

mice trial

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mice trial Load data and install packages

```
##  
## Attaching package: 'mice'  
  
## The following object is masked from 'package:stats':  
##  
## filter  
  
## The following objects are masked from 'package:base':  
##  
## cbind, rbind
```

Here are necessary functions to run the mice. These functions are there to handle data by e.g., calculating a mask to introduce missingness into a data set without missingness present, normalize data, and also calculate the RMSE. These functions are based on the functions used in the GAIN(<https://doi.org/10.48550/arXiv.1806.02920>) paper.

```
# This function generates a mask for introducing the missing values  
missing <- function(p, no, dim) {  
  mm <- matrix(runif(no*dim),no,dim)  
  mask <- ifelse((mm < p),1,NA)  
  return(mask)  
}  
  
# this function normalize the data  
normalization <- function(data, parameters){  
  
  data_norm <- sweep(data, 2, parameters[,1], "-")  
  data_norm <- sweep(data_norm, 2, parameters[,2], "/")  
}  
  
# this function calculate the RMSE  
rmse_loss <- function(ori_data, imputed_data, data_m){  
  
  #I changed this part because I was running into a problem since i already normalized so with the prev  
  
  # Ensure that the original data and imputed data are already normalized
```

```

if (is.null(parameters)) {
  parameters <- parameters_norm(ori_data) # Calculate parameters only if not provided
}

# Normalize the data if parameters are not passed (initial normalization)
ori_data <- normalization(ori_data, parameters)
imputed_data <- normalization(imputed_data, parameters)

# Only for missing values
nominator <- sum(((1-data_m) * ori_data - (1-data_m) * imputed_data)**2)
denominator <- sum(1-data_m)

rmse <- sqrt(nominator/denominator)

return(rmse)
}

```

Introducing missing data

```

set.seed(123)

# Introduce missing values
mask <- missing(0.2, nrow(data), ncol(data))

spam_data_with_missing <- data * mask

```

Impute missing data

```

# Impute missing values using mice
imputed_data <- mice(spam_data_with_missing, m = 5, maxit = 5, method = 'pmm')
# Extract the complete dataset after imputation
spam_data_imputed <- complete(imputed_data)

```

Calculate the overall rmse

```

# RMSE calculation function
rmse <- function(original, imputed) {
  sqrt(mean((original - imputed)^2, na.rm = TRUE))
}

# Calculate RMSE for each column and get an average
rmse_values <- sapply(names(data), function(col) {
  rmse(data[[col]], spam_data_imputed[[col]])
})

```

```

})
rmse_overall <- mean(rmse_values, na.rm = TRUE)

print(rmse_overall)

```

```
## [1] 17.2708
```

I forgot to normalize the data, which is probably why the rmse is so high(the RMSE is related to the scale of the data lol). SO lets go again:))

Normalize

```

set.seed(123) # For reproducibility

# Calculate the normalization parameters
parameters_norm <- function(data) {
  mean_sd <- apply(data, 2, function(x) c(mean = mean(x, na.rm = TRUE), sd = sd(x, na.rm = TRUE)))
  return(t(mean_sd)) # returns a matrix with means and sds
}

# Get parameters for normalization
parameters <- parameters_norm(data)

# Normalize the data using the function built above
data_normalized <- normalization(data, parameters)

```

Introduce missingness

```

set.seed(123)
# Introduce missing values
##mask <- missing(0.2, nrow(data_normalized), ncol(data_normalized))

data_with_missing <- data_normalized * mask

```

Imputing missing data

```

mice_imputed <- mice(as.data.frame(data_with_missing), m = 1, maxit = 5)
imputed_data <- complete(mice_imputed)

```

Calculate rmse

```
#I forgot there was already a function to calculate the RMSE above so I will use it from now on
# Calculate RMSE
rmse <- rmse_loss(data_normalized, imputed_data, mask)
print(paste("RMSE:", rmse))
```

```
## [1] "RMSE: NA"
```

```
# returns NA so got to change the code of the mask
```

```
mask_rmse <- ifelse(is.na(mask), 0, 1) # Convert NA to 0, keeping valid entries as 1
```

```
# Calculate RMSE again
```

```
rmse <- rmse_loss(data_normalized, imputed_data, mask_rmse)
print(paste("RMSE:", rmse))
```

```
## [1] "RMSE: 3.99704543094645"
```

```
#looks better but still above 1, this might be due to different normmalization techniques
```

