

Dec, 2015

Review TADA

CC model

De novo model

Grids of
parameters

De novo

Case-control

Estimate
parameters

Constrained
optimization

MCMC

Dec, 2015

February 10, 2016

Review TADA

CC model

De novo model

Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC

- Review TADA (Transmission And De novo Association) model.
- Test the likelihood values of TADA on grids of parameters on **D0**.
- Estimate parameters using box-constrained optimization and MCMC on **D1** and **D2**:

D0. De Rubeis, Silvia, et al. "Synaptic, transcriptional and chromatin genes disrupted in autism." Nature 515.7526 (2014): 209-215.

D1. He, Xin, et al. "Integrated model of de novo and inherited genetic variants yields greater power to identify risk genes." PLoS Genet 9.8 (2013): e1003671.

D2. Only the FMRP gene set from the data set **D0**.
From Darnell: 842 genes.

Review TADA

CC model

De novo model

Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC

Let π be the fraction of risk genes in all genes.

Main parameters		Variants (LoF and mis3)
$\left\{ \begin{array}{l} \textit{Mutation rate } (\mu) \\ \textit{Relative risk } (\gamma) \\ \textit{Population frequency } (q) \end{array} \right.$	\Rightarrow	$\left\{ \begin{array}{l} \text{De novo mutation} \\ \text{Transmitted variations} \\ \text{Variants in case-control studies} \end{array} \right.$

For each i^{th} gene, TADA uses a Bayesian approach to test the hypothesis

$H_0 : \gamma_i = 1$ against the alternative $H_1 : \gamma_i \neq 1$

\Rightarrow A fraction π of risk genes (per total genes) follows the H_1 model.

The model incorporates information across genes, assumming that:

- Relative risk γ :
 $\gamma \sim \text{Gamma}(\bar{\gamma} * \beta, \beta)$.
- Population frequency of variants q :
 - Risk genes: $q_1 \sim \text{Gamma}(\rho_1, \nu_1)$
 - Normal genes: $q_0 \sim \text{Gamma}(\rho_0, \nu_0)$

=> Need to estimate $\bar{\gamma}, \beta, \rho_1, \nu_1, \rho_0, \nu_0, \pi$.

With each type of data/variants (x), at each gene:

$$P(x|\text{parameteres}) = \pi P(x|H_1) + (1 - \pi)P(x|H_0)$$

Two types of mutations are tested: Loss-of-function (LoF) and probably damaging (Mis3).

Review TADA

CC model

De novo model

Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC

Test two models:

External product

$$P(x|parameters) = \prod_{i=1}^m \left[\pi P(x_{i_{LoF}}|H_1) + (1 - \pi)P(x_{i_{LoF}}|H_0) \right] \left[\pi P(x_{i_{mis3}}|H_1) + (1 - \pi)P(x_{i_{mis3}}|H_0) \right]$$

Internal product

$$P(x|parameters) = \prod_{i=1}^m \left[\pi P(x_{i_{LoF}}|H_1)P(x_{i_{mis3}}|H_1) + (1 - \pi)P(x_{i_{LoF}}|H_0)P(x_{i_{mis3}}|H_0) \right]$$

Bayes factor

$$BF = \frac{P(x|H_1)}{P(x|H_0)} = \frac{P(x_{LoF}|H_1)P(x_{mis3}|H_1)}{P(x_{LoF}|H_0)P(x_{mis3}|H_0)}$$

$$p_{dn} = 2 * \mu\gamma$$

$$p_{control} = q$$

$$p_{case} = q\gamma$$

Model for case-control data

Review TADA

CC model

De novo model

Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC

Relative risks:

$$\gamma|H_1 \sim \text{Gamma}(\bar{\gamma} * \beta, \beta)$$

Frequency of variants:

$$q|H_1 \sim \text{Gamma}(\rho, \nu)$$

$$q|H_0 \sim \text{Gamma}(\rho_0, \nu_0)$$

The model:

$$P(x|H_0) = \int p(x|q, \gamma = 1)p(q|H_0)dq$$

$$P(x|H_1) = \int p(x|q, \gamma)p(q|H_1)p(\gamma|H_1)dq d\gamma$$

Model for case-control data (cont)

