

# a RepSeq data analysis tutorial

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**Abstract.** In this work, we follow a RepSeq data analysis tutorial.

## 1 Introduction

In this work, we follow tutorial, which covers some analysis of RepSeq data.

We use the samples from study "Diversity and clonal selection in the human T-cell repertoire" [1]. Using information about T-cell subpopulations and phenotypes, we can attempt to get immunological properties from unlabeled samples.

sample	donor	status	subset	phenotype
s1	D1	CMV-	CD8	memory
s2	D2	CMV+	CD8	naive
s3	D1	CMV+	CD8	memory
s4	D2	CMV-	CD4	memory
s5	D2	CMV+	CD8	memory
s6	D2	CMV-	CD4	memory
s7	D1	CMV+	CD8	memory
s8	D1	CMV-	CD4	memory
s9	D2	CMV+	CD8	memory
s10	D2	CMV-	CD4	memory
s11	D2	CMV+	CD8	memory
s12	D2	CMV+	CD8	memory
s13	D2	CMV+	CD8	naive
s14	D2	CMV+	CD8	memory
s15	D2	CMV-	CD8	naive
s16	D2	CMV-	CD4	naive

Table 1: Summarizing results

## References

- [1] Age and T-cell repertoire Qian Qi, Yi Liu, Yong Cheng, Jacob Glanville, David Zhang, Ji-Yeun Lee, Richard A. Olshen, Cornelia M. Weyand, Scott D. Boyd, Jörg J. Goronzy Proceedings of the National Academy of Sciences Sep 2014, 111 (36) 13139-13144; DOI: 10.1073/pnas.1409155111