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An introduction to CFTK, the co-fractionation toolkit

CFTK, the co-fractionation toolkit, is an R package designed for the analysis of co-fractionation mass spectrometry (CF-MS) data. CFTK provides convenient and flexible implementations of many of the most common analysis tasks that investigators working with CF-MS data seek to perform. These include loading CF-MS data and known protein complexes into R, preprocessing the data, filtering low-quality chromatograms, evaluating data quality, scoring proteins with similar patterns of fractionation, and integrating data across multiple replicates using a machine-learning approach.

This vignette demonstrates the major functionality of the CFTK package through application to an example dataset. The CF-MS data was obtained from Kirkwood *et al.*, 2013 (1), who profiled 40 size exclusion chromatography (SEC) fractions from human osteosarcoma (U2OS) cells, in three biological replicates. The raw data was obtained from the ProteomeXchange, under accession PXD001220, and reprocessed with MaxQuant (version 1.6.5.0), using default parameters. All of the data analyzed in this vignette is available from the `data-raw` folder on the GitHub repository, at <https://github.com/fosterlab/CFTK> (<https://github.com/fosterlab/CFTK>).

The code presented in this vignette assumes that you have set your working directory to the location of the CFTK package. This can be accomplished using the `setwd` function. For example, if you are using a Linux or macOS machine and have downloaded the CFTK package to a directory named `git` inside your home directory, run the following command:

```
setwd("~/git/CFTK")
```

Adjust the path to the CFTK package directory as needed.

The code in this vignette also makes use of functions from the `magrittr`, `dplyr`, and `purrr` packages, which are installed along with the CFTK package. Load these packages before running this code, and set `stringsAsFactors` to `FALSE`, using the following command:

```
library(magrittr)
library(dplyr)
library(purrr)
options(stringsAsFactors = FALSE)
```

Loading CF-MS data from MaxQuant

CFTK is agnostic to the specific pipeline used to search and quantify raw mass spectrometric data. However, it does provide a convenience function to import CF-MS chromatograms searched using MaxQuant (2), by parsing MaxQuant `proteinGroups.txt` files. This functionality is implemented in the `read_maxquant()` function, which allows the user to import chromatograms using multiple different quantitation modes (providing, of course, that the information is present in the file), including iBAQ, MaxLFQ, MS1 intensity, spectral counts, and isotopologue ratios. The function also provides a method to map protein groups to genes, using information contained in the `Gene names` column of the `proteinGroups.txt` file. To read the first replicate from PXD001220, using the label-free quantitation implemented in MaxLFQ and mapping protein groups to gene names, run the following function:

```
filepath = "data-raw/PXD001220/repl/proteinGroups.txt.gz"
mat = read_maxquant(filepath, quant_mode = "MaxLFQ", identifiers = 'genes')
dim(mat)
```

```
## [1] 5229 40
```

```
str(mat)
```

```
## num [1:5229, 1:40] 0 2021400 0 0 0 ...
## - attr(*, "dimnames")=List of 2
## ..$ : chr [1:5229] "A2ML1" "AAAS" "AACS" "AAGAB" ...
## ..$ : chr [1:40] "LFQ.intensity.PT1541S1F00" "LFQ.intensity.PT1541S1F01"
"LFQ.intensity.PT1541S1F02" "LFQ.intensity.PT1541S1F03" ...
## - attr(*, "gene_map")='data.frame': 5229 obs. of 2 variables:
## ..$ gene : chr [1:5229] "A2ML1" "AAAS" "AACS" "AAGAB" ...
## ..$ protein_group: chr [1:5229] "A8K2U0" "Q9NRG9;F8VZ44;H3BU82;Q9NRG9-2"
"Q86V21;Q86V21-2" "Q6PD74-2;Q6PD74;H0YL49" ...
```

