Rcpi: R/Bioconductor Package as an Integrated Informatics Platform in Drug Discovery

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Contents

1. Introduction

The **Rcpi** package (Xiao *et al.* 2014a) presented in this manual offers an R/Bioconductor package emphasizing the comprehensive integration of bioinformatics and chemoinformatics into a molecular informatics platform for drug discovery.

Rcpi implemented and integrated the state-of-the-art protein sequence descriptors and molecular descriptors/fingerprints with R. For protein sequences, the **Rcpi** package could

- Calculate six protein descriptor groups composed of fourteen types of commonly used structural and physicochemical descriptors that include 9,920 descriptors.

- Calculate profile-based protein representation derived by PSSM (Position-Specific Scoring Matrix).

- Calculate six types of generalized scales-based descriptors derived by various dimensionality reduction methods for proteochemometric (PCM) modeling.

- Parallellized pairwise similarity computation derived by protein sequence alignment and Gene Ontology (GO) semantic similarity measures within a list of proteins.

For small molecules, the **Rcpi** package could

- Calculate 307 molecular descriptors (2D/3D), including constitutional, topological, geometrical, and electronic descriptors, etc.

- Calculate more than ten types of molecular fingerprints, including FP4 keys, E-state fingerprints, MACCS keys, etc., and parallelized chemical similarity search.

- Parallelized pairwise similarity computation derived by fingerprints and maximum common substructure search within a list of small molecules.

By combining various types of descriptors for drugs and proteins in different methods, interaction descriptors representing protein-protein or compound-protein interactions could be conveniently generated with **Rcpi**, including:

- Two types of compound-protein interaction (CPI) descriptors

- Three types of protein-protein interaction (PPI) descriptors

Several useful auxiliary utilities are also shipped with **Rcpi**:

- Parallelized molecule and protein sequence retrieval from several online databases, like PubChem, ChEMBL, KEGG, DrugBank, UniProt, RCSB PDB, etc.

- Loading molecules stored in SMILES/SDF files and loading protein sequences from FASTA/PDB files

- Molecular file format conversion

The computed protein sequence descriptors, molecular descriptors/fingerprints, interaction descriptors and pairwise similarities are widely used in various research fields relevant to drug disvery, primarily bioinformatics, chemoinformatics, proteochemometrics and chemogenomics.

The **Rcpi** package is available from Bioconductor (http://bioconductor.org), visit http://bioconductor.org/packages/release/bioc/html/Rcpi.html for more details. This vignette corresponds to **Rcpi** Release 3 and was typeset on 2015-04-16.

To install the **Rcpi** package in R, simply type

```
source('http://bioconductor.org/biocLite.R')
biocLite('Rcpi')
```

To make the **Rcpi** package fully functional (especially the Open Babel related functionalities), we recommend the users also install the *Enhances* packages by using:

```
source('http://bioconductor.org/biocLite.R')
biocLite('Rcpi', dependencies = c('Imports', 'Enhances'))
```

Several dependencies of the **Rcpi** package may require some system-level libraries, check the corresponding manuals of these packages for detailed installation guides.

2. Applications in Bioinformatics

For bioinformatics research, **Rcpi** calculates commonly used descriptors and proteochemometric (PCM) modeling descriptors for protein sequences. **Rcpi** also computes pairwise similarities derived by GO semantic similarity and sequence alignment.

2.1. Predicting Protein Subcellular Localization

Protein subcellular localization prediction involves the computational prediction of where a protein resides in a cell. It is an important component of bioinformatics-based prediction of protein function and genome annotation, and could also aid us to identify novel drug targets.

Here we use the subcellular localization dataset of human proteins presented in the study of Chou and Shen (2008) for a demonstration. The complete dataset includes 3134 protein sequences (2750 different proteins), classified into 14 human subcellular locations. We select two classes of proteins as our benchmark dataset. Class 1 contains 325 *extracell* proteins, and class 2 includes 307 *mitochondrion* proteins.

First, we load the **Rcpi** package, then read the protein sequences stored in two separated FASTA files with readFASTA():

```
require(Rcpi)

# load FASTA files
extracell = readFASTA(system.file('vignettedata/extracell.fasta',
                                  package = 'Rcpi'))
mitonchon = readFASTA(system.file('vignettedata/mitochondrion.fasta',
                                  package = 'Rcpi'))
```

To read protein sequences stored in PDB format files, use `readPDB()` instead. The loaded sequences will be stored as two lists in R, and each component in the list is a character string representing one protein sequence. In this case, there are 325 *extracell* protein sequences and 306 *mitonchon* protein sequences:

```
length(extracell)
```

```
## [1] 325
```

```
length(mitonchon)
```

```
## [1] 306
```

To assure that the protein sequences only have the twenty standard amino acid types which is required for the descriptor computation, we use the `checkProt()` function in **Rcpi** to do the amino acid type sanity checking and remove the *non-standard* sequences:

```
extracell = extracell[(sapply(extracell, checkProt))]
mitonchon = mitonchon[(sapply(mitonchon, checkProt))]

length(extracell)
```

```
## [1] 323
```

```
length(mitonchon)
```

```
## [1] 304
```

Two protein sequences were removed from each class. For the remaining sequences, we calculate the amphiphilic pseudo amino acid composition (APAAC) descriptor (Chou 2005) and make class labels for classification modeling.

```
# calculate APAAC descriptors
x1 = t(sapply(extracell, extractProtAPAAC))
x2 = t(sapply(mitonchon, extractProtAPAAC))
x  = rbind(x1, x2)

# make class labels
labels = as.factor(c(rep(0, length(extracell)), rep(1, length(mitonchon))))
```

In **Rcpi**, the functions of commonly used descriptors for protein sequences and proteochemometric (PCM) modeling descriptors are named after `extractProt...()` and `extractPCM...()`.

