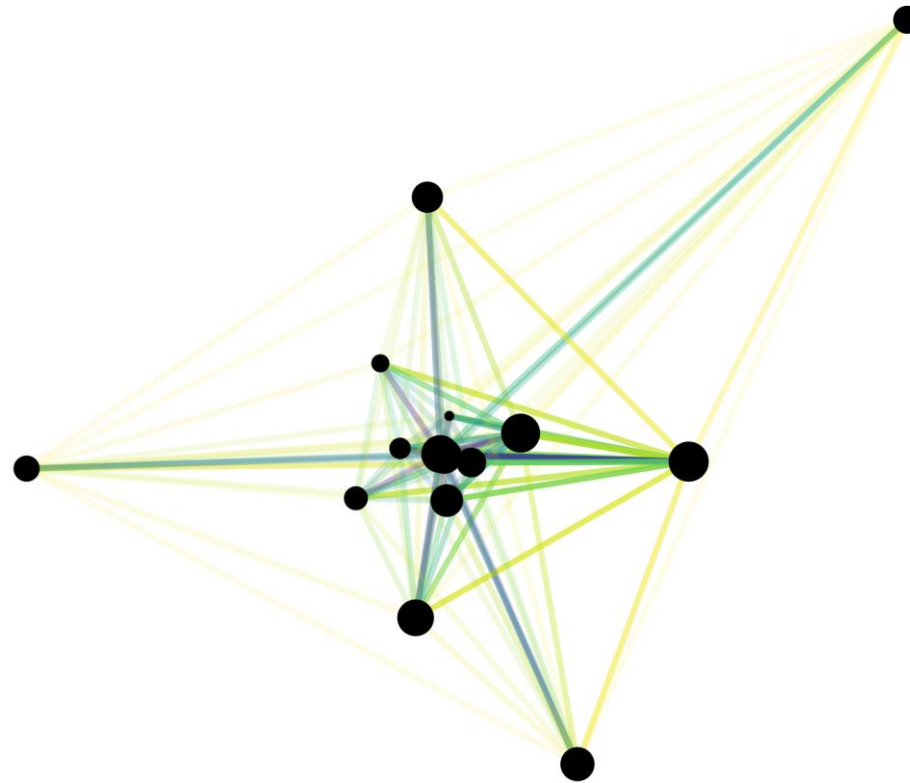


Introduction to STAN for dyadic edge regression models

Winter Workshop on complex systems 2025



We do

1. Highlight the potential of STAN
2. Introducing the basics of STAN
3. Mixture models and varying effects

Networks are often assumed as given, but should be considered as random realizations of underlying data generating processes (domain specific knowledge)

Propagate uncertainty from edges to network metrics

We do

1. Highlight the potential of STAN
2. Introducing the basics of STAN
3. Mixture models and varying effects

Networks are often assumed as given, but should be considered as random realizations of underlying data generating processes (domain specific knowledge)

Propagate uncertainty from edges to network metrics

We don't

Revise Bayesian statistics

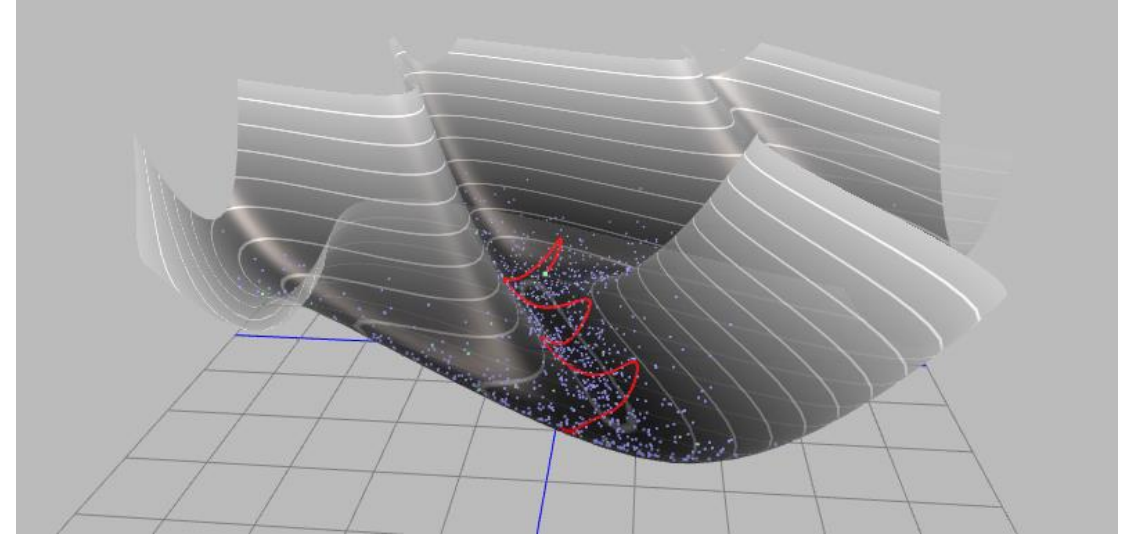
Bayesian workflow:

1. Prior and posterior predictive simulations
2. MCMC convergence diagnostics
3. Hypothesis testing

What is STAN?

Probabilistic programming language

Allows to fit a *wide* variety of statistical models through MCMC (Hamiltonian Monte Carlo NUTS)



Download STAN:

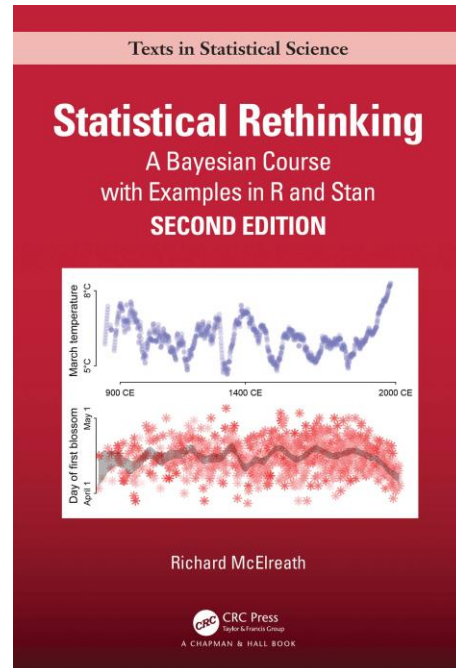
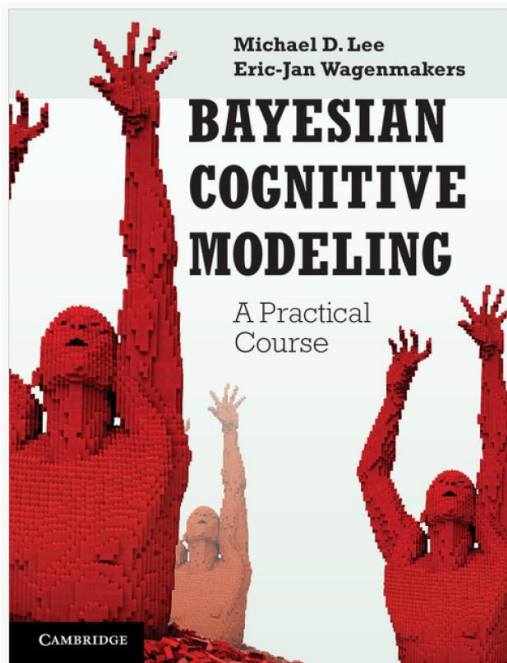
<https://mc-stan.org/install/>

Learn STAN:

<https://mc-stan.org/learn-stan/tutorials.html>

<https://mc-stan.org/learn-stan/case-studies.html>

<https://www.youtube.com/@rmcelreath>

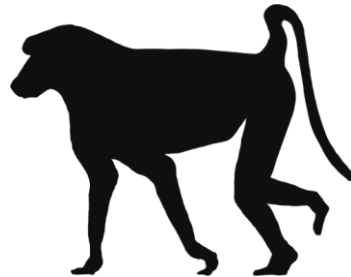


Research problem

Data:

Troop of 15 baboons with dominance rank.