Because the `read_maxquant` function wraps the base R function `read.delim`, the filepath can also be a remote URL. For instance, if we wished to read a `proteinGroups.txt` file hosted on the server “my-website.com”, we could simply pass in the full URL of the file instead:

```
filepath = "http://my-website.com/maxquant/PXD001220/repl/proteinGroups.txt.gz"
mat = read_maxquant(filepath, quant_mode = "MaxLFQ", identifiers = 'genes')
```

As mentioned, CFTK is not limited to MaxQuant outputs, but can work with chromatograms obtained from any database search program. For alternative search programs, CFTK simply expects a numeric matrix, with proteins in rows and fractions in columns. Please note that this matrix must have

rownames set in order to link calculated features or predicted interactions to the proteins identified within the CF-MS experiment.

During the development of the CFTK package, we systematically re-analyzed 206 published CF-MS experiments using MaxQuant. The processed chromatograms obtained from this re-analysis are available from Zenodo, at <https://zenodo.org/record/4106578#.X--haulKh24> (<https://zenodo.org/record/4106578#.X--haulKh24>). In this upload, separate chromatogram matrices are provided for each protein quantification method implemented in MaxQuant (e.g., iBAQ vs. MaxLRFQ). A sample of the chromatograms available from Zenodo is also available in the `data-raw` directory. To read one of these chromatograms into R as a numeric matrix for use with the CFTK, enter the following command:

```
mat = read.delim("data-raw/zenodo/PXD001220/rep1/iBAQ.tsv.gz") %>%
  as.matrix()
```

To keep only the first UniProt accession associated with each protein group, enter the following command:

```
rownames(mat) %<>% gsub(";.*$", "", .)
```

Loading known protein complexes from CORUM

Investigators often seek to compare CF-MS data to known protein complexes for a variety of purposes. For this reason, CFTK provides a convenience function to read protein complex data distributed through the CORUM database (3), using the `read_corum()` function, although CFTK is similarly agnostic to the source of known protein complexes (or binary protein-protein interactions) used for CF-MS data analysis. This function allows the user to map complex subunits to either UniProt accessions, Entrez gene IDs, or gene names. CFTK also provides a variety of functions to convert protein complex data between various R data structures, including tidy data frames, lists, adjacency matrices, and pairwise data frames enumerating all intra-complex interactions.

To read the 'core' set of CORUM protein complexes, mapping subunits to their gene symbols, run the following function:

```
corum = read_corum("data-raw/CORUM/coreComplexes.txt.gz", identifiers = 'gene_name')
head(corum)
```

```
## # A tibble: 6 x 2
##   complex          subunit
##   <chr>            <chr>
## 1 BCL6-HDAC4 complex BCL6
## 2 BCL6-HDAC4 complex HDAC4
## 3 BCL6-HDAC5 complex BCL6
## 4 BCL6-HDAC5 complex HDAC5
## 5 BCL6-HDAC7 complex BCL6
## 6 BCL6-HDAC7 complex HDAC7
```

The `read_corum()` function returns a data frame in which the first column contains complex names, and the second column contains complex subunits. Often, however, we need to convert this data into a different format. For example, we might wish to convert this data frame into a list, where each entry represents a protein complex and contains a vector of its subunits. This can be achieved using the function `as_annotation_list()`:

```
complex_list = as_annotation_list(corum, 'complex', 'subunit')
str(complex_list[1:5])
```

```
## List of 5
## $ (E.F.G) complex                                : chr [1:
3] "SNRPE" "SNRPF" "SNRPG"
## $ (ER)-localized multiprotein complex, Ig heavy chains associated: chr [1:1
0] "Pdla4" "Hsp90b1" "P4hb" "Hspa5" ...
## $ 12S U11 snRNP                                  : chr [1:1
5] "SNRPB" "SNRPE" "SNRPF" "SNRPG" ...
## $ 14-3-3 gamma-CXCR2 complex, unstimulated        : chr [1:
2] "CXCR2" "YWHAG"
## $ 17S U2 snRNP                                    : chr [1:3
3] "U2SURF" "DHX15" "SF3B1" "DNAJC8" ...
```

