

# mRMRe: an R package for parallelized mRMR ensemble feature selection

Nicolas De Jay<sup>1</sup>, Simon Papillon-Cavanagh<sup>1</sup>, Catharina Olsen<sup>2</sup>,  
Gianluca Bontempi<sup>2</sup>, and Benjamin Haibe-Kains<sup>1</sup>

<sup>1</sup>Bioinformatics and Computational Biology Laboratory,  
Institut de recherches cliniques de Montréal, Montreal, Quebec,  
Canada

<sup>2</sup>Machine Learning Group, Université Libre de Bruxelles,  
Brussels, Belgium

November 3, 2017

## Contents

<b>1</b>	<b>Introduction</b>	<b>2</b>
1.1	Installation and Settings . . . . .	2
1.2	Requirements . . . . .	2
<b>2</b>	<b>Measures of Association</b>	<b>2</b>
2.1	Mutual Information Matrix . . . . .	2
2.2	Correlations . . . . .	4
<b>3</b>	<b>mRMR Feature Selection</b>	<b>5</b>
3.1	Classic mRMR . . . . .	5
3.2	Ensemble mRMR . . . . .	5
<b>4</b>	<b>Causality Inference</b>	<b>6</b>
<b>5</b>	<b>Session Info</b>	<b>6</b>

# 1 Introduction

*mRMRe* is an R package for parallelized mRMR ensemble feature selection.

## 1.1 Installation and Settings

*mRMRe* requires that *Rcpp* is installed. These should be installed automatically when you install *mRMRe*. Install *mRMRe* from CRAN or Bioconductor using *biocLite* function.

```
> install.packages("mRMRe")
```

Load *mRMRe* into your current workspace:

```
> library(mRMRe)
```

The *mRMRe* package allows its users to set the number of threads it will use for computations. One should may consider the following method to avoid crowding computing clusters, or fully utilize them.

```
> set.thread.count(2)
```

Load the example dataset *cgps* into your current workspace:

```
> data(cgps)
> data.annot <- data.frame(cgps.annot)
> data.cgps <- data.frame(cgps.ic50, cgps.ge)
```

## 1.2 Requirements

*mRMRe* has only been tested on Windows and Linux platforms. It requires that the *openMP* C library be installed on the hosts on which the package is intended to run.

# 2 Measures of Associtation

## 2.1 Mutual Information Matrix

*mRMRe* offers a fully parallelized implementation to compute the Mutual Information Matrix (MIM). The object *data\_cgps* should be a dataframe with

samples/observations in rows and features/variables in columns. The method supports the following column types: "numeric" ("integer" or "double"), "ordered factor" and "Surv". Mutual information (MI) between two columns is estimated using a linear approximation based on correlation such that MI is estimated as  $I(x, y) = -\frac{1}{2} \ln(1 - \rho(x, y)^2)$ , where  $I$  and  $\rho$  respectively represent the MI and correlation coefficient between features  $x$  and  $y$ . Correlation between continuous variables can be computed using either Pearson's or Spearman's estimators, while Cramer's V and Somers' Dxy index are used for correlation between discrete variables and between continuous variables and survival data, respectively.

```
> ## Test on a dummy dataset.
>
> # Create a dummy data set
> library(survival)
> df <- data.frame(
+   "surv1" = Surv(runif(100),
+                 sample(0:1, 100, replace = TRUE)),
+   "cont1" = runif(100),
+   "disc1" = factor(sample(1:5, 100, replace = TRUE),
+                   ordered = TRUE),
+   "surv2" = Surv(runif(100),
+                 sample(0:1, 100, replace = TRUE)),
+   "cont2" = runif(100),
+   "cont3" = runif(100),
+   "surv3" = Surv(runif(100),
+                 sample(0:1, 100, replace = TRUE)),
+   "disc2" = factor(sample(1:5, 100, replace = TRUE),
+                   ordered = TRUE))
> dd <- mRMR.data(data = df)
> # Show a partial mutual information matrix.
> print(mim(subsetData(dd, 1:4, 1:4)))
```

	surv1	cont1	disc1	surv2
surv1	0.0000000	0.0000000	Inf	0.0000000
cont1	0.0000000	Inf	0.1061395	Inf
disc1	Inf	0.1061395	Inf	0.2231436
surv2	0.2231436	Inf	0.2231436	0.0000000

```

> ## Test on the 'cgps' dataset, where the
> ## variables are all of continuous type.
>
> dd <- mRMR.data(data = data.cgps)
> dd <- subsetData(dd, 1:10, 1:10)
> # Uses Spearman as correlation estimator
> spearman_mim <- mim(dd, continuous_estimator = "spearman")
> print(spearman_mim[1:4, 1:4])

```

```

           cgps.ic50 geneid_3310 geneid_2978 geneid_6352
cgps.ic50           Inf 0.025796493 0.000900719 0.108915849
geneid_3310 0.025796493           Inf 0.017968244 0.002227175
geneid_2978 0.000900719 0.017968244           Inf 0.050207046
geneid_6352 0.108915849 0.002227175 0.050207046           Inf

