Classification of regulatory sequences using machine learning techniques

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Introduction

Melanoma is a very aggressive cancer that is very therapy-resistant due to its high degree of heterogeneity and plasticity. Despite the great efforts put into the field of melanoma treatment, resulting in great advances, many challenges remain. The major challange in fighting melanoma relapse continues to be the tumor heterogeneity. To be able to adress this issue therapeutically, the underlying mechanisms of heterogeneity need to be characterized. In this paper, a distinction between two major types of melanoma cells is made: invasive and proliferative.(Verfaillie et al. 2015; Shannan et al. 2015)

Transcriptional reprogramming of melanoma cells in proliferative state into melanoma cells with invasive characteristics is a critical event at the origin of metastatic spreading of melanoma.

Transcriptomic, open chromatin and histone modification maps of melanoma cultures were constructed, revealing thousands of active cis-regulatory regions, both for proliferative and invasive cells. We posited that it should be possible to discern which cis-regulatory regions are useful for the classification of cell states in melanoma samples if such states are truly distinct in terms of regulatory landscape.

Methods

Results and discussion

References

Shannan et al. 2015. "Heterogeneity in Melanoma." *Cancer Treatment and Research.*

Verfaillie et al. 2015. "Decoding the Regulatory Landscape of Melanoma Reveals Teads as Regulators of the Invasive Cell State." *Nature Communications.*