Alternatively, we might wish to enumerate all possible pairs of proteins that are members of the same protein complex. From a list of protein complexes, we can construct a pairwise data frame of intra-complex pairs using the function `to_pairwise_df()`:

```
complex_pairs = to_pairwise_df(complex_list)
head(complex_pairs)
```

```
## # A tibble: 6 x 2
##   protein_A protein_B
##   <chr>      <chr>
## 1 SNRPE      SNRPF
## 2 SNRPE      SNRPG
## 3 SNRPF      SNRPG
## 4 Cabp1      Dnajb11
## 5 Cabp1      Hsp90b1
## 6 Cabp1      Hspa5
```

Finally, we might wish to create an adjacency matrix, in which each cell represents a potential protein-protein interaction and intra-complex pairs are marked as ones. This can be done from the pairwise data frame using the function `to_adjacency_matrix()`:

```
complex_adj = to_adjacency_matrix(complex_pairs)
str(complex_adj)
```

```
## num [1:5163, 1:5163] 0 1 0 0 0 0 0 0 0 0 ...
## - attr(*, "dimnames")=List of 2
## ..$ : chr [1:5163] "SNRPE" "SNRPF" "Cabp1" "Dnajb11" ...
## ..$ : chr [1:5163] "SNRPE" "SNRPF" "Cabp1" "Dnajb11" ...
```

These different representations of protein complexes are used by various functions throughout the CFTK package.

Loading functional annotations from the Gene Ontology

CFTK also provides a utility function to read protein function annotations from the Gene Ontology in GAF format, implemented in the function `read_gaf()`. This function also allows users to filter the GO: for instance, by removing annotations with less reliable or potentially recursive evidence codes, such as 'IEA' (inferred by electronic annotation) or 'IPI' (inferred from physical interaction). To read Gene Ontology annotations for human, removing interactions with the code 'IEA', run the following function:

```
goa = read_gaf("data-raw/GO/goa_human.gaf.gz", filter_evidence = "IEA")
head(goa)
```

```
## # A tibble: 6 x 17
##   DB      `DB Object ID` `DB Object Symb... Qualifier `GO ID` `DB:Reference`
##   <chr> <chr>          <chr>          <chr>    <chr>    <chr>
## 1 UniP... A0A024RBG1      NUDT4B          <NA>    GO:000... GO_REF:0000052
## 2 UniP... A0A075B6P5      IGKV2-28        <NA>    GO:000... Reactome:R-HS...
## 3 UniP... A0A075B6P5      IGKV2-28        <NA>    GO:000... Reactome:R-HS...
## 4 UniP... A0A075B6P5      IGKV2-28        <NA>    GO:000... Reactome:R-HS...
## 5 UniP... A0A075B6P5      IGKV2-28        <NA>    GO:000... Reactome:R-HS...
## 6 UniP... A0A075B6P5      IGKV2-28        <NA>    GO:000... Reactome:R-HS...
## # ... with 11 more variables: `Evidence Code` <chr>, `With (or) From` <chr>,
## #   Aspect <chr>, `DB Object Name` <chr>, `DB Object Synonym` <chr>, `DB Obj
## #   Type` <chr>, Taxon <chr>, Date <dbl>, `Assigned By` <chr>, `Annotation
## #   Extension` <lgl>, `Gene Product Form ID` <lgl>
```

CFTK also provides a convenience function, `go_roots()`, which returns a vector containing the Gene Ontology codes for 'biological process', 'molecular function', and 'cellular compartment'. This function can be used to filter these terms, which are usually considered uninteresting, from the set of annotations:

```
goa %<>% filter(!`GO ID` %in% go_roots())
```

