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 (Stevenson et al. 2024)). Specifically, we will fit models to dataset 1 from (Miletić et al. 2025), which corresponds to the 'choice, short [CS]' condition from (Wagenmakers, Farrell, and Ratcliff 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 (note that you will also need the Hmisc package installed):

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

# This is some code that contains plotting functions used later on in this tutorial
code_url <- paste0(
  "https://raw.githubusercontent.com/StevenM1/",
  "dynamic_tutorial/refs/heads/main/plotting_utils.R")
source(code_url)

# Load in the data
data_url <- paste0(
  "https://github.com/StevenM1/dynamic_tutorial/",
  "raw/refs/heads/main/datasets/dataset_1.RData")
load(url(data_url))

# 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* tutoial (Stevenson et al. 2024). We will set up two baseline models: first using a racing diffusion model (RDM), and then using a Wiener diffusion model (WDM), which is the diffusion decision model (DDM) without between-trial variabilities (sometimes called the 'simple' 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:

```r
# 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
```

```r
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:
  custom: Custom C++ kernel: provided via register_trend().
  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 = d1 * c + d2 * c^2
  poly3: Cubic polynomial: k = d1 * c + d2 * c^2 + d3 * c^3
  poly4: Quartic polynomial: k = d1 * c + d2 * c^2 + d3 * c^3 + d4 * c^4
  delta: Standard delta rule kernel: k = q[i].
         Updates q[i] = q[i-1] + alpha * (c[i-1] - q[i-1]).
         Parameters: q0 (initial value), alpha (learning rate).
  delta2kernel: Dual kernel delta rule: k = q[i].
          Combines fast and slow learning rates
          and switches between them based on dSwitch.
          Parameters: q0 (initial value), alphaFast (fast learning rate),
          propSlow (alphaSlow = propSlow * alphaFast), dSwitch (switch threshold).
  delta2lr: Dual learning rate delta rule: k = q[i].
          Like the standard delta rule, but with separate
          learning rates for positive and negative prediction errors.
          Parameters: q0 (initial value), alphaPos (learning rate for positive PEs),
          alphaNeg (learning rate for negative PEs).

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

Phase 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, 'phase', 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`, `t0`, `s`, (and `A`, its omission in the design above causes it to be fixed to zero) parameters per accumulator remain. However, in many applications, the parameter of interest is defined as a between-accumulator difference (e.g., `v_lMd` 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 `phase='premap'` (the default).

There is an important caveat here. By default, *EMC2* estimates some parameters with a lower bound (e.g., non-decision time, thresholds, RDM's drift rates) on a log scale, and other parameters with both a lower and upper bound on a 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 by trying to impose a linear trend on thresholds in case of the RDM:

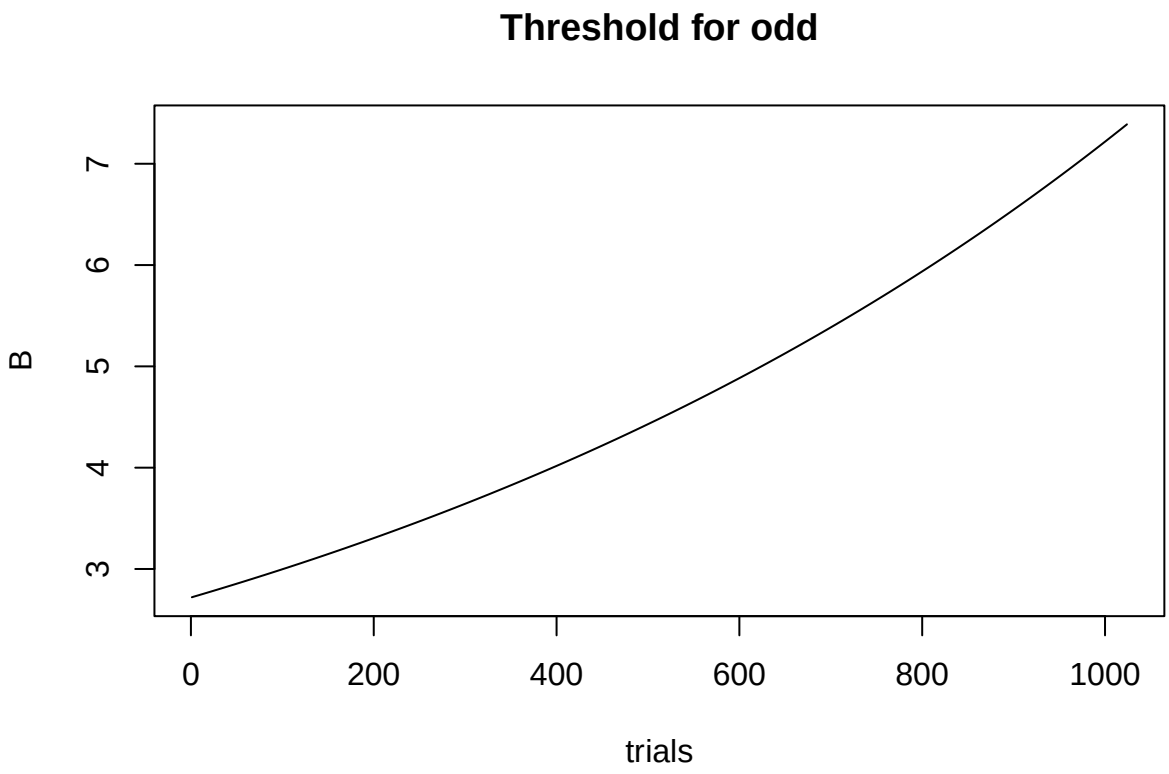
```r
# Add a 'trials' column specifying trial number
dat <- EMC2:::add_trials(dat)

# Rescale the effect of this covariate to a larger parameter range to help
# sampling and interpretation (there are 1024 trials so the corresponding
# estimated parameter (B.w, see below) indexes the change from start to
# finish of the experiment).
dat$trials2 <- dat$trials/1024
lin_trend <- make_trend(cov_names='trials2',
                        kernels = 'lin_incr',
                        par_names='B',
                        bases='lin',
                        phase='premap')

design_RDM_lin_B <- design(model=RDM,
                           data=dat,
                           contrast=list(lM=ADmat),
                            # specify relevant covariate columns
                           covariates='trials2',
                           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 rescaled trials on thresholds: $B_t = B_0 + B.w * trials2$. Let's define a set of parameters and look at the resulting trial-by-trial thresholds:

```r
emc <- 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, emc=emc,
           par_name='B', subject=1,
           # filter here is a function that selects only the rows in the dadm
           # corresponding to the 'odd' accumulator
           filter = function(data) data$lR == "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()` can be used to clarify:

```
mapped_pars(design_RDM_lin_B)
```

```
$B

 intercept  : 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',
                         phase='posttransform')
```

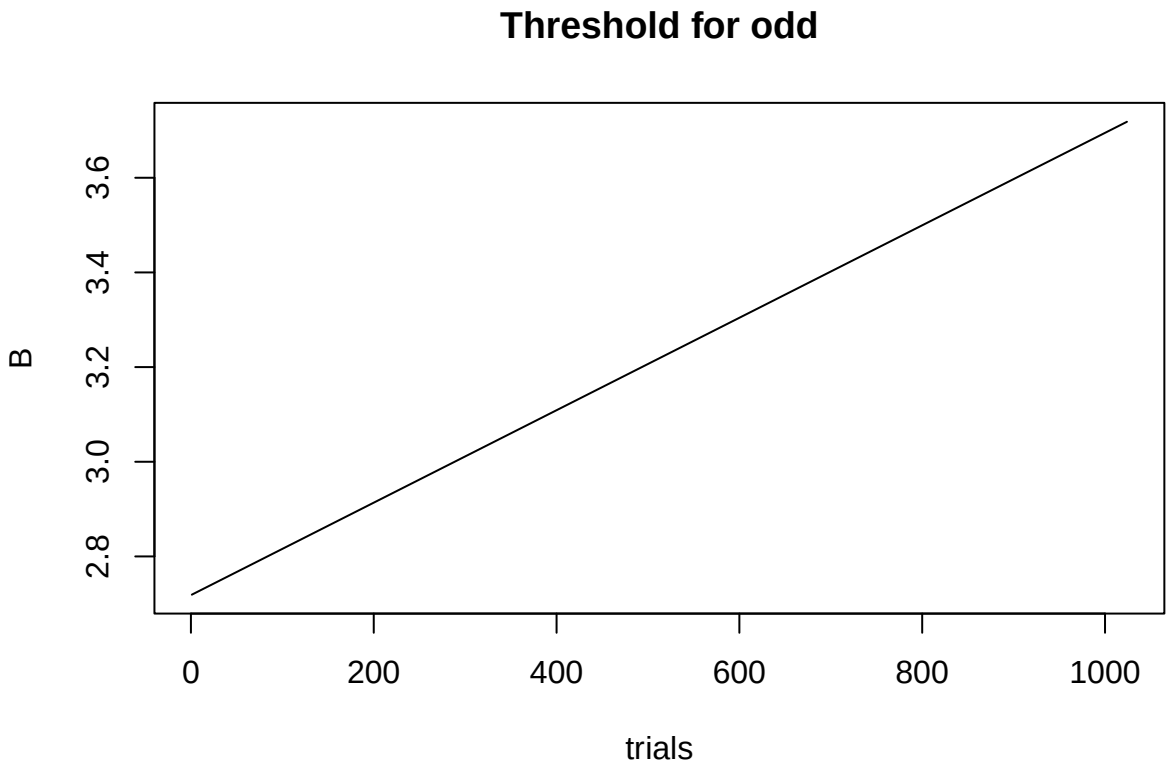
```
design_RDM_lin_B2 <- design(model=RDM,
                            data=dat,
                            contrast=list(lM=ADmat),
                            covariates='trials2',
                            matchfun=function(d) d$S==d$lR,
                            formula=list(B ~ 1, v ~ lM, t0 ~ 1),
                            trend=lin_trend2)
```

```
 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

 intercept  : 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)
```

```
emc <- 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, emc=emc,
           par_name='B', subject=1,
           filter=function(data) data$lR == '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',
                         phase='premap')  # 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)
```

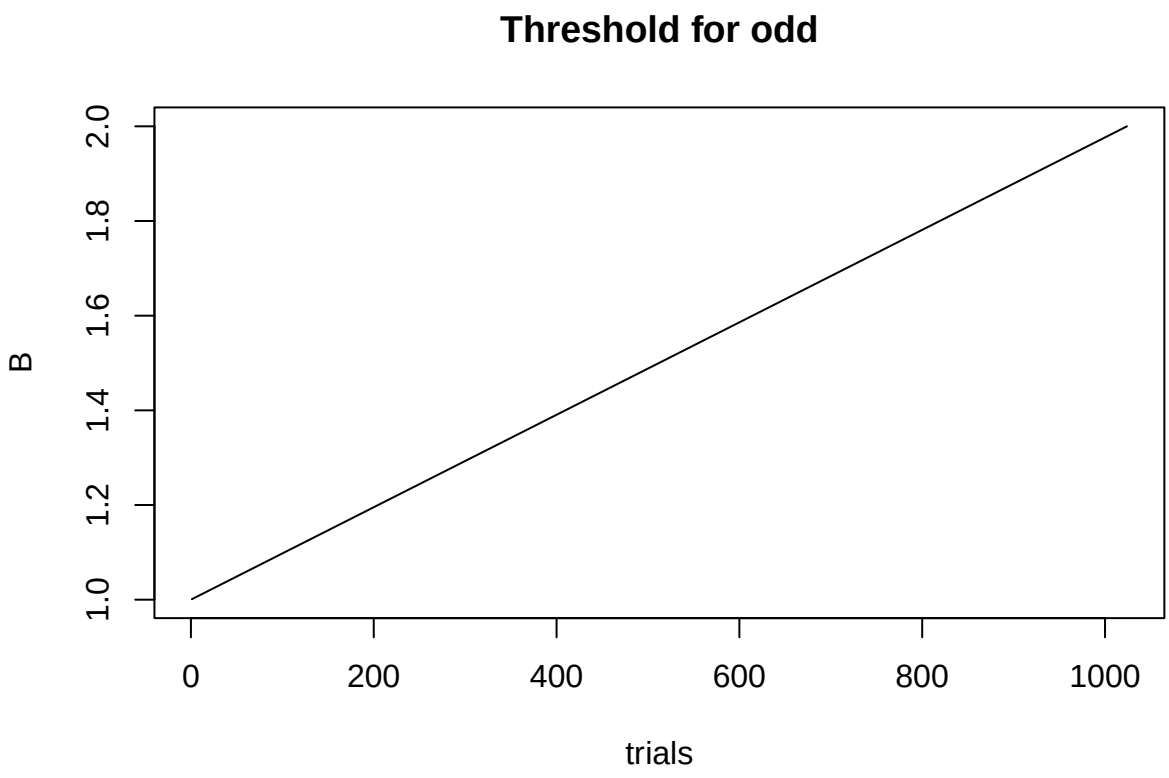
```
 Sampled Parameters:
[1] "B"     "v"     "v_lMd" "t0"    "B.w"

