REXPOSOME: A BIOCONDUCTOR PACKAGE FOR CHARACTERIZING MULTIPLE ENVIRONMENTAL FACTORS AND ITS ASSOCIATION WITH DIFFERENT OMICS BIOMARKERS AND DISEASE

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ISGlobal
Barcelona
Institute for
Global Health

BACKGROUND

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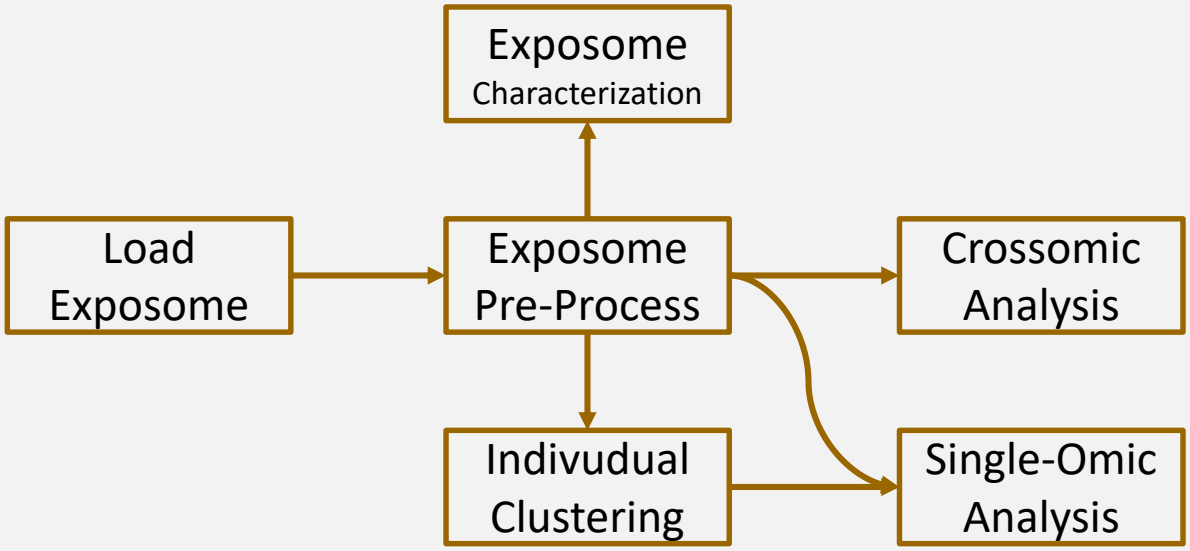
The HELIX Project – characterize early-life exposure and association with major health outcomes trough omic data analysis