Review TADA

CC model

De novo model

Grids of
parametersDe novo
Case-controlEstimate
parametersConstrained
optimization
MCMC

For simplicity, let $q|H_1 = q|H_0 = q \sim \text{Gamma}(\rho, \nu)$,

we will calculate the conditional distribution of variants in cases on total variants of cases and controls.

$$X_{\text{case}} \sim \text{Pois}(\lambda_1); X_{\text{control}} \sim \text{Pois}(\lambda_0)$$

$$\text{With } \lambda_1 = N_{\text{case}} * q * \gamma; \lambda_0 = N_{\text{control}} * q$$

$$X = X_{\text{case}} + X_{\text{control}}$$

$$X \sim \text{Pois}(\lambda_1 + \lambda_0)$$

Question:

1) should let $q = \epsilon * q_0$.

2) Relationship between q and μ .

Model for case-control data (cont2)

Review TADA

CC model

De novo model

Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC

At the i^{th} gene,

$$P(X_{case} = k | X = n) = \frac{P(X_{case}=k, X=n)}{P(X=n)} = \frac{P(X_{case}=k, X_{contro}=n-k)}{P(X=n)}$$

$$= \frac{\frac{e^{-\lambda_1} \lambda_1^k}{k!} \frac{e^{-\lambda_0} \lambda_0^{n-k}}{(n-k)!}}{\frac{e^{-(\lambda_1+\lambda_0)} (\lambda_1+\lambda_0)^n}{n!}}$$

$$= \frac{n!}{(n-k)! k!} \frac{\lambda_1^k \lambda_0^{n-k}}{(\lambda_1+\lambda_0)^n} = C_n^k p^k (1-p)^{n-k}$$

With

$$p = \frac{\lambda_1}{\lambda_1 + \lambda_0} = \frac{N_{case} q \gamma}{N_{case} q \gamma + N_{control} q} = \frac{N_{case} \gamma}{N_{case} \gamma + N_{control}}$$

Review TADA

CC model

De novo model

Grids of
parametersDe novo
Case-controlEstimate
parametersConstrained
optimization
MCMC

- First way (**Poisson distribution**)

$$X_{dn}|H_1 \sim \text{Pois}(2N_{dn}\mu\gamma)$$

$$X_{dn}|H_0 \sim \text{Pois}(2N_{dn}\mu)$$

- Second way (**Binomial distribution**)

$$X_{dn}|H_1 \sim \text{Binomial}(N_{dn}, 2 * \mu\gamma)$$

$$X_{dn}|H_0 \sim \text{Binomial}(N_{dn}, 2 * \mu)$$

With

Relative risk:

$$\gamma \sim \text{Gamma}(\bar{\gamma} * \beta_{dn}, \beta_{dn})$$

Review TADA

CC model

De novo model

Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC

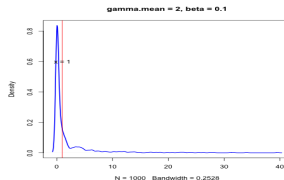
Can we simultaneously estimate all parameters based data + prior information from publications? \Rightarrow it will be easier to incorporate other information.

Some simple steps last month:

- \Rightarrow Re-write likelihood functions with two types of model.
- \Rightarrow Check there are overlapping intervals π between different variants.
- \Rightarrow Test whether we can constrain parameterers to estimate simultaneously.

Some issues we have had:

- Internal OR external models.
- Constrain relative risks (γ).
 - Some relative risk parameters imply substantial proportions of protective genes.



- Improve the calculation of mutation rates for each genes/annotations.
- Use adjusted counts as data.
- Improve algorithm (eliminate numerical integration).

Grid on each data type

- Denovo LoF.
- Denovo Mis3.
- Case-control LoF.

