

Multi-omic data analysis

Juan R Gonzalez

BRGE - Bioinformatics Research Group in Epidemiology
Barcelona Institute for Global Health (ISGlobal)
e-mail: juanr.gonzalez@isglobal.org
<http://www.creal.cat/brge>

- 1 Introduction
- 2 One omic dataset: dimensionality reduction
- 3 Integrating two or more omic datasets
- 4 Take home messages

Outline

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Introduction

- Understanding the genetic basis of complex traits is an open question for many researchers
- Recent advances in technology has made this problem even more complex by incorporating other pieces of information such as neuroimaging, daily measurements of environmental exposures among others
- The main challenge is to analyze the vast amount of data that is being generated, particularly how to integrate information from different tables

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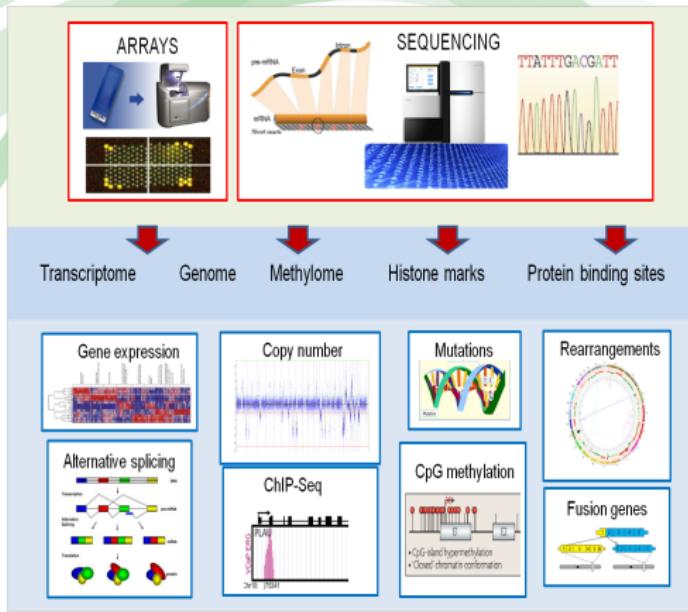
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- Recent advances in technology have made this problem even more complex by incorporating other pieces of information such as neuroimaging, daily measurements of environmental exposures among others
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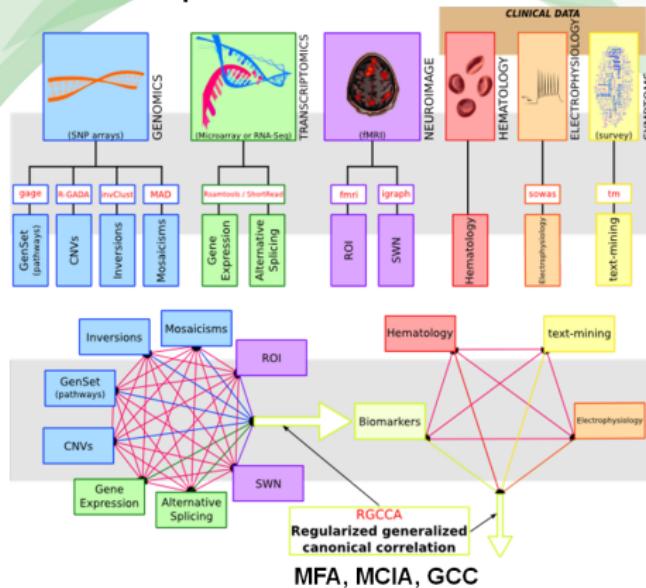


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Introduction

Supervised



Introduction

- Data integration (Integrative bioinformatics, integrated analysis, crossomics, multi-dataset analysis, data fusion, ...) is being crucial in Bioinformatics/Biology/Epidemiology
- Data integration may refer to different aspects
 - Computational combination of data (sets)
 - Simultaneous analysis of different variables from different tables, different time points, different tissues, ...
 - Provide biological insights by using information from existing databases (ENCODE, GTEx, KEGG, ...)
- Here we mean the process by which different types of omic data are combined as predictor variables to allow more thorough and comprehensive modelling of complex traits or phenotypes

Introduction

- **Multi-staged analysis:** Involves integrating information using a stepwise or hierarchical analysis approach
- **Meta-dimensional analysis:** Refers to the concept of integrating multiple different data types to build a multivariate model associated with a given outcome

Multi-staged analysis

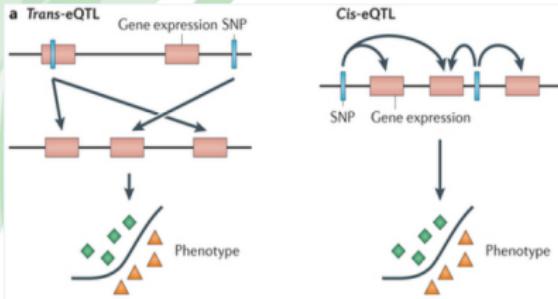
- **Genomic variation analysis approaches:** Triangle approach
 - ① SNPs are associated with the phenotype of interest and filtered based on p-values
 - ② Significant SNPs are tested for association with another level of omic data (i.e eQTLs)
 - ③ Omic data used in step 2 are then tested for correlation with phenotype of interest
- **Domain knowledge-guided approaches:** Integration of functional and pathway information
 - ① Significant results (regions of interest) are annotated in databases such as ENCODE, Roadmap Epigenomic Project, KEGG, ...
 - ② We can determine whether those regions are within pathways and/or overlapping with functional units, such as transcription factors binding, hyper- or hypo-methylated regions
 - ③ Overlapping regions are then correlated with the phenotype of interest
 - ④ The main limitation is that this method is biased by current knowledge

Multi-staged analysis

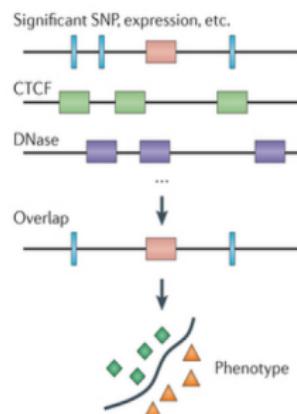
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Types of multi-staged analyses

(a) Genomic variation analysis



(b) Domain knowledge-guided



Genomic variation example

ARTICLES

nature
biotechnology

Epigenome-wide association data implicate DNA methylation as an intermediary of genetic risk in rheumatoid arthritis

