

Introducing the hermes package for RNA-seq data

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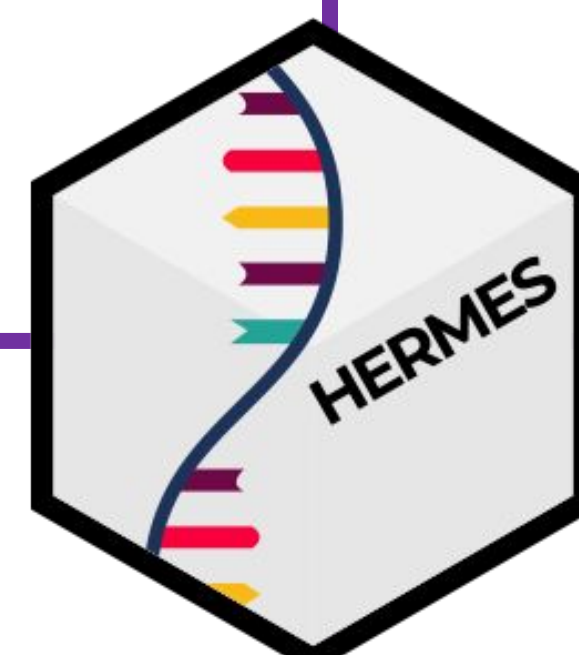
Background

- RNA-seq data is now a more commonly collected next-generation sequencing (NGS) biomarker available in many drug development projects in the pharmaceutical industry.
- [teal](#) is a general Shiny framework for analyzing clinical trial data. Development started 4 years ago - now it is used in production in many clinical trials across Roche and is starting to be used in other companies.
- [hermes](#) objectives were:
 - Production package which can be easily and robustly be used across projects.
 - Open source and publish on [Bioconductor](#) to give opportunity for external contributors and meet high quality requirements.
 - Democratize the analyses by enabling scientists with minimal R programming skills to look at the data - by developing [teal modules](#) powering Shiny apps.



Methods

- We worked as an agile SCRUM team, with most developers rotating from other projects. Daily standup meetings, and issue and PR tracking via GitHub Kanban boards.
- [teal](#) was modified substantially in order to directly take MultiAssayExperiment objects as input, as it can then take our HermesData input easily.
- [hermes](#) is based firmly on Bioconductor and CRAN standards, by using packages such as SummarizedExperiment, ggplot2, etc. It can easily be extended for custom use cases given the modular classes and methods design.
- [teal.modules.hermes](#) was developed subsequently - this Shiny layer is as thin as possible, such that all scientific logic is in hermes. Automated shiny tests are used for long-term maintainability. It is easy to add custom modules.



Features

- Annotate gene information from a central database (e.g. Biomart, or internal databases via add-on package).
- Add standard quality control (QC) flags to genes and samples.
- Filter the data set (genes, samples, required annotations).
- Normalize the counts (DESeq2 or voom).
- Quickly produce descriptive plots (static and dynamic).
- Perform principal components analysis.
- Produce a QC report (Rmd template for RStudio knitr).
- Perform differential expression analysis (different methods).

Getting Started

hermes from Bioconductor 3.15:

```
BiocManager::install("hermes")
vignette("introduction")
```

teal.modules.hermes from GitHub:

```
Sys.setenv(GITHUB_PAT = "your_pat_here")
remotes::install_github(
  "insightsengineering/teal.modules.hermes@*release"
)
```

Look at the [example Shiny app](#) →



Acknowledgments

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Example App with teal.modules.hermes modules