 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

 intercept  : 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)
```

```
emc <- 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, emc=emc,
```

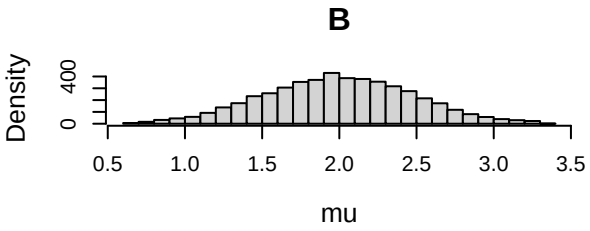
```
            par_name='B', subject=1,
            filter=function(data) data$lR == 'odd', main='Threshold for odd')
```

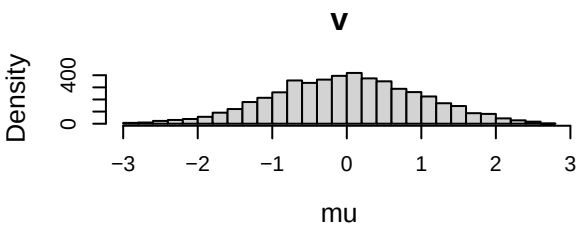


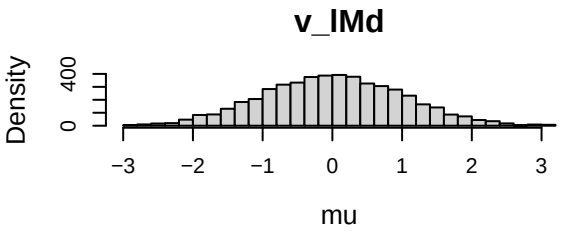
This leads to the expected linear effect. As a cautionary note, keep in mind that the default priors in *EMC2* are Gaussian distributions centered on 0 with unit variance. Since many cognitive model parameters cannot be negative (and by default *EMC2* will still enforce that, see help for the bound argument in `?design`), 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.

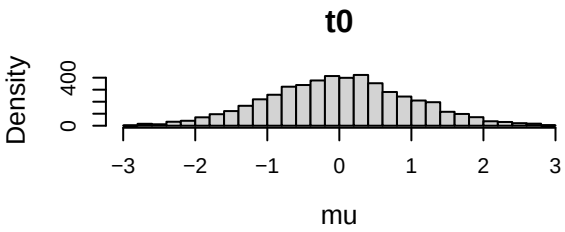
With all that in mind, we can now start sampling our first model. We set a N(2,0.5) prior on the threshold B to reduce the prior density on negative thresholds. This is a somewhat subjective choice based on earlier experience, so it reflects our (but perhaps not your) prior belief. The rest of the priors are left to their default N(0,1) – on the scale on which they are sampled – except B.w, where we set a tight N(0,0.1) prior.

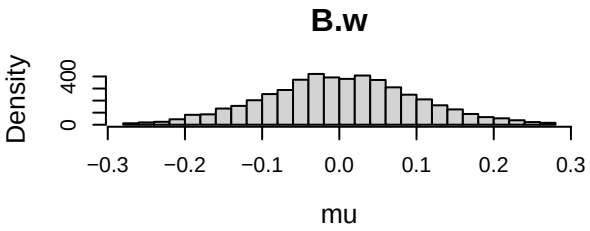
```
prior_linB <- prior(design_RDM_lin_B3,
                    mu_mean=c(B=2, B.w=0), mu_sd=c(B=0.5,B.w=0.1))
emc <- make_emc(dat, design=design_RDM_lin_B3, prior_list = prior_linB)
# Priors on parameters as defined in the p_vector:
plot(prior_linB, map=FALSE)
```



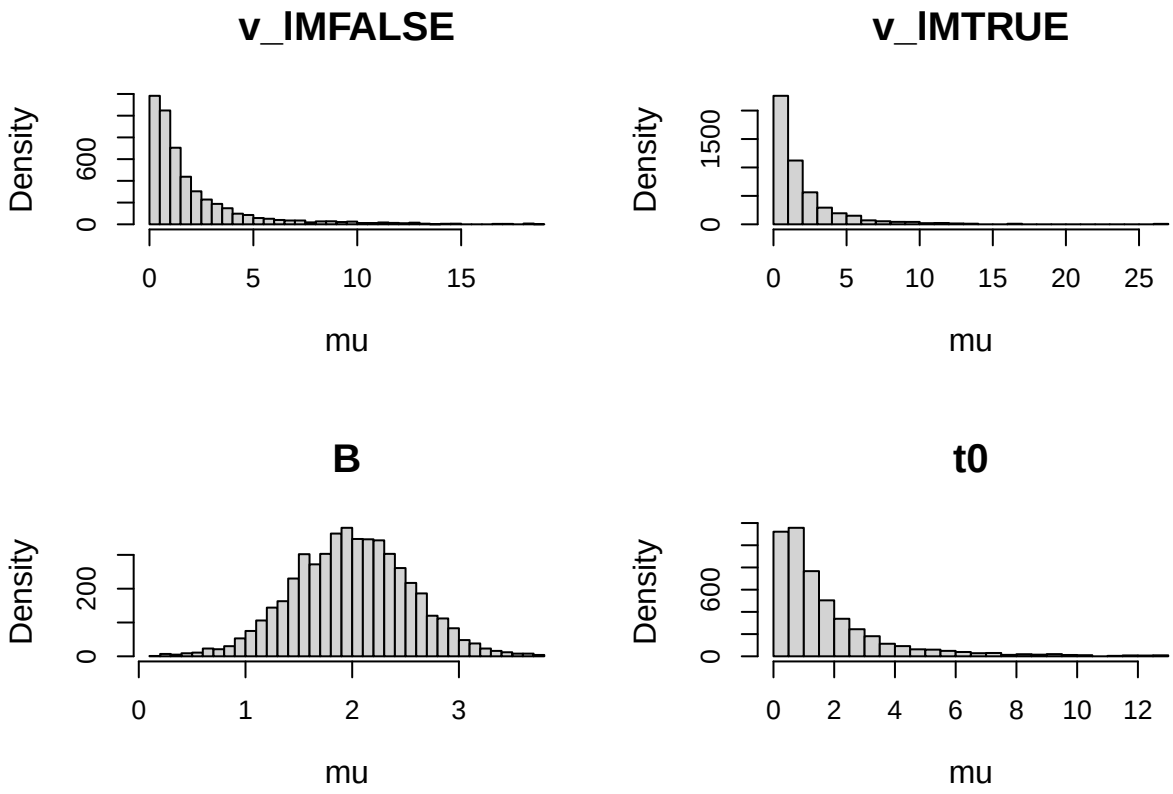








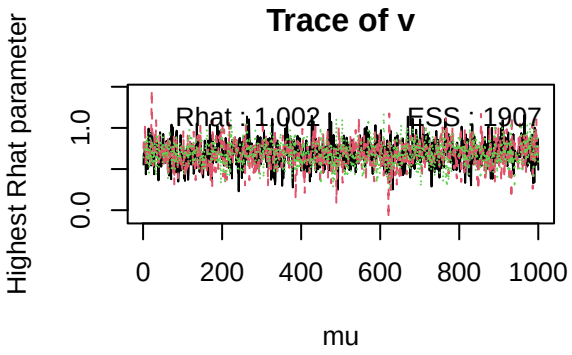

```r
# Implied priors after mapping and transforming
plot(prior_linB, map=TRUE,
     covariates=data.frame(trials2=seq(0, 1, length.out=1024)))
```

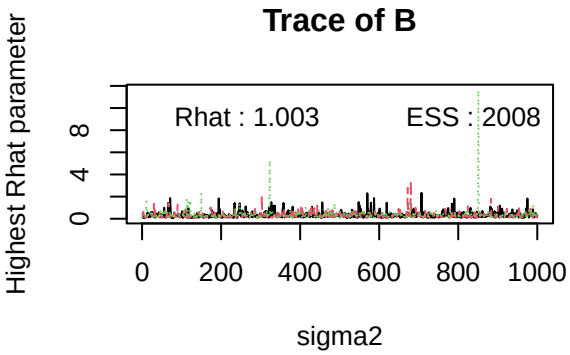


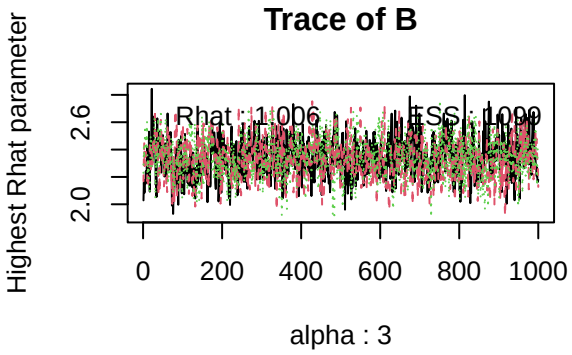

```
emc <- fit(emc, cores_per_chain=3, cores_for_chains=3,
                fileName='./samples/ds1_linB.RData')
```

```
check(emc)
```

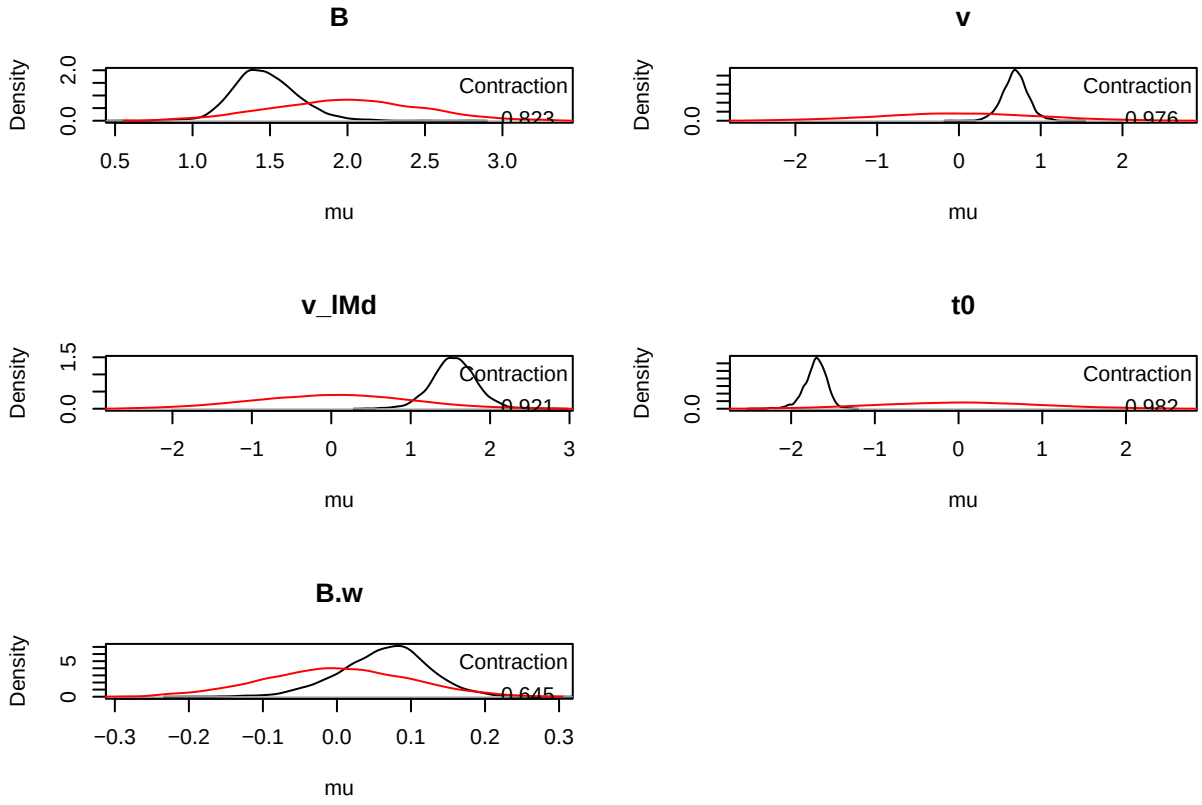
```
Iterations:
     preburn burn adapt sample
[1,]       0    0     0   1000
[2,]       0    0     0   1000
[3,]       0    0     0   1000

 mu
            B        v    v_lMd       t0      B.w
Rhat    1.001    1.002    1.001    1.001    1.001
ESS  2298.000 1907.000 2061.000 1956.000 2521.000

 sigma2
            B        v    v_lMd       t0      B.w
Rhat    1.003    1.003    1.001    1.002    1.001
ESS  2008.000 1384.000 1692.000 1429.000 1054.000

 alpha highest Rhat : 3
            B        v    v_lMd      t0      B.w
Rhat    1.006    1.005    1.004   1.006    1.005
ESS  1099.000 1425.000 1509.000 927.000 1400.000
```








