University of Antwerp
Faculty of Social Sciences

Objective rating method: Entropy

Speech intelligibility estimation

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What are we going to talk about?

1. Preliminars

Research question

Research question

On two fronts:

1. Can comparative judgement (CJ) methods be used to assess speech intelligibility (SI)?,
   To investigate this wee need:
   - an objective measure of SI
2. where CJ stands versus absolute holistic judgement (HJ) methods?,
   In terms of:
   - validity
   - reliability
   - statistical efficiency
   - time efficiency

Objective measure of SI

the most objective (we know of) measure of SI comes from a transcription task:

1. transcribe children's utterances (made by multiple judges),
2. align transcriptions at the utterance level,
3. calculate an entropy measure (H), per utterance per child:

$$H = H(\mathbf{p}) = \frac{-\sum_{i=1}^{n} p_i \cdot \log_2(p_i)}{\log_2(N)}$$

4. characteristics of H [3, 7]
   - bounded in $[0, 1]$ space,
   - utterances with more agreement are more intelligible, and therefore $H \to 0$,
   - utterances with low agreement are less intelligible, and therefore $H \to 1$.

1. Preliminars

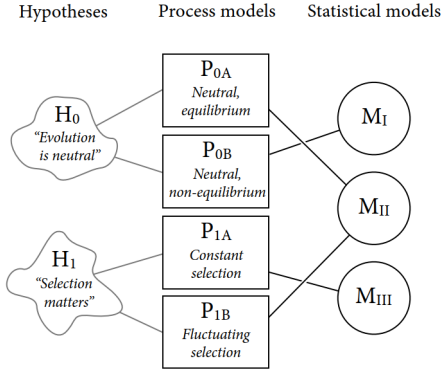
Research hypothesis production

A typical scientific lab

What is needed / deal with[a]

1. Quality of theory
2. Quality of data
3. Reliable procedures and code
4. Quality of data analysis
5. Documentation
6. Reporting

[a] Figure extracted from McElreath [11]



Research hypothesis production[1]

Well known challenges

- Insufficient data
- Wrong population
- Measurement error
- Selection bias
- Confounding

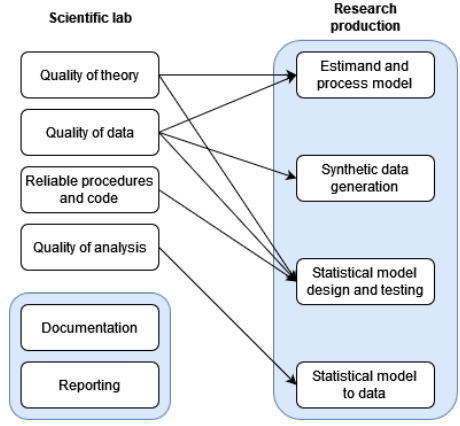
Known challenges in our research;

- Insufficient data (possibly)
- Wrong population
- Measurement error
- Selection bias
- Confounding

[1] Hernán [9], lesson 4

Research hypothesis schematics[2]

a. Estimand and process model
b. Synthetic data generation
c. Statistical model design and testing
d. Apply statistical model to data



[2]McElreath [12], lecture 20, Pearl [13]. Follow Fogarty et al. [8] on item (c).

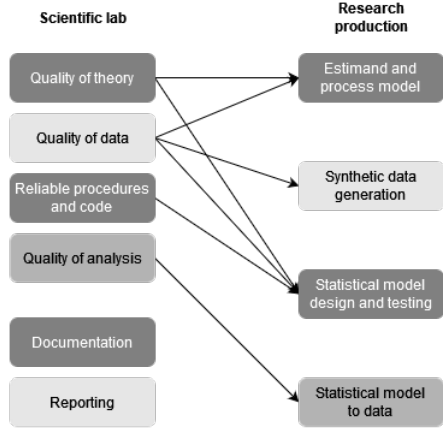
Why do we need to follow this?

Because the improvement of:

- A clear definition of the estimand and process model (assumptions).
- An improved the reliability of your procedures.
- As a documentation procedure.

leads to:

- A sound analysis and results (even when we cannot answer our question).
- An improved planning to get data.

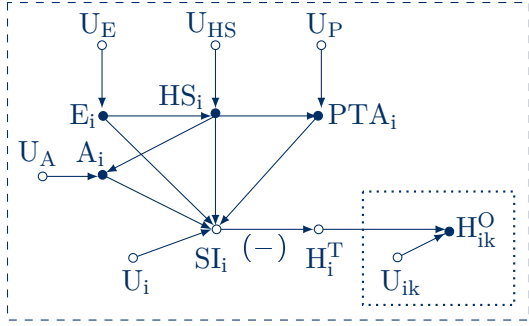


2. Research hypothesis procedure

Estimand and process model

The theory behind our research

- H_{ik} = (observed) entropy replicates
- H_i = (latent) "true" entropy
- SI_i = (latent) SI score
  (inversely related to H_i^T)
- A_i = "hearing" age (minimum)
- E_i = etiology of disease
- HS_i = hearing status
- PTA_i = pure tone average
  (standardized)
- variables assumed independent,
  beyond the described relationships,



