

# Package: imv (via r-universe)

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**Title** Model Comparison via the 'InterModel Vigorish' ('IMV')

**Version** 0.3

**Description** Computes the 'InterModel Vigorish' ('IMV'), a metric for comparing the predictive accuracy of two models for binary outcomes. The 'IMV' is derived from the expected value of a bettor using one model's predicted probabilities against those of a competing model, and is estimated via k-fold cross-validation. Methods are provided for generalized linear models, mixed-effects models ('lme4'), and item response theory models ('mirt'). See <[doi:10.1371/journal.pone.0316491](https://doi.org/10.1371/journal.pone.0316491)>.

**Depends** R (>= 3.5.0)

**Suggests** lme4, mirt, testthat (>= 3.0.0)

**License** MIT + file LICENSE

**RoxygenNote** 7.3.1

**Language** en-US

**NeedsCompilation** no

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imv *Cross-validated IMV for comparing two models*

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### Description

S3 generic that computes the InterModel Vigorish (IMV) between a baseline model `m0` and an enhanced model `m1` via `k`-fold cross-validation. For each fold, both models are refit on the training partition and evaluated on the held-out partition; the IMV is computed from those out-of-fold predictions.

`imv.default` provides an escape hatch for unsupported model types via `predict_fn`: in that case the original fitted models are used (without refitting) to obtain predictions on each test fold.

### Usage

```
imv(m0, m1, ...)

## S3 method for class 'glm'
imv(m0, m1, data = NULL, nfold = 4, predict_fn = NULL, y = NULL, ...)

## Default S3 method:
imv(m0, m1, data = NULL, nfold = 4, predict_fn = NULL, y = NULL, ...)
```

### Arguments

<code>m0</code>	Baseline model.
<code>m1</code>	Enhanced model.
<code>data</code>	Data frame used for cross-validation. May be omitted for model classes that store training data internally (e.g., objects from <code>glm()</code> or <code>lme4::glmer()</code> ).
<code>nfold</code>	Number of cross-validation folds (default 4).
<code>predict_fn</code>	Optional function with signature <code>function(model, newdata)</code> returning a numeric vector of predicted probabilities. When supplied, <code>imv.default</code> is invoked and models are not refit per fold.
<code>y</code>	Character string naming the binary outcome column in <code>data</code> . Required when <code>predict_fn</code> is supplied; otherwise inferred from the model formula.
<code>...</code>	Additional arguments passed to methods.

### Value

A named list with four elements:

**folds**  Numeric vector of per-fold IMV values (length `nfold`).

**mean**  Mean IMV across folds.

**sd**  Standard deviation of per-fold IMVs.

**ci**  Named numeric vector of length 2: a 95% interval computed as  $\text{mean} \pm 1.96 * (\text{sd} / \sqrt{\text{nfold}})$ .

## References

Domingue, B. W., Rahal, C., Faul, J., Freese, J., Kanopka, K., Rigos, A., Stenhaug, B., & Tripathi, A. S. (2025). The InterModel Vigorish (IMV) as a flexible and portable approach for quantifying predictive accuracy with binary outcomes. *PloS one*, 20(3), e0316491. <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0316491>

## See Also

[imv.binary](#), [imv.glmerMod](#), [imv.SingleGroupClass](#)