Yun Liu^{1,2,12}, Martin J Aryee^{1,3,12}, Leonid Padyukov^{4,5,12}, M Daniele Fallin^{1,6,7,12}, Espen Hesselberg^{4,5},
Arni Runarsson^{1,2}, Lovisa Reinarius⁸, Nathalie Acevedo⁹, Margaret Taub^{1,6}, Marcus Ronninger^{4,5},
Klementy Shchetynsky^{4,5}, Annika Scheynius⁹, Juha Kere⁸, Lars Alfredsson¹⁰, Lars Klareskog^{4,5},
Tomas J Ekström^{5,11} & Andrew P Feinberg^{1,2,6}

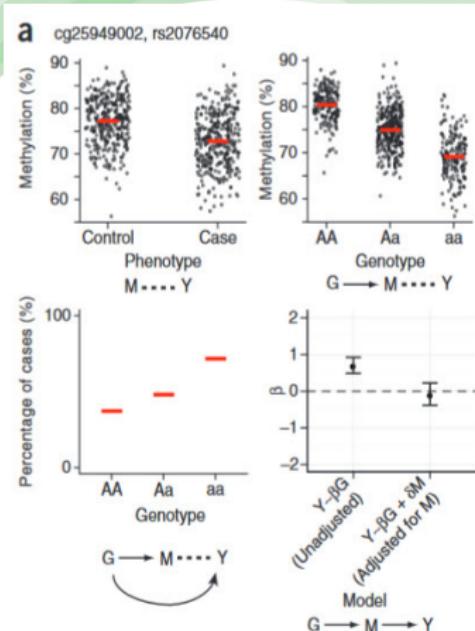
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Genomic variation example



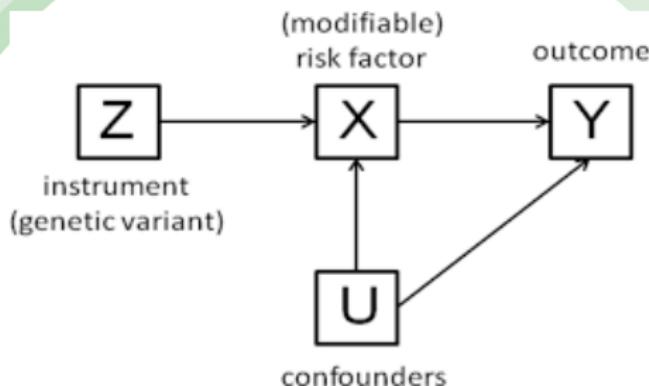
Genomic variation example

- Mendelian randomization
- Conditional Independent test (CIT)

MR: https://cran.r-project.org/web/packages/MendelianRandomization/vignettes/Vignette_MR.pdf

CIT: <https://cran.r-project.org/web/packages/cit/>

Mendelian randomization



Conditional Independent Test (CIT)

A) Independencia / Asociación



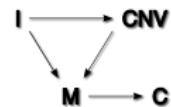
B) Causal



C) Causal / Asociación



D) Complejo



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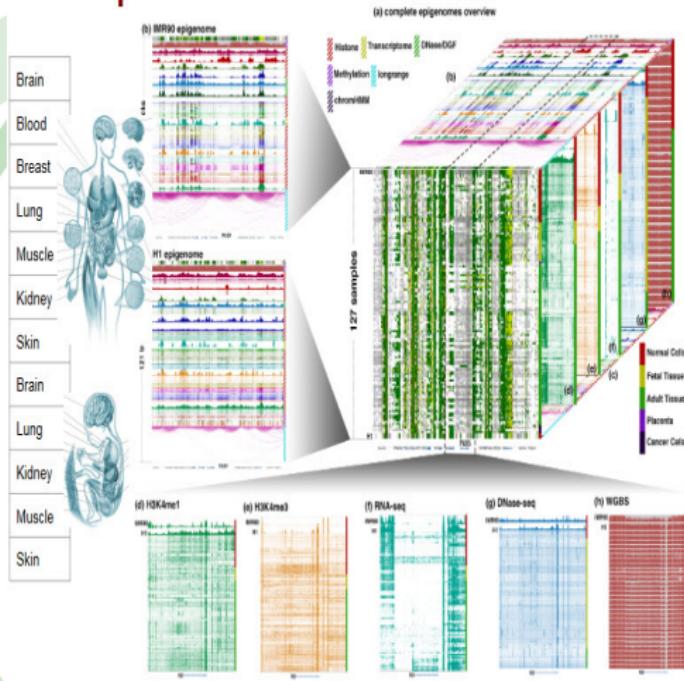
One omic dataset: dimensionality reduction

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Domain knowledge-guided

The Map!



The RoadMap Epigenomics

- Marking of functional genomic elements
- Environmental exposures
- Understanding development and differentiation
- Regenerative medicine (stem and iPS cells)
- Human disease
- Interpreting GWAS
- Biomarkers, diagnostics and therapies
- Exploring cross-talk between epigenomic mechanisms

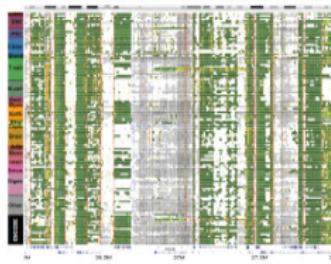
Domain knowledge-guided

Using Epigenomic Data to Interpret GWAS Data

Gene variants in
human disease



Epigenomic data for many
normal human cell/tissue types



- 77% of disease variants are in/near enhancer elements or promoters*
- Variants are in regulatory regions NOT protein coding regions
- Generate hypotheses about function



Introduction

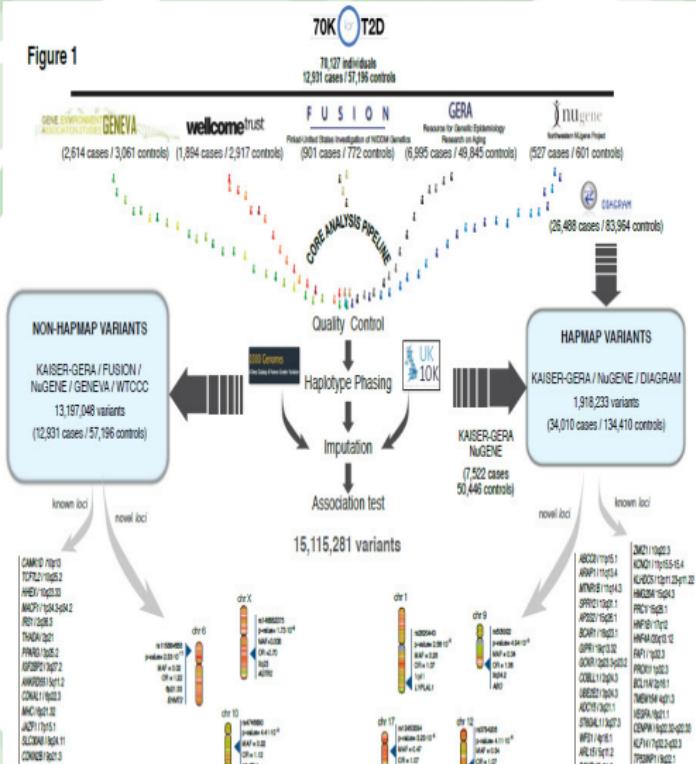
One omic dataset: dimensionality reduction