For 20 days, we know the number of hours two individuals are doing the same behaviour



Research problem

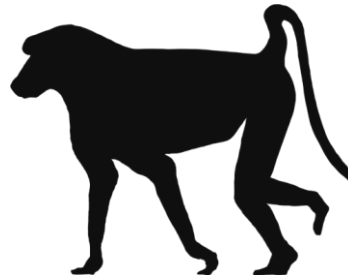
Data:

Troop of 15 baboons with dominance rank.

For 20 days, we know the number of hours two individuals are doing the same behaviour

Research questions:

1. What is the effect of dominance on pairwise synchrony, i.e., the probability a pair is performing the same behaviour?
2. What is the individual centrality in synchrony network?



Research problem

Data:

Troop of 15 baboons with dominance rank.

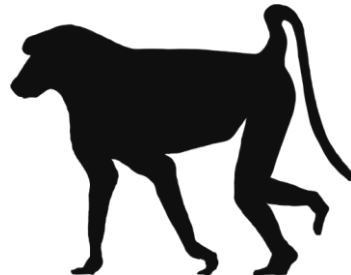
For 20 days, we know the number of hours two individuals are doing the same behaviour.

Research questions:

1. What is the effect of dominance on pairwise synchrony, i.e., the probability a pair is performing the same behaviour?
2. What is the individual centrality in synchrony network?

Complications:

Different number of observations for every pair. Sometimes troop splits, but we do not know the number of subgroups, when the troop splits, and who goes where



Model

$$y_i \sim \text{binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i)\text{binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = 2\alpha_2 + ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{bernulli}(\theta)$$

y_i : number of hours the pair was synchronized on observation i

λ_i : pair is together (1) or not (0)

α_1 : synchrony when pair is separated

α_2 : individual baseline synchrony

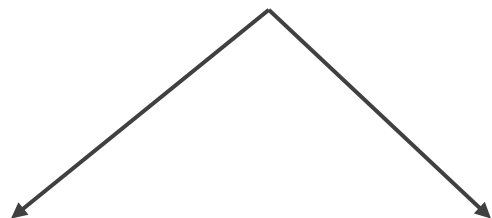
β : effect of dominance

$ID_{k,j}$: effect of individual k and j involved in observation i (ID is a vector)

θ : probability the pair is together (*mixture probability*)

Model

Mixture model: more than one data generating process



$$y_i \sim \text{binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i) \text{binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = 2\alpha_2 + ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{bernulli}(\theta)$$

y_i : number of hours the pair was synchronized on observation i

λ_i : pair is together (1) or not (0)

α_1 : synchrony when pair is separated

α_2 : individual baseline synchrony

β : effect of dominance

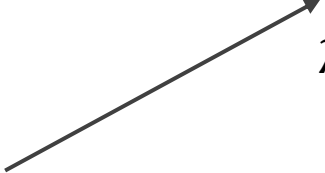
$ID_{k,j}$: effect of individual k and j involved in observation i (ID is a vector)

θ : probability the pair is together (*mixture probability*)

Model

$$y_i \sim \text{binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i) \text{binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = 2\alpha_2 + \boxed{ID_{k[i]} + ID_{j[i]}} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{bernulli}(\theta)$$


Dyadic regression: control for non-independency of edges belonging to a node by including a node effect (in *causal inference* terminology: close backdoor path)

Hart et al., 2023

y_i : number of hours the pair was synchronized on observation i

λ_i : pair is together (1) or not (0)

α_1 : synchrony when pair is separated

α_2 : individual baseline synchrony

β : effect of dominance

$ID_{k,j}$: effect of individual k and j involved in observation i (ID is a vector)

θ : probability the pair is together (*mixture probability*)

STAN implementation

STAN works by defining the model through “blocks” and finding the “posterior surface” by defining log likelihood of each observation

$$y_i \sim \text{binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i)\text{binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = 2\alpha_2 + ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{bernulli}(\theta)$$

```
data {  
  ?  
}  
  
parameters {  
  ?  
}  
  
model {  
  ?  
}
```

Data block

$$y_i \sim \text{binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i)\text{binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = 2\alpha_2 + ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{bernulli}(\theta)$$

Which variables are data?

Data block

$$y_i \sim \text{binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i) \text{binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = 2\alpha_2 + ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{bernulli}(\theta)$$

```
data {  
  int<lower=0> N; // number of data points  
  int<lower=0> N_ind; // number of individuals  
  int<lower=0> n_hours_same[N]; // number of hours in which both individuals are performing the same behaviour  
  int<lower=0> id_1[N]; // first individual of edge  
  int<lower=0> id_2[N]; // second individual of edge  
  vector<lower=0,upper=1>[N] dominance_1; // dominance first individual  
  vector<lower=0,upper=1>[N] dominance_2; // dominance second individual  
}
```

STAN is explicitly typed compiled language which requires variable declaration and definition
For more on data types: <https://mc-stan.org/docs/reference-manual/types.html>

Data block

$$y_i \sim \text{binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i) \text{binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = 2\alpha_2 + ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

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```
data {  
  int<lower=0> N; // number of data points  
  int<lower=0> N_ind; // number of individuals  
  int<lower=0> n_hours_same[N]; // number of hours in which both individuals are performing the same behaviour  
  int<lower=0> id_1[N]; // first individual of edge Integer arrays  
  int<lower=0> id_2[N]; // second individual of edge  
  vector<lower=0,upper=1>[N] dominance_1; // dominance first individual Real vectors supports  
  vector<lower=0,upper=1>[N] dominance_2; // dominance second individual linear algebra operations  
}
```

STAN is explicitly typed compiled language which requires variable declaration and definition
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Data block

$$y_i \sim \text{binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i) \text{binomial}(n = 24, \alpha_1)$$

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$$\lambda_i \sim \text{bernulli}(\theta)$$

```
data {  
  int<lower=0> N; // number of data points  
  int<lower=0> N_ind; // number of individuals  
  int<lower=0> n_hours_same[N]; // number of hours in which both individuals are performing the same behaviour  
  int<lower=0> id_1[N]; // first individual of edge  
  int<lower=0> id_2[N]; // second individual of edge  
  vector<lower=0,upper=1>[N] dominance_1; // dominance first individual  
  vector<lower=0,upper=1>[N] dominance_2; // dominance second individual  
}
```

```
transformed data {  
  // Centralize predictors |  
  vector[N] dominance_1_c = dominance_1 - mean(dominance_1);  
  vector[N] dominance_2_c = dominance_2 - mean(dominance_2);  
}
```

- Centralizing predictors increases sampling performance
- Response is a random variable and as such should not be centralized
- Data blocks evaluated once

Parameters block

Parameters → “unknown quantities”

$$y_i \sim \text{binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i) \text{binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = 2\alpha_2 + ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{bernulli}(\theta)$$

Which variables are the parameters?

Parameters block

Parameters → “unknown quantities”

$$y_i \sim \text{binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i) \text{binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = 2\alpha_2 + ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{bernulli}(\theta)$$

