

metaboprep: an R package for pre-analysis data description and processing of metabolomics data

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Introduction

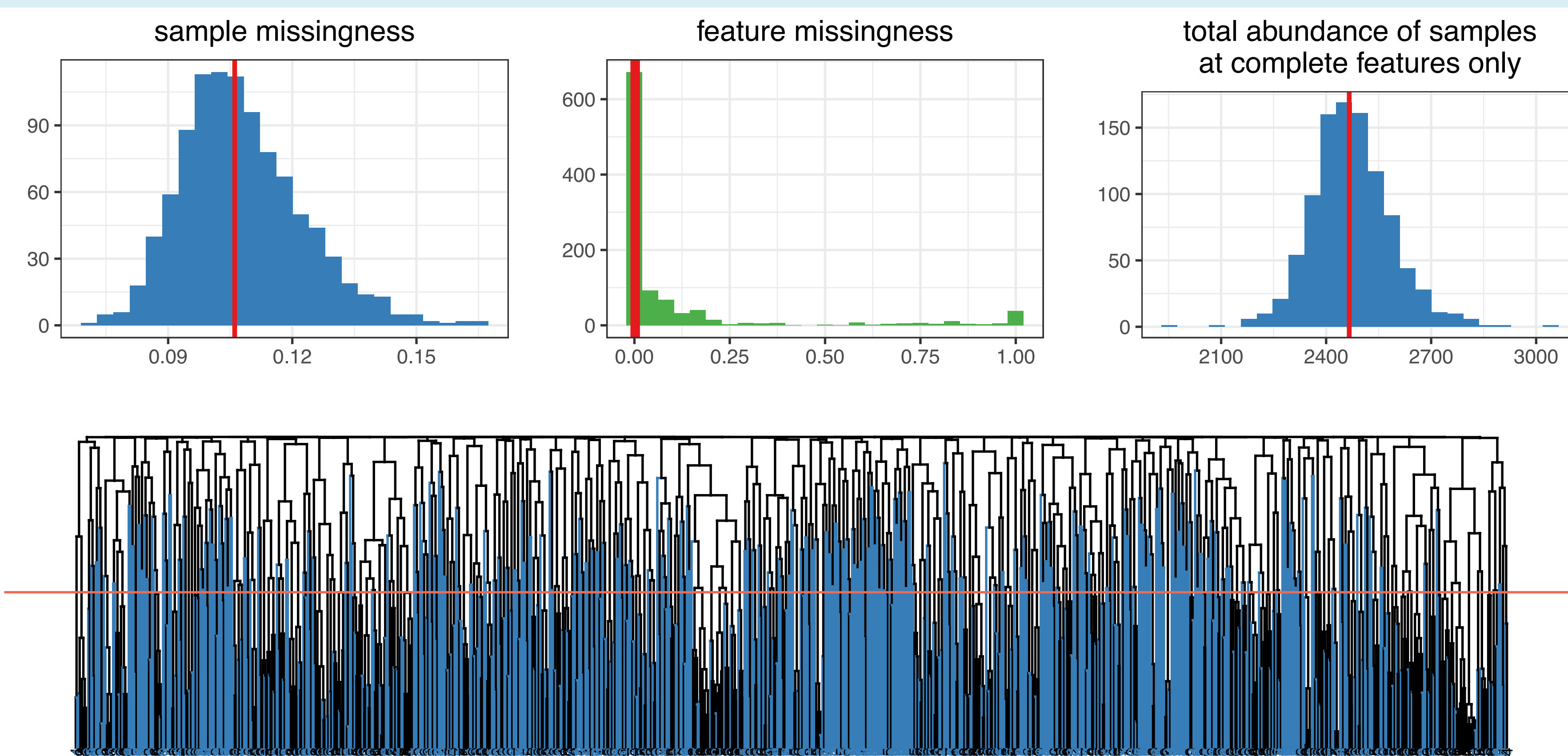
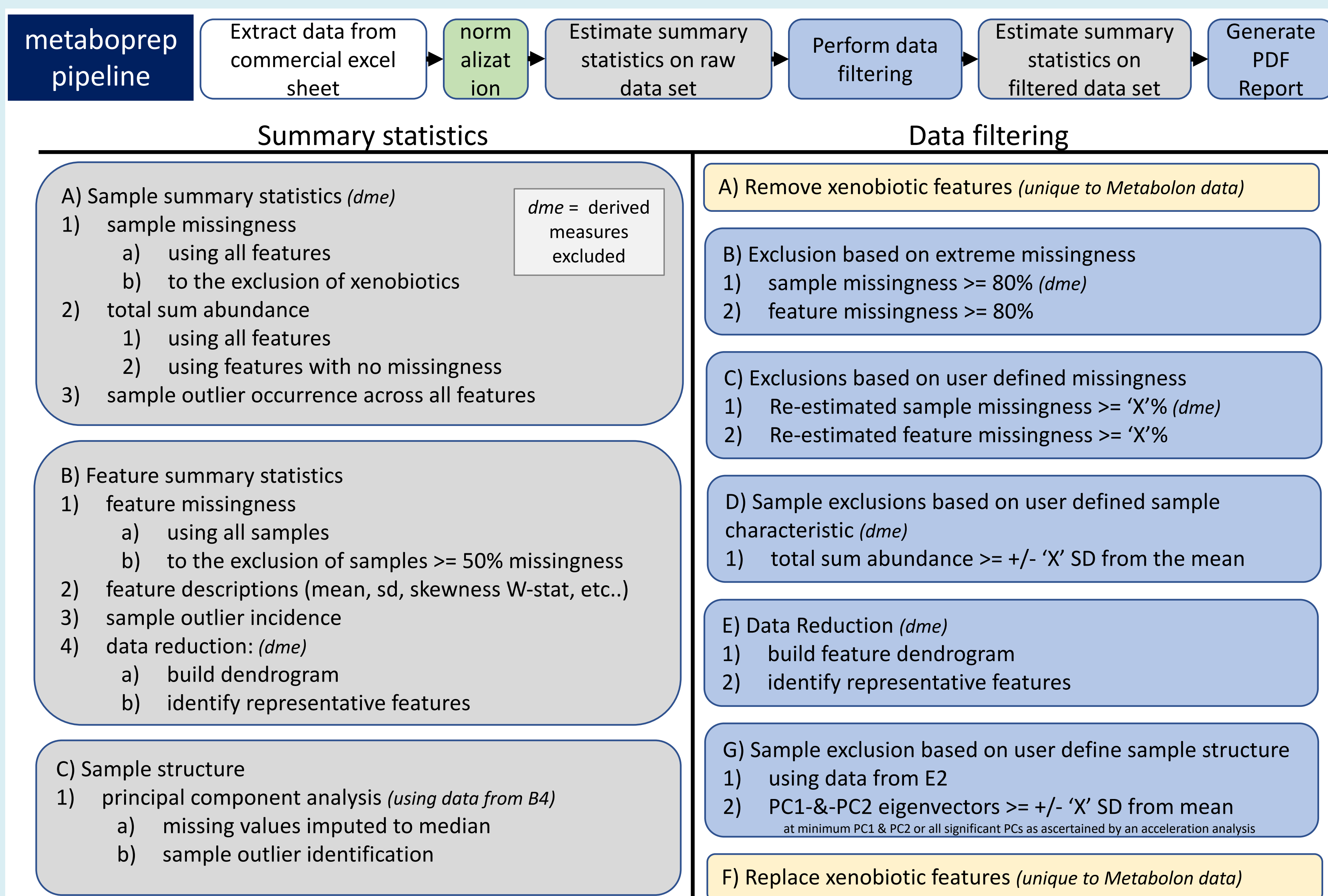
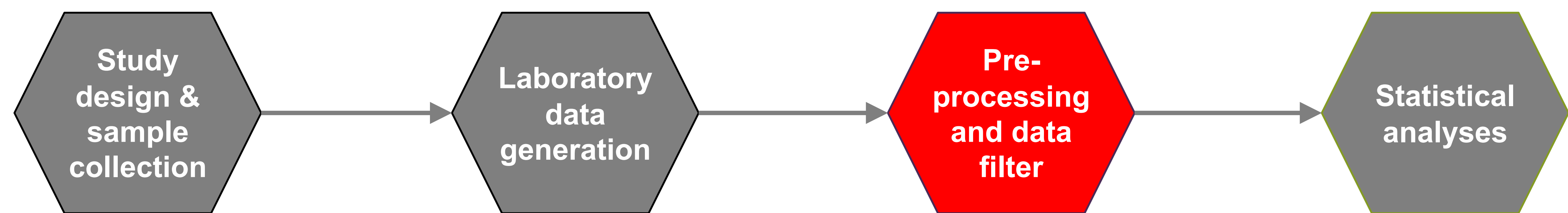
- Metabolomics is an increasingly common part of health research.
- Even when working with high quality curated datasets, there is a need for pre-analytical data processing.
- While some **pre-processing** steps are common, we identified a lack of standardization and reporting transparency for these procedures.

Aim

To produce a **single, flexible** pre-processing pipeline to enable **reproducible** and **transparent pre-processing** of metabolomics data.

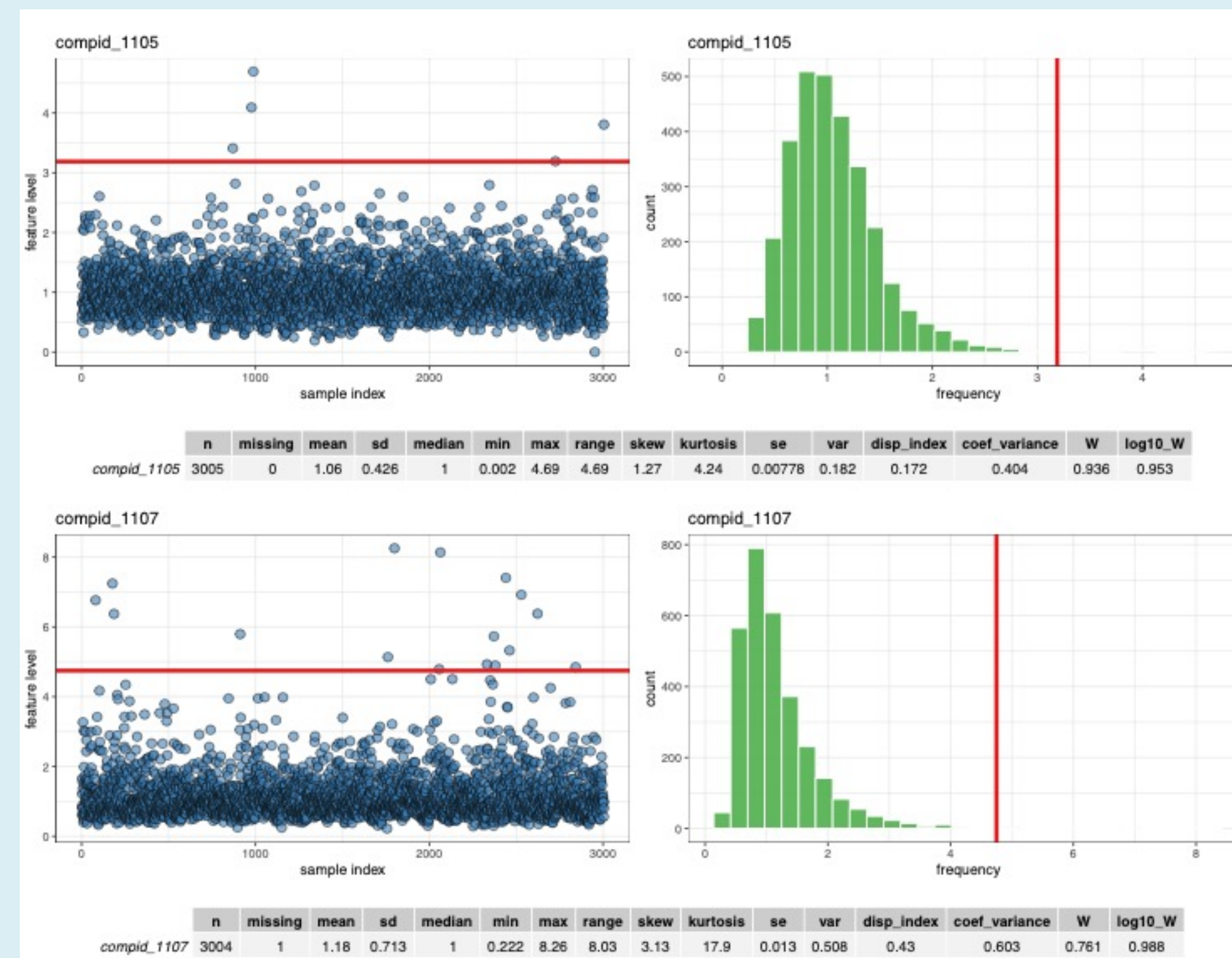
Conclusion

We created *metaboprep*, an openly available and citable R package available on GitHub.
<https://github.com/MRCIEU/metaboprep>

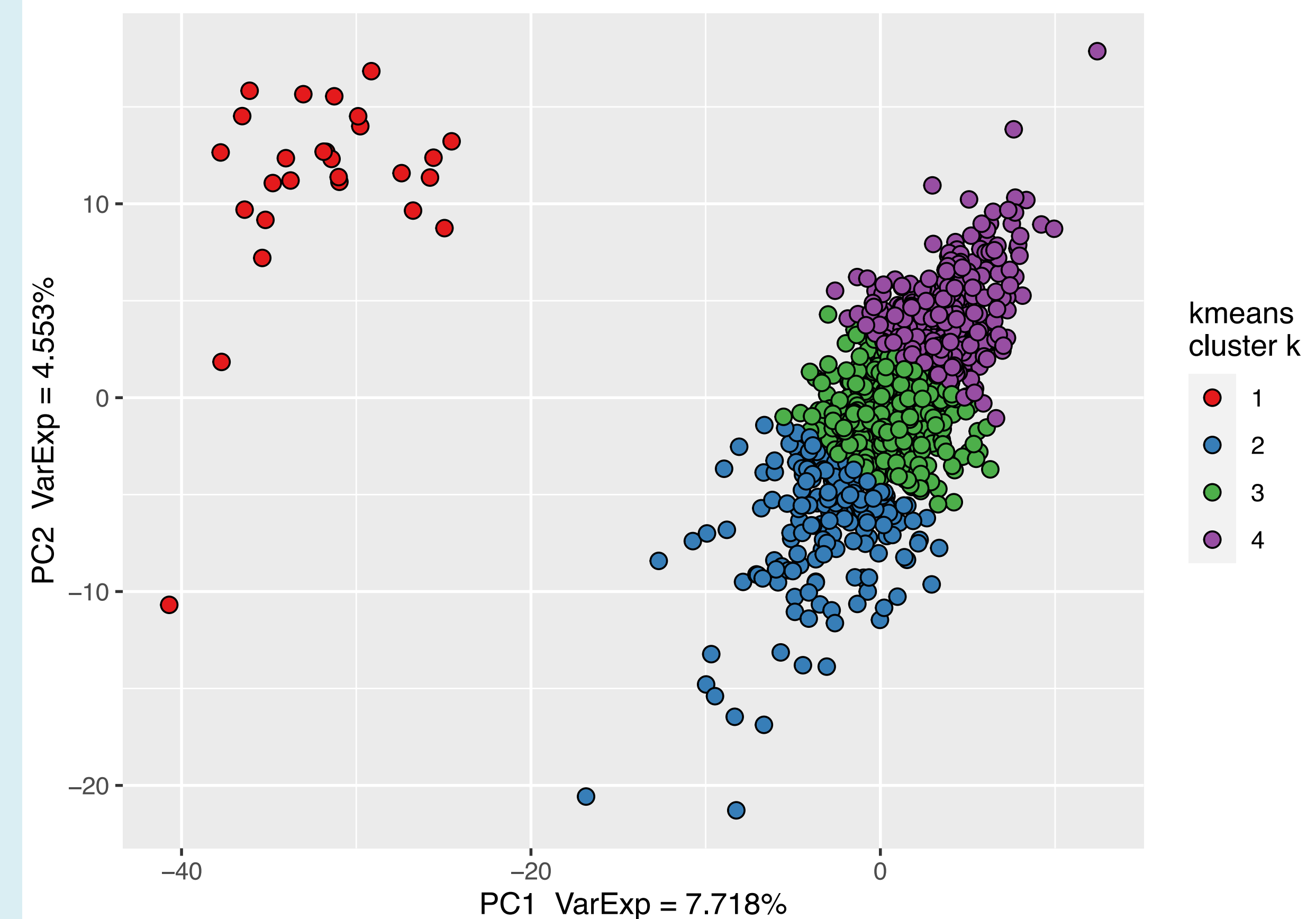


The *metaboprep* package:

1. **Reads in** and processes (un)targeted metabolomics data and exports in tab-delimited format;
2. Provides useful **summary data** in the form of tab-delimited text file and html report;
3. Performs **data filtering** using a standard pipeline and user-defined thresholds.



Principal components 1-&-2 using 514 representative metabolites



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Systems biology
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All feedback is welcome!

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