Cohort	#Sample
BiB	14 000
EDEN	2 000
INMA	2 500
KANC	4 000
MoBa	8 000
RHEA	1 500

From the total (+30 000), 1 200 will get omic data

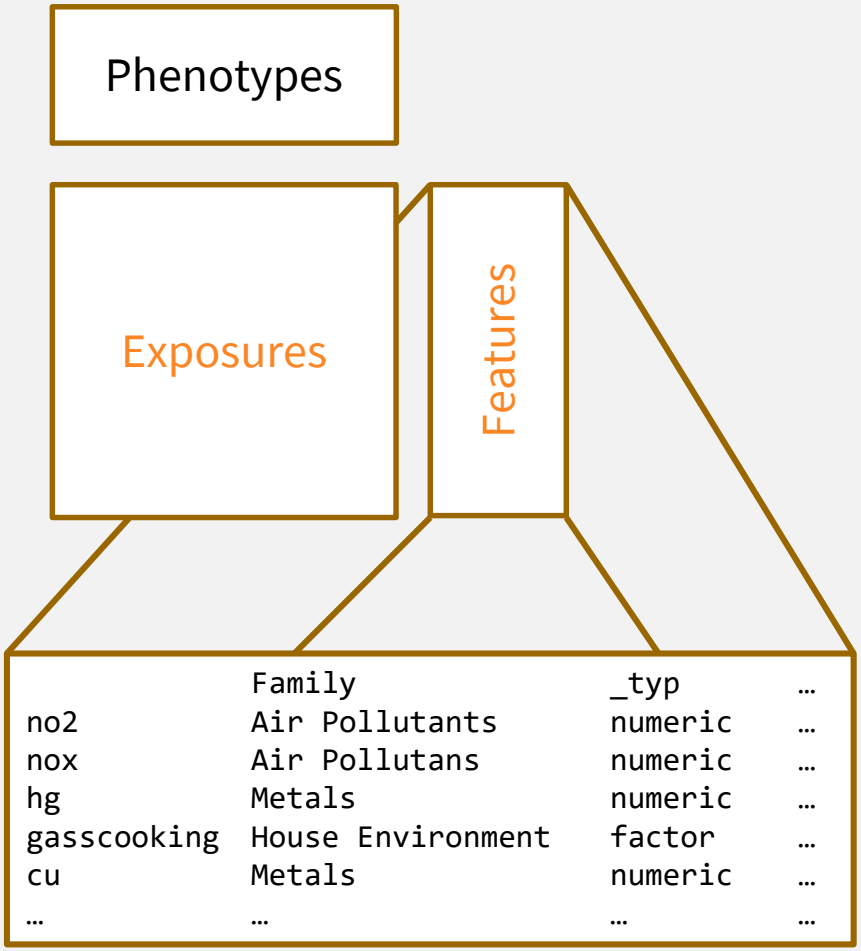
Transcriptome, Methylome, Proteome & Metabolome

REXPOSOME - WORKFLOW



REXPOSOME – INTERNAL STRUCTURES (1/2)

- *ExposomeSet*



- *eSet* based class
  - Exposures can be both *numerical* and *factor*
  - Adds a restriction to *fData*:
    - It must contain a column with “family definition”

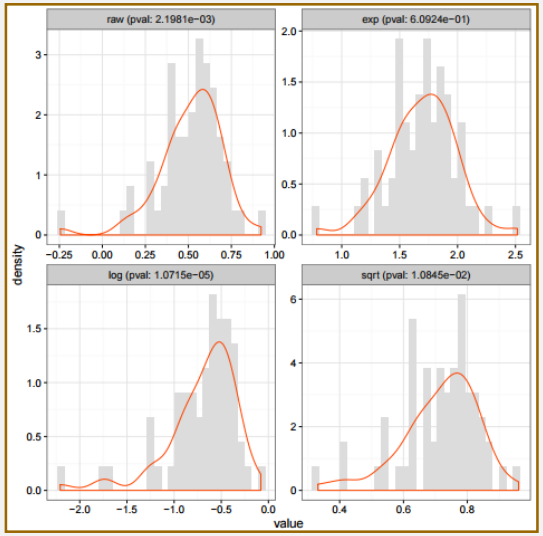
REXPOSOME – EXPOSOMESET'S METHODS

Load Exposome

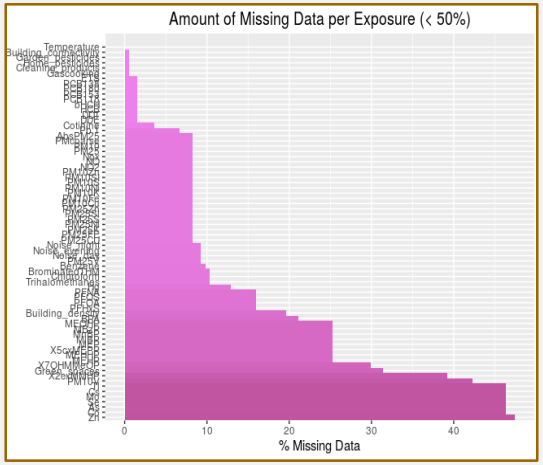
from files → read_exposome
from *data.frames* → load_exposome