Next, we will split the data into a 75% training set and a 25% test set.

```
# split training and test set
set.seed(1001)
tr.idx = c(sample(1:nrow(x1), round(nrow(x1) * 0.75)),
           sample(nrow(x1) + 1:nrow(x2), round(nrow(x2) * 0.75)))
te.idx = setdiff(1:nrow(x), tr.idx)
x.tr   = x[tr.idx, ]
x.te   = x[te.idx, ]
y.tr   = labels[tr.idx]
y.te   = labels[te.idx]
```

We will train a random forest classification model on the training set with 5-fold cross-validation, using the **randomForest** package.

```
require(randomForest)
rf.fit = randomForest(x.tr, y.tr, cv.fold = 5)
print(rf.fit)
```

The training result is:

```
## Call:
##  randomForest(x = x.tr, y = y.tr, cv.fold = 5)
##                Type of random forest: classification
##                      Number of trees: 500
## No. of variables tried at each split: 8
##
##         OOB estimate of  error rate: 25.11%
## Confusion matrix:
##     0   1 class.error
## 0 196  46   0.1900826
## 1  72 156   0.3157895
```

With the model trained on the training set, we predict on the test set and plot the ROC curve with the **pROC** package, as is shown in figure 1.

```
# predict on test set
rf.pred = predict(rf.fit, newdata = x.te, type = 'prob')[, 1]

# plot ROC curve
require(pROC)
plot.roc(y.te, rf.pred, col = '#0080ff', grid = TRUE, print.auc = TRUE)
```

The area under the ROC curve (AUC) is:

```
## Call:
## plot.roc.default(x = y.te, predictor = rf.pred, col = "#0080ff",
##                  grid = TRUE, print.auc = TRUE)
##
## Data: rf.pred in 81 controls (y.te 0) > 76 cases (y.te 1).
## Area under the curve: 0.8697
```
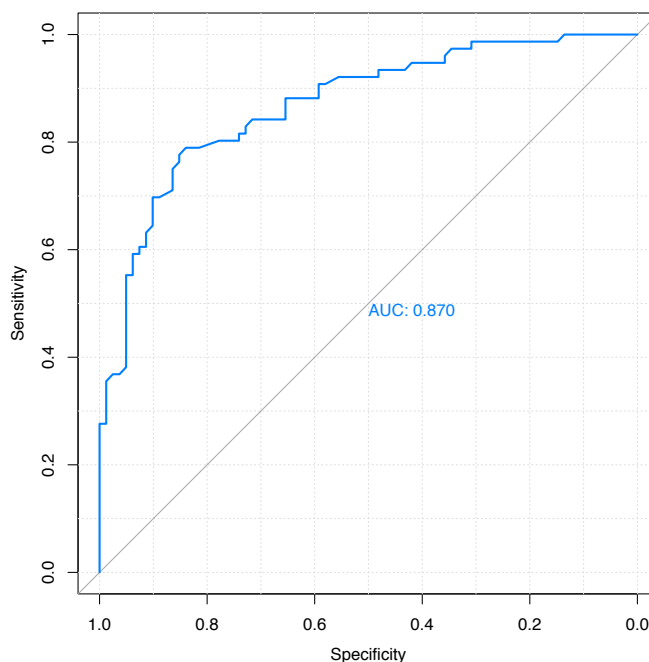
Figure 1: ROC curve for the test set of protein subcellular localization data

3. Applications in Chemoinformatics

For chemoinformatics research, **Rcpi** calculates various types of molecular descriptors/fingerprints, and computes pairwise similarities derived by fingerprints and maximum common substructure search. **Rcpi** also provides the `searchDrug()` function for parallelized molecular similarity search based on these similarity types.

3.1. Regression Modeling in QSRR Study of Retention Indices

In Yan *et al.* (2012), a quantitative structure-retention relationship study was performed for 656 flavor compounds on four stationary phases of different polarities, using constitutional, topological and geometrical molecular descriptors. The gas chromatographic retention indices (RIs) of these compounds were accurately predicted using linear models. Here we choose the molecules and their RIs of one stationary phase (OV101) as our benchmark dataset.

Since it would be rather tedious to implement the complete cross-validation procedures, the R package **caret** is used here. To run the R code below, users need to install the **caret** package and the required predictive modeling packages first. The **caret** package provides a unified interface for the modeling tuning task across different statistical machine learning packages. It is particularly helpful in QSAR modeling, for it contains tools for data splitting, pre-processing, feature selection, model tuning and other functionalities.

Just like the last section, we load the **Rcpi** package, and read the molecules stored in a SMILES file:

require(Rcpi)

```
RI.smi = system.file('vignettedata/FDAMDD.smi', package = 'Rcpi')
RI.csv = system.file('vignettedata/RI.csv', package = 'Rcpi')

x.mol = readMolFromSmi(RI.smi, type = 'mol')
x.tab = read.table(RI.csv, sep = '\t', header = TRUE)
y     = x.tab$RI
```

The `readMolFromSmi()` function is used for reading molecules from SMILES files, for molecules stored in SDF files, use `readMolFromSDF()` instead.

The CSV file `RI.csv` contains tabular data for the retention indices, compound name, and odor information of the compounds. Here we only extracted the RI values by calling `x.tab$RI`.

After the molecules were properly loaded, we calculate several selected molecular descriptors. The corresponding functions for molecular descriptor calculation are all named after `extractDrug...()` in **Rcpi**:

```
# calculate selected molecular descriptors
x = suppressWarnings(cbind(
    extractDrugALOGP(x.mol),
    extractDrugApol(x.mol),
    extractDrugECI(x.mol),
    extractDrugTPSA(x.mol),
    extractDrugWeight(x.mol),
    extractDrugWienerNumbers(x.mol),
    extractDrugZagrebIndex(x.mol)))
```

After the descriptors were calculated, the result `x` would be an R data frame, each row represents one molecule, and each column is one descriptor (predictor). The Rcpi package integrated the molecular descriptors and chemical fingerprints calculated by the **rcdk** package (Steinbeck *et al.* 2003) and the **ChemmineOB** package (Horan and Girke 2013).