LoF de novo

Review TADA

CC model

De novo model

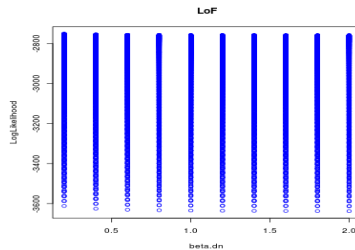
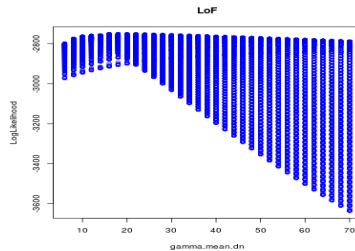
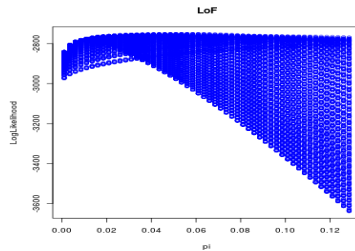
Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC



LoF de novo: top log LLK

Review TADA

CC model

De novo model

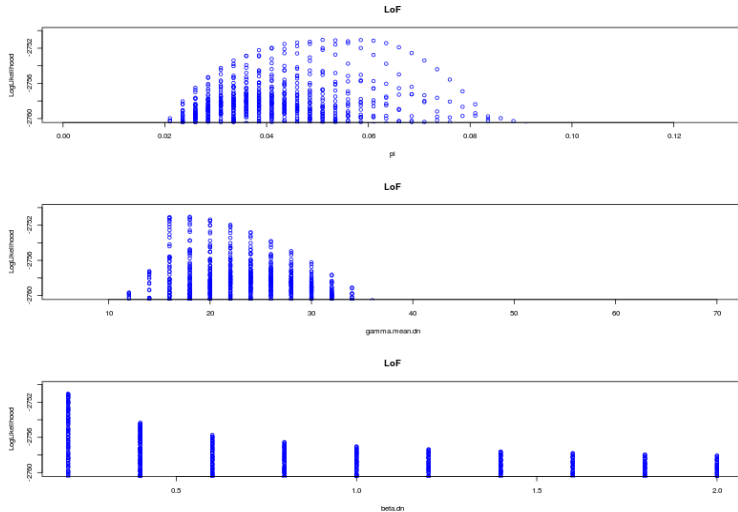
Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