Exposome Pre-Process

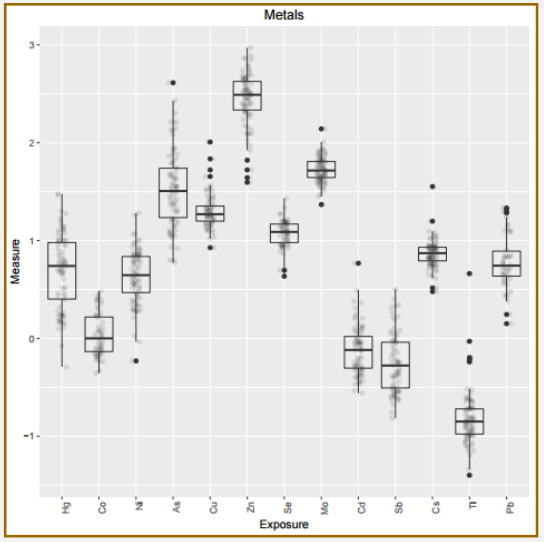
plotHistogram



plotMissings



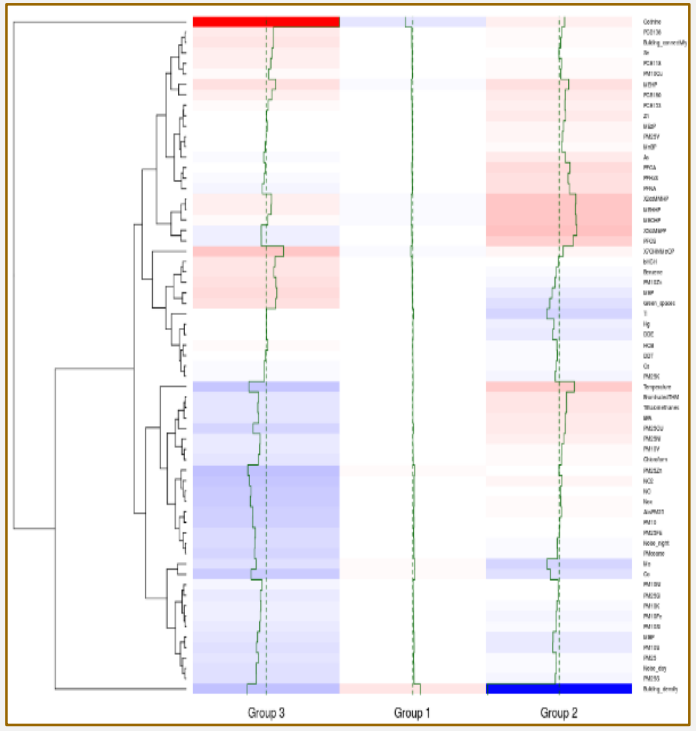
plotFamily



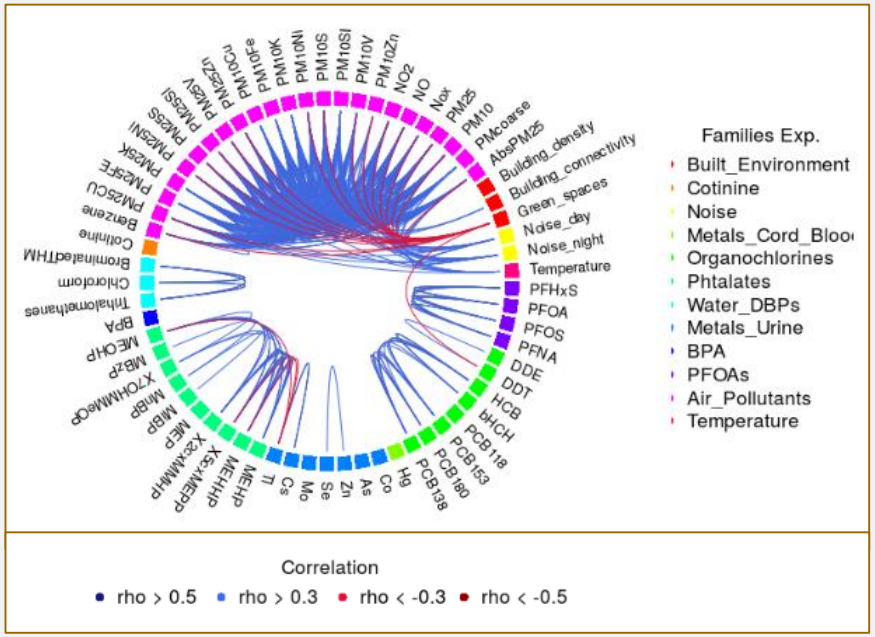
REXPOSOME – EXPOSOMESET'S METHODS

Indivudual Clustering & Exposome Characterization

plotClustering

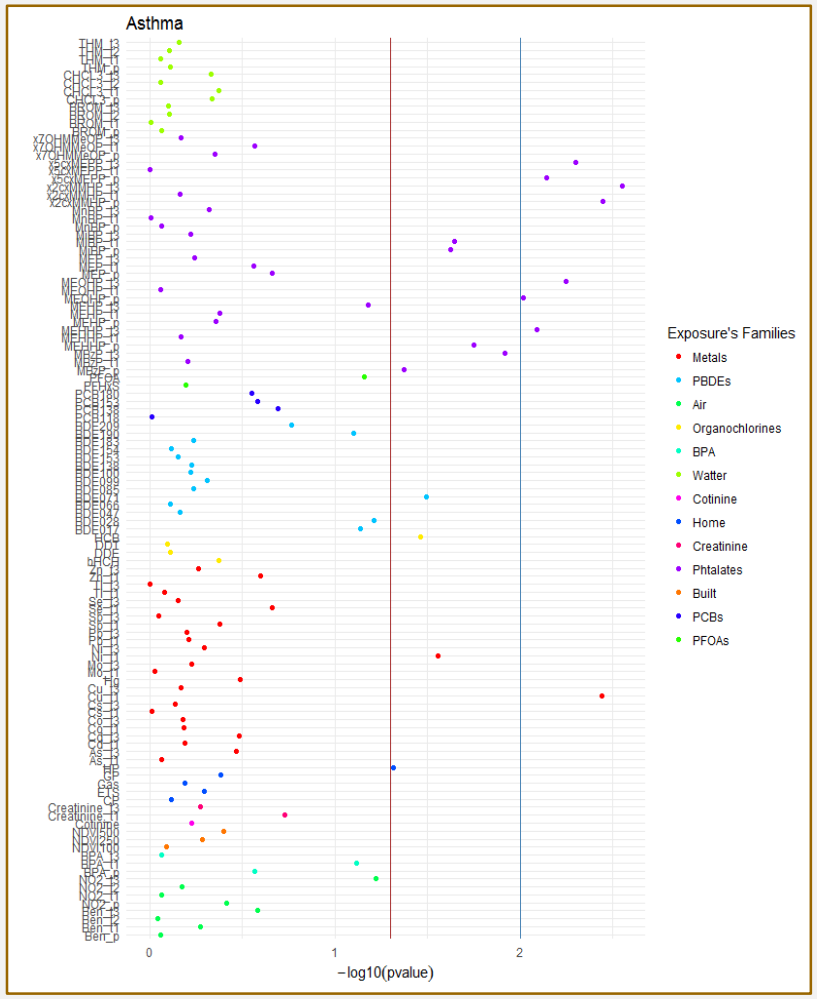


plotCorrelation



