Integrating and visualising multi-omics data with the `{moiraine}` R package

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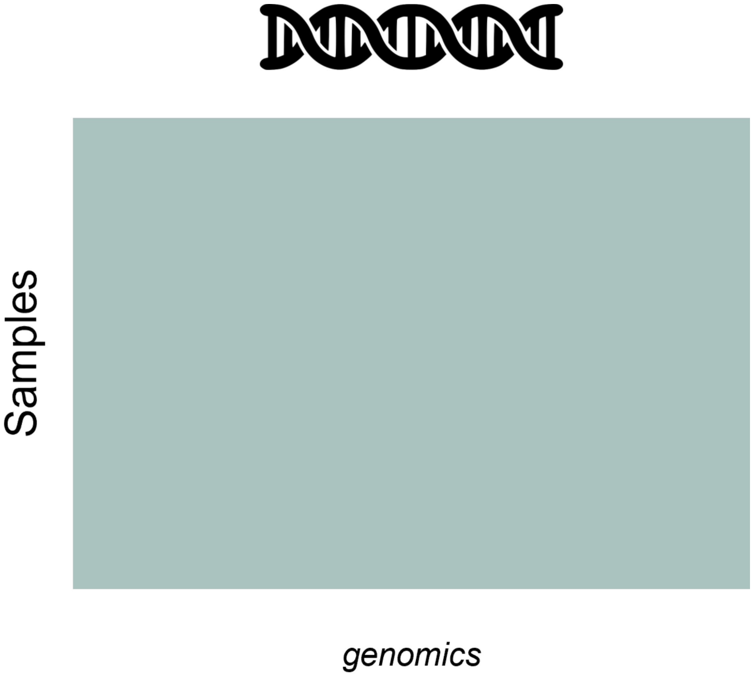
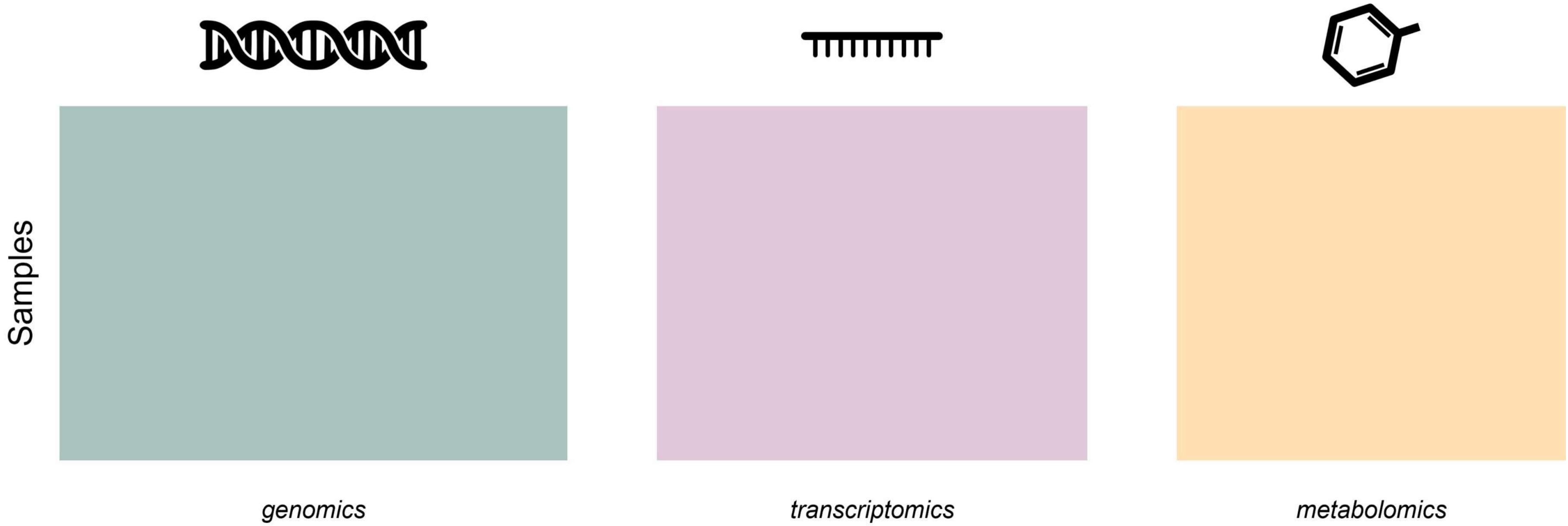
Multi-omics data