## Examples

```
## --- glm -----
set.seed(1)
x <- rnorm(100)
y <- rbinom(100, 1, plogis(x))
df <- data.frame(x = x, y = y)
m0 <- glm(y ~ 1, df, family = "binomial")
m1 <- glm(y ~ x, df, family = "binomial")
result <- imv(m0, m1, nfold = 2)
result$mean
result$ci

## --- custom predict_fn (escape hatch for unsupported model types) ---
pfn <- function(model, newdata) predict(model, newdata, type = "response")
result <- imv(m0, m1, data = df, y = "y", predict_fn = pfn, nfold = 2)
result$mean

## --- glmer (requires lme4) -----
if (requireNamespace("lme4", quietly = TRUE)) {
  data(sleepstudy, package = "lme4")
  sleepstudy$slow <- as.integer(sleepstudy$Reaction > 300)
  m0 <- lme4::glmer(slow ~ (1 | Subject), sleepstudy, family = binomial)
  m1 <- lme4::glmer(slow ~ Days + (1 | Subject), sleepstudy, family = binomial)
  imv(m0, m1)
}

## --- mirt (requires mirt) -----
if (requireNamespace("mirt", quietly = TRUE)) {
  resp <- mirt::expand.table(mirt::LSAT7)
  mod1 <- mirt::mirt(resp, 1, "Rasch", verbose = FALSE) # 1PL
  mod2 <- mirt::mirt(resp, 1, verbose = FALSE) # 2PL
  imv(mod1, mod2)
}
```

---

imv.binary

*Compute IMV for binary outcomes*


---

### Description

Computes the InterModel Vigorish (IMV) comparing baseline predictions  $p_1$  to enhanced predictions  $p_2$  for binary outcomes  $y$ . A positive value indicates that  $p_2$  predicts better than  $p_1$  out of sample; a negative value indicates the reverse.

### Usage

```
## S3 method for class 'binary'
imv(m0, m1, p2, sigma = 1e-04, ...)
```

### Arguments

<code>m0</code>	Integer or numeric vector of binary outcomes (0/1), preferably from a held-out test set.
<code>m1</code>	Numeric vector of baseline predicted probabilities (same length as <code>m0</code> ).
<code>p2</code>	Numeric vector of enhanced predicted probabilities (same length as <code>m0</code> ).
<code>sigma</code>	Small positive constant used to clip probabilities away from 0 and 1 to avoid numerical issues. Default <code>1e-4</code> .
<code>...</code>	Currently unused. Accepted for consistency with the <code>imv</code> generic.

### Value

A scalar IMV value. Positive values favour  $p_2$ ; negative values favour  $p_1$ .

### References

Domingue, B. W., Rahal, C., Faul, J., Freese, J., Kanopka, K., Rigos, A., Stenhaug, B., & Tripathi, A. S. (2025). The InterModel Vigorish (IMV) as a flexible and portable approach for quantifying predictive accuracy with binary outcomes. *PLoS one*, 20(3), e0316491. <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0316491>

### See Also

[imv](#)

### Examples

```
set.seed(1)
x <- rnorm(1000)
y <- rbinom(length(x), 1, plogis(x))
df <- data.frame(x = x, y = y)
m <- glm(y ~ x, df, family = "binomial")
pr <- predict(m, data.frame(x = x), type = "response")
imv.binary(y, mean(y), pr)
```

imv.glmMod

*Cross-validated IMV for binomial mixed-effects models***Description**

Computes the InterModel Vigorish (IMV) for binomial mixed-effects models fit with `lme4::glmer()` via k-fold cross-validation. Both models are refit on each training fold; predictions on the held-out fold use `allow.new.levels = TRUE` to handle random-effect levels not seen during training.

Only binomial family models are supported.

**Usage**

```
## S3 method for class 'glmMod'
imv(m0, m1, data = NULL, nfold = 4, predict_fn = NULL, y = NULL, ...)
```

**Arguments**

<code>m0</code>	A <code>glmMod</code> object (binomial family) serving as the baseline model.
<code>m1</code>	A <code>glmMod</code> object (binomial family) serving as the enhanced model. Must be fit to the same data as <code>m0</code> .
<code>data</code>	Optional data frame. If <code>NULL</code> , extracted from <code>model.frame(m1)</code> .
<code>nfold</code>	Number of cross-validation folds. Default 4.
<code>predict_fn</code>	Ignored for this method.
<code>y</code>	Ignored for this method; the outcome is inferred from the model formula.
<code>...</code>	Currently unused. Accepted for consistency with the generic.

