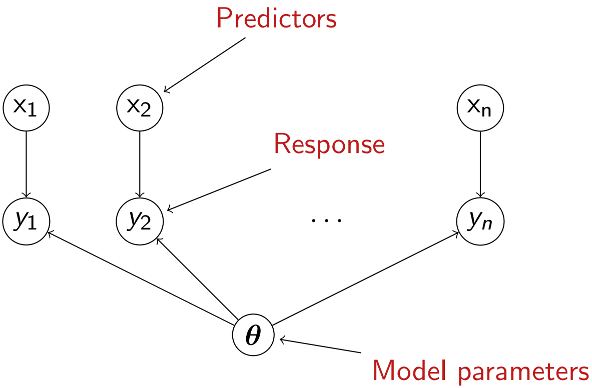
Mixed-effects/hierarchical GLMs

The non-hierarchical GLM picture:



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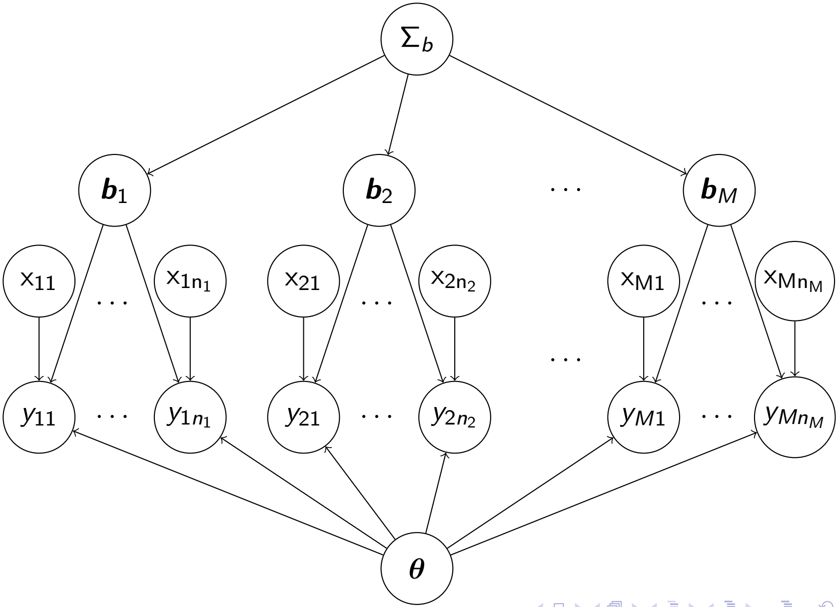

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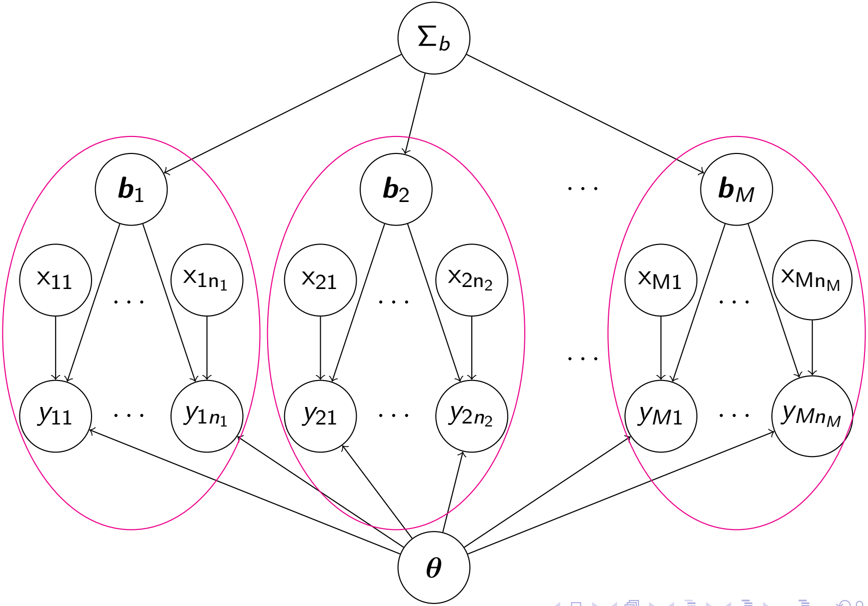

