AMBARTI models for agricultural experiments

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Agenda

- Additive Main Effect interaction (AMMI) models
- AMMI + BART = AMBARTI
- Simulation (AMMI and AMBARTI)
- Next steps
- Appendix

Additive Main effects and Multiplicative Interactions (AMMI)

Linear–bilinear models are frequently used to analyse two-way data such as genotype-by-environment data.

An example of this class of models is the AMMI model:

$$y_{ij} = \mu + \alpha_i + \beta_j + \sum_{q=1}^{Q} \lambda_q \gamma_{iq} \delta_{jq} + \epsilon_{ij}, \quad \epsilon_{ij} \sim \mathcal{N}\left(0, \tau^{-1}\right),$$

where α_i is the effect of genotype and β the effect of environment.

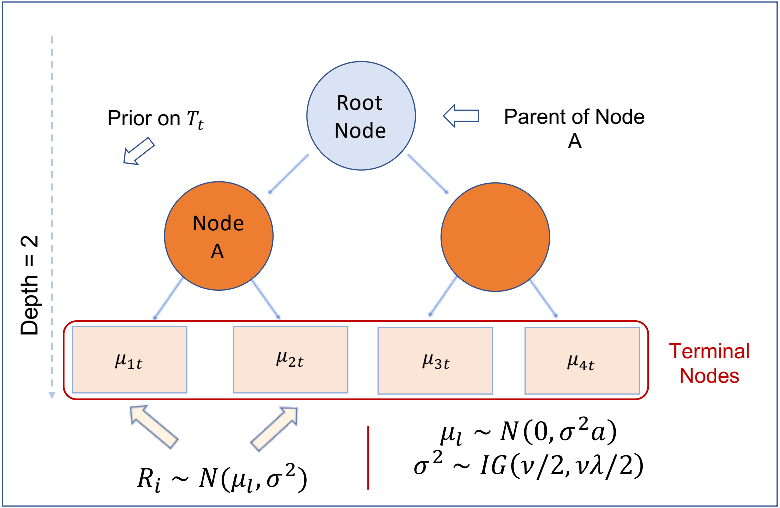
Additive Main effects and Multiplicative Interactions (AMMI)

The following priors are assumed in its Bayesian version (Josse et al, JABES, 2014):

$$
\begin{aligned}
\mu &\sim \mathrm{N}\left(m, s_\mu^2\right), \\
\alpha_i &\sim \mathrm{N}\left(0, s_g^2\right), \\
\beta_j &\sim \mathrm{N}\left(0, s_e^2\right), \\
(\lambda_q)_{q=1,\ldots,Q} &\sim \text{ ordered sample of } Q \text{ independent } \mathrm{N}^+\left(0, s_\lambda^2\right), \\
\gamma_{1q} &\sim \mathrm{N}^+(0,1) \quad \text{ for } q = 1, \ldots, Q, \\
\gamma_{iq} &\sim \mathrm{N}(0,1) \quad \text{ for } i > 1 \text{ and } q = 1, \ldots, Q, \\
\delta_{jq} &\sim \mathrm{N}(0,1) \quad \text{ for } j \geq 1 \text{ and } q = 1, \ldots, Q, \\
\sigma_E &\sim \mathrm{U}\left(0, S_{\mathrm{ME}}\right).
\end{aligned}
$$

Additive Main Effect Bayesian Additive Regression Tree Interaction models (AMBARTI)

BART



Prior on T_t
Root Node
Parent of Node A
Node A
Depth = 2
μ_{1t}
μ_{2t}
μ_{3t}
μ_{4t}
Terminal Nodes
$R_i \sim N(\mu_l, \sigma^2)$
$\mu_l \sim N(0, \sigma^2 a)$
$\sigma^2 \sim IG(\nu/2, \nu\lambda/2)$

AMMI + BART

BART is a flexible tree-based method that can be used for predicting when there are interactions and non-linear relationships.