```
parameters {  
  // intercepts  
  ordered[2] alpha;  
  // fixed effect  
  real beta;  
  // hyperparameters  
  real<lower=0> sigma_id;  
  // mixture mixing parameter  
  real<lower=0,upper=1> theta;  
  // random effects  
  vector[N_ind] id_z;  
}
```

Parameters block

Parameters → “unknown quantities”

$$y_i \sim \text{binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i) \text{binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = 2\alpha_2 + ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{bernulli}(\theta)$$

Missing values can be imputed by including them in the parameters block

ordered is a data type to solve non-identifiability of mixture models (and HMMs)

It would be possible to swap values of p_i and α_1 , and change $\theta \rightarrow 1 - \theta$

```
parameters {  
  // intercepts  
  ordered[2] alpha;  
  // fixed effect  
  real beta;  
  // hyperparameters  
  real<lower=0> sigma_id;  
  // mixture mixing parameter  
  real<lower=0,upper=1> theta;  
  // random effects  
  vector[N_ind] id_z;  
}
```

Model block

$$y_i \sim \text{Binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i) \text{Binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = 2\alpha_2 + ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{Bernulli}(\theta)$$

Model block

$$y_i \sim \text{Binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i)\text{Binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = 2\alpha_2 + ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{Bernulli}(\theta)$$

$$\theta \sim \text{Beta}(4, 4)$$

$$\beta \sim \text{Normal}(0, 5)$$

$$\alpha_1 \sim \text{Normal}(0, 5)$$

Priors

- Priors' distribution depend on parameters' domain
- Priors' parameters are chosen through prior predictive simulations and domain-specific knowledge
- Wise choice of priors' parameters allow *regularization*

Model block

$$y_i \sim \text{Binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i) \text{Binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = 2\alpha_2 + ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{Bernulli}(\theta)$$

$$\theta \sim \text{Beta}(4, 4)$$

$$\beta \sim \text{Normal}(0, 5)$$

$$\alpha_1 \sim \text{Normal}(0, 5)$$

Varying effects

$$ID \sim \text{Normal}(\alpha_2, \sigma_{ID})$$

$$\alpha_2 \sim \text{Normal}(0, 5)$$

Hyperparameters

$$\sigma_{ID} \sim \text{Exponential}(0.1)$$

- Priors' distribution depend on parameters' domain
- Priors' parameters are chosen through prior predictive simulations and domain-specific knowledge
- Wise choice of priors' parameters allow *regularization*
- Varying effects consist in letting the data inform the parameters of prior → automatic regularization

Model block

Non-centered parametrization

$$ID \sim \text{Normal}(\alpha_2, \sigma_{ID})$$

$$\alpha_2 \sim \text{Normal}(0, 5)$$

$$\sigma_{ID} \sim \text{Exponential}(0.1)$$



$$ID.z \sim \text{Normal}(0, 1)$$

$$ID = ID.z + \alpha_2 * \sigma_{ID}$$

$$\alpha_2 \sim \text{Normal}(0, 5)$$

$$\sigma_{ID} \sim \text{Exponential}(0.1)$$

Non-centered parametrization increases sampling performance

Non-centered parametrization for multidimensional normal distributions more complicated (involves Cholesky decomposition) but very necessary

<https://www.youtube.com/watch?v=DPnLb5EaCkA&t=3977s>

Find the log-likelihood of each observation

Model block executed each time gradient is computed

```
transformed parameters { // Back-transform centered parametrization.
  vector[N_ind] transformed_id = sigma_id * id_z + alpha[2];
}

model {
  // Priors
  // fixed effect
  alpha[1] ~ normal(-1, 5);
  beta ~ normal(0, 5);
  // Hyperparameters
  alpha[2] ~ normal(0, 5);
  sigma_id ~ exponential(0.1);
  // mixture mixing probability
  theta ~ beta(4, 4);
  // random effects
  target += normal_lpdf(id_z | 0, 1);

  // Model
  for(i in 1:N) { // for every observation
    real p = transformed_id[id_1[i]] + transformed_id[id_2[i]] + beta * (dominance_1_c[i] + dominance_2_c[i]);
    target += log_sum_exp( // marginalize likelihood.
      log(theta) + binomial_logit_lpmf(n_hours_same[i] | 24, p), // "process" 1 : the pair is in the same location
      log(1 - theta) + binomial_logit_lpmf(n_hours_same[i] | 24, alpha[1]) // "process" 2 : the pair is in a different location
    );
  }
}
```

$$y_i \sim \text{Binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i) \text{Binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

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$$\alpha_1 \sim \text{Normal}(-1, 5)$$

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$$ID.z \sim \text{Normal}(0, 1)$$

$$ID = ID.z + \alpha_2 * \sigma_{ID}$$

$$\alpha_2 \sim \text{Normal}(0, 5)$$

$$\sigma_{ID} \sim \text{Exponential}(0.1)$$

Find the log-likelihood of each observation

```
transformed parameters { // Back-transform centered parametrization.
  vector[N_ind] transformed_id = sigma_id * id_z + alpha[2];
}
```

```
model {
  // Priors
  // fixed effect
  alpha[1] ~ normal(-1, 5);
  beta ~ normal(0, 5);
  // Hyperparameters
  alpha[2] ~ normal(0, 5);
  sigma_id ~ exponential(0.1);
  // mixture mixing probability
  theta ~ beta(4, 4);
  // random effects
  target += normal_lpdf(id_z | 0, 1);
}
```

To let the data inform priors of varying effects likelihood must be specified

```
// Model
for(i in 1:N) { // for every observation
  real p = transformed_id[id_1[i]] + transformed_id[id_2[i]] + beta * (dominance_1_c[i] + dominance_2_c[i]);
  target += log_sum_exp( // marginalize likelihood.
    log(theta) + binomial_logit_lpmf(n_hours_same[i] | 24, p), // "process" 1 : the pair is in the same location
    log(1 - theta) + binomial_logit_lpmf(n_hours_same[i] | 24, alpha[1]) // "process" 2 : the pair is in a different location
  );
}
```

$$y_i \sim \text{Binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i)\text{Binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{Bernulli}(\theta)$$

$$\theta \sim \text{Beta}(4, 4)$$

$$\beta \sim \text{Normal}(0, 5)$$

$$\alpha_1 \sim \text{Normal}(-1, 5)$$

$$\alpha_2 \sim \text{Normal}(0, 5)$$

$$ID.z \sim \text{Normal}(0, 1)$$

$$ID = ID.z + \alpha_2 * \sigma_{ID}$$

$$\alpha_2 \sim \text{Normal}(0, 5)$$

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Find the log-likelihood of each observation

```
transformed parameters { // Back-transform centered parametrization.
  vector[N_ind] transformed_id = sigma_id * id_z + alpha[2];
}

model {
  // Priors
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  alpha[1] ~ normal(-1, 5);
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  // Hyperparameters
  alpha[2] ~ normal(0, 5);
  sigma_id ~ exponential(0.1);
  // mixture mixing probability
  theta ~ beta(4, 4);
  // random effects
  target += normal_lpdf(id_z | 0, 1);

  // Model
  for(i in 1:N) { // for every observation
    real p = transformed_id[id_1[i]] + transformed_id[id_2[i]] + beta * (dominance_1_c[i] + dominance_2_c[i]);
    target += log_sum_exp( // marginalize likelihood.
      log(theta) + binomial_logit_lpmf(n_hours_same[i] | 24, p), // "process" 1 : the pair is in the same location
      log(1 - theta) + binomial_logit_lpmf(n_hours_same[i] | 24, alpha[1]) // "process" 2 : the pair is in a different location
    );
  }
}
```

Priors consistent
with
the ordered type

$$y_i \sim \text{Binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i)\text{Binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{Bernulli}(\theta)$$

$$\theta \sim \text{Beta}(4, 4)$$

$$\beta \sim \text{Normal}(0, 5)$$

$$\alpha_1 \sim \text{Normal}(-1, 5)$$

$$\alpha_2 \sim \text{Normal}(0, 5)$$

$$ID.z \sim \text{Normal}(0, 1)$$

$$ID = ID.z + \alpha_2 * \sigma_{ID}$$

$$\alpha_2 \sim \text{Normal}(0, 5)$$

$$\sigma_{ID} \sim \text{Exponential}(0.1)$$

Find the log-likelihood of each observation