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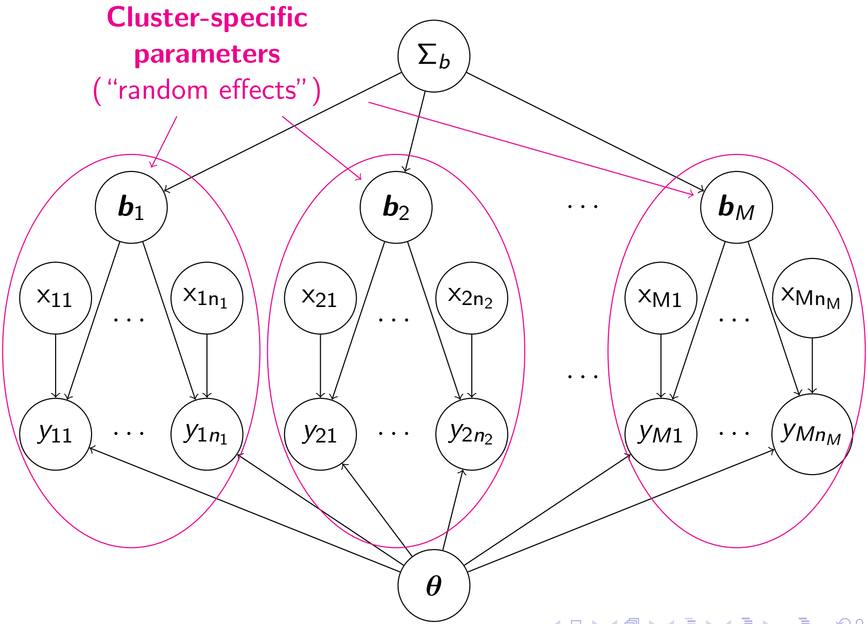

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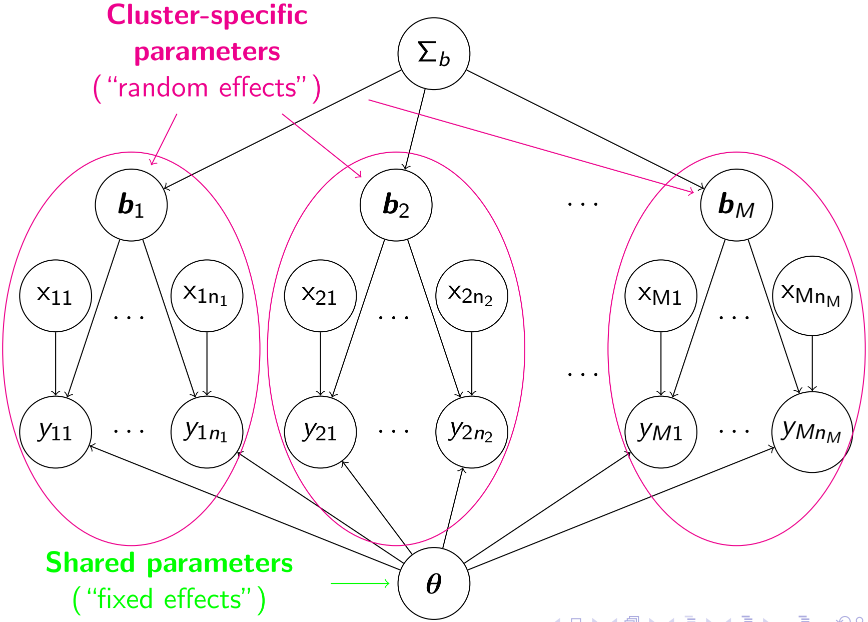