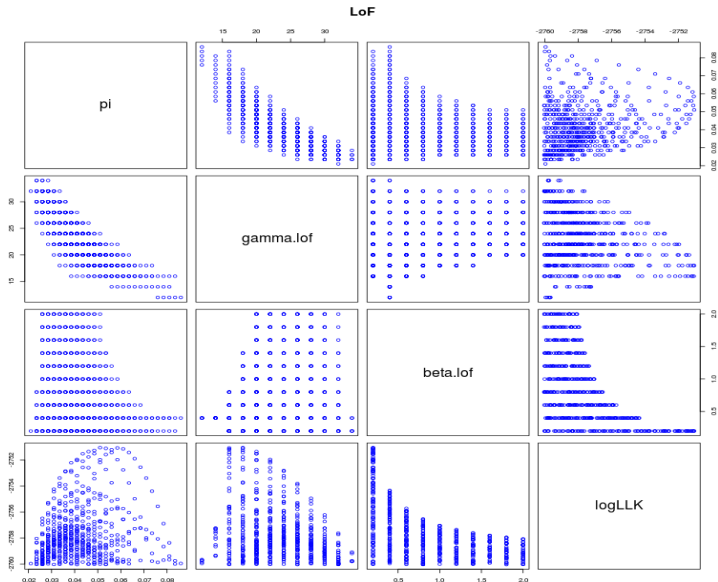
MCMC



LoF de novo: check correlations between hyperparameters

Review TADA

De novo



Mis3 de novo

Review TADA

CC model

De novo model

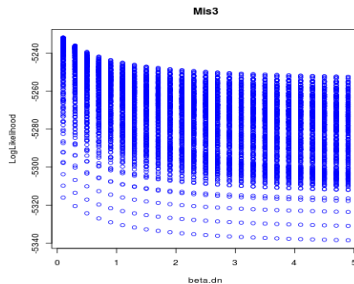
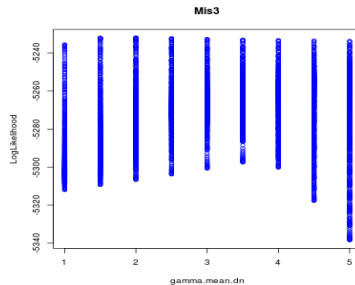
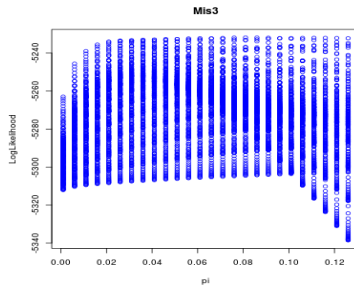
Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC



Mis3 de novo: top LLK less than 0.6% protective variants.

Review TADA

CC model

De novo model

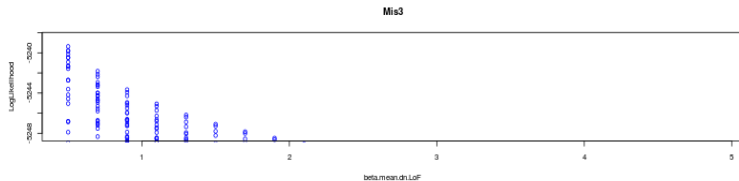
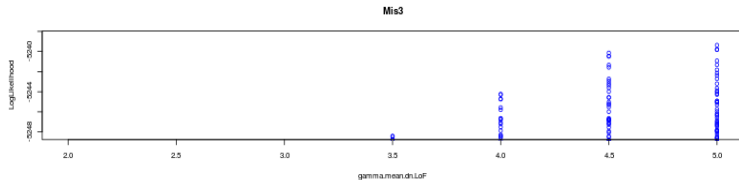
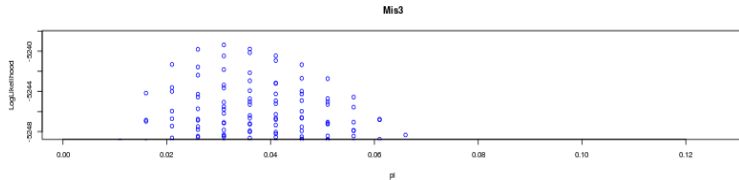
Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC



Dec, 2015

Review TADA

CC model

De novo model

Grids of
parameters

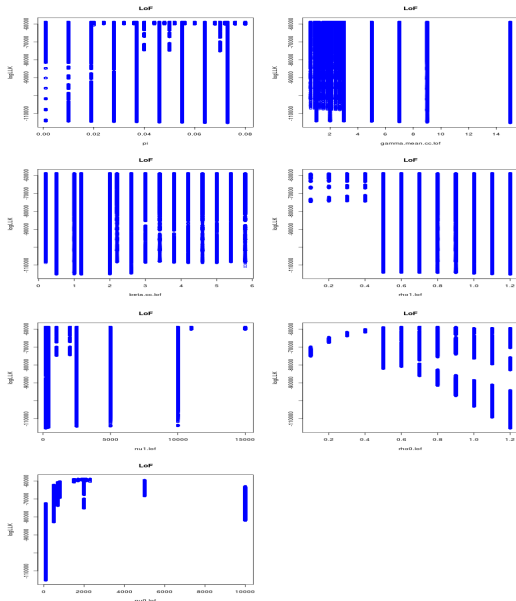
De novo

Case-control

Estimate
parameters

Constrained
optimization

MCMC



LoF case-control

Review TADA

CC model

De novo model

Grids of
parameters

De novo

Case-control

**Estimate
parameters**

Constrained
optimization

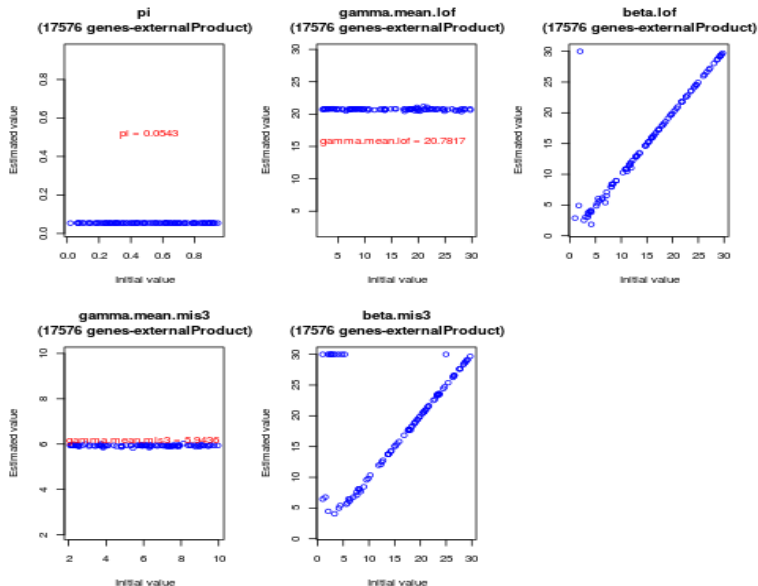
MCMC

Estimate parameters

Use intervals of hyperparameters to set uniform priors for hyperparameters.

Constrained optimization

- ① A set of random initial values was used \Rightarrow they can converge to approximately optimal values.
- ② Some different algorithms (built in R) are used.

Test ([external](#)) for de novo data: LoF + mis3 for D1!

Review TADA

CC model

De novo model

Grids of
parameters

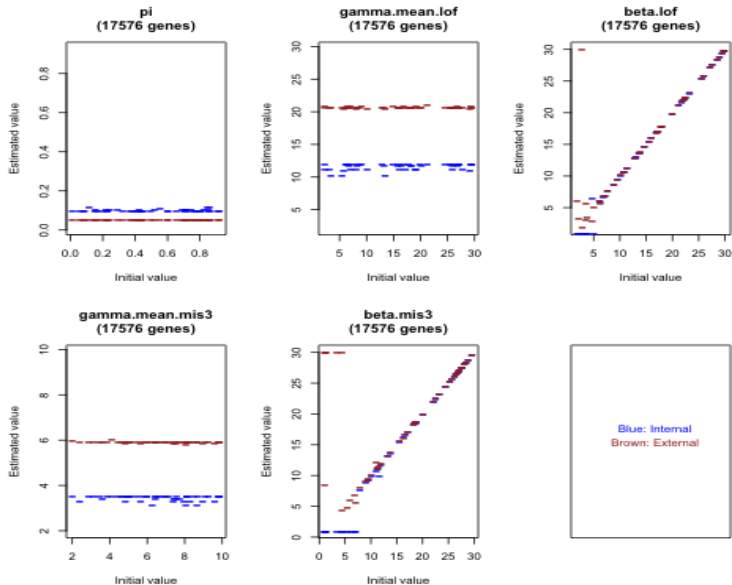
De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC

Test (internal/external) for de novo data: LoF + mis3 for D1!



Review TADA

CC model

De novo model

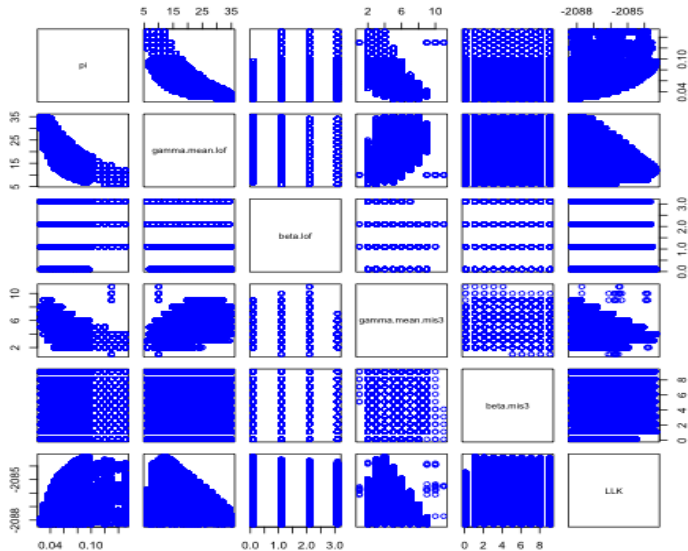
Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC

Grid top LLK ([internal](#)) for de novo data: LoF + mis3 for D1!