```

```

> # Uses Pearson as correlation estimator
> pearson_mim <- mim(dd, continuous_estimator = "pearson")
> print(pearson_mim[1:4, 1:4])

```

```

           cgps.ic50 geneid_3310 geneid_2978 geneid_6352
cgps.ic50           Inf 0.02104964 7.541758e-05 0.09249434
geneid_3310 2.104964e-02           Inf 2.450671e-02 0.02740061
geneid_2978 7.541758e-05 0.02450671           Inf 0.05790450
geneid_6352 9.249434e-02 0.02740061 5.790450e-02           Inf

```

## 2.2 Correlations

The mRMRe package offers an efficient, stratified and weighted implementation of the major correlation estimators: Cramer's V, Somers Dxy index (based on the concordance index), Pearson, Spearman correlation coefficients.

```

> # Compute c-index between feature 1 and 2
> correlate(cgps.ge[, 1], cgps.ge[, 2], method = "cindex")
> # Compute Cramer's V
> x <- sample(factor(c("CAT_1", "CAT_2", "CAT_3"),
+                   ordered = TRUE), 100, replace = TRUE)
> y <- sample(factor(c("CAT_1", "CAT_2"),
+                   ordered = TRUE), 100, replace = TRUE)
> correlate(x, y, method = "cramersv")

```

```

> # Compute Pearson coefficient with random strata and
> # sample weights between features 1 and 2
> strata <- sample(factor(c("STRATUM_1", "STRATUM_2",
+                          "STRATUM_3"),
+                          ordered = TRUE),
+                          nrow(cgps.ge), replace = TRUE)
> weights <- runif(nrow(cgps.ge))
> correlate(cgps.ge[, 1], cgps.ge[, 2], strata = strata,
+          weights = weights, method = "pearson")

```

### 3 mRMR Feature Selection

mRMR offers a highly efficient implementation of the mRMR feature selection [2, 4]. The two crucial aspects of our implementation consists first, in parallelizing the key steps of the algorithm and second, in using a lazy procedure to compute only the part of the MIM that is required during the search for the best set of features (instead of estimating the full MIM).

#### 3.1 Classic mRMR

Here is an example of the classic mRMR feature selection [2].

```

> dd <- mRMR.data(data = data.cgps)
> mRMR.classic(data = dd, target_indices = c(1),
+             feature_count = 30)

```

#### 3.2 Ensemble mRMR

```

> dd <- mRMR.data(data = data.cgps)
> # For mRMR.classic-like results
> mRMR.ensemble(data = dd, target_indices = c(1),
+             solution_count = 1, feature_count = 30)
> # For mRMR.ensemble-like results
> mRMR.ensemble(data = dd, target_indices = c(1),
+             solution_count = 5, feature_count = 30)

```

## 4 Causality Inference

The mRMRe package allows one to infer causality through the use of the co-information lattice method [1, 3].

```
> ensemble <- mRMR.ensemble(data = dd, target_indices = c(1),
+                             solution_count = 5,
+                             feature_count = 10)
> causality(ensemble)
```

## 5 Session Info

- R Under development (unstable) (2017-10-05 r73475), x86\_64-pc-linux-gnu
- Locale: LC\_CTYPE=en\_US.UTF-8, LC\_NUMERIC=C, LC\_TIME=en\_US.UTF-8, LC\_COLLATE=en\_US.UTF-8, LC\_MONETARY=en\_US.UTF-8, LC\_MESSAGES=C, LC\_PAPER=en\_US.UTF-8, LC\_NAME=C, LC\_ADDRESS=C, LC\_TELEPHONE=C, LC\_MEASUREMENT=en\_US.UTF-8, LC\_IDENTIFICATION=C
- Running under: Debian GNU/Linux 9 (stretch)
- Matrix products: default
- BLAS/LAPACK: /usr/lib/libopenblas-r0.2.19.so
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: igraph 1.1.2, mRMRe 2.0.7, survival 2.41-3
- Loaded via a namespace (and not attached): compiler 3.5.0, grid 3.5.0, lattice 0.20-35, magrittr 1.5, Matrix 1.2-11, pkgconfig 2.0.1, splines 3.5.0, tools 3.5.0

## References

- [1] A J Bell. The co-information lattice. In S Amari, A Cichocki, S Makino, and N Murata, editors, *Proceedings of the Fifth International Workshop on Independent Component Analysis and Blind Signal Separation: ICA 2003*, 2003.
- [2] Chris Ding and Hanchuan Peng. Minimum redundancy feature selection from microarray gene expression data. *Journal of bioinformatics and computational biology*, 3(2):185–205, April 2005.
- [3] W McGill. Multivariate information transmission. *IEEE Transactions on Information Theory*, 4(4):93–111, September 1954.
- [4] P. E. Meyer, C. Schretter, and Gianluca Bontempi. Information-Theoretic Feature Selection in Microarray Data Using Variable Complementarity. *Selected Topics in Signal Processing, IEEE Journal of*, 2(3):261–274, 2008.