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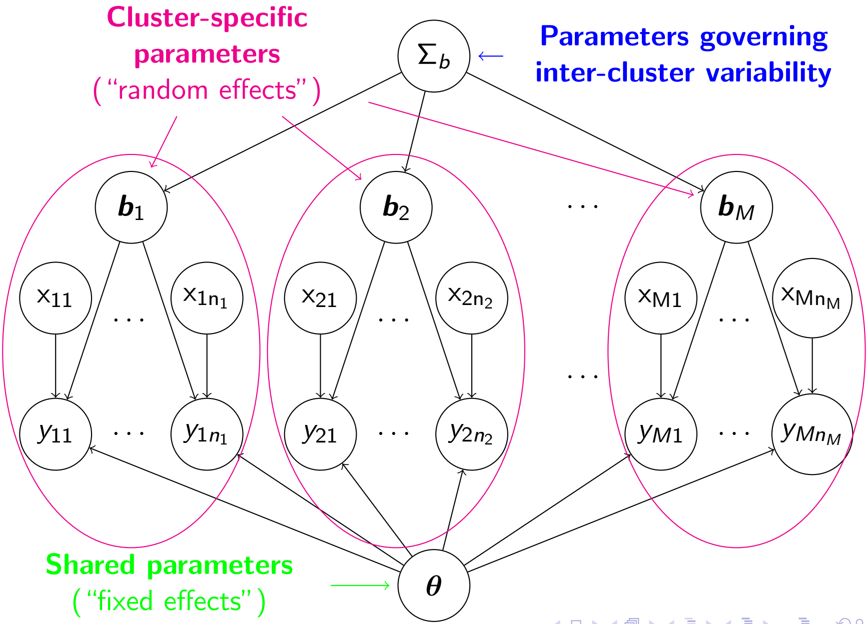

Multi-level Models I

An example of a multi-level model:

- Back to your lexical-decision experiment
  `tpozt` *Word or non-word?*
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- Additionally, different participants in your study may also have:
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- You want to draw inferences about all these things at the same time

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- This is invaluable for achieving deeper understanding of both your analysis and your data

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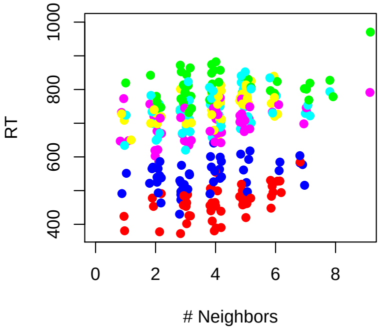
```
## simulate some data
> sigma.b <- 125       # inter-subject variation larger than
> sigma.e <- 40        # intra-subject, inter-trial variation
> alpha <- 500
> beta <- 12
> M <- 6                            # number of participants
> n <- 50                           # trials per participant
> b <- rnorm(M, 0, sigma.b)         # individual differences
> nneighbors <- rpois(M*n,3) + 1    # generate num. neighbors
> subj <- rep(1:M,n)
> RT <- alpha + beta * nneighbors + # simulate RTs!
    b[subj] + rnorm(M*n,0,sigma.e)  #
```

Multi-level Models III: simulating data



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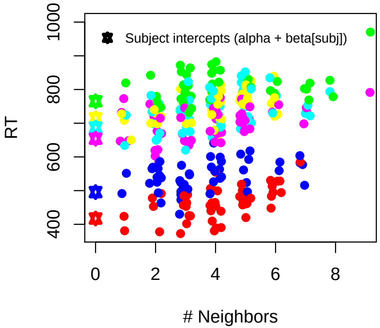

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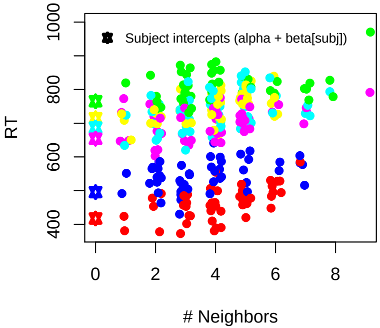

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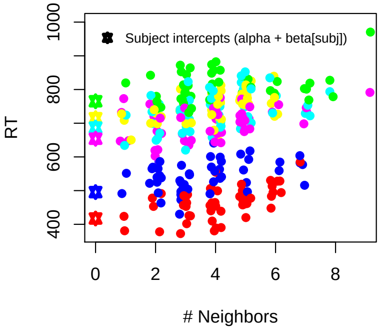