Omics data: High-throughput measurement of molecular layer across biological samples

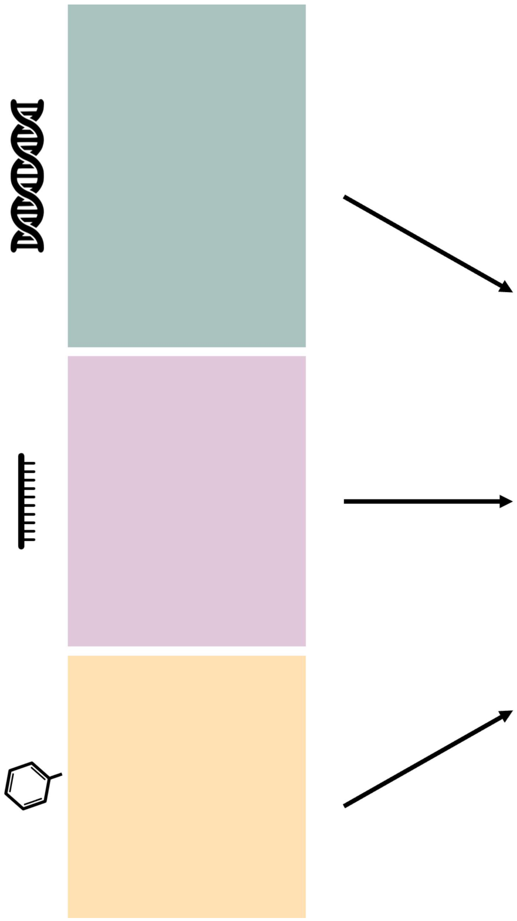


Multi-omics data

Multi-omics data: Different omics layers measured on the same biological samples



Multi-omics integration



Multi-omics integration methods:

- DIABLO – `{mixOmics}`
- MOFA – `{MOFA2}`
- MCIA – `{omicade4}`
- omeSOM
- MFA – `{FactoMineR}`
- …

Technical challenges

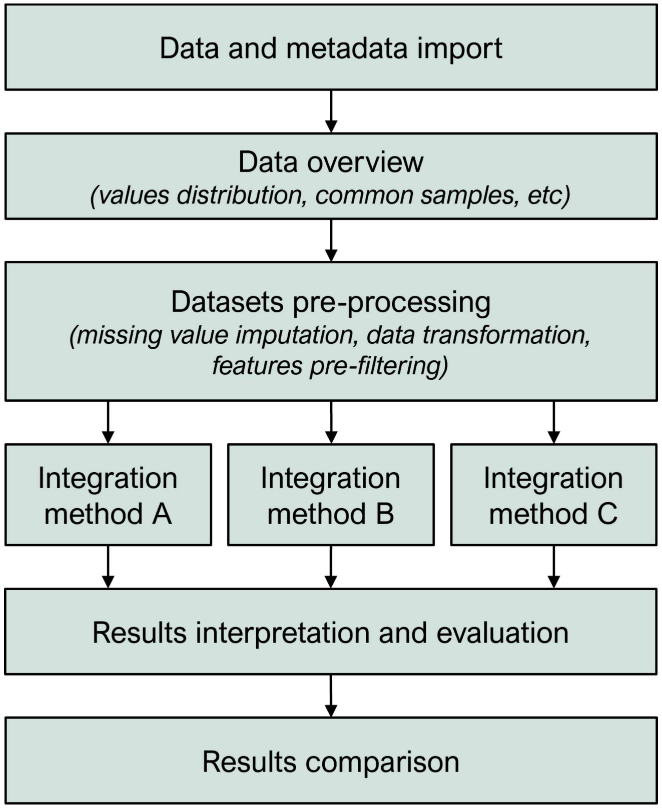
Different requirements for input data format