General causal diagram

$$P(\mathbf{U}) = P(U_{ik}, U_i, U_A, U_E, U_{HS}, U_P)$$
$$= P(U_{ik})P(U_i)P(U_A)P(U_E)P(U_{HS})P(U_P)$$

Probabilistic (causal) model

First form

$$
\begin{aligned}
\mathrm{H}^{\mathrm{O}}_{\mathrm{ik}} &\leftarrow \mathrm{f}(\mathrm{H}^{\mathrm{T}}_{\mathrm{i}}, \mathrm{U}_{\mathrm{ik}}) \\
\mathrm{H}^{\mathrm{T}}_{\mathrm{i}} &\leftarrow \mathrm{f}(\mathrm{SI}_{\mathrm{i}}) \\
\mathrm{SI}_{\mathrm{i}} &\leftarrow \mathrm{f}(\mathrm{HS}_{\mathrm{i}}, \mathrm{A}_{\mathrm{i}}, \mathrm{E}_{\mathrm{i}}, \mathrm{PTA}_{\mathrm{i}}, \mathrm{U}_{\mathrm{i}}) \\
\\
\\
\mathrm{HS}_{\mathrm{i}} &\leftarrow \mathrm{f}(\mathrm{U}_{\mathrm{HS}}) \\
\mathrm{A}_{\mathrm{i}} &\leftarrow \mathrm{f}(\mathrm{U}_{\mathrm{A}}) \\
\mathrm{E}_{\mathrm{i}} &\leftarrow \mathrm{f}(\mathrm{U}_{\mathrm{E}}) \\
\mathrm{PTA}_{\mathrm{i}} &\leftarrow \mathrm{f}(\mathrm{U}_{\mathrm{P}}) \\
\mathrm{U} &\sim \mathrm{P}(\mathbf{U})
\end{aligned}
$$

(a) general structural model

$$
\begin{aligned}
\mathrm{H}^{\mathrm{O}}_{\mathrm{ik}} &\sim \mathrm{BetaProp}(\mathrm{H}^{\mathrm{T}}_{\mathrm{i}}, \mathrm{M}_{\mathrm{ik}}) \\
\mathrm{H}^{\mathrm{T}}_{\mathrm{i}} &= \mathrm{inv\_logit}(-\mathrm{SI}_{\mathrm{i}}) \\
\mathrm{SI}_{\mathrm{i}} &\sim \mathrm{Normal}(\mu_{\mathrm{SI}}, \sigma_{\mathrm{Ui}}) \\
\mu_{\mathrm{SI}} &= \alpha + \alpha_{\mathrm{HS[i]}} + \alpha_{\mathrm{E[i]}} \\
&\quad + \beta_{\mathrm{A,HS[i]}}(\mathrm{A}_{\mathrm{i}} - \bar{\mathrm{A}}) + \beta_{\mathrm{P}}\mathrm{PTA}_{\mathrm{i}} \\
\mathrm{HS}_{\mathrm{i}} &\sim \mathrm{data} \\
\mathrm{A}_{\mathrm{i}} &\sim \mathrm{data} \\
\mathrm{E}_{\mathrm{i}} &\sim \mathrm{data} \\
\mathrm{PTA}_{\mathrm{i}} &\sim \mathrm{data} \\
\mathrm{U} &\sim \mathrm{unobservable}
\end{aligned}
$$

(a) general probabilistic model

Probabilistic (causal) model

First form

Notice,

- α, $\alpha_{\text{HS[i]}}$, $\alpha_{\text{E[i]}}$, $\beta_{\text{A,HS[i]}}$, β_{P} are structural parameters (as in SEM)
- U_{ik} = replicates measurement error U_{i} = between child SI variability
- variability of U_{ik} is modeled by M_{ik} variability of U_{i} is modeled by σ_{Ui}

$$
\begin{aligned}
\text{H}^{\text{O}}_{\text{ik}} &\sim \text{BetaProp}(\text{H}^{\text{T}}_{\text{i}}, \text{M}_{\text{ik}}) \\
\text{H}^{\text{T}}_{\text{i}} &= \text{inv\_logit}(-\text{SI}_{\text{i}}) \\
\text{SI}_{\text{i}} &\sim \text{Normal}(\mu_{\text{SI}}, \sigma_{\text{Ui}}) \\
\mu_{\text{SI}} &= \alpha + \alpha_{\text{HS[i]}} + \alpha_{\text{E[i]}} \\
&\quad + \beta_{\text{A,HS[i]}}(\text{A}_{\text{i}} - \bar{\text{A}}) + \beta_{\text{P}}\text{PTA}_{\text{i}} \\
\text{HS}_{\text{i}} &\sim \text{data} \\
\text{A}_{\text{i}} &\sim \text{data} \\
\text{E}_{\text{i}} &\sim \text{data} \\
\text{PTA}_{\text{i}} &\sim \text{data} \\
\text{U} &\sim \text{unobservable}
\end{aligned}
$$