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Domain knowledge-guided

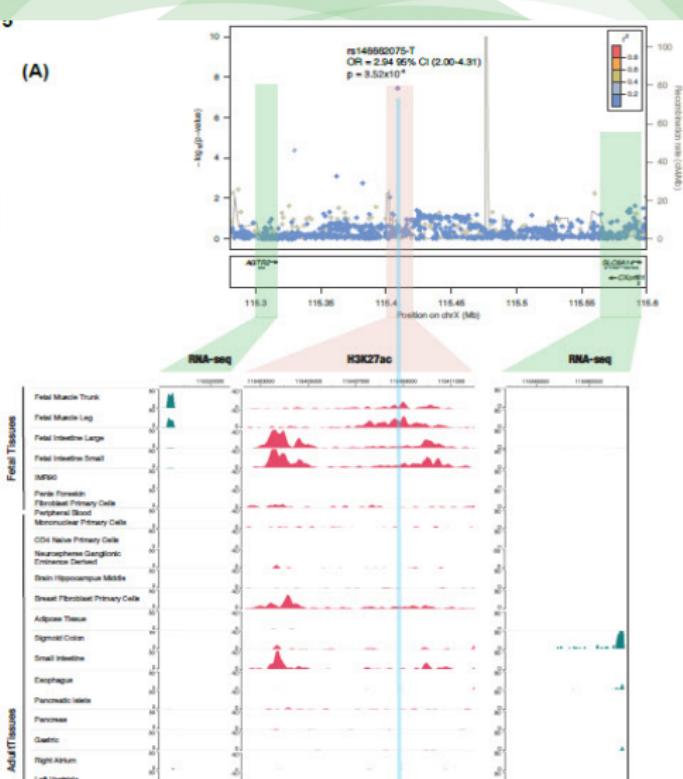
Figure 1



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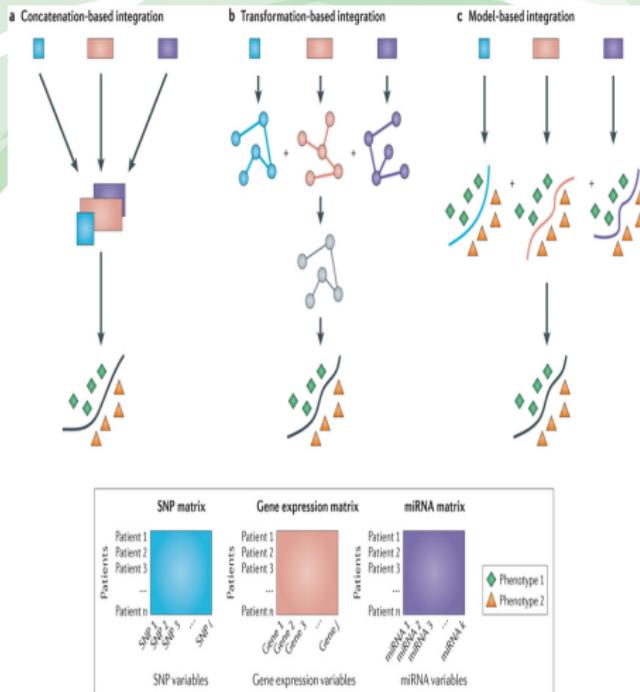
Domain knowledge-guided



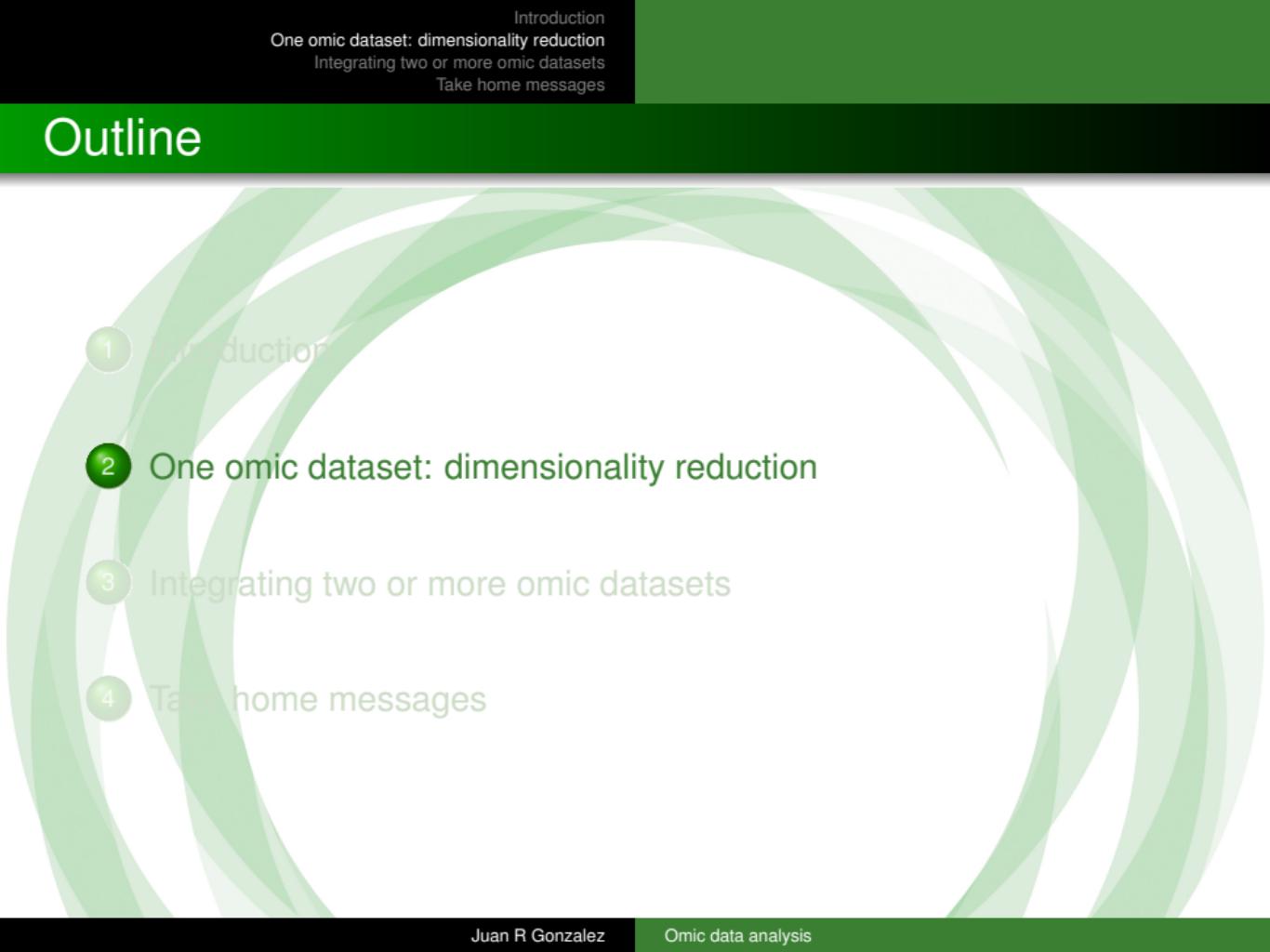
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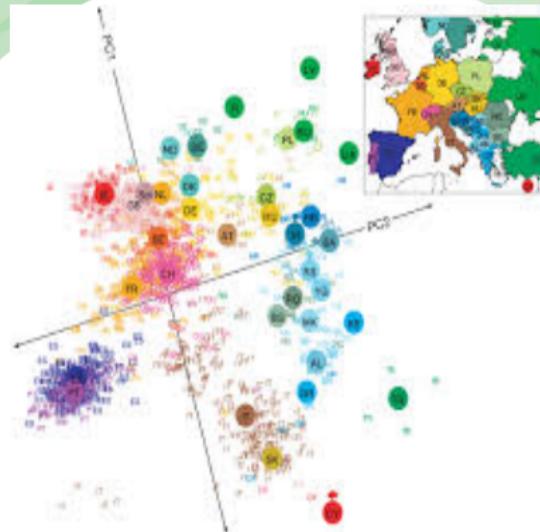
Types of meta-dimensional analyses



