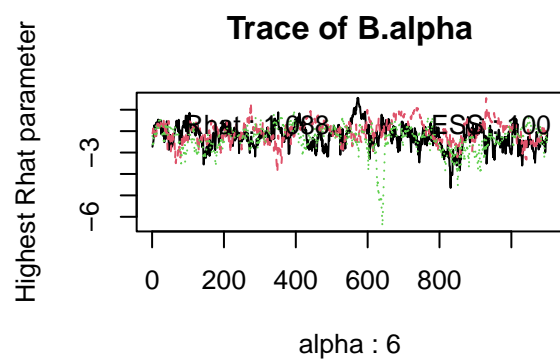
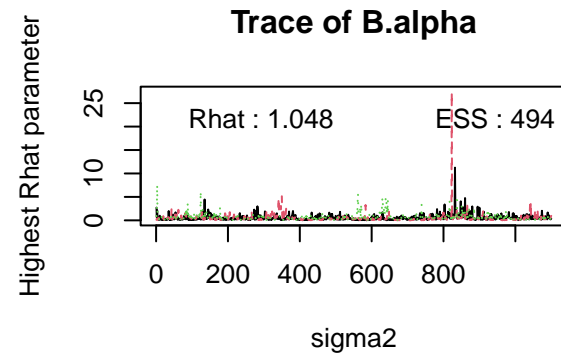
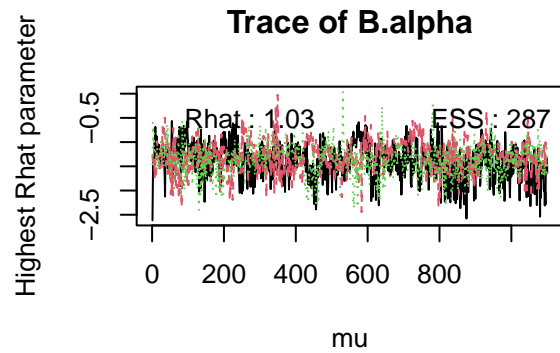
Iterations:

	preburn	burn	adapt	sample
[1,]	0	0	0	1100
[2,]	0	0	0	1100
[3,]	0	0	0	1100

mu	B	v	v_lMd	t0	s_lMd	B.w	B.alpha
Rhat	1.019	1.007	1.008	1.006	1.004	1.009	1.03
ESS	235.000	1176.000	1154.000	1757.000	1656.000	764.000	287.00

sigma2	B	v	v_lMd	t0	s_lMd	B.w	B.alpha
Rhat	1.046	1.016	1.014	1.004	1.01	1.004	1.048
ESS	483.000	966.000	1178.000	996.000	1026.00	1108.000	494.000

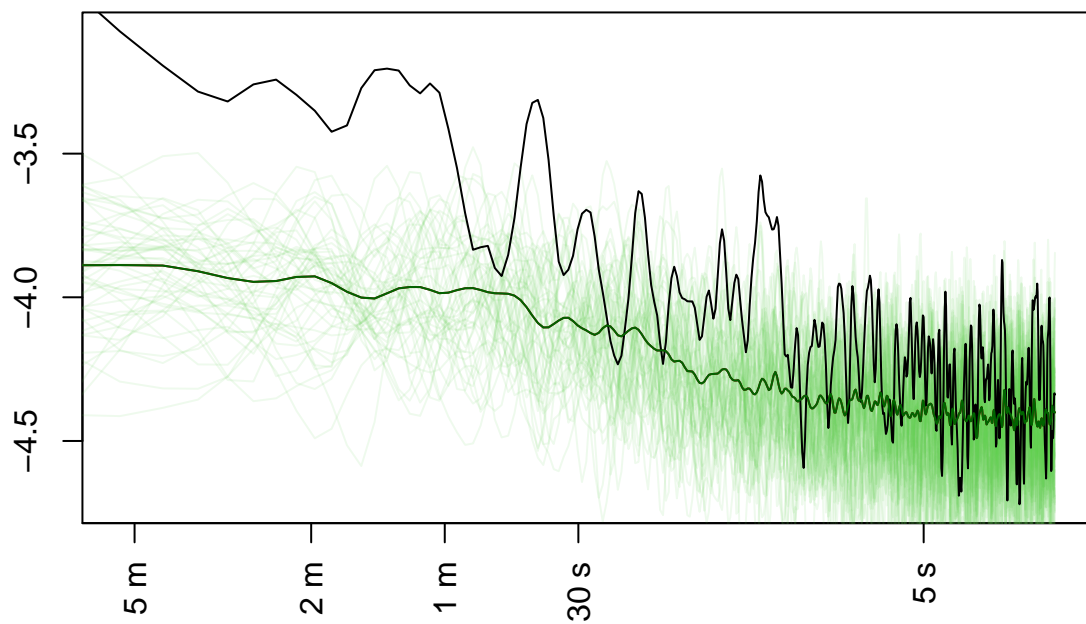
alpha highest Rhat : 6							
	B	v	v_lMd	t0	s_lMd	B.w	B.alpha
Rhat	1.008	1.006	1.006	1.007	1.002	1.01	1.088
ESS	194.000	866.000	1004.000	1193.000	1365.000	169.00	100.000



```
pp <- predict(samplers, n_cores=10, conditional_on_data=FALSE)
save(pp, file='./samples/ds1_FM_pps.RData')
```

Fluency memory provides an explanation for the slower fluctuations in the observed response times. One useful way to visualize these is by creating a power spectrum of the RT data. We provide a convenience function that does this for the data and the posterior predictives of the estimated model:

```
# convenience function to plot the spectrum
plotSpectrum(dat=dat, pp=pp, trial_duration=1.265) # mean trial duration of this task was 1.265 s, wh
```

which demonstrates that fluency can account for the fluctuations that are moderate to fast, but not the slowest fluctuations.