(a) general probabilistic model

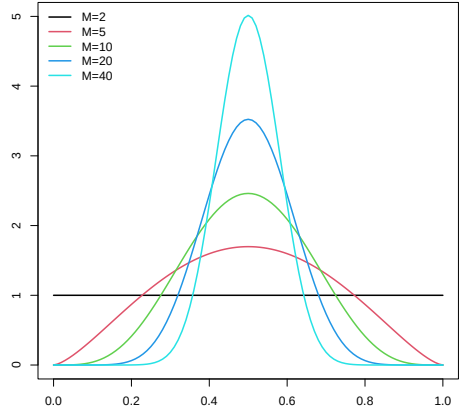
Probabilistic (causal) model

Express variability in BetaProp

$$
\begin{aligned}
H^{O}_{ik} &\sim \text{BetaProp}(H^{T}_{i}, M_{ik}) \\
H^{T}_{i} &= \alpha/(\alpha+\beta) \\
M_{ik} &= \alpha+\beta
\end{aligned}
$$

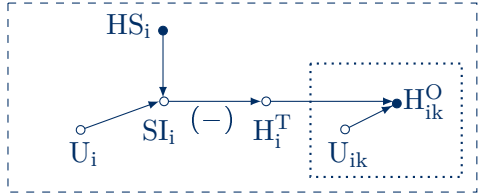
$$
\begin{aligned}
\alpha &= H^{T}_{i} \cdot M_{ik} \\
\beta &= (1-H^{T}_{i}) \cdot M_{ik}
\end{aligned}
$$

$$
\begin{aligned}
\alpha &= 0.5 \cdot 2 \\
\beta &= (1-0.5) \cdot 2
\end{aligned}
$$

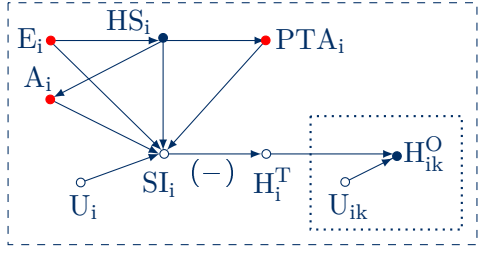


Interested in two effects

1. total effects model inherits:
   - children's characteristics that lead to the fitting of specific apparatus,
   - the (convenience of) sample selection (fixed with post-stratification)
2. to do the last, we stratify for all variables that explain variability, ergo, use a direct effects model
3. two levels: replicates (k), children (i), denoted by discontinuous squares



(b) total effects



(a) direct effects

Probabilistic (causal) model

Second form

$$
\begin{aligned}
\mathrm{H}^{\mathrm{O}}_{\mathrm{ik}} &\leftarrow \mathrm{f}(\mathrm{H}^{\mathrm{T}}_{\mathrm{i}}, \mathrm{U}_{\mathrm{ik}}) \\
\mathrm{H}^{\mathrm{T}}_{\mathrm{i}} &\leftarrow \mathrm{f}(\mathrm{SI}_{\mathrm{i}}) \\
\mathrm{SI}_{\mathrm{i}} &\leftarrow \mathrm{f}(\mathrm{HS}_{\mathrm{i}}, \mathrm{A}_{\mathrm{i}}, \mathrm{E}_{\mathrm{i}}, \mathrm{PTA}_{\mathrm{i}}, \mathrm{U}_{\mathrm{i}}) \\
\\
\mathrm{HS}_{\mathrm{i}} &\leftarrow \mathrm{f}(\mathrm{U}_{\mathrm{HS}}) \\
\mathrm{A}_{\mathrm{i}} &\leftarrow \mathrm{f}(\mathrm{U}_{\mathrm{A}}) \\
\mathrm{E}_{\mathrm{i}} &\leftarrow \mathrm{f}(\mathrm{U}_{\mathrm{E}}) \\
\mathrm{PTA}_{\mathrm{i}} &\leftarrow \mathrm{f}(\mathrm{U}_{\mathrm{P}}) \\
\mathrm{U} &\sim \mathrm{P}(\mathbf{U})
\end{aligned}
$$

(a) general structural model

$$
\begin{aligned}
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\mathrm{H}^{\mathrm{T}}_{\mathrm{i}} &= \mathrm{inv\_logit}(-\mathrm{SI}_{\mathrm{i}}) \\
\mathrm{SI}_{\mathrm{i}} &= \mathrm{a}_{\mathrm{i}} + \alpha + \alpha_{\mathrm{HS[i]}} + \alpha_{\mathrm{E[i]}} \\
&\quad + \beta_{\mathrm{A,HS[i]}}(\mathrm{A}_{\mathrm{i}} - \bar{\mathrm{A}}) + \beta_{\mathrm{P}}\mathrm{PTA}_{\mathrm{i}} \\
\mathrm{a}_{\mathrm{i}} &\sim \mathrm{Normal}(0, \sigma_{\mathrm{Ui}}) \\
\mathrm{HS}_{\mathrm{i}} &\sim \mathrm{data} \\
\mathrm{A}_{\mathrm{i}} &\sim \mathrm{data} \\
\mathrm{E}_{\mathrm{i}} &\sim \mathrm{data} \\
\mathrm{PTA}_{\mathrm{i}} &\sim \mathrm{data} \\
\mathrm{U} &\sim \mathrm{unobservable}
\end{aligned}
$$