- Participant-level clustering is easily visible
- This reflects the fact that inter-participant variation (125ms) is larger than inter-trial variation (40ms)
- And the effects of neighborhood density are also visible

Statistical inference with multi-level models

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- We *have* data and we need to infer a model
  - Specifically, the "fixed-effect" parameters α, β, and σ_ϵ, plus the parameter governing inter-subject variation, σ_b
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  - e.g., hypothesis tests about effects of neighborhood density: can we reliably infer that β is $\{$non-zero, positive, ...$\}$?
- Fortunately, we can use the same principles as before to do this:
  - The principle of maximum likelihood
  - Or Bayesian inference

Fitting a multi-level model using maximum likelihood

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> print(m,corr=F)
[...]
Random effects:
 Groups      Name        Variance Std.Dev.
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Number of obs: 1760, groups: participant, 44

Fixed effects:
                   Estimate Std. Error t value
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- Inter-participant variability σ_b is what's new:
  - Variability in average RT in the population from which the participants were drawn has standard deviation 70.18ms

Inferences about cluster-level parameters

$$RT_{ij} = \alpha + \beta x_{ij} + \overbrace{b_i}^{\sim N(0,\sigma_b)} + \overbrace{\epsilon_{ij}}^{\text{Noise}\sim N(0,\sigma_\epsilon)}$$

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- The BLUPS are the conditional modes of b_i—the choices that maximize the above probability

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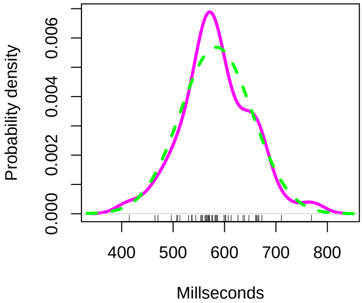
- The BLUP participant-specific “average” RTs for this dataset are black lines on the base of this graph



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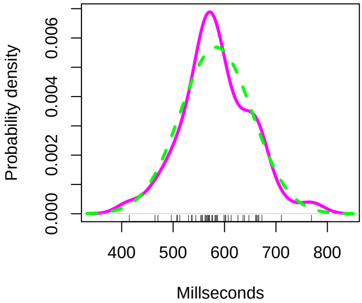

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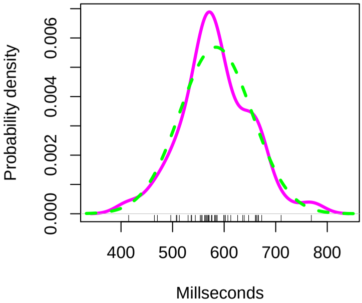

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These three numbers jointly characterize $\widehat{\Sigma}_b$

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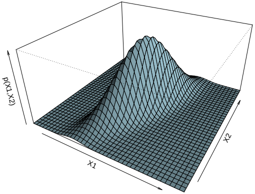
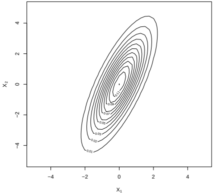
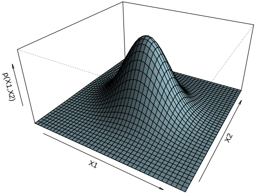
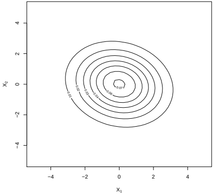
- The results of the `lmer()` fit are saying that the maximum-likelihood estimate of the covariance matrix Σ_b governing participant-specific variability is

$$\widehat{\Sigma_b} = \begin{pmatrix} 70.20 & -0.3097 \\ -0.3097 & 4.41 \end{pmatrix}$$

Inference about cluster-level parameters V

- Visualizing some multivariate normal distributions:

