2023

Using the GLIPH2 algorithm to analyze TCR specificity in cancer patients

SUPERVISOR: NICOLAI JUUL BIRKBAK

CHRISTIAN BJØDSTRUP RYGAARD, 201806127

Abstract

T-cells play a crucial role in the fight for survival against cancer, as they play a pivotal role in the recognition and elimination of cancerous cells. However, this would not be possible without the T-cell receptor (TCR). Through the use of TCR sequencing, it is possible to cluster TCR sequences of similar specificities and in extension of that, find out which epitopes occupy the immune system during cancer treatment. Gaining insight into this can potentially improve treatment for individual patients in the future by using biomarkers.
In this thesis the TCR clustering algorithm GLIPH2 is used to create a pipeline for gauging TCR antigen specificities in bladder cancer patients.

Table of contents

Abstract..1
Introduction..3
  T-cells and T-cell receptors..3
  GLIPH2..5
  Aim of the study..5
Methods..7
  Introduction to the dataset..7
  GLIPH2..7
  TCR targets..8
  Statistical tests..8
  Diversity measures..8
  Additional statistical analysis..9
Results..10
  Pipeline of the analysis..10
  Overview analysis of the data..11
  GLIPH2 analysis..16
Discussion..25
  Non-GLIPH analysis..25
  GLIPH2 analysis..25
    Baseline and non-baseline..25
    Relapse and non-relapse..26
    Big and non-big..26
    CMV and EBV..26
  Concluding remarks..27
References..28
Acknowledgements..30
Supplementary..30