

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, 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 have an 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