Covariance matrix	Perspective plot	Contour plot
$\Sigma_b = \begin{pmatrix} 1 & 0.75 \\ 0.75 & 4 \end{pmatrix}$		
$\Sigma_b = \begin{pmatrix} 2.5 & -0.13 \\ -0.13 & 2 \end{pmatrix}$		

Inference about cluster-level parameters VI

- In 2D we often visually summarize a multivariate normal distribution with a CHARACTERISTIC ELLIPSE

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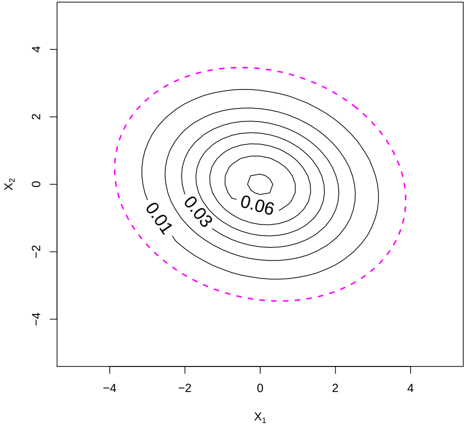

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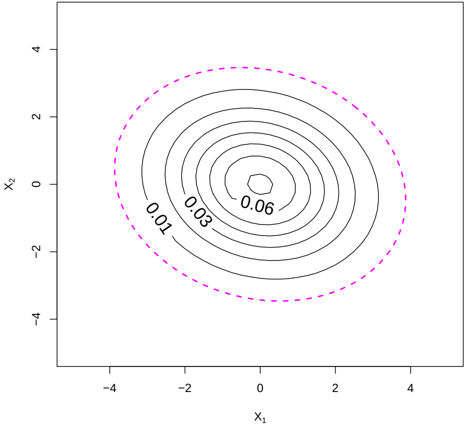
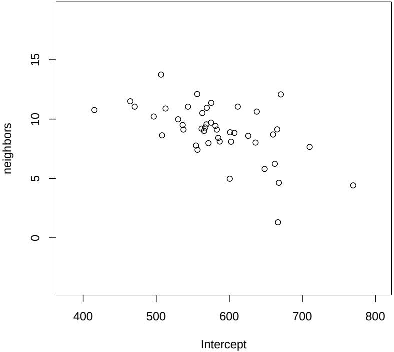


- This ellipse contains a certain proportion (here & conventionally, 95%) of the probability mass for the distribution in question

Inference about cluster-level parameters VII



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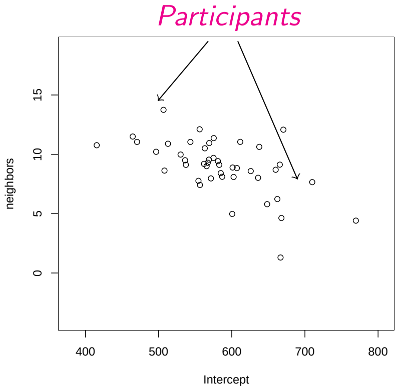

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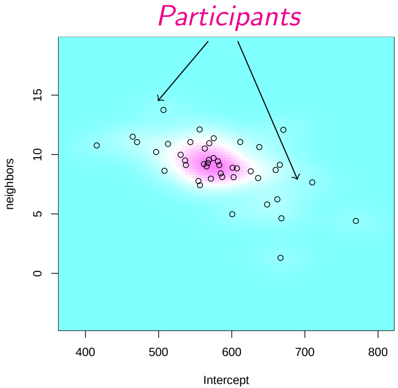

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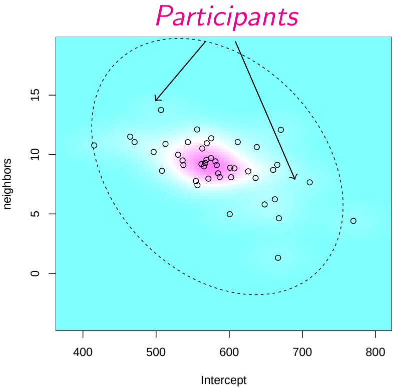