Next, a partial least squares model will be fitted with the **pls** and **caret** package. The cross-validation setting is 5-fold repeated CV (repeat for 10 times).

```
# regression on training set
require(caret)
require(pls)

# cross-validation settings
ctrl = trainControl(method = 'repeatedcv', number = 5, repeats = 10,
                    summaryFunction = defaultSummary)

# train pls model
set.seed(1002)
pls.fit = train(x, y, method = 'pls', tuneLength = 10, trControl = ctrl,
                metric = 'RMSE', preProc = c('center', 'scale'))
```

```
# print cross-validation result
print(pls.fit)
```

The cross-validation result is:

```
## Partial Least Squares
##
## 297 samples
##  10 predictors
##
## Pre-processing: centered, scaled
## Resampling: Cross-Validated (5 fold, repeated 10 times)
##
## Summary of sample sizes: 237, 237, 237, 238, 239, 238, ...
##
## Resampling results across tuning parameters:
##
##   ncomp  RMSE   Rsquared  RMSE SD  Rsquared SD
##   1      104    0.884     9.44     0.0285
##   2      86.4   0.92      6.99     0.0194
##   3      83.8   0.924     6.56     0.0185
##   4      79.6   0.931     6.98     0.0194
##   5      76.3   0.937     7.45     0.0187
##   6      74.7   0.94      6.85     0.0162
##   7      73.7   0.941     6.75     0.0159
##   8      73.5   0.942     6.5      0.0142
##   9      72.5   0.944     6.18     0.0137
##
## RMSE was used to select the optimal model using  the smallest value.
## The final value used for the model was ncomp = 9.
```

We see that the RMSE of the PLS regression model was decreasing when the number of principal components (`ncomp`) was increasing. We can plot the components and RMSE to helps us select the desired number of principal components used in the model.

```
# Components vs RMSE
print(plot(pls.fit, asp = 0.5))
```

From figure 2, we consider that selecting six or seven components is acceptable. At last, we plot the experimental RIs and the predicted RIs to see if the model fits well on the training set (Figure 3):

```
# plot experimental RIs vs predicted RIs
plot(y, predict(pls.fit, x), xlim = range(y), ylim = range(y),
     col = '#0080ff', xlab = 'Experimental RIs', ylab = 'Predicted RIs')
abline(a = 0, b = 1)
```
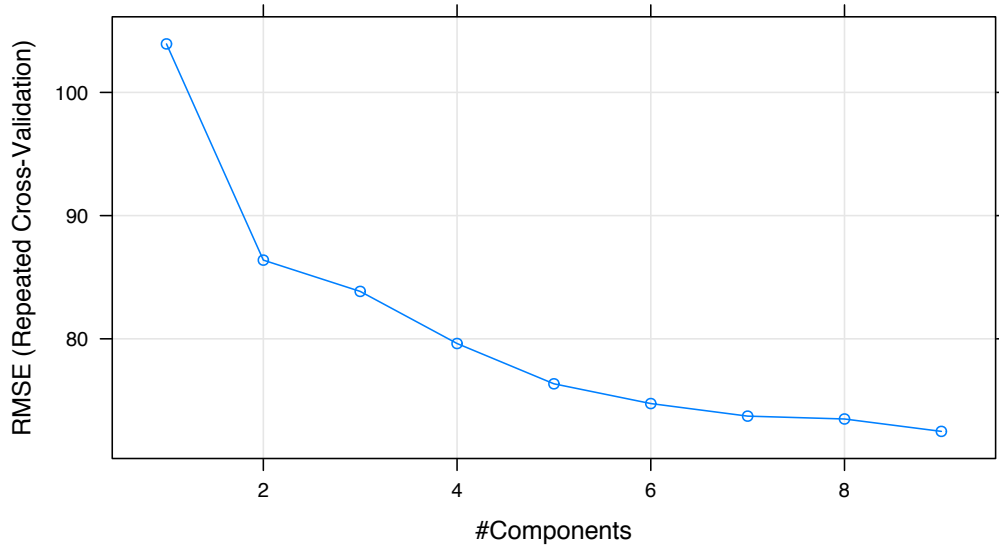
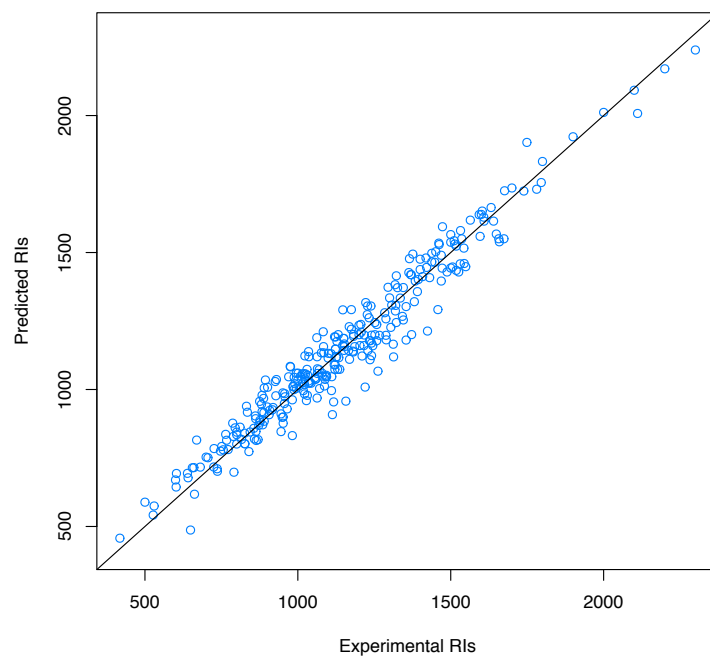Figure 2: Number of principal components vs. RMSE for the PLS regression model

Figure 3: Experimental RIs vs. Predicted RIs

3.2. In Silico Toxicity Classification for Drug Discovery

In the perspective of quantitative pharmacology, the successful discovery of novel drugs depends on the pharmacokinetics properties, like **a**bsorption, **d**istribution, **m**etabolism, and **e**xcretion. In addition, the potential **t**oxicity of chemical compounds is taken into account. QSAR or QSPR methods are usually employed to predict the ADME/T qualities of potential drug candidates.