$$y_{ij}|\mathbf{x}_{ij}, \mathcal{T}, \mathcal{M}, \Theta, \sigma^2 \sim \mathrm{N}\left(\alpha_i + \beta_j + \sum_{t=1}^{T} h(\mathbf{x}_{ij}, \mathcal{M}_t, \mathcal{T}_t), \sigma^2\right),$$

where y_{ij} is the yield for genotype i and environment j, and α_i and β_j are the genotype and environment effects, respectively.

$$\begin{aligned}
\mu_{t\ell}|\mathcal{T}_t &\sim \mathrm{N}(\mu_\mu = 0, \sigma_\mu^2), \\
\alpha_i|\mathcal{T}_t &\sim \mathrm{N}(\mu_g, \sigma_g^2), \\
\beta_j|\mathcal{T}_t &\sim \mathrm{N}(\mu_e, \sigma_e^2), \\
\sigma_g^2 &\sim \mathrm{IG}(a_g, b_g), \\
\sigma_e^2 &\sim \mathrm{IG}(a_e, b_e), \\
\sigma^2 &\sim \mathrm{IG}(a, b).
\end{aligned}$$

Interesting fact. . .

Bayesian AMMI - Postprocessing (Josse et al, 2014)

Recall that

$$\mu_{ij} = \hat{y}_{ij} = \hat{\mu} + \hat{\alpha}_i + \hat{\beta}_j + \sum_{q=1}^{Q} \hat{\lambda}_q \hat{\gamma}_{iq} \hat{\delta}_{jq}.$$

"This means that, concretely, S matrices of size $I \times J$ are available as draws from the posterior distributions of the μ_{ij}. Thus, it is possible to apply a postprocessing on each matrix $(s = 1, ..., S)$ performing the classical procedure (in accordance with the chosen constraints): each matrix is centered by row and by column, and an SVD is applied on the resulting matrix. Consequently, for each s, new parameters (μ, α, β, γ, δ, λ_q) meeting the constraints are available. Consequently, draws in the posterior distribution of the parameters (taking the S new values) are available. Such a postprocessing makes it easier to interpret the results."

Simulation: AMMI scenarios (20 combinations)

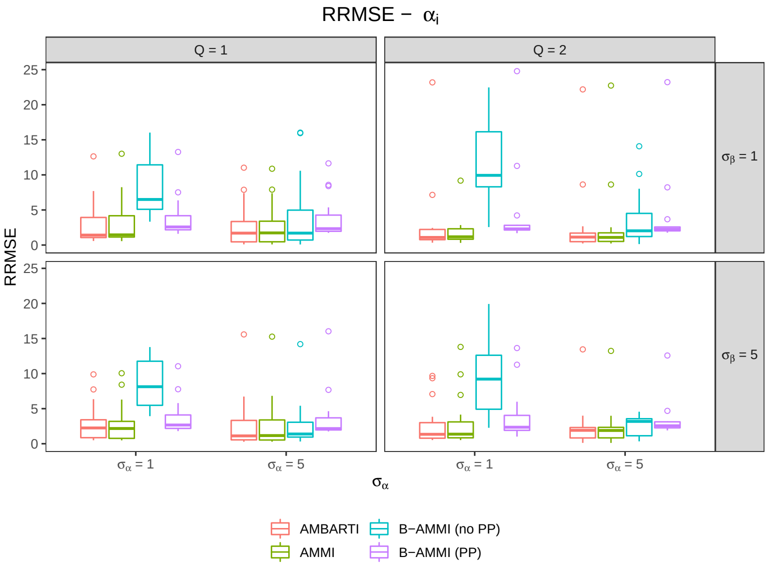
We consider the following setting to generate a set of simulated data sets:

$$y_{ij} = \mu + \alpha_i + \beta_j + \sum_{q=1}^{Q} \lambda_q \gamma_{iq} \delta_{jq} + \epsilon_{ij}, \quad \epsilon_{ij} \sim \mathcal{N}\left(0, \tau^{-1}\right),$$