Different formatting of results

Unequal visualisation capabilities

The `{moiraine}` R package

- Construction of reproducible multi-omics data integration pipelines
- Comparison of results from several integration methods



https://github.com/Plant-Food-Research-Open/moiraine/

Three key features of `{moiraine}`

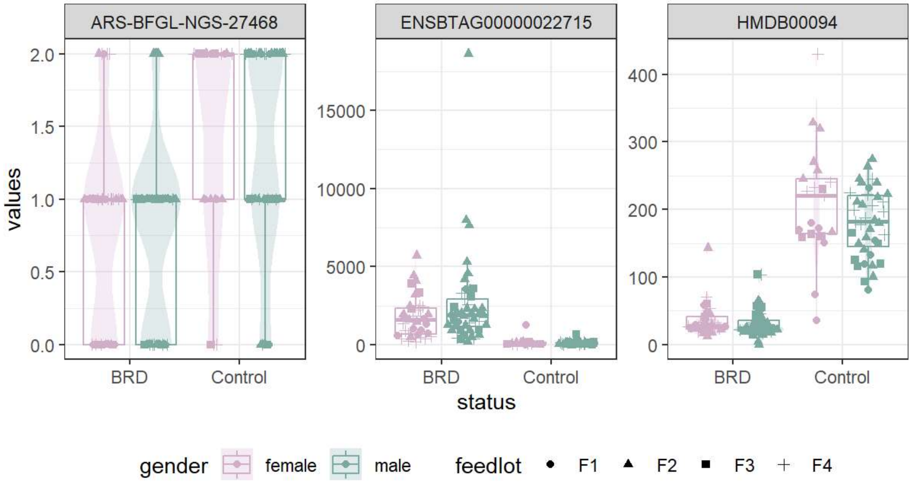
Storing data with `{MultiDataSet}`

Using the `{MultiDataSet}` package to store omics datasets and related metadata in one R object:

```r
mo_set
```

```
Object of class 'MultiDataSet'
 . assayData: 3 elements
    . snps: 23036 features, 139 samples
    . rnaseq: 20335 features, 143 samples
    . metabolome: 55 features, 139 samples
 . featureData:
    . snps: 23036 rows, 13 cols
    . rnaseq: 20335 rows, 15 cols
    . metabolome: 55 rows, 16 cols
 . rowRanges:
    . snps: YES
    . rnaseq: YES
    . metabolome: NO
 . phenoData:
    . snps: 139 samples, 10 cols
    . rnaseq: 143 samples, 10 cols
    . metabolome: 139 samples, 10 cols
```

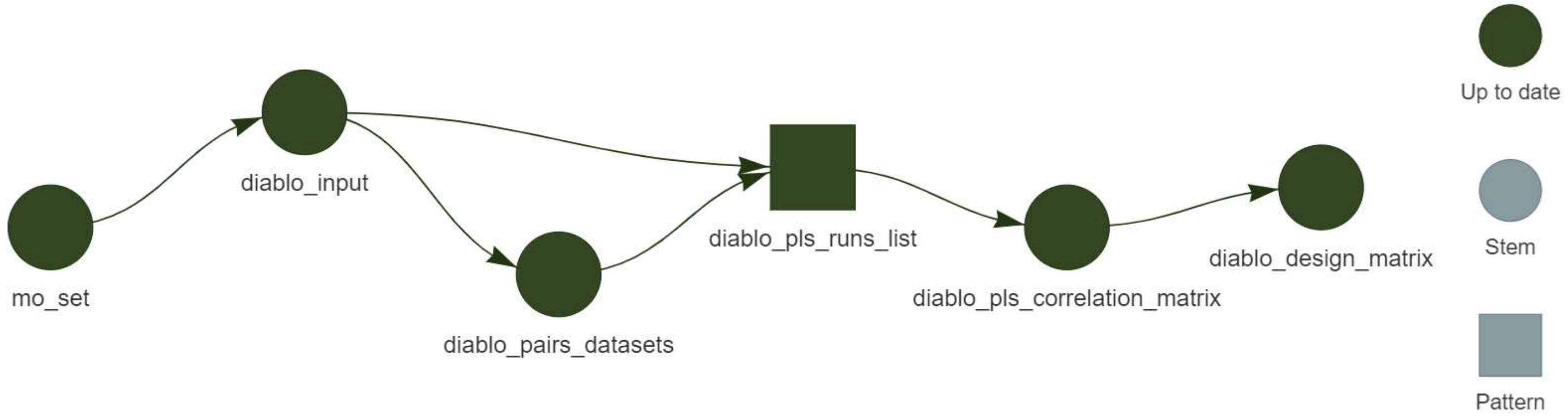
```r
plot_data_covariate(
  mo_set,
  covariate = "status",
  features = c("ARS-BFGL-NGS-27468",
               "ENSBTAG00000022715",
               "HMDB00094"),
  colour_by = "gender",
  shape_by = "feedlot"
)
```