Review TADA

CC model

De novo model

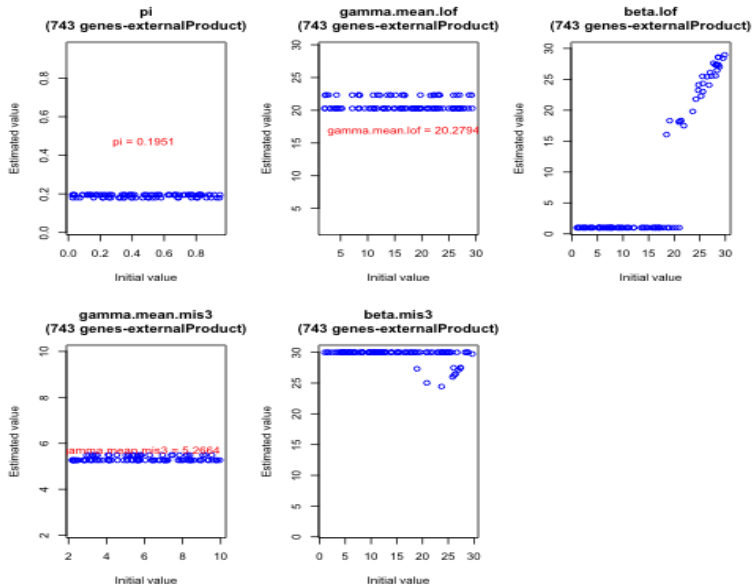
Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC

Test ([external](#)) for de novo data: LoF + mis3 for D2 (the FMRP gene set)!

Review TADA

CC model

De novo model

Grids of
parameters

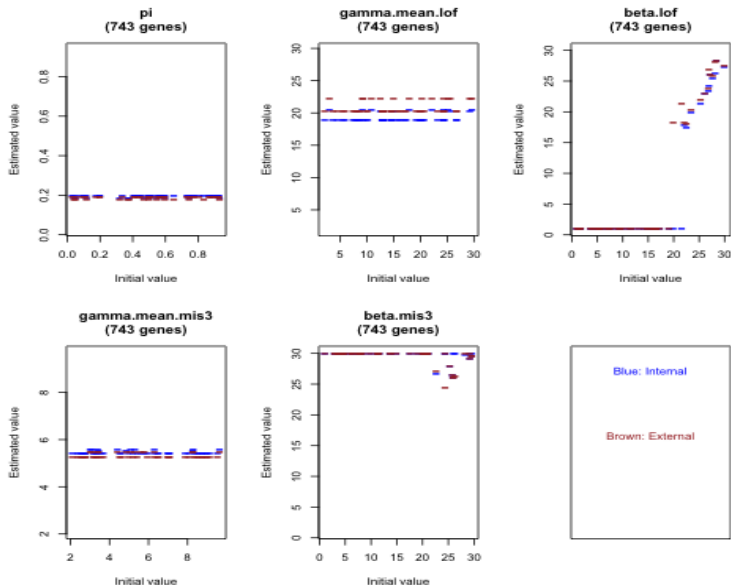
De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC

Test (internal/external) for de novo data: LoF + mis3 for D2 (the FMRP gene set)!



Review TADA

CC model

De novo model

Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC

MCMC for D1: **external** product.