```
transformed parameters { // Back-transform centered parametrization.  
  vector[N_ind] transformed_id = sigma_id * id_z + alpha[2];  
}
```

```
model {  
  // Priors  
  // fixed effect  
  alpha[1] ~ normal(-1, 5);  
  beta ~ normal(0, 5);  
  // Hyperparameters  
  alpha[2] ~ normal(0, 5);  
  sigma_id ~ exponential(0.1);  
  // mixture mixing probability  
  theta ~ beta(4, 4);  
  // random effects  
  target += normal_lpdf(id_z | 0, 1);
```

To find
likelihood of
mixture model
marginalize
over data
generating
processes

```
// Model  
for(i in 1:N) { // for every observation
```

```
  real p = transformed_id[id_1[i]] + transformed_id[id_2[i]] + beta * (dominance_1_c[i] + dominance_2_c[i]);  
  target += log_sum_exp( // marginalize likelihood.  
    log(theta) + binomial_logit_lpmf(n_hours_same[i] | 24, p), // "process" 1 : the pair is in the same location  
    log(1 - theta) + binomial_logit_lpmf(n_hours_same[i] | 24, 1 - p) // "process" 2 : the pair is in a different location  
  );  
}
```

$$y_i \sim \text{Binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i)\text{Binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{Bernulli}(\theta)$$

$$\theta \sim \text{Beta}(4, 4)$$

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$$\alpha_1 \sim \text{Normal}(-1, 5)$$

$$\alpha_2 \sim \text{Normal}(0, 5)$$

$$ID.z \sim \text{Normal}(0, 1)$$

$$ID = ID.z + \alpha_2 * \sigma_{ID}$$

$$\alpha_2 \sim \text{Normal}(0, 5)$$

$$\sigma_{ID} \sim \text{Exponential}(0.1)$$

Find the log-likelihood of each observation

```
transformed parameters { // Back-transform centered parametrization.
  vector[N_ind] transformed_id = sigma_id * id_z + alpha[2];
}
```

```
model {
  // Priors
  // fixed effect
  alpha[1] ~ normal(-1, 5);
  beta ~ normal(0, 5);
  // Hyperparameters
  alpha[2] ~ normal(0, 5);
  sigma_id ~ exponential(0.1);
  // mixture mixing probability
  theta ~ beta(4, 4);
  // random effects
  target += normal_lpdf(id_z | 0, 1);

  // Model
  for(i in 1:N) { // for every observation
    real p = transformed_id[id_1[i]] + transformed_id[id_2[i]] + beta * (dominance_1_c[i] + dominance_2_c[i]);
    target += log_sum_exp( // marginalize likelihood.
      log(theta) + binomial_logit_lpmf(n_hours_same[i] | 24, p), // "process" 1 : the pair is in the same location
      loglm(theta) + binomial_logit_lpmf(n_hours_same[i] | 24, alpha[1]) // "process" 2 : the pair is in a different location
    );
  }
}
```

Computationally stable:
 $\log_sum_exp()$ → sum probabilities
 $\loglm()$ → 1 - probability

$$y_i \sim \text{Binomial}(n = 24, p_i)(\lambda_i) + (1 - \lambda_i)\text{Binomial}(n = 24, \alpha_1)$$

$$\text{logit}(p_i) = ID_{k[i]} + ID_{j[i]} + \beta(d_{k[i]} + d_{j[i]})$$

$$\lambda_i \sim \text{Bernulli}(\theta)$$

$$\theta \sim \text{Beta}(4, 4)$$

$$\beta \sim \text{Normal}(0, 5)$$

$$\alpha_1 \sim \text{Normal}(-1, 5)$$

$$\alpha_2 \sim \text{Normal}(0, 5)$$

$$ID.z \sim \text{Normal}(0, 1)$$

$$ID = ID.z + \alpha_2 * \sigma_{ID}$$

$$\alpha_2 \sim \text{Normal}(0, 5)$$

$$\sigma_{ID} \sim \text{Exponential}(0.1)$$

Generated quantities block

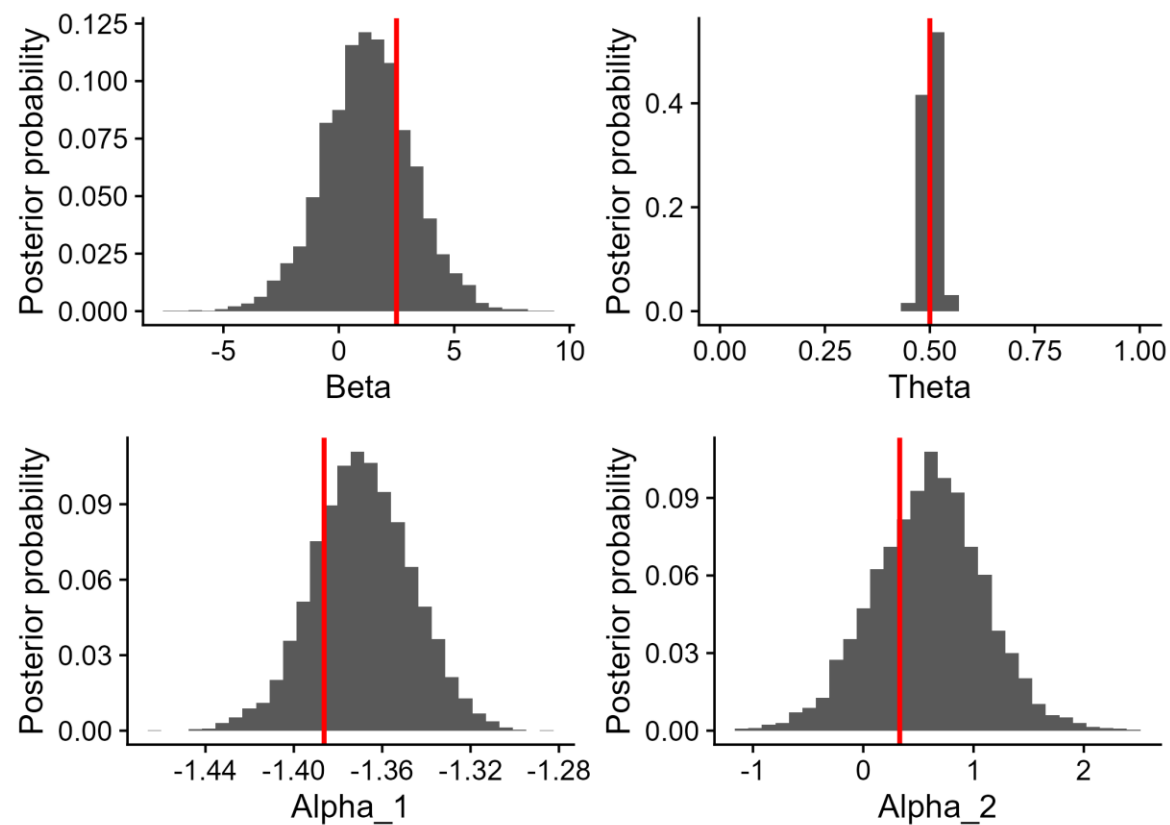
Block executed for each MCMC sample