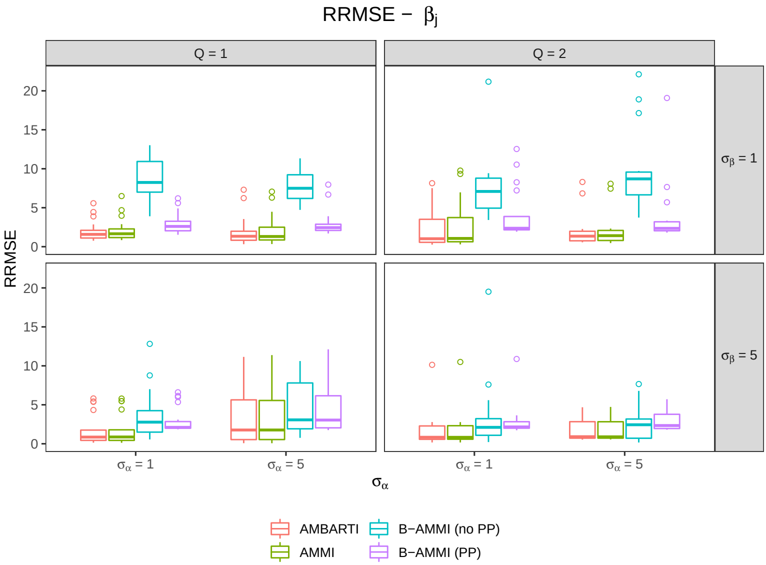
where

- $\mu = 100$, $\tau = 1$.
- $I = J = 10$ (without repetitions).
- $\beta_j \sim \mathrm{N}(0, s_e)$, with $s_e = c(1, 5)$.
- $\alpha_i \sim \mathrm{N}(0, s_g)$, with $s_g = c(1, 5)$.
- $Q = c(1, 2, 3)$, with $\lambda = c(8, 12, [8, 12], [10, 12], [8, 10, 12])$.
- We used RMSE (Root Mean Squared Error) and RRMSE (Relative Root Mean Squared Error).

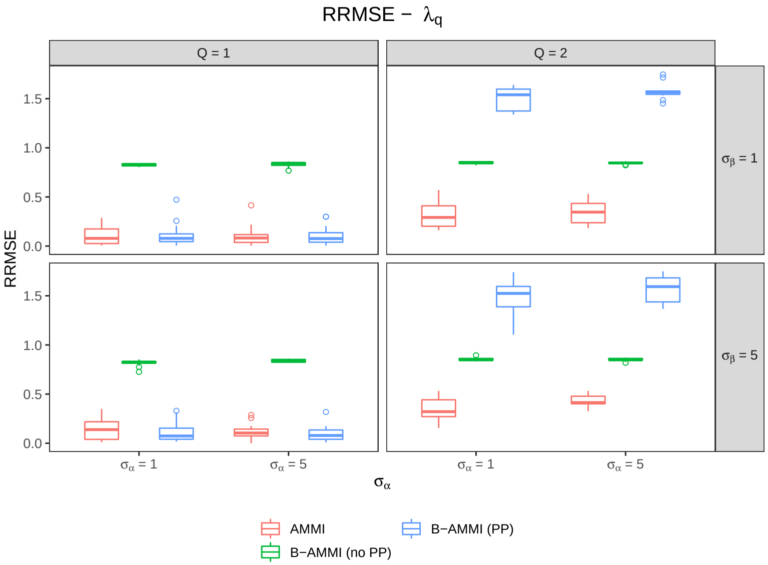
Simulation AMMI ($y_{ij} = \mu + \alpha_i + \beta_j + \sum_{q=1}^{Q} \lambda_q \gamma_{iq} \delta_{jq}$)



Simulation AMMI ($y_{ij} = \mu + \alpha_i + \beta_j + \sum_{q=1}^{Q} \lambda_q \gamma_{iq} \delta_{jq}$)



Simulation AMMI ($y_{ij} = \mu + \alpha_i + \beta_j + \sum_{q=1}^{Q} \lambda_q \gamma_{iq} \delta_{jq}$)



