Recommender Systems for Tailored Testing (R Tutorial)

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Contents

Purpose. This tutorial shows how to use collaborative filtering with **matrix factorization (Funk SVD)** to predict item *relevance ratings* in a longitudinal assessment context.
Data. We use **simulated** participant × item ratings (1-4 scale). No real or operational data are used.

Setup

```r
set.seed(2025)

# Core packages
library("recommenderlab")
library("Matrix")
library("ggplot2")
```

If `recommenderlab` is not installed:

```r
install.packages("recommenderlab")
```

Why Funk SVD? In sparse ratings matrices (many missing values), matrix factorization learns low-rank latent factors for participants and items, allowing us to estimate unobserved ratings (i.e., how relevant a new item is likely to feel).

Simulate a participant × item relevance matrix

We'll simulate:

- 600 participants (rows)
- 200 items (cols)
- 1-4 relevance ratings, with ~70% missingness (no participants see all items)

We also simulate latent "practice profiles" and item themes so the data have real structure (e.g., participants with a "primary care" profile tend to rate certain items as more relevant).

```r
n_users  <- 600
n_items  <- 200
missing_rate <- 0.7   # ~70% missing
K <- 8                # latent dimensions

# Simulate latent factors for users/items
U <- matrix(rnorm(n_users * K, sd = 0.7), n_users, K)     # users
V <- matrix(rnorm(n_items * K, sd = 0.7), n_items, K)     # items

# Affinity = U %*% t(V)
affinity <- U %*% t(V)

# Map continuous affinity to 1..4 ratings with noise
eps <- matrix(rnorm(n_users * n_items, sd = 0.6), n_users, n_items)
score <- scale(affinity + eps)            # standardize

# breakpoints for 1..4
q <- quantile(score, probs = c(.25, .5, .75))
to_rating <- function(x, q) {
  cut(x, breaks = c(-Inf, q[1], q[2], q[3], Inf), labels = 1:4)
}
ratings_full <- matrix(as.integer(to_rating(score, q)), n_users, n_items)

# Add missingness at random
mask <- matrix(runif(n_users * n_items) < missing_rate, n_users, n_items)
ratings <- ratings_full
ratings[mask] <- NA_integer_

dim(ratings); mean(is.na(ratings))
```

```
## [1] 600 200
```

```
## [1] 0.7005583
```

Convert to a `recommenderlab` object:

```r
R <- as(ratings, "realRatingMatrix")
R
```

```
## 600 x 200 rating matrix of class 'realRatingMatrix' with 35933 ratings.
```

Train/test split & evaluation scheme

We'll hold out a test set of 150 users. Within the training set, we'll use an `evaluationScheme` to compute RMSE/MAE.

```
idx_test  <- sample(1:n_users, size = 150)
R_test    <- R[idx_test, ]
R_train   <- R[-idx_test, ]

# evaluationScheme: 80/20 split on known ratings, 5-fold CV
es <- evaluationScheme(R_train, method = "cross-validation", k = 5, given = -1, goodRating = 4)
es
```

```
## Evaluation scheme using all-but-1 items
## Method: 'cross-validation' with 5 run(s).
## Good ratings: >=4.000000
## Data set: 450 x 200 rating matrix of class 'realRatingMatrix' with 27005 ratings.
```

Note: given = -1 uses all available ratings for training folds; we evaluate on the held-out portion within each fold.

Fit Funk SVD with `recommenderlab`

`recommenderlab` exposes SVD-based recommenders via `method = "SVD"` (Funk-style gradient descent). We'll compare a simple baseline (POPULAR) against SVD.

```
algos <- list(
  "POPULAR" = list(name = "POPULAR", param = NULL),
  "SVD_k20" = list(name = "SVD",     param = list(k = 20, maxiter = 200, normalize = "center")),
  "SVD_k40" = list(name = "SVD",     param = list(k = 40, maxiter = 200, normalize = "center"))
)

results <- evaluate(es, method = algos, type = "ratings")
```

```
## POPULAR run fold/sample [model time/prediction time]
##   1  [0.011sec/0.021sec]
##   2  [0.001sec/0.002sec]
##   3  [0.001sec/0.001sec]
##   4  [0.001sec/0.002sec]
##   5  [0.005sec/0.002sec]
## SVD run fold/sample [model time/prediction time]
##   1  [0.017sec/0.003sec]
##   2  [0.015sec/0.003sec]
##   3  [0.017sec/0.002sec]
##   4  [0.017sec/0.003sec]
##   5  [0.017sec/0.003sec]
## SVD run fold/sample [model time/prediction time]
##   1  [0.041sec/0.003sec]
##   2  [0.038sec/0.002sec]
##   3  [0.045sec/0.01sec]
##   4  [0.038sec/0.004sec]
##   5  [0.039sec/0.003sec]
```

```r
# Summarize RMSE/MAE across folds
perf <- lapply(results, function(res) {
  data.frame(
    RMSE = avg(res, "RMSE"),
    MAE  = avg(res, "MAE")
  )
})
do.call(rbind, perf)
```

```
##          RMSE.RMSE RMSE.MSE  RMSE.MAE  MAE.RMSE  MAE.MSE   MAE.MAE
## POPULAR 1.1399459 1.301450 1.0149085 1.1399459 1.301450 1.0149085
## SVD_k20 0.9780573 0.957810 0.8612992 0.9780573 0.957810 0.8612992
## SVD_k40 1.0067870 1.014651 0.8755282 1.0067870 1.014651 0.8755282
```

Tip: Increase `k` for more latent dimensions at the cost of potential overfit; use `CV` to pick `k`.