(a) general probabilistic model

2. Research hypothesis procedure

Synthetic data generation

Idealized data[3]

Simulation data can serve as [10, 11],

1. A place where to test your model, on multiple purposes,
   - parameter recovery
   - power
2. A reflection of a population,
   - De Raeve [6]: 70 HI/CI, 130 HI/HA
   - Our idealized data: 150 NH, 70 HI/CI, 130 HI/HA
3. A reflection of a hypothesis,
   - size of effects

```
(sim_name=NULL, # file_name ne
sim_save=NULL, # file_save ne
seed=NULL, # seed
I=350, # experimental units (
K=10, # replicates (utterance
p=c(0.50, 0.175, 0.325), # ch
par=list( m_i=0, s_i=0.5, # h
          m_M=10, s_M=NULL, #
          a=0,
          aE=rep(0,4),
          aHS=c(0.4,0,-0.4),
          bP=-0.1,
          bA=0.15,
          bAHS=rep(0,3) ) ){
```

[3] more details in file: 1_2_E_sim_fun.R

Idealized data

About the size of the effects
(in logits, no previous info)

1. aE $= 0$, ordered by severity
   ($\text{cor}(\text{E}, \text{HS}) \approx 1$, ordering might not be possible) ,
2. aHS $= -0.4$, difference between NH children and HI/CI,
3. bP $= -0.1$, per PTA unit
   ($+10$ PTA units $\Rightarrow -1$ logit),
4. bA $= -0.15$, per A unit, above the minimum
   ($+10$ A units $\Rightarrow +1.5$ logits),

```
(sim_name=NULL, # file_name ne
sim_save=NULL, # file_save ne
seed=NULL, # seed
I=350, # experimental units (
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p=c(0.50, 0.175, 0.325), # ch
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          aHS=c(0.4,0,-0.4),
          bP=-0.1,
          bA=0.15,
          bAHS=rep(0,3) ) ){
```

Idealized data

1. variables are generated in a random fashion
2. between children SI variability are defined by the random effects

```r
# 1. true data ####
dT = data.frame(matrix(NA, nrow=I, ncol=1))
names(dT) = c('child_id')
dT$child_id = 1:I


# assigning children to groups
n = round( p*I )
if( sum(n) != I ){
  if( I - sum(n[c(1,3)]) > n[2] ){
    n[2] = I - sum(n[c(1,3)]) # to sum the right amount
  } else {
    n[3] = I - sum(n[c(1,3)]) # to sum the right amount
  }
}


# generating covariates
if(!is.null(seed)){
  set.seed(seed+1)
}
dT$HS = c( rep(1, n[1]), rep(2, n[2]), rep(3, n[3]))
dT$A = round( rnorm( sum(n), 5, 1) )
dT$A = with(dT, ifelse(A>7, 7, A) )

dT$E = c( rep(1, n[1]), # no way to know true effects
          sample(2:3, size=n[2], replace=T),
          sample(3:4, size=n[3], replace=T))

dT$PTA = c( round(rnorm(n[1], 60, 15)), # first 12 NH
            round(rnorm(n[2], 90, 15)), # next 10
            round(rnorm(n[3], 110, 15))) # last 10


# children's random effects
if(!is.null(seed)){
  set.seed(seed-1)
}
par$re_i = rnorm(I, par$m_i, par$s_i)
dT$re_i = par$re_i # children's random effects (between SI v
```

Idealized data

1. we use second form of the probabilistic model
2. “true’ entropy (Ht) is inversely related to SI
3. we simulate measurement error through M from BetaProp() distribution.