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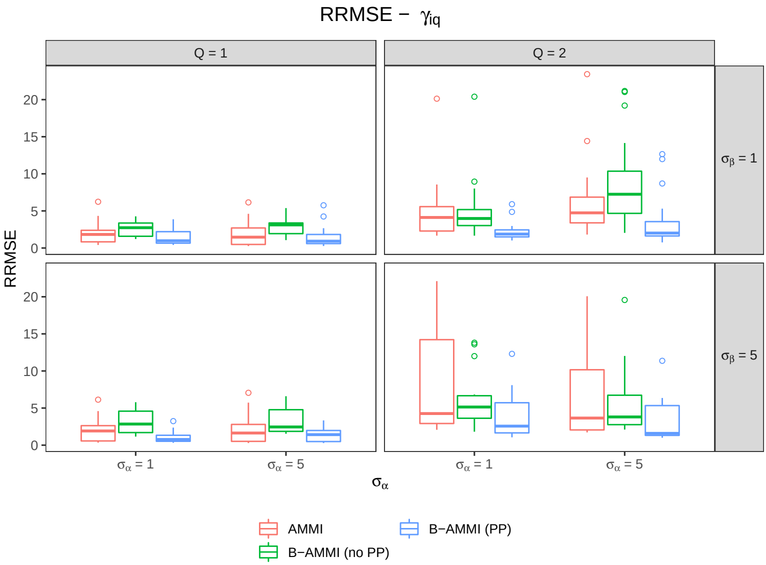

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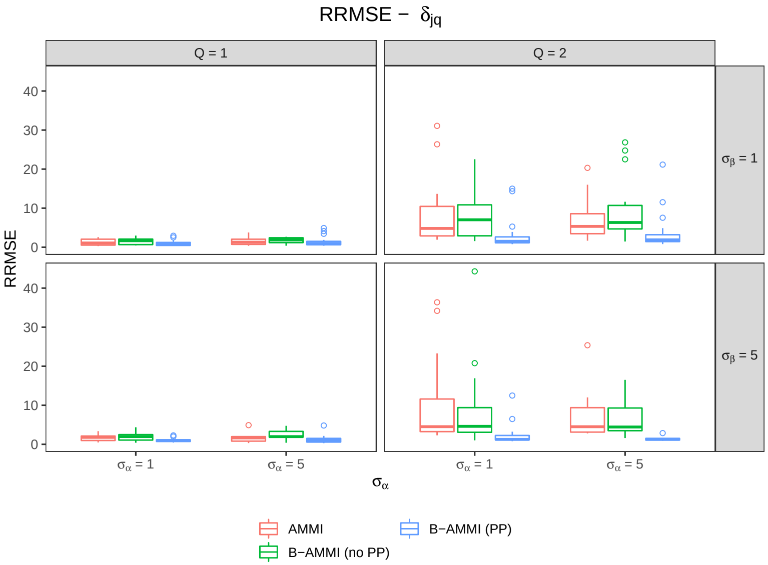

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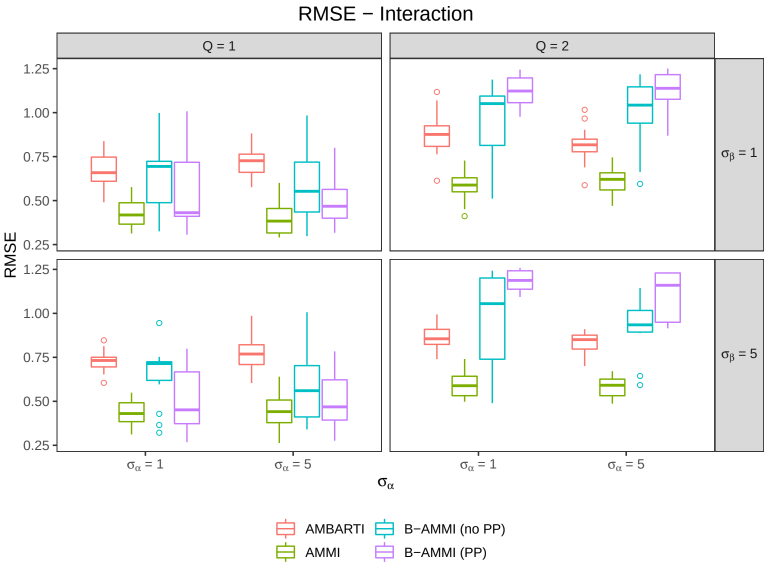