To create a list in which each entry is a GO term, and contains a vector of all proteins annotated to that GO term, we can again make use of the function `as_annotation_list()`:

```
go_ann = as_annotation_list(goa, 'GO ID', 'DB Object Symbol')
str(go_ann[1:5])
```

```
## List of 5
## $ GO:0000002: chr [1:11] "OPA1" "SLC25A4" "TYMP" "LONP1" ...
## $ GO:0000003: chr [1:4] "MMP23B" "GNRH1" "LIN9" "GNRH2"
## $ GO:0000010: chr [1:2] "PDSS1" "PDSS2"
## $ GO:0000012: chr [1:8] "TNP1" "LIG4" "ERCC6" "ERCC8" ...
## $ GO:0000014: chr [1:10] "ERCC1" "MRE11" "SETMAR" "RAD50" ...
```

Preprocessing CF-MS data

Having read one or more CF-MS datasets into an R session, CFTK now provides several functions to pre-process the data. Low-quality chromatograms can be removed with the `filter_matrix()` function, which removes proteins not quantified in a certain minimum number of fractions. These typically represent a minority of identified proteins but in some cases, can account for a substantial fraction:

```
dim(mat)
```

```
## [1] 5229 40
```

```
mat %<>% filter_matrix(min_fractions = 4)
dim(mat)
```

```
## [1] 3641 40
```

Missing values are ubiquitous in CF-MS data, occurring for example in SEC data because proteins do not participate in any macromolecular complexes at the approximate molecular weight of a particular fraction, and can be handled in several different ways. CFTK provides the

`sanitize_missing_values()` and `replace_missing_values()` functions to deal with missing values. The first, `sanitize_missing_values()`, identifies `NA`s, `NaN`s, infinite values, and zeroes, and replaces them all with `NA`s. The second, `replace_missing_values()`, both enforces this consistent representation of missing data and then optionally replaces them either with zeroes, or random near-zero noise. To treat all missing values as zeroes, run the following command:

```
mat %<>% replace_missing_values(missing = 'zero')
```

Finally, CFTK also provides the `transform_matrix()` function to normalize the matrix, although we suggest that this function should be used sparingly and only when appropriate. This can be achieved either by log-transformation (because CF-MS data is approximately log-normally distributed), or quantile normalization. Users must be cautious about the order in which these operations are performed. For instance, replacing missing values with zeroes must be done *after* log-transformation, or this transformation may introduce a large number of `-Inf` values. Similarly, users wishing to treat missing values as zeroes should perform quantile normalization only *after* this step is complete. We suggest the following order of operations:

- i. filter the matrix
- ii. log-transform chromatograms (optional)
- iii. handle missing values

Identifying co-eluting protein pairs

One of the central tasks in CF-MS data analysis is to identify pairs (or groups) of proteins with similar patterns of elution across a chromatographic separation. This is commonly achieved using ubiquitous measures of association such as the Pearson correlation or Euclidean distance. In addition to these, CFTK implements a total of 24 measures of association that have been proposed for CF-MS or more general ‘-omics’ data analysis. These can be applied to obtain a square matrix, scoring the similarity of every protein pair in the experiment, using the `score_pairs()` function. For example, to score all protein pairs using the Bray-Curtis distance, enter the following command:

```
pairs = score_pairs(mat, metric = 'bray_curtis')
str(pairs)
```

```
## num [1:3641, 1:3641] 0 -0.962 -1 -0.91 -0.999 ...
## - attr(*, "dimnames")=List of 2
## ..$ : chr [1:3641] "AAAS" "AAK1" "AAMDC" "AAR2" ...
## ..$ : chr [1:3641] "AAAS" "AAK1" "AAMDC" "AAR2" ...
```

