Integrative cross-omics and cross-context analysis elucidates molecular links underlying genetic effects on complex traits

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Introduction

This vignette provides an introduction to the `X.ING` package. The R package `X.ING` implements the X-ING method for cross-omics and cross-context analysis.

To install the development version of the `X.ING` package, please load the `devtools` package first. Note that `X.ING` requires the `CCA`, `RGCCA`, `Rcpp`, and `RcppArmadillo` packages.

To install this package, run the following command in R

```
library(devtools)
install_github("ylustat/X.ING")
```

Load the package using the following command:

```
library("X.ING")
```

```
##
## Attaching package: 'X.ING'
```

```
## The following objects are masked from 'package:base':
##
##     scale, unique
```

This vignette depends on R packages `MendelianRandomization`, `ggplot2` and `tidyverse`, you can load these packages using the following command:

```
suppressMessages(library("tidyverse"))
suppressMessages(library("pROC"))
suppressMessages(library("MASS"))
library("ggplot2")
library("MendelianRandomization")
library("RGCCA")
```

Fit XING using simulated data

The main function of the `X.ING` package is `XING()`. In this section, we fit `XING` function using simulated data (provided in the package) as an example to illustrate the basic usage of `XING`. The example data is a list with two elements, where `z` is a list of z-scores and `gamma` is a list of true underlying association status. `1` in `gamma` indicates the presence of non-zero effect and `0` indicates the absence of effect. We have three sets of data available in the example data (L=3). The number of contexts are 10, 8, and 6, respectively.

```
data("example_data")
length(example$z)
```

```
## [1] 3
```

```
sapply(example$z, dim)
```

```
##      [,1] [,2] [,3]
## [1,] 6000 6000 6000
## [2,]   10    8    6
```

The proportion of true associations are ~0.04.

```
sapply(example$gamma, mean)
```

```
## [1] 0.04265000 0.03893750 0.03922222
```

The X-ING takes the z-score list as input. It automatically use CCA (when L=2) for GCCA (when L>2) for the multi-view learning. Afterwards, it applies PCA to extract shared patterns across contexts for each omics. A simplest application where two sets of z-scores are analyzed:

```
z <- example$z
res <- XING(z_list = z[1:2])
```

The output includes posterior probabilities (`alpha`) and posterior means (`mu`):

```
names(res)
```

```
## [1] "mu"    "alpha"
```

```
lengths(res)
```

```
##    mu alpha
##     2     2
```

AUC can be calculated based on the posterior probability and true association status

```
gamma <- example$gamma

mapply(function(g,pp) auc(c(g),c(pp), quiet = T), gamma[1:2], res$alpha)
```

```
## [1] 0.9361313 0.9296026
```

It switches to GCCA (implemented in RGCCA package) if L>2 (note that the computation speed may substantially slowed):

```
z <- example$z
res <- XING(z_list = z)
```

Similar to the previous example, the output also includes posterior probabilities (`alpha`) and posterior means (`mu`):

```
names(res)
```

```
## [1] "mu"    "alpha"
```

```
lengths(res)
```

```
##    mu alpha
##     3     3
```

And the corresponding AUCs:

```
mapply(function(g,pp) auc(c(g),c(pp), quiet = T), gamma, res$alpha)
```

```
## [1] 0.9449007 0.9282614 0.9002920
```

Users may specify the sample overlap matrix $\widehat{\boldsymbol{R}}$ through thr `Lambda_list` parameter. The number of canonical coefficients to keep, and the number of PCs can be specified by `CC` and `PC_list`. For example,

```
res <- XING(z_list = z, CC = 4, PC_list = c(4,3,2), Lambda_list = lapply(sapply(z,ncol),diag))
mapply(function(g,pp) auc(c(g),c(pp), quiet = T), gamma, res$alpha)
```

```
## [1] 0.9027015 0.9012925 0.8088504
```

To reduce computation time, user may specify the iteration time via `iterT`. Also, the `tolerance` parameter controls the criterion for convergence of the GCCA algorithm. A smaller `tolerance` may lead to substantially longer computation time.