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One omic dataset: dimensionality reduction



One omic dataset: dimensionality reduction

- Used to study tissue, cell attributes or cancer signatures with regard to abundance of mRNAs, proteins and metabolites
- Given an omic data set X , which is a $n \times p$ matrix, of n individuals and p features

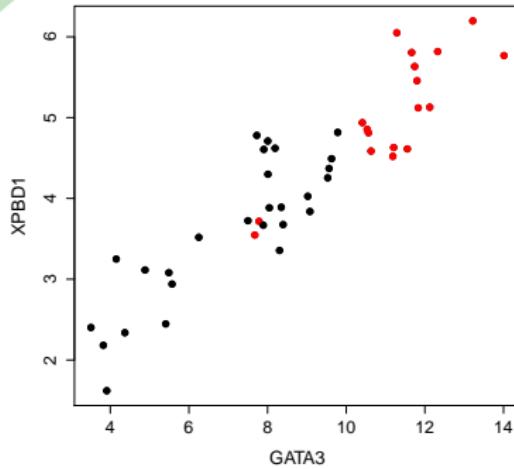
$$X = (x_1, x_2, \dots, x_p)$$

- we look for new variables that are linear combinations of the original variables $f = q_1 X_1 + q_2 X_2 + \dots + q_p X_p$ or $f = Xq$ where q are known as loadings.
- We introduce the restriction that for i th component, q 's should maximize the variance components of f 's

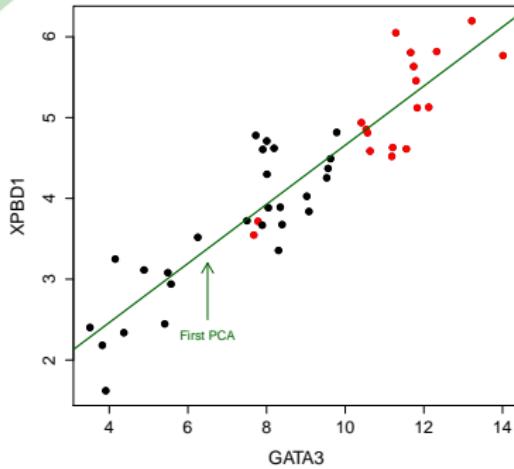
$$\arg \max_{q^i} \text{var}(Xq^i)$$

and q 's have to be orthogonal to each other.

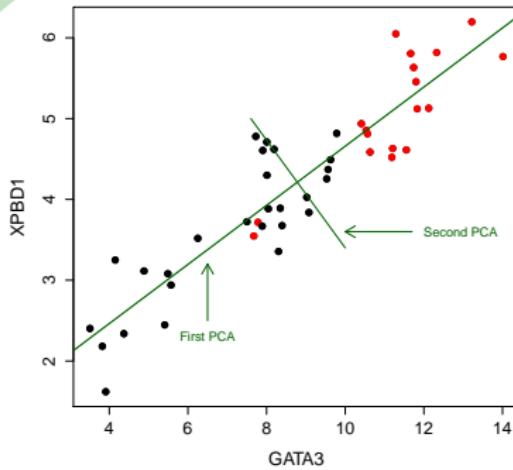
One omic dataset: dimensionality reduction



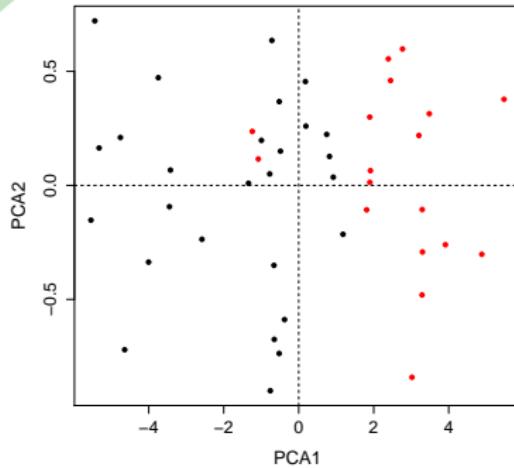
One omic dataset: dimensionality reduction