The complete list of all 24 metrics can be accessed using the `metrics()` function.

```
metrics()
```

```
## Bayesian correlation Biweight midcorrelation
## "bayes_cor" "bicor"
## Co-dependency index Bray-Curtis distance
## "binomial" "bray_curtis"
## Canberra distance Cosine distance
## "canberra" "cosine"
## Dice coefficient Distance correlation
## "dice" "distance_cor"
## Euclidean distance GENIE3
## "euclidean" "GENIE3"
## Hamming distance Jaccard index
## "hamming" "jaccard"
## Kendall correlation Manhattan distance
## "kendall" "manhattan"
## Mutual information Pearson correlation
## "MI" "pearson"
## Proportionality (phi) Profile correlation
## "phi_s" "profile_cor"
## Proportionality (rho) Spearman correlation
## "rho_p" "spearman"
## treeClust Weighted cross-correlation
## "treeClust" "wccor"
## Weighted rank correlation Zero-inflated Kendall correlation
## "weighted_rank" "zi_kendall"
```

The matrix of protein pairs can itself be filtered to replace pairs of proteins that were not *jointly* detected in some minimum number of fractions with `NA`s, using the `filter_pairs()` function. For instance, to mask protein pairs that did not co-occur in at least one fraction, enter the following command:

```
pairs0 = filter_pairs(pairs, mat, min_pairs = 1)
```

Combining information across replicates

While the `score_pairs()` function implements a number of different approaches to scoring co-eluting protein pairs within a single CF-MS experiment, investigators generally collect multiple CF-MS replicates from the same biological system in order to enable more robust network inference. The standard workflow for combining information across multiple replicates involves the application of a machine-learning workflow to score interacting protein pairs, by learning from a dataset of known protein complexes. (The same workflow can be applied to integrate evidence from multiple features within a single CF-MS replicate). Briefly, after calculating one or more measures of association (or ‘features’) for each protein pair in each replicate, these features are merged across replicates to create a single, consolidated data frame scoring every possible protein pair. Then, a ‘gold standard’ set of protein-protein interactions is loaded—for example, intra-complex interactions from the CORUM database. The ‘gold standard’ is split into a number of folds, and a series of machine-learning classifiers are trained on the features using the gold standard, with each fold excluded one at a time. The trained classifiers are used to compute the likelihood that all protein pairs *not* overlapping with the training set are interacting, based on the same CF-MS features. Protein pairs are then sorted by their mean classifier score across all folds, in descending order, to obtain a ranked list of all candidate protein-protein interactions.

Implementing the workflow described above using CFTK proceeds as follows. First, features for every protein pair must be calculated and merged into a single data frame. This can be done by repeatedly applying the `score_pairs()` function to calculate various features of interest, then merging them using the `merge_features()` function. The use of this function is demonstrated below to concatenate the Pearson correlation and Euclidean distance in a single replicate:

```
pairs1 = score_pairs(mat, metric = 'pearson')
pairs2 = score_pairs(mat, metric = 'euclidean')
feature_df = merge_features(list(pairs1, pairs2))
head(feature_df)
```

```
##   protein_A protein_B   feature.x feature.y
## 1      AAAS      AAK1 -0.09411139 -23260111
## 2      AAAS      AAMDC -0.08536994 -87324269
## 3      AAK1      AAMDC -0.11300250 -90066078
## 4      AAAS      AAR2 -0.07592153  -7575923
## 5      AAK1      AAR2 -0.11634107 -22942817
## 6      AAMDC      AAR2 -0.16347969 -87333061
```

Alternatively, if only a single measure of association is of interest, this can be calculated for a list of CF-MS matrices using the `calculate_features()` function. For instance, to calculate the Pearson correlation for three matrices simultaneously, run the following command:


```

replicates = c('rep1', 'rep2', 'rep3')
filepaths = file.path("data-raw/PXD001220", replicates, "proteinGroups.txt.gz")
mats = map(filepaths, read_maxquant, quant_mode = "MaxLFQ", identifiers = 'genes')
feature_df = calculate_features(mats, metric = 'pearson')
head(feature_df)