```
plot_pars(emc)
```



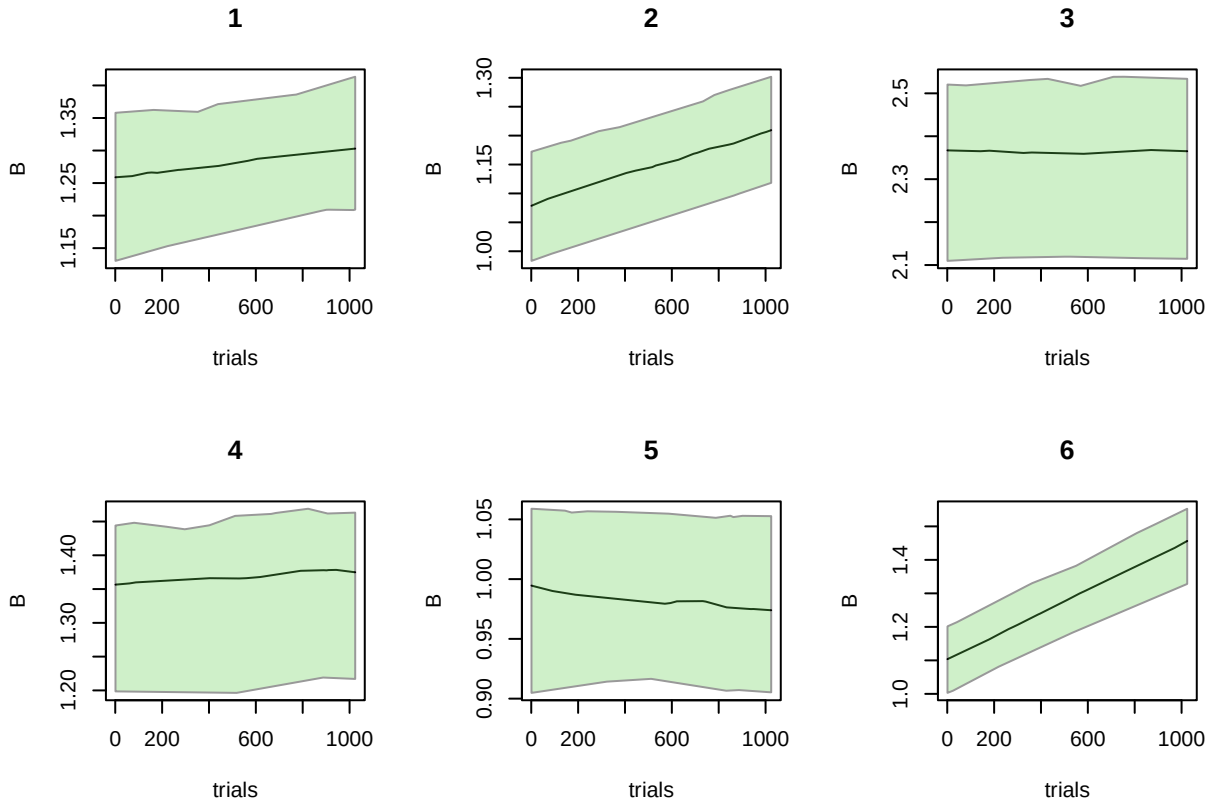

```
credint(emc)
```

```
$mu
         2.5%    50%  97.5%
B       1.108  1.456  1.916
v       0.377  0.689  1.006
v_lMd   0.990  1.545  2.092
t0     -2.019 -1.700 -1.478
B.w    -0.063  0.068  0.176
```

On a group-level, we find a small (not credible) positive `B.w` – on average, in this dataset, thresholds appear to increase by ~0.07 over the course of 1024 trials. We can now generate posterior predictives, and while doing that, ask *EMC2* to return the mapped and transformed parameters, which will allow us to visualize the fitted thresholds over trials. Here we see that although there is little change for some participants, for others (e.g, 6) the change is more substantial.

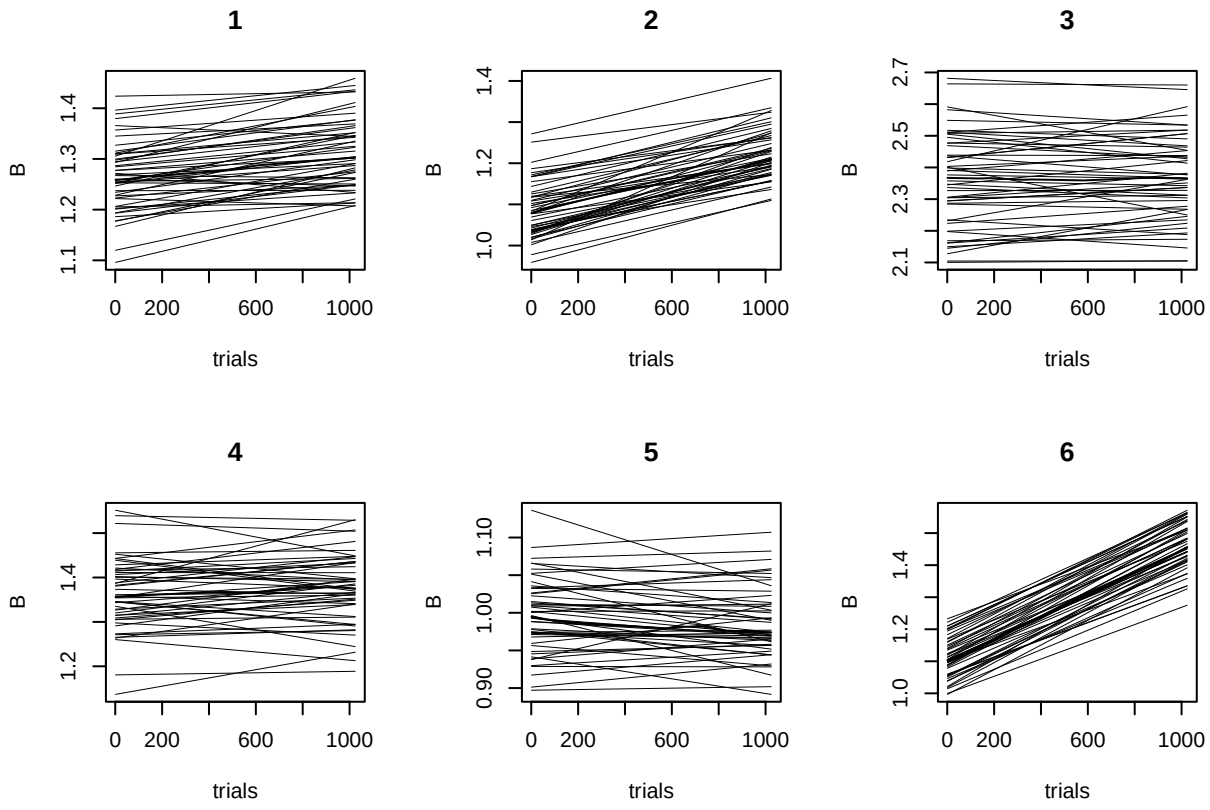
```
# By setting return_trialwise_parameters to TRUE, we obtain the parameters
# of each iteration as an attribute in the returned object (pp).
pp <- predict(emc, n_cores=9, return_trialwise_parameters=TRUE)
par(mfrow=c(2,3))
for(subject in 1:6) {
  plot_trend(attr(pp, 'trialwise_parameters'), emc=emc,
             par_name='B', subject=subject,
             filter = function(data) data$lR == 'odd',
```

```
              main=subject)
}
```



Here, the green shaded area indicated the 95% credible interval of the posterior on the threshold for each trial. We can also plot the individual thresholds of each posterior predictive separately as lines:

```
par(mfrow=c(2,3))
for(subject in 1:6) {
  plot_trend(attr(pp, 'trialwise_parameters'), emc=emc,
             par_name='B', subject=subject,
             filter = function(data) data$lR == 'odd',
             main=subject, pp_shaded=FALSE)
}
```



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 kernels that enforce either an increase or decrease. 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 ~ lM, t0 ~ 1),
                          trend=trend_exp_incr)
```

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

 Design Matrices:
$B
 B
```

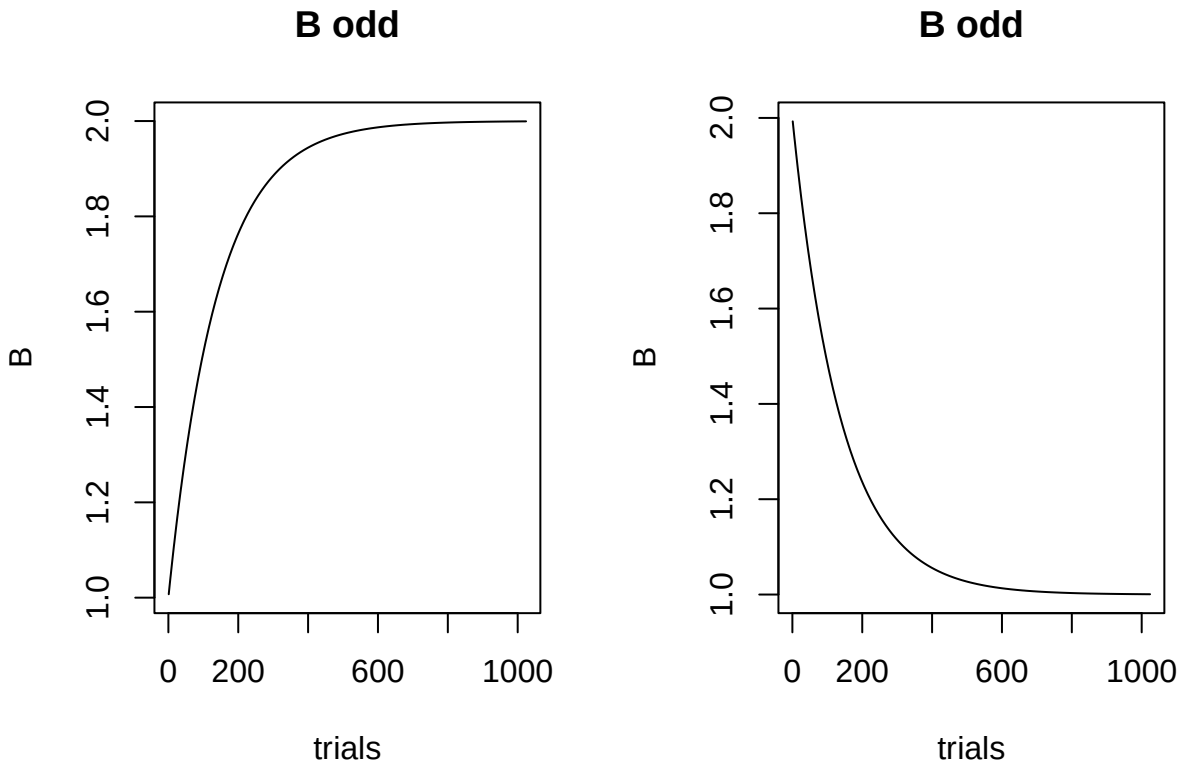
```
 1

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

$t0
 t0
  1

$B.w
 B.w
   1

$B.d_ei
 B.d_ei
      1

$A
 A
 1

$s
 s
 1
```

```r
design_exp_decr <- 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 ~ lM, t0 ~ 1),
                          trend=trend_exp_decr)
```

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

 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

$B.d_ed
 B.d_ed
      1

$A
 A
 1

$s
 s
 1
```

```r
emc_incr <- make_emc(dat, design_exp_incr)
emc_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, emc=emc_incr,
           par_name='B', subject=1, filter = function(data) data$lR == 'odd',
           main='B odd')
plot_trend(p_vector_decr, emc=emc_decr,
           par_name='B', subject=1, filter = function(data) data$lR == 'odd',
           main='B 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` (i.e., the ability to discriminate odd from even) 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)
```

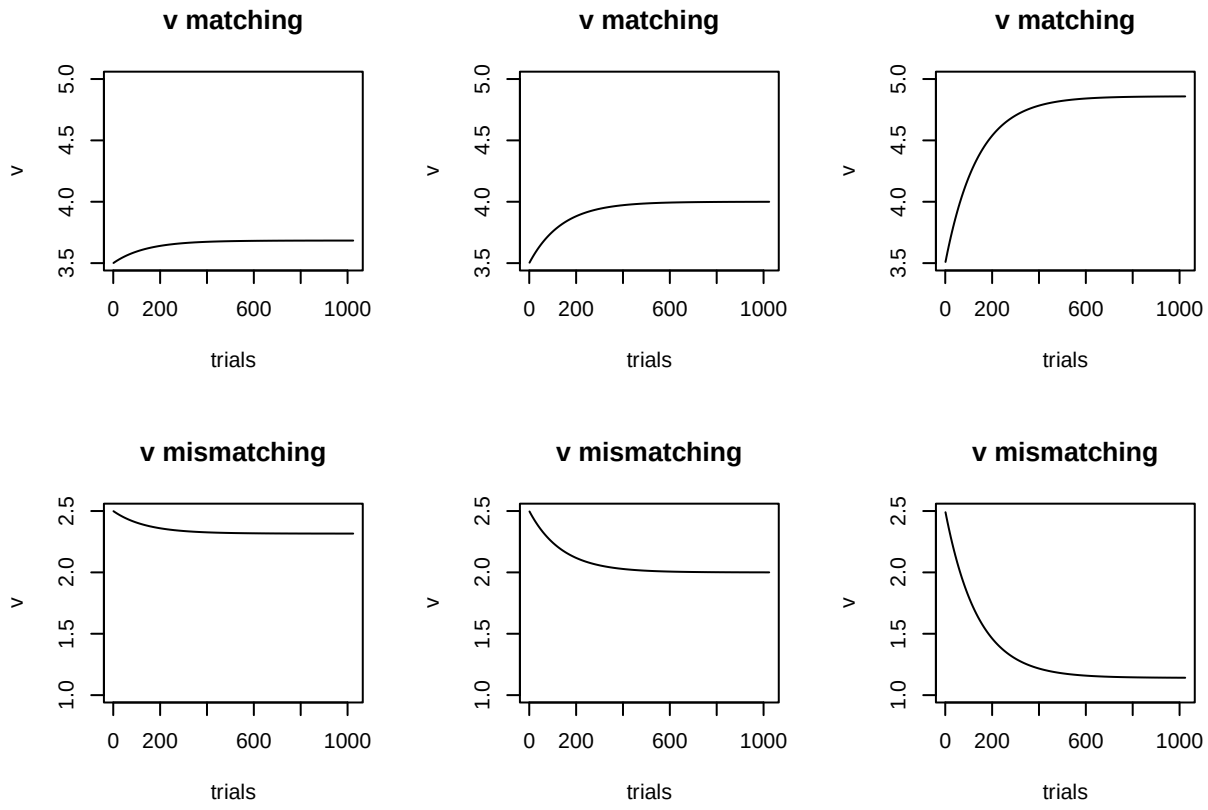
```
 Sampled Parameters:
[1] "B"          "v"          "v_lMd"      "t0"         "v_lMd.w"
[6] "v_lMd.d_ei"

 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))
```

```
emc_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, emc=emc_incr, par_name='v',
           subject=1, filter = function(data) data$lM == TRUE,
           main='v matching', ylim=c(3.5,5))
plot_trend(p_vector1, emc=emc_incr, par_name='v',
```

```
            subject=1, filter = function(data) data$lM == FALSE,
            main='v mismatching', ylim=c(1, 2.5))
plot_trend(p_vector2, emc=emc_incr, par_name='v',
            subject=1, filter = function(data) data$lM == TRUE,
            main='v matching', ylim=c(3.5,5))
plot_trend(p_vector2, emc=emc_incr, par_name='v',
            subject=1, filter = function(data) data$lM == FALSE,
            main='v mismatching', ylim=c(1, 2.5))
plot_trend(p_vector3, emc=emc_incr, par_name='v',
            subject=1, filter = function(data) data$lM == TRUE,
            main='v matching', ylim=c(3.5,5))
plot_trend(p_vector3, emc=emc_incr, par_name='v',
            subject=1, filter = function(data) data$lM == FALSE,
            main='v mismatching', 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

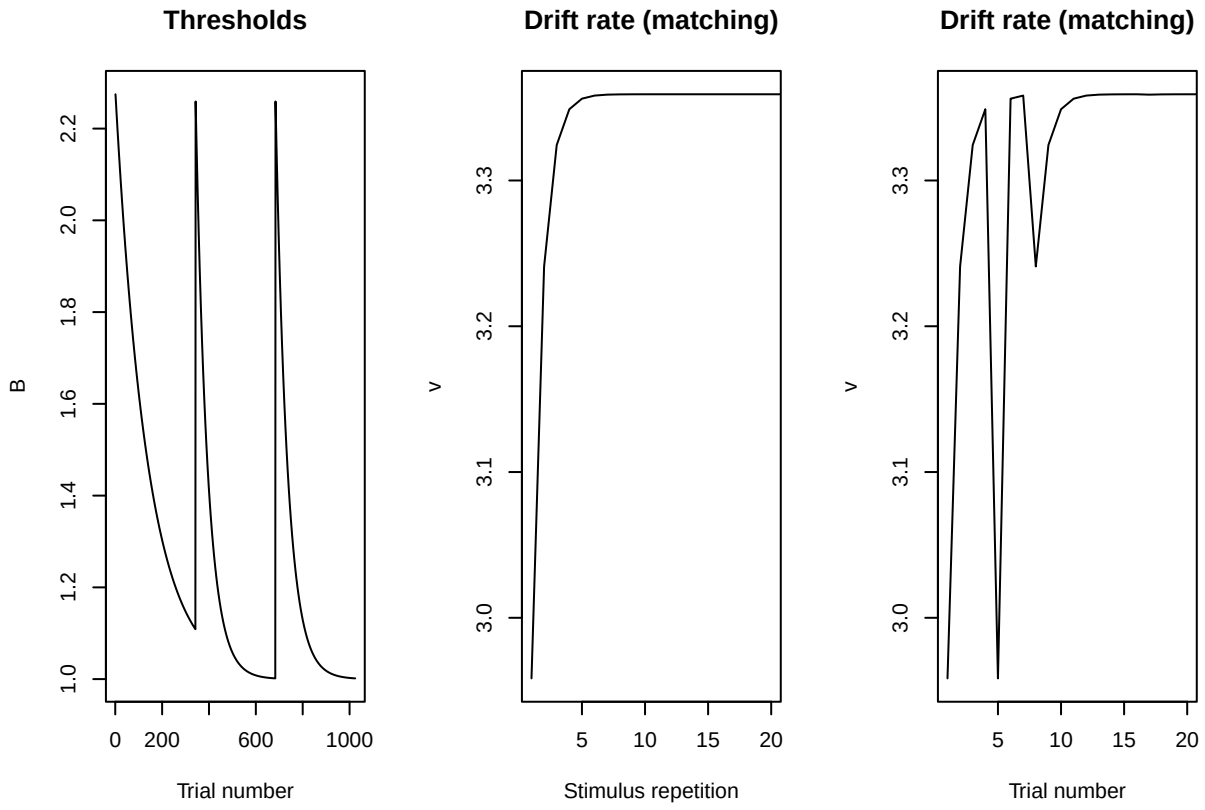
purposes we can simulate such effects:

```
# 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)/1024
}
# 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
```

```r
emc_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, emc=emc_multitrend, par_name='B',
           subject=1, filter = function(data) data$lR == 'odd',
           main='Thresholds', xlab='Trial number')
plot_trend(p_vector, emc=emc_multitrend, par_name='v',
           subject=1, filter = function(data) data$lM == TRUE,
           main='Drift rate (matching)', on_x_axis='stimulus_repetition',
           xlab='Stimulus repetition', xlim=c(1,20))
plot_trend(p_vector, emc=emc_multitrend, par_name='v',
           subject=1, filter = function(data) data$lM == TRUE,
           main='Drift rate (matching)', xlab='Trial number', xlim=c(1,20))
```




```
mapped_pars(design_multitrend)
```

```
$B

 intercept  : 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 illustrates how the thresholds decrease within each block (at different rates between blocks), 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. Many functions 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 polynomial basis around the mean of the covariate (allowing there to be changes in the direction of the trend, which is not possible if the covariate is always positive). 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 ~ lM, t0 ~ 1),
                      trend=trend_poly)
```

```
 Sampled Parameters:
[1] "B"     "v"     "v_lMd" "t0"    "B.d1"  "B.d2"  "B.d3"  "B.d4"

 Design Matrices:
$B
 B
 1

$v
    lM v v_lMd
  TRUE 1   0.5
```

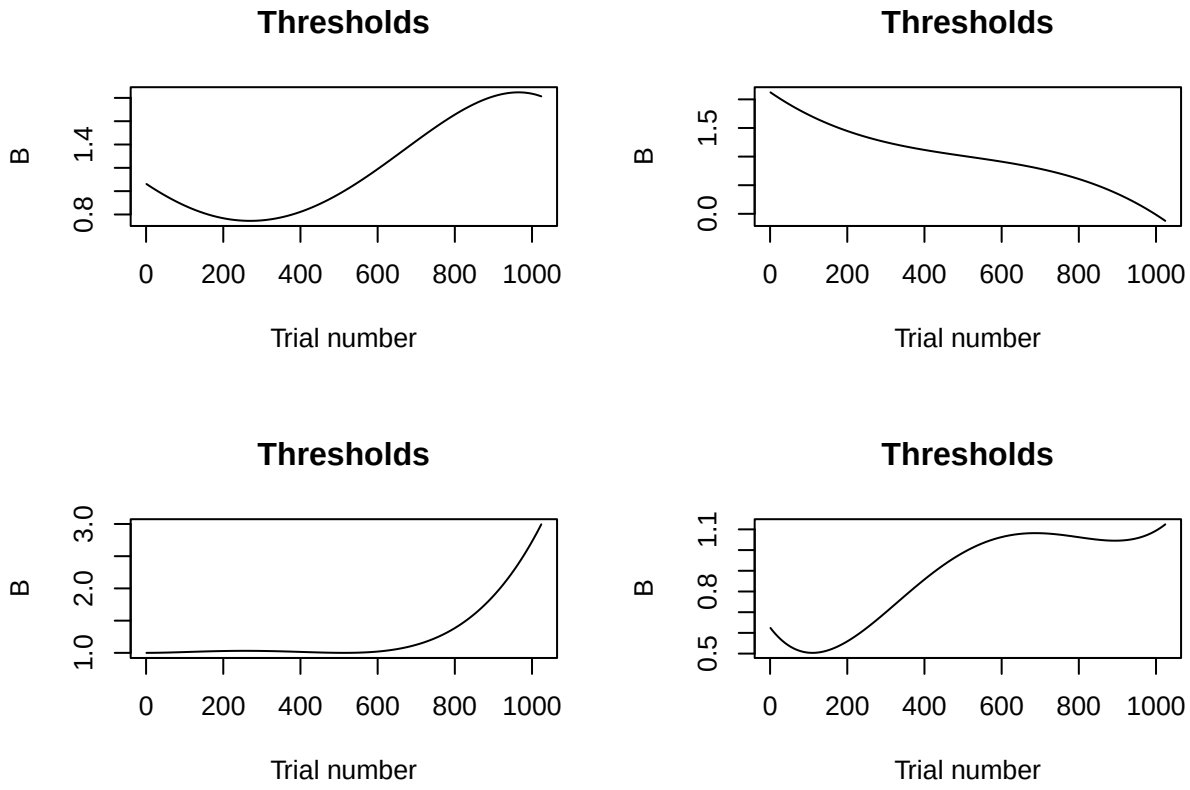
```
 FALSE 1  -0.5

$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

 intercept  : 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)
```

```
emc_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)
```

```r
par(mfrow=c(2,2))
plot_trend(p_vector1, emc=emc_poly, par_name='B',
           subject=1, filter = function(data) data$lR == 'odd',
           main='Thresholds', xlab='Trial number')
plot_trend(p_vector2, emc=emc_poly, par_name='B',
           subject=1, filter = function(data) data$lR == 'odd',
           main='Thresholds', xlab='Trial number')
plot_trend(p_vector3, emc=emc_poly, par_name='B',
           subject=1, filter = function(data) data$lR == 'odd',
           main='Thresholds', xlab='Trial number')
plot_trend(p_vector4, emc=emc_poly, par_name='B',
           subject=1, filter = function(data) data$lR == 'odd',
           main='Thresholds', xlab='Trial number')
```



Mechanisms of dynamics: Stimulus memory

Models with dynamic mechanisms (as opposed to the descriptions of dynamics in the last section) often 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 Miletić 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 recode as 1 (even) and -1 (odd) and use in 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 a belief that both stimuli occur equally often.

For now, let us assume that stimulus memory influences the relative thresholds: the threshold for the even accumulator increases, and the odd threshold decreases (by the same amount). To achieve this, we need to parametrise thresholds with the same mean-difference parametrisation 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',
                       phase = "premap")
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
```

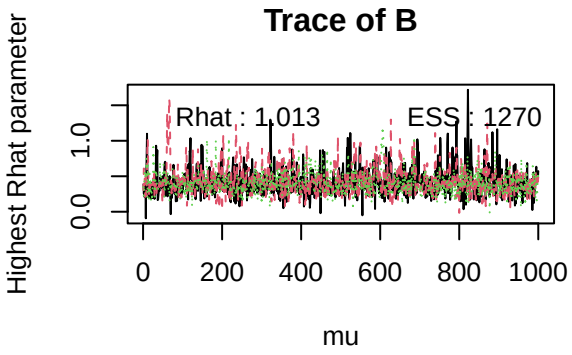
We can now apply a similar prior to B as above, and fit the model. Note that data compression is turned off automatically, since the delta rule needs to be applied to the covariate on each trial individually.

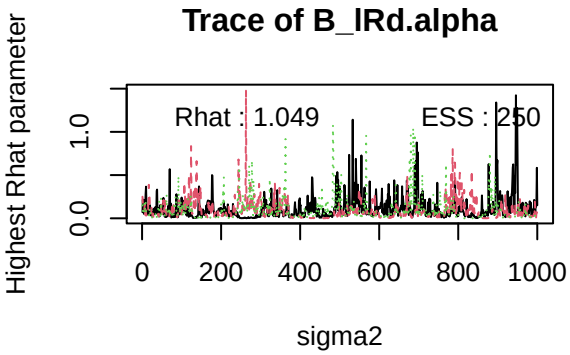
```
prior_SMB <- prior(design_RDM_SM, mu_mean=c(B=2), mu_sd=c(B=0.5))
emc <- make_emc(dat, design=design_RDM_SM, prior_list = prior_SMB)
```

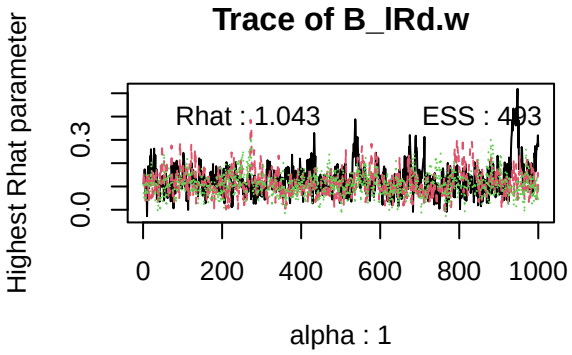
```
emc <- fit(emc, cores_per_chain=3, cores_for_chains=3,
           fileName='./samples/ds1_SMB.RData')
```

```
check(emc)
```

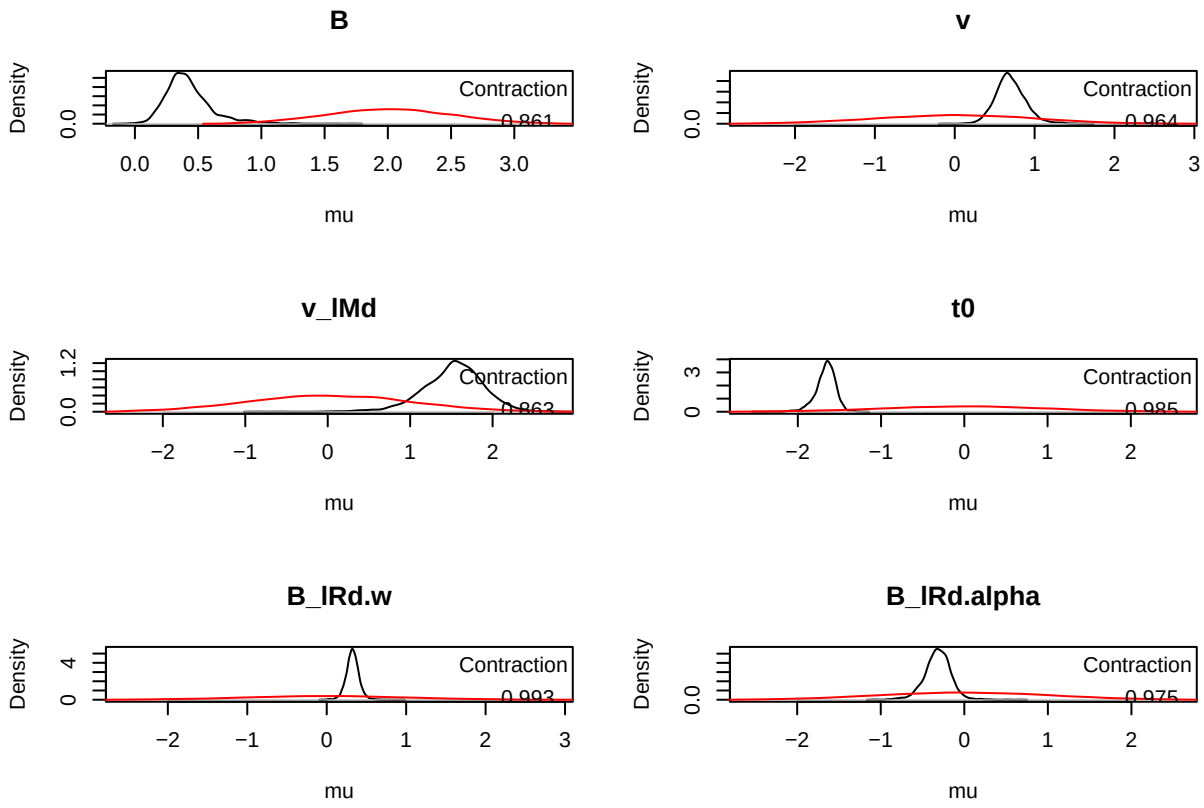
```
Iterations:
     preburn burn adapt sample
[1,]       0    0     0   1000
[2,]       0    0     0   1000
[3,]       0    0     0   1000

 mu
            B        v v_lMd       t0  B_lRd.w B_lRd.alpha
Rhat    1.013    1.001     1    1.003    1.004       1.012
ESS  1270.000 1738.000  1616 1624.000 1590.000     691.000

 sigma2
            B        v    v_lMd       t0  B_lRd.w B_lRd.alpha
Rhat    1.011    1.003    1.002    1.004    1.019       1.049
ESS  1058.000 1372.000 1278.000 1151.000 1081.000     250.000

 alpha highest Rhat : 1
            B       v   v_lMd       t0 B_lRd.w B_lRd.alpha
Rhat    1.002   1.004   1.003    1.004   1.043       1.034
ESS  1540.000 906.000 908.000 2125.000 493.000     285.000
```








```
plot_pars(emc)
```