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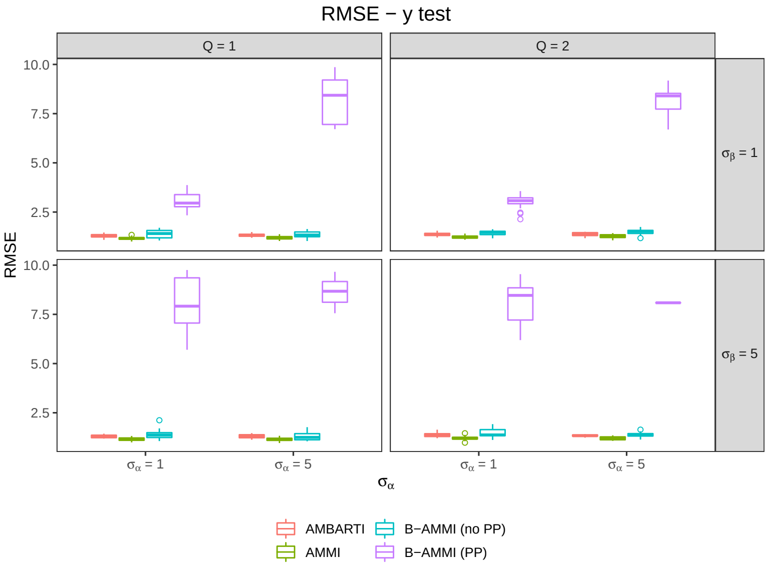

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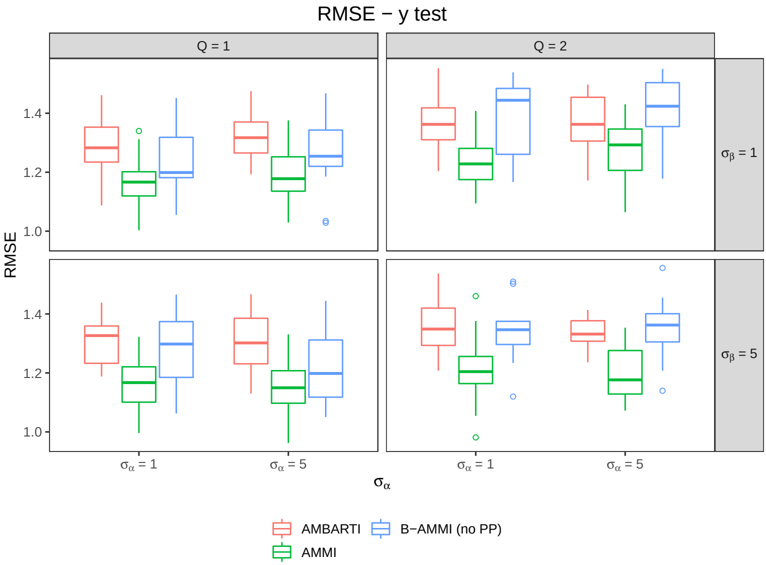


Simulation: AMBARTI scenarios (4 combinations)