In the study of Cao *et al.* (2012b), quantitative structure-toxicity relationship (QSTR) models were established for classifying five toxicity datasets. Here we use the maximum recommended daily dose dataset (FDAMDD) from FDA Center for Drug Evaluation and Research as our benchmark dataset.

First, load the drug molecules stored in a SMILES file into R:

```
require(Rcpi)

fdamdd.smi = system.file('vignettedata/FDAMDD.smi', package = 'Rcpi')
fdamdd.csv = system.file('vignettedata/FDAMDD.csv', package = 'Rcpi')

x.mol = readMolFromSmi(fdamdd.smi, type = 'mol')
x.smi = readMolFromSmi(fdamdd.smi, type = 'text')
y     = as.factor(paste0('class', scan(fdamdd.csv)))
```

The object `x.mol` is used for computing the MACCS and E-state fingerprints, the object `x.smi` is used for computing the FP4 fingerprints. The 0-1 class labels stored in `FDAMDD.csv` indicates whether the drug molecule has high toxicity or not.

Then we calculate three different types of molecular fingerprints (E-state, MACCS, and FP4) for the drug molecules:

```
# calculate molecular fingerprints
x1 = extractDrugEstateComplete(x.mol)
x2 = extractDrugMACCSComplete(x.mol)
x3 = extractDrugOBFP4(x.smi, type = 'smile')
```

As the nature of fingerprint-based structure representation, the calculated 0-1 matrix `x1`, `x2`, and `x3` will be very sparse. Since there are several columns have nearly exactly the same value for all the molecules, we should remove them with `nearZeroVar()` in **caret** before modeling, and split our training set and test set:

```
# Remove near zero variance variables
require(caret)
x1 = x1[, -nearZeroVar(x1)]
x2 = x2[, -nearZeroVar(x2)]
x3 = x3[, -nearZeroVar(x3)]

# split training and test set
set.seed(1003)
```

```
tr.idx = sample(1:nrow(x1), round(nrow(x1) * 0.75))
te.idx = setdiff(1:nrow(x1), tr.idx)
x1.tr  = x1[tr.idx, ]
x1.te  = x1[te.idx, ]
x2.tr  = x2[tr.idx, ]
x2.te  = x2[te.idx, ]
x3.tr  = x3[tr.idx, ]
x3.te  = x3[te.idx, ]
y.tr   = y[tr.idx]
y.te   = y[te.idx]
```

On the training sets, we will train three classification models separately using SVM (RBF kernel), using the **kernlab** package and **caret** package. The cross-validation setting is 5-fold repeated CV (repeat for 10 times). Then print the cross-validation result.

```
# svm classification on training sets
require(kernlab)

# cross-validation settings
ctrl = trainControl(method = 'cv', number = 5, repeats = 10,
                    classProbs = TRUE,
                    summaryFunction = twoClassSummary)

# SVM with RBF kernel
svm.fit1 = train(x1.tr, y.tr, method = 'svmRadial', trControl = ctrl,
                 metric = 'ROC', preProc = c('center', 'scale'))
svm.fit2 = train(x2.tr, y.tr, method = 'svmRadial', trControl = ctrl,
                 metric = 'ROC', preProc = c('center', 'scale'))
svm.fit3 = train(x3.tr, y.tr, method = 'svmRadial', trControl = ctrl,
                 metric = 'ROC', preProc = c('center', 'scale'))

# print cross-validation result
print(svm.fit1)
print(svm.fit2)
print(svm.fit3)
```

The training result when using E-state fingerprints:

```
## Support Vector Machines with Radial Basis Function Kernel
##
## 597 samples
##  23 predictors
##   2 classes: 'class0', 'class1'
##
## Pre-processing: centered, scaled
## Resampling: Cross-Validated (5 fold)
##
## Summary of sample sizes: 478, 479, 477, 477, 477
##
## Resampling results across tuning parameters:
##
##   C     ROC    Sens   Spec   ROC SD   Sens SD  Spec SD
##   0.25  0.797  0.7    0.765  0.0211   0.0442   0.00666
##   0.5   0.808  0.696  0.79   0.0173   0.059    0.0236
##   1     0.812  0.703  0.781  0.0191   0.0664   0.0228
```

```
##
## Tuning parameter 'sigma' was held constant at a value of 0.02921559
## ROC was used to select the optimal model using  the largest value.
## The final values used for the model were sigma = 0.0292 and C = 1.
```

We could see that after removing the near zero variance predictors, there are only 23 predictors left for the original length 79 E-state fingerprints.

The training result when using MACCS keys:

```
## Support Vector Machines with Radial Basis Function Kernel
##
## 597 samples
## 126 predictors
##   2 classes: 'class0', 'class1'
##
## Pre-processing: centered, scaled
## Resampling: Cross-Validated (5 fold)
##
## Summary of sample sizes: 477, 477, 477, 478, 479
##
## Resampling results across tuning parameters:
##
##   C     ROC    Sens   Spec   ROC SD  Sens SD  Spec SD
##   0.25  0.834  0.715  0.775  0.0284  0.0994   0.0589
##   0.5   0.848  0.726  0.79   0.0299  0.065    0.0493
##   1     0.863  0.769  0.793  0.0307  0.0229   0.0561
##
## Tuning parameter 'sigma' was held constant at a value of 0.004404305
## ROC was used to select the optimal model using  the largest value.
## The final values used for the model were sigma = 0.0044 and C = 1.
```

There are 126 predictors left for the original length 166 MACCS keys after removing the near zero variance predictors. The model performance by AUC values is slightly better than using the E-state fingerprints.

The training result when using FP4 fingerprints:

```
## Support Vector Machines with Radial Basis Function Kernel
##
## 597 samples
##  58 predictors
##   2 classes: 'class0', 'class1'
##
## Pre-processing: centered, scaled
## Resampling: Cross-Validated (5 fold)
##
## Summary of sample sizes: 478, 478, 477, 478, 477
##
## Resampling results across tuning parameters:
##
##   C     ROC    Sens   Spec   ROC SD  Sens SD  Spec SD
##   0.25  0.845  0.769  0.746  0.0498  0.0458   0.0877
##   0.5   0.856  0.744  0.777  0.0449  0.0148   0.0728
##   1     0.863  0.751  0.777  0.0428  0.036    0.0651
##
## Tuning parameter 'sigma' was held constant at a value of 0.01077024
## ROC was used to select the optimal model using  the largest value.
## The final values used for the model were sigma = 0.0108 and C = 1.
```

There are 58 predictors left for the original length 512 FP4 fingerprints after the screening. The model performance by AUC values is almost the same comparing to using MACCS keys, and better than using E-state fingerprints.