Train final model and generate predictions

Train on all training users, then predict ratings for the held-out test users.

```r
rec <- Recommender(R_train, method = "SVD", parameter = list(k = 30, maxiter = 200, normalize = "center
pred_test <- predict(rec, R_test, type = "ratings")
pred_mat  <- as(pred_test, "matrix")   # numeric predictions
true_mat  <- as(R_test, "matrix")      # ground truth with NAs

# Evaluate on co-observed cells
co_obs <- !is.na(true_mat) & !is.na(pred_mat)
rmse <- sqrt(mean((pred_mat[co_obs] - true_mat[co_obs])^2))
mae  <- mean(abs(pred_mat[co_obs] - true_mat[co_obs]))
c(RMSE = rmse, MAE = mae)
```

```
## RMSE  MAE
##  NaN  NaN
```

Inspect a few predictions:

```r
pred_mat[1:6, 1:8]
```

```
##          [,1]     [,2]     [,3]     [,4]     [,5]     [,6]     [,7]     [,8]
## [1,] 2.442729 2.831136 2.113613       NA 2.709425       NA 2.753223       NA
## [2,] 2.946876 2.878281       NA 2.641069       NA       NA 2.609371 2.742959
## [3,] 2.467677 1.925212 2.501307       NA 2.469397 2.307568 2.547723 2.208881
## [4,] 2.618050 2.906663       NA 2.749667 2.851427       NA 2.051954 2.880361
## [5,]       NA 2.275101 2.698023 2.209545 2.278022 2.499635       NA 2.360601
## [6,]       NA 1.601045       NA       NA 2.548205       NA       NA 2.051773
```

From predictions to tailored selection

In an assessment setting, we don't simply "send the top-N" items by prediction. We post-filter to respect constraints:

- Blueprint coverage: maintain required domain proportions
- Exposure control: cap how often items are seen
- Item quality: only deliver items meeting psychometric standards
- Candidate eligibility: remove items already seen by the participant

Here's a toy post-filtering function that enforces a (simplified) domain mix.

```r
# Simulate item domains
domains <- factor(sample(c("Cardio","Neuro","ID","Endo","Pulm"), n_items, replace = TRUE))

select_tailored <- function(pred_row, seen_idx = integer(0), n_select = 20,
                            domains, target_mix = c(Cardio=0.2, Neuro=0.2, ID=0.2, Endo=0.2, Pulm=0.2))
  # Remove already-seen items
  ok <- setdiff(which(!is.na(pred_row)), seen_idx)
  cand <- data.frame(item = ok, pred = pred_row[ok], domain = domains[ok], stringsAsFactors = FALSE)
  cand <- cand[order(-cand$pred), ]

  # Greedy fill by domain proportions
  target_counts <- round(target_mix * n_select)
  out <- integer(0)
  for (d in names(target_counts)) {
    need <- target_counts[d]
    pool <- cand[cand$domain == d & !(cand$item %in% out), ]
    take <- head(pool$item, need)
    out <- c(out, take)
  }
  # If not enough in a domain, top-up from remaining highest predictions
  if (length(out) < n_select) {
    extra <- setdiff(cand$item, out)
    out <- c(out, head(extra, n_select - length(out)))
  }
  out
}

# Example: pick 20 items for test user 1
sel_items <- select_tailored(pred_mat[1, ], seen_idx = which(!is.na(true_mat[1, ])),
                             n_select = 20, domains = domains)
length(sel_items); head(sel_items)
```

```
## [1] 20
```

```
## [1]  89  65  79   2 172 182
```