One omic dataset: dimensionality reduction

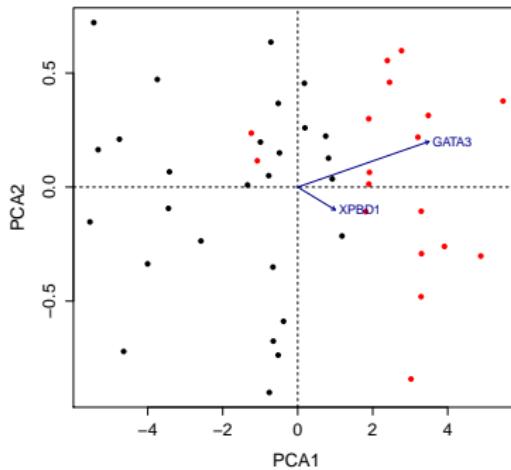


One omic dataset: dimensionality reduction



One omic dataset: dimensionality reduction

Data visualization: biplot



One omic dataset: dimensionality reduction

- There are other techniques such as: Principal co-ordinate analysis (PCoA), correspondence analysis (CA) and nonsymmetrical correspondence analysis (NSCA).
- They can be applied to other types of data (e.g. non-continuous). PCoA can also be applied to binary or count data.
- PCA is designed to analyze multi-normal distributed data. If data are skewed, contain extreme outliers, or display nonlinear trends, other methods such as Multidimensional Scaling (MDS)
- Nonnegative matrix factorization (NMF) and Independent Component Analysis (ICA) are applied when orthogonality or independence across components are not hold.

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One omic dataset: dimensionality reduction

- Solving the problem for the i -th component

$$\arg \max_{q^i} \text{var}(Xq^i)$$

uses SVD decomposition and it requires an inversion step that can be problematic when $p \gg n$

- Several extensions based on regularization step or L-1 penalization (Least Absolute Shrinkage and Selection Operator, LASSO) can be applied
- Sparse, penalized and regularized extensions of PCA and related methods have been proposed in omic data analysis, recently (sPCA)

Multi-omic real data

- Data from the Cancer Genome Atlas (TCGA) will be analyzed.
- A subset of the TCGA breast cancer study from Nature 2012 publication have been selected.
- Data
<https://tcga-data.nci.nih.gov/docs/publications/brcal>
- Available data are: miRNA, miRNAPrecursor, RNAseq, Methylation, proteins from a RPPA array, and GISTIC SNP calls (CNA and LOH). Clinical data are also available.

Multi-omic real data

Data can be loaded into R by executing:

```
load("data/breast_TCGA_subset_multi_omic.RData")
summary(breast_multi)
```

```
##                                     Length Class      Mode
## miRNA                           79   data.frame  list
## miRNAPrecursor                   79   data.frame  list
## RNAseq                          791580 -none-    numeric
## Methyl                          79   data.frame  list
## RPPA                            79   data.frame  list
## LOH                             996348 -none-    numeric
## CNA                            934649 -none-    numeric
## clin                           29   data.frame  list
```

PCA analysis

```
require(ade4)
dim(breast_multi$RNAseq)

## [1] 10020      79

breastPCA<-dudi.pca(breast_multi$RNAseq,
                      scannf=FALSE, nf=5)
```

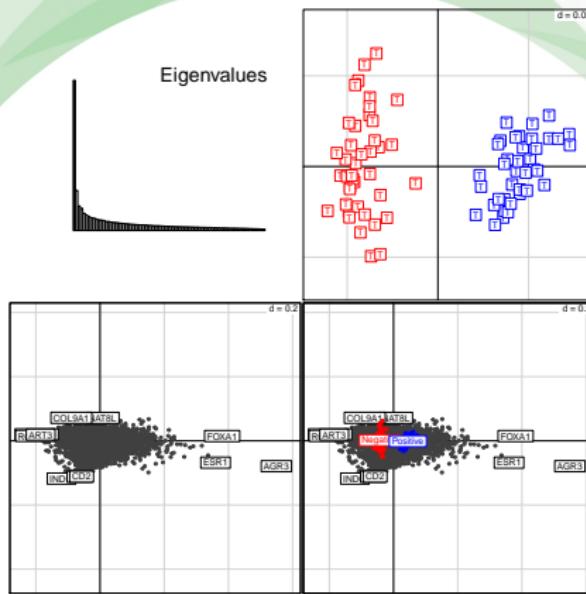
PCA analysis

There is a BioC package called made4 which is a wrapper around ade4 that utilizes Bioconductor data classes (such as Expression Set to help visualizing the results). The key function is `ord`. The panels show plots of eigenvalues, projections of samples, projections of genes and biplot.

```
require(made4)
```

```
group<-droplevels(breast_multi$clin$ER.Status)
out <- ord(breast_multi$RNAseq, classvec=group)
plot(out, nlab=3, arraylabels=rep("T", 79))
```

PCA analysis

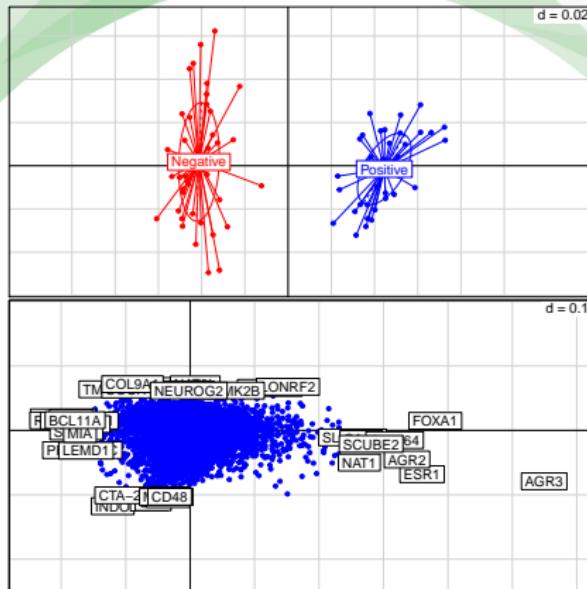


PCA analysis

Sample and genes projections can also be plotted using another wrapper around `ade4` package. By default the top-10 more important genes for each axis are highlighted.

```
par(mfrow=c(2,1))
plotarrays(out$ord$co, classvec=group)
plotgenes(out, col="blue")
```

