Maximum Mean Discrepancy in High-Dimensional Biology

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Text of abstract

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Keywords: keyword 1; keyword 2; keyword 3

Highlights: These are the highlights.

# 1 Specific Aims

**Aim 1: Apply MMD to high-dimensional biological data**

**Aim 2: Create an R package that implements MMD methods**

Current R software for MMD methods doesn’t provide significance thresholds. Gretton’s website hosts Matlab software that implements the methods in Gretton et al. (2012), Gretton et al. (2009) and Gretton et al. (2006). We will create an R package with Rcpp (Eddelbuettel and François, 2011). We’ll implement the methods in R and C++ before assembling the code into a well documented, user-friendly R package (R Core Team, 2021).

# 2 Background and Significance

The last twenty years have seen an explosion in the volume and dimensionality of molecular biology data. Following the sequencing of the human genome, technologies such as DNA sequencing, RNA sequencing, and single-cell RNA sequencing proliferated. The new experimental designs and high dimension of modern biological data require parallel development of new statistical methods and computational tools for their analysis. Maximum mean discrepancy (MMD) is a new statistical tool with novel mathematical properties (Borgwardt et al., 2006; Gretton et al., 2012, 2009, 2006). We propose to explore its mathematical and statistical properties and to apply MMD methods in the analysis of high-dimensional biological data.

MMD is a statistical method for determining whether two high-dimensional samples arise from distinct distributions. Throughout this document, we use the term “sample” to refer to measurements on a collection of subjects from a single group. In introductory statistics courses, one often studies Student’s t-test (Student, 1908) when discerning whether two samples come from the same distribution. Implicit to the t-test is the assumption that the two samples arise from normal distributions with a single, common variance parameter.

# 3 Approach

# 4 Methods

# 5 Results

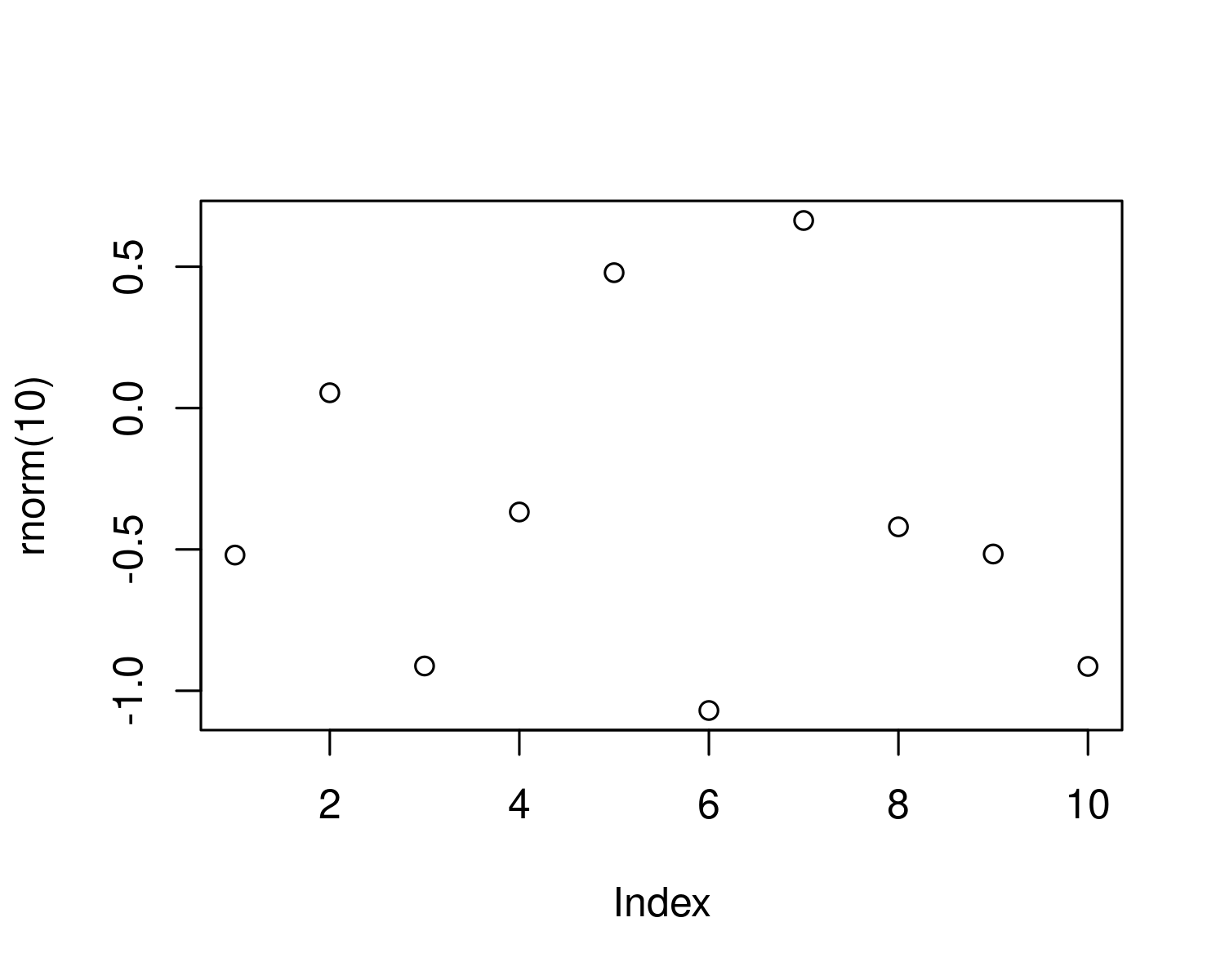


Figure 5.1: A plot of random numbers

Figure 5.1 shows how we can have a caption and cross-reference for a plot

Here is an example of inline code 3.14 in the middle of a sentence.

# 6 Discussion

# 7 Conclusion

# 8 Acknowledgements

# 9 References

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### 9.0.1 Colophon

This report was generated on 2021-05-08 19:54:05 using the following computational environment and dependencies:

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#> system x86\_64, linux-gnu   
#> ui X11   
#> language (EN)   
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#> ctype en\_US.UTF-8   
#> tz America/New\_York   
#> date 2021-05-08   
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#> checkmate 2.0.0 2020-02-06 [1] CRAN (R 4.0.1)   
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#> [4] /usr/lib/R/library

The current Git commit details are:

#> Local: main /home/fred/work/professional-development/mmdproject  
#> Remote: main @ origin (https://github.com/fboehm/mmdproject.git)  
#> Head: [00c7e72] 2021-05-08: added software Aim