REXPOSOME – EXPOSOMESET'S METHODS

Exposome Characterization

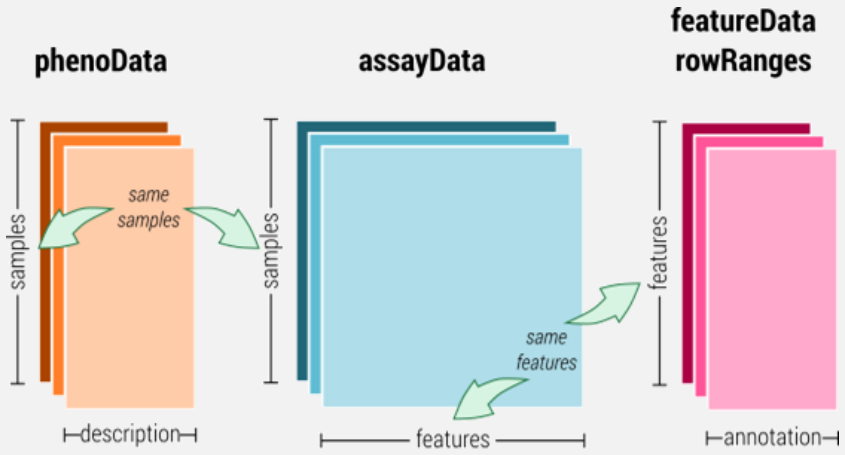


Exposure-Wide Association Study

ExWAS

REXPOSOME – INTERNAL STRUCTURES (2/2)

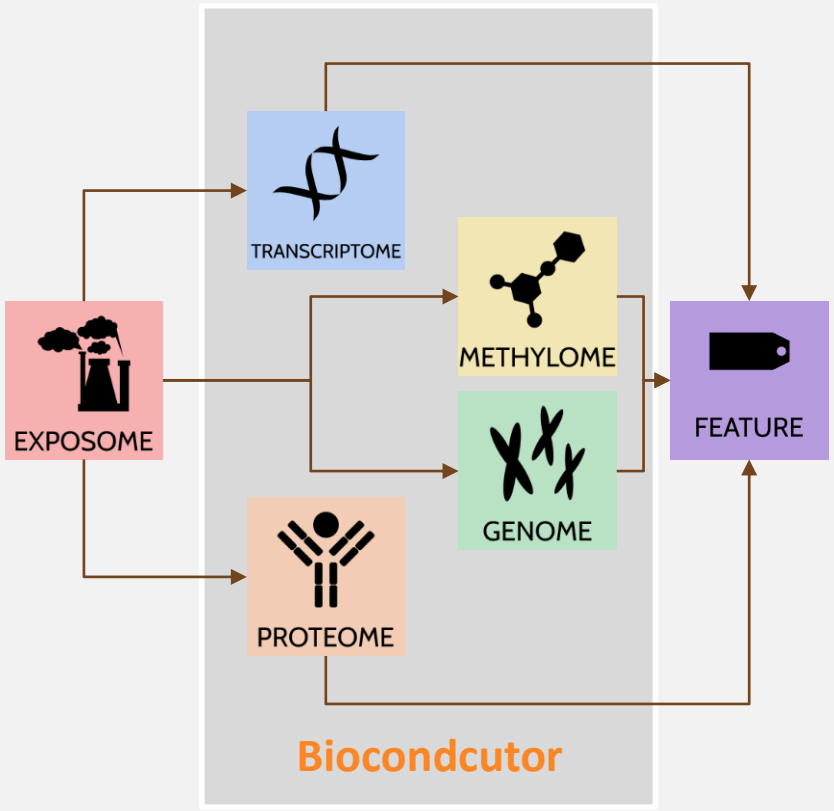
- *ExposomeSet*
- *MultiDataSet*[*]



- *add_exp* → *ExposomeSet* & *ExposomeClust*

[*]: *Hernandez-Ferrer et al.*; ***MultiDataSet: an R package for encapsulating multiple data sets with application to omic data integration***; BMC Bioinf [tentatively accepted]

REXPOSOME – MULTIDATASET'S METHODS



- Single Omic Analysis

  (Exposome-Omic Data Association)

  - **Exposure** Association to Transcriptome, Methylome and Proteome
  - **Health Outome** Association to Genome, Transcriptome, Methylome and Proteome