We find excellent convergence properties, especially given learning rate parameters are often hard to estimate. 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 (this can take a while to run):

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

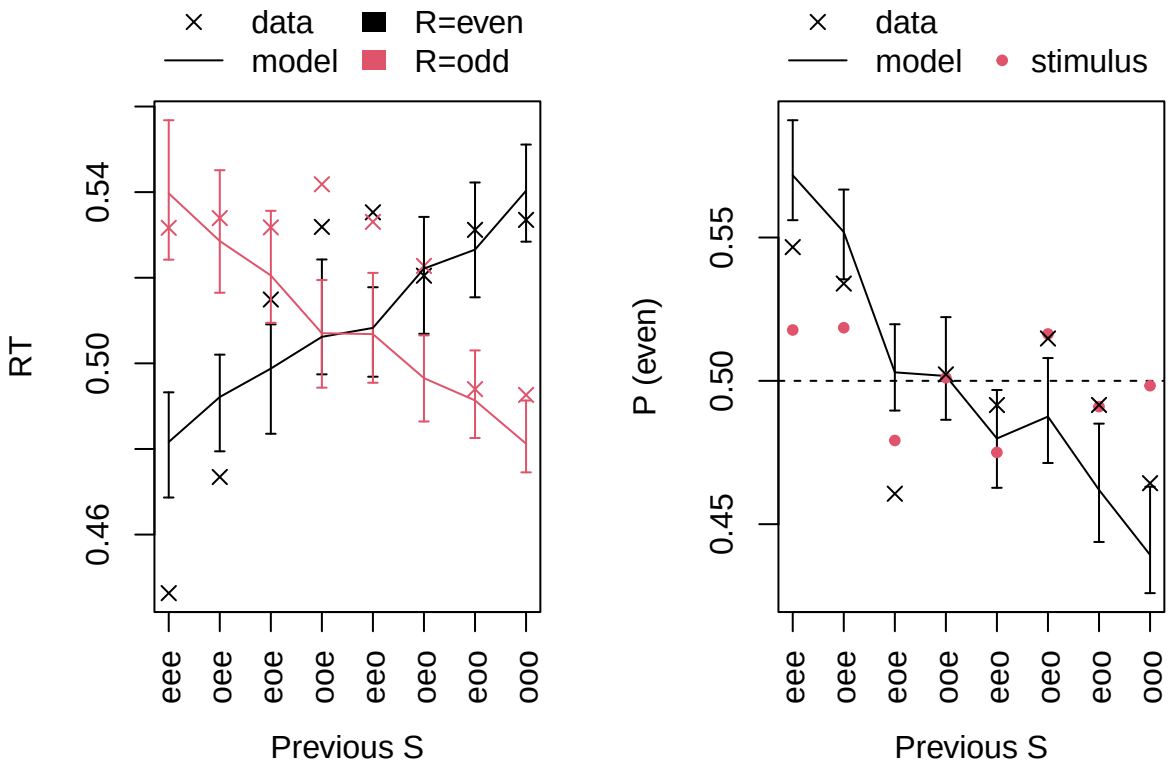
```
$mu
           2.5%   50% 97.5%
v_lMFALSE 0.819 0.965 1.120
v_lMTRUE  4.239 4.352 4.470
B_lReven  1.304 1.359 1.425
B_lRodd   1.305 1.359 1.425
t0        0.200 0.208 0.215
```

Hence, we find a group-wise mean learning rate of ~0.38, and the threshold of the odd accumulator is 0.323 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(emc, n_cores=9,
              # for plotting purposes below, this argument is added:
              return_trialwise_parameters=TRUE)
save(pp, file='./ds1_SMB_pps.RData')
```

```r
load('./ds1_SMB_pps.RData')

# this is a convience function that is not part of EMC2. For help, inspect the
# first lines after calling plot_history_effects (omitting the parentheses),
# which document its use
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 (e.g., ooo = odd, odd, odd; ooe = odd, odd, even; etc, where the right-most letter in the string indicates the most recent trial). The RT 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 crosses demonstrates that participants are more likely (~.55) to choose 'even' if the previous three trials were 'even'. The red circles are important as a quality check. If the stimuli are generated truly randomly, the red circles should be approximately at 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 black crosses deviating more from 0.5 compared to red circles.

Advanced note: at

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 emc object to see that the covariate `Stim1` is indeed the same across accumulators in each trial:

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

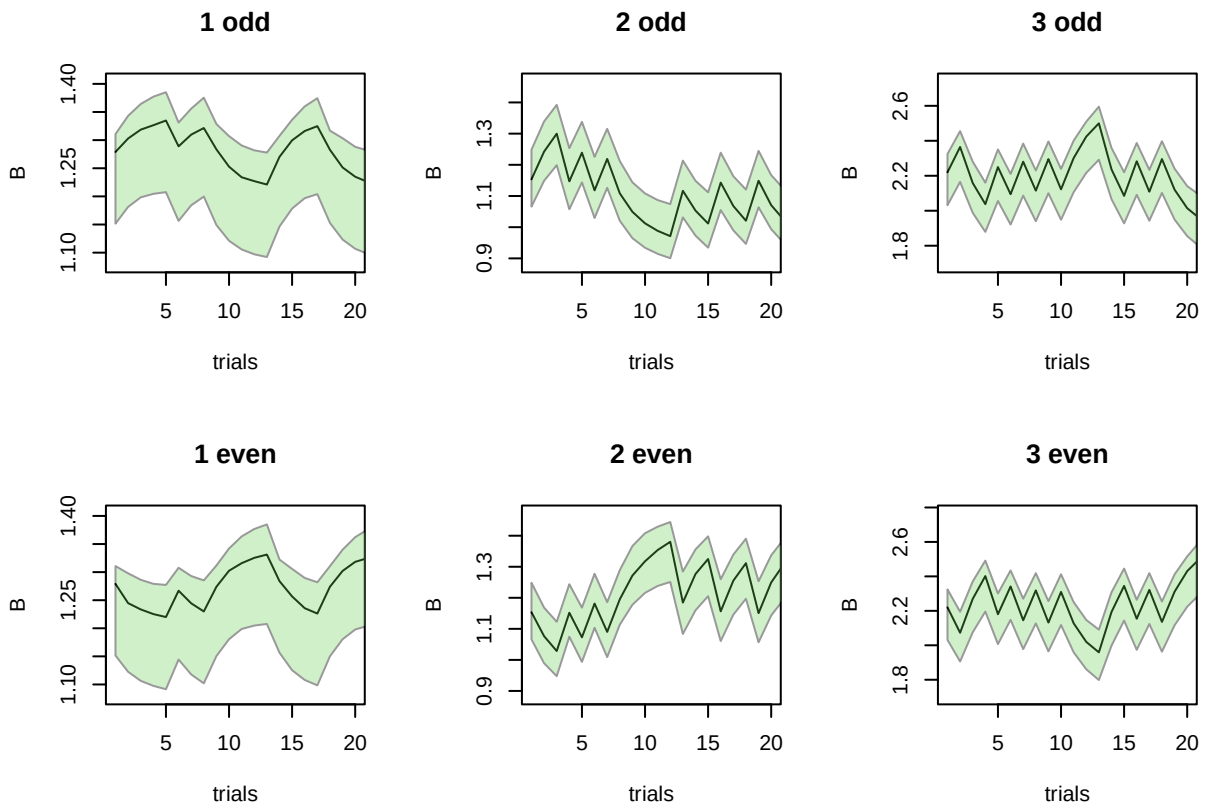
```
  subjects    S    R        rt trials trials2 block trial_in_block
1        1 even even 0.5333333      1   0.001     1          0.001
2        1 even even 0.5333333      1   0.001     1          0.001
3        1 even even 0.4166667      2   0.002     1          0.002
4        1 even even 0.4166667      2   0.002     1          0.002
5        1 even even 0.5000000      3   0.003     1          0.003
6        1 even even 0.5000000      3   0.003     1          0.003
  stimulus_repetition   tctrd Stim1   lR    lM winner
1                   1 -0.5115     1 even  TRUE   TRUE
2                   1 -0.5115     1  odd FALSE  FALSE
3                   2 -0.5105     1 even  TRUE   TRUE
4                   2 -0.5105     1  odd FALSE  FALSE
5                   3 -0.5095     1 even  TRUE   TRUE
6                   3 -0.5095     1  odd FALSE  FALSE
```

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, 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. By setting 'at='lR'', the Q-value is only updated at the first level of the factor in 'lR', and the resulting Q-value is carried over to the other levels of 'lR'. <!– 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, and therefore 'lR' is the default setting for 'at'. The DDM marks an exception, since it assumes one accumulator per trial, so has no 'lR' factor, as we demonstrate below. Additionally, advanced use cases might need to set 'at=NULL'.

As before, we can plot the trial-wise parameters with `plot_trend()`. Let's zoom in on the even and odd thresholds of the first three subject for the first 20 trials:

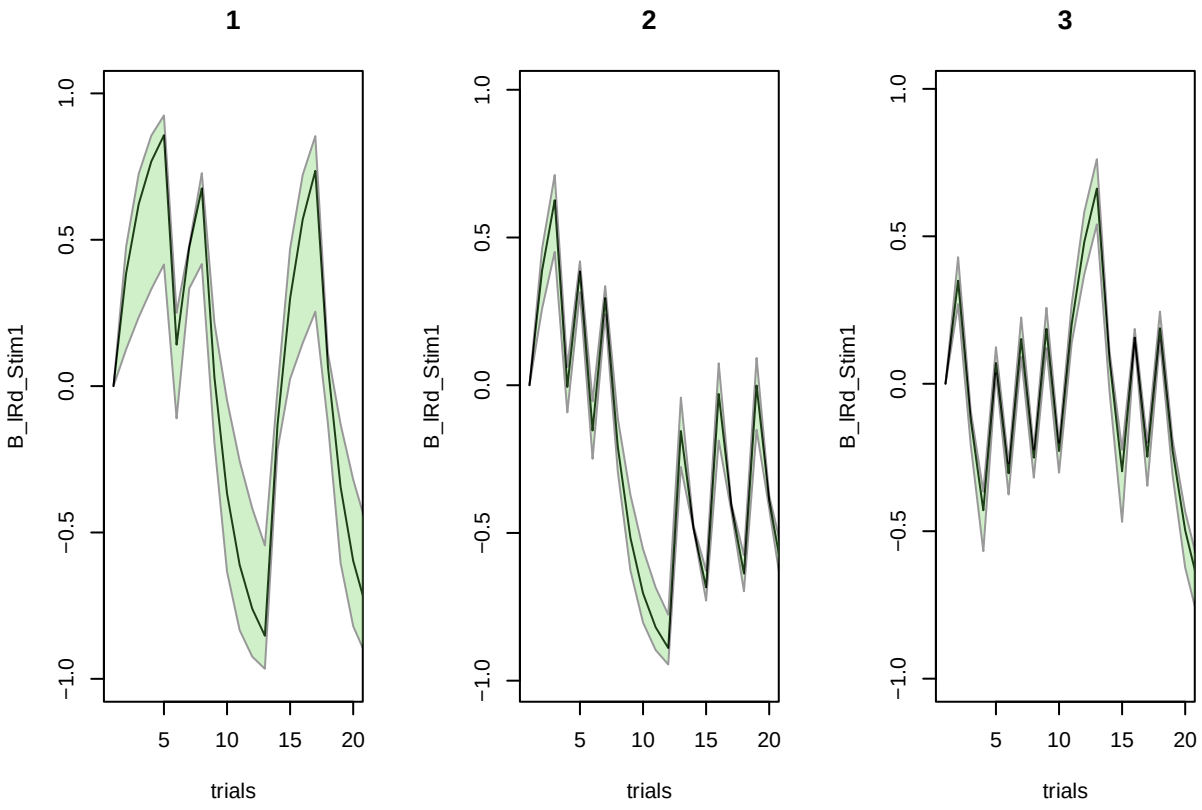
```
par(mfcol=c(2,3))
for(subject in 1:3) {
  plot_trend(attr(pp, 'trialwise_parameters'), emc=emc,
             par_name='B', subject=subject,
             filter= function(data) data$lR == 'odd',
             main=paste0(subject, ' odd'), xlim=c(1,20))
  plot_trend(attr(pp, 'trialwise_parameters'), emc=emc,
             par_name='B', subject=subject,
             filter= function(data) data$lR == 'even',
             main=paste0(subject, ' even'), xlim=c(1,20))
```

```
}
```



Alternatively, we can plot the evolution of the Q-values themselves. Note that `predict()` was run with another argument: `return_trialwise_parameters`, which returns the updated covariates as an attribute. We can use this as follows:

```
par(mfcol=c(1,3))
for(subject in 1:3) {
  plot_trend(attr(pp, 'trialwise_parameters'), emc=emc,
             par_name='B_lRd_Stim1', subject=subject,
             main=subject,
             xlim=c(1,20))
}
```



Repetition/alternation memory

The stimulus-memory mechanism accounts for what (Jones et al. 2013) termed *first-degree* recency effects: They depend on stimulus identity (e.g., 'odd' or 'even'). There are also *second-degree* recency effects, which depend on sequential properties - i.e., whether stimuli are repetitions or alternations of those stimuli before. It is easy to implement such a mechanism with a delta rule as well. If we code the stimuli as $S_t \in -1, 1$, then the multiplication $S_{t-1}S_t$ indicates if trial t repeats (outcome 1) or alternates (outcome -1) trial $t-1$. Let's hypothesize that participants keep track of the repetition rate using a repetition memory (RM). That could make use of the delta rule:

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

Q_{RM} is a latent representation for the belief that the stimulus will repeat itself. We could hypothesize that, if participants believe that the stimulus is repeating, the threshold corresponding the choice option that repeats the previous stimulus is lower compared to the one that alternates - and vice versa. To implement this, we need to parametrise the thresholds as repeat/alternate:

$$B_{repeat} = B_{mean} + B_{lR2d}$$
$$B_{alternate} = B_{mean} - B_{lR2d}$$

Like before, we are making use of an advantage-difference parametrisation for the thresholds here, but the difference B_{lR2d} parameter here codes accumulators by whether they repeat or alternate the previous stimuli. This B_{lR2d} term is the parameter influenced by the updated covariate. Since we do not necessarily expect an across-trial *mean* difference between thresholds, we set B_{lR2d} itself as a constant to 0.

