Multiway Classification with Real Data

Matthew Asisgress

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In this demonstration, we apply the R package **cpfa** (Asisgress, 2025) to the MNIST dataset (LeCun, Cortes, and Burges, 1998; LeCun et al., 2002). We show how to use the package to distinguish between the digits of 2 and 3, a binary classification problem.

MNIST

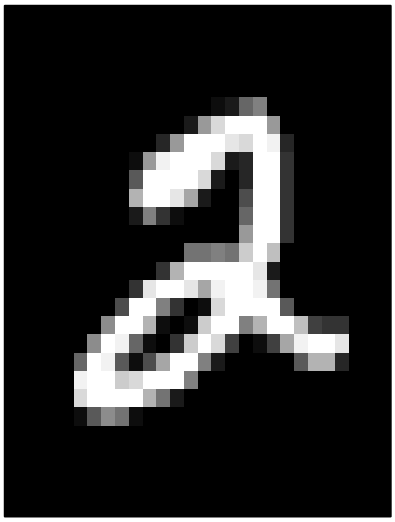
The MNIST dataset consists of 70,000 grayscale images of handwritten digits from 0 to 9. We use the R package **dslabs** (Irizarry and Gill, 2025) to download the dataset. We subset to only 2000 images from the original training set. The images include 980 images of the digit 2 and 1020 images of the digit 3.

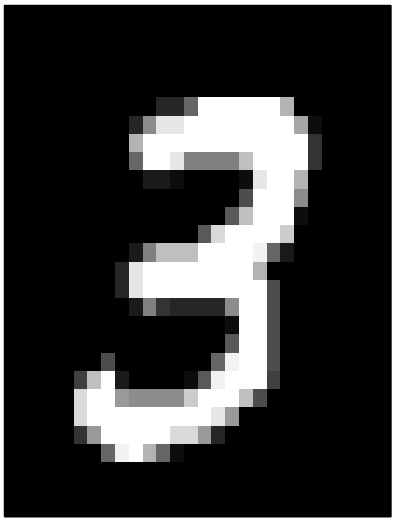
Download

```
# load library
library(dslabs)

# download MNIST data and subset training set to digits of 2 or 3
mnist <- read_mnist()
inde <- which(mnist$train$labels %in% c(2, 3))
images <- mnist$train$images[inde, ]
labels <- mnist$train$labels[inde]

# restructure data into a three-way array and prepare labels
X0 <- array(images, c(nrow(images), 28, 28))
y0 <- as.factor(as.numeric(as.factor(labels)) - 1)

# subset to first 2000 images
ind <- 1:2e3
X <- X0[ind, , ]
y <- y0[ind]
```

We plot and examine an example of the digit 2 and an example of the digit 3.

```
# plot example of digit 2 and digit 3
par(mfrow = c(1, 2))
pdigit <- function(imat) {
  m <- t(apply(imat, 2, rev))
  image(m, col = gray(seq(0, 1, 0.05)), xaxt = "n", yaxt = "n")
}
pdigit(t(X[which(y == 0)[1], , ])); pdigit(t(X[which(y == 1)[1], , ]))
```





