

pRocessomics: a new bioinformatic tool suite designed for -omics research(ers)

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How will I handle my new data??!



I don't want to wait for my bioinformatician forever. I want my analysis now, but my life is more than computers, R, and data processing!

Restarting R session...

```
Loading required package: rCIR
> m <- ggplot(proteins, aes(treatments, fill=class))
Error: could not find function "ggplot"
> m + geom_bar()
Error: could not find function "geom_bar"
> library(ggplot2)
> m <- ggplot(proteins, aes(treatment, fill=class))
> m + geom_bar()
Error in .Call("loop_apply", as.integer(n), f, env):
"loop_apply" not resolved from current namespace
```

= Frustration!!



But I do need a state-of-the-art pipeline for my research

Someone should tell my pal about

pRocessomics

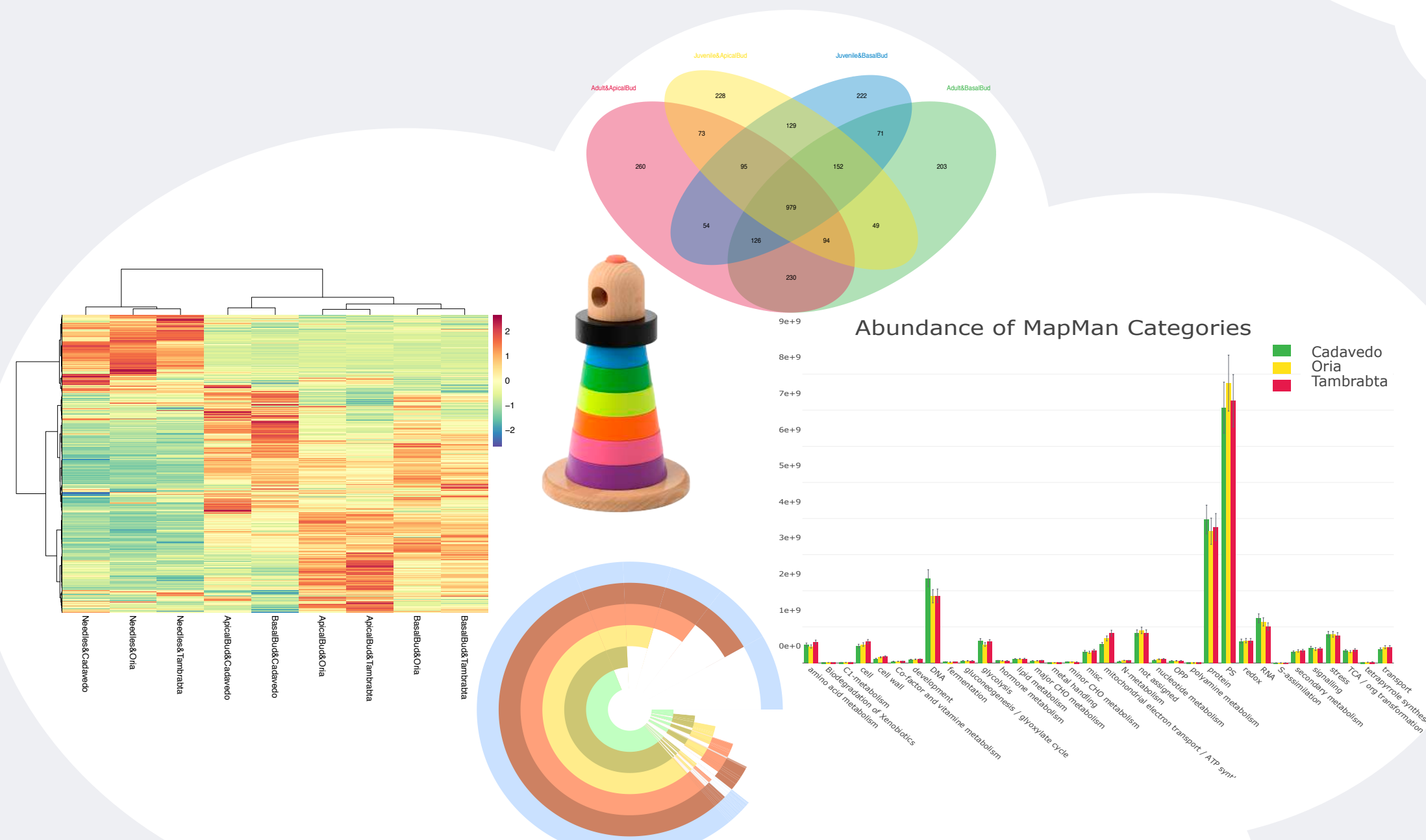
It has all we need to process our datasets in a way we can understand