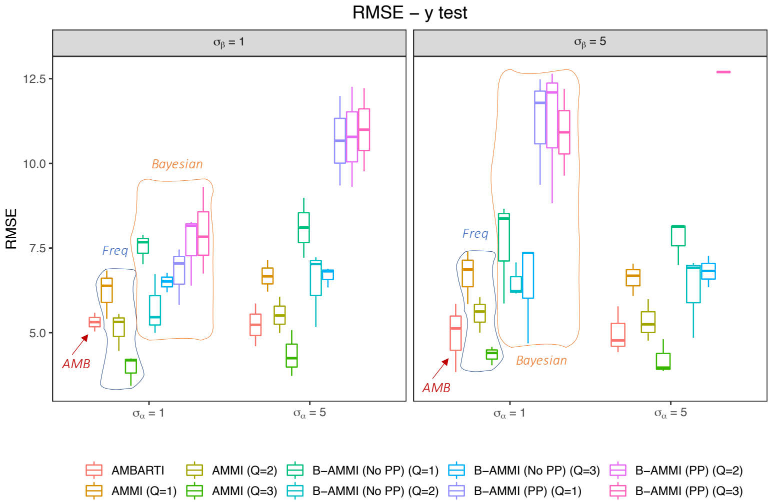
We consider the following setting to generate a set of simulated data sets:

$$y_{ij}|\mathbf{x}_{ij}, \mathcal{T}, \mathcal{M}, \Theta, \sigma^2 \sim \mathrm{N}\left(\alpha_i + \beta_j + \sum_{t=1}^{T} h(\mathbf{x}_{ij}, \mathcal{M}_t, \mathcal{T}_t), \sigma^2\right),$$

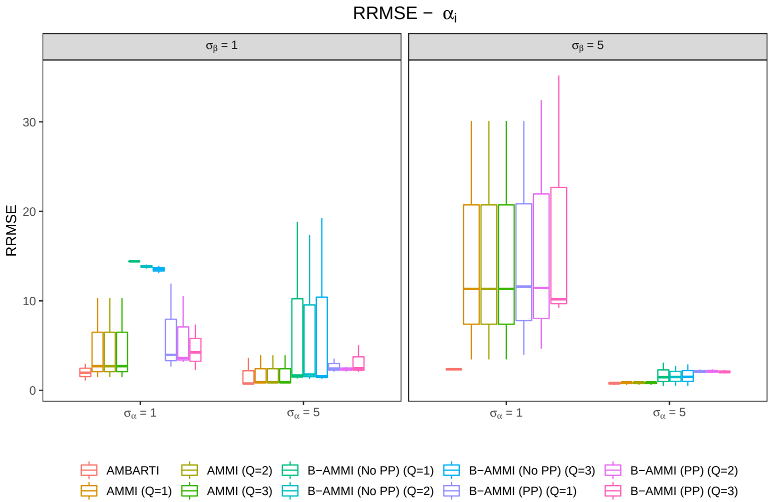
where y_{ij} is the yield for genotype i and environment j, and α_i and β_j are the genotype and environment effects, respectively.

- $\sigma^2 = 1,\ T = 200.$
- $I = J = 10$ (without repetitions).
- $\mu_{t\ell}|\mathcal{T}_t \sim \mathrm{N}(\mu_\mu = 0, \sigma^2_\mu = 3),$
- $\beta_j \sim \mathrm{N}(0, s_e)$, with $s_e = c(1, 5)$.
- $\alpha_i \sim \mathrm{N}(0, s_g)$, with $s_g = c(1, 5)$.

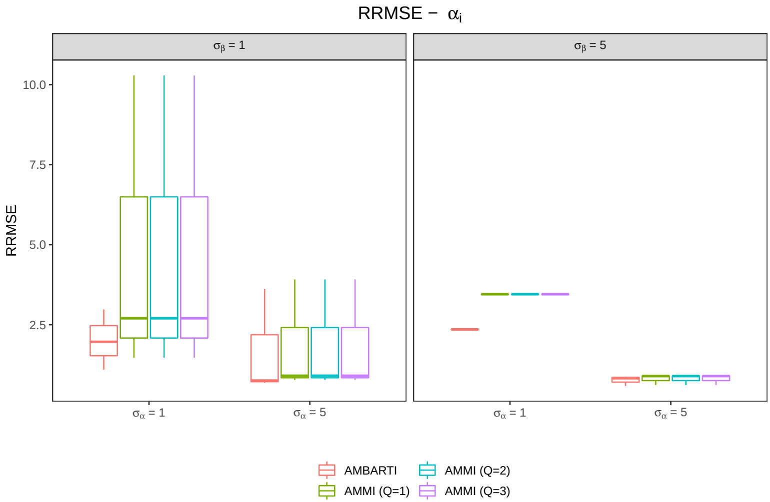
Simulation AMBARTI ($y_{ij} = \alpha_i + \beta_j + \sum_{t=1}^{T} h(\mathbf{x}_{ij}, \mathcal{M}_t, \mathcal{T}_t)$)