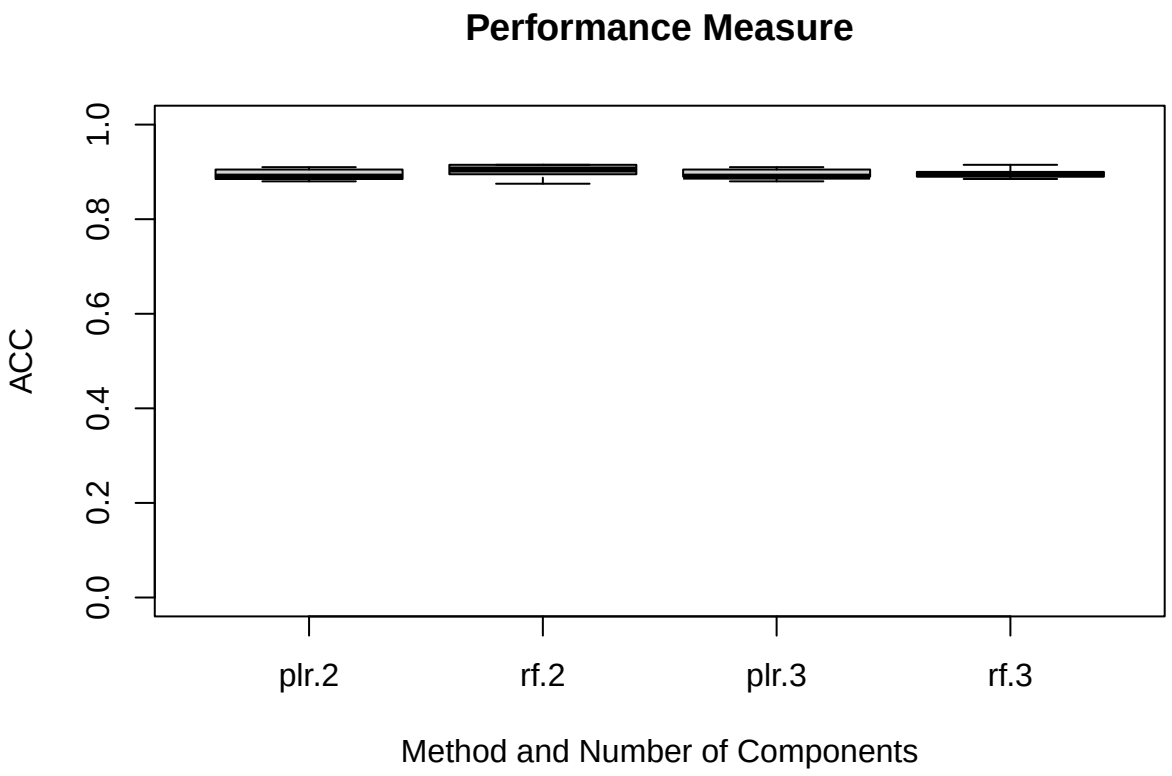
Analysis

We load the R package **cpfa** and initialize the tensor model. First, the data array is a regular three-way array, so we set `model <- "parafac"` to use a Parafac model. Note that the Parafac2 model can be used for ragged tensors. Second, we initialize the number of components to fit for the model by setting `nfac <- c(2, 3)` in order to fit both a two-component Parafac model and a three-component Parafac model. We set `nstart <- 10` to allow for 10 random starts in the Parafac alternating least squares algorithm fit by R package **multiway** (Helwig, 2025), upon which R package **cpfa** depends. Third, we specify the constraint desired for each array mode using `const`. Note that numerous constraint options are available; after loading **cpfa**, type `const()` in the R console to access a constraint options list provided through R package **CMLS** (Helwig, 2025). Fourth, we use `cmode <- 1` to specify that the classification mode is the first mode of the input array (i.e., the mode connected to the class labels).

We next initialize classification methods. First, we use `method = c("PLR", "RF")` to employ penalized logistic regression (PLR) and random forest (RF) classifiers for this problem. See `help(cpfa)` for other options and for references associated with these classifiers. Second, we specify that the problem is a binary classification problem by setting `family <- "binomial"`. Third, we use 10-fold cross-validation (CV) in our inner training, setting `nfolds <- 10`; and fourth, we set `nrep <- 5` to perform five outer train-test splits of our data. Fifth, we set `ratio <- 0.9` to specify that each outer training set will contain a proportion of 0.9 of the full input data while the outer testing set will contain 0.1 of the data. Finally, we specify ranges for tuning parameters alpha (PLR), the number of trees (RF), and node size (RF), wrapping them into a list called `parameters`.

```
# load library
library(cpfa)

# set seed
set.seed(500)

# initialize Parafac model
model <- "parafac"
nfac <- c(2, 3)
nstart <- 10
const <- c("uncons", "uncons", "uncons")
cmode <- 1

# initialize classification
method <- c("PLR", "RF")
```

```r
family <- "binomial"
nfolds <- 10
nrep <- 5
ratio <- 0.9

# initialize tuning parameters
alpha <- seq(0, 1, length = 8)
ntree <- c(400, 600, 800, 1000)
nodesize <- c(4, 8, 16, 32)
parameters <- list(alpha = alpha, ntree = ntree, nodesize = nodesize)

# implement train-test splits with inner k-fold CV to optimize classification
outputR <- cpfa(x = X, y = y, model = model, nfac = nfac, nstart = nstart,
                const = const, cmode = cmode, method = method,
                family = family, nfolds = nfolds, nrep = nrep, ratio = ratio,
                parameters = parameters, type.out = "descriptives",
                seeds = NULL, plot.out = TRUE, parallel = FALSE,
                verbose = FALSE)
```