- Correlation visible in participant-specific BLUPs

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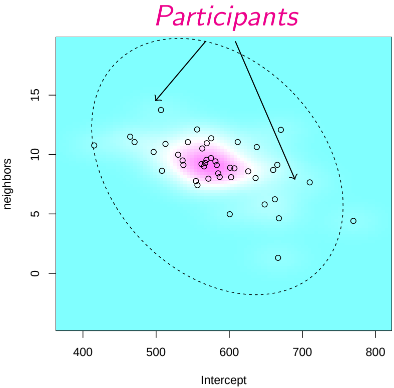

- Correlation visible in participant-specific BLUPs
- Participants who were faster overall also tend to be more affected by neighborhood density

$$\widehat{\Sigma_b} = \begin{pmatrix} 70.20 & -0.3097 \\ -0.3097 & 4.41 \end{pmatrix}$$

Bayesian inference for multilevel models

$$\boxed{P(\{\beta_i\}, \sigma_b, \sigma_\epsilon | Y) = \frac{\overbrace{P(Y|\{\beta_i\}, \sigma_b, \sigma_\epsilon)}^{\text{Likelihood}}\overbrace{P(\{\beta_i\}, \sigma_b, \sigma_\epsilon)}^{\text{Prior}}}{P(Y)}}$$

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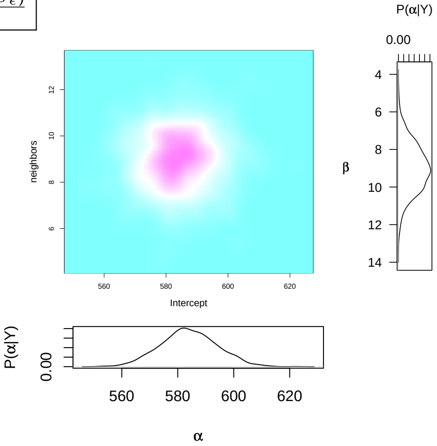

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- There are two situations:
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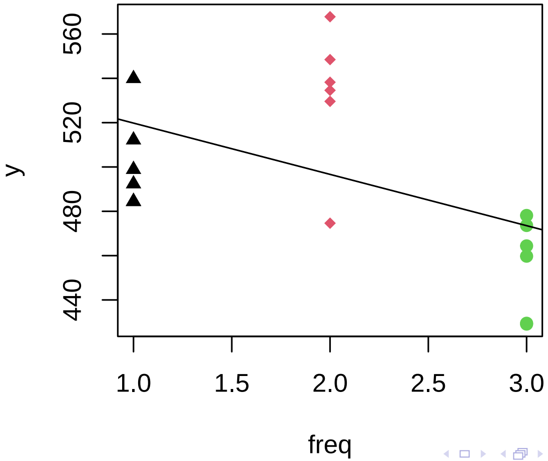
  2. When the value that a fixed effect takes *varies within some or all clusters*

Predictors varying between clusters

Hypothetical relationship observed for three words:



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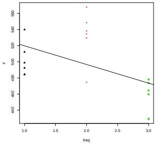

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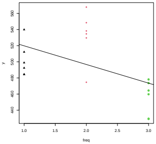

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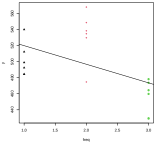

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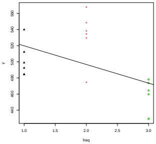

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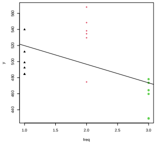

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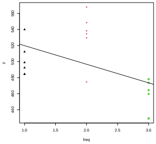