We predict on the test sets with the established models, and plot the ROC curves in one figure, as is shown in figure 4.

```
# predict on test set
svm.pred1 = predict(svm.fit1, newdata = x1.te, type = 'prob')[, 1]
svm.pred2 = predict(svm.fit2, newdata = x2.te, type = 'prob')[, 1]
svm.pred3 = predict(svm.fit3, newdata = x3.te, type = 'prob')[, 1]

# generate colors
require(RColorBrewer)
pal = brewer.pal(3, 'Set1')

# ROC curves of different fingerprints
require(pROC)
plot(smooth(roc(y.te, svm.pred1)), col = pal[1], grid = TRUE)
plot(smooth(roc(y.te, svm.pred2)), col = pal[2], grid = TRUE, add = TRUE)
plot(smooth(roc(y.te, svm.pred3)), col = pal[3], grid = TRUE, add = TRUE)
```
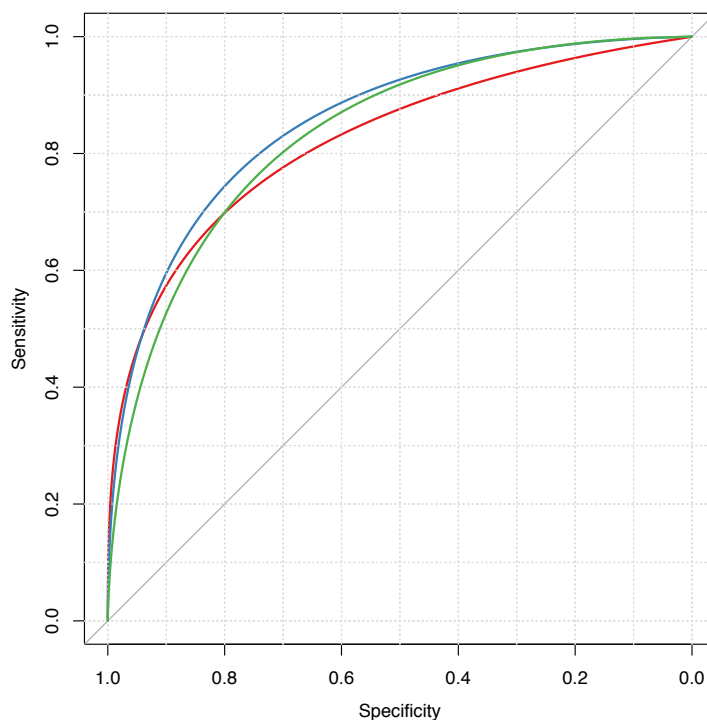

Figure 4: Smoothed ROC curves for different fingerprint types

3.3. Clustering of Molecules Based on Structural Similarities

Apart from supervised methods (classification and regression), unsupervised approaches, like clustering, is also widely applied in the quantitative research of drugs.

In reality, there are usually too many chemical compounds available for identifying drug-like

molecules. Thus it would be attractive using clustering methods to aid the selection of a representative subset of all available compounds. For a clustering approach that groups compounds together by their structural similarity, applying the principle *similar compounds have similar properties* means that we only need to test the representative compounds from each individual cluster, rather than do the time-consuming complete set of experiments, and this should be sufficient to understand the structure-activity relationships of the whole compound set.

The **Rcpi** package provides easy-to-use functions for computing the similarity between small molecules derived by molecular fingerprints and maximum common substructure search.

As a example, the SDF file `tyrphostin.sdf` below is a database composed by searching *tyrphostin* in PubChem and filtered by *Lipinski's rule of five*. We load this SDF file into R using `readMolFromSDF()`:

```
require(Rcpi)
mols = readMolFromSDF(system.file('compseq/tyrphostin.sdf', package = 'Rcpi'))
```

Then compute the E-state fingerprints for all the molecules using `extractDrugEstate()`, and calculate their pairwise similarity matrix with `calcDrugFPSim()`:

```
simmat = diag(length(mols))

for (i in 1:length(mols)) {
 for (j in i:length(mols)) {
   fp1 = extractDrugEstate(mols[[i]])
   fp2 = extractDrugEstate(mols[[j]])
   tmp = calcDrugFPSim(fp1, fp2, fptype = 'compact', metric = 'tanimoto')
   simmat[i, j] = tmp
   simmat[j, i] = tmp
 }
}
```

For the computed similarity matrix `simmat`, we will try to do hierarchical clustering with it, then visualize the clustering result:

```
mol.hc = hclust(as.dist(1 - simmat), method = 'ward')

require(ape)  # for tree-like visualization
clus5 = cutree(mol.hc, 5)  # cut dendrogram into 5 clusters

# generate colors
require(RColorBrewer)
pal5 = brewer.pal(5, 'Set1')
plot(as.phylo(mol.hc), type = 'fan', tip.color = pal5[clus5],
     label.offset = 0.1, cex = 0.7)
```