Results

We examine classification performance metrics of error (`err`) and overall accuracy (`acc`) for each model and for each classifier. We also examine, averaged across outer train-test splits, the optimal tuning parameters chosen (i.e., that minimized misclassification error) for each classifier.

```r
# examine classification performance measures - median across train-test splits
outputR$descriptive$median[, 1:2]
```

```
##            err   acc
## fac.2plr 0.110 0.890
```

```
## fac.2rf  0.095 0.905
## fac.3plr 0.110 0.890
## fac.3rf  0.105 0.895
```

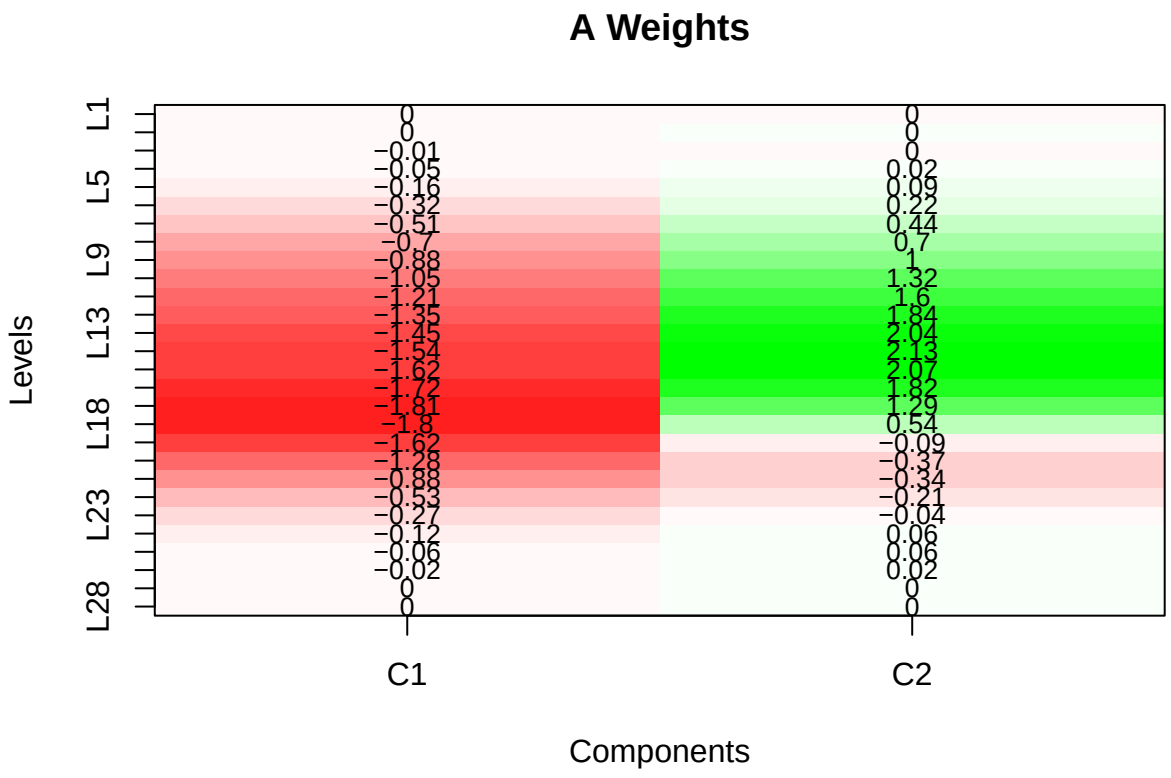
```
# examine optimal tuning parameters averaged across train-test splits
outputR$mean.opt.tune
```