```

```

##   protein_A protein_B  pearson.x  pearson.y  pearson
## 1    A2ML1    AAAS -0.04712832         NA -0.02564103
## 2    A2ML1    AACS -0.04246607         NA -0.04556039
## 3     AAAS    AACS -0.07805282 -0.06936836 -0.04556039
## 4    A2ML1   AAGAB -0.04072171         NA -0.07851446
## 5     AAAS   AAGAB -0.07484668 -0.04305747 -0.07851446
## 6     AACS   AAGAB -0.06744234 -0.04130934  0.42458579

```

These two functions can be mixed and matched: for example, to calculate *two* measures of association per replicate, we could run the `calculate_features()` function again, then run `merge_features()`, like so:

```

feature_df1 = feature_df
feature_df2 = calculate_features(mats, metric = 'euclidean')
feature_df = merge_features(list(feature_df1, feature_df2))
head(feature_df)

```

```

##   protein_A protein_B  pearson.x  pearson.y  pearson euclidean.x
## 1    A2ML1    AAAS -0.04712832         NA -0.02564103    -5862973
## 2    A2ML1    AACS -0.04246607         NA -0.04556039   -14988257
## 3     AAAS    AACS -0.07805282 -0.06936836 -0.04556039   -15794796
## 4    A2ML1   AAGAB -0.04072171         NA -0.07851446    -3897018
## 5     AAAS   AAGAB -0.07484668 -0.04305747 -0.07851446    -6325701
## 6     AACS   AAGAB -0.06744234 -0.04130934  0.42458579   -15175240
##   euclidean.y euclidean
## 1           NA -22801490
## 2           NA -31431462
## 3   -33866995 -21714889
## 4           NA -27568896
## 5   -4420671 -15609088
## 6   -33682918 -19576405

```

When features are obtained from multiple replicates, there will typically be missing values, because not all proteins are quantified in all replicates. Some classifiers, such as the naive Bayes, can naturally handle these missing values. However, most will throw an error if missing values are included in the input. The `impute_missing_features()` function can be used to replace these missing values with the median value for that feature, plus or minus some random noise:

```

feature_df %<>% impute_missing_features()

```

Having calculated a series of features for this experiment, we are now ready to provide it as input to the cross-validation procedure, along with the complexes from the CORUM database that we loaded in above. This procedure is implemented in the `score_interactions()` function, which allows the

user to specify the number of cross-validation folds to perform (the default is 10) and select a classifier (one of 'NB' for naive Bayes, 'RF' for random forest, 'SVM' for support vector machine, or 'LR' for logistic regression). The `score_interactions()` function also allows the user to control the way in which cross-validation is performed. Specifically, the 'gold standard' complexes can be divided into folds that are disjoint either with respect to individual protein subunits (argument `split_by = 'proteins'`), or with respect to pairwise interactions (`split_by = 'pairs'`). Although splitting complexes by interacting pairs provides more data to the classifier, it can lead to overfitting. These cross-validation procedures are implemented in the `split_by()` function.

To run the `score_interactions()` function, enter the following command. (Note that this can take quite a while to run, depending on the size of the dataset, classifier selection, and number of cross-validation folds, so the code below is not run within this vignette).

```
## not run
interactions = score_interactions(feature_df, complex_pairs, n_folds = 3, classifier = 'NB')
```

This concludes the demonstration of the main functionality in the CFTK package. For more information, explore the R documentation, and please do not hesitate to contact us with any error reports at <http://github.com/fosterlab/CFTK/issues> (<http://github.com/fosterlab/CFTK/issues>).

References

1. Kirkwood KJ, Ahmad Y, Larance M, Lamond AI (2013) Characterization of native protein complexes and protein isoform variation using size-fractionation-based quantitative proteomics. *Mol Cell Proteomics* 12(12):3851–3873.
2. Tyanova S, Temu T, Cox J (2016) The MaxQuant computational platform for mass spectrometry-based shotgun proteomics. *Nat Protoc* 11(12):2301–2319.
3. Giurgiu M, et al. (2019) CORUM: The comprehensive resource of mammalian protein complexes—2019. *Nucleic Acids Res* 47(D1):D559–D563.