Reproducible pipelines with `{targets}`

Uses the `{targets}` package to build reproducible analysis pipelines

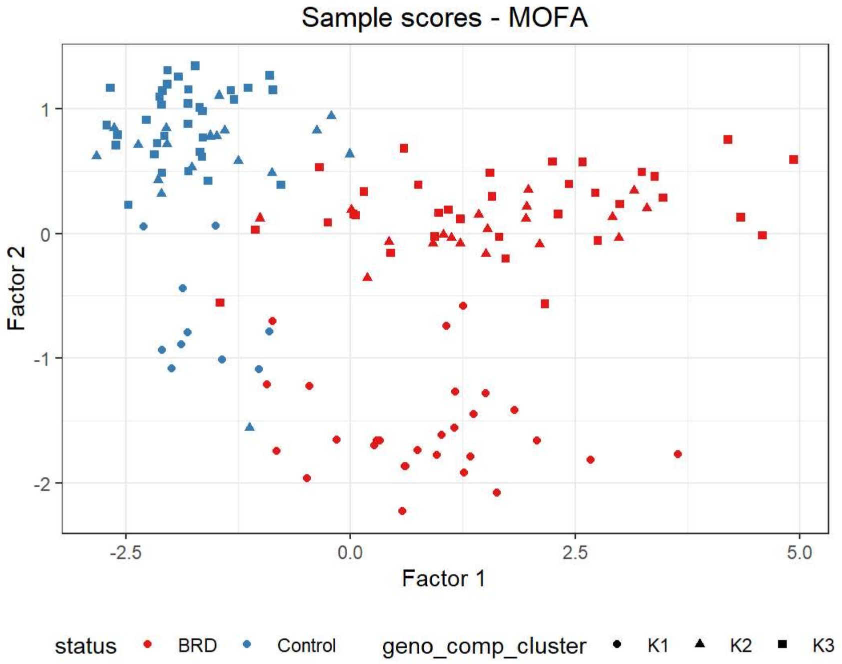
e.g. automates multi-step processes such as estimation of a parameter of interest:



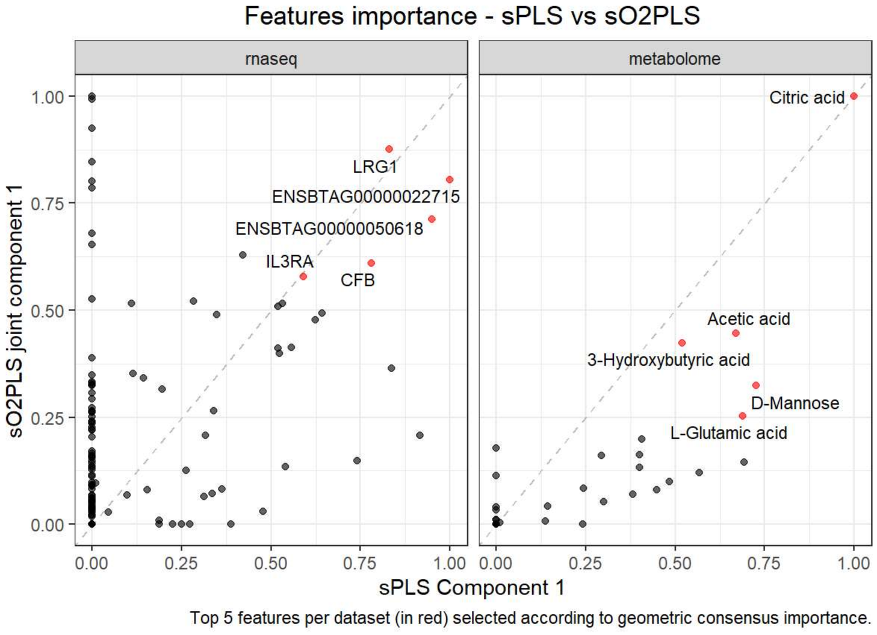
Consistent formatting of integration output

Converts methods’ output into S3 object for storing dimension reduction results

Results interpretation:



Methods comparison:



Top 5 features per dataset (in red) selected according to geometric consensus importance.

Thank you for your attention!

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