

A RepSeq data analysis tutorial

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

1 Introduction

In this work, we followed tutorial [1], which covers some analysis of RepSeq data.

We use the samples from study "Diversity and clonal selection in the human T-cell repertoire" [2]. Using information about T-cell subpopulations and phenotypes, we have an attempt to get immunological properties from unlabeled samples.

sample	donor	status	subset	phenotype
s1	D2	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] <https://github.com/antigenomics/repseq-annotation-tutorial>
- [2] 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