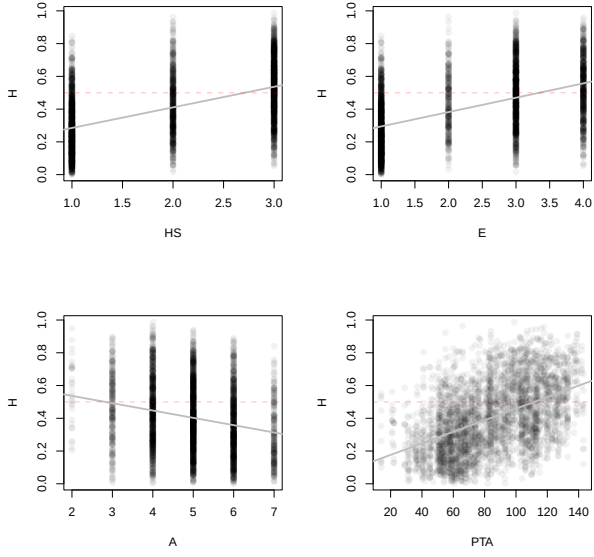
```
# linear predictor / SI index
dT$SI = with(dT, re_i + par$a + par$aE[E] + par$aHS[HS] +
               par$bA*(A - min(A)) +
               par$bAHS[HS]*(A - min(A)) +
               par$bP*c( standardize(PTA) ) )

# true entropy
dT$Ht = inv_logit(-dT$SI) # true entropy (SI -> Ht: negativ


# variability of H
if(!is.null(seed)){
  set.seed(seed+2)
}
if( is.numeric(par$m_M) & !is.numeric(par$s_M) ){
  par$M = rep(par$m_M, I)
} else{
  par$M = round( rlnorm(I, meanlog=par$m_M, sdlog= par$s_M)
}
dT$M = par$M # same df for all children (not same shape!!)


# rounding
dT[,6:ncol(dT)] = round( dT[,6:ncol(dT)], 5)



# 2. observed data ####
N = I*K
dO = data.frame(matrix(NA, nrow=N, ncol=3))
names(dO) = c('child_id','utt_id','H')
dO$child_id = rep(1:I, each=K)
dO$utt_id = rep(1:K, I)

# generating observed H
# i=1
if(!is.null(seed)){
  set.seed(seed-2)
}
```

Idealized data

1. we simulate replicate measures of entropy (H)
2. we storage all relevant parameters and data

```
for(i in 1:I){

  # identify data
  idx = dO$child_id == i

  # linear predictor
  dO$H[idx] = rbeta2(n=K, prob=dT$Ht[i], theta=dT$M[i])
}

# round
dO$H = round( dO$H, 5)


# 3. list data ####
dL = list(
  # dimensions
  N = nrow(dO), # observations
  I = max(dO$child_id), # children
  K = max(dO$utt_id), # utterances

  # category numbers
  cHS = max(dT$HS),
  cE = max(dT$E),

  # child's data
  HS = dT$HS,
  Am = with(dT, A-min(A) ), # centered at minimum
  E = dT$E,
  sPTA = c( standardize( dT$PTA ) ),

  # observed data
  H = with(dO, ifelse(H==0, 0.0001, ifelse(H==1, 0.9999, H)) ),
  cid = dO$child_id,
  uid = dO$utt_id
)


# 4. save data ####
mom = list(dS=list( dT=dT, dO=dO, par=par), dL=dL)
```

Example


H
0.0
0.2
0.4
0.6
0.8
1.0
1.0
1.5
2.0
2.5
3.0
HS
H
0.0
0.2
0.4
0.6
0.8
1.0
1.0
1.5
2.0
2.5
3.0
3.5
4.0
E
H
0.0
0.2
0.4
0.6
0.8
1.0
2
3
4
5
6
7
A
H
0.0
0.2
0.4
0.6
0.8
1.0
20
40
60
80
100
120
140
PTA

2. Research hypothesis procedure

Statistical model design and testing

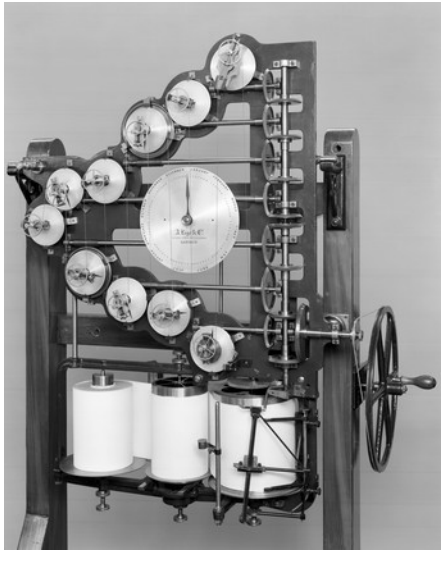
Model design and test[4]

Purpose:

- to have reliable procedures,
- to maintain a clear documentation,
- to have a sound analysis

Procedure:

- step by step, instantiating one difficulty at the time
- use probabilistic assumptions defined in estimand and process model
- is like running synthetic data generation backwards

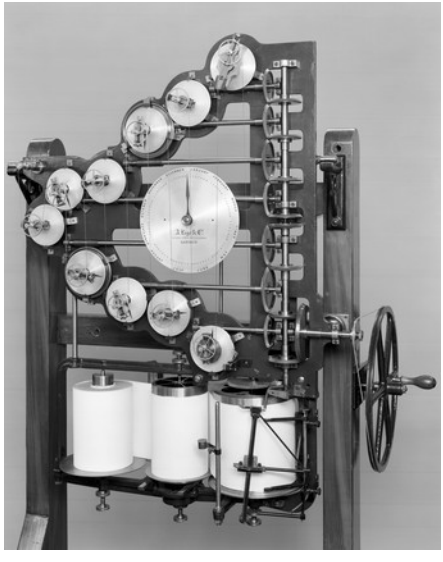


[4] Following Fogarty et al. [8]