PCA analysis



PCA analysis

A list of variables with higher loadings on axes can be obtained using the following function

```
ax1 <- topgenes(out, axis=1, n=5)
ax2 <- topgenes(out, axis=2, n=5)
cbind(ax1, ax2)

##           ax1          ax2
## [1,] "ROPN1B"    "SH3GL2"
## [2,] "ROPN1"     "SLITRK6"
## [3,] "FOXA1"      "LONRF2"
## [4,] "SFRP1"      "IL7R"
## [5,] "ESR1"        "INDO"
## [6,] "AGR3"        "NAT8L"
## [7,] "AGR2"        "UBD"
## [8,] "Clorf64"    "CD2"
## [9,] "ART3"        "CD69"
## [10,] "BCL11A"     "COL9A1"
```

Sparse PCA analysis

Witten D, Tibshirani R, Hastie T (Biostatistics, 2009, 10(3):515-534) presented a penalized matrix decomposition for computing a rank-K approximation for a matrix based on L1-penalization. The method is also extended to Canonical Correlation Analysis (CCA).

```
require(PMA)
dd <- t(breast_multi$RNAseq)
sout <- SPC(dd, sumabsv=3,
            K=2, orth=TRUE)

## 12345678910
## 1234567891011121314151617181920
```

NOTE: `sumabsv` argument controls the degree of sparsity. It can be tuned by using `SPC.cv` function

Sparse PCA analysis

```
rownames(sout$u) <- rownames(dd)
rownames(sout$v) <- colnames(dd)
head(sout$u)

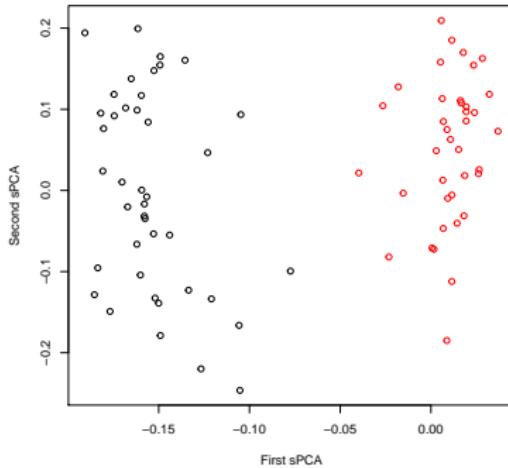
##           [,1]      [,2]
## TCGA-C8-A12V -0.1266630 -0.2198702
## TCGA-A2-A0ST -0.1052587 -0.2464092
## TCGA-E2-A159 -0.1057203 -0.1662398
## TCGA-BH-A0BW -0.1335251 -0.1229296
## TCGA-A2-A0SX -0.1520058 -0.1327320
## TCGA-AR-A1AI -0.1768082 -0.1491056

head(sout$v)

##      [,1] [,2]
## CREB3L1    0   0
## PNMA1     0   0
## MMP2      0   0
## C10orf90   0   0
## GPR98     0   0
## APBB2     0   0
```

Sparse PCA analysis

```
plot(sout$u, type="n", xlab="First sPCA", ylab="Second sPCA")
points(sout$u, col=as.numeric(group))
```



Sparse PCA analysis

```
ss <- sout$v[,1]
ss[ss!=0]

##      FSIP1      ROPN1B      SLC44A4      ROPN1      FOXA1      SCGB2A2
## 0.12976786 -0.20047758  0.09854402 -0.22180706  0.35283734  0.02914304
##      CA12      HORMAD1      TFF3      ABCC11      ESR1      AGR3
## 0.08389962 -0.11978720  0.01092539  0.01843790  0.26810418  0.69491639
##      AGR2      Clorf64      SCUBE2      ART3
## 0.29917578  0.23368898  0.05023190 -0.18825577

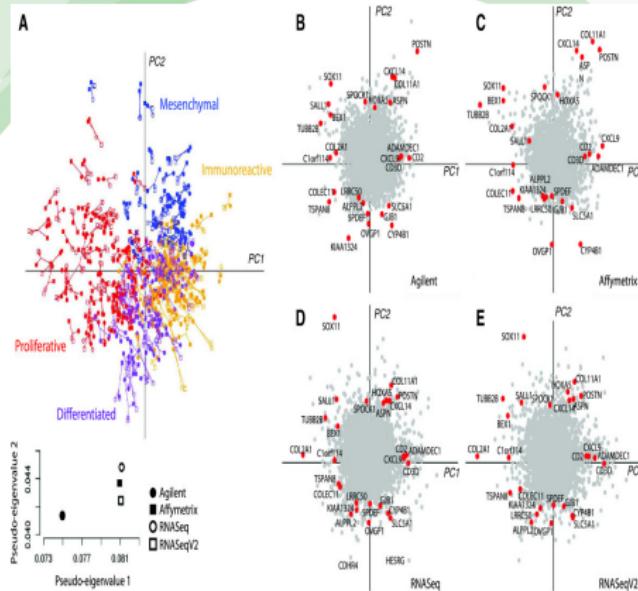
ax1

## [1] "ROPN1B"   "ROPN1"    "FOXA1"    "SFRP1"    "ESR1"    "AGR3"    "AGR2"
## [8] "Clorf64"  "ART3"     "BCL11A"
```

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One omic dataset: dimensionality reduction



Integrating two or more omic datasets

- There are methods based on dimension reduction techniques: generalized SVD, Co-Inertia Analysis (CIA), sparse or penalized extensions of Partial Least Squares (PLS), Canonical Correlation (CCA), Multiple Factor Analysis (MFA), Generalized Canonical Correlation (GCA)
- There are methods that are based on path modelling: structural equation models (SEM)
- Regularized Generalized Canonical Correlation (RGCA) provides a unified framework for different approaches (Tenenhaus, M. and Tenenhaus, A. Psychometrika, 2011, 76(2):257-284). Other methods are special cases of RGCA.
- RGCA integrates a feature selection method, named sparse GCCA (SGCCA) (Tenenhaus, A et al. Biostatistics, 2014, 15(3):669-83).

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Integrating two or more omic datasets

- Canonical Correlation can be seen as an extension of PCA for more than two tables X and Y
- The two datasets can be decomposed as:

$$f = Xp$$

$$g = Yq$$

where p and q are the loading vectors

- CCA searches for association or correlations among X and Y by

$$\arg \max_{p^i q^i} \text{cor}(Xp^i Yq^i)$$

for the i -th component

- Xp^i and Yq^i are known as canonical variates and their correlations are the canonical correlations.