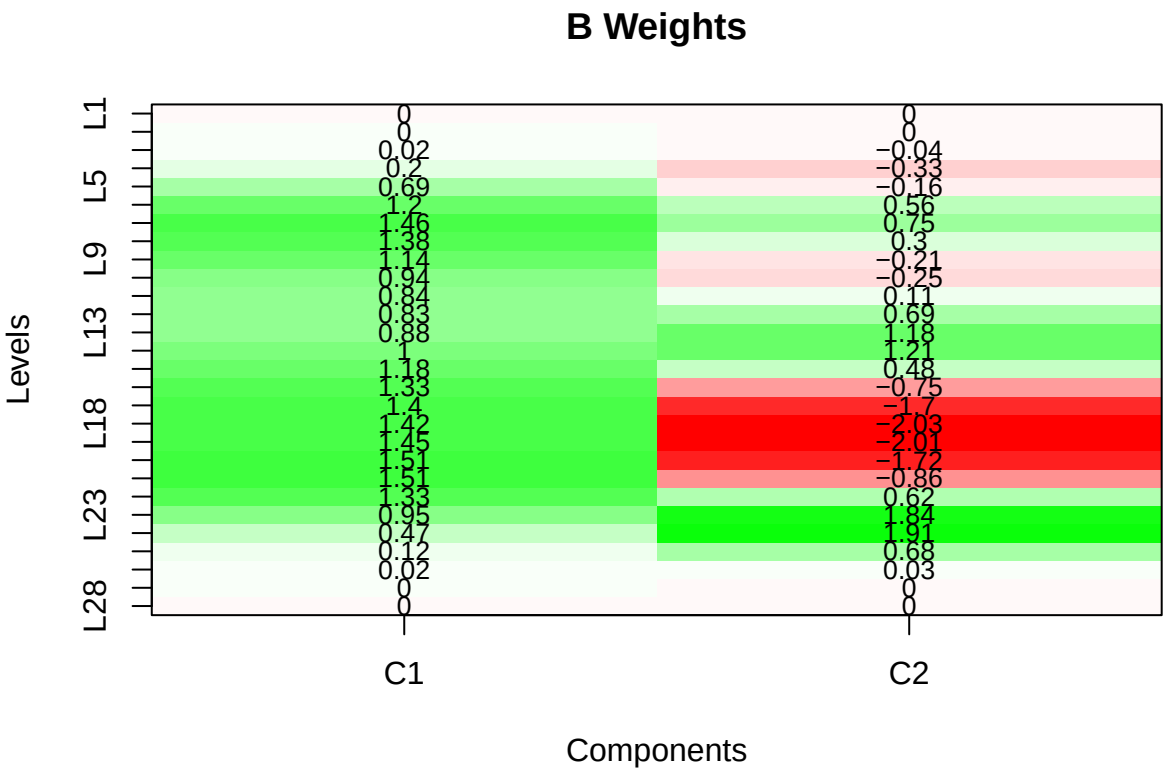
```
##   nfac      alpha   lambda gamma cost ntree nodesize size decay rda.alpha delta
## 1    2 0.11428571 2.350755    NA   NA   600     32.0   NA    NA        NA    NA
## 2    3 0.02857143 6.256281    NA   NA   680     10.4   NA    NA        NA    NA
##   eta max.depth subsample nrounds
## 1  NA        NA        NA      NA
## 2  NA        NA        NA      NA
```

Using 2000 images, we can see that classification accuracy values are close to 0.9 for both two-component and three-component models. The two-component Parafac model with the RF classifier performed best. In addition, we can see average optimal tuning parameters for each classifier. Note that PLR optimized lambda internally.

Next, we use the function `plotcpfa`. The function does two things: (1) it fits the optimal model among those fit using function `cpfa`; and (2) it plots the component weights from the non-classification modes. Note that, for the Parafac2 model, the function does not plot A mode weights as these are allowed to vary within each level of the classification mode. From the component weights, we can search for relationships between the levels of mode A or B and the model components. In this case, mode A corresponds to the horizontal axis of the images (when viewing the images as those above) while mode B corresponds to the vertical axis of the images.

```
# set seed
set.seed(500)

# plot heatmaps of component weights for optimal model
results <- plotcpfa(outputR, nstart = 10, ctol = 1e-6, verbose = FALSE)
```





Examining the first component for the A mode (horizontal), weights are stronger between levels 5-24. Looking at the B mode (vertical), a similar pattern is seen: weights are stronger in the middle between levels 4-25. Then, whether viewed from the A mode or B mode perspective, this first component appears to be a general component showing the presence of non-zero values, distinguishing empty outer parts of images from inner parts. Likely, the 2 and 3 digits have systematic differences in the presence of non-zero values in these areas.

Examining the second component for the A mode, weights are stronger near and around level 14 where there appears to be a greater presence of zero values in digit 3 compared to digit 2 near this level. A similar pattern is seen in the B mode around levels 18 and 19 with more non-zero values for 2, compared to 3, around these levels. Taken together between the modes, this component could be identifying the closed circle present in the digit 2, which differs from the open or half circle seen in digit 3.

References

Asisgress, M. (2025). cpfa: Classification with Parallel Factor Analysis. R package version 1.2-2, https://CRAN.R-project.org/package=cpfa.

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Irizarry, R., Gill, A. (2025). dslabs: Data Science Labs. R package version 0.9.0, https://CRAN.R-project.org/package=dslabs.

LeCun, Y., Bottou, L., Bengio, Y., and Haffner, P. (2002). Gradient-based learning applied to document recognition. Proceedings of the IEEE, 86(11), 2278–2324.

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