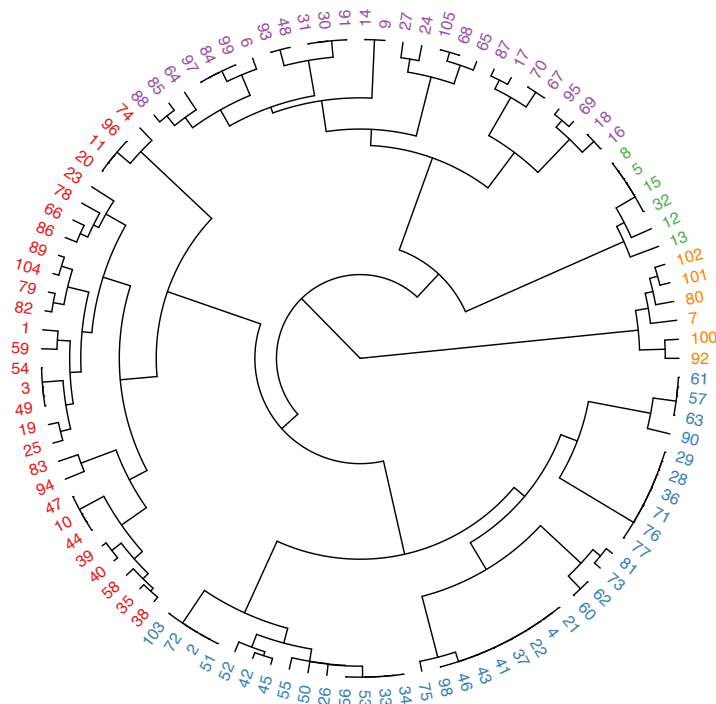The clustering result for these molecules is shown in figure 5.

Figure 5: Tree visualization of molecular clustering result

3.4. Structure-Based Chemical Similarity Searching

Structure-based chemical similarity searching ranks molecules in a database by their similarity degree to one query molecule structure. The numerical similarity value is usually computed based on the molecular fingerprints with selected metrics or by maximum common structure search. It is one of the core techniques for ligand-based virtual screening in drug discovery.

The SDF file `DB00530.sdf` below is retrieved from DrugBank, the drug ID DB00530 is *Erlotinib*, which is a reversible tyrosine kinase inhibitor. Given this molecule as the query molecule, we will do a similarity searching in the database `tyrphostin.sdf` presented in the last subsection.

```
require(Rcpi)


mol   = system.file('compseq/DB00530.sdf', package = 'Rcpi')
moldb = system.file('compseq/tyrphostin.sdf', package = 'Rcpi')
```

We could do parallelized drug molecular similarity search with the `searchDrug()` function in **Rcpi**. Here we choose the search criterion to be MACCS keys with cosine similarity, FP2 fingerprints with tanimoto similarity, and maximum common substructure search with tanimoto similarity.

```
rank1 = searchDrug(mol, moldb, cores = 4, method = 'fp',
                fptype = 'maccs', fpsim = 'tanimoto')
```

```
rank2 = searchDrug(mol, moldb, cores = 4, method = 'fp',
                   fptype = 'fp2', fpsim = 'cosine')
rank3 = searchDrug(mol, moldb, cores = 4, method = 'mcs',
                   mcssim = 'tanimoto')
```

The returned search result is stored as a numerical vector, each element's name is the molecule number in the database, and the value is the similarity value between the query molecule and this molecule. We shall print the top search results here:

```
head(rank1)
##        92       100        83       101         1        36
## 0.6491228 0.6491228 0.5882353 0.5660377 0.5000000 0.4861111


head(rank2)
##       100        92        83       101        94        16
## 0.8310005 0.8208663 0.5405856 0.5033150 0.4390790 0.4274081


head(rank3)
##        92       100        23        39        94        64
## 0.7000000 0.7000000 0.4000000 0.4000000 0.4000000 0.3783784
```

The **Rcpi** package also integrated the functionality of converting molecular file formats. For example, we could convert the SDF files to SMILES files using `convMolFormat()`. Since the No. 92 molecule ranks the highest in the three searches performed, we will calculate the similarity derived by maximum common substructure search between the query molecule and the No. 92 molecule using `calcDrugMCSSim()`:

```
# convert SDF format to SMILES format
convMolFormat(infile = mol, outfile = 'DB00530.smi', from = 'sdf', to = 'smiles')
convMolFormat(infile = moldb, outfile = 'tyrphostin.smi', from = 'sdf', to = 'smiles')


smi1 = readLines('DB00530.smi')
smi2 = readLines('tyrphostin.smi')[92]  # select No.92 molecule in database
calcDrugMCSSim(smi1, smi2, type = 'smile', plot = TRUE)
```

The MCS search result is stored in a list, which contains the original MCS result provided by the **fmcsR** package (Wang *et al.* 2013), the Tanimoto coefficient and the overlap coefficient.

```
## [[1]]
## An instance of "MCS"
##  Number of MCSs: 1
##  530: 29 atoms
##  4705: 22 atoms
##  MCS: 18 atoms
##  Tanimoto Coefficient: 0.54545
##  Overlap Coefficient: 0.81818
##
## [[2]]
## Tanimoto_Coefficient
```

```
##            0.5454545
##
## [[3]]
## Overlap_Coefficient
##            0.8181818
```

By using `calcDrugMCSSim(..., plot = TRUE)`, the maximum common substructure of the two molecules is presented in figure 6.
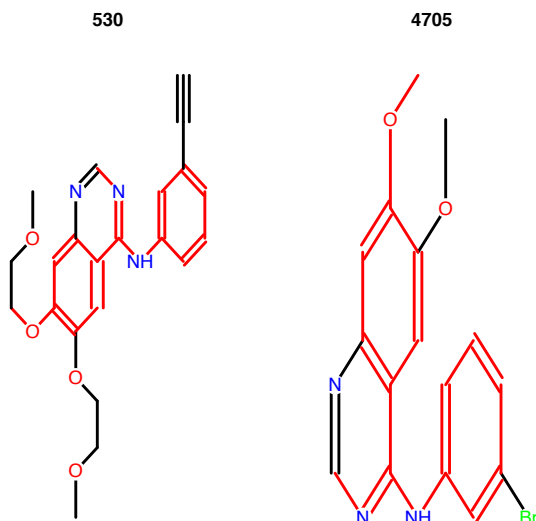

Figure 6: Maximum common structure of the query molecule and No.92 molecule in the chemical database (SDF file)

4. Applications in Chemogenomics

For chemogenomics modeling, **Rcpi** calculates compound-protein interaction (CPI) descriptors and protein-protein interaction (PPI) descriptors.

