

ivd: An R Package for Individual Variance Detection using Spike-and-Slab Priors

Summary

Research in fields such as psychology and education typically focus on average performance of unit (e.g., a student or a school), but the *consistency* or variability of that performance can also carry important information about the units of study [@raudenbush1987jes, @leckie_mixed-effects_2023, rast_modeling_2012]. Standard statistical approaches often treat within-cluster variability as a nuisance parameter or assume it is constant across groups. The `ivd` package implements the Spike-and-Slab Mixed-Effects Location Scale Model (SS-MELSM) as a Bayesian framework for explicitly modeling and detecting heterogeneous residual variances.

`ivd` enables users to estimate models for both means (location) and within-cluster variability (scale) simultaneously. It uses a spike-and-slab prior on the scale random effects as a probabilistic selection tool, distinguishing clusters with typical variability (shrunk to the population mean, the spike) from those with atypical variability (the slab) [@mitchell_bayesian_1988]. This approach identifies individual units that differ significantly from the norm, such as schools with unusually consistent or inconsistent test scores, or patients with highly stable or unstable symptoms [@leckie_modeling_2014].

Statement of Need

Standard mixed-effects models partition variance into between-group and within-group components, typically assuming the within-group residual variance (σ^2) is homogeneous across all groups [@raudenbush_hierarchical_2002]. While Mixed-Effects Location Scale Models (MELSM) relax this assumption by allowing σ^2 to vary as a function of covariates and random effects [@hedeker_application_2008], they do not inherently provide a decision rule for identifying *which* specific units deviate significantly from the average consistency.

In `ivd`, MELSMs are extended through the SS-MELSM approach, which computes a Posterior Inclusion Probability (PIP) for each cluster's scale random effect. The model simultaneously estimates fixed and random effects for both

location and scale. For the scale, the residual standard deviation σ_{ij} is modeled as a log-linear function of covariates. The scale intercept's random effects are subject to a spike-and-slab prior, with a binary indicator δ_{jk} determining inclusion. A high PIP for δ_j provides strong evidence that the unit belongs to the slab distribution, corresponding to a larger Bayes factor for including the k th random effect for the j th school [@rodriguez_who_2022, @williams_putting_2021]. PIPs are calculated as the proportion of MCMC samples where $\delta_{jk} = 1$.

The package provides a user-friendly interface for NIMBLE [@de_valpine_programming_2017], enabling users to fit SS-MELSMs with standard R formula syntax, without custom BUGS or NIMBLE code. Since languages like Stan do not directly support discrete parameters, implementing these models can be challenging for applied researchers. The main function, `ivd()`, accepts two formulas: `location_formula` for the mean structure and `scale_formula` for within-cluster variance. `ivd` also uses the future package [@bengtsson_2021] to enable parallel processing of MCMC chains.

Analysis and Visualization

The `summary()` function returns the fixed effects for both location and scale, along with the PIPs for the random scale effects. Convergence of each estimate is summarised with computation of \hat{R} , and estimation efficiency by the effective sample size [@vehtariRankNormalization2021].

To help detect atypical units, the package offers several visualization methods, specified by the `type` argument in the `plot()` function. The default, `pip`, highlights units exceeding a set probability threshold (default 0.75). `funnel` shows the relationship between PIP and estimated within-cluster standard deviation, while `outcome` displays the interaction between average performance and consistency. For MCMC convergence diagnostics, the `codaplot()` function provides trace and density plots for selected parameters.

Model Comparison

Model comparison is supported using the Widely Applicable Information Criterion (WAIC), which is computed during estimation by default (`WAIC = TRUE`). Additionally, `ivd` stores the pointwise log-likelihood matrix, allowing compatibility with the `loo` package [@loo] for predictive accuracy assessment using Pareto smoothed importance sampling Leave-one-out cross-validation (PSIS-LOO) [@vehtari_practical_2017].