Review TADA

CC model

De novo model

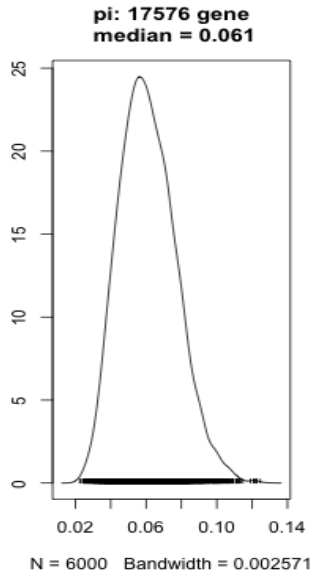
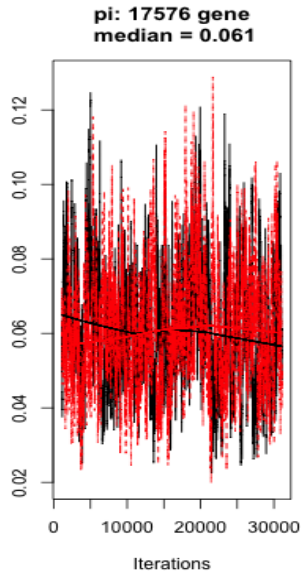
Grids of
parameters

De novo

Case-control

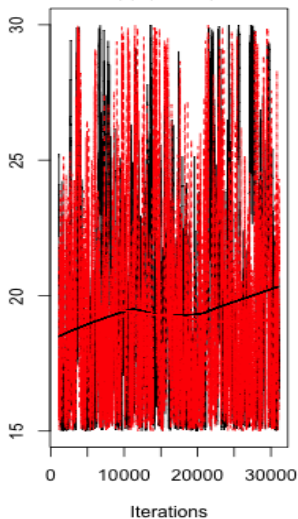
Estimate
parametersConstrained
optimization

MCMC

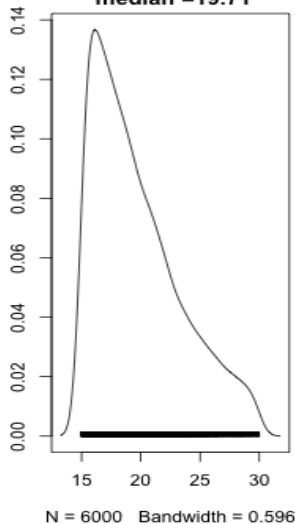


MCMC for D1: external product.

LoF.gamma.mean.denovo
17576 gene
median =19.71



LoF.gamma.mean.denovo
17576 gene
median =19.71



Review TADA

CC model

De novo model

Grids of
parameters

De novo

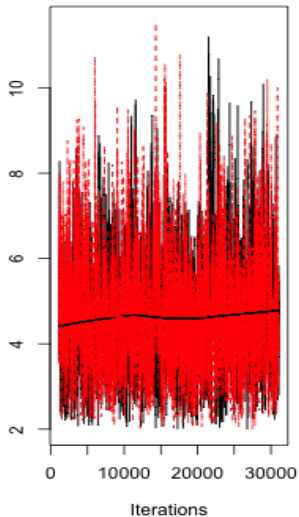
Case-control

Estimate
parametersConstrained
optimization

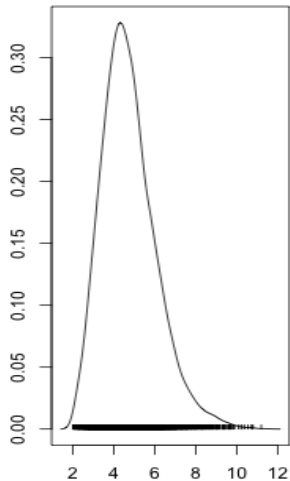
MCMC

MCMC for D1: external product.