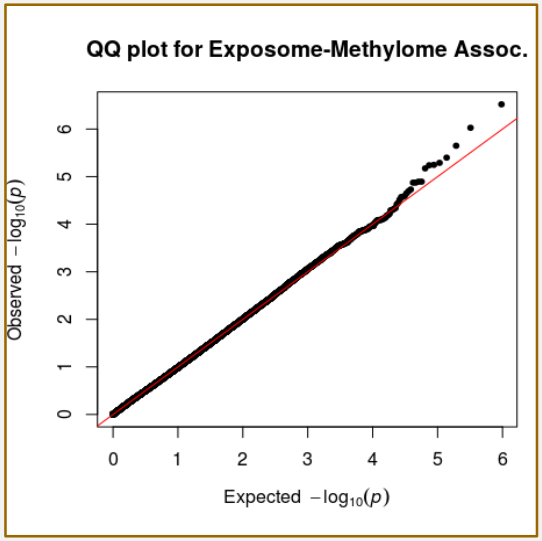
- Crossomics

  (Exposome-Omic Data Integration)

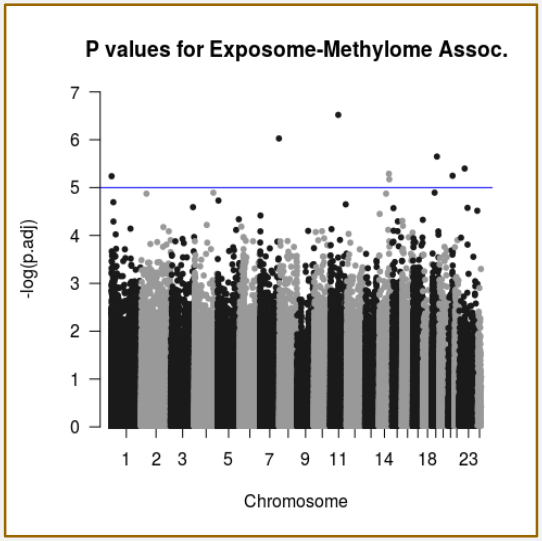
  - Supervised (2 datasets)
  - Non-Supervised (N datasets)