**Value**

A named list with four elements:

**folds**  Numeric vector of per-fold IMV values (length `nfold`).

**mean**  Mean IMV across folds.

**sd**  Standard deviation of per-fold IMVs.

**ci**  Named numeric vector of length 2: a 95% interval computed as  $\text{mean} \pm 1.96 * (\text{sd} / \sqrt{\text{nfold}})$ .

**References**

Domingue, B. W., Rahal, C., Faul, J., Freese, J., Kanopka, K., Rigos, A., Stenhaug, B., & Tripathi, A. S. (2025). The InterModel Vigorish (IMV) as a flexible and portable approach for quantifying predictive accuracy with binary outcomes. *PLoS one*, 20(3), e0316491. <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0316491>

**See Also**

[imv](#), [imv.binary](#)

**Examples**

```

if (requireNamespace("lme4", quietly = TRUE)) {
  data(sleepstudy, package = "lme4")
  sleepstudy$slow <- as.integer(sleepstudy$Reaction > 300)

  m0 <- lme4::glmer(slow ~ (1 | Subject), sleepstudy, family = binomial)
  m1 <- lme4::glmer(slow ~ Days + (1 | Subject), sleepstudy, family = binomial)
  imv(m0, m1)
}

```

---

imv.SingleGroupClass *Cross-validated IMV for mirt IRT models*

---

**Description**

Computes the InterModel Vigorish (IMV) for item response theory models fit with the `mirt` package via response-level  $k$ -fold cross-validation. Fold splits are at the individual response level: each held-out observation is a single person-by-item pair, and ability is estimated from the remaining responses for that person.

When a single model is supplied ( $m1 = \text{NULL}$ ), predictions from  $m0$  are compared to item-level prevalence rates (the null model). When two models are supplied,  $m0$  serves as the baseline and  $m1$  as the enhanced model.

Only dichotomous response models are supported.

**Usage**

```

## S3 method for class 'SingleGroupClass'
imv(m0, m1 = NULL, data = NULL, nfold = 5,
    predict_fn = NULL, y = NULL,
    fscores.options = list(method = "EAP"),
    whole.matrix = TRUE,
    remove.nonvarying.items = TRUE,
    remove.allNA.rows = TRUE, ...)

```

**Arguments**

<code>m0</code>	A <code>SingleGroupClass</code> model object returned by <code>mirt::mirt()</code> .
<code>m1</code>	An optional second <code>SingleGroupClass</code> model fit to the same data as <code>m0</code> . When <code>NULL</code> , <code>m0</code> is compared to item prevalence.
<code>data</code>	Not used for <code>mirt</code> models. Accepted for consistency with the generic.
<code>nfold</code>	Number of cross-validation folds (default 5).
<code>predict_fn</code>	Not used for <code>mirt</code> models. Accepted for consistency with the generic.
<code>y</code>	Not used for <code>mirt</code> models. Accepted for consistency with the generic.
<code>fscores.options</code>	Named list of additional arguments passed to <code>mirt::fscores()</code> . Default is <code>list(method = "EAP")</code> .

<code>whole.matrix</code>	Logical (default TRUE). When TRUE, fold assignment is repeated until every training partition contains all participants and all items, ensuring that models can be re-identified on each fold. Ignored when <code>m1 = NULL</code> .
<code>remove.nonvarying.items</code>	Logical (default TRUE). Drop items with no response variance from each training fold's response matrix.
<code>remove.allNA.rows</code>	Logical (default TRUE). Drop persons whose responses are entirely missing from a training fold's response matrix.
<code>...</code>	Currently unused.

### Value

A named list with four elements:

**folds**  Numeric vector of per-fold IMV values (length `nfold`).

**mean**  Mean IMV across folds.

**sd**  Standard deviation of per-fold IMVs.

**ci**  Named numeric vector of length 2: a 95% interval computed as  $\text{mean} \pm 1.96 * (\text{sd} / \sqrt{\text{nfold}})$ .