Simulation AMBARTI ($y_{ij} = \alpha_i + \beta_j + \sum_{t=1}^{T} h(\mathbf{x}_{ij}, \mathcal{M}_t, \mathcal{T}_t)$)



Simulation AMBARTI ($y_{ij} = \alpha_i + \beta_j + \sum_{t=1}^{T} h(\mathbf{x}_{ij}, \mathcal{M}_t, \mathcal{T}_t)$)



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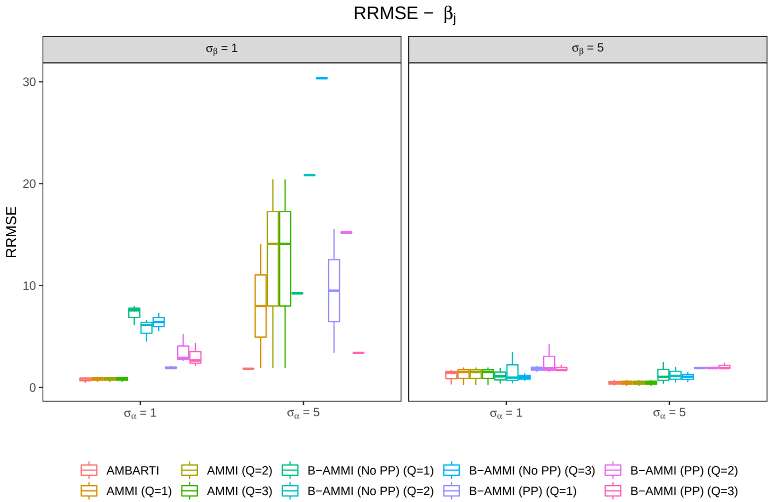
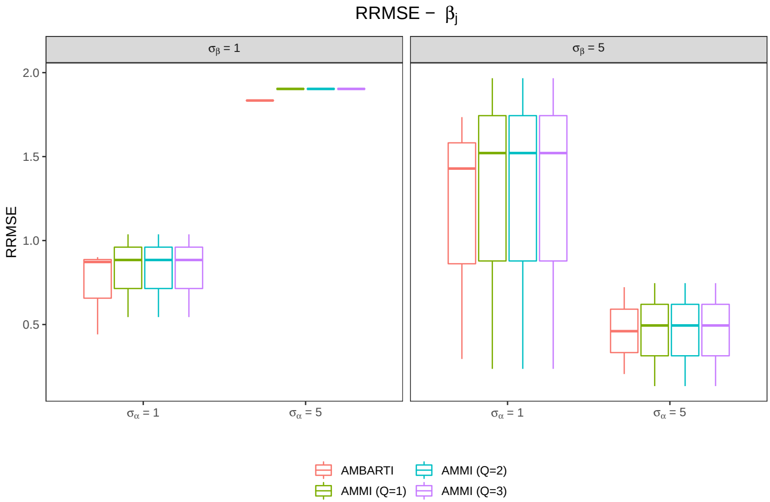


Simulation AMBARTI ($y_{ij} = \alpha_i + \beta_j + \sum_{t=1}^{T} h(\mathbf{x}_{ij}, \mathcal{M}_t, \mathcal{T}_t)$)



Next steps

1. Adapt our implementation to simulate large (> 15) I and J. We have another idea...
2. Perform more simulations considering large I and J.
3. Analyse real data sets.

That's all, folks! Thank you!