Model design and test

We evaluate,

- the probabilistic model implementation [11, 2] (centered and non-centered versions)
- prior predictive
- "health" of MCMC chains
- parameter recovery
- posterior predictive
- power



Probabilistic model

starts with,

- the simplest model
- the simplest data generating procedure

```
transformed parameters{
    vector[I] SI;          // SI index (per child)
    vector[I] Ht;          // true entropy (per chi

    SI = a + re_i;         // linear predictor
    Ht = inv_logit(-SI);   // average entropy (SI -
}
model{

    // hyperpriors
    m_i ~ normal( 0 , 0.2 );
    s_i ~ exponential( 1 );

    // priors
    a ~ normal( 0 , 0.2 );
    re_i ~ normal( m_i , s_i );

    // likelihood
    for(n in 1:N){
      H[n] ~ beta_proportion( Ht[cid[n]] , 10 );
    }
}
```

Probabilistic model

try,

- the centered and non-centered parametrization

```
transformed parameters{
    vector[I] re_i;       // random intercepts (per
    vector[I] SI;         // SI index
    vector[I] Ht;         // true entropy (per child

    re_i = m_i + s_i*z_re;// non-centered RE
    SI = a + re_i;        // linear predictor
    Ht = inv_logit(-SI);  // average entropy (SI ->
}
model{

    // hyperpriors
    m_i ~ normal( 0 , 0.2 );
    s_i ~ exponential( 1 );

    // priors
    a ~ normal( 0 , 0.2 );
    z_re ~ std_normal();

    // likelihood
    for(n in 1:N){
      H[n] ~ beta_proportion( Ht[cid[n]] , 10 );
    }
}
```

Probabilistic model

escalate,

- complexity of model
- traits of the data

```
transformed parameters{
    vector[I] SI;          // SI index (per child)
    vector[I] Ht;          // true entropy (per chil

    // linear predictor
    for(i in 1:I){
      SI[i] = re_i[i] + a + aHS[HS[i]] +
        bA*Am[i] + bP*sPTA[i];
      // no multicollinearity between E and HS
    }

    // average entropy (SI -> Ht: negative)
    Ht = inv_logit(-SI);  // average entropy (SI ->
}
model{

    // hyperpriors
    m_i ~ normal( 0 , 0.2 );
    s_i ~ exponential( 1 );

    // priors
    a ~ normal( 0 , 0.2 );
    re_i ~ normal( m_i , s_i );
    //aE ~ normal( 0 , 0.5 );
    aHS ~ normal( 0 , 0.5 );
    bP ~ normal( 0 , 0.3 );
    bA ~ normal( 0 , 0.3 );
    m_M ~ lognormal( 1.5 , 0.5 );

    // likelihood
    for(n in 1:N){
      H[n] ~ beta_proportion( Ht[cid[n]] , m_M );
    }
}
```

Probabilistic model

We tested 5 random effects models:
(from 5 synthetic data types)
(centered, and non-centered)

- only intercept, M = 10,
- causal model, M = 10,
- causal model, M per individual,
- no known process,
- causal model with interaction, M per individual,

```
transformed parameters{
    vector[I] SI;          // SI index (per child)
    vector[I] Ht;          // true entropy (per child)

    // linear predictor
    for(i in 1:I){
      SI[i] = re_i[i] + a + aHS[HS[i]] +
        bA*Am[i] + bP*sPTA[i];
      // no multicollinearity between E and HS
    }

    // average entropy (SI -> Ht: negative)
    Ht = inv_logit(-SI);  // average entropy (SI -> H
}
model{

    // hyperpriors
    m_i ~ normal( 0 , 0.2 );
    s_i ~ exponential( 1 );

    // priors
    a ~ normal( 0 , 0.2 );
    re_i ~ normal( m_i , s_i );
    //aE ~ normal( 0 , 0.5 );
    aHS ~ normal( 0 , 0.5 );
    bP ~ normal( 0 , 0.3 );
    bA ~ normal( 0 , 0.3 );
    m_M ~ lognormal( 1.5 , 0.5 );

    // likelihood
    for(n in 1:N){
      H[n] ~ beta_proportion( Ht[cid[n]] , m_M );
    }
}
```

Prior predictive

Priors and hyper-priors

- In the probabilistic (causal) model there were no priors for our parameters,
- To decide our priors we follow McElreath [11]: "priors are part of the assumptions, and should be inspected as such",
- We will evaluate the implications of our priors on the outcome scale. We have three outcomes scales: SI_i, H_i^T, and H_{ik}^O

Priors

$$
\begin{aligned}
a_i &\sim \text{Normal}(\mu_a, \sigma_a) \\
M_i &\sim \text{LogNormal}(\mu_M, \sigma_M) \\
\alpha &\sim \text{Normal}(0, 0.2) \\
\alpha_{HS[i]} &\sim \text{Normal}(0, 0.3) \\
\alpha_{E[i]} &\sim \text{Normal}(0, 0.3) \\
\beta_{A,HS[i]} &\sim \text{Normal}(0, 0.3) \\
\beta_P &\sim \text{Normal}(0, 0.3)
\end{aligned}
$$