```
generated quantities {  
  // Classify observation as same or different location  
  vector[N] prob_same;  
  for(i in 1:N) { // the mixture probability of a data point is the likelihood multiplied by the mixture probability normalized over the mixtures  
    real p = transformed_id[id_1[i]] + transformed_id[id_2[i]] + beta * (dominance_1_c[i] + dominance_2_c[i]);  
    real mixture_1 = binomial_logit_lpmf(n_hours_same[i] | 24, p) + log(theta);  
    real mixture_2 = binomial_logit_lpmf(n_hours_same[i] | 24, alpha[1]) + log1m(theta);  
    prob_same[i] = exp(mixture_1 - log_sum_exp(mixture_1, mixture_2));  
  }  
  // Generate edge posterior  
  matrix[N_ind, N_ind] edges;  
  for(ind_1 in 1:N_ind) {  
    for(ind_2 in 1:N_ind) {  
      edges[ind_1, ind_2] = inv_logit(transformed_id[ind_1] + transformed_id[ind_2] + beta * (dominance_1_c[ind_1] + dominance_2_c[ind_2]));  
    }  
  }  
  // Generate centrality posterior  
  vector[N_ind] centrality;  
  for(ind_1 in 1:N_ind) {  
    centrality[ind_1] = 0;  
    for(ind_2 in 1:N_ind) {  
      centrality[ind_1] += edges[ind_1, ind_2];  
    }  
  }  
  centrality /= N_ind;  
}
```

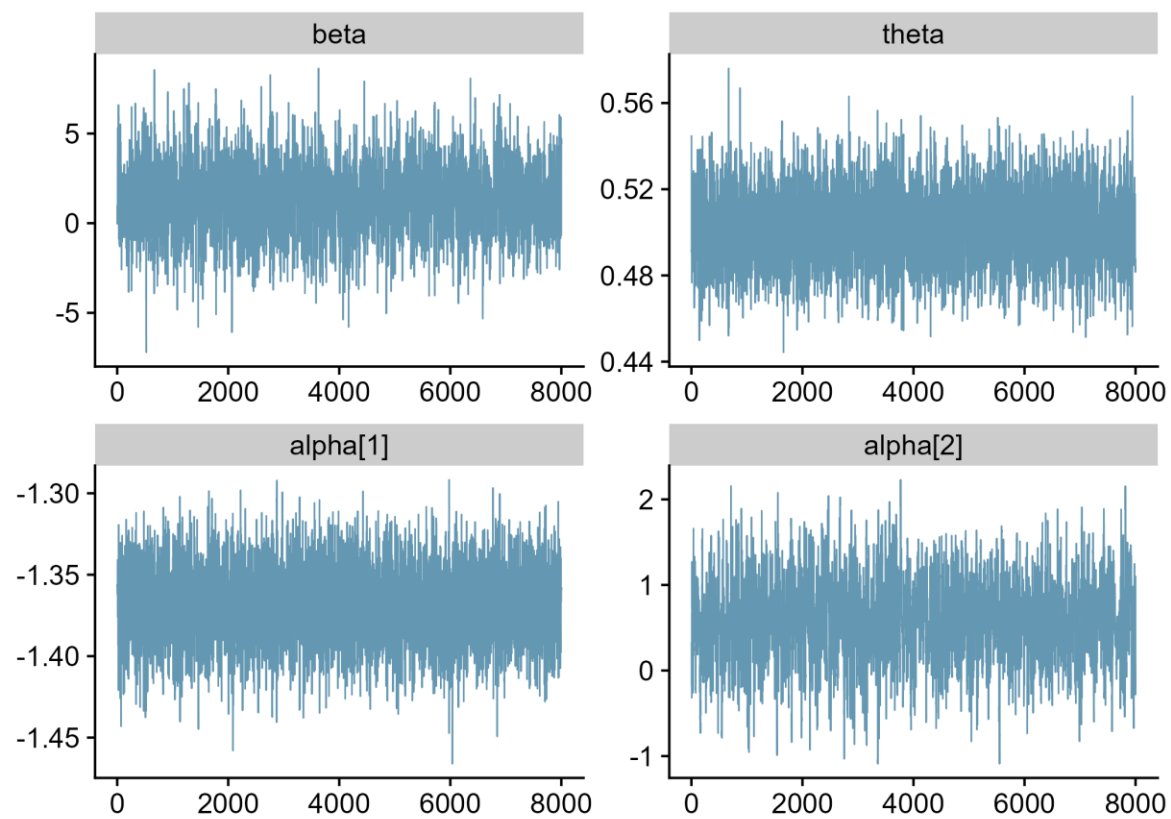
Mixture models perform unsupervised classification

To find the posterior for a data point belonging to a specific data generating process, multiply the likelihood times the mixture probability and normalize over the data generating processes

Results

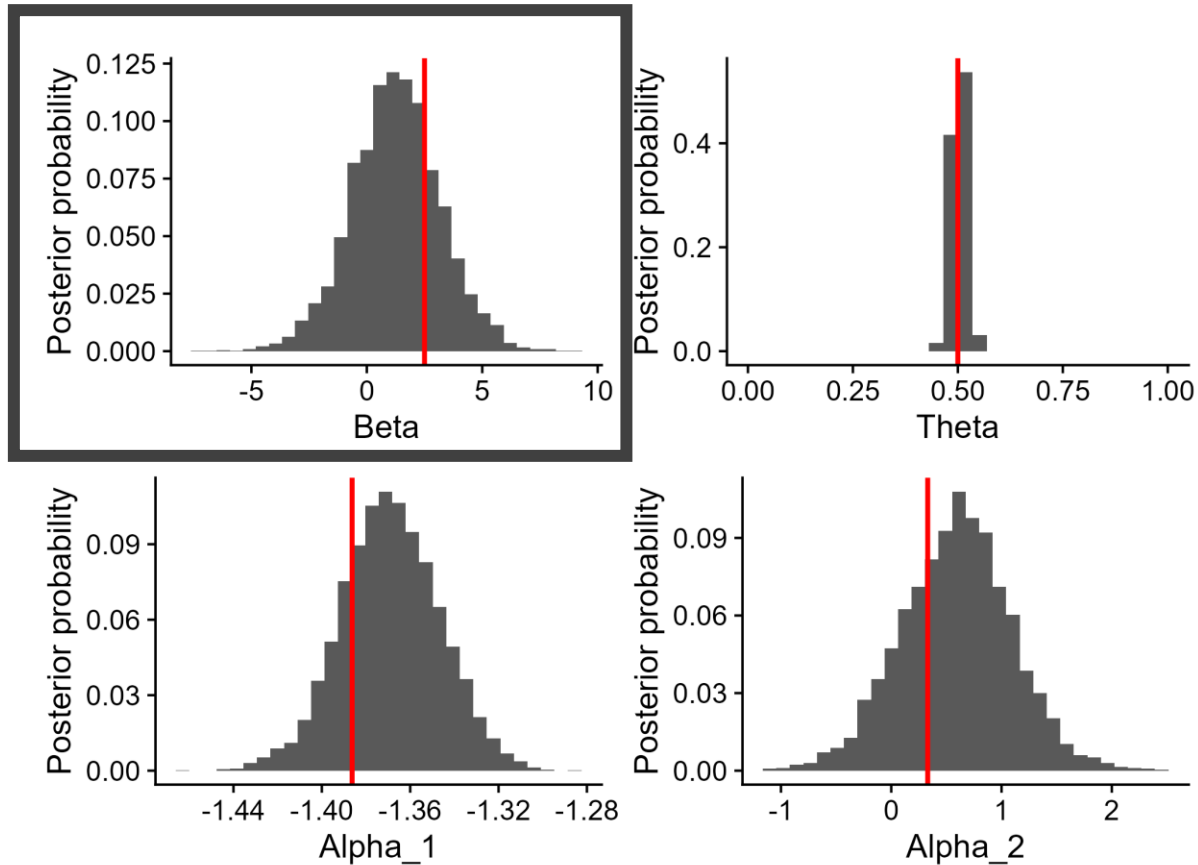


Parameters used to generate data