Usage Example

The following example demonstrates the workflow with the `saeb` dataset included in the package. Here, students' mathematics proficiency is modeled within

schools, predicting both mean achievement and residual variability as functions of student and school socioeconomic status (SES).

```
library(ivd)
library(data.table)

## Prepare data: separate within- and between-school SES effects
data(saeb)
school_ses <- saeb[, .(school_ses = mean(student_ses, na.rm = TRUE)), by = school_id]
saeb <- saeb[school_ses, on = "school_id"]
saeb$student_ses <- saeb$student_ses - saeb$school_ses
saeb$school_ses <- c(scale(saeb$school_ses, scale = FALSE))

## Fit the Spike-and-Slab MELSM
model <- ivd(
  location_formula = math_proficiency ~ student_ses * school_ses + (1|school_id),
  scale_formula     = ~ student_ses * school_ses + (1|school_id),
  data              = saeb,
  niter             = 2000,
  nburnin          = 1000,
  WAIC              = TRUE,
  workers           = 2
)

## Summarize results
summary(model)

## Visualizations
## Identify schools with unusual variability (PIP > 0.75)
plot(model, type = "pip")

## Inspect the relationship between PIP and within-cluster SD
plot(model, type = "funnel")

## Check convergence for the intercept
codaplot(model, parameters = "Intc")
```

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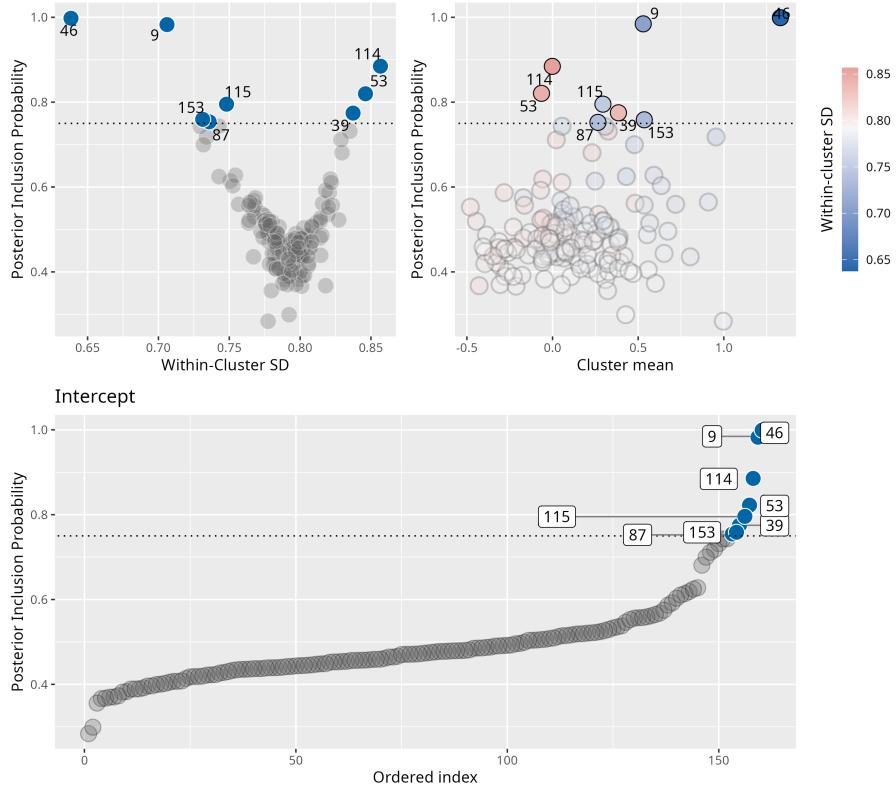


Figure 1: Scatter plots show posterior inclusion probability (PIP) for the scale random intercept. Panel A plots PIP against the estimated within-cluster standard deviation (SD), with the y-axis as PIP and the x-axis as within-cluster SD. Panel B plots PIP against estimated math achievement scores, with the x-axis showing math achievement scores. Panel C shows PIPs for each school, sorted on the horizontal axis. The dotted horizontal line denotes the PIP threshold of 0.75.