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

$$B_{lR2d,t} = B_{lR2d} + w_{RM} \cdot Q_{RM,t}$$

Again introducing a weighting parameter: w_{RM}.

Let's implement this step by step. First, let's add $S_{t-1}S_t$ to the data, as `dat$Stim2`. This will be our new covariate. It should affect `B_lR2d` with a linear basis. Contrary to `lR`, the `lR2` factor is not automatically created by *EMC2*, so we must pass a function to design that creates it for us.

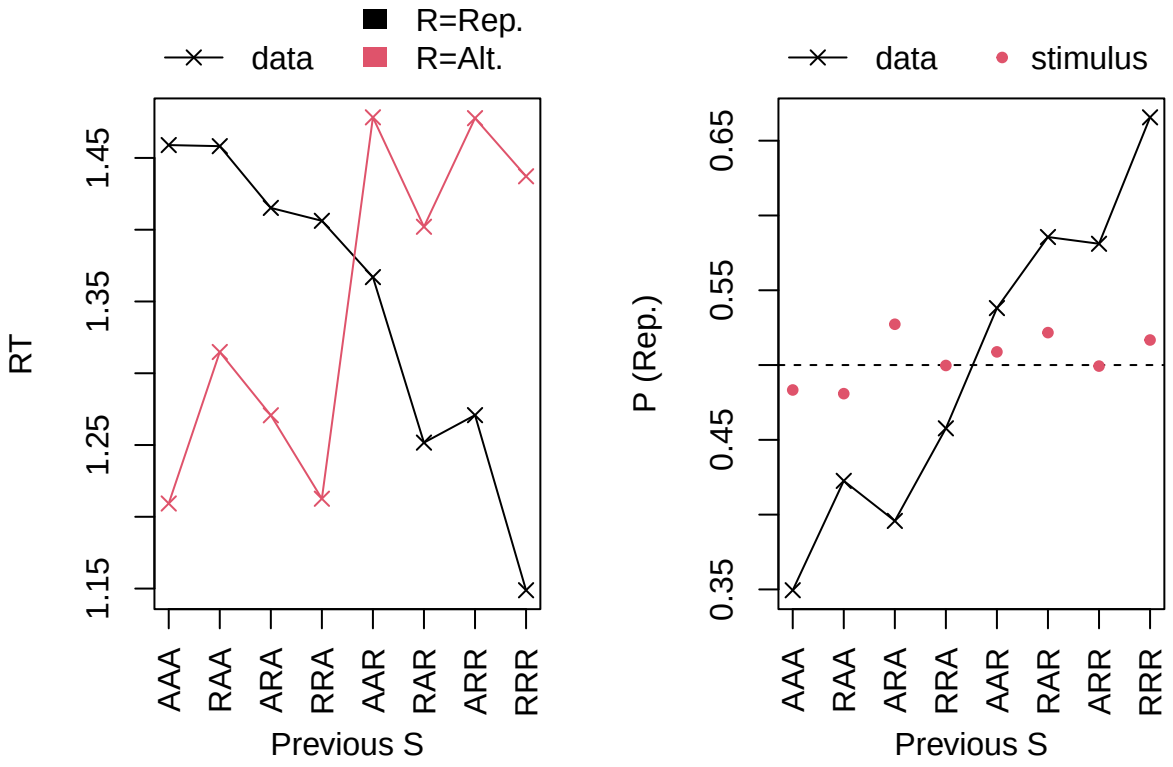
```
dat$Stim1 <- ifelse(dat$S=='even', 1, -1)      # S_{t}
dat$Stim2 <- dat$Stim1*Hmisc::Lag(dat$Stim1,1) # S_{t-1}S_{t}
RM_trend <- make_trend(cov_names=c('Stim2'),
                       kernels = 'delta',
                       par_names='B_lR2d',
                       bases='lin',
                       phase = "premap")
ADmat <- matrix(c(-.5,.5), ncol=1, dimnames=list(NULL,'d'))
make_lR2 <- function(x) {
  # note that we need to use lag 2, since the dadm has one row per accumulator
  lR2 <- as.numeric(x$lR)==as.numeric(Hmisc::Lag(x$S,2))
  # The first trial has no repeat/alternate.
  # However, since we set B_lR2d.q0, we can set lR2 for this trial
  # arbitrarily TRUE or FALSE -- B_lR2d_{1} is always 0.
  lR2[is.na(lR2)] <- TRUE
  factor(lR2, levels=c(1,0), labels=c('rep', 'alt'))
}

design_RDM_RM <- design(model=RDM,
                        data=dat,
                        contrast=list(lM=ADmat, lR=ADmat, lR2=ADmat),
                        covariates='Stim2',
                        functions=list(lR2=make_lR2),
                        matchfun=function(d) d$S==d$lR,
                        formula=list(B ~ lR2, v ~ lM, t0 ~ 1),
                        trend=RM_trend,
                        constants=c('B_lR2d'=0, 'B_lR2d.q0'=0))
```

```
 Sampled Parameters:
[1] "B"            "v"            "v_lMd"        "t0"           "B_lR2d.w"
[6] "B_lR2d.alpha"

 Design Matrices:
$B
 lR2 B B_lR2d
 rep 1   -0.5
 alt 1    0.5

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

$t0
```

```
 t0
  1

$B_lR2d.w
 B_lR2d.w
        1

$B_lR2d.q0
 B_lR2d.q0
         1

$B_lR2d.alpha
 B_lR2d.alpha
            1

$A
 A
 1

$s
 s
 1
```

Before fitting, we might want to simulate some data to test whether simulated data indeed demonstrates second-degree recency effects.

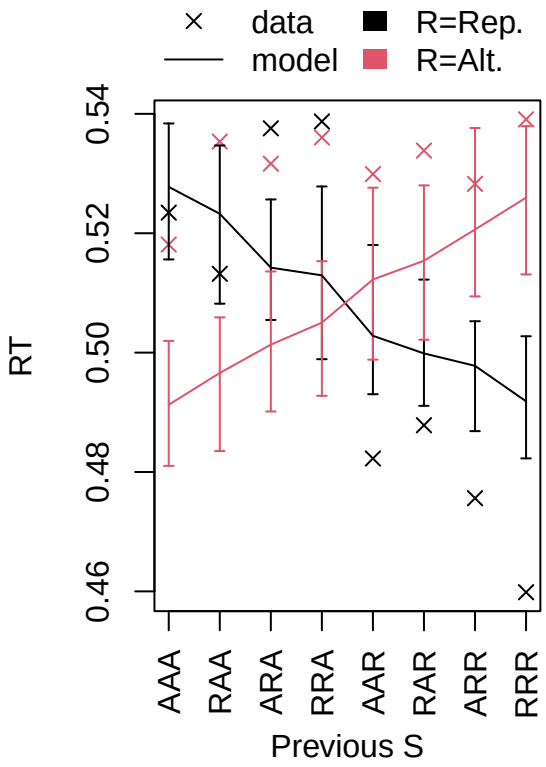
```r
p_vector <- sampled_pars(design_RDM_RM)
p_vector[1:6] <- c(log(2), log(1), .5, log(.15), 2, qnorm(0.1))
simDat <- make_data(p_vector, design_RDM_RM, data=dat)
# the plot_history_effects()-function takes an additional argument:
# degree, which can be 1 for first-degree or 2 for second-degree
# effects
plot_history_effects(dat=simDat, degree=2)
```

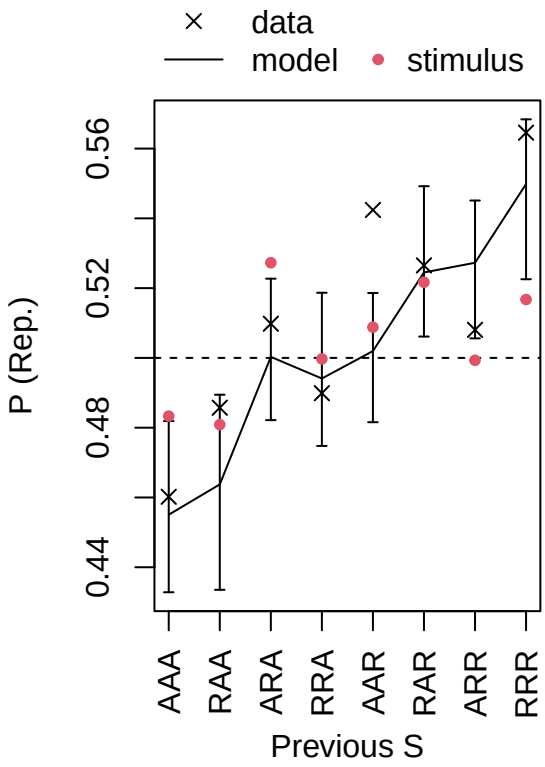


Which generates the expected pattern: if the previous trials were repeats, the model predicts participants are more likely to repeat on the current trial. Furthermore, a 'repeat' response would be faster than an 'alternate' response. Now let's fit the model to see the strength of these effects in real data:

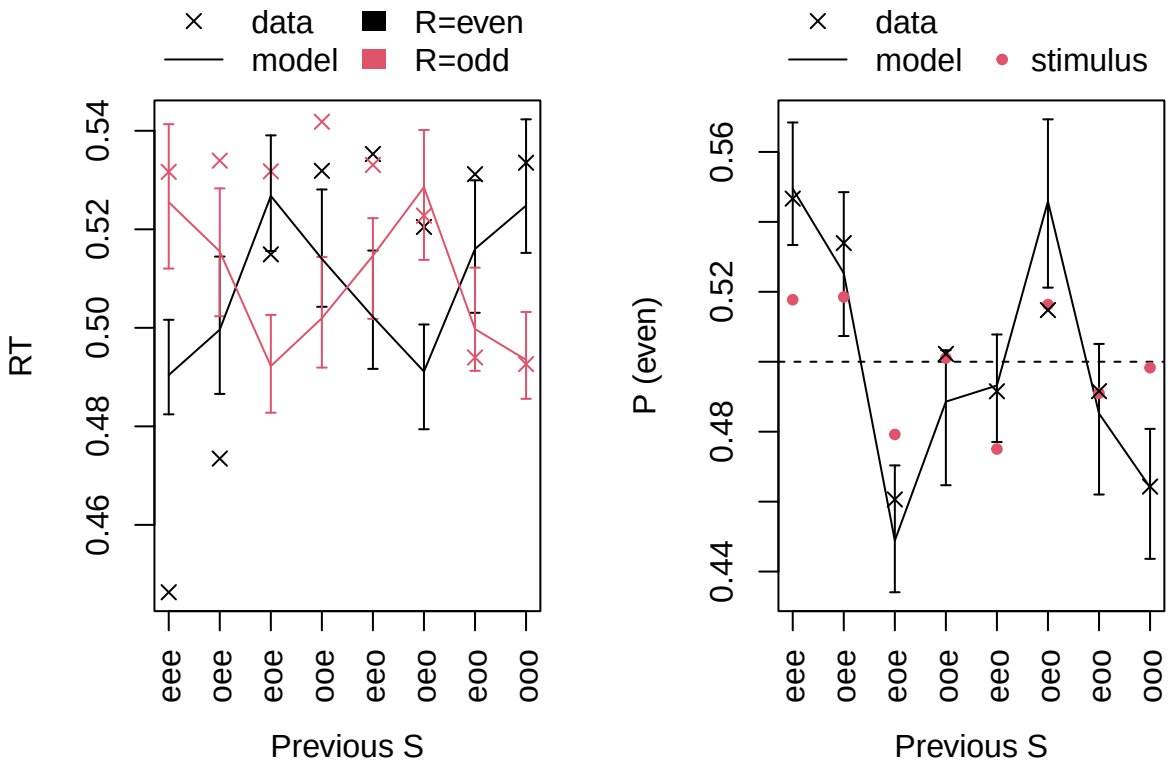
```
emc <- make_emc(dat, design=design_RDM_RM)
emc <- fit(emc, cores_per_chain=3, cores_for_chains=3,
           fileName='./samples/ds1_RMB.RData')
pp <- predict(emc, n_cores=10)
save(pp, file='./samples/ds1_RMB_pps.RData')
```

```
plot_history_effects(dat, pp, degree=2)
```






```
plot_history_effects(dat, pp, degree=1)
```