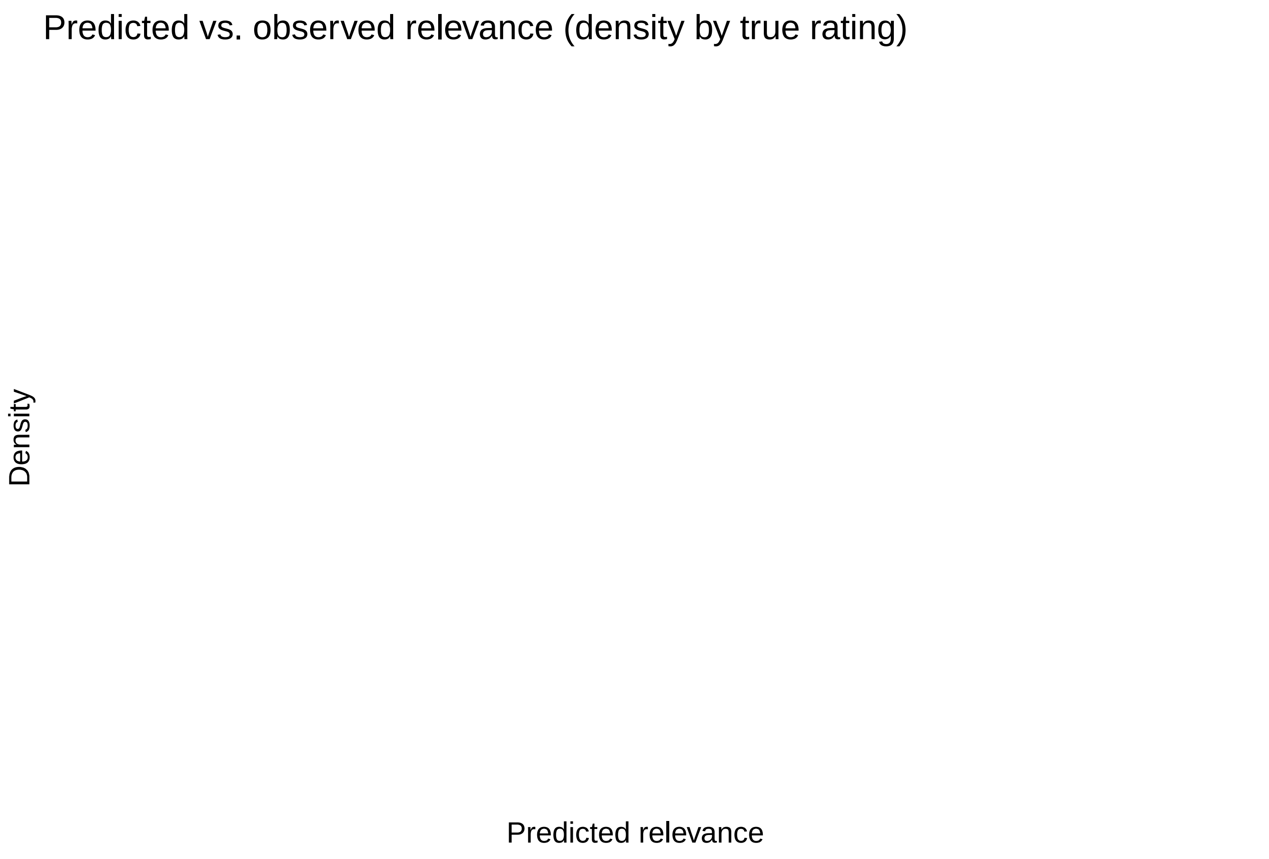
Interpreting predictions (face validity checks)

It helps to visualize how predictions separate 1–4 "true" ratings.

```r
# Sample co-observed cells for plotting
co_idx <- which(co_obs, arr.ind = TRUE)
samp   <- co_idx[sample(nrow(co_idx), size = min(8000, nrow(co_idx))), , drop = FALSE]
```

```r
df_plot <- data.frame(
  pred = pred_mat[samp],
  true = factor(true_mat[samp], levels = 1:4)
)

ggplot(df_plot, aes(x = pred, fill = true)) +
  geom_density(alpha = 0.35) +
  labs(x = "Predicted relevance", y = "Density", fill = "Observed rating",
       title = "Predicted vs. observed relevance (density by true rating)") +
  theme_minimal()
```



You should see higher predictions shifting toward higher observed ratings—i.e., monotonic separation.

Cold-start and drift (practical considerations)

- Item cold-start: New items with no ratings can borrow information from content features (e.g., tags, blueprint domain) via hybrid models, or by seeding with pilot ratings.
- User cold-start: For brand-new participants, use population priors, brief "warm-up" questions, or side info (practice profile) to initialize.
- Concept drift: Re-train on a cadence (e.g., quarterly) and monitor prediction error over time.

Fairness & psychometric guardrails (assessment context)

- Even with good accuracy, governance matters. In assessments:

- Blueprint adherence: Item selection must guarantee domain coverage.
- Score comparability: If scores are used, maintain comparability via equating/linking; personalization must not change score meaning.
- Fairness checks: Routinely evaluate subgroup RMSE/MAE and calibration (e.g., by practice setting, geography, training cohort). Investigate/mitigate gaps.
- Exposure & security: Cap exposures, control for leakage, and rotate forms/items appropriately.
- Transparency: Document the algorithm, inputs, re-training cadence, and monitoring plan.

What "good enough" looks like

No model is perfect. You want:

- Consistent lift over baseline (e.g., SVD vs. POPULAR) on RMSE/MAE.
- Face-valid separation of predictions by observed rating.
- Operational impact: higher average relevance after deployment without violating blueprint/fairness constraints.