REXPOSOME – MULTIDATASET'S METHODS

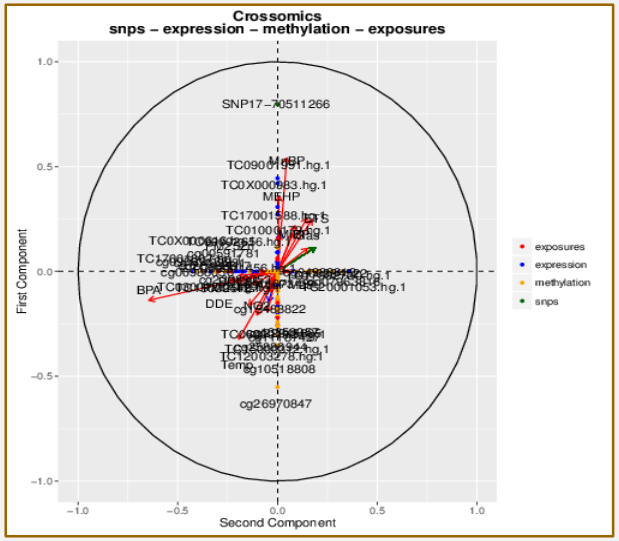
plotAssociation



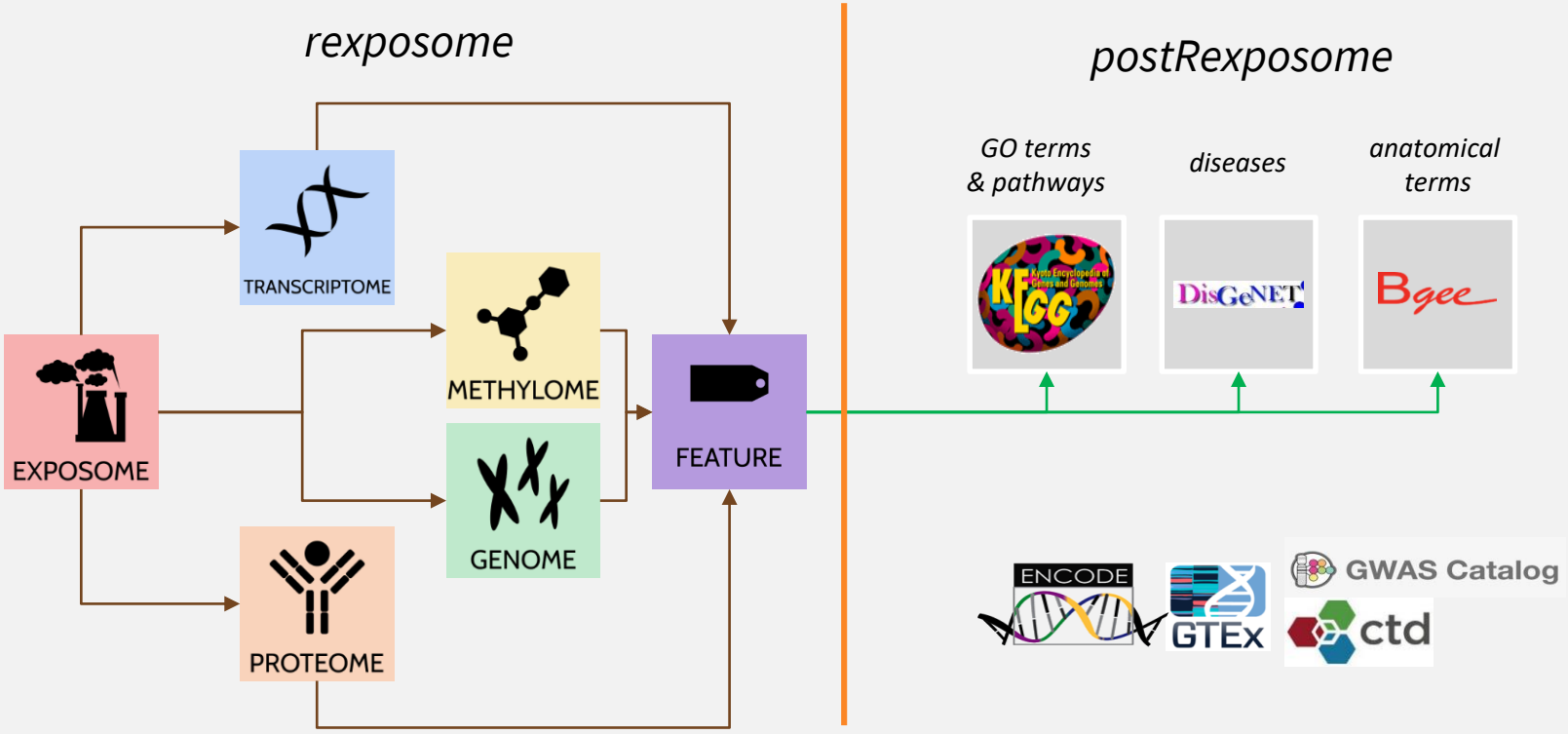
plotAssociation



plotIntegration



REXPOSOME & POSTREXPOSOME



rexposome allows to analyses each pair of exposome-omic data sets and obtain a list of significant associated features, that can be used to translate the significance from feature to *pathways level*, *disease level*, *cell type level*, *functional level* and *tissue level* in **postRexposome**

REXPOSOME & POSTREXPOSOME

- *rexposome*
  - **public beta**
  - https://github.com/carleshf/rexposome
- *postRexposome*
  - **private alpha**
- *MultiDataSet*
  - **published in Bioconductor**

BIOINFORMATIC RESEARCH GROUP IN EPIDEMIOLOGY

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THANKS!

Any questions?

You can contact me at:

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```
def success(dedication, persistence, passion):
  dedication += 1 # dedicate yourself
  persistence += 1 # be persistent
  passion = True # have passion

  if passion == True:
    magic = dedication + persistence
    return magic
  else:
    magic = 0
    return magic

# love it. make mistakes. learn. keep grinding.
```