Hyper-priors

$$
\begin{aligned}
\mu_a &\sim \text{Normal}(0, 0.2) \\
\sigma_a &\sim \text{Exp}(1) \\
\mu_M &\sim \text{Normal}(0, 0.5) \\
\sigma_M &\sim \text{Exp}(1)
\end{aligned}
$$

Prior predictive

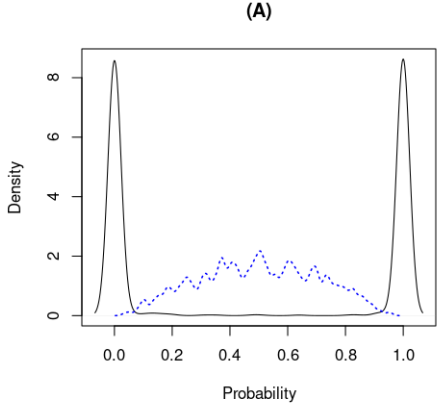
Undesired assumptions can easily creep in non-linear models[a]
Example:

(black line)

$$\theta \sim \mathrm{N}(0, 100)$$
$$\mathrm{logit}(\mathrm{p}) = \theta$$

(blue line)

$$\theta \sim \mathrm{N}(0, 1)$$
$$\mathrm{logit}(\mathrm{p}) = \theta$$



[a] Figure extracted from Rivera [14].

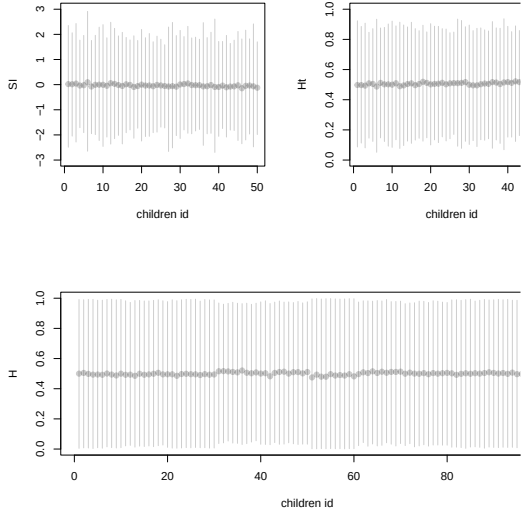
Prior predictive

What our priors imply?

NO undesired assumption has crept in:

- the SI_i scale,
- the H_i^T scale,
- the H_{ik}^O scale

i.e. the scales' full space can be reached by (a combination of) the parameters



“Health” of MCMC chains

The MCMC chains achieve,

- good convergence
- good mixing
- lack of autocorrelation

same results on the n_eff and RHat statistics.

“Health” of MCMC chains

The MCMC chains achieve,

- good convergence
- good mixing
- lack of autocorrelation

same results on the n_eff and RHat statistics.

chains2.pdf

“Health” of MCMC chains

The non-centered parametrization has,

- better n_eff
  (denoting lack of autocorrelation)
- better Rhat
  (denoting good convergence)
- better mixing
  (inspected visually, not shown)

chain_stat.pdf

Parameter recovery

On idealized data

The model,

- recovers the parameters in the right scale,
- most of the “true” parameters are inside of the compatibility intervals (CI)
- contrast are approximately correct

Posterior predictive

But how well reproduces the data?,

The model with less working assumptions[a],

- captures the variability of the replicates,
- provides a “true” H and SI

More complex models,

- captures even better the data, but might overfit,
- avoid overfit when the model is fit to the data (ITA [1, 4])

[a] random effects causal model, with M = 10

Power

Equivalent prior sampling method [18, 10]

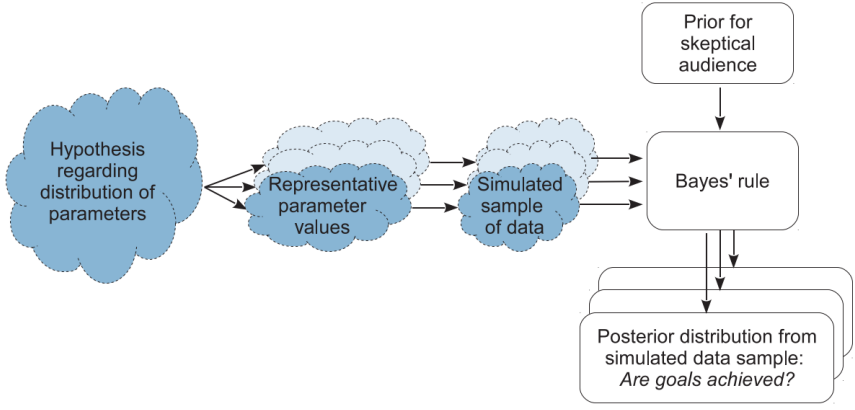
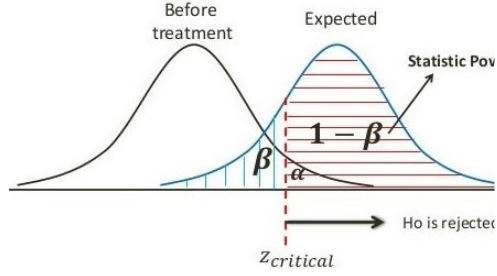


Figure: Flow of information in a power analysis, in which simulated data come from random hypothetical parameters. Extracted from Kruschke [10].