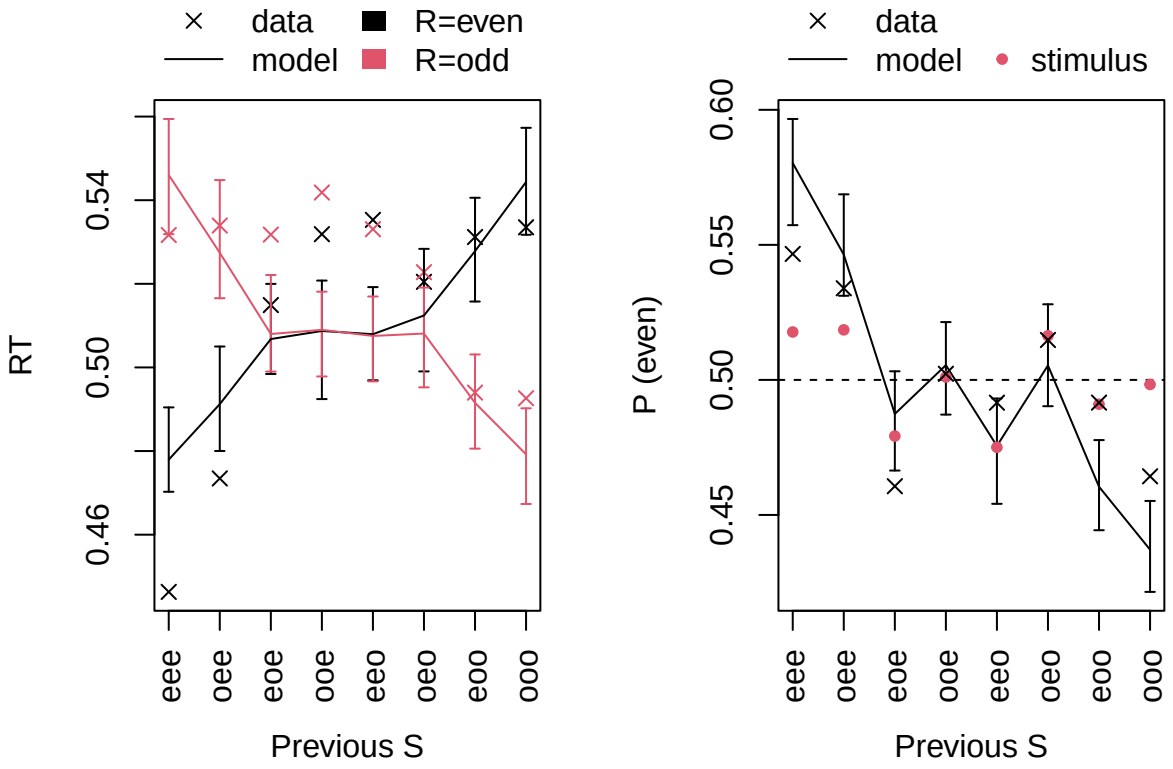


The second-degree recency effects are fitted okay, but the first-degree effects now seem off. Perhaps a combination would work best.

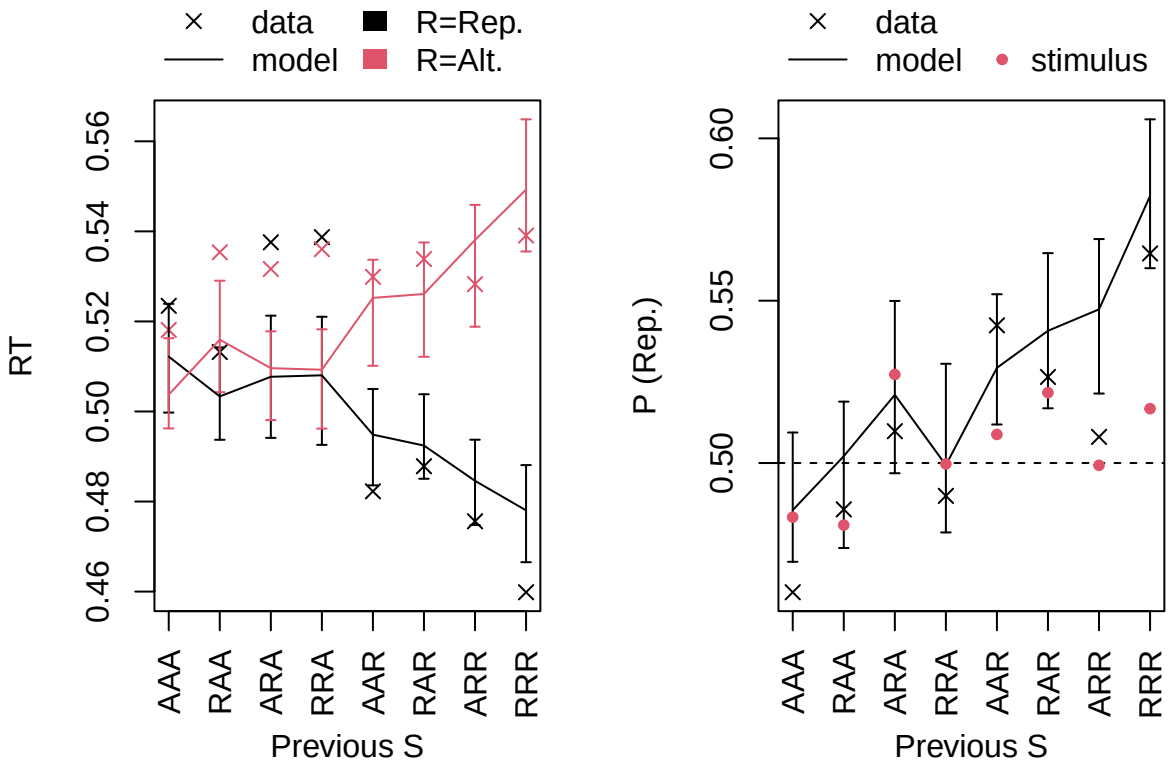
```
dat$Stim1 <- ifelse(dat$S=='even', 1, -1)
dat$Stim2 <- dat$Stim1*Hmisc::Lag(dat$Stim1,1)
SM_RM_trend <- make_trend(cov_names=c('Stim1', 'Stim2'),
                          kernels = c('delta', 'delta'),
                          par_names=c('B_lRd', 'B_lR2d'),
                          bases=c('lin', 'lin'),
                          phase = "premap")

design_RDM_RM <- design(model=RDM,
                        data=dat,
                        contrast=list(lM=ADmat, lR=ADmat, lR2=ADmat),
                        covariates=c('Stim1', 'Stim2'),
                        functions=list(lR2=function(x) {
                          lR2 <- as.numeric(x$lR)==as.numeric(Hmisc::Lag(x$S,2))
                          lR2[is.na(lR2)] <- TRUE
                          factor(lR2, levels=c(1,0), labels=c('rep', 'alt'))
                        }),
                        matchfun=function(d) d$S==d$lR,
                        formula=list(B ~ lR2+lR, v ~ lM, t0 ~ 1),
                        trend=SM_RM_trend,
                        constants=c('B_lR2d'=0, 'B_lR2d.q0'=0,
                                    'B_lRd'=0, 'B_lRd.q0'=0))
```

```
emc <- make_emc(dat, design=design_RDM_RM)
emc <- fit(emc, cores_per_chain=6, cores_for_chains=3,
           fileName='./samples/ds1_SMB_RMB.RData')
pp <- predict(emc, n_cores=10)
save(pp, file='./samples/ds1_SMB_RMB_pps.RData')
```

```
plot_history_effects(dat, pp, degree=1)
```




```
plot_history_effects(dat, pp, degree=2)
```



Although the alternation effects are relatively small in this dataset, formal model comparison suggests that the inclusion of the RM mechanism sufficiently improves the quality of fit to warrant the additional model complexity:

```
emc_SMB <- get(load('./samples/ds1_SMB.RData'))
emc_SMB_RMB <- get(load('./samples/ds1_SMB_RMB.RData'))
compare(list('SM'=emc_SMB, 'SM+RM'=emc_SMB_RMB))
```

```
         MD wMD   DIC wDIC  BPIC wBPIC EffectiveN meanD Dmean  minD
SM    -6923   0 -7027    0 -6943     0         85 -7112 -7139 -7196
SM+RM -6955   1 -7097    1 -7004     1         93 -7190 -7210 -7282
```

Stimulus memory: DDM and drift rate effects

The examples above mimic Miletić et al. (2025) by using 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 Wiener diffusion model (a DDM without between-trial variabilities) instead and hypothesize that drift rates rather than start points are biased. This can be implemented as follows:

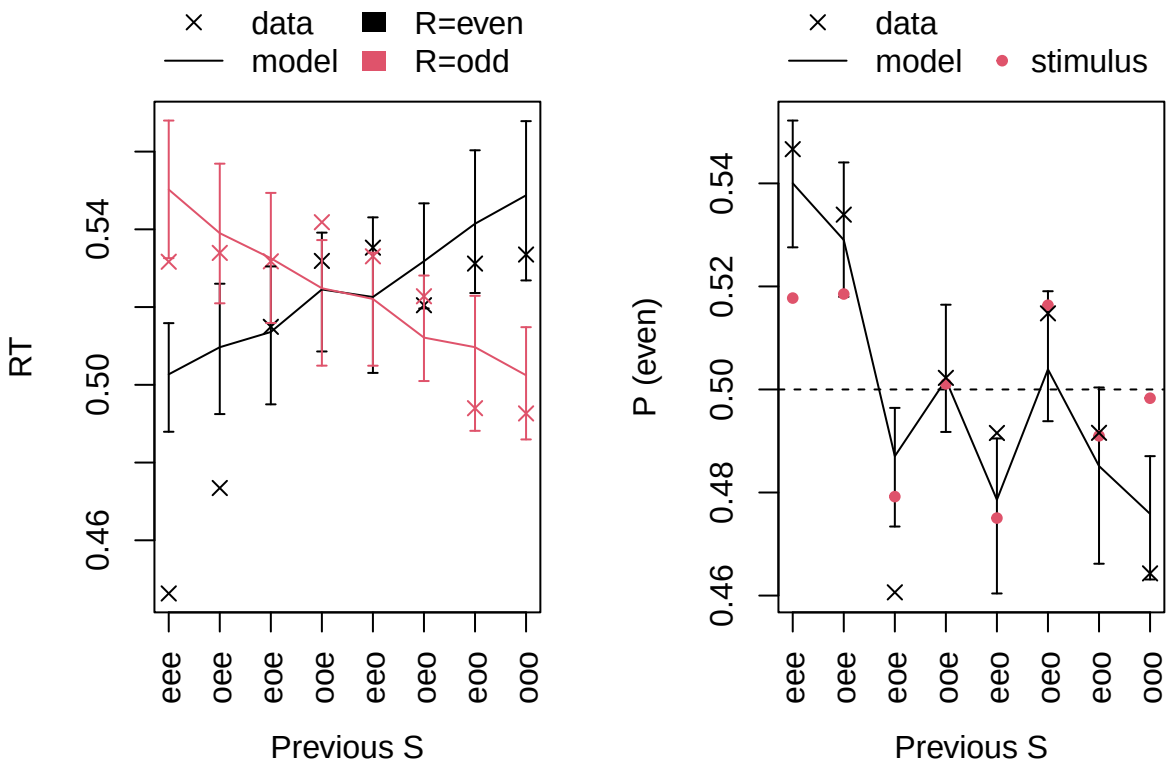
```
trend_SM_DDM <- make_trend(cov_names='Stim1',
                           kernels = 'delta',
                           par_names='v',
                           bases='lin',
                           phase = "premap",
                           at = NULL)
Smat <- matrix(c(-1,1), nrow = 2,dimnames=list(NULL,"dif"))
```

```
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)

# 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.
emc <- make_emc(dat, design=design_DDM)
emc <- fit(emc, cores_per_chain=3, cores_for_chains=3,
           fileName='./samples/ds1_SMv_DDM.RData')
```

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

```
pp_ddm <- predict(emc, 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'))))
```

```
       MD wMD   DIC wDIC  BPIC wBPIC EffectiveN meanD Dmean  minD
rdm -6923   1 -7027    1 -6943     1         85 -7112 -7139 -7196
ddm -5273   0 -5362    0 -5291     0         72 -5434 -5448 -5506
```

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 is important when simulating new data - the covariate in question is not the *empirically-observed* accuracy on any given trial, but the *newly-simulated* accuracy.