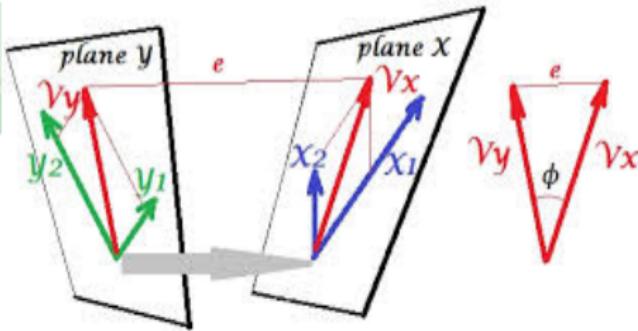
Integrating two or more omic datasets

- ($p >> n$) is an issue. Additionally, there is often presence of multicollinearity within both sets of variables that requires a regularization step.
- This may be accomplished by adding a ridge penalty, that is, adding a multiple of the identity matrix to the correlation/covariance matrix.

$$\arg \max_{p^i q^i} \text{cor}(X p^i Y q^i) + \lambda I$$

- A sparse solution (filtering the number of variables) is the solution: pCCA, sCCA, CCA-I1, CCA-EN, CCA-group sparse have been used to integrate two omic data.

Integrating two or more omic datasets



V_y and V_x are selected to maximize:

- Correlation (CCA)
- Squared Covariance (CIA)

$$\arg \max_{p^i q^i} \text{cov}^2(X p^i Y q^i)$$

Co-Inertia

- CIA does not require an inversion step of the covariance matrix; thus, regularization or penalization implementation is not required
- CIA can deal with disperse variables
- CIA does consider quantitative or qualitative variables
- Can weight cases
- The method provides the RV coefficient. This is a measure of global similarity between the datasets, and is a number between 0 and 1. The closer it is to 1 the greater the global similarity between the two datasets.

Canonical Correlation: gene expression and proteins

```
require(CCA)
df1 <- t(breast_multi$RNAseq) [,1:1000]
df2 <- t(breast_multi$RPPA)
```

```
resCC <- cc(df1, df2)
```

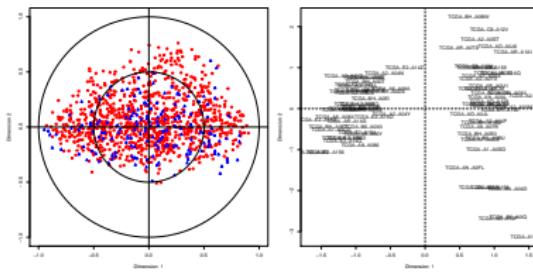
Error en chol.default(Bmat) :
la submatriz de orden 81 no es definida positiva

```
resRCC <- rcc(df1, df2, 0.2, 0.1)
```

```
regul <- estim.regul(df1, df2)
resRCC2 <- rcc(df1, df2, regul$lambda1, regul$lambda2)
```

```
plt.cc(resRCC)
```

Canonical Correlation: gene expression and proteins



Canonical Correlation: gene expression and proteins

```
require(PMA)
ddlist <- list(df1, df2)
perm.out <- MultiCCA.permute(ddlist,
                               type=c("standard", "standard"),
                               trace=FALSE)

resMultiCCA <- MultiCCA(ddlist,
                         penalty=perm.out$bestpenalties,
                         ws=perm.out$ws.init,
                         type=c("standard", "standard"),
                         ncomponents=1, trace=FALSE, standardize=TRUE)
```

Canonical Correlation: gene expression and proteins

```
rownames(resMultiCCA$ws[[1]]) <- colnames(df1)
rownames(resMultiCCA$ws[[2]]) <- colnames(df2)
head(resMultiCCA$ws[[1]])

##                [,1]
## CREB3L1      0.03812575
## PNMA1        0.04078831
## MMP2         0.02402715
## C10orf90   -0.02896362
## GPR98        0.04723420
## APBB2        0.06279879

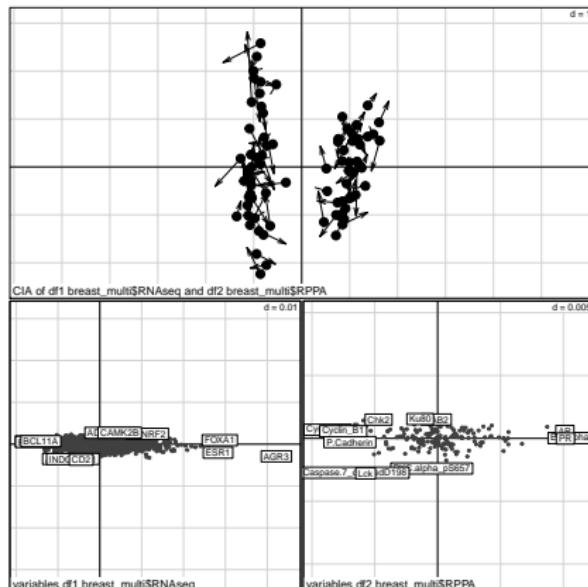
head(resMultiCCA$ws[[2]])

##                [,1]
## c.Myc       -0.07099252
## HER3        0.02652238
## XBP1        0.00000000
## Fibronectin 0.01527691
## PAI.1       -0.02319958
## p21         0.02415011
```

Co-inertia: gene expression and proteins

```
resCIA <- cia(breast_multi$RNaseq, breast_multi$RPPA)
```

```
plot(resCIA, classvec=group, nlab=3, clab=0, cpoint=3 )
```



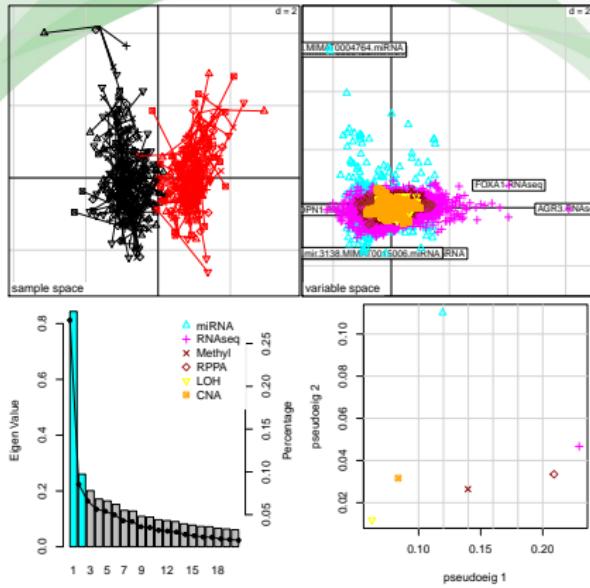
More than two tables

```
require(omicade4)
resMCIA <- mcia( breast_multi[ c(1,3,4,5,6,7) ] )

plot(resMCIA, axes=1:2, sample.lab=FALSE, sample.legend=FALSE,
phenovec=group, gene.nlab=2,
df.color=c("cyan", "magenta", "red4", "brown", "yellow", "orange")
df.pch=2:7)

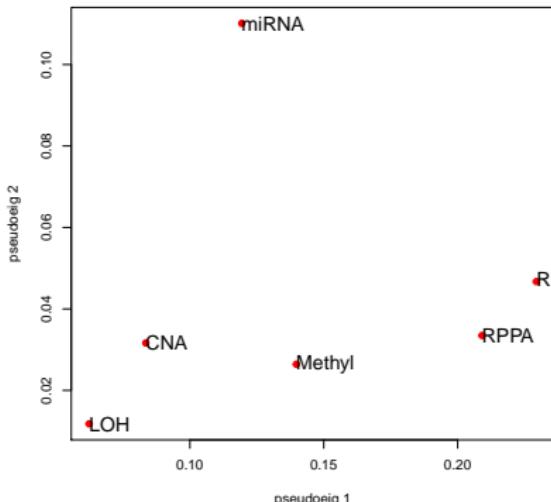
## Error in xy.coords(x, y, xlabel, ylabel, log): 'x' is a
list, but does not have components 'x' and 'y'
```