Power

Equivalent prior sampling method

1. generate idealized data
2. generate parameters' distribution (with Bayes theorem)
3. simulate data sample (variability in data and parameters)
4. apply models to simulated data (include priors)
5. evaluate desire goals
   - reject the null hypothesis
   - affirm predicted value
   - achieve precision in estimate
6. repeat procedure (to approximate power)



Power

Equivalent prior sampling method

1. ~~generate idealized data~~
2. ~~generate parameters' distribution~~ (with Bayes theorem)
3. simulate data sample (variability in data and parameters)
4. apply models to simulated data (include priors)
5. evaluate desire goals
   - reject the null hypothesis
   - affirm predicted value
   - achieve precision in estimate
6. repeat procedure (to approximate power)

```
Epower( power_save=file.path(getwd(), 'sim_chain'), # po
        sim_name='Hbeta_sim2_power.RData', # file_save n
        sim_save=file.path(getwd(), 'sim_data'), # file_
        model_name='Hbeta_NC_sim2', # model for which we
        model_in=file.path(getwd(), 'sim_models'), # loc
        model_out=file.path(getwd(), 'sim_chain'), # loc
        Nsim=100, # number of simulation for power
        I_grid = c(48, 60), # experimental units (childr
        K_grid = c(10, 20), # replicates (utterances)
        p=C(0.34, 0.33, 0.33), # children prop. on each
        par_int=c('aHS','bP','bA','m_i','s_i','m_M','SI'
        par_cont=c('aHS','SI') ) # parameters to contras
```

Power

Equivalent prior sampling method

1. ~~generate idealized data~~
2. ~~generate parameters' distribution~~ (with Bayes theorem)
3. ~~simulate data sample~~ (variability in data and parameters)
4. ~~apply models to simulated data~~ (include priors)
5. evaluate desire goals[a]
   - reject the null hypothesis
   - affirm predicted value
   - achieve precision in estimate
6. repeat procedure (to approximate power)

```
(true_par,
cuts=c(0,0.1,0.2,0.5,0.8,1.2,2), # based
rvalues=c(0.2,0.2,0.15,0.3,0.3,0.4,0.8))
```

Effect size	*d*
Very small	0.01
Small	0.20
Medium	0.50
Large	0.80
Very large	1.20
Huge	2.0

[a] region of practical equivalence (ROPE) [10], effect sizes [5, 15]

Power results

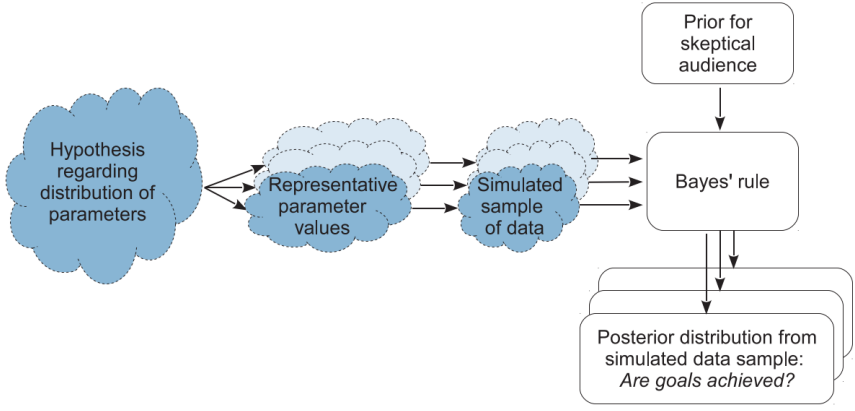


Figure: Flow of information in a power analysis, in which simulated data come from random hypothetical parameters. Extracted from Kruschke [10].

2. Research hypothesis procedure

Apply statistical model to data

What we have so far

1. measure:
   replicated entropies H^{O}_{ik}
2. estimand:
   SI index, SEM parameters, contrasts
3. structural models:
   total and direct effects
4. probabilistic models:
   three possible fitting models
5. statistical models:
   works as intended
6. power:
   enough
7. model to data:
   to select the most fitting model

Point 7 uses
Information Theoretic Approach [1, 4]

1. ~~hypothesis into statistical models~~,
2. select among competing models,
3. make inferences based on one or multiple models.

We select models according to information criteria,

1. WAIC [17]
2. PSIS [16]

Competing models

```
(true_par,
cuts=c(0,0.1,0.2,0.5,0.8,1.2,2), # based
rvalues=c(0.2,0.2,0.15,0.3,0.3,0.4,0.8))
```

Effect size	*d*
Very small	0.01
Small	0.20
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3. References

3. References

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