Redo the normalization

So the results above show that the RMSE is still outside of the [0,1] scale, which has been used for the GAIN. This means the two values are not comparable. I noticed looking back at the code that a different normalization has been used than the one provided above. They used the minmax normalization so that the scale is [0,1] instead of the scale I had above [-1,1]. Fixing the normalization and keeping everything else in place should fix the problem and make our RMSE comparable to the one from GAIN:))

```
normalization <- function(data, parameters = NULL) {
  # If no parameters are provided, calculate min and max for each column
  if (is.null(parameters)) {
    min_val <- apply(data, 2, min, na.rm = TRUE)
    max_val <- apply(data, 2, max, na.rm = TRUE)

    # Normalize data using min-max formula
    norm_data <- sweep(data, 2, min_val, "-")
    norm_data <- sweep(norm_data, 2, max_val - min_val, "/")

    # Return normalized data and the min/max parameters for future renormalization
    return(list(norm_data = norm_data, parameters = list(min_val = min_val, max_val = max_val)))
  } else {
    min_val <- parameters$min_val
    max_val <- parameters$max_val

    # Normalize using pre-calculated min and max values
    norm_data <- sweep(data, 2, min_val, "-")
    norm_data <- sweep(norm_data, 2, max_val - min_val, "/")

    return(norm_data)
  }
}
```

```

norm_ <- normalization(data)
norm_data <- norm_$norm_data
parameters <- norm_$parameters # parameters is a list, containing min_val and max

norms <- normalization(data, parameters)

```

Introduce missingness

```

set.seed(123)

# Introduce missing values by using the same mask generated above
#mask <- missig(0.2, nrow(norms), ncol(norms))

data_with_missing_2 <- norms * mask

```

Imputing missing data

```

mice_imputed <- mice(as.data.frame(data_with_missing_2), m = 1, maxit = 5)
imputed_data <- complete(mice_imputed)

```

Calculate rmse

```

# Calculate RMSE
rmse <- rmse_loss(norms, imputed_data, mask)
print(paste("RMSE:", rmse))

## [1] "RMSE: NA"

# returns NA so got to change the code of the mask

mask_rmse <- ifelse(is.na(mask), 0, 1) # Convert NA to 0, keeping valid entries as 1

# Calculate RMSE again
rmse <- rmse_loss(norms, imputed_data, mask_rmse)
print(paste("RMSE:", rmse))

## [1] "RMSE: 0.0119416829808488"

```

the (hopefully) final rmse is 0.012 where as the one from gain is 0.051. So just by comparing these two numbers it looks like mice did perform better, i do not know whether it is okay to make that statement yet though. It is important to note that while the mask is generated in the same fashion, it is not ensured that it is the same mask. so we are not imputing the same missing values...

To deal with this I extracted the mask for the spam.csv data the GAIN team used for the default spam.csv file. So running the MICE now with the exact same missing data set, we should be able to properly compare the results of the two imputation techniques.

```
#loading the mask file
mask <- read.csv("mask.csv")
```

MinMax normalization

```
normalization <- function(data, parameters = NULL) {
  # If no parameters are provided, calculate min and max for each column
  if (is.null(parameters)) {
    min_val <- apply(data, 2, min, na.rm = TRUE)
    max_val <- apply(data, 2, max, na.rm = TRUE)

    # Normalize data using min-max formula
    norm_data <- sweep(data, 2, min_val, "-")
    norm_data <- sweep(norm_data, 2, max_val - min_val, "/")

    # Return normalized data and the min/max parameters for future renormalization
    return(list(norm_data = norm_data, parameters = list(min_val = min_val, max_val = max_val)))
  } else {
    min_val <- parameters$min_val
    max_val <- parameters$max_val

    # Normalize using pre-calculated min and max values
    norm_data <- sweep(data, 2, min_val, "-")
    norm_data <- sweep(norm_data, 2, max_val - min_val, "/")

    return(norm_data)
  }
}

norm_ <- normalization(data)
norm_data <- norm_$norm_data
parameters <- norm_$parameters # parameters is a list, containing min_val and max

norms <- normalization(data, parameters)
```

Introduce missingness

```
set.seed(123)

# Introduce missing values by using the same mask generated above
# Convert 0's in the mask to NA
mask[mask == 0] <- NA

data_m <- norms * mask
```

Imputing missing data

```
mice_imputed <- mice(data_m, m = 1, maxit = 5)
imputed_data <- complete(mice_imputed)
```

Calculate rmse

```
# Calculate RMSE
rmse <- rmse_loss(norms, imputed_data, mask)
print(paste("RMSE:", rmse))
```

```
## [1] "RMSE: NA"
```

```
# returns NA so got to change the code of the mask

mask_rmse <- ifelse(is.na(mask), 0, 1) # Convert NA to 0, keeping valid entries as 1

# Calculate RMSE again
rmse <- rmse_loss(norms, imputed_data, mask_rmse)
print(paste("RMSE:", rmse))
```

```
## [1] "RMSE: 0.011046514378707"
```

The RMSE obtained using the same data set with the same mask, which has been extracted from GAIN, is now 0.11, compared to 0.053. So the difference stayed around the same. This is not completely reproducible because every time the GAIN script is run the mask is being randomly obtained, but for this example we had the same mask. It is also questionable whether comparing the RMSE's is the best way to compare the two methods of imputing missing data.