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Science Foundation Ireland sfi For what's next

Appendix

Simulation: full model (4 combinations)

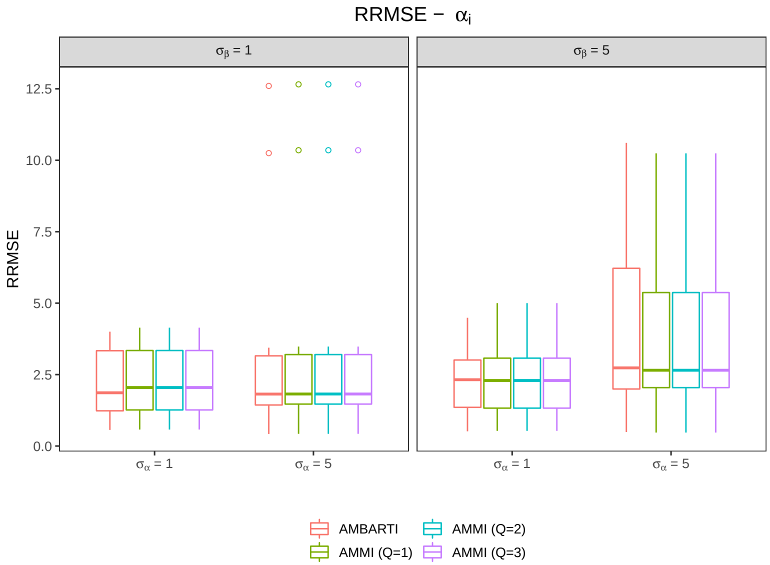
We consider the following setting to generate a set of simulated data sets:

$$y_{ij} = \mu + \alpha_i + \beta_j + \alpha_i \times \beta_j + \epsilon_{ij}, \quad \epsilon_{ij} \sim \mathcal{N}\left(0, \tau^{-1}\right),$$

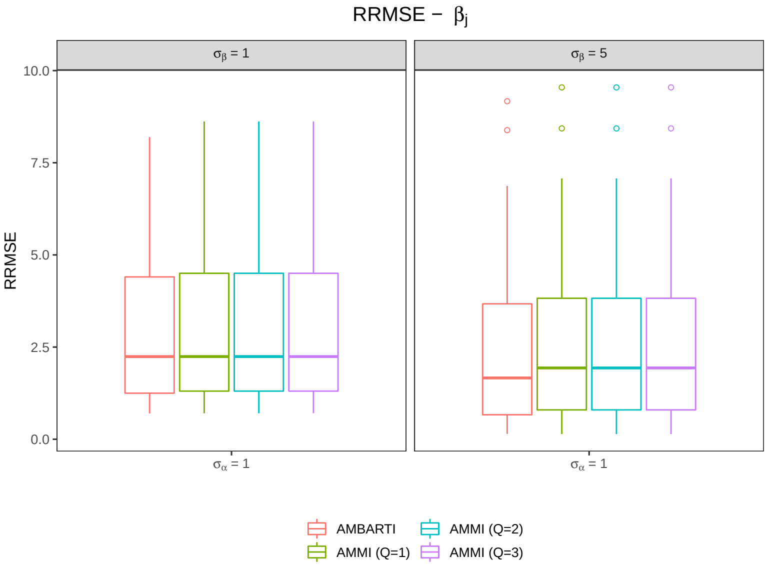
where

- $\mu = 100$, $\tau = 1$.
- $I = J = 10$ (without repetitions).
- $\beta_j \sim \mathrm{N}(0, s_e)$, with $s_e = c(1, 5)$.
- $\alpha_i \sim \mathrm{N}(0, s_g)$, with $s_g = c(1, 5)$.

Simulation full model ($y_{ij} = \alpha_i + \beta_j + \alpha_i \times \beta_j$)



Simulation full model ($y_{ij} = \alpha_i + \beta_j + \alpha_i \times \beta_j$)



Simulation full model ($y_{ij} = \alpha_i + \beta_j + \alpha_i \times \beta_j$)