4.1. Predicting Drug-Target Interaction by Integrating Chemical and Genomic Spaces

The prediction of novel interactions between drugs and target proteins is a key area in genomic drug discovery. In this example, we use the G protein-coupled receptor (GPCR) dataset provided by Yamanishi *et al.* (2008) as our benchmark dataset.

A drug-target interaction network can be naturally modeled as a bipartite graph, where the nodes are target proteins or drug molecules and edges (only drugs and proteins could be connected by edges) represent drug-target interactions. Initially, the graph only contains edges describing the *real* drug-target interactions determined by experiments or other ways. In this example, all real drug-target interaction pairs (i.e., 635 drug-target interactions) are used as the positive samples. For negative samples we select random, non-interacting pairs from these drugs and proteins. They are constructed as follows:

1. Separate the pairs in the above positive samples into single drugs and proteins;

2. Re-couple these singles into pairs in a way that none of them occurs in the corresponding positive dataset.

Ten generated negative sets were used in Cao *et al.* (2012a), here we only use one of them for a demonstration. The drug ID and target ID is stored in `GPCR.csv`. The first column is KEGG protein ID, and the second column is KEGG drug ID. The first 635 rows is the positive set, and the last 635 rows is the negative set.

```
require(Rcpi)
```

```
gpcr = read.table(system.file('vignettedata/GPCR.csv', package = 'Rcpi'),
                  header = FALSE, as.is = TRUE)
```

Get a glimpse of the data:

```
head(gpcr)
```

```
##            V1      V2
## 1 hsa:10161 D00528
## 2 hsa:10800 D00411
## 3 hsa:10800 D01828
## 4 hsa:10800 D05129
## 5 hsa:11255 D00234
## 6 hsa:11255 D00300
```

We will visualize the network first. Figure 7 shows the connection pattern for the GPCR drug-target interaction network in the form of an *arc diagram*.

```
require(igraph)
require(arcdiagram)
require(reshape)

g = graph.data.frame(gpcr[1:(nrow(gpcr)/2), ], directed = FALSE)
edgelist = get.edgelist(g)
vlabels  = V(g)$name
vgroups  = c(rep(0, 95), rep(1, 223))
vfill    = c(rep('#8B91D4', 95), rep('#B2C771', 223))
vborders = c(rep('#6F74A9', 95), rep('#8E9F5A', 223))
degrees  = degree(g)

xx = data.frame(vgroups, degrees, vlabels, ind = 1:vcount(g))
yy = arrange(xx, desc(vgroups), desc(degrees))
new.ord = yy$ind

arcplot(edgelist, ordering = new.ord, labels = vlabels,
        cex.labels = 0.1, show.nodes = TRUE,
```

```
          col.nodes = vborders, bg.nodes = vfill,
          cex.nodes = log10(degrees) + 0.1,
          pch.nodes = 21, line = -0.5, col.arcs = hsv(0, 0, 0.2, 0.25))
```
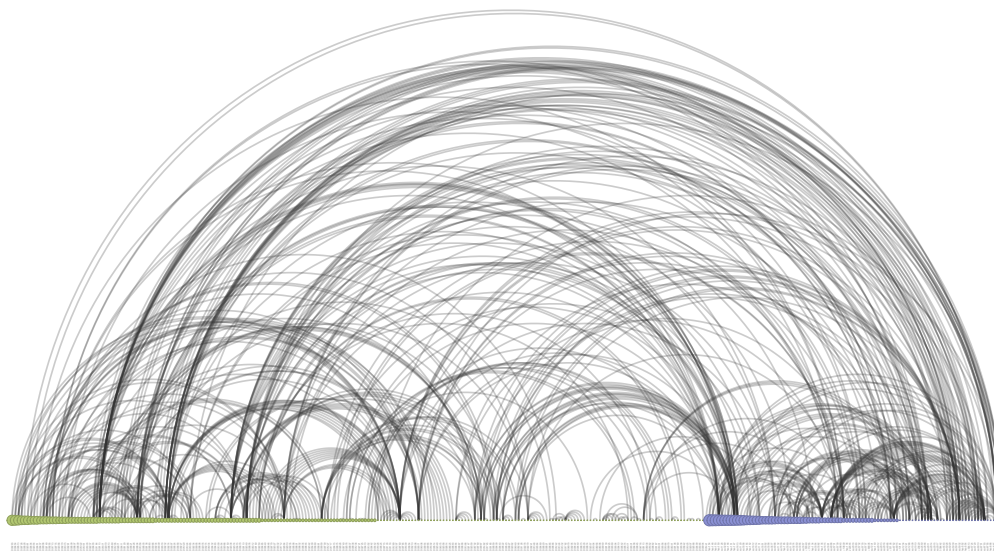

Figure 7: Arc diagram visualization of the GPCR drug-target interaction network

An arc diagram visualize the nodes in the network in a one-dimensional layout, while using circular arcs to represent edges. With a good ordering of nodes, it is easy to identify cliques and bridges.

Next, we will download the target protein sequences (in FASTA format) and drug molecule (in SMILES format) from the KEGG database, in parallel:

```
require(Rcpi)

gpcr   = read.table(system.file('vignettedata/GPCR.csv', package = 'Rcpi'),
                    header = FALSE, as.is = TRUE)

protid = unique(gpcr[, 1])
drugid = unique(gpcr[, 2])

protseq = getSeqFromKEGG(protid, parallel = 5)
drugseq = getSmiFromKEGG(drugid, parallel = 50)
```

If the connection is slow or accidentally interrupts, just try more times until success.

The functions in **Rcpi** named after `getMolFrom...()` and `getSmiFrom...()` supports the parallelized retrieval of (drug) molecules from PubChem, ChEMBL, CAS, KEGG, and DrugBank. The functions named after `getSeqFrom...()`, `getFASTAFrom...()` and `getPDBFrom...()` supports the parallelized retrieval of proteins from UniProt, KEGG and RCSB PDB. The functions `getDrug()` and `getProt()` are two integrated wrapper functions for downloading the molecules and protein sequences from these online databases.