More than two tables

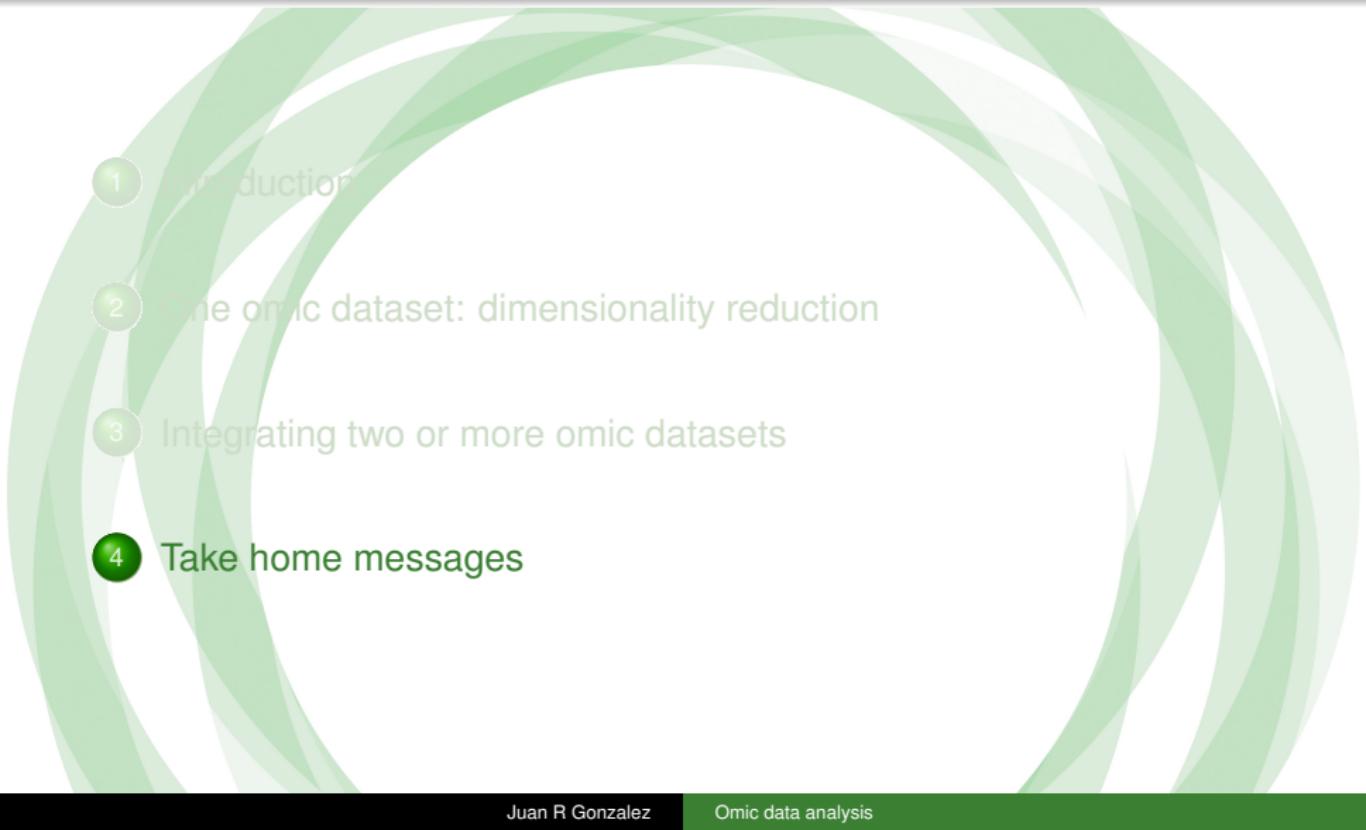


More than two tables

```
plot(resMCIA$mcoa$cov2, xlab = "pseudoeig 1",  
     ylab = "pseudoeig 2", pch=19, col="red")  
text(resMCIA$mcoa$cov2, labels=rownames(resMCIA$mcoa$cov2),  
     cex=1.4, adj=0)
```



Outline

- 
- 1 Introduction
 - 2 One omic dataset: dimensionality reduction
 - 3 Integrating two or more omic datasets
 - 4 Take home messages

Concluding remarks

Correlation $Y = X$

Multiple correlation $Y = X_1 X_2 X_3 \cdots X_k$

Canonical correlation $Y_1 Y_2 Y_3 \cdots Y_j = X_1 X_2 X_3 \cdots X_k$

- Co-inertia analysis (CIA) is similar to CCA but it optimizes the squared covariance between the eigenvectors while CC optimizes the correlation.
- CIA can be applied to datasets where the number of variables (genes) far exceeds the number of samples (arrays) such is the case in several omic data, while CCA requires a regularized version to be implemented.
- Sparse and regularized methods require a tuning parameter. This makes these methods computing demanding.

Take home messages

- Multivariate methods are purely descriptive methods that do not test a hypothesis to generate a p-value.
- They are not optimized for variable of biomarkers discovery, though the introduction of sparsity in variable loadings may help in the selection of variables for downstream analyses.
- Number of variables in omic data is a challenge to traditional visualization tools. New R packages including `ggord` are being developed to address this issue.
- Dynamic visualization is possible using `ggvis`, `ploty`, `explor` and other packages.
- Projection in the same space of variable annotation (GO or Reactome) may help to determine gene sets or pathways associated with our traits.