Mis3.gamma.mean.denovo
17576 gene
median = 4.74



Mis3.gamma.mean.denovo
17576 gene
median = 4.74



N = 6000 Bandwidth = 0.2048

Review TADA

CC model

De novo model

Grids of
parameters

De novo

Case-control

Estimate
parameters

Constrained
optimization

MCMC

MCMC for **D2** (the FMRP gene set,)

Review TADA

CC model

De novo model

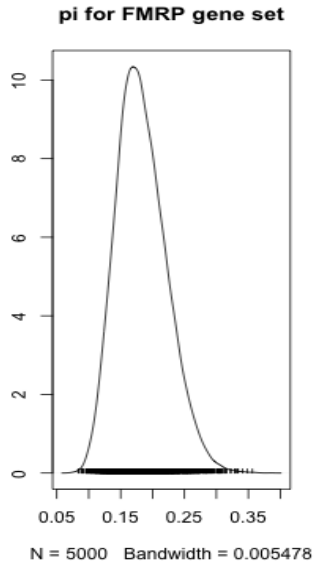
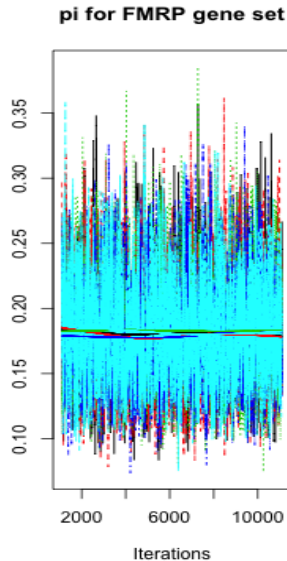
Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC



MCMC for **D2** (the FMRP gene set,)

Review TADA

CC model

De novo model

Grids of
parameters

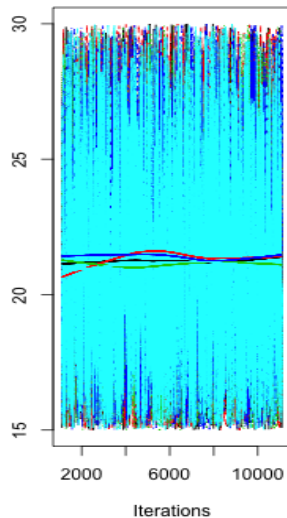
De novo

Case-control

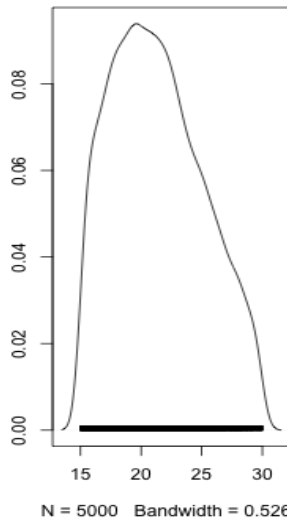
Estimate
parametersConstrained
optimization

MCMC

LoF.gamma.mean.denovo

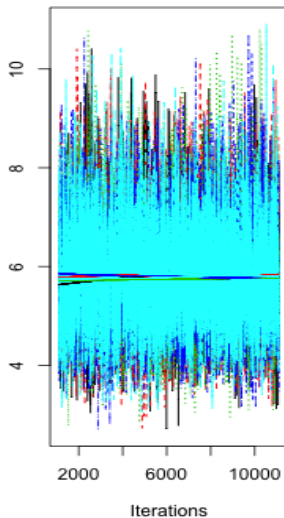


LoF.gamma.mean.denovo

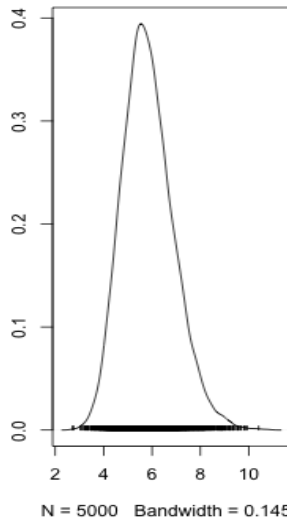


MCMC for **D2** (the FMRP gene set,)

Mis3.gamma.mean.denovo



Mis3.gamma.mean.denovo



Review TADA

CC model

De novo model

Grids of
parameters

De novo

Case-control

Estimate
parametersConstrained
optimization

MCMC