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After the sequences were downloaded, we could calculate the protein sequence descriptors and molecular descriptors for the targets and drugs:

```
x0.prot = cbind(t(sapply(unlist(protseq), extractProtAPAAC)),
                t(sapply(unlist(protseq), extractProtCTriad)))

x0.drug = cbind(extractDrugEstateComplete(readMolFromSmi(textConnection(drugseq))),
                extractDrugMACCSComplete(readMolFromSmi(textConnection(drugseq))),
                extractDrugOBFP4(drugseq, type = 'smile'))
```

Since the descriptors is only for the *uniqued* drug and target list, we need to generate the full descriptor matrix for the training data:

```
# generate drug x / protein x / y
x.prot = matrix(NA, nrow = nrow(gpcr), ncol = ncol(x0.prot))
x.drug = matrix(NA, nrow = nrow(gpcr), ncol = ncol(x0.drug))
for (i in 1:nrow(gpcr)) x.prot[i, ] = x0.prot[which(gpcr[, 1][i] == protid), ]
for (i in 1:nrow(gpcr)) x.drug[i, ] = x0.drug[which(gpcr[, 2][i] == drugid), ]

y = as.factor(c(rep('pos', nrow(gpcr)/2), rep('neg', nrow(gpcr)/2)))
```

Generate drug-target interaction descriptors using `getCPI()`.

```
x = getCPI(x.prot, x.drug, type = 'combine')
```

The pairwise interaction is another useful type of representation in drug-target prediction, protein-protein interaction prediction and related research. **Rcpi** also provides `getPPI()` to generate protein-protein interaction descriptors. `getPPI()` provides three types of interactions while `getCPI()` provides two types. The argument `type` is used to control this:

- Compound-Protein Interaction (CPI) Descriptors

  For compound descriptor vector $d_1^{1 \times p_1}$ and the protein descriptor vector $d_2^{1 \times p_2}$, there are two methods for construction of descriptor vector d for compound-protein interaction:

  1. `'combine'` - combine the two feature matrix, d has $p_1 + p_2$ columns;
  2. `'tensorprod'` - column-by-column (pseudo)-tensor product type interactions, d has $p_1 \times p_2$ columns.

- Protein-Protein Interaction (PPI) Descriptors

  For interaction protein A and protein B, let $d_1^{1 \times p}$ and $d_2^{1 \times p}$ be the descriptor vectors. There are three methods to construct the protein-protein interaction descriptor d:

  1. `'combine'` - combine the two descriptor matrix, d has $p + p$ columns;
  2. `'tensorprod'` - column-by-column (pseudo)-tensor product type interactions, d has $p \times p$ columns;

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3. `'entrywise'` - entrywise product and entrywise sum of the two matrices, then combine them, d has $p + p$ columns.

Train a random forest classification model with 5-fold repeated CV:

```
require(caret)
x = x[, -nearZeroVar(x)]

# cross-validation settings
ctrl = trainControl(method = 'cv', number = 5, repeats = 10,
                    classProbs = TRUE,
                    summaryFunction = twoClassSummary)

# train a random forest classifier
require(randomForest)
set.seed(1006)
rf.fit = train(x, y, method = 'rf', trControl = ctrl,
               metric = 'ROC', preProc = c('center', 'scale'))
```

Print the cross-validation result:

```
print(rf.fit)
```

```
## Random Forest
##
## 1270 samples
##  562 predictors
##    2 classes: 'neg', 'pos'
##
## Pre-processing: centered, scaled
## Resampling: Cross-Validated (5 fold)
##
## Summary of sample sizes: 1016, 1016, 1016, 1016, 1016
##
## Resampling results across tuning parameters:
##
##   mtry  ROC    Sens   Spec   ROC SD  Sens SD  Spec SD
##   2     0.83   0.726  0.778  0.0221  0.044    0.0395
##   33    0.882  0.795  0.82   0.018   0.0522   0.0443
##   562   0.893  0.822  0.844  0.0161  0.0437   0.0286
##
## ROC was used to select the optimal model using  the largest value.
## The final value used for the model was mtry = 562.
```

Predict on the training set (for demonstration purpose only) and plot ROC curve.

```
rf.pred = predict(rf.fit$finalModel, x, type = 'prob')[, 1]

require(pROC)
plot(smooth(roc(y, rf.pred)), col = '#0080ff', grid = TRUE, print.auc = TRUE)
```
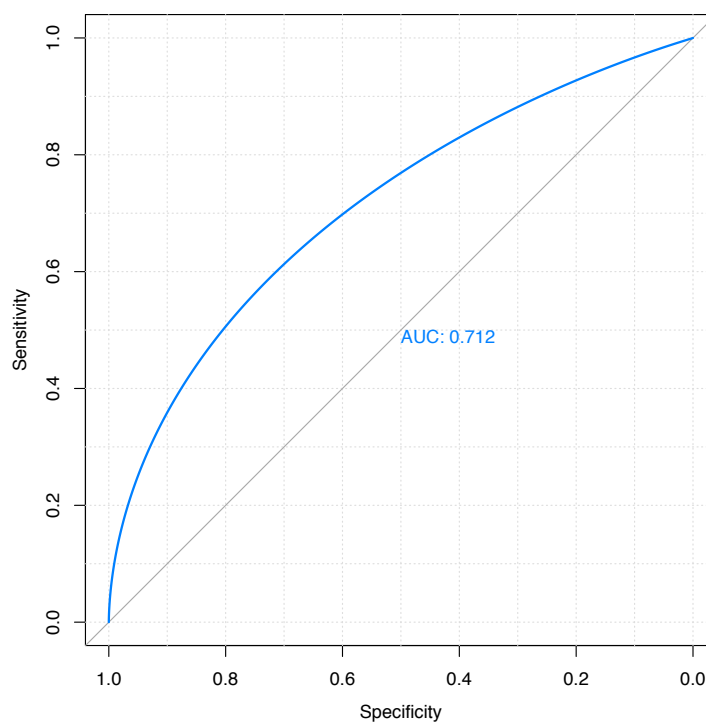
The ROC curve is shown in figure 8.

Figure 8: ROC curve for predicting on the training set of the GPCR drug-target interaction dataset using random forest

Acknowledgments

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