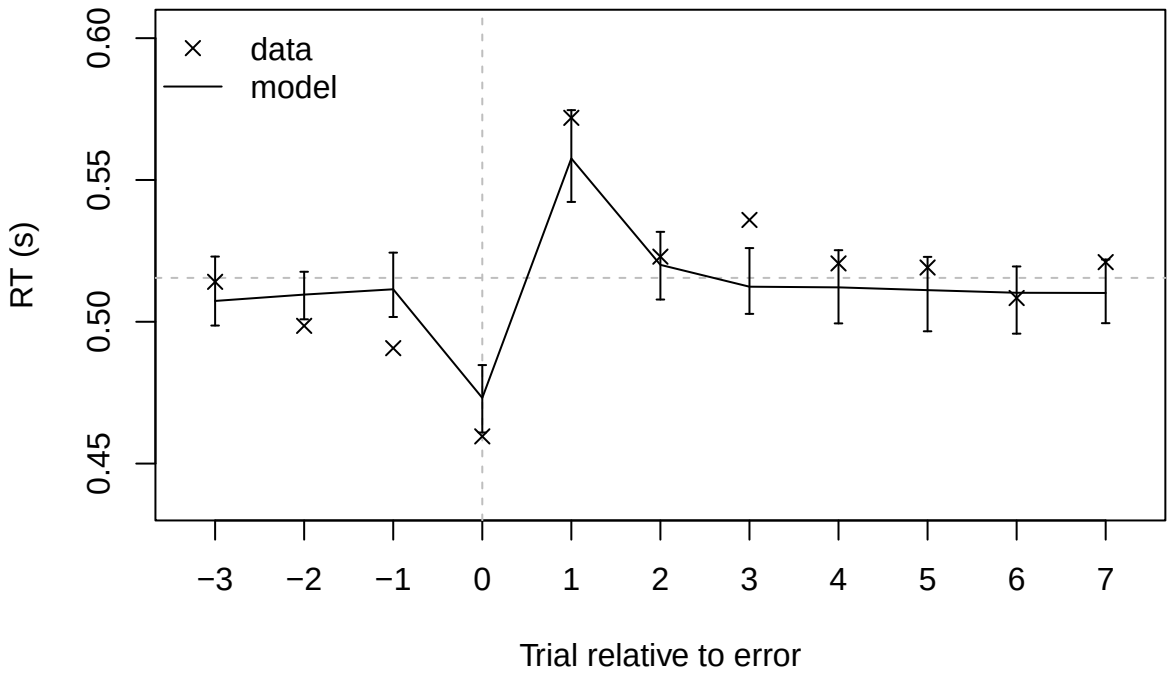
For this reason, it is useful to have *EMC2* calculate accuracy with a function rather than specifying it in the dataframe (in which case it would be treated as a static experimental factor). The function is applied when generating posterior predictives, ensuring that the accuracy of the *simulated* data is used as a covariate.

```
AM_trend <- make_trend(cov_names='error',
                       kernels = 'delta',
                       par_names='v',
                       bases='lin',
                       phase = "premap")
design_RDM_AM <- design(model=RDM,
                        data=dat,
                        contrast=list(lM=ADmat, lR=ADmat),
                        functions=list(error=function(x) x$S!=x$R),
                        matchfun=function(d) d$S==d$lR,
                        transform=list(lower=c(v.alpha=0.01)),
                        formula=list(B ~ 1, v ~ lM, t0 ~ 1, s~lM),
                        trend=AM_trend,
                        constants=c('v.q0'=0, 's'=1))
# NB1: we allow within-trial noise s to vary with accumulator
# match (correct/incorrect), which will allow us to capture the
# relative speed of errors.

# NB2: in this case, we are not estimating v on the natural scale:
mapped_pars(design_RDM_AM)
# This is because the AM mechanism can push drift rates on individual trials
# to negative values when applied on the natural scale.
# Since the RDM has no known analytic likelihood for negative drift rates these
# are excluded by the RDM model using its bound attribute (see RDM()$bound), but
# 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.
# The cognitive interpretation remains similar.

emc <- make_emc(dat, design=design_RDM_AM)
emc <- fit(emc, cores_per_chain=3, cores_for_chains=3,
           fileName='./samples/ds1_AM.RData')
credint(emc)
```

Accuracy memory can explain error-related effects such as 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. As mentioned above, 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. Because vectorisation is not possible in this case, this way of simulating data is much slower. ## NOTE TO SELF – DOUBLE CHECK IF AUTOMATED DETECTION STILL WORKS AS STATED HERE!!! ## ## ANDREW it worked for me here! ##

```
emc <- get(load('./samples/ds1_AM.RData'))

pp <- predict(emc, n_cores=40, conditional_on_data=FALSE)
save(pp, file='./samples/ds1_AM_pps.RData')
```

```
# this is a convience function that is not part of EMC2. For help, inspect the
# first lines after calling plot_error_effects (omitting the parentheses),
# which document its use
plot_error_effects(dat, pp)
```



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.

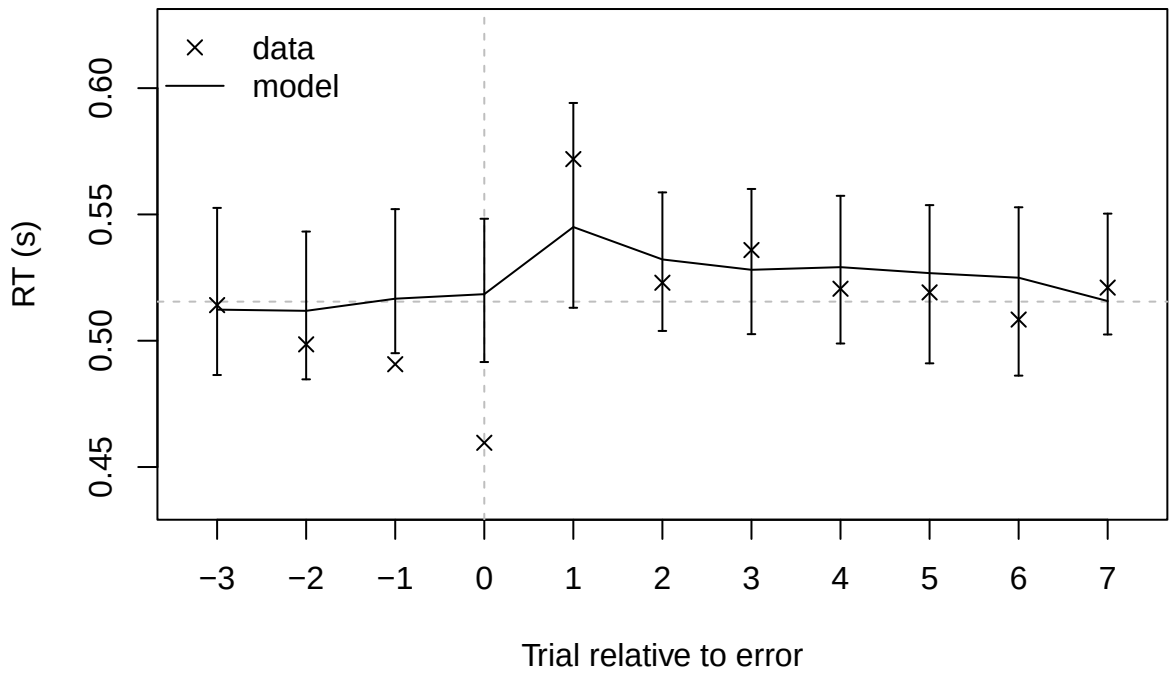
```
trend_AM_DDM <- make_trend(cov_names='error',
                           kernels = 'delta',
                           par_names='a',
                           bases='lin',
                           phase='posttransform',
                           at=NULL)
Smat <- matrix(c(-1,1), nrow = 2,dimnames=list(NULL,"dif"))
design_DDM <- design(model=DDM,
                     data=dat,
                     functions=list(error=function(x) x$S!=x$R),
```

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

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

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

```
emc <- get(load('./samples/ds1_AMa_DDM.RData'))
pp_ddm <- predict(emc, n_cores=40, conditional_on_data=FALSE)
save(pp_ddm, file='./samples/ds1_AMa_DDM_pps.RData')
```

```
plot_error_effects(dat, pp_ddm)
```




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

```
       MD wMD   DIC wDIC  BPIC wBPIC EffectiveN meanD Dmean  minD
rdm -6888   1 -7018    1 -6926     1         93 -7111 -7119 -7204
ddm -5298   0 -5390    0 -5315     0         76 -5466 -5498 -5541
```

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 approximates mean speed, which can be used as a proxy for difficulty, as processing efficiency will be lower for difficult trials relative to easy trials. Formally, $Q_{FM,t+1} = Q_{FM,t} + \alpha_{FM}(b_t/rt_t - Q_{FM,t})$.

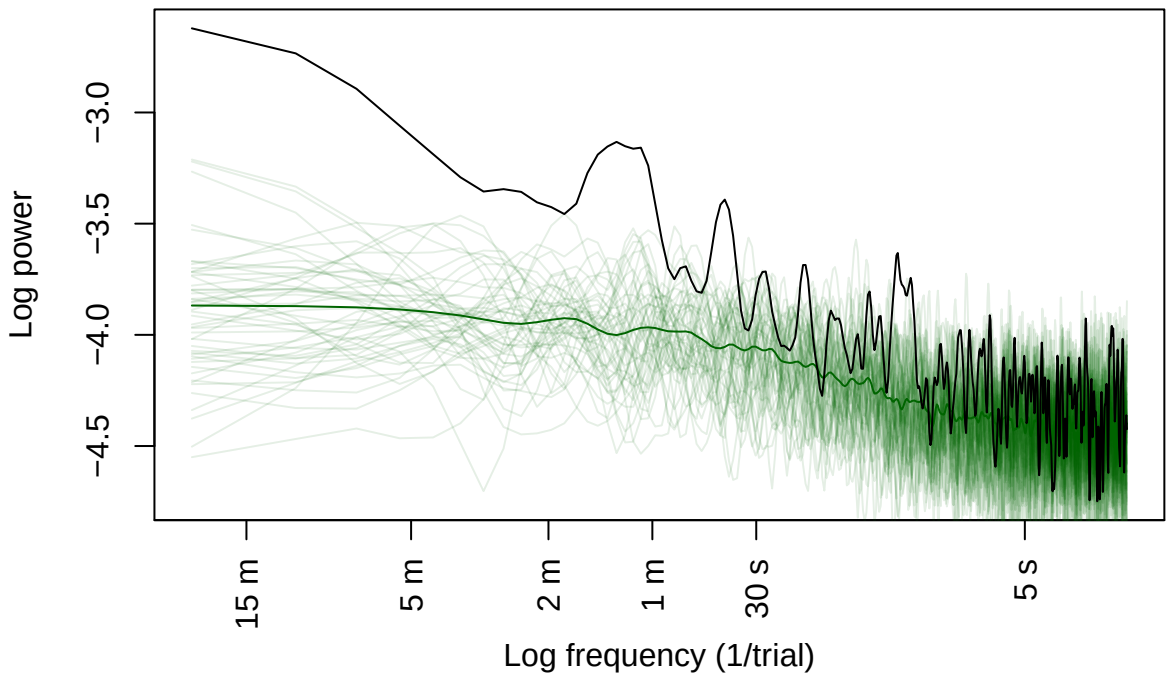
Here, we implement this using a custom kernel. Note that when we load a custom-kernel emc object from disk we need to reinitialize C pointers (see ?fix_custom_kernel_pointers).

```
tf <- tempfile(fileext = ".cpp")
writeLines(c(
  "// [[Rcpp::depends(EMC2)]]",
  "#include <Rcpp.h>",
  "#include \"EMC2/userfun.hpp\"",
  "",
  "// Example: two params (q0, alpha) and three inputs (rt, B, weight)",
  "Rcpp::NumericVector custom_kernel(Rcpp::NumericMatrix kernel_pars, ",
  "                                  Rcpp::NumericMatrix input) {",
  "  // assume kernels_pars(q0, alpha) and inputs(rt, B, weight)",
  "  int n = input.nrow();",
  "  Rcpp::NumericVector q(n);",
  "  Rcpp::NumericVector B_t(n);",
  "  Rcpp::NumericVector pe(n);",
  "  // B_t = B + w*Q_t for trial 1",
  "  q[0] = kernel_pars(0,0);",
  "  B_t[0] = input(0, 1) + input(0, 2)*q[0];",
  "  for (int i = 1; i < n; ++i) {",
  "    // 'prediction error' = B_t/rt_t - Q_t ",
  "    pe[i-1] = (B_t[i-1] / input(i-1,0)) - q[i-1];",
  "    // update: Q_t = Q_t-1 + alpha_t-1 * pe_t-1",
  "    q[i] = q[i-1] + kernel_pars(i-1,1) * pe[i-1];",
  "    // Apply base to B to get the correct threshold for ",
  "    // next trial (needed for PE calculation)",
  "    B_t[i] = input(i,1) + input(i,2) * q[i];",
  "  }",
  "  return q;",
  "}",
  "",
  "// Export pointer maker for registration",
  "// [[Rcpp::export]]",
  "SEXP EMC2_make_custom_kernel_ptr();",
  "EMC2_MAKE_PTR(custom_kernel)"
), tf)

ct <- register_trend(
  trend_parameters = c("q0", "alpha"),
  file = tf,
  transforms = c(q0 = "identity", alpha = "pnorm"),
  base = "lin"
)
```

```
trend_FM=make_trend(par_names='B',
                    cov_names=c('rt'),
                    kernels='custom',
                    par_input=list(c('B', 'B.w')),
                    bases = NULL,          # uses ct$base (here: lin)
                    custom_trend = ct)

ADmat <- matrix(c(-.5,.5), ncol=1, dimnames=list(NULL,'d'))
dat <- EMC2:::add_trials(dat)
design_FM <- design(model=RDM,
                    data=dat,
                    covariates=c('rt'),
                    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, # NB1
                                's'=log(1)),

                    trend=trend_FM)
# NB1: Why q0=3? When fitting a static RDM,
# the mean fit threshold over mean RT ratio is very roughly 3
# in this dataset. It serves as a reasonable place to start
prior_FM <- prior(design_FM, mu_mean=c('B'=2), mu_sd=c('B'=0.5))
emc <- make_emc(dat, design=design_FM, compress=FALSE, prior_list=prior_FM)
emc <- fit(emc, cores_per_chain=3, cores_for_chains=3,
           fileName='samples/ds1_FM.RData')

load('./samples/ds1_FM.RData')
emc <- fix_custom_kernel_pointers(emc, trend_FM)
check(emc)
pp <- predict(emc, n_cores=40, conditional_on_data=FALSE, n_post = 50,
              return_trialwise_parameters=TRUE)

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
plot_spectrum(dat=dat, pp=pp, trial_duration=1.265)
```




```
# mean trial duration of this task was 1.265 s,
# which we use to determine the periods
```

The spectrum shows that fluency can account for the much of the power in fluctuations that are moderate to fast, but not the slowest fluctuations. Note that we supplied the mean trial duration to determine the periods, which are then plotted on the x axis. If this is not supplied the x axis is instead log(frequency).

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