### References

Domingue, B. W., Rahal, C., Faul, J., Freese, J., Kanopka, K., Rigos, A., Stenhaug, B., & Tripathi, A. S. (2025). The InterModel Vigorish (IMV) as a flexible and portable approach for quantifying predictive accuracy with binary outcomes. *PloS one*, 20(3), e0316491. <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0316491>

### See Also

[imv](#), [imv.binary](#)

### Examples

```
if (requireNamespace("mirt", quietly = TRUE)) {
  set.seed(1)
  resp <- mirt::expand.table(mirt::LSAT7)

  # Single model vs prevalence baseline
  mod1 <- mirt::mirt(resp, 1, "Rasch", verbose = FALSE)
  imv(mod1)

  # Two models
  mod2 <- mirt::mirt(resp, 1, verbose = FALSE)
  imv(mod1, mod2)

  # Priors specified as a variable are handled correctly
  my_prior <- list(a1 = c(0, 1, 0.25, 3))
  mod3 <- mirt::mirt(resp, 1, prior.list = my_prior, verbose = FALSE)
  imv(mod3)
```

}

---

`imv0glm`*IMV for a GLM compared to a prevalence baseline*

---

## Description

Legacy function. Computes the IMV for a fitted `glm` model against a null model (intercept only) via `k`-fold cross-validation. Both the full and null models are refit on each training fold and evaluated on the held-out fold.

For new code, prefer `imv(m0, m1)` with an explicit null model as `m0`.

## Usage

```
imv0glm(m, nfold = 5)
```

## Arguments

<code>m</code>	A <code>glm</code> object fit with a binomial family. Must have been called with an explicit data argument.
<code>nfold</code>	Number of cross-validation folds. Default 5.

## Value

A numeric vector of length `nfold` containing the per-fold IMV values.

## References

Domingue, B. W., Rahal, C., Faul, J., Freese, J., Kanopka, K., Rigos, A., Stenhaug, B., & Tripathi, A. S. (2025). The InterModel Vigorish (IMV) as a flexible and portable approach for quantifying predictive accuracy with binary outcomes. *PLoS one*, 20(3), e0316491. <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0316491>

## See Also

[imv](#), [imv.binary](#)

## Examples

```
set.seed(1)
x <- rnorm(1000)
y <- rbinom(length(x), 1, plogis(x))
df <- data.frame(x = x, y = y)
m <- glm(y ~ x, df, family = "binomial")
imv0glm(m)
```

---

`imvglm.rmvar`*IMV for a GLM versus the same model with one variable removed*

---

### Description

Legacy function. Computes the IMV comparing a full `glm` model to a reduced model with `var.nm` dropped from the formula, via `k`-fold cross-validation. Both models are refit on each training fold and evaluated on the held-out fold.

For new code, prefer constructing both models explicitly and calling `imv(m0, m1)`.

### Usage

```
imvglm.rmvar(m, nfold = 5, var.nm)
```

### Arguments

<code>m</code>	A <code>glm</code> object fit with a binomial family. Must have been called with an explicit data argument.
<code>nfold</code>	Number of cross-validation folds. Default 5.
<code>var.nm</code>	Character string naming the variable to remove from the formula. Must match exactly the term as it appears in the original <code>glm</code> call.

### Value

A numeric vector of length `nfold` containing the per-fold IMV values. The reduced model (without `var.nm`) serves as the baseline; the full model serves as the enhanced model. A positive mean indicates that `var.nm` improves out-of-sample prediction.

### References

Domingue, B. W., Rahal, C., Faul, J., Freese, J., Kanopka, K., Rigos, A., Stenhaus, B., & Tripathi, A. S. (2025). The InterModel Vigorish (IMV) as a flexible and portable approach for quantifying predictive accuracy with binary outcomes. *PLoS one*, 20(3), e0316491. <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0316491>

### See Also

[imv](#), [imv.binary](#)

### Examples

```
set.seed(1)
x <- rnorm(1000)
z <- rnorm(1000)
y <- rbinom(length(x), 1, plogis(x))
df <- data.frame(x = x, z = z, y = y)
m <- glm(y ~ x + z, df, family = "binomial")
imvglm.rmvar(m, var.nm = "z")
```

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