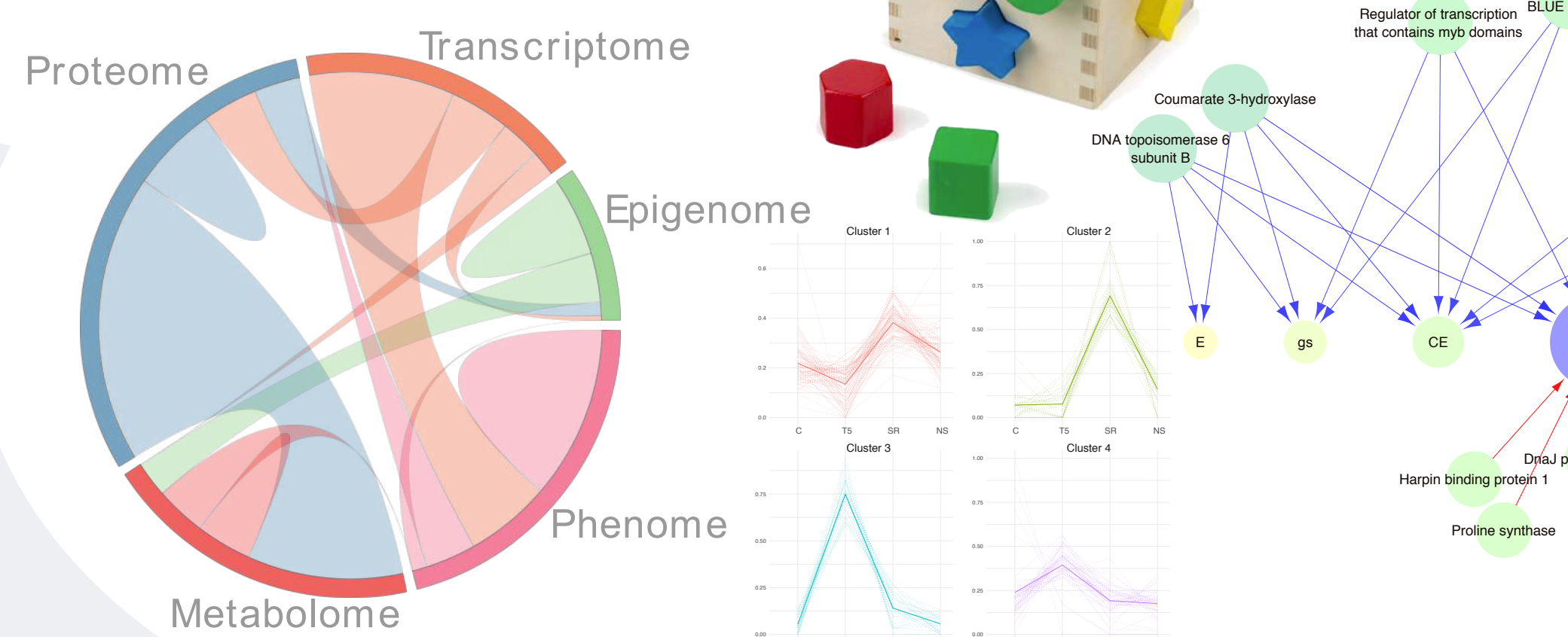
Data analysis made easier and more powerful than never before

Key Features of pRocessomics:

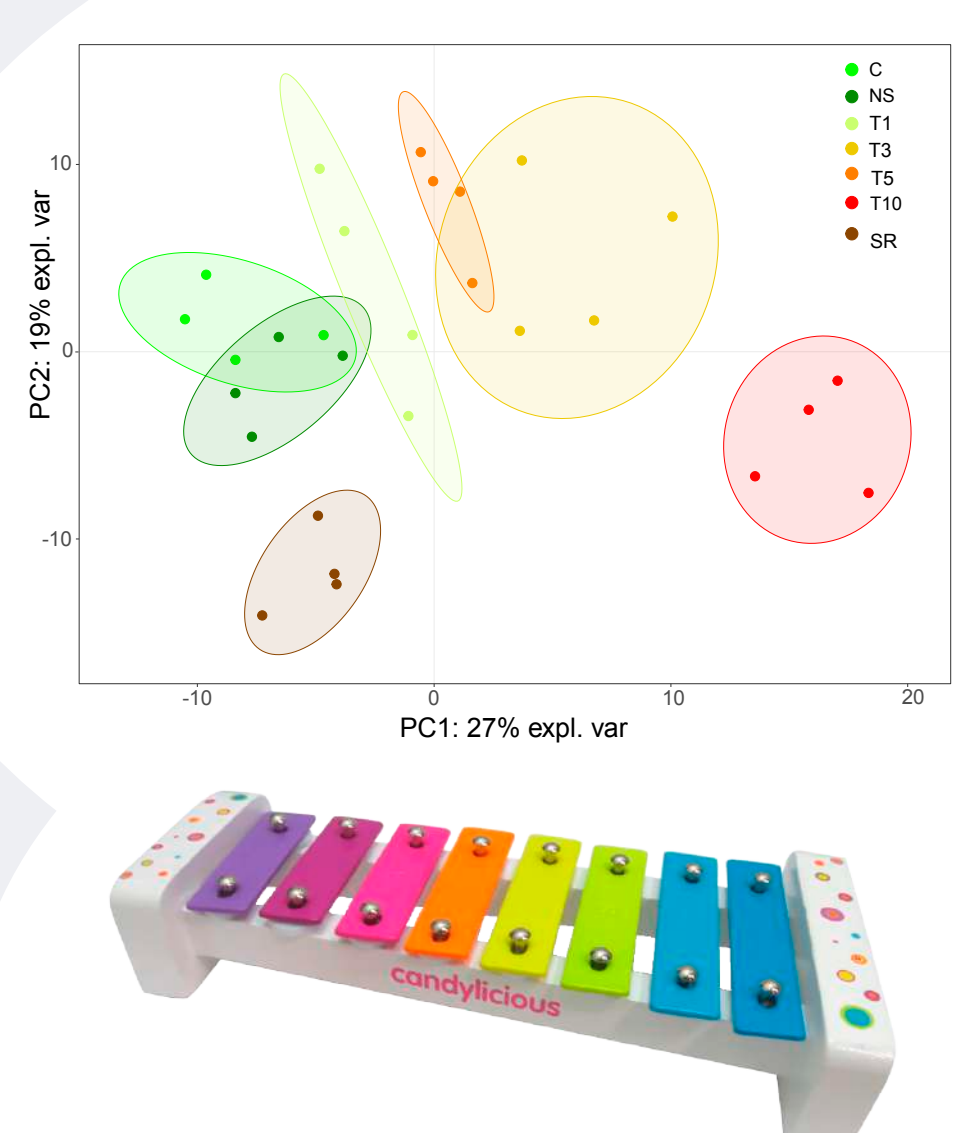
- Guided analysis and data preprocessing steps
- Possibility of integrative analysis of multiple omics
- Powerful statistical capabilities: exploratory, uni- and multivariate analyses. Dimensionality reduction
- Integration of biological annotations
- Ready to publish table export
- Beautiful figures, fully customizable and interactive
- Everything with less than 5 lines of source code.
- Graphical user interface coming soon.



Meaningful representation of data: univariate, heatmaps, Venn, ...



Integration of different omic levels, Circos, Networks... Cytoscape ready exports



Dimension reduction: quick and colorful. Biologically annotated (I)PCAs, PLSSs, DAs and MCOA

'Wanna try it?? check QR!

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