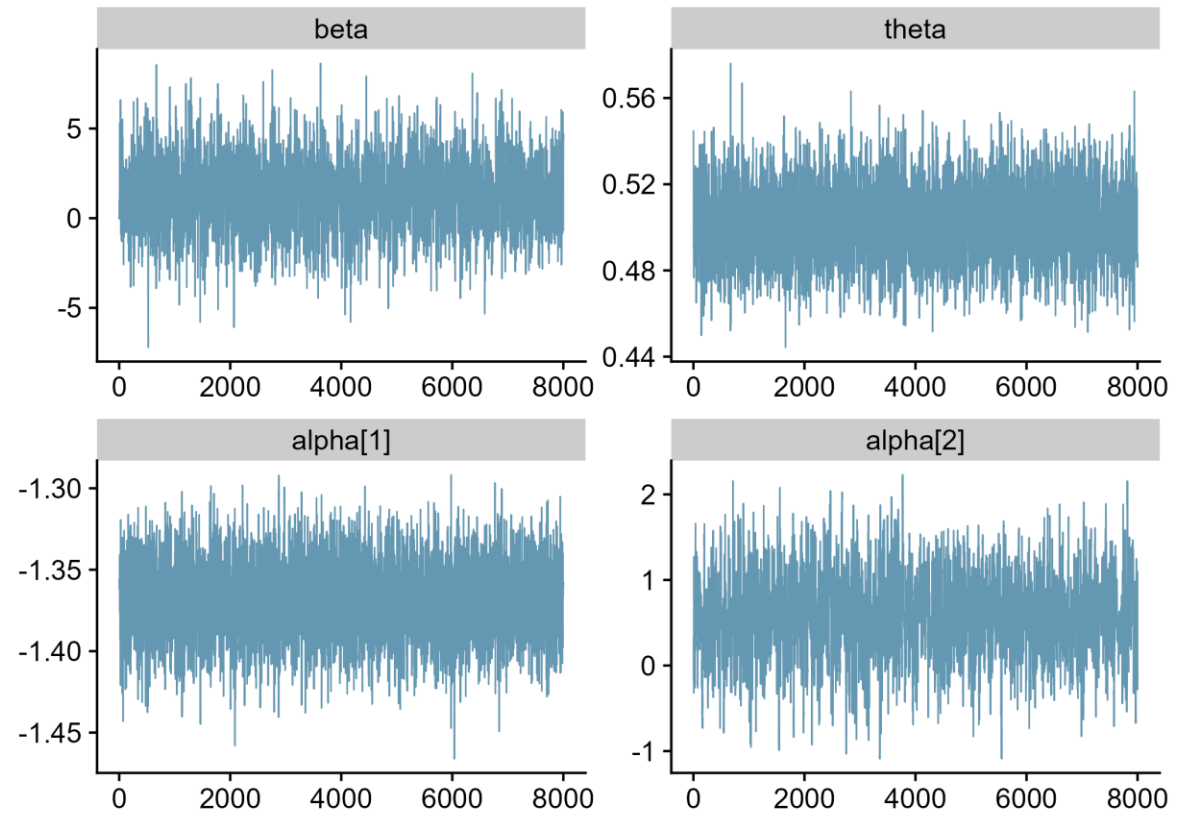


MCMC diagnostics

What is the effect of dominance on pairwise synchrony?

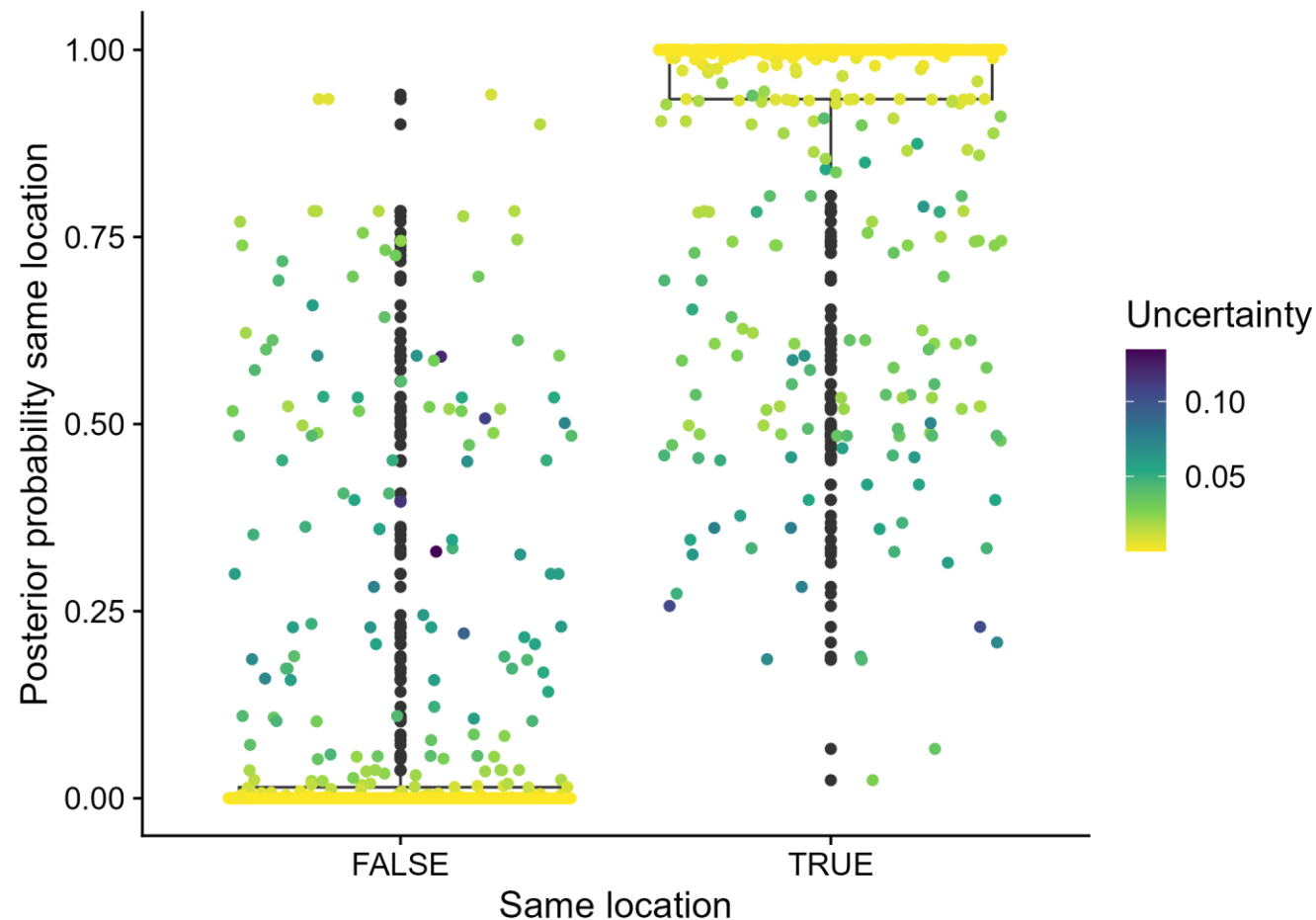
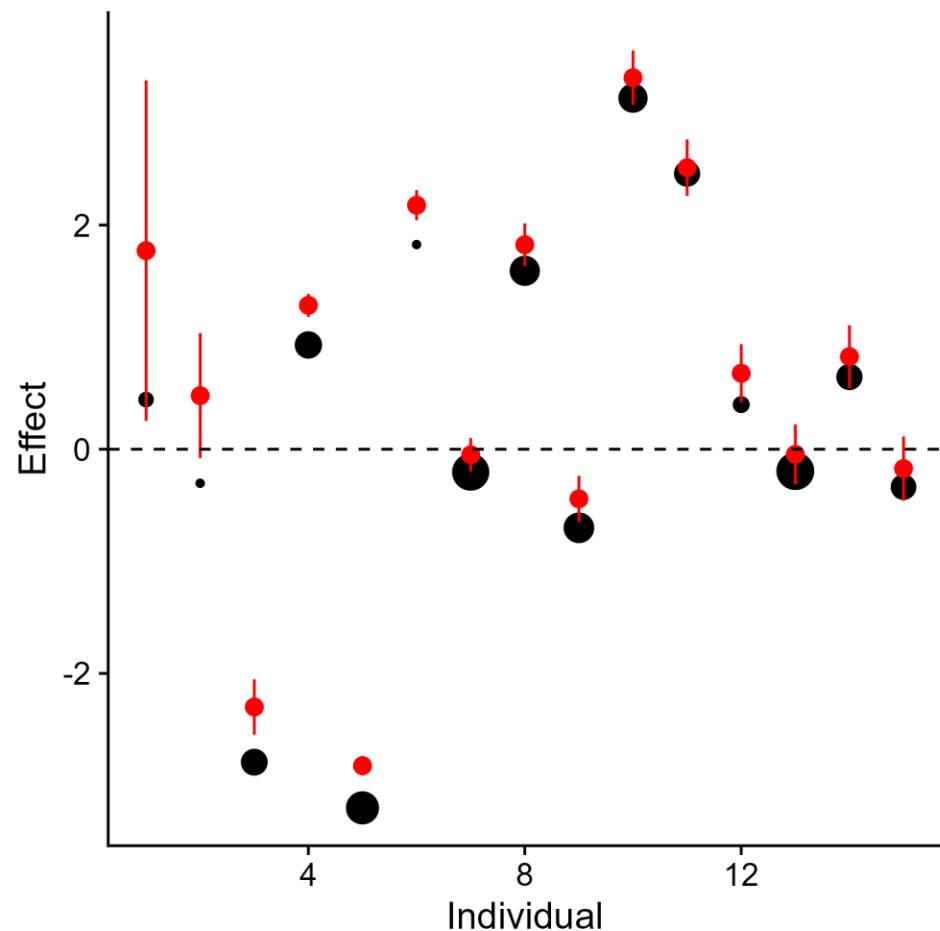


Parameter used to generate data



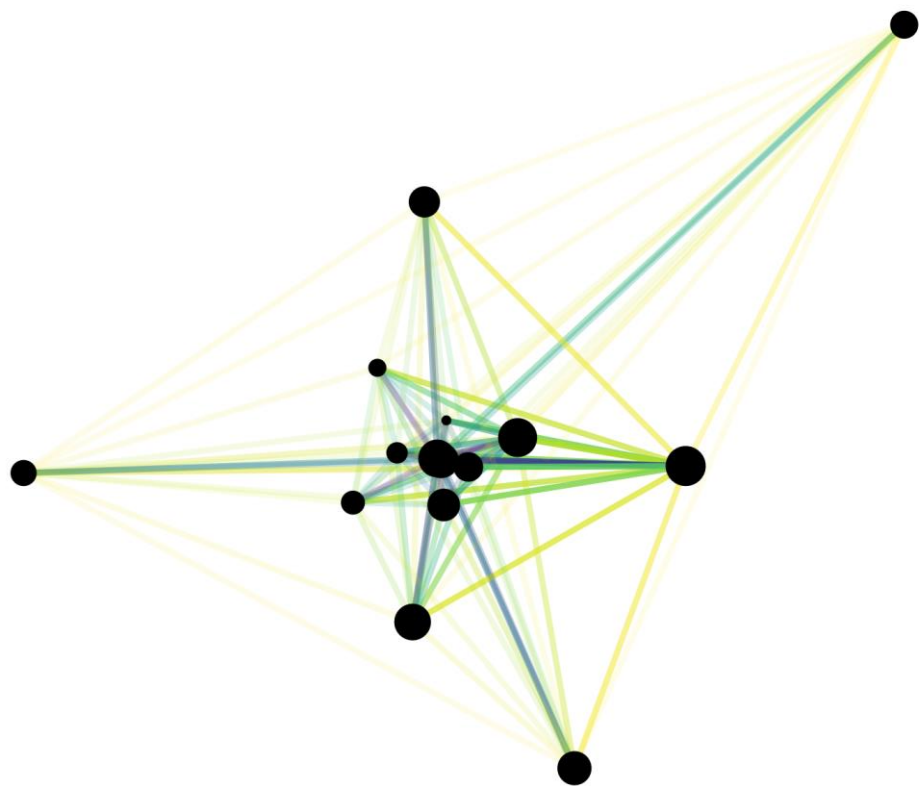
MCMC diagnostics

Results

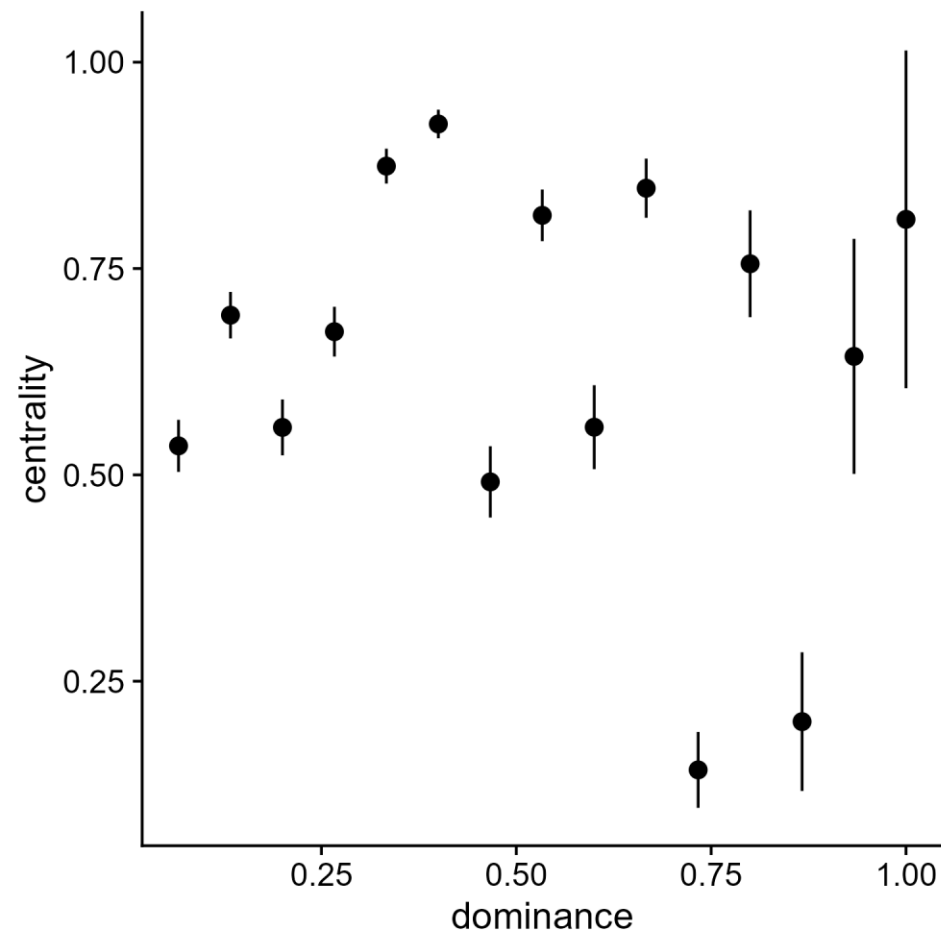


- Successful unsupervised classification
- Uncertainty is SD of posterior
- All derived quantities have a posterior, not only parameters – propagation of uncertainty

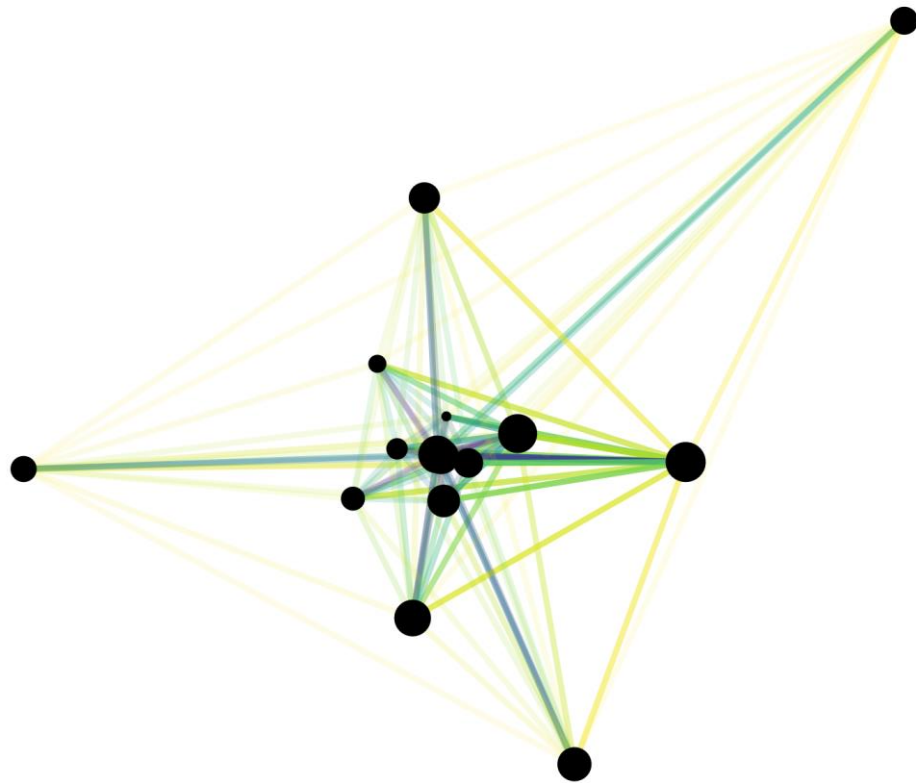
Results



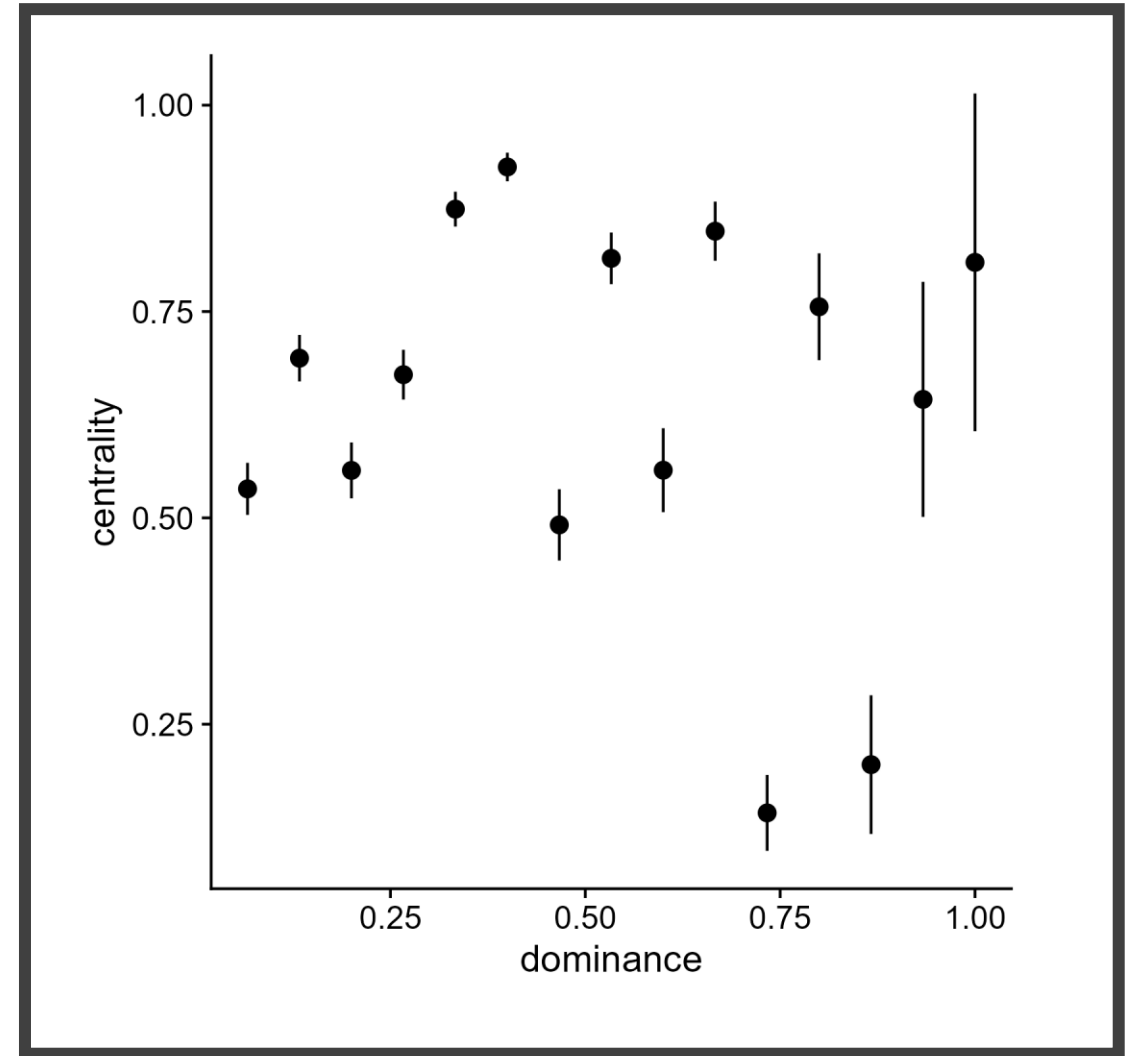
Color is posterior median
Transparency is posterior SD
Node size is dominance



What is the individual centrality in synchrony network?



Color is posterior median
Transparency is posterior sd
Node size is dominance



Uncertainty propagated from edges to node level metric

Examples of other STAN usage

Reinforcement learning



RESEARCH ARTICLE



Risk-sensitive learning is a winning strategy for leading an urban invasion

Alexis J Breen^{1*†}, Dominik Deffner^{2,3*}

Hidden Markov Models

nature communications



Article

<https://doi.org/10.1038/s41467-024-47010-3>

Collective incentives reduce over-exploitation of social information in unconstrained human groups

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Gaussian processes

RESEARCH ARTICLE

Inference in social networks



BISoN: A Bayesian framework for inference of social networks

Jordan Hart¹ | Michael Nash Weiss^{2,3} | Daniel Franks^{4,5} | Lauren Brent⁶