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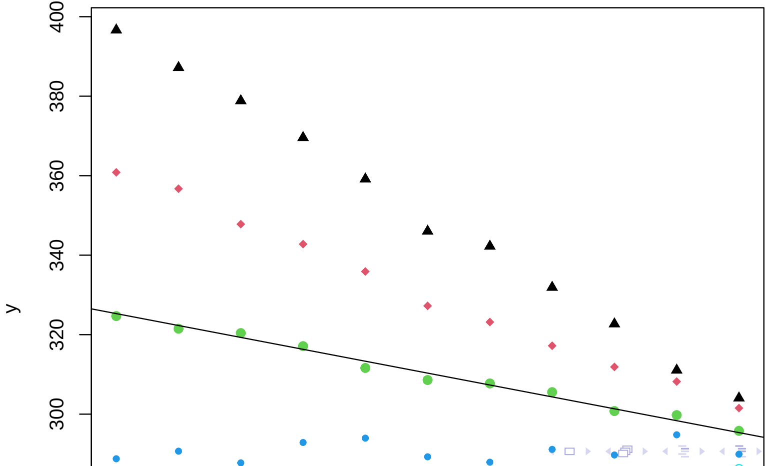
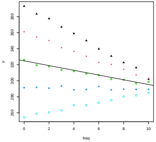
- But the probability that the observed means would have this monotonicity would still be $\frac{1}{6}$
- To address this issue we need a random intercept
- Our model will wind up answering the question of whether there is a systematic trend across words for frequency sensitivity, *above and beyond idiosyncratic variation among*

Predictors varying within clusters

Hypothetical frequency-based responses for five different individual participants:



Predictors varying within clusters I



- It looks like we have good evidence for frequency-sensitivity of the response

Predictors varying within clusters II

- Classic question: *above and beyond idiosyncratic sensitivities of different individuals to context-driven predictability*, are predictable words in general named faster than unpredictable words?
- In mixed-effects models, this implies a need for a random by-speaker slope in our null-hypothesis model
- Inferences about the fixed effect will wind up meaning, *is there a systematic effect of word frequency, above and beyond idiosyncratic speaker-specific sensitivities to word frequency?*

The nonwords experiment

- The **?** experiment had many different participants and many different nonwords

```
response ~ X + (1 | Word) + (1 + X | Participant)
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- Finally, models differing in random effects structure alone can *in principle* be compared with likelihood-ratio tests
  - However, these results can be either conservative or anti-conservative, so take them with a grain of salt

Results for the nonword-recognition experiment

```
##
## Attaching package:  'ellipse'
## The following object is masked from
'package:graphics':
##
##     pairs
## Loading required package:  Matrix
```

```
dat$X <- dat$neighbors
m2 <- lmer(time ~ X + (1 + X | participant) + (1|target), dat,REML=F)

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
control$checkConv, :  Model failed to converge with max|grad| =
0.0021026 (tol = 0.002, component 1)

print(m2,corr=F)

## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: time ~ X + (1 + X | participant) + (1 | target)
##    Data: dat
```

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- **This position has been widely** (though not universally) **accepted by the field, and we continue to advocate for it**

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  - ... *were* generally arrogant and rude.
- The question of theoretical interest for our data is whether the processing penalty induced by disambiguation of the RC attachment would show up immediately (before potentially biasing semantic content of the RC shows up).

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$$\textit{John}\ \overbrace{\textit{babysat/detested}}^{\text{V}}\ \textit{the children of the musician who}\ \overbrace{\textit{was/were}}^{\text{B}}\ \textcolor{red}{\textit{generally}}\ \textit{arrogant and rude}$$

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  $\overbrace{\textit{was/were}}^{\text{B}}$ *generally arrogant and rude*

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- These factors are crossed in the experiment, and both within-subject

A controlled experiment III

- Results of a maximal LME fit:

```
## boundary (singular) fit:  see help('isSingular')
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: rt ~ V * A + (V * A | subj) + (V * A | item)
##    Data: d
##       AIC       BIC    logLik  deviance  df.resid
## 12527.408 12647.990 -6238.704 12477.408       894
## Random effects:
##  Groups   Name        Std.Dev. Corr
##  subj     (Intercept) 129.496
##           V            21.820  -0.82
##           A             4.939  -0.94  0.96
##           V:A         111.507  -0.48  0.90  0.75
##  item     (Intercept)  38.996
##           V            45.339  -0.80
##           A            40.787   0.06 -0.64
##           V:A          74.371   0.04  0.56 -1.00
##  Residual             196.208
## Number of obs: 919, groups:  subj, 55; item, 20
## Fixed Effects:
## (Intercept)            V            A          V:A
##    470.4938     -33.7621      -0.1967     -85.0056
## optimizer (nloptwrap) convergence code: 0 (OK) ; 0 optimizer warnings; 1 lme4 warnings
```

A controlled experiment III

- Likelihood-ratio-based hypothesis testing for a fixed effect:

```
## boundary (singular) fit:  see help('isSingular')
```

```
rt.lmer.null <- lmer(rt ~ V + A + ( V*A | subj)  + ( V*A | item),
  data=d,REML=F)
```

```
print(anova(rt.lmer.full,rt.lmer.null))

## Data: d
## Models:
## rt.lmer.null: rt ~ V + A + (V * A | subj) + (V * A | item)
## rt.lmer.full: rt ~ V * A + (V * A | subj) + (V * A | item)
##              npar   AIC   BIC  logLik deviance  Chisq Df Pr(>Chisq)
## rt.lmer.null   24 12531 12647 -6241.5    12483
## rt.lmer.full   25 12527 12648 -6238.7    12477 5.5137  1    0.01887
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Bayesian fitting of mixed models with brms

```
## Loading 'brms' package (version 2.21.0).  Useful
instructions
## can be found by typing help('brms').  A more
detailed introduction
## to the package is available through
vignette('brms_overview').
##
## Attaching package:  'brms'
## The following object is masked from
'package:lme4':
##
##     ngrps
## The following object is masked from
'package:stats':
##
##     ar
## Compiling Stan program...
```

Bayesian fitting of mixed models with brms

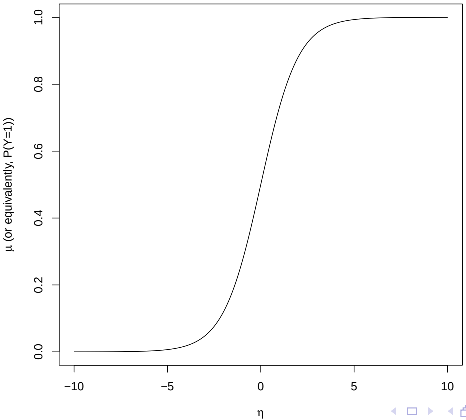
```
summary(rt.brm.full)

##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: rt ~ V * A + (V * A | subj) + (V * A | item)
##    Data: d (Number of observations: 919)
##   Draws: 4 chains, each with iter = 2000; warmup = 1000;
##          total post-warmup draws = 4000
##
## Multilevel Hyperparameters:
## ~item (Number of levels: 20)
##                      Estimate Est.Error l-95% CI u-95% CI
## sd(Intercept)           43.45     11.67    23.25    69.27
## sd(V)                   44.00     22.12     3.94    89.83
## sd(A)                   34.50     21.44     2.15    80.39
## sd(V:A)                 71.18     42.53     3.76   159.64
## cor(Intercept,V)        -0.39      0.34    -0.91     0.39
```

Mixed logit models

Recall the inverse logit function that we used for logistic regression:

$$\mu = \frac{e^{\eta}}{1 + e^{\eta}}$$



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$$P(Y=y|\mu) = \begin{cases} \mu & y=1 \\ 1-\mu & y=0 \\ 0 & \text{otherwise} \end{cases}$$

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- And linear predictor

$$\eta = \mathrm{X}\boldsymbol{\beta} + \mathrm{Zb}$$

  where b is multivariate-normal distributed:

$$\mathrm{b} \sim N(0, \Sigma_{\mathrm{b}})$$

References I

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- Note that so-called "p_{MCMC}" is NOT a p-value in the Neyman-Pearson sense!
- Weakness, both in practice and in principle: the alternative hypothesis is never actually used (except indirectly in determining optimal acceptance and rejection regions)

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- So for me, the p-value of your experiment serves as a rough indicator of how small $P(D|H_0)$ may be
- Technically, such a measure doesn't need to be a true Neyman-Pearson p-value (p_{MCMC} falls into this category)