


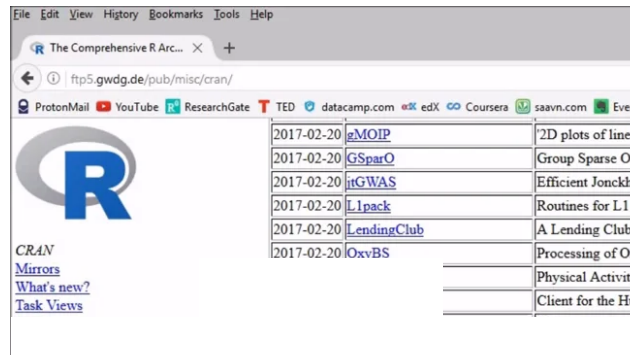
Module 2.3: Learn - Professional Development

Overview

For this week's lesson in professional development and research skills, we will show you how to search for R packages that you can use to do specific analyses. This includes specific resources you can look at as well as techniques to help search the internet more effectively.

Searching for useful R packages

The **Comprehensive R Archive Network**  (<https://cran.r-project.org/>) (better known as “CRAN”) is a network where developers submit packages to the CRAN repository which contains standard packages available for installation to ensure reproducibility across all users. Developers are constantly creating extensions and overall, contributing hundreds of packages each month to a repository that already contains tens of thousands. Let's look at best practices for navigating for useful R packages.



Video. Searching for packages in R.

This video will show you how to find packages for specific functions in R.

View Transcript. (<https://canvas.asu.edu/courses/122165/files/54792250?wrap=1>)_ [↓](https://canvas.asu.edu/courses/122165/files/54792250/download?download_frd=1)
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The CRAN website lists [available packages by name and links to index pages that contain information on](https://cran.r-project.org/web/packages/available_packages_by_name.html) (https://cran.r-project.org/web/packages/available_packages_by_name.html). You can easily search this page by using Windows or 'Cmd + F' on Mac. If we know which packages we are searching for, we can install them directly in R outlined in Section 2.2: Learn Coding.

Remember last week how we recommended you can also search in scientific literature by using literary search engine **Scholar** [\(https://scholar.google.com/\)](https://scholar.google.com/) or **ASU Library One Search** (<https://search.lib.asu.edu/>). For example, I searched for differential expression package by searching 'differential expression package' in Google Scholar (you will have access without paying if you are signed into your ASU google ID).

Google Scholar

Q

Articles

About 727,000 results (0.08 sec)

Any time

Since 2022

Since 2021

Since 2018

Custom range...

Sort by relevance

Sort by date

Any type

Review articles

☐ include patents
☒ include citations

☐ Create alert

edgeR: a Bioconductor **package** for differential expression analysis of digital gene expression data

[HTML] oup.com

MD Robinson, DJ McCarthy, GK Smyth - bioinformatics, 2010 - academic.oup.com

... edgeR is a Bioconductor software **package** for examining **differential expression** of replicated count data. An overdispersed Poisson model is used to account for both biological and ...

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[PDF] Differential expression of RNA-Seq data at the gene level—the DESeq **package**

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S Anders, W Huber - Heidelberg, Germany: European Molecular ..., 2012 - genomatix.de

... The **package** DESeq provides methods to test for **differential expression** by use of the negative ... This vignette explains the use of the **package**. For an exposition of the statistical method, ...

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[HTML] limma powers differential expression analyses for RNA-sequencing and microarray studies

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ME Ritchie, B Phipson, DI Wu, Y Hu... - Nucleic acids ..., 2015 - academic.oup.com

... The **package** contains particularly strong facilities for reading, normalizing and exploring ... First, the **package** can now perform both **differential expression** and **differential** splicing ...

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Data quality aware analysis of differential expression in RNA-seq with NOISeq R/Bioc **package**

[HTML] oup.com

S Tarazona, P Furió-Tarí, D Turrà, AD Pietro... - Nucleic acids ..., 2015 - academic.oup.com

... Within each block, the **package** offers both ... **package** includes an option for easily generating

Figure. Google Scholar search results for differential expression packages.

If we click any of the links, we can look at the packages recommended by the authors, review data visualizations whether or not we want to use these packages on our own dataset. One thing to consider is the number that cor This shows how many other publications referenced the article and can be telling of the effectiveness of the pack scientific papers are probably the best source for finding packages relevant to your work, we can also visit the rel favorite results or search for tutorials on YouTube to look for additional packages. Let’s continue to practice readi reviewing the preprint that inspired our research question.

How to read a scientific article (continued from 1.3)

Assignment

In **Module 1.3: Learn Professional development** (<https://canvas.asu.edu/courses/122165/pages/module-1-dot-3-development>), you learned how to efficiently read a scientific article. The basis of the research aims of this course is that are differentially expressed female versus male placentas. To help you understand the samples and data we give you context for the analytical question we are asking, we would like you to read the manuscript describing this primarily by Dr. Kimberly Olney who was a graduate student in Dr. Wilson's lab and co-authored by Dr. Seema Patel. This is the research efforts during this course.

Olney, K. C., Plaisier, S. B., Phung, T. N., Silasi, M., Perley, L., O'Bryan, J., ... & Wilson, M. A. (2022). Sex chromosome term placenta are conserved in adult tissues. bioRxiv. <https://www.biorxiv.org/content/10.1101/2022.08.08.503197v1>

This manuscript describes how gene expression for two batches of placenta samples collected by Yale Biobank was analyzed using RNA sequencing. Data processing parameters including trimming parameters were determined using previous work from the Wilson lab. Having seen that the RNA sequencing reads were of high quality using FastQC, the parameters used were deemed acceptable and processed gene expression data (counts) was used as input into the differential gene expression analysis. Results were described in the figures of the paper.

There is one small thing we wanted to point out between the manuscript and the data we generated for this course project that investigates the effect of trimming on differential gene expression analysis using sex differences in the placenta. In the manuscript, two batches of placenta tissues were collected and the batch was incorporated into the differential gene expression analysis. In our course, we generated data sets using only the first batch of placenta tissues to avoid worry about factoring in any batch effects. This is why you will see less samples in our data than there were in the manuscript. The reason we are pointing this out is that this is the level of scrutiny you will be reading the papers with when you are using them to enhance your own research. Reading papers about techniques or data you want to apply requires you to pay very close attention to what is the same or different between your work and the study you are reading about so that you can pull out the information.

Module 2.3 Additional Resources

- Comprehensive R Archive Network (CRAN)  (<https://cran.r-project.org/>)
- CRAN: Packages listed by name  (https://cran.